



# Full wwPDB X-ray Structure Validation Report ⓘ

Nov 13, 2017 – 07:49 PM EST

PDB ID : 4V4K  
Title : Bacteriophage P22 Portal Protein bound to middle Tail Factor GP4. This file contain the second biological assembly  
Authors : Olia, A.S.; Cingolani, G.  
Deposited on : unknown  
Resolution : 3.25 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)

A user guide is available at

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030345
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20030345

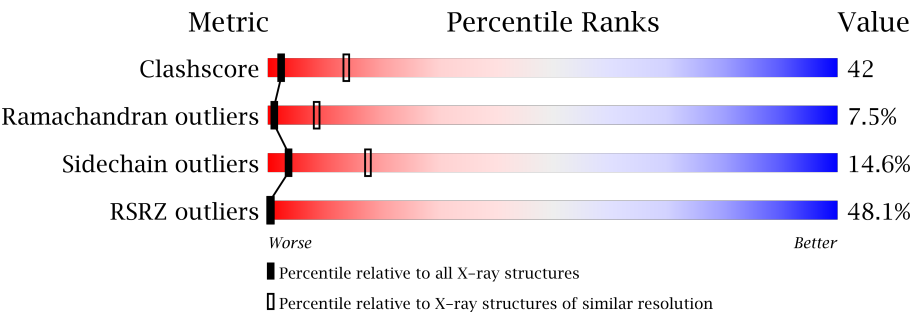
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.25 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	112137	2036 (3.32-3.20)
Ramachandran outliers	110173	2000 (3.32-3.20)
Sidechain outliers	110143	1998 (3.32-3.20)
RSRZ outliers	101464	1861 (3.32-3.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	602	<div><div>47%</div><div><div>38%</div><div>44%</div><div>12%</div><div>• 5%</div></div></div>
1	B	602	<div><div>50%</div><div><div>38%</div><div>44%</div><div>12%</div><div>• 5%</div></div></div>
1	C	602	<div><div>48%</div><div><div>37%</div><div>45%</div><div>12%</div><div>• 5%</div></div></div>
1	D	602	<div><div>43%</div><div><div>38%</div><div>44%</div><div>12%</div><div>• 5%</div></div></div>
1	E	602	<div><div>45%</div><div><div>38%</div><div>45%</div><div>12%</div><div>• 5%</div></div></div>
1	F	602	<div><div>43%</div><div><div>38%</div><div>43%</div><div>12%</div><div>• 5%</div></div></div>
1	G	602	<div><div>45%</div><div><div>38%</div><div>44%</div><div>12%</div><div>• 5%</div></div></div>

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Mol	Chain	Length	Quality of chain
1	H	602	
1	I	602	
1	J	602	
1	K	602	
1	L	602	
1	M	602	
1	N	602	
1	O	602	
1	P	602	
1	Q	602	
1	R	602	
1	S	602	
1	T	602	
1	U	602	
1	V	602	
1	W	602	
1	X	602	
2	Y	166	
2	Z	166	
2	a	166	
2	b	166	
2	c	166	
2	d	166	
2	e	166	
2	f	166	

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Mol	Chain	Length	Quality of chain
2	g	166	
2	h	166	
2	i	166	
2	j	166	
2	k	166	
2	l	166	
2	m	166	
2	n	166	
2	o	166	
2	p	166	
2	q	166	
2	r	166	
2	s	166	
2	t	166	
2	u	166	
2	v	166	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 135120 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called PORTAL PROTEIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	M	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	N	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	O	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	P	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	Q	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	R	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	S	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	T	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	U	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	V	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	W	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	X	569	Total	C	N	O	S	Se	0	0	0
			4564	2871	786	887	4	16			
1	A	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	B	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	C	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	D	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	E	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	F	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	G	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	H	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	I	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	J	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	K	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			
1	L	569	Total	C	N	O	S	Se	0	0	0
			4553	2865	783	885	4	16			

- Molecule 2 is a protein called PACKAGED DNA STABILIZATION PROTEIN GP4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	k	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	l	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	m	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	n	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	o	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	p	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	q	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	r	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	s	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	t	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	u	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	v	145	Total	C	N	O	S	0	0	0
			1052	654	182	211	5			
2	Y	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	Z	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	a	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	b	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	c	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	d	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	e	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	f	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	g	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	h	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	i	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			
2	j	146	Total	C	N	O	S	0	0	0
			1048	652	179	212	5			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
k	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
l	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
m	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
n	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
o	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
p	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
q	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
r	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
s	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
t	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
u	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
v	141	PRO	ALA	ENGINEERED MUTATION	UNP P26746
Y	150	PRO	ALA	ENGINEERED	UNP P26746

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Chain	Residue	Modelled	Actual	Comment	Reference
Z	150	PRO	ALA	ENGINEERED	UNP P26746
a	150	PRO	ALA	ENGINEERED	UNP P26746
b	150	PRO	ALA	ENGINEERED	UNP P26746
c	150	PRO	ALA	ENGINEERED	UNP P26746
d	150	PRO	ALA	ENGINEERED	UNP P26746
e	150	PRO	ALA	ENGINEERED	UNP P26746
f	150	PRO	ALA	ENGINEERED	UNP P26746
g	150	PRO	ALA	ENGINEERED	UNP P26746
h	150	PRO	ALA	ENGINEERED	UNP P26746
i	150	PRO	ALA	ENGINEERED	UNP P26746
j	150	PRO	ALA	ENGINEERED	UNP P26746

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	M	21	Total O 21 21	0	0
3	N	21	Total O 21 21	0	0
3	O	21	Total O 21 21	0	0
3	P	21	Total O 21 21	0	0
3	Q	21	Total O 21 21	0	0
3	R	21	Total O 21 21	0	0
3	S	21	Total O 21 21	0	0
3	T	21	Total O 21 21	0	0
3	U	21	Total O 21 21	0	0
3	V	21	Total O 21 21	0	0
3	W	21	Total O 21 21	0	0
3	X	21	Total O 21 21	0	0
3	A	22	Total O 22 22	0	0
3	B	22	Total O 22 22	0	0

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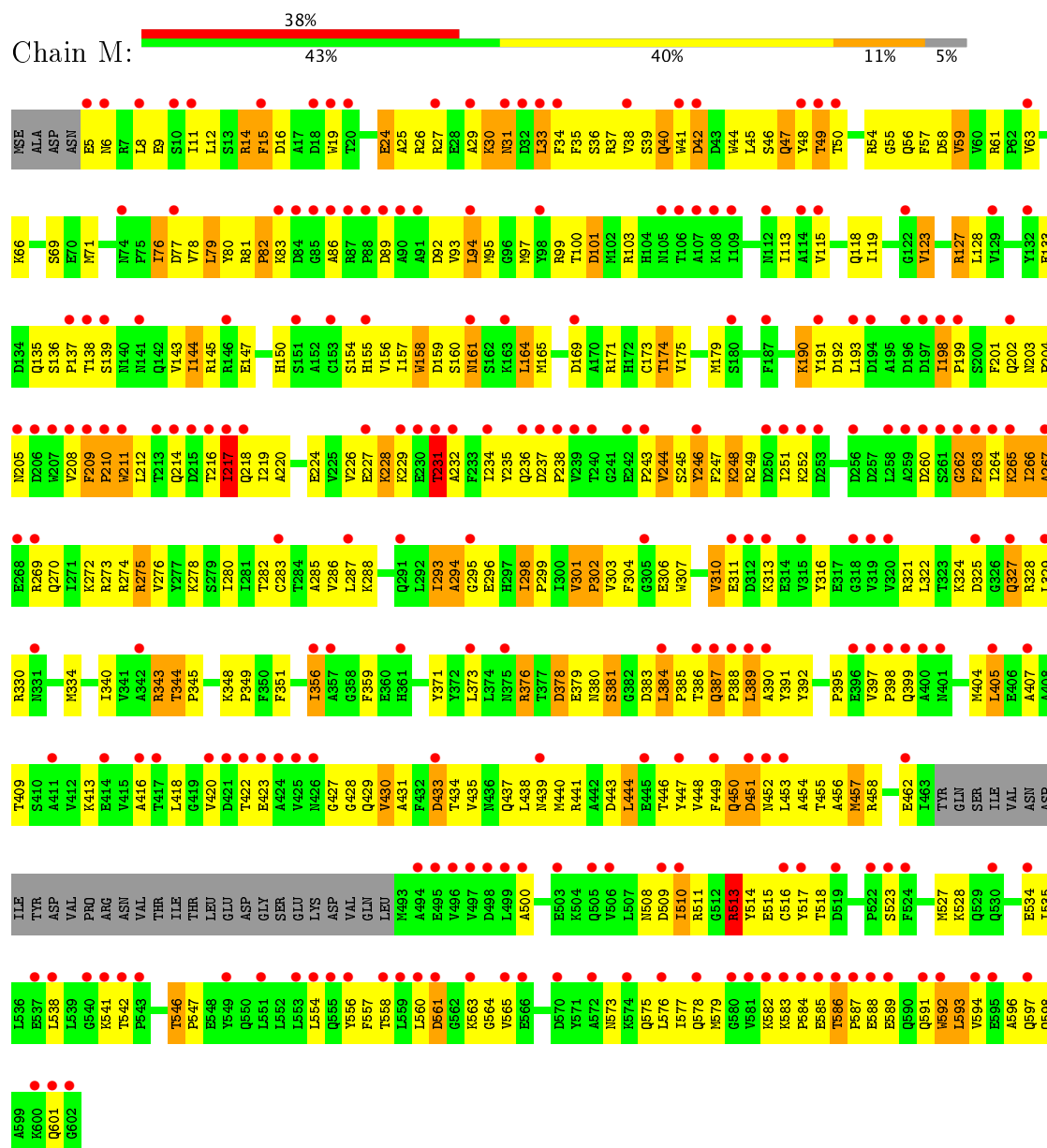
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	22	Total 22	O 22	0	0
3	D	22	Total 22	O 22	0	0
3	E	22	Total 22	O 22	0	0
3	F	22	Total 22	O 22	0	0
3	G	22	Total 22	O 22	0	0
3	H	22	Total 22	O 22	0	0
3	I	22	Total 22	O 22	0	0
3	J	22	Total 22	O 22	0	0
3	K	22	Total 22	O 22	0	0
3	L	22	Total 22	O 22	0	0

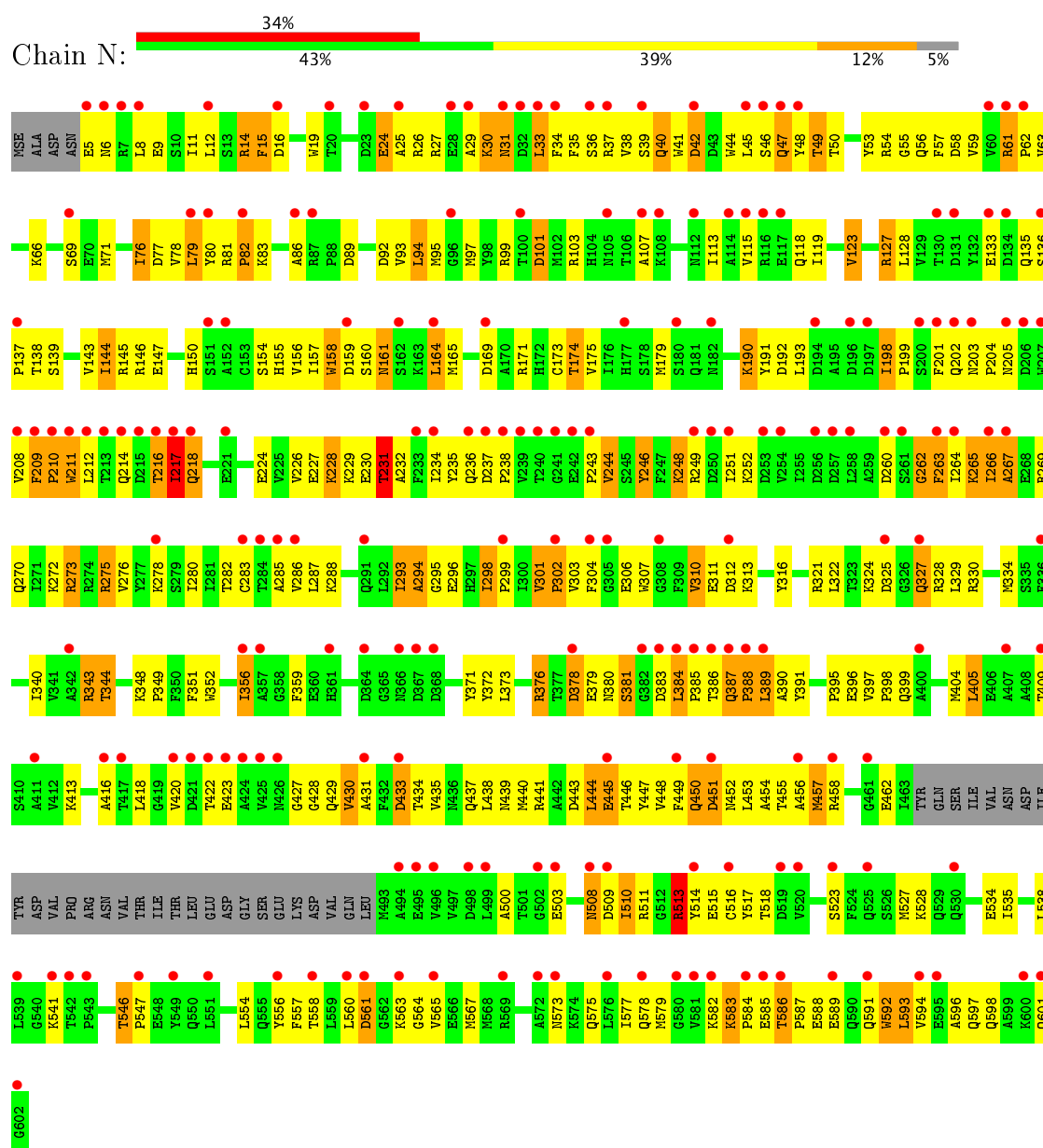
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

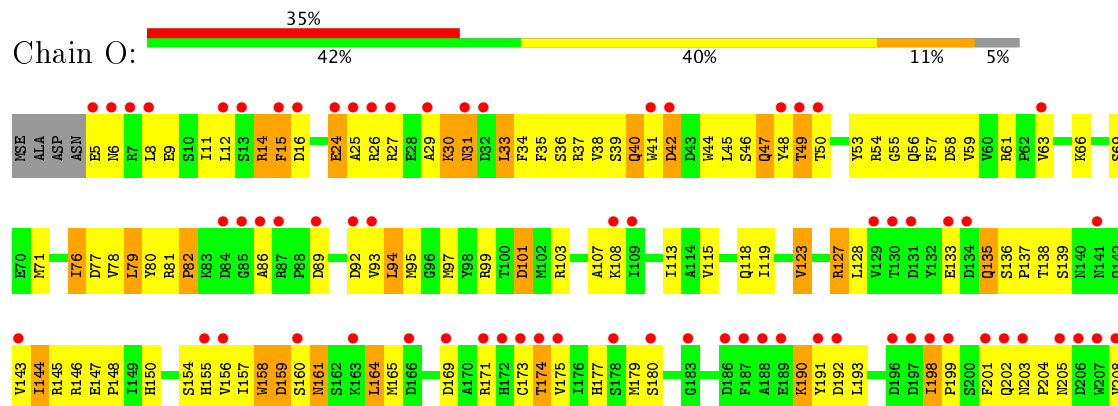
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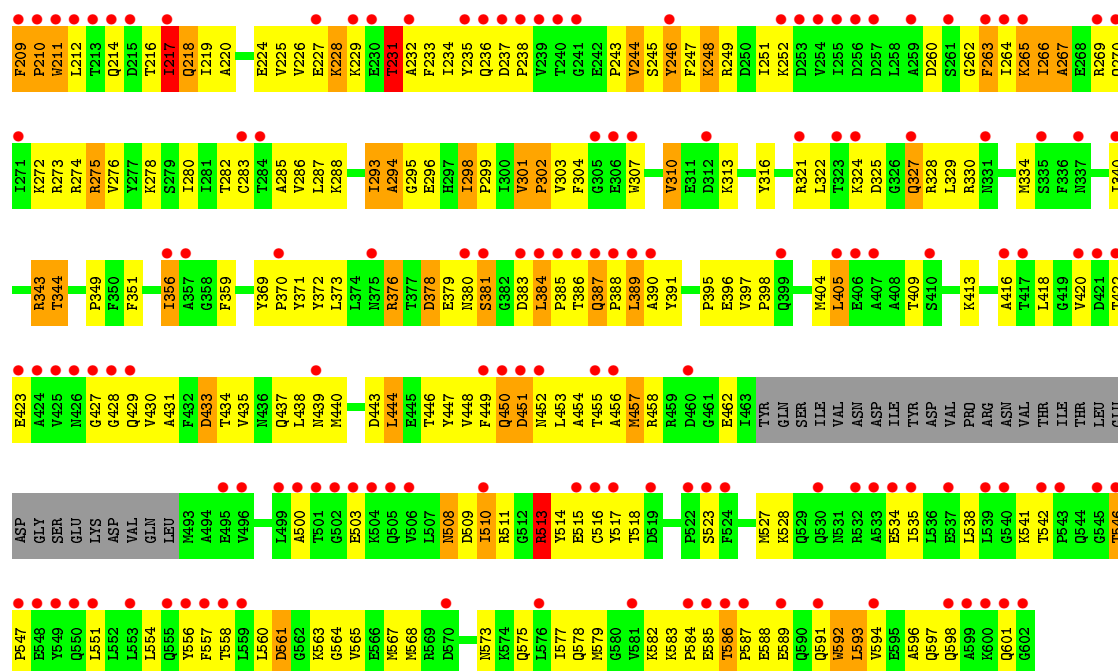


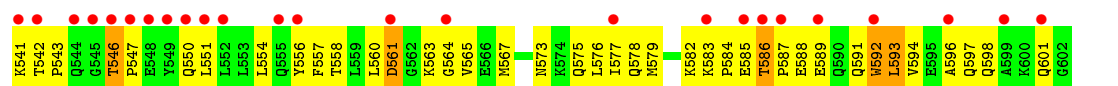
#### • Molecule 1: PORTAL PROTEIN



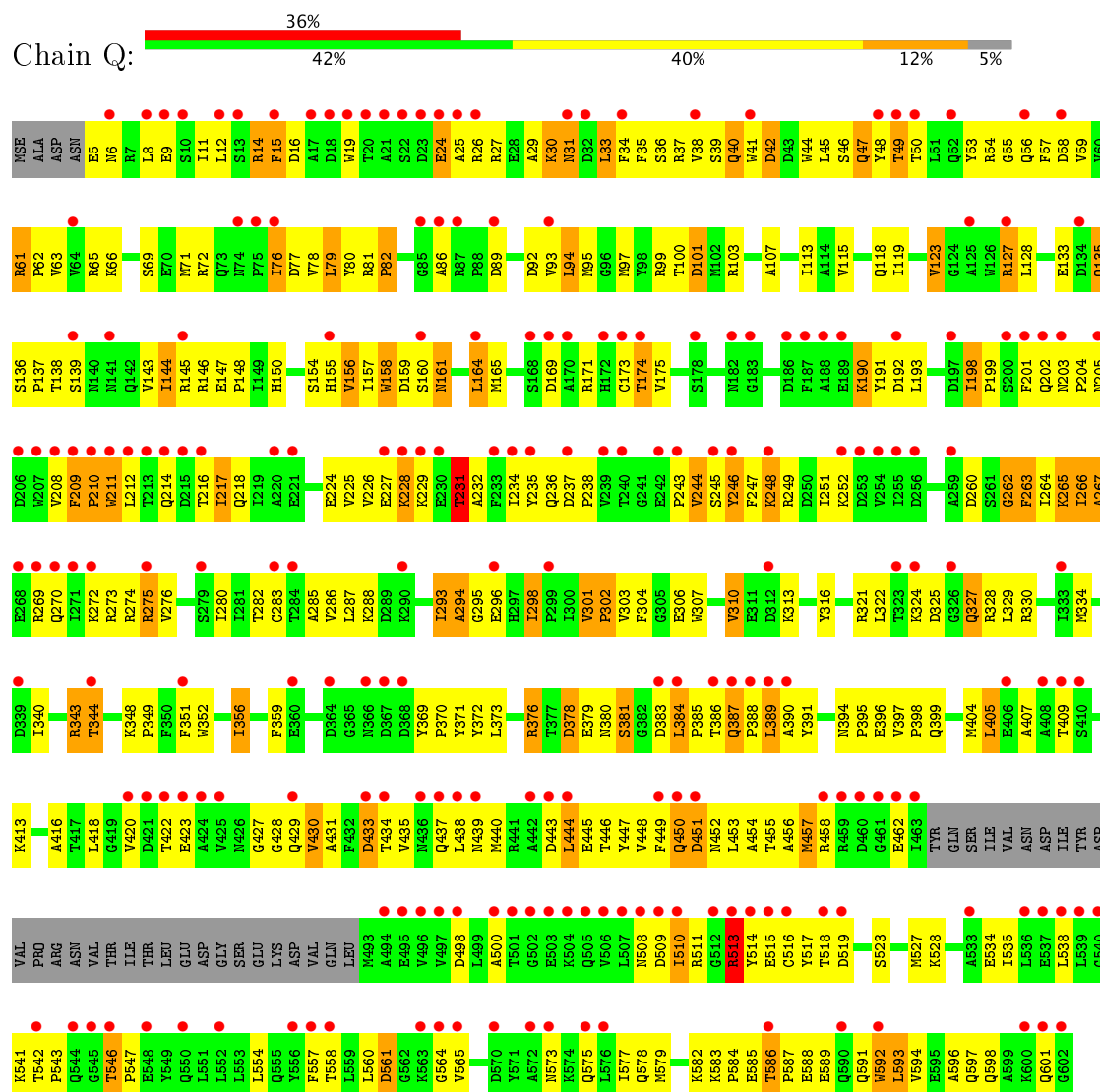
● Molecule 1: PORTAL PROTEIN



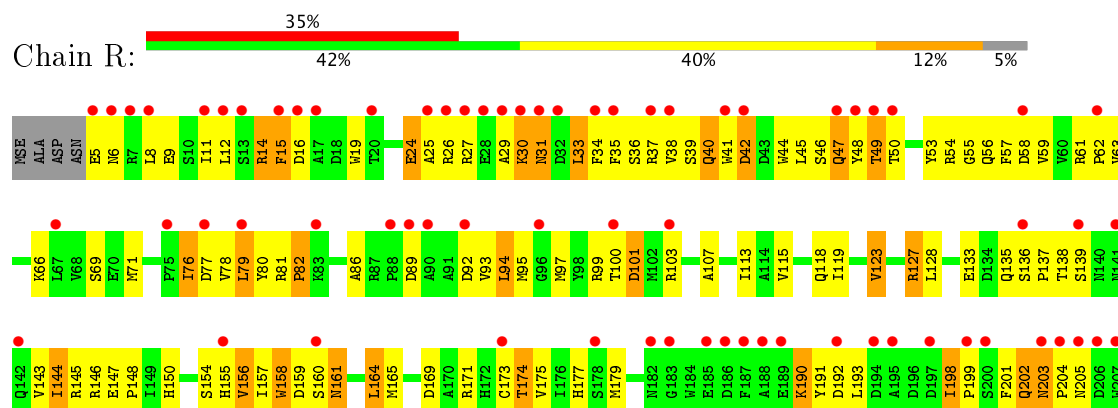


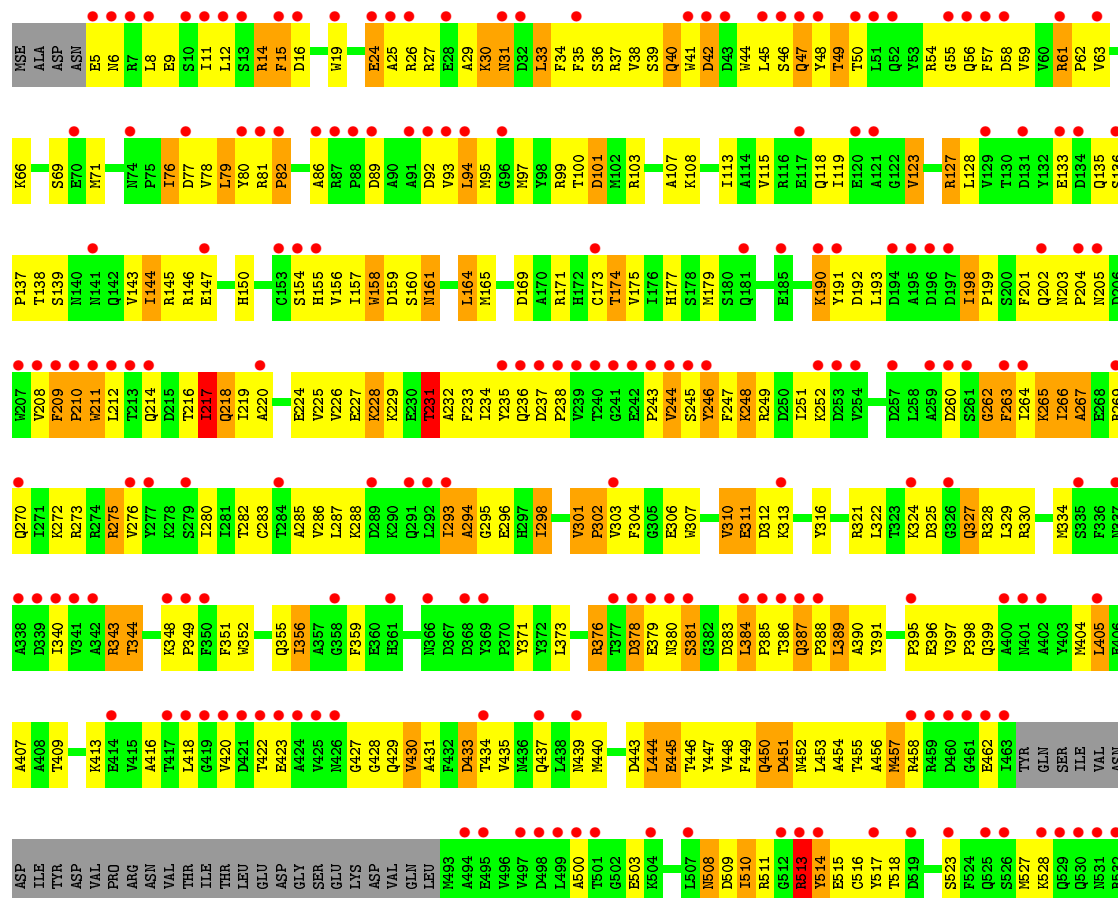


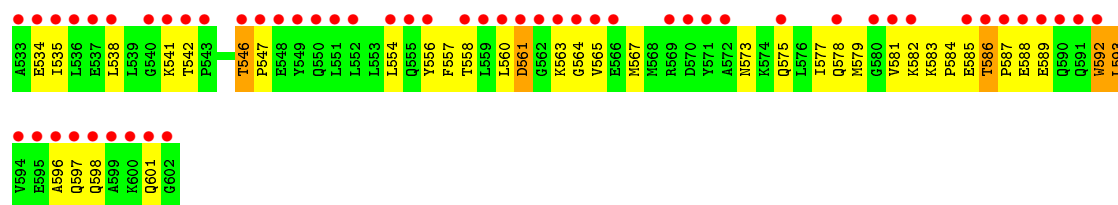
### • Molecule 1: PORTAL PROTEIN



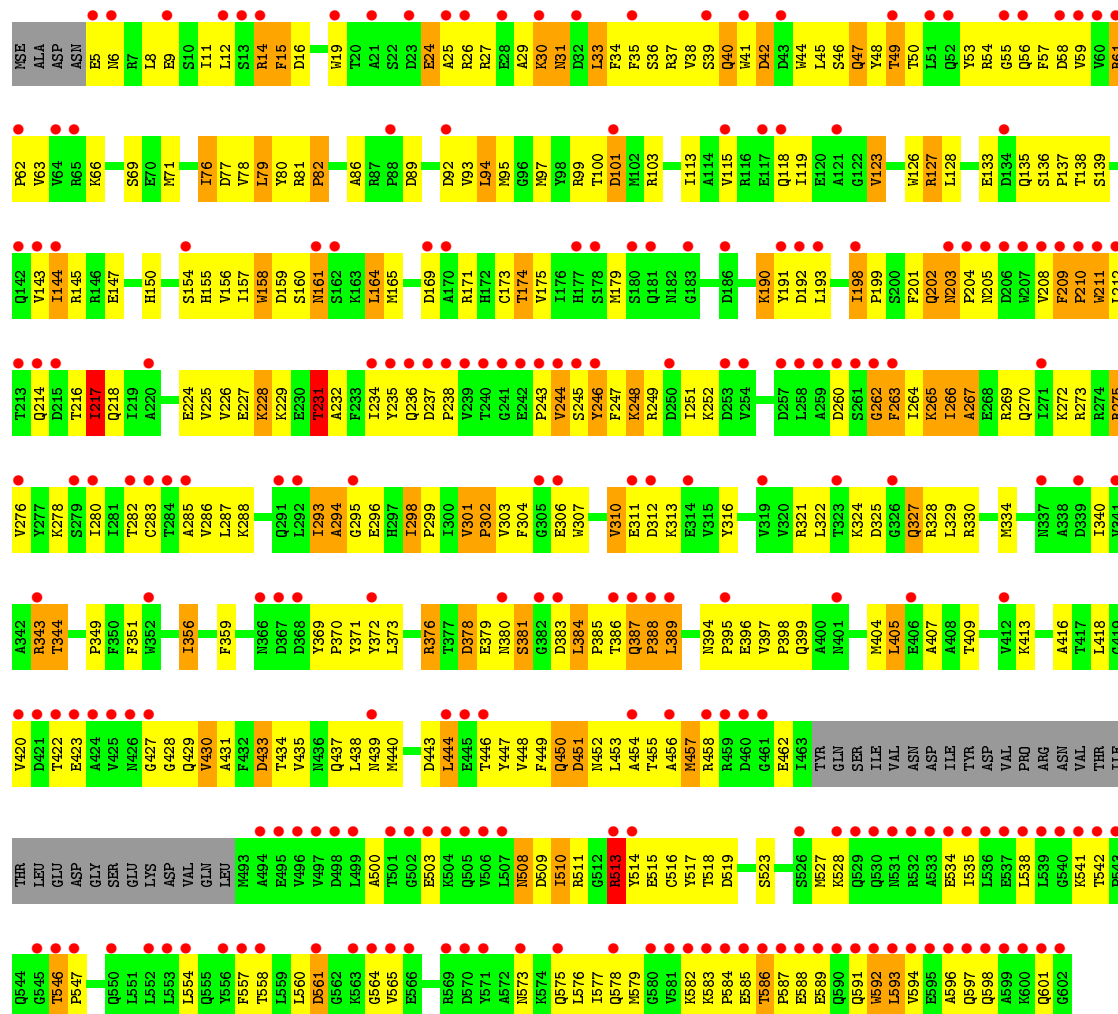
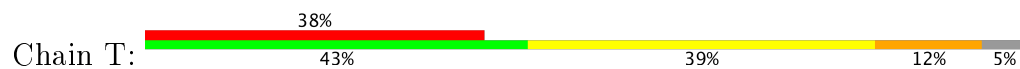
### • Molecule 1: PORTAL PROTEIN



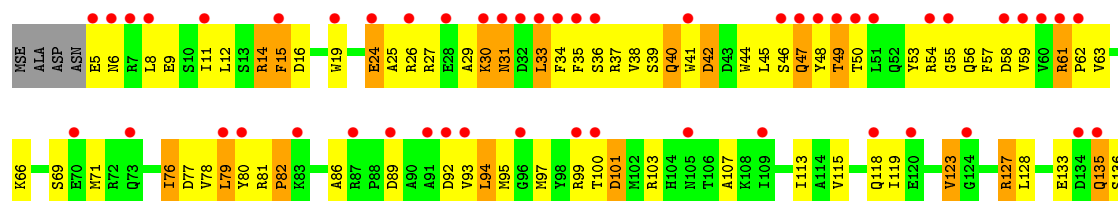
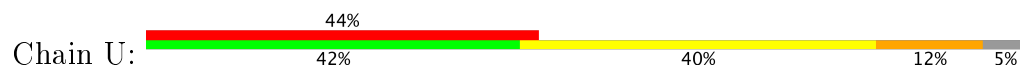


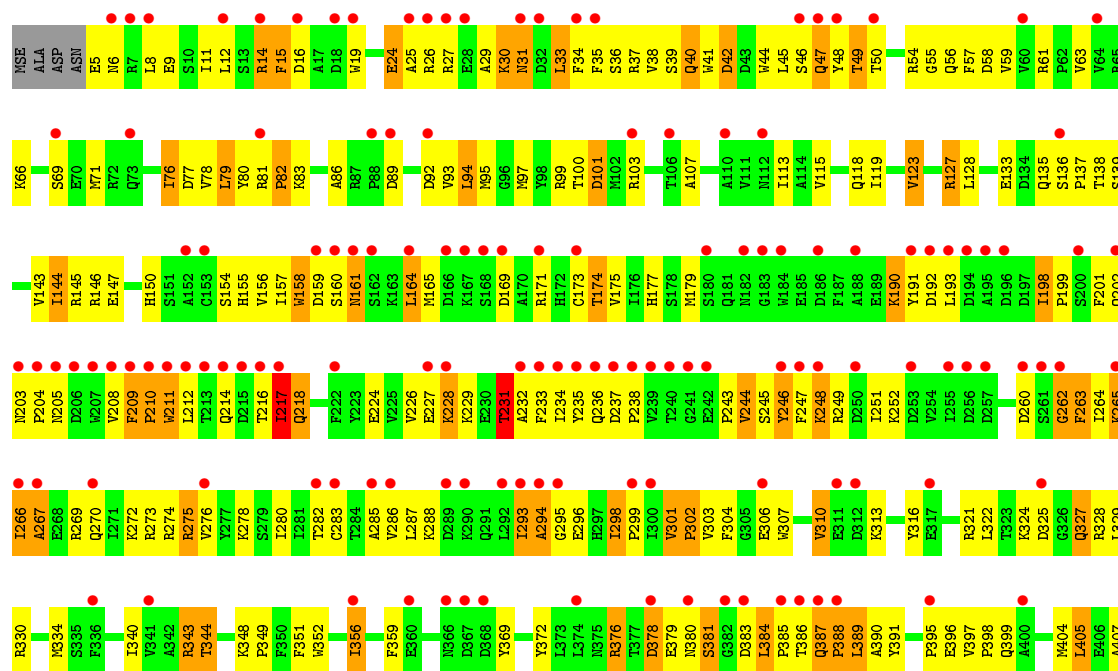


### • Molecule 1: PORTAL PROTEIN

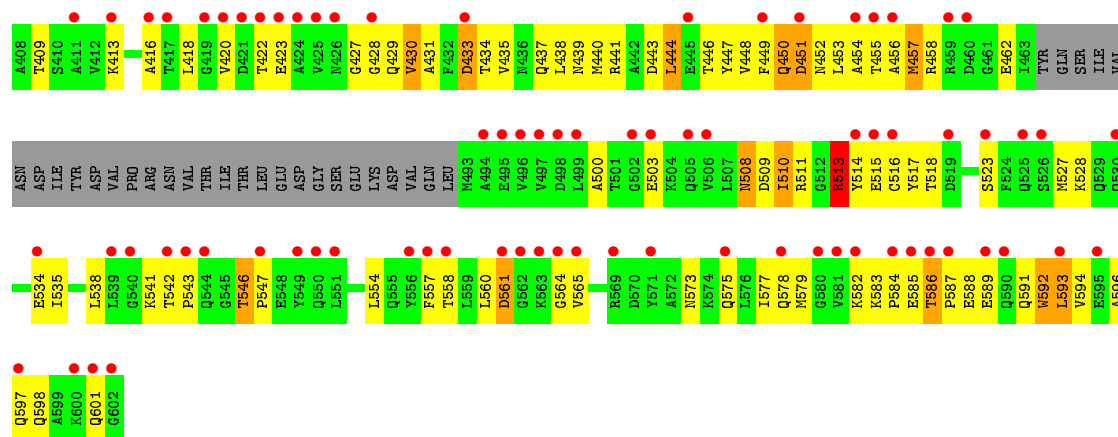


### • Molecule 1: PORTAL PROTEIN

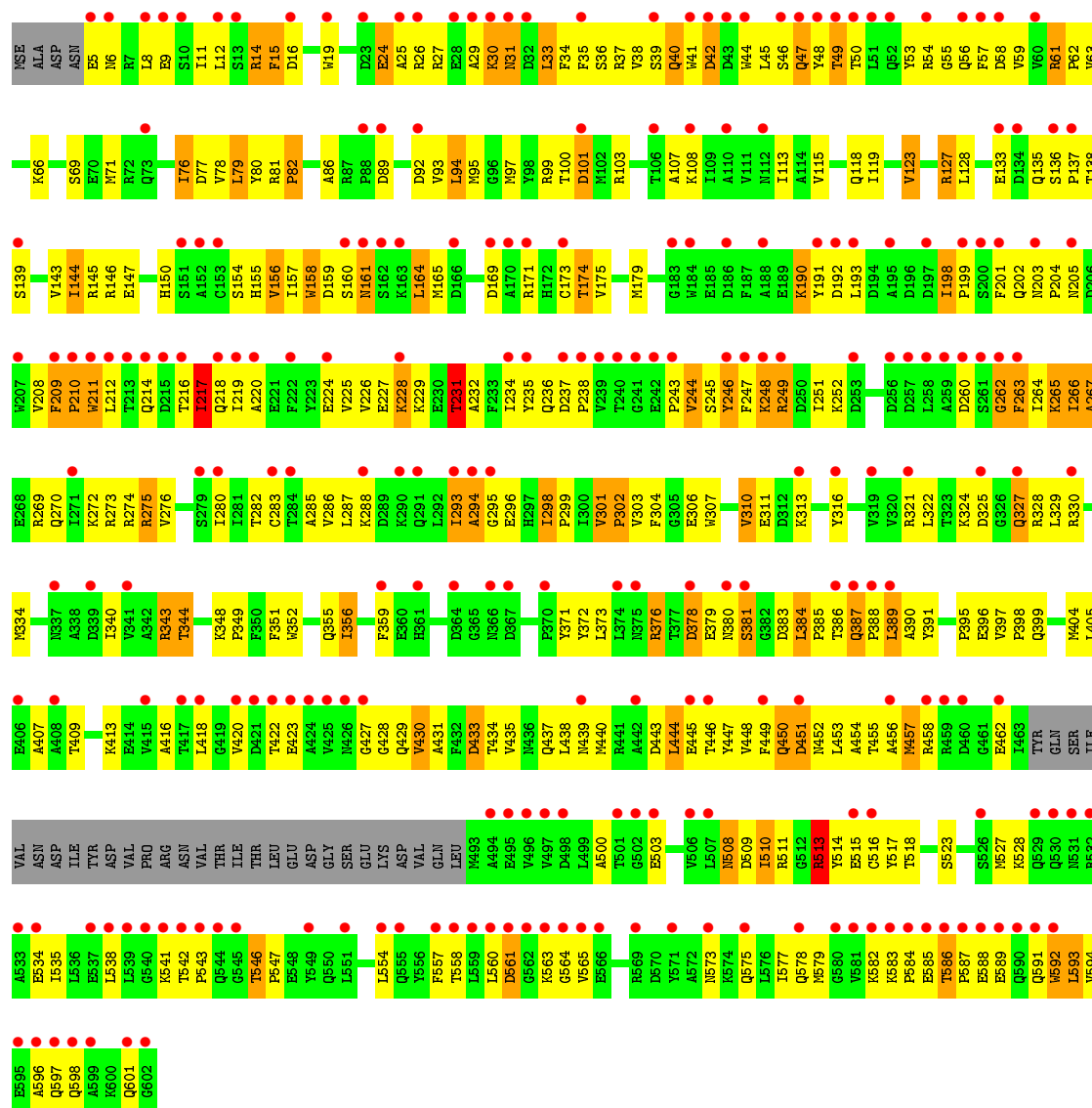
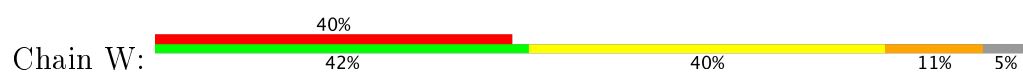








### • Molecule 1: PORTAL PROTEIN

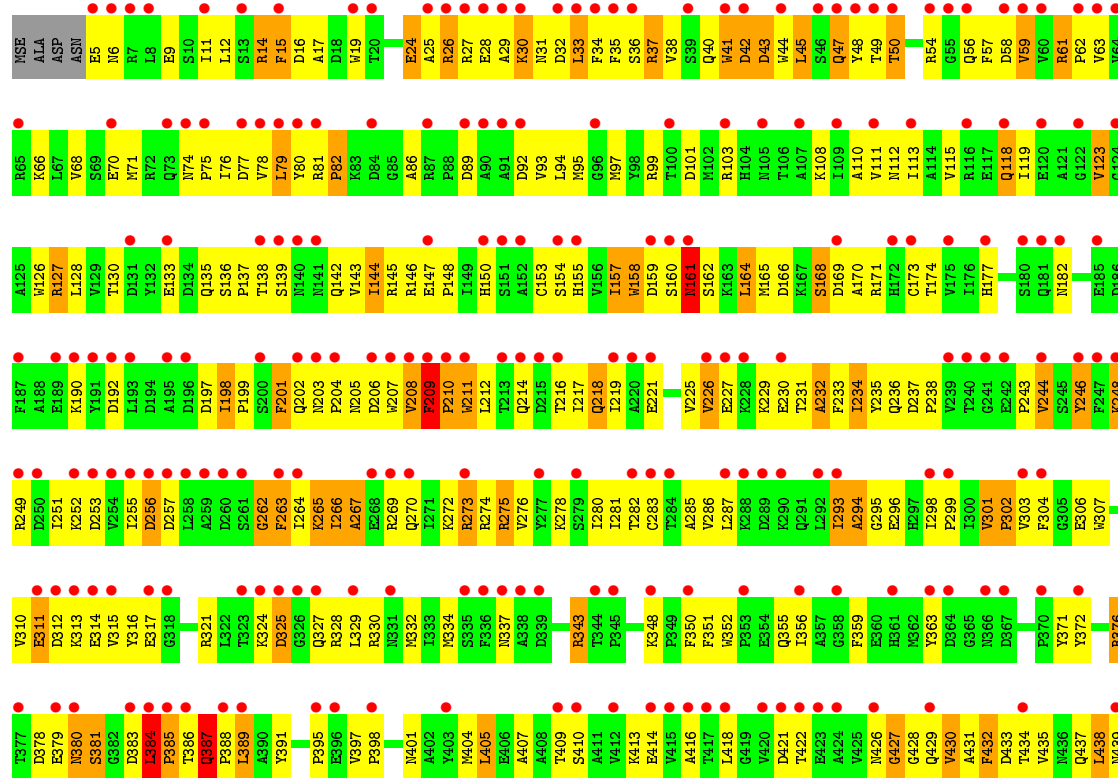


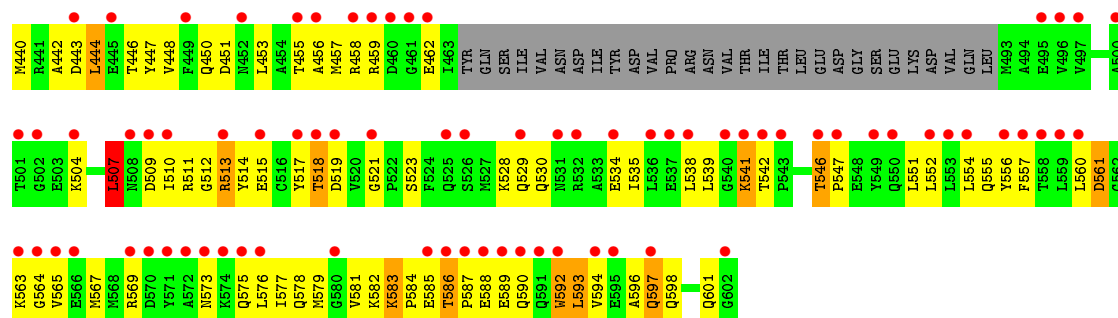
Chain X:

Chain A:

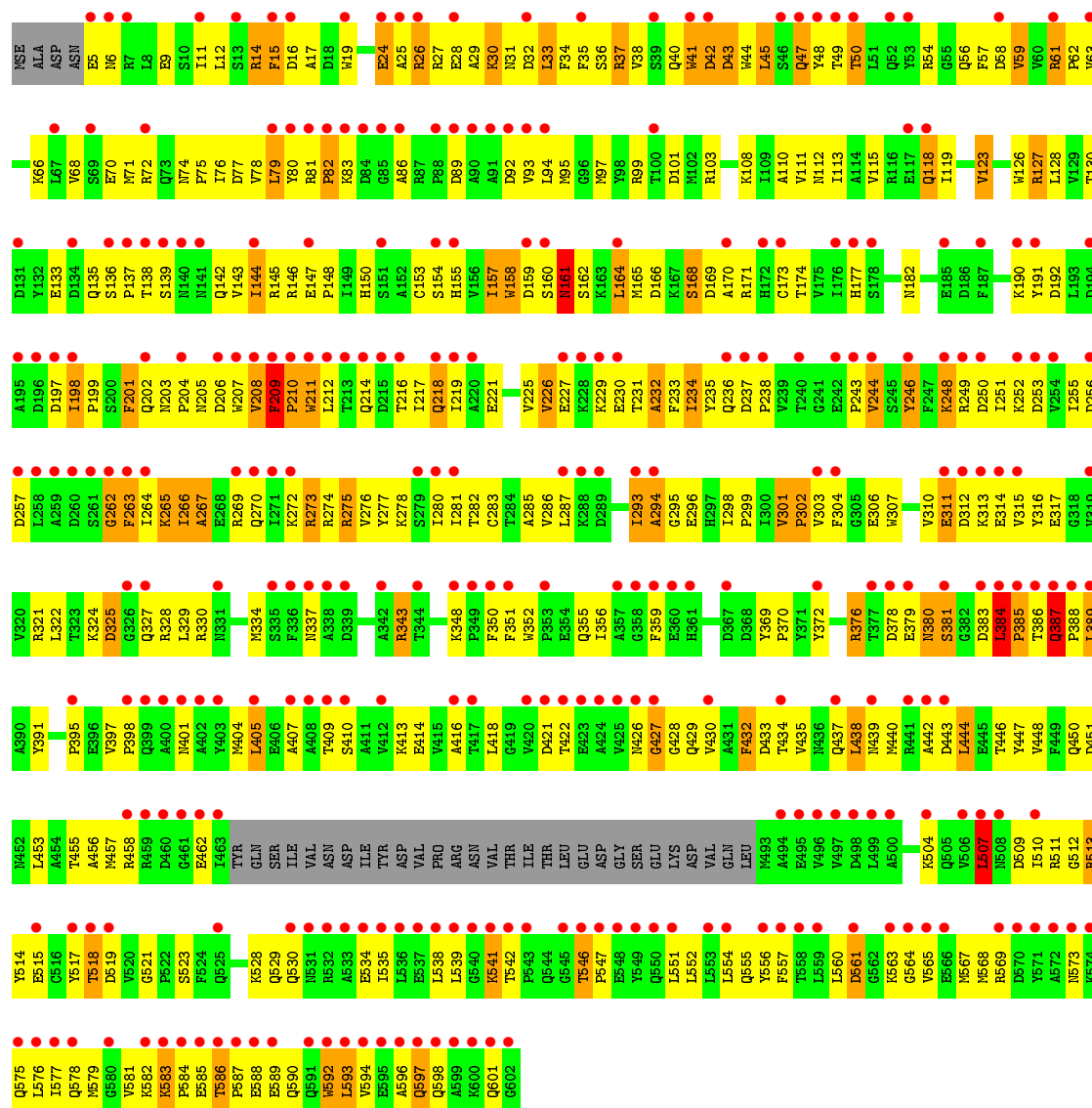
47% 38% 44% 12% 5%

Amino Acid	Count
P82	1
V63	1
K66	1
L67	1
V68	1
S69	1
E70	1
M71	1
R72	1
T73	1
M74	1
P75	1
I76	1
D77	1
V78	1
L79	1
Y80	1
R81	1
P82	1
A86	1
R87	1
P88	1
D89	1
D92	1
V93	1
L94	1
M95	1
G96	1
M97	1
Y98	1
K99	1
T100	1
D101	1
M102	1
R103	1
H104	1
N105	1
T106	1
A107	1
K108	1
I109	1
V110	1
V111	1
N112	1
I113	1
A114	1
V115	1
Q118	1
I119	1
G122	1
V123	1
G124	1
A125	1
K126	1
R127	1
L128	1
V129	1
T130	1
E133	1
D134	1
Q135	1
S136	1
K137	1
P138	1
T139	1
S140	1
M141	1
Q142	1
V143	1
I144	1
R145	1
K146	1
E147	1
P148	1
I149	1
H150	1
C153	1
S154	1
H155	1
V156	1
I157	1
M158	1
D159	1
S160	1
M161	1
S162	1
K163	1
L164	1
M165	1
D166	1
K167	1
S168	1
D169	1
A170	1
R171	1
H172	1
T174	1
H177	1
M182	1
G183	1
H184	1
D185	1
H186	1
F187	1
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H189	1
K190	1
Y191	1
D192	1
L193	1

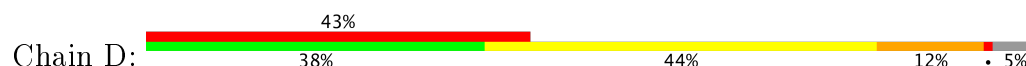


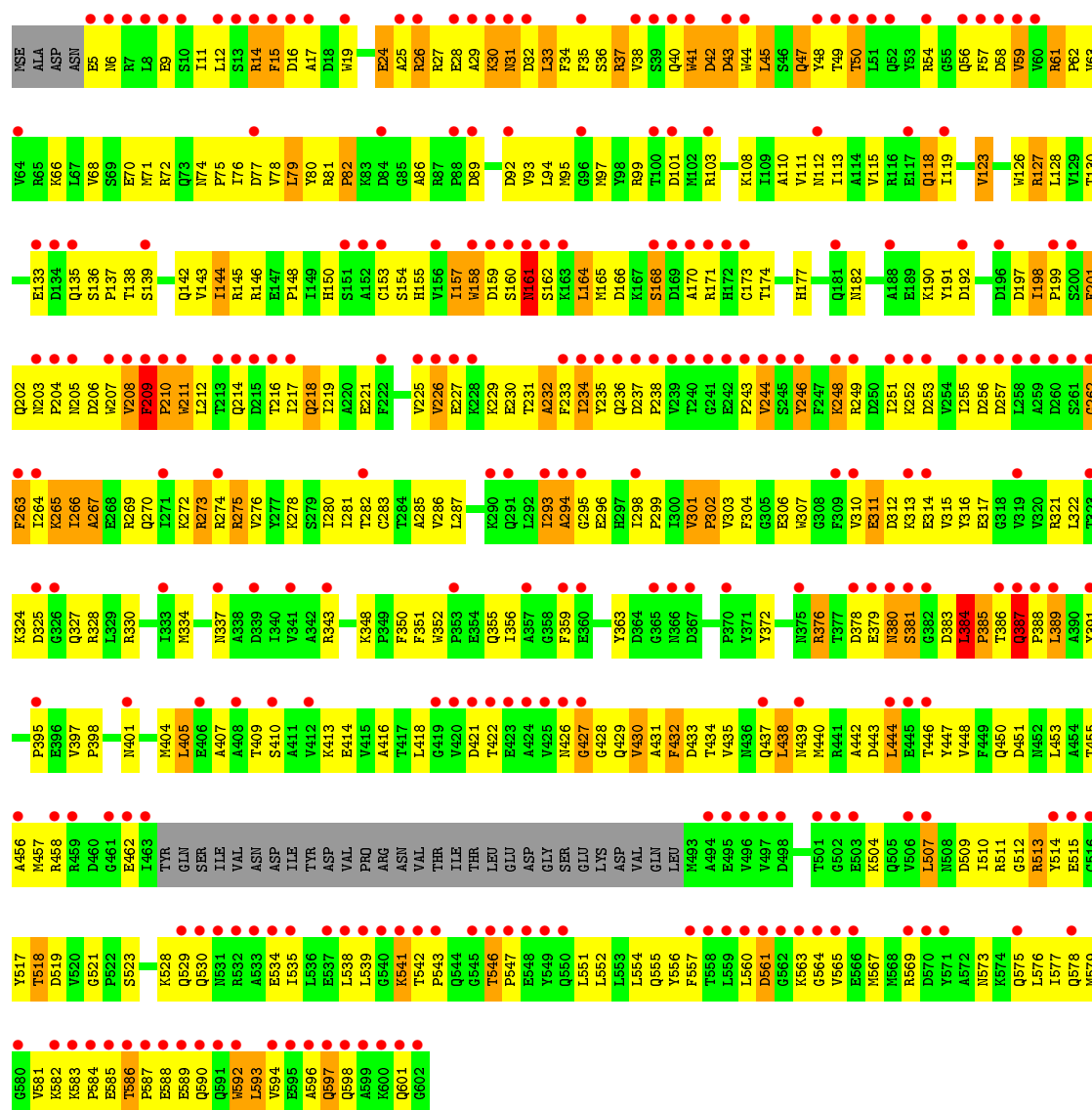


• Molecule 1: PORTAL PROTEIN

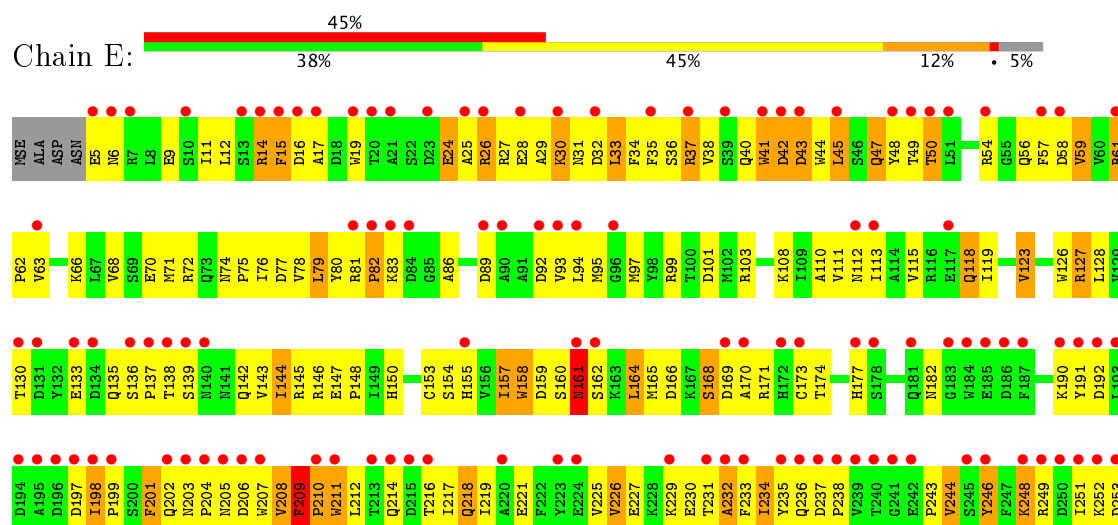


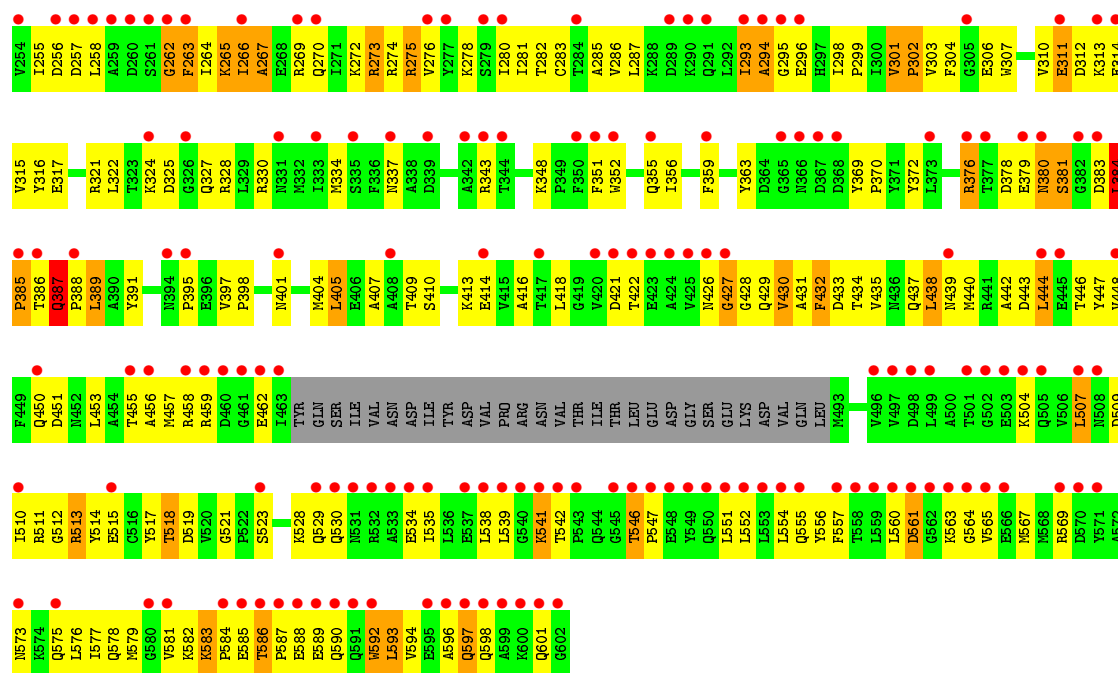
• Molecule 1: PORTAL PROTEIN



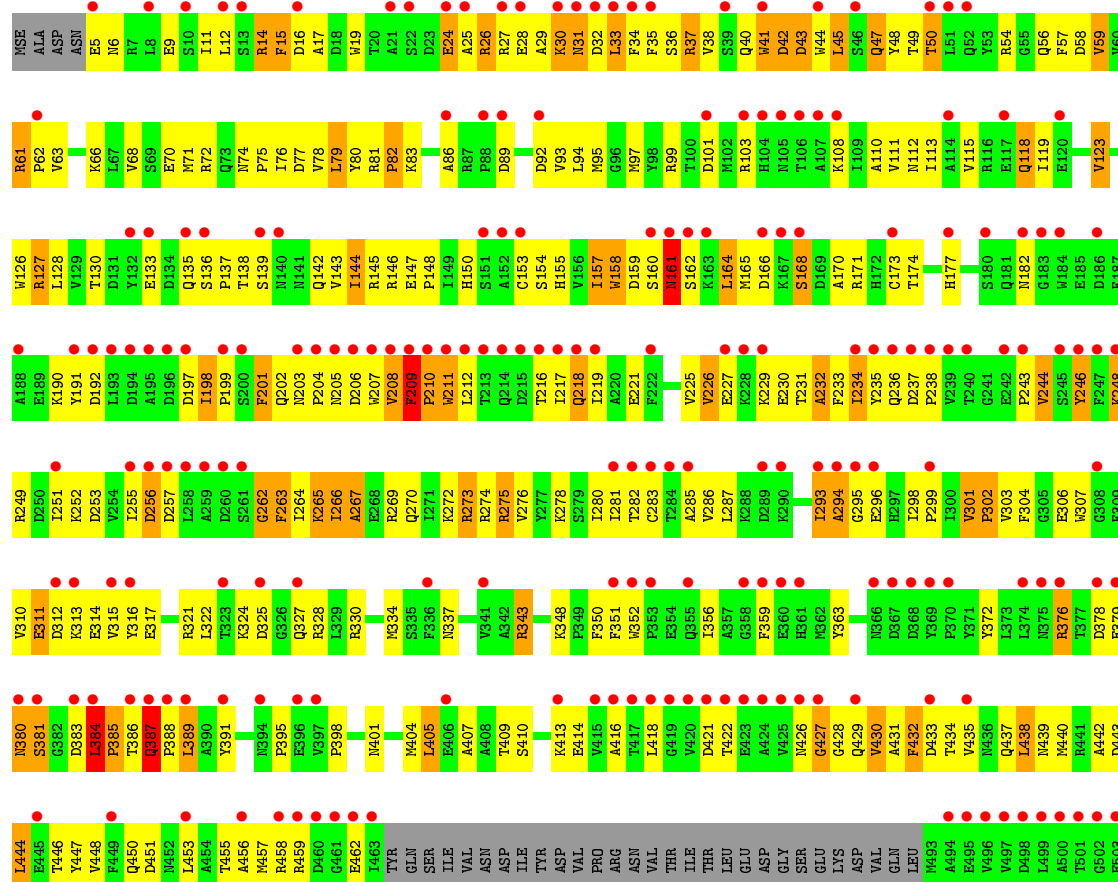
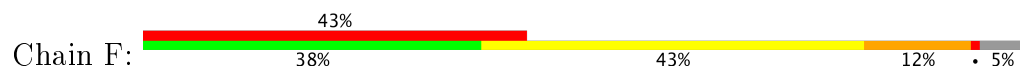


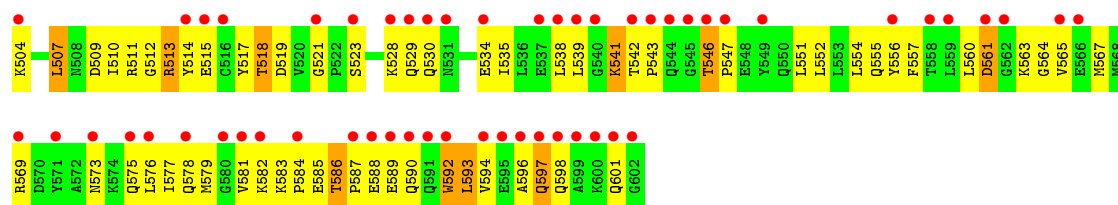
• Molecule 1: PORTAL PROTEIN



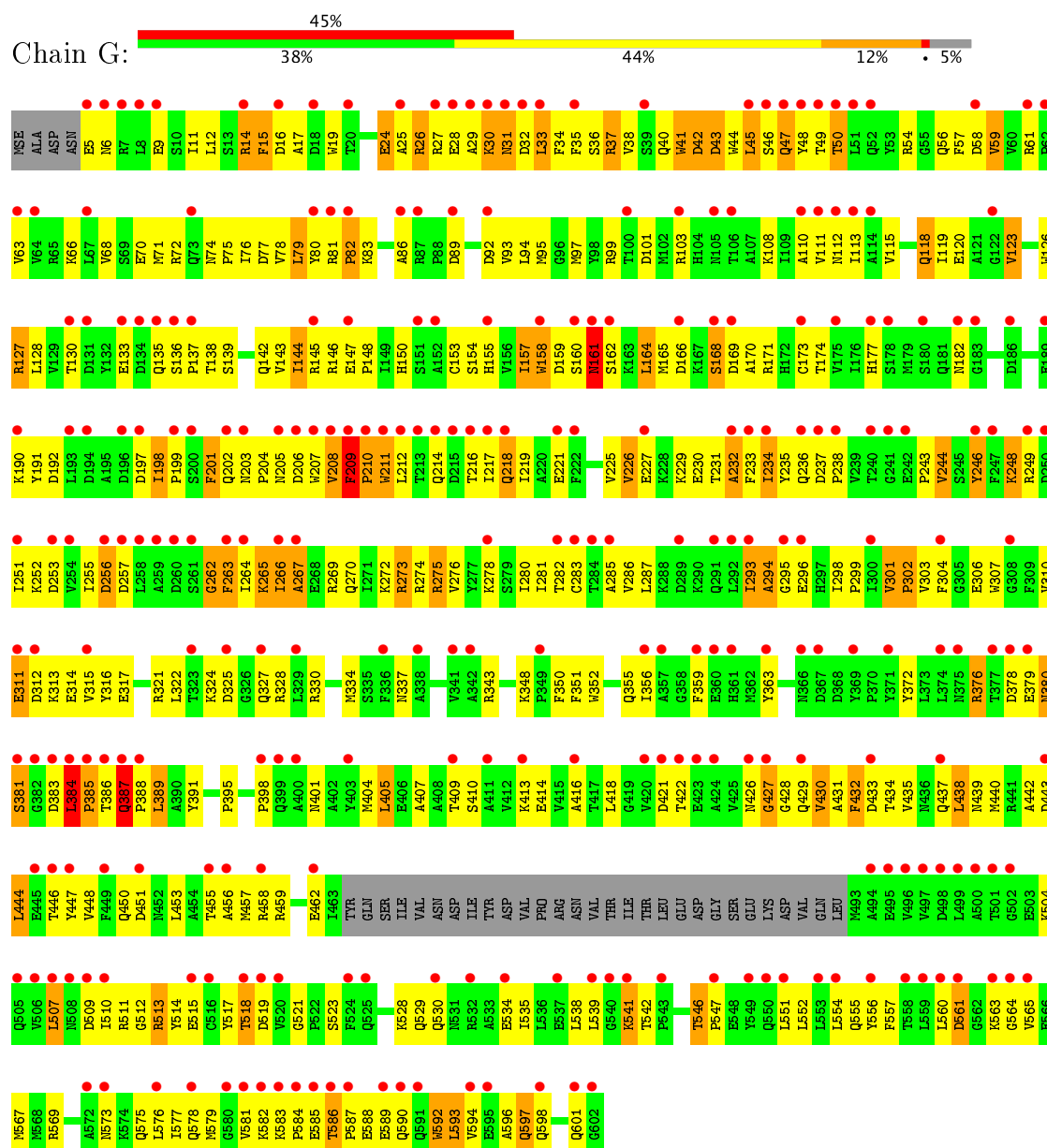


- Molecule 1: PORTAL PROTEIN

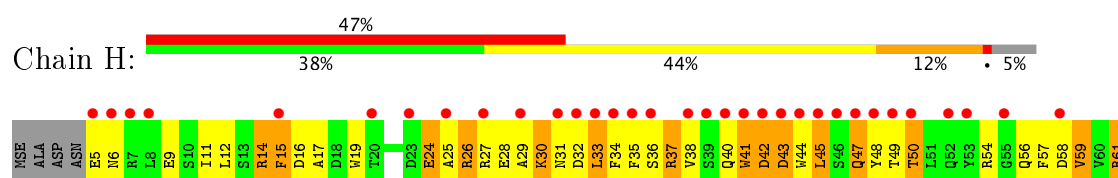


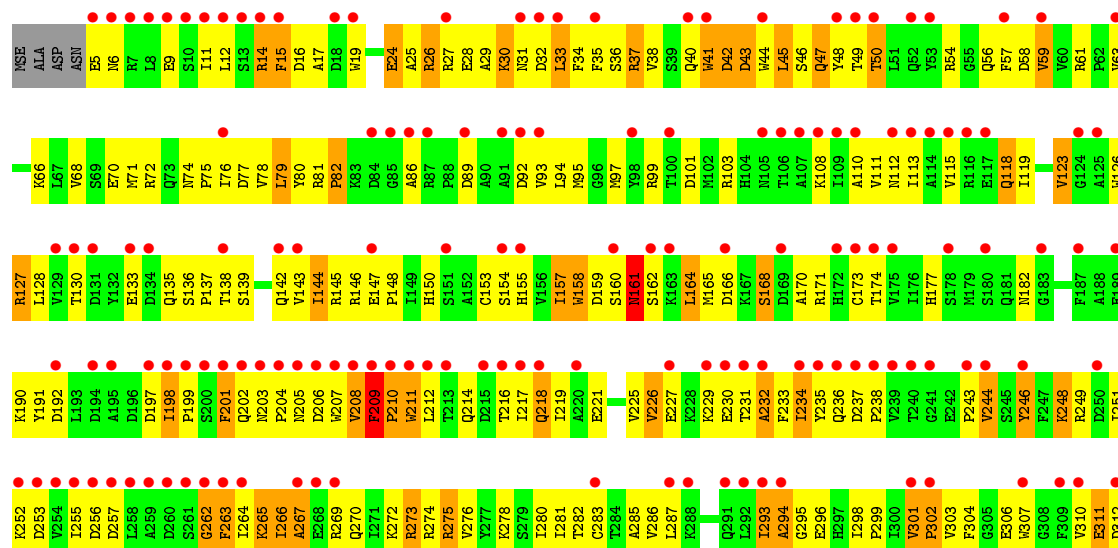


### • Molecule 1: PORTAL PROTEIN

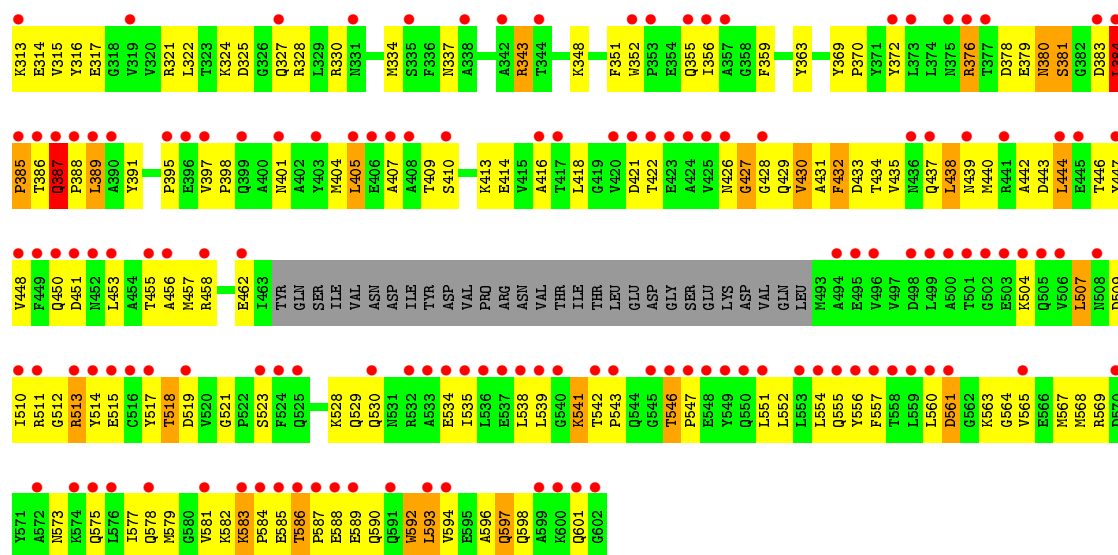


### • Molecule 1: PORTAL PROTEIN

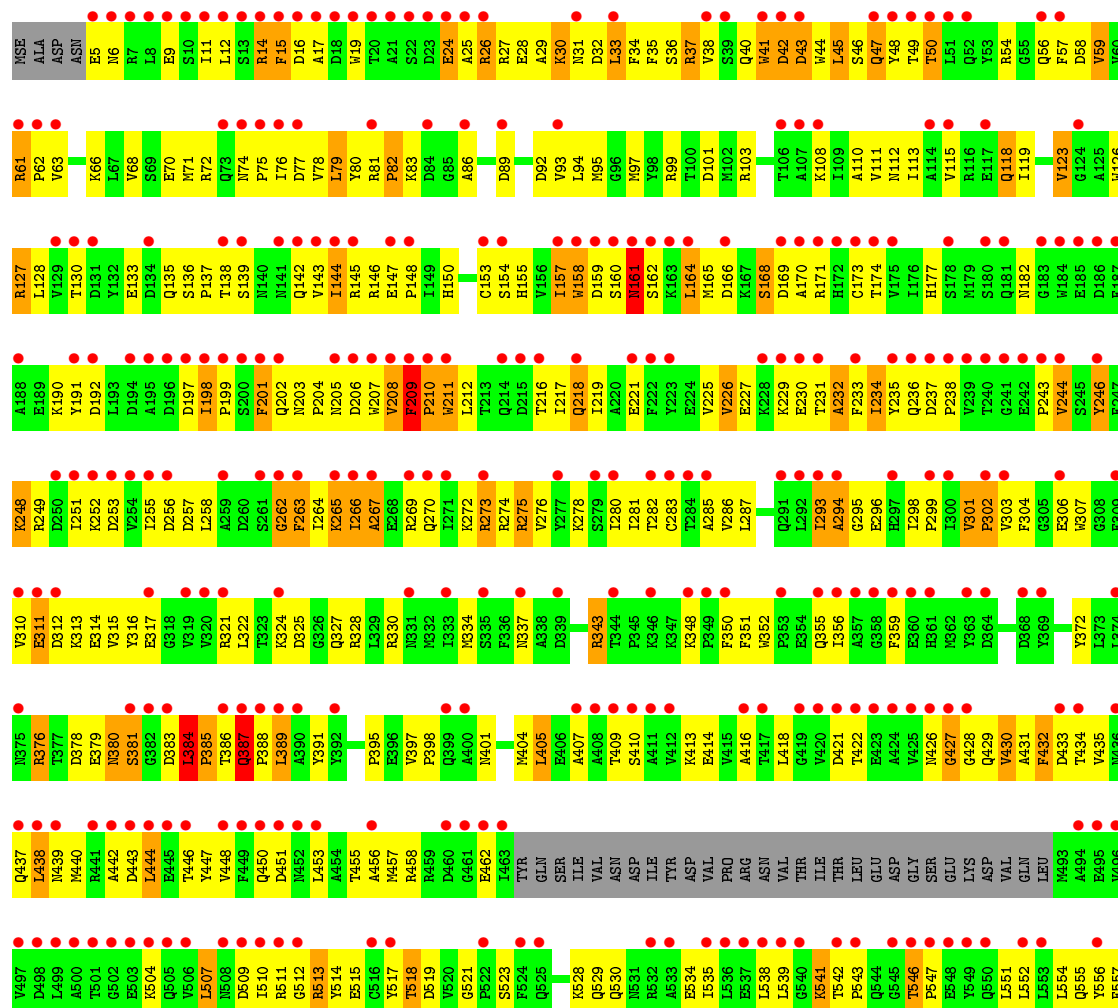






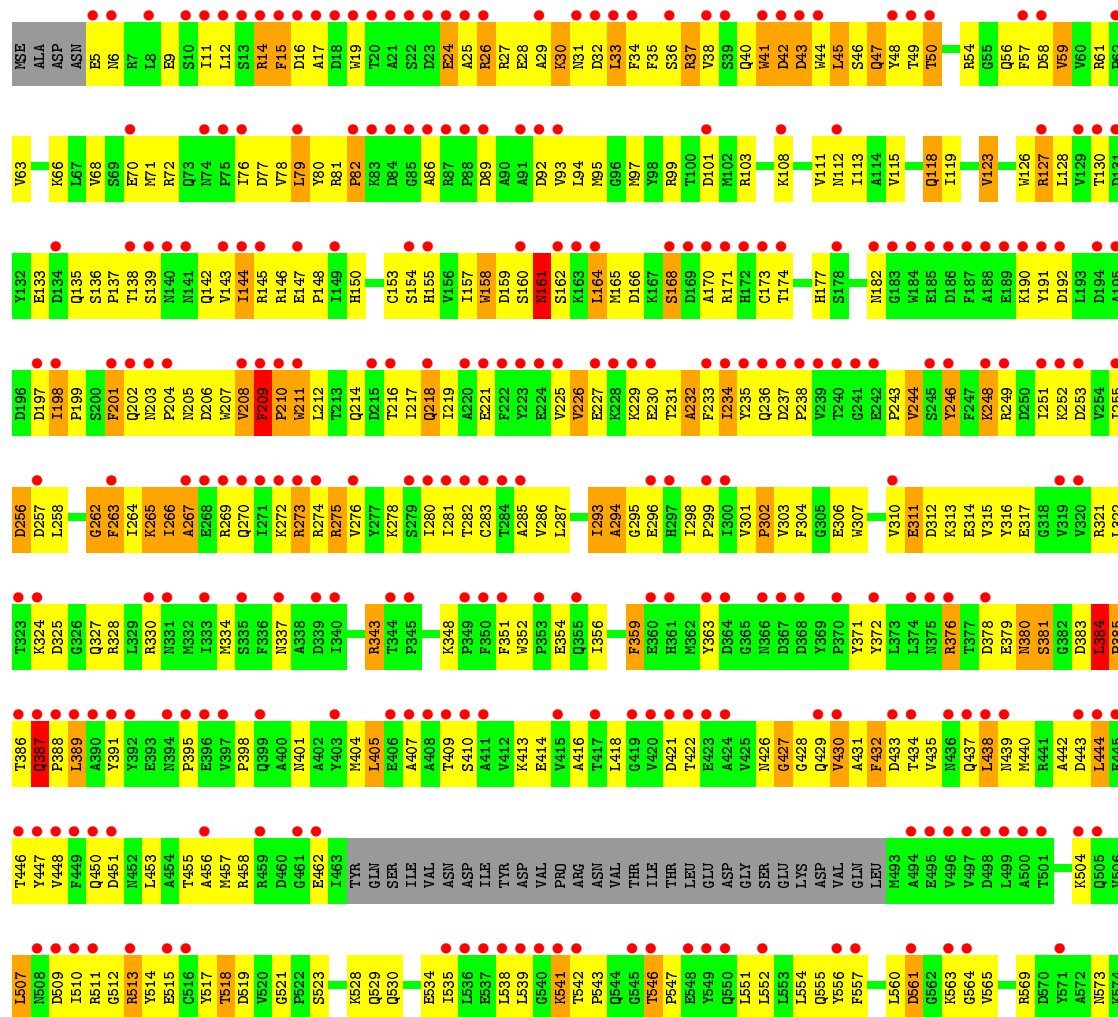
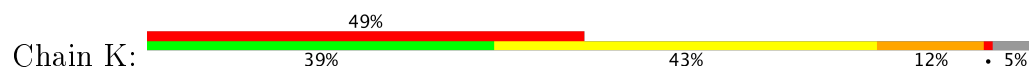


### • Molecule 1: PORTAL PROTEIN

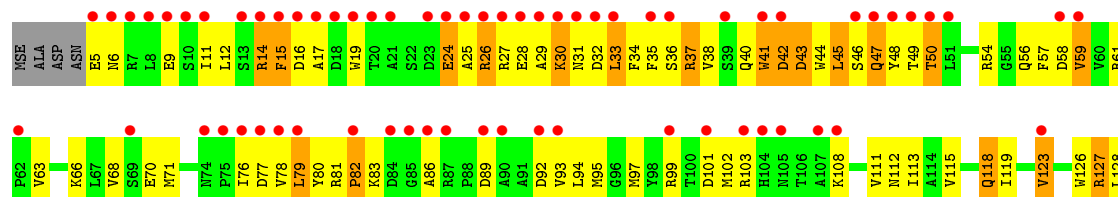
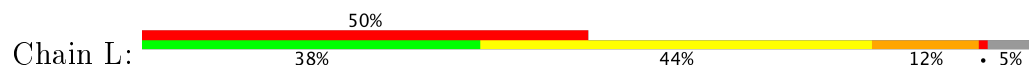




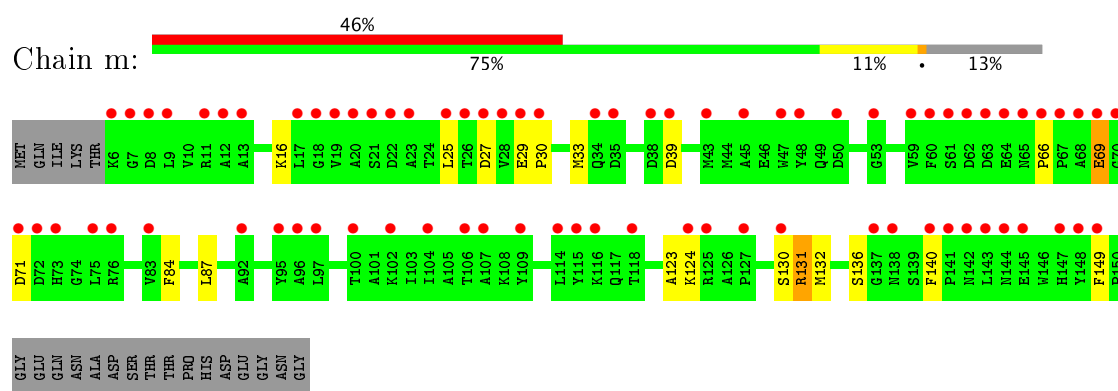
### • Molecule 1: PORTAL PROTEIN



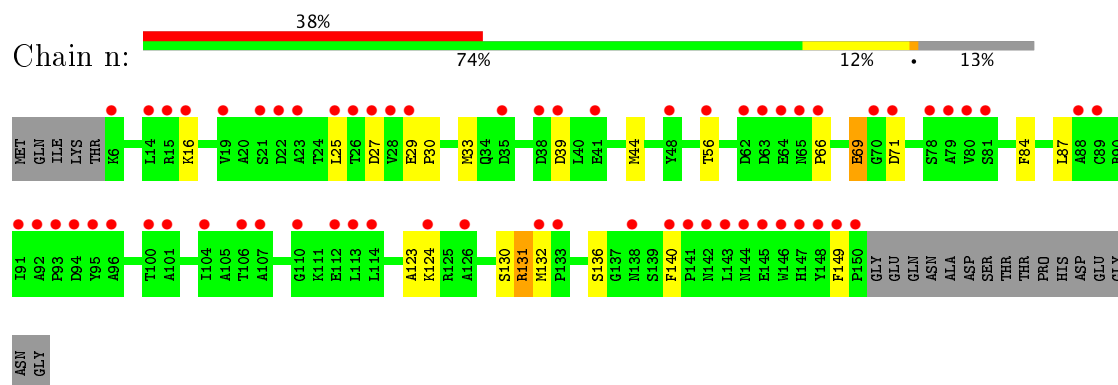
### • Molecule 1: PORTAL PROTEIN



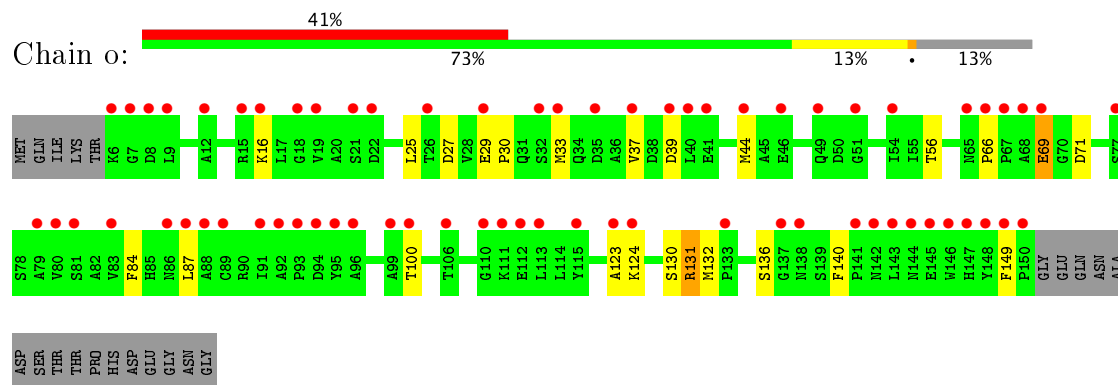




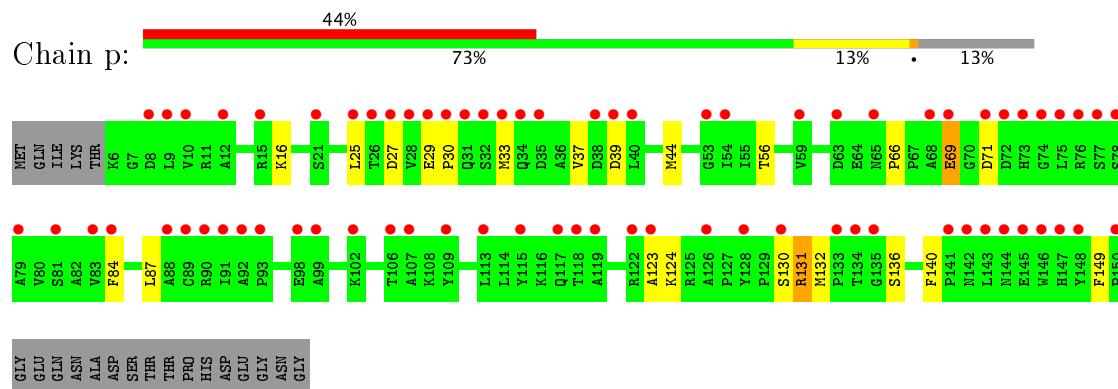
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



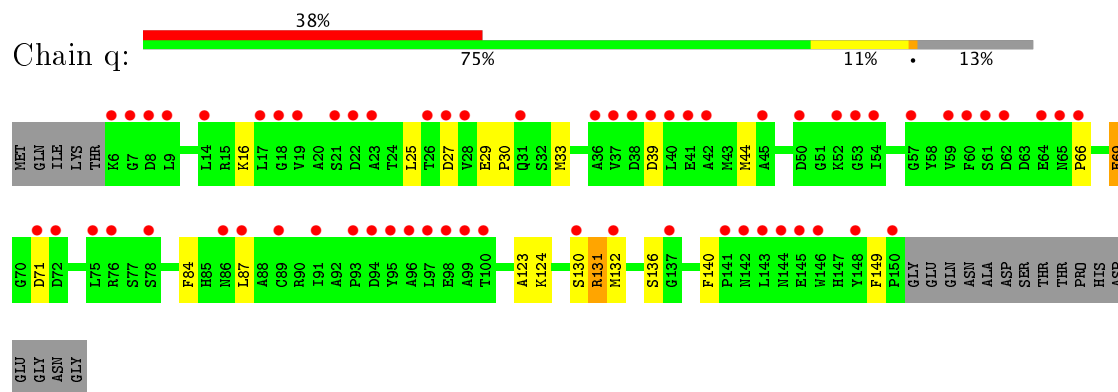
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



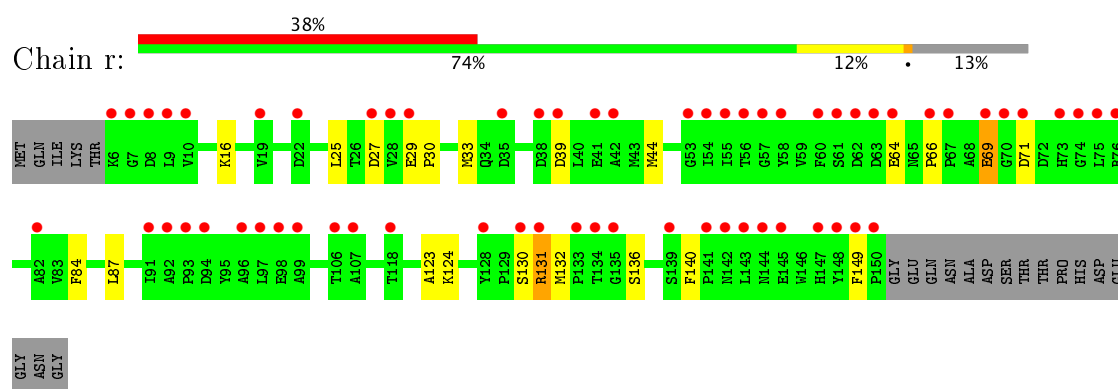
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



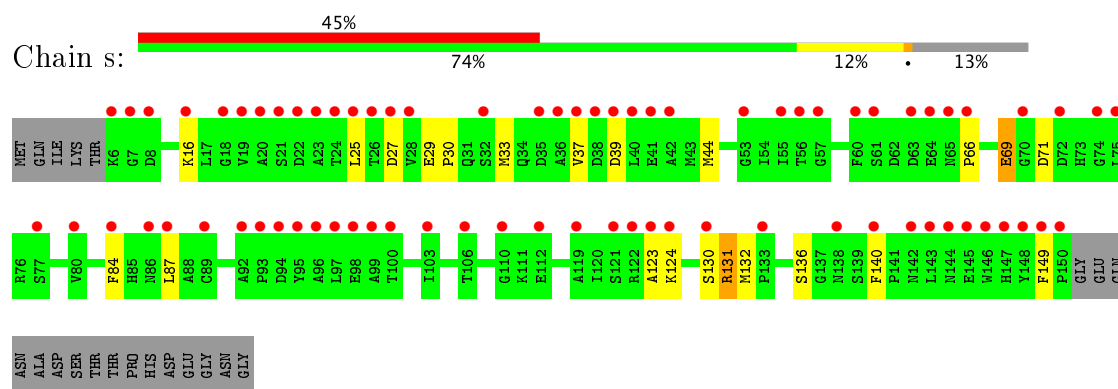
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



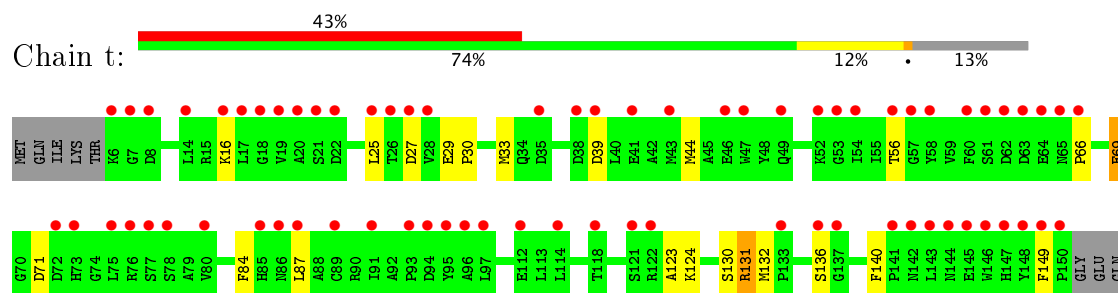
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



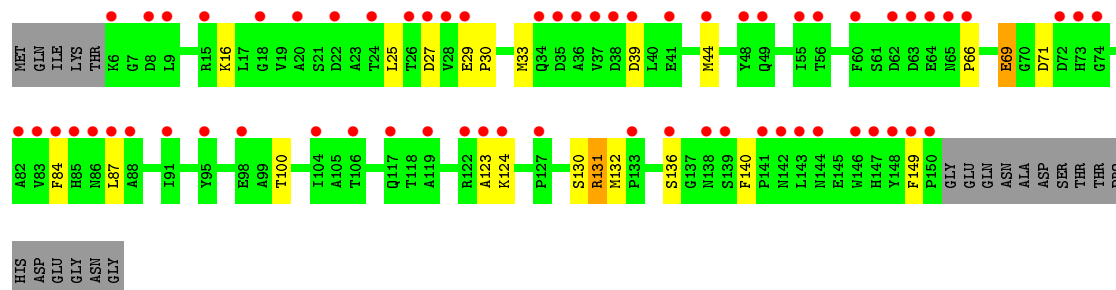
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



ASN  
ALA  
ASP  
SER  
THR  
PRO  
HIS  
ASP  
GLU  
GLY  
ASN  
GLY

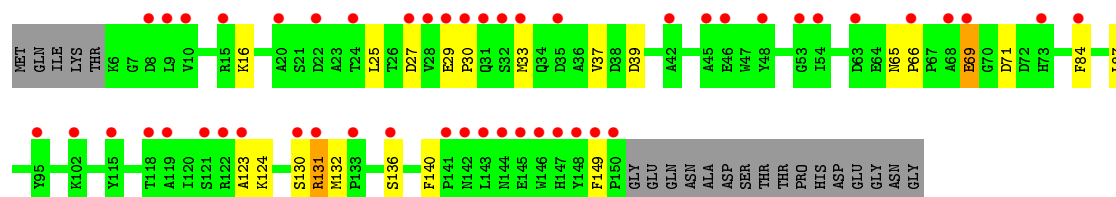
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain u: 39% 74% 12% 13%



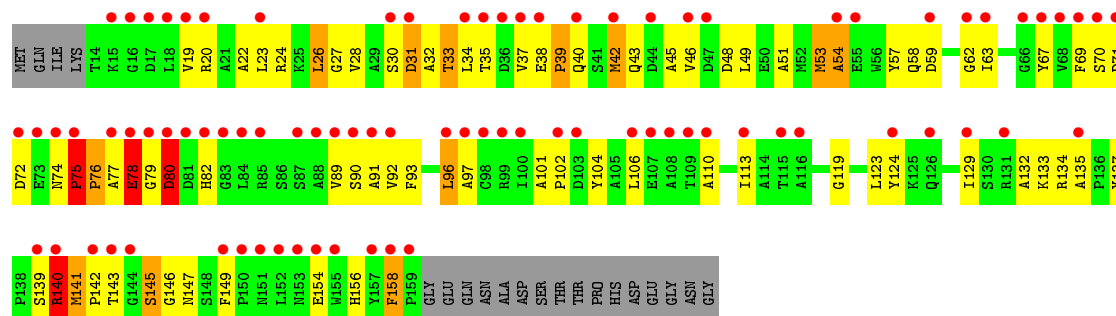
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain v: 30% 74% 12% 13%



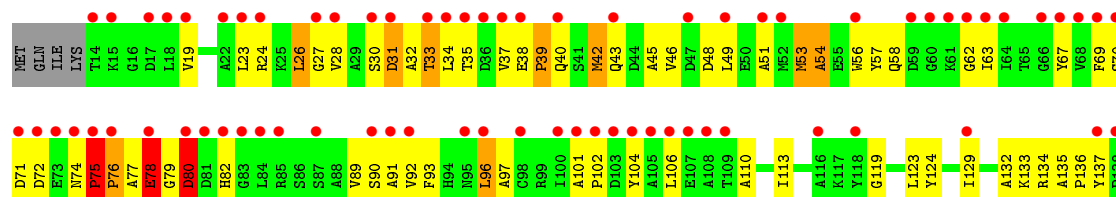
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

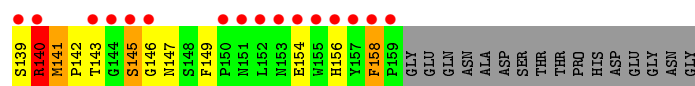
Chain Y: 51% 40% 38% 7% 12%



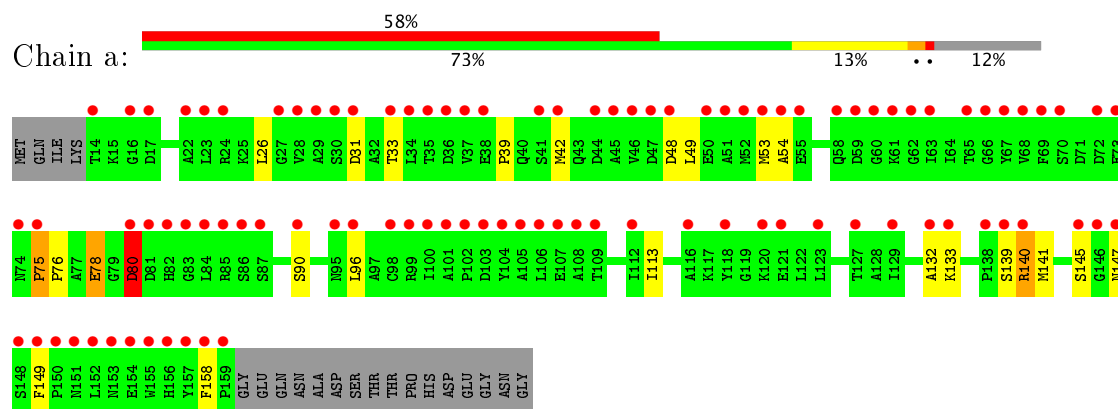
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

Chain Z: 52% 41% 37% 7% 12%

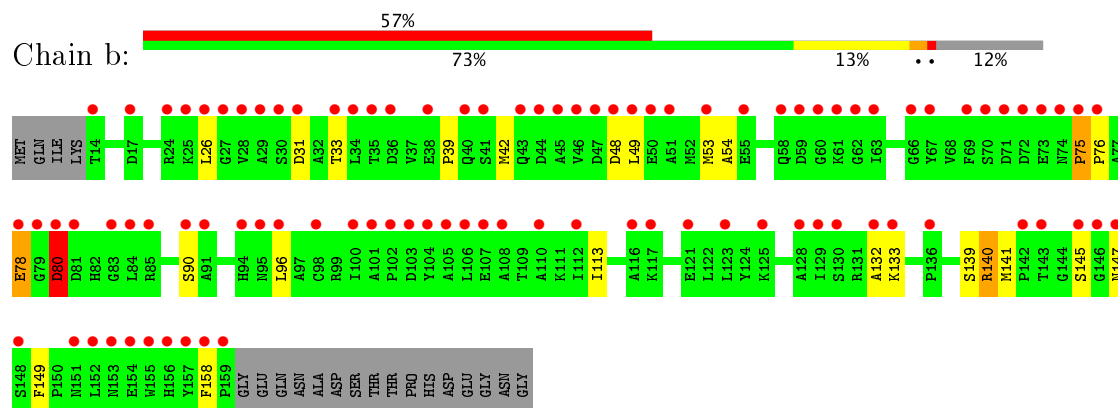




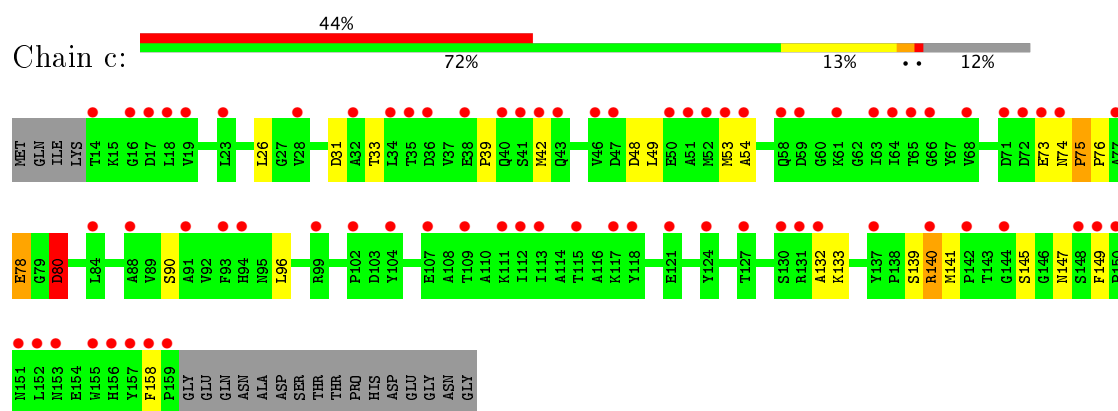
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



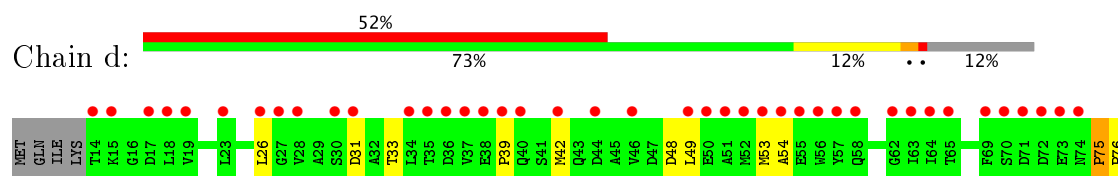
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

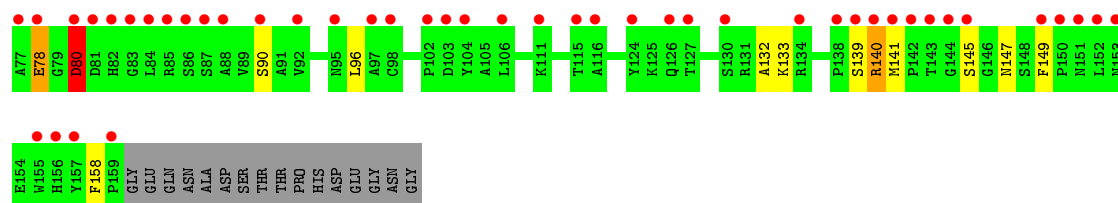


• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

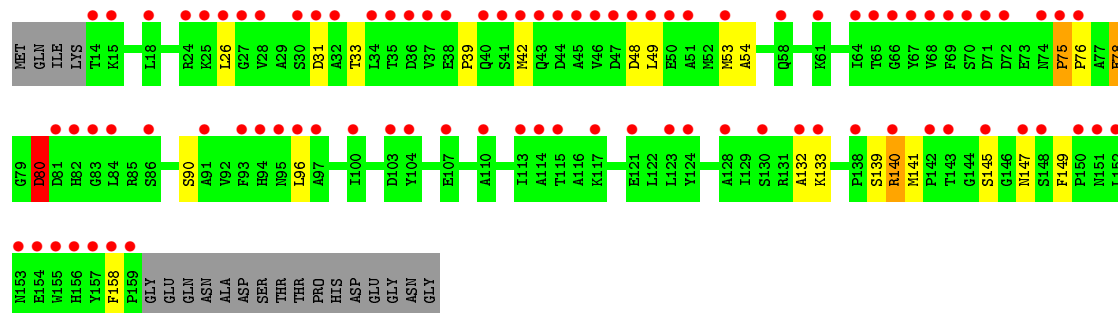
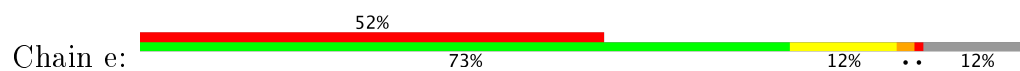


• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4

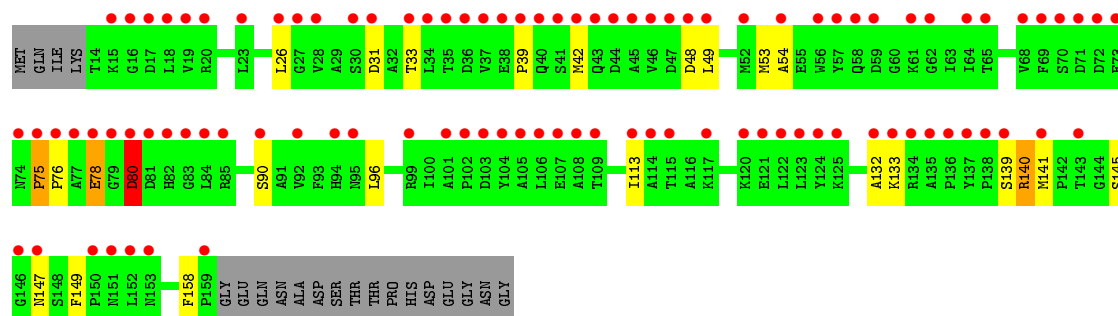




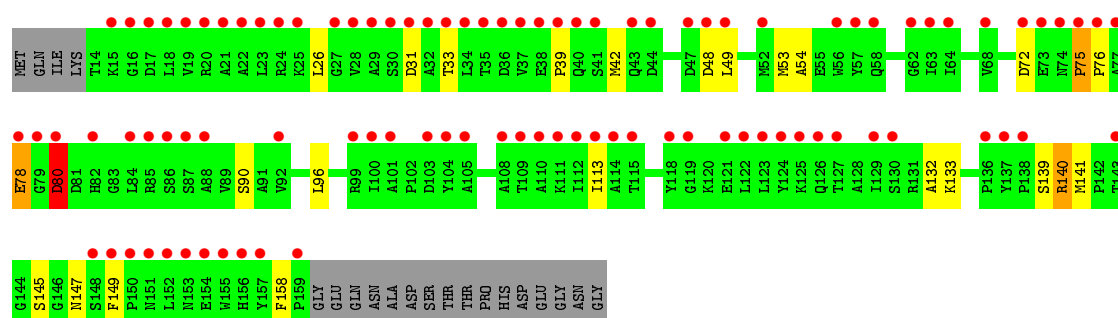
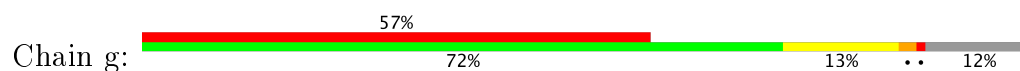
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



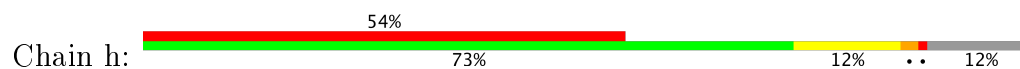
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



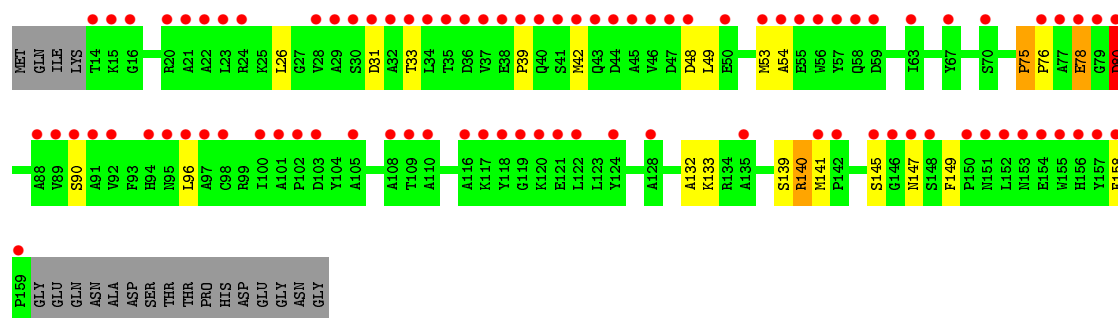
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



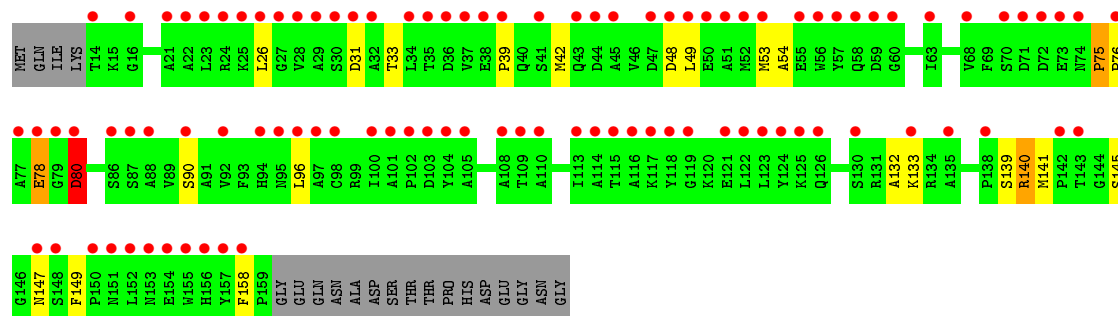
• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



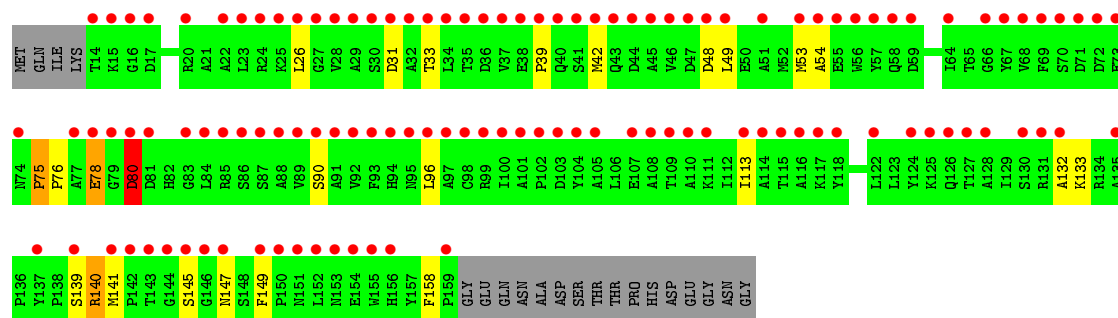




• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



• Molecule 2: PACKAGED DNA STABILIZATION PROTEIN GP4



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	170.17Å 253.28Å 282.73Å 90.00° 90.68° 90.00°	Depositor
Resolution (Å)	19.99 – 3.25 78.75 – 3.23	Depositor EDS
% Data completeness (in resolution range)	59.7 (19.99-3.25) 91.6 (78.75-3.23)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.15	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.88 (at 3.26Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE: 1.5_2)	Depositor
R, $R_{free}$	0.222 , 0.236 0.282 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	65.0	Xtriage
Anisotropy	1.241	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.31 , 107.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	0.025 for h,-k,-l	Xtriage
$F_o, F_c$ correlation	0.77	EDS
Total number of atoms	135120	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	92.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality

### 5.1 Standard geometry

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	A	0.35	0/4635	0.54	0/6265
1	B	0.35	0/4635	0.54	0/6265
1	C	0.35	0/4635	0.54	0/6265
1	D	0.35	0/4635	0.54	0/6265
1	E	0.35	0/4635	0.54	0/6265
1	F	0.35	0/4635	0.54	0/6265
1	G	0.35	0/4635	0.54	0/6265
1	H	0.35	0/4635	0.54	0/6265
1	I	0.35	0/4635	0.54	0/6265
1	J	0.35	0/4635	0.54	0/6265
1	K	0.35	0/4635	0.54	0/6265
1	L	0.35	0/4635	0.54	0/6265
1	M	0.31	0/4646	0.51	0/6278
1	N	0.32	0/4646	0.51	0/6278
1	O	0.32	0/4646	0.50	0/6278
1	P	0.32	0/4646	0.51	0/6278
1	Q	0.32	0/4646	0.51	0/6278
1	R	0.32	0/4646	0.51	0/6278
1	S	0.31	0/4646	0.51	0/6278
1	T	0.31	0/4646	0.50	0/6278
1	U	0.31	0/4646	0.51	0/6278
1	V	0.32	0/4646	0.51	0/6278
1	W	0.31	0/4646	0.55	2/6278 (0.0%)
1	X	0.31	0/4646	0.50	0/6278
2	Y	0.37	0/1067	0.84	4/1452 (0.3%)
2	Z	0.37	0/1067	0.85	4/1452 (0.3%)
2	a	0.37	0/1067	0.84	4/1452 (0.3%)
2	b	0.37	0/1067	0.84	4/1452 (0.3%)
2	c	0.37	0/1067	0.84	4/1452 (0.3%)
2	d	0.37	0/1067	0.84	4/1452 (0.3%)
2	e	0.37	0/1067	0.84	4/1452 (0.3%)
2	f	0.37	0/1067	0.84	4/1452 (0.3%)
2	g	0.37	0/1067	0.84	4/1452 (0.3%)
2	h	0.37	0/1067	0.84	4/1452 (0.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
2	i	0.37	0/1067	0.85	4/1452 (0.3%)
2	j	0.37	0/1067	0.84	4/1452 (0.3%)
2	k	0.32	0/1071	0.52	0/1455
2	l	0.33	0/1071	0.52	0/1455
2	m	0.33	0/1071	0.51	0/1455
2	n	0.33	0/1071	0.51	0/1455
2	o	0.33	0/1071	0.51	0/1455
2	p	0.33	0/1071	0.51	0/1455
2	q	0.32	0/1071	0.51	0/1455
2	r	0.36	0/1071	0.51	0/1455
2	s	0.32	0/1071	0.52	0/1455
2	t	0.32	0/1071	0.51	0/1455
2	u	0.31	0/1071	0.51	0/1455
2	v	0.32	0/1071	0.51	0/1455
All	All	0.34	0/137028	0.56	50/185400 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
1	M	0	1
1	N	0	1
1	O	0	1
1	P	0	1
1	Q	0	1
1	R	0	1
1	S	0	1
1	T	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
1	U	0	1
1	V	0	1
1	W	0	1
1	X	0	1
All	All	0	24

There are no bond length outliers.

All (50) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	i	80	ASP	N-CA-CB	17.19	141.54	110.60
2	d	80	ASP	N-CA-CB	17.18	141.52	110.60
2	Z	80	ASP	N-CA-CB	17.17	141.51	110.60
2	Y	80	ASP	N-CA-CB	17.17	141.50	110.60
2	e	80	ASP	N-CA-CB	17.17	141.50	110.60
2	a	80	ASP	N-CA-CB	17.17	141.50	110.60
2	j	80	ASP	N-CA-CB	17.17	141.50	110.60
2	b	80	ASP	N-CA-CB	17.16	141.48	110.60
2	f	80	ASP	N-CA-CB	17.16	141.48	110.60
2	g	80	ASP	N-CA-CB	17.16	141.48	110.60
2	c	80	ASP	N-CA-CB	17.15	141.48	110.60
2	h	80	ASP	N-CA-CB	17.14	141.45	110.60
1	W	249	ARG	NE-CZ-NH2	-15.09	112.75	120.30
2	a	75	PRO	C-N-CD	-9.11	100.57	120.60
2	c	75	PRO	C-N-CD	-9.09	100.60	120.60
2	Z	75	PRO	C-N-CD	-9.09	100.61	120.60
2	f	75	PRO	C-N-CD	-9.08	100.62	120.60
2	i	75	PRO	C-N-CD	-9.08	100.62	120.60
2	Y	75	PRO	C-N-CD	-9.08	100.62	120.60
2	e	75	PRO	C-N-CD	-9.08	100.62	120.60
2	g	75	PRO	C-N-CD	-9.08	100.62	120.60
2	j	75	PRO	C-N-CD	-9.08	100.63	120.60
2	b	75	PRO	C-N-CD	-9.07	100.64	120.60
2	d	75	PRO	C-N-CD	-9.07	100.64	120.60
2	h	75	PRO	C-N-CD	-9.07	100.65	120.60
2	f	80	ASP	N-CA-C	-8.92	86.93	111.00
2	g	80	ASP	N-CA-C	-8.91	86.93	111.00
2	i	80	ASP	N-CA-C	-8.91	86.94	111.00
2	Z	80	ASP	N-CA-C	-8.91	86.95	111.00
2	Y	80	ASP	N-CA-C	-8.90	86.96	111.00
2	e	80	ASP	N-CA-C	-8.90	86.97	111.00
2	c	80	ASP	N-CA-C	-8.90	86.97	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	d	80	ASP	N-CA-C	-8.90	86.98	111.00
2	b	80	ASP	N-CA-C	-8.89	86.98	111.00
2	j	80	ASP	N-CA-C	-8.89	86.99	111.00
2	h	80	ASP	N-CA-C	-8.89	87.00	111.00
2	a	80	ASP	N-CA-C	-8.89	87.00	111.00
1	W	249	ARG	NE-CZ-NH1	7.82	124.21	120.30
2	a	31	ASP	CB-CG-OD2	5.22	123.00	118.30
2	i	31	ASP	CB-CG-OD2	5.22	123.00	118.30
2	Z	31	ASP	CB-CG-OD2	5.21	122.99	118.30
2	c	31	ASP	CB-CG-OD2	5.21	122.99	118.30
2	j	31	ASP	CB-CG-OD2	5.20	122.98	118.30
2	d	31	ASP	CB-CG-OD2	5.20	122.98	118.30
2	Y	31	ASP	CB-CG-OD2	5.18	122.97	118.30
2	g	31	ASP	CB-CG-OD2	5.18	122.97	118.30
2	b	31	ASP	CB-CG-OD2	5.18	122.96	118.30
2	f	31	ASP	CB-CG-OD2	5.17	122.95	118.30
2	e	31	ASP	CB-CG-OD2	5.15	122.94	118.30
2	h	31	ASP	CB-CG-OD2	5.12	122.91	118.30

There are no chirality outliers.

All (24) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	231	THR	Peptide
1	B	231	THR	Peptide
1	C	231	THR	Peptide
1	D	231	THR	Peptide
1	E	231	THR	Peptide
1	F	231	THR	Peptide
1	G	231	THR	Peptide
1	H	231	THR	Peptide
1	I	231	THR	Peptide
1	J	231	THR	Peptide
1	K	231	THR	Peptide
1	L	231	THR	Peptide
1	M	231	THR	Peptide
1	N	231	THR	Peptide
1	O	231	THR	Peptide
1	P	231	THR	Peptide
1	Q	231	THR	Peptide
1	R	231	THR	Peptide
1	S	231	THR	Peptide

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Mol	Chain	Res	Type	Group
1	T	231	THR	Peptide
1	U	231	THR	Peptide
1	V	231	THR	Peptide
1	W	231	THR	Peptide
1	X	231	THR	Peptide

## 5.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4553	0	4351	430	0
1	B	4553	0	4351	437	2
1	C	4553	0	4351	432	4
1	D	4553	0	4351	423	0
1	E	4553	0	4351	430	0
1	F	4553	0	4351	428	0
1	G	4553	0	4351	430	0
1	H	4553	0	4351	424	0
1	I	4553	0	4351	433	0
1	J	4553	0	4351	430	0
1	K	4553	0	4351	431	0
1	L	4553	0	4351	441	0
1	M	4564	0	4368	365	0
1	N	4564	0	4368	375	5
1	O	4564	0	4368	363	0
1	P	4564	0	4368	371	0
1	Q	4564	0	4368	373	0
1	R	4564	0	4368	385	0
1	S	4564	0	4368	364	3
1	T	4564	0	4368	366	0
1	U	4564	0	4368	374	0
1	V	4564	0	4368	368	0
1	W	4564	0	4368	364	1
1	X	4564	0	4368	364	0
2	Y	1048	0	957	111	0
2	Z	1048	0	957	108	0
2	a	1048	0	957	0	0
2	b	1048	0	957	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	c	1048	0	957	0	4
2	d	1048	0	957	0	0
2	e	1048	0	957	0	0
2	f	1048	0	957	0	0
2	g	1048	0	957	0	1
2	h	1048	0	957	0	0
2	i	1048	0	957	0	0
2	j	1048	0	957	0	0
2	k	1052	0	975	0	0
2	l	1052	0	975	0	0
2	m	1052	0	975	0	0
2	n	1052	0	975	0	0
2	o	1052	0	975	0	0
2	p	1052	0	975	0	0
2	q	1052	0	975	0	0
2	r	1052	0	975	0	3
2	s	1052	0	975	0	0
2	t	1052	0	975	0	0
2	u	1052	0	975	0	0
2	v	1052	0	975	0	3
3	A	22	0	0	1	0
3	B	22	0	0	1	0
3	C	22	0	0	1	0
3	D	22	0	0	1	0
3	E	22	0	0	2	0
3	F	22	0	0	2	0
3	G	22	0	0	1	0
3	H	22	0	0	2	0
3	I	22	0	0	1	0
3	J	22	0	0	2	0
3	K	22	0	0	2	0
3	L	22	0	0	2	0
3	M	21	0	0	4	0
3	N	21	0	0	4	0
3	O	21	0	0	3	0
3	P	21	0	0	5	0
3	Q	21	0	0	5	0
3	R	21	0	0	4	0
3	S	21	0	0	4	0
3	T	21	0	0	5	0
3	U	21	0	0	3	0
3	V	21	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	W	21	0	0	4	0
3	X	21	0	0	4	0
All	All	135120	0	127812	9241	13

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 42.

All (9241) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:32:ALA:O	2:Z:33:THR:CG2	1.82	1.27
2:Y:32:ALA:O	2:Y:33:THR:CG2	1.82	1.26
2:Z:32:ALA:O	2:Z:33:THR:HG23	1.12	1.26
2:Y:32:ALA:O	2:Y:33:THR:HG23	1.12	1.24
2:Z:28:VAL:HG21	2:Z:96:LEU:CD1	1.68	1.23
2:Y:28:VAL:HG21	2:Y:96:LEU:CD1	1.68	1.21
2:Z:53:MET:CE	2:Z:92:VAL:HG12	1.72	1.20
2:Y:53:MET:CE	2:Y:92:VAL:HG12	1.72	1.18
1:D:78:VAL:HG21	1:D:444:LEU:HD11	1.28	1.16
1:J:78:VAL:HG21	1:J:444:LEU:HD11	1.28	1.16
1:L:78:VAL:HG21	1:L:444:LEU:HD11	1.29	1.15
2:Y:53:MET:CE	2:Y:92:VAL:CG1	2.24	1.15
1:E:78:VAL:HG21	1:E:444:LEU:HD11	1.29	1.15
2:Z:53:MET:CE	2:Z:92:VAL:CG1	2.24	1.15
1:B:78:VAL:HG21	1:B:444:LEU:HD11	1.28	1.15
1:I:78:VAL:HG21	1:I:444:LEU:HD11	1.29	1.15
1:H:78:VAL:HG21	1:H:444:LEU:HD11	1.29	1.15
2:Z:28:VAL:CG1	2:Z:97:ALA:HA	1.77	1.14
2:Y:28:VAL:CG1	2:Y:97:ALA:HA	1.77	1.14
2:Z:42:MET:HG3	2:Z:42:MET:O	1.42	1.13
1:G:78:VAL:HG21	1:G:444:LEU:HD11	1.28	1.13
1:C:78:VAL:HG21	1:C:444:LEU:HD11	1.28	1.12
1:Q:560:LEU:HD13	1:R:82:PRO:HD2	1.31	1.12
2:Y:42:MET:HG3	2:Y:42:MET:O	1.42	1.11
1:K:78:VAL:HG21	1:K:444:LEU:HD11	1.28	1.11
1:K:560:LEU:HD13	1:L:82:PRO:HD2	1.29	1.11
1:A:139:SER:HB3	1:A:455:THR:HG23	1.34	1.10
1:F:139:SER:HB3	1:F:455:THR:HG23	1.34	1.10
1:A:78:VAL:HG21	1:A:444:LEU:HD11	1.29	1.09
1:H:139:SER:HB3	1:H:455:THR:HG23	1.34	1.09
2:Z:28:VAL:HG13	2:Z:97:ALA:CA	1.83	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:14:ARG:HA	1:L:14:ARG:HE	1.19	1.08
2:Y:53:MET:HE1	2:Y:92:VAL:CG1	1.79	1.08
2:Z:28:VAL:HG21	2:Z:96:LEU:HD13	1.36	1.08
2:Z:31:ASP:OD2	2:Z:93:PHE:HE2	1.36	1.08
1:F:78:VAL:HG21	1:F:444:LEU:HD11	1.29	1.08
1:G:139:SER:HB3	1:G:455:THR:HG23	1.34	1.08
1:K:139:SER:HB3	1:K:455:THR:HG23	1.34	1.08
1:E:14:ARG:HE	1:E:14:ARG:HA	1.19	1.07
2:Y:28:VAL:HG13	2:Y:97:ALA:CA	1.83	1.07
1:F:14:ARG:HA	1:F:14:ARG:HE	1.19	1.07
1:L:139:SER:HB3	1:L:455:THR:HG23	1.34	1.07
1:G:14:ARG:HA	1:G:14:ARG:HE	1.19	1.07
2:Y:28:VAL:HG21	2:Y:96:LEU:HD13	1.35	1.07
2:Z:53:MET:HE1	2:Z:92:VAL:CG1	1.81	1.07
1:J:139:SER:HB3	1:J:455:THR:HG23	1.34	1.06
1:N:78:VAL:HG21	1:N:444:LEU:HD11	1.37	1.06
1:V:78:VAL:HG21	1:V:444:LEU:HD11	1.35	1.06
1:X:78:VAL:HG21	1:X:444:LEU:HD11	1.38	1.06
1:I:41:TRP:CZ3	1:I:42:ASP:HB2	1.90	1.06
1:C:139:SER:HB3	1:C:455:THR:HG23	1.34	1.06
1:D:41:TRP:CZ3	1:D:42:ASP:HB2	1.91	1.06
1:U:78:VAL:HG21	1:U:444:LEU:HD11	1.37	1.06
1:J:560:LEU:HD13	1:K:82:PRO:HD2	1.34	1.06
1:K:41:TRP:CZ3	1:K:42:ASP:HB2	1.91	1.06
1:F:41:TRP:CZ3	1:F:42:ASP:HB2	1.91	1.05
1:J:41:TRP:CZ3	1:J:42:ASP:HB2	1.91	1.05
2:Y:28:VAL:CG1	2:Y:97:ALA:CA	2.34	1.05
1:H:41:TRP:CZ3	1:H:42:ASP:HB2	1.90	1.05
1:C:41:TRP:CZ3	1:C:42:ASP:HB2	1.90	1.05
1:K:14:ARG:HE	1:K:14:ARG:HA	1.18	1.05
1:L:41:TRP:CZ3	1:L:42:ASP:HB2	1.91	1.05
1:S:14:ARG:HA	1:S:14:ARG:HE	1.21	1.05
1:T:78:VAL:HG21	1:T:444:LEU:HD11	1.37	1.05
1:A:41:TRP:CZ3	1:A:42:ASP:HB2	1.90	1.05
1:G:41:TRP:CZ3	1:G:42:ASP:HB2	1.91	1.05
1:B:139:SER:HB3	1:B:455:THR:HG23	1.34	1.04
1:B:41:TRP:CZ3	1:B:42:ASP:HB2	1.91	1.04
1:C:14:ARG:HE	1:C:14:ARG:HA	1.19	1.04
1:E:139:SER:HB3	1:E:455:THR:HG23	1.34	1.04
1:M:14:ARG:HE	1:M:14:ARG:HA	1.21	1.04
2:Y:31:ASP:OD2	2:Y:93:PHE:HE2	1.36	1.04

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:28:VAL:CG1	2:Z:97:ALA:CA	2.34	1.04
1:O:78:VAL:HG21	1:O:444:LEU:HD11	1.38	1.04
1:X:14:ARG:HA	1:X:14:ARG:HE	1.22	1.04
1:E:41:TRP:CZ3	1:E:42:ASP:HB2	1.90	1.04
1:O:14:ARG:HE	1:O:14:ARG:HA	1.23	1.03
1:A:41:TRP:CE3	1:A:42:ASP:N	2.26	1.03
1:D:41:TRP:CE3	1:D:42:ASP:N	2.26	1.03
1:D:82:PRO:HD2	1:E:560:LEU:HD13	1.37	1.03
1:I:139:SER:HB3	1:I:455:THR:HG23	1.34	1.03
1:N:14:ARG:HA	1:N:14:ARG:HE	1.21	1.03
1:R:78:VAL:HG21	1:R:444:LEU:HD11	1.36	1.03
1:F:41:TRP:CE3	1:F:42:ASP:N	2.26	1.03
1:H:560:LEU:HD13	1:I:82:PRO:HD2	1.40	1.03
1:Q:78:VAL:HG21	1:Q:444:LEU:HD11	1.38	1.03
1:W:78:VAL:HG21	1:W:444:LEU:HD11	1.36	1.03
1:D:14:ARG:HE	1:D:14:ARG:HA	1.19	1.03
1:E:41:TRP:CE3	1:E:42:ASP:N	2.26	1.03
1:M:78:VAL:HG21	1:M:444:LEU:HD11	1.37	1.03
1:P:78:VAL:HG21	1:P:444:LEU:HD11	1.39	1.02
1:W:14:ARG:HA	1:W:14:ARG:HE	1.23	1.02
1:A:14:ARG:HA	1:A:14:ARG:HE	1.19	1.02
1:H:41:TRP:CE3	1:H:42:ASP:N	2.26	1.02
1:L:41:TRP:CE3	1:L:42:ASP:N	2.26	1.02
1:G:41:TRP:CE3	1:G:42:ASP:N	2.26	1.02
1:A:82:PRO:HD2	1:L:560:LEU:HD13	1.38	1.02
1:B:14:ARG:HA	1:B:14:ARG:HE	1.19	1.02
1:K:41:TRP:CE3	1:K:42:ASP:N	2.26	1.02
1:I:41:TRP:CE3	1:I:42:ASP:N	2.26	1.02
1:B:41:TRP:CE3	1:B:42:ASP:N	2.26	1.02
1:N:82:PRO:HD2	1:V:560:LEU:HD13	1.38	1.02
1:D:139:SER:HB3	1:D:455:THR:HG23	1.34	1.01
1:F:560:LEU:HD13	1:G:82:PRO:HD2	1.42	1.01
1:J:41:TRP:CE3	1:J:42:ASP:N	2.26	1.01
1:H:14:ARG:HA	1:H:14:ARG:HE	1.19	1.01
1:C:41:TRP:CE3	1:C:42:ASP:N	2.26	1.01
1:V:82:PRO:HD2	1:W:560:LEU:HD13	1.42	1.01
1:U:14:ARG:HA	1:U:14:ARG:HE	1.21	1.01
1:V:14:ARG:HA	1:V:14:ARG:HE	1.21	1.01
1:I:14:ARG:HA	1:I:14:ARG:HE	1.19	1.01
1:R:14:ARG:HA	1:R:14:ARG:HE	1.21	1.01
1:Q:14:ARG:HE	1:Q:14:ARG:HA	1.23	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:14:ARG:HA	1:J:14:ARG:HE	1.19	1.01
1:T:546:THR:HG23	1:T:547:PRO:HD3	1.43	1.01
2:Z:53:MET:HE1	2:Z:92:VAL:HG12	1.01	1.01
1:S:78:VAL:HG21	1:S:444:LEU:HD11	1.38	1.00
1:D:158:TRP:HE3	1:D:173:CYS:HG	1.01	1.00
1:C:58:ASP:O	1:C:59:VAL:HG12	1.62	1.00
1:P:14:ARG:HE	1:P:14:ARG:HA	1.23	1.00
1:T:14:ARG:HE	1:T:14:ARG:HA	1.22	1.00
1:B:58:ASP:O	1:B:59:VAL:HG12	1.62	1.00
1:D:560:LEU:HD13	1:F:82:PRO:HD2	1.44	1.00
1:J:58:ASP:O	1:J:59:VAL:HG12	1.62	1.00
1:Q:546:THR:HG23	1:Q:547:PRO:HD3	1.43	1.00
2:Z:24:ARG:O	2:Z:28:VAL:HG23	1.60	1.00
1:A:58:ASP:O	1:A:59:VAL:HG12	1.62	0.99
1:W:546:THR:HG23	1:W:547:PRO:HD3	1.44	0.99
1:G:158:TRP:HE3	1:G:173:CYS:HG	1.03	0.99
1:K:58:ASP:O	1:K:59:VAL:HG12	1.62	0.99
1:G:58:ASP:O	1:G:59:VAL:HG12	1.62	0.99
1:H:58:ASP:O	1:H:59:VAL:HG12	1.62	0.99
1:F:58:ASP:O	1:F:59:VAL:HG12	1.62	0.99
1:K:158:TRP:HE3	1:K:173:CYS:HG	1.03	0.99
2:Y:24:ARG:O	2:Y:28:VAL:HG23	1.61	0.99
1:L:158:TRP:HE3	1:L:173:CYS:HG	1.05	0.99
1:O:546:THR:HG23	1:O:547:PRO:HD3	1.44	0.99
1:V:546:THR:HG23	1:V:547:PRO:HD3	1.44	0.99
1:E:58:ASP:O	1:E:59:VAL:HG12	1.62	0.99
1:T:560:LEU:HD13	1:W:82:PRO:HD2	1.41	0.99
1:X:248:LYS:HB3	1:X:511:ARG:HH11	1.25	0.98
1:U:82:PRO:HD2	1:X:560:LEU:HD13	1.45	0.98
1:P:560:LEU:HD13	1:Q:82:PRO:HD2	1.43	0.98
1:R:248:LYS:HB3	1:R:511:ARG:HH11	1.27	0.98
1:S:248:LYS:HB3	1:S:511:ARG:HH11	1.29	0.98
1:C:158:TRP:HE3	1:C:173:CYS:HG	1.00	0.98
1:I:58:ASP:O	1:I:59:VAL:HG12	1.62	0.98
1:L:58:ASP:O	1:L:59:VAL:HG12	1.62	0.98
1:W:248:LYS:HB3	1:W:511:ARG:HH11	1.28	0.98
1:M:248:LYS:HB3	1:M:511:ARG:HH11	1.28	0.98
1:O:158:TRP:HB3	1:O:173:CYS:HA	1.46	0.98
1:V:15:PHE:HZ	1:V:283:CYS:HG	1.12	0.98
1:D:58:ASP:O	1:D:59:VAL:HG12	1.62	0.97
1:P:158:TRP:HE3	1:P:173:CYS:HG	0.98	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:46:VAL:HG11	2:Y:77:ALA:HB1	1.45	0.97
1:U:248:LYS:HB3	1:U:511:ARG:HH11	1.28	0.97
1:R:546:THR:HG23	1:R:547:PRO:HD3	1.44	0.97
1:A:158:TRP:HE3	1:A:173:CYS:HG	1.00	0.97
1:M:330:ARG:HH21	1:M:409:THR:HG21	1.29	0.97
1:T:248:LYS:HB3	1:T:511:ARG:HH11	1.27	0.97
2:Z:46:VAL:HG11	2:Z:77:ALA:HB1	1.45	0.97
1:V:158:TRP:HB3	1:V:173:CYS:HA	1.44	0.97
2:Y:53:MET:HE2	2:Y:92:VAL:HG11	1.47	0.97
1:F:34:PHE:HZ	1:F:328:ARG:NH2	1.63	0.96
1:N:546:THR:HG23	1:N:547:PRO:HD3	1.45	0.96
1:A:41:TRP:CZ3	1:A:42:ASP:CB	2.49	0.96
1:H:41:TRP:CZ3	1:H:42:ASP:CB	2.48	0.96
1:E:41:TRP:CZ3	1:E:42:ASP:CB	2.48	0.96
1:H:34:PHE:HZ	1:H:328:ARG:NH2	1.63	0.96
1:M:546:THR:HG23	1:M:547:PRO:HD3	1.47	0.96
2:Y:53:MET:HE1	2:Y:92:VAL:HG12	0.99	0.96
1:J:34:PHE:HZ	1:J:328:ARG:NH2	1.63	0.96
1:S:546:THR:HG23	1:S:547:PRO:HD3	1.45	0.96
1:W:158:TRP:HB3	1:W:173:CYS:HA	1.45	0.96
2:Z:53:MET:HE2	2:Z:92:VAL:CG1	1.94	0.96
1:C:41:TRP:CZ3	1:C:42:ASP:CB	2.49	0.96
1:L:41:TRP:CZ3	1:L:42:ASP:CB	2.49	0.96
1:J:41:TRP:CZ3	1:J:42:ASP:CB	2.49	0.96
1:O:248:LYS:HB3	1:O:511:ARG:HH11	1.29	0.96
1:B:41:TRP:CZ3	1:B:42:ASP:CB	2.49	0.96
1:I:34:PHE:HZ	1:I:328:ARG:NH2	1.63	0.96
1:P:158:TRP:HB3	1:P:173:CYS:HA	1.45	0.96
1:S:158:TRP:HB3	1:S:173:CYS:HA	1.47	0.96
1:T:330:ARG:HH21	1:T:409:THR:HG21	1.31	0.96
2:Z:34:LEU:O	2:Z:35:THR:HG23	1.66	0.96
1:E:158:TRP:HE3	1:E:173:CYS:HG	1.00	0.96
1:B:34:PHE:HZ	1:B:328:ARG:NH2	1.63	0.95
1:K:41:TRP:CZ3	1:K:42:ASP:CB	2.49	0.95
1:E:34:PHE:HZ	1:E:328:ARG:NH2	1.63	0.95
1:F:41:TRP:CZ3	1:F:42:ASP:CB	2.49	0.95
1:V:248:LYS:HB3	1:V:511:ARG:HH11	1.29	0.95
1:X:330:ARG:HH21	1:X:409:THR:HG21	1.30	0.95
1:F:158:TRP:HE3	1:F:173:CYS:HG	1.00	0.95
1:G:34:PHE:HZ	1:G:328:ARG:NH2	1.63	0.95
1:O:330:ARG:HH21	1:O:409:THR:HG21	1.31	0.95

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:41:TRP:CZ3	1:I:42:ASP:CB	2.49	0.95
2:Z:53:MET:HE2	2:Z:92:VAL:HG11	1.46	0.95
1:X:546:THR:HG23	1:X:547:PRO:HD3	1.46	0.95
1:C:34:PHE:HZ	1:C:328:ARG:NH2	1.63	0.95
1:D:41:TRP:CZ3	1:D:42:ASP:CB	2.49	0.95
1:G:41:TRP:CZ3	1:G:42:ASP:CB	2.49	0.95
1:U:158:TRP:HB3	1:U:173:CYS:HA	1.49	0.95
1:X:158:TRP:HB3	1:X:173:CYS:HA	1.48	0.95
1:D:34:PHE:HZ	1:D:328:ARG:NH2	1.63	0.94
1:I:158:TRP:HE3	1:I:173:CYS:HG	1.00	0.94
1:K:561:ASP:HB2	1:L:89:ASP:HA	1.46	0.94
1:Q:158:TRP:HB3	1:Q:173:CYS:HA	1.49	0.94
1:Q:248:LYS:HB3	1:Q:511:ARG:HH11	1.29	0.94
1:R:560:LEU:HD13	1:X:82:PRO:HD2	1.49	0.94
1:K:560:LEU:HD22	1:L:82:PRO:HG2	1.49	0.94
1:L:34:PHE:HZ	1:L:328:ARG:NH2	1.63	0.94
2:Y:34:LEU:O	2:Y:35:THR:HG23	1.65	0.94
1:A:89:ASP:HA	1:L:561:ASP:HB2	1.49	0.94
1:P:248:LYS:HB3	1:P:511:ARG:HH11	1.27	0.94
1:S:330:ARG:HH21	1:S:409:THR:HG21	1.30	0.94
1:A:34:PHE:HZ	1:A:328:ARG:NH2	1.63	0.94
1:T:158:TRP:HB3	1:T:173:CYS:HA	1.44	0.94
2:Z:71:ASP:HB2	2:Z:75:PRO:HD2	1.50	0.94
1:G:560:LEU:HD13	1:H:82:PRO:HD2	1.50	0.94
1:E:546:THR:HG23	1:E:547:PRO:HD3	1.50	0.94
1:V:330:ARG:HH21	1:V:409:THR:HG21	1.28	0.94
1:D:546:THR:HG23	1:D:547:PRO:HD3	1.50	0.94
1:R:330:ARG:HH21	1:R:409:THR:HG21	1.32	0.94
1:S:158:TRP:HE3	1:S:173:CYS:HG	0.96	0.94
1:K:34:PHE:HZ	1:K:328:ARG:NH2	1.63	0.94
1:U:546:THR:HG23	1:U:547:PRO:HD3	1.46	0.94
1:G:139:SER:HB3	1:G:455:THR:CG2	1.98	0.93
1:M:158:TRP:HB3	1:M:173:CYS:HA	1.50	0.93
1:P:330:ARG:HH21	1:P:409:THR:HG21	1.32	0.93
1:P:546:THR:HG23	1:P:547:PRO:HD3	1.46	0.93
1:Q:561:ASP:HB2	1:R:89:ASP:HA	1.50	0.93
1:R:158:TRP:HB3	1:R:173:CYS:HA	1.48	0.93
1:I:139:SER:HB3	1:I:455:THR:CG2	1.98	0.93
1:C:546:THR:HG23	1:C:547:PRO:HD3	1.50	0.93
1:N:158:TRP:HB3	1:N:173:CYS:HA	1.48	0.93
1:C:139:SER:HB3	1:C:455:THR:CG2	1.98	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:546:THR:HG23	1:F:547:PRO:HD3	1.50	0.93
1:M:560:LEU:HD13	1:O:82:PRO:HD2	1.50	0.93
2:Z:28:VAL:HG21	2:Z:96:LEU:HB3	1.49	0.93
1:J:158:TRP:HE3	1:J:173:CYS:HG	1.01	0.93
1:L:139:SER:HB3	1:L:455:THR:CG2	1.98	0.93
1:F:14:ARG:NE	1:F:14:ARG:HA	1.83	0.93
1:F:139:SER:HB3	1:F:455:THR:CG2	1.98	0.93
1:N:248:LYS:HB3	1:N:511:ARG:HH11	1.30	0.93
1:H:158:TRP:HE3	1:H:173:CYS:HG	1.00	0.93
1:N:15:PHE:HZ	1:N:283:CYS:HG	1.07	0.93
1:U:330:ARG:HH21	1:U:409:THR:HG21	1.29	0.93
1:W:330:ARG:HH21	1:W:409:THR:HG21	1.32	0.93
2:Y:71:ASP:HB2	2:Y:75:PRO:HD2	1.50	0.93
2:Y:78:GLU:HA	2:Y:78:GLU:OE1	1.69	0.93
1:B:546:THR:HG23	1:B:547:PRO:HD3	1.50	0.93
1:E:139:SER:HB3	1:E:455:THR:CG2	1.98	0.92
1:N:158:TRP:HE3	1:N:173:CYS:HG	0.92	0.92
1:A:139:SER:HB3	1:A:455:THR:CG2	1.98	0.92
1:H:139:SER:HB3	1:H:455:THR:CG2	1.98	0.92
1:Q:330:ARG:HH21	1:Q:409:THR:HG21	1.31	0.92
1:B:139:SER:HB3	1:B:455:THR:CG2	1.98	0.92
1:G:546:THR:HG23	1:G:547:PRO:HD3	1.50	0.92
1:N:330:ARG:HH21	1:N:409:THR:HG21	1.33	0.92
2:Y:34:LEU:O	2:Y:35:THR:CG2	2.17	0.92
2:Z:78:GLU:HA	2:Z:78:GLU:OE1	1.69	0.92
1:B:158:TRP:HE3	1:B:173:CYS:HG	1.00	0.92
1:H:14:ARG:HA	1:H:14:ARG:NE	1.83	0.92
1:W:158:TRP:HE3	1:W:173:CYS:HG	0.94	0.92
1:J:139:SER:HB3	1:J:455:THR:CG2	1.98	0.92
1:D:139:SER:HB3	1:D:455:THR:CG2	1.98	0.92
1:A:14:ARG:HA	1:A:14:ARG:NE	1.83	0.92
1:N:89:ASP:HA	1:V:561:ASP:HB2	1.48	0.92
1:A:546:THR:HG23	1:A:547:PRO:HD3	1.50	0.92
2:Y:31:ASP:OD2	2:Y:93:PHE:CE2	2.22	0.92
1:G:14:ARG:NE	1:G:14:ARG:HA	1.83	0.91
1:T:158:TRP:HE3	1:T:173:CYS:HG	0.96	0.91
1:W:144:ILE:HG12	1:W:447:TYR:HE1	1.35	0.91
1:K:139:SER:HB3	1:K:455:THR:CG2	1.98	0.91
2:Y:28:VAL:HG21	2:Y:96:LEU:HB3	1.49	0.91
1:R:158:TRP:HE3	1:R:173:CYS:HG	0.95	0.91
1:U:158:TRP:HE3	1:U:173:CYS:HG	0.93	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:31:ASP:OD2	2:Z:93:PHE:CE2	2.22	0.91
2:Z:34:LEU:O	2:Z:35:THR:CG2	2.17	0.91
1:D:14:ARG:NE	1:D:14:ARG:HA	1.83	0.91
1:H:546:THR:HG23	1:H:547:PRO:HD3	1.50	0.91
1:X:158:TRP:HE3	1:X:173:CYS:HG	0.93	0.91
1:N:46:SER:H	1:N:48:TYR:HE2	1.19	0.91
1:O:46:SER:H	1:O:48:TYR:HE2	1.19	0.91
1:P:144:ILE:HG12	1:P:447:TYR:HE1	1.35	0.91
1:L:546:THR:HG23	1:L:547:PRO:HD3	1.50	0.91
1:X:46:SER:H	1:X:48:TYR:HE2	1.19	0.91
2:Z:53:MET:CE	2:Z:92:VAL:HG11	2.00	0.91
2:Z:32:ALA:C	2:Z:33:THR:HG23	1.91	0.91
1:O:158:TRP:HE3	1:O:173:CYS:HG	0.94	0.90
1:W:173:CYS:SG	1:W:298:ILE:HD12	2.12	0.90
2:Y:32:ALA:C	2:Y:33:THR:HG23	1.91	0.90
1:S:46:SER:H	1:S:48:TYR:HE2	1.19	0.90
1:X:15:PHE:HZ	1:X:283:CYS:HG	1.14	0.90
1:I:546:THR:HG23	1:I:547:PRO:HD3	1.50	0.90
1:V:144:ILE:HG12	1:V:447:TYR:HE1	1.34	0.90
1:K:546:THR:HG23	1:K:547:PRO:HD3	1.50	0.90
1:M:144:ILE:HG12	1:M:447:TYR:HE1	1.34	0.90
2:Y:53:MET:CE	2:Y:92:VAL:HG11	2.00	0.90
1:N:144:ILE:HG12	1:N:447:TYR:HE1	1.34	0.90
1:V:46:SER:H	1:V:48:TYR:HE2	1.16	0.90
1:J:546:THR:HG23	1:J:547:PRO:HD3	1.50	0.90
1:N:229:LYS:HA	1:N:272:LYS:HA	1.52	0.89
1:C:560:LEU:HD13	1:E:82:PRO:HD2	1.53	0.89
1:K:14:ARG:NE	1:K:14:ARG:HA	1.83	0.89
1:Q:144:ILE:HG12	1:Q:447:TYR:HE1	1.35	0.89
1:U:144:ILE:HG12	1:U:447:TYR:HE1	1.38	0.89
1:C:14:ARG:HA	1:C:14:ARG:NE	1.83	0.89
1:E:94:LEU:HA	1:E:97:MSE:HE2	1.55	0.89
1:I:14:ARG:HA	1:I:14:ARG:NE	1.83	0.89
1:J:560:LEU:HD22	1:K:82:PRO:HG2	1.52	0.89
1:B:94:LEU:HA	1:B:97:MSE:HE2	1.55	0.89
1:D:94:LEU:HA	1:D:97:MSE:HE2	1.55	0.89
1:K:94:LEU:HA	1:K:97:MSE:HE2	1.55	0.89
1:T:46:SER:H	1:T:48:TYR:HE2	1.18	0.89
1:C:94:LEU:HA	1:C:97:MSE:HE2	1.55	0.89
1:F:41:TRP:HE3	1:F:42:ASP:N	1.70	0.89
1:O:144:ILE:HG12	1:O:447:TYR:HE1	1.36	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:165:MSE:HG3	1:R:307:TRP:CE3	2.08	0.89
1:C:41:TRP:CE3	1:C:42:ASP:HB2	2.09	0.89
1:B:564:GLY:HA2	1:C:554:LEU:HD21	1.53	0.89
1:G:94:LEU:HA	1:G:97:MSE:HE2	1.55	0.89
1:R:144:ILE:HG12	1:R:447:TYR:HE1	1.36	0.89
1:T:165:MSE:HG3	1:T:307:TRP:CE3	2.07	0.89
1:I:560:LEU:HD13	1:J:82:PRO:HD2	1.53	0.88
1:W:273:ARG:HH22	1:W:453:LEU:HD11	1.38	0.88
1:A:94:LEU:HA	1:A:97:MSE:HE2	1.55	0.88
1:J:561:ASP:HB2	1:K:89:ASP:HA	1.52	0.88
1:M:46:SER:H	1:M:48:TYR:HE2	1.19	0.88
1:K:25:ALA:O	1:K:29:ALA:HB3	1.74	0.88
2:Y:53:MET:HE2	2:Y:92:VAL:CG1	1.96	0.88
1:B:41:TRP:CE3	1:B:42:ASP:HB2	2.09	0.88
1:I:94:LEU:HA	1:I:97:MSE:HE2	1.55	0.88
1:Q:229:LYS:HA	1:Q:272:LYS:HA	1.55	0.88
1:V:158:TRP:HE3	1:V:173:CYS:HG	0.93	0.88
1:Q:158:TRP:HE3	1:Q:173:CYS:HG	0.92	0.88
1:R:14:ARG:HA	1:R:14:ARG:NE	1.87	0.88
1:R:46:SER:H	1:R:48:TYR:HE2	1.20	0.88
1:S:144:ILE:HG12	1:S:447:TYR:HE1	1.36	0.88
1:C:25:ALA:O	1:C:29:ALA:HB3	1.74	0.88
1:E:41:TRP:CE3	1:E:42:ASP:HB2	2.09	0.88
1:I:41:TRP:HE3	1:I:42:ASP:N	1.70	0.88
2:Z:28:VAL:HG21	2:Z:96:LEU:HD12	1.54	0.88
1:D:41:TRP:CE3	1:D:42:ASP:HB2	2.09	0.88
1:H:94:LEU:HA	1:H:97:MSE:HE2	1.55	0.88
1:J:14:ARG:HA	1:J:14:ARG:NE	1.83	0.88
1:L:25:ALA:O	1:L:29:ALA:HB3	1.74	0.88
1:M:158:TRP:HE3	1:M:173:CYS:HG	0.93	0.88
1:P:229:LYS:HA	1:P:272:LYS:HA	1.55	0.88
1:B:14:ARG:HA	1:B:14:ARG:NE	1.83	0.88
1:Q:46:SER:H	1:Q:48:TYR:HE2	1.18	0.88
1:W:165:MSE:HG3	1:W:307:TRP:CE3	2.08	0.88
1:V:173:CYS:SG	1:V:298:ILE:HD12	2.13	0.88
1:L:41:TRP:HE3	1:L:42:ASP:N	1.70	0.88
2:Z:23:LEU:HA	2:Z:26:LEU:HG	1.55	0.88
1:G:41:TRP:CE3	1:G:42:ASP:HB2	2.09	0.87
1:I:37:ARG:HH21	1:I:37:ARG:HB3	1.39	0.87
1:J:25:ALA:O	1:J:29:ALA:HB3	1.74	0.87
1:S:165:MSE:HG3	1:S:307:TRP:CE3	2.09	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:37:ARG:HB3	1:A:37:ARG:HH21	1.40	0.87
1:D:41:TRP:HE3	1:D:42:ASP:N	1.70	0.87
1:E:25:ALA:O	1:E:29:ALA:HB3	1.74	0.87
1:F:25:ALA:O	1:F:29:ALA:HB3	1.74	0.87
1:L:41:TRP:CE3	1:L:42:ASP:HB2	2.09	0.87
1:F:94:LEU:HA	1:F:97:MSE:HE2	1.55	0.87
1:J:94:LEU:HA	1:J:97:MSE:HE2	1.55	0.87
1:L:94:LEU:HA	1:L:97:MSE:HE2	1.55	0.87
1:T:144:ILE:HG12	1:T:447:TYR:HE1	1.37	0.87
1:T:229:LYS:HA	1:T:272:LYS:HA	1.56	0.87
1:A:41:TRP:CE3	1:A:42:ASP:HB2	2.09	0.87
1:D:82:PRO:HG2	1:E:560:LEU:HD22	1.57	0.87
1:H:25:ALA:O	1:H:29:ALA:HB3	1.74	0.87
1:J:41:TRP:HE3	1:J:42:ASP:N	1.70	0.87
1:V:229:LYS:HA	1:V:272:LYS:HA	1.55	0.87
1:W:229:LYS:HA	1:W:272:LYS:HA	1.56	0.87
2:Y:28:VAL:HG21	2:Y:96:LEU:HD12	1.55	0.87
1:B:25:ALA:O	1:B:29:ALA:HB3	1.74	0.87
1:A:560:LEU:HD13	1:B:82:PRO:HD2	1.54	0.87
1:G:25:ALA:O	1:G:29:ALA:HB3	1.74	0.87
1:L:14:ARG:HA	1:L:14:ARG:NE	1.83	0.87
1:B:40:GLN:O	1:B:41:TRP:HB2	1.75	0.87
1:E:41:TRP:HE3	1:E:42:ASP:N	1.70	0.87
1:G:37:ARG:HH21	1:G:37:ARG:HB3	1.39	0.87
1:H:41:TRP:CE3	1:H:42:ASP:HB2	2.09	0.87
1:I:40:GLN:O	1:I:41:TRP:HB2	1.75	0.87
1:K:41:TRP:CE3	1:K:42:ASP:HB2	2.09	0.87
1:V:165:MSE:HG3	1:V:307:TRP:CE3	2.10	0.87
1:F:37:ARG:HH21	1:F:37:ARG:HB3	1.40	0.87
1:A:25:ALA:O	1:A:29:ALA:HB3	1.74	0.87
1:E:14:ARG:NE	1:E:14:ARG:HA	1.83	0.87
1:F:41:TRP:CE3	1:F:42:ASP:HB2	2.09	0.87
1:B:37:ARG:HB3	1:B:37:ARG:HH21	1.40	0.87
1:O:165:MSE:HG3	1:O:307:TRP:CE3	2.10	0.87
1:P:46:SER:H	1:P:48:TYR:HE2	1.18	0.87
1:Q:173:CYS:SG	1:Q:298:ILE:HD12	2.14	0.87
1:S:173:CYS:SG	1:S:298:ILE:HD12	2.15	0.87
1:F:40:GLN:O	1:F:41:TRP:HB2	1.75	0.86
1:M:165:MSE:HG3	1:M:307:TRP:CE3	2.10	0.86
1:N:14:ARG:NE	1:N:14:ARG:HA	1.87	0.86
1:N:173:CYS:SG	1:N:298:ILE:HD12	2.14	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:273:ARG:HH22	1:Q:453:LEU:HD11	1.39	0.86
1:V:14:ARG:HA	1:V:14:ARG:NE	1.87	0.86
1:D:25:ALA:O	1:D:29:ALA:HB3	1.74	0.86
1:D:89:ASP:HA	1:E:561:ASP:HB2	1.56	0.86
1:E:37:ARG:HH21	1:E:37:ARG:HB3	1.39	0.86
1:R:229:LYS:HA	1:R:272:LYS:HA	1.55	0.86
1:W:46:SER:H	1:W:48:TYR:HE2	1.18	0.86
1:I:25:ALA:O	1:I:29:ALA:HB3	1.74	0.86
1:S:15:PHE:HZ	1:S:283:CYS:HG	1.16	0.86
1:I:41:TRP:CE3	1:I:42:ASP:HB2	2.09	0.86
1:S:273:ARG:HH22	1:S:453:LEU:HD11	1.39	0.86
1:C:37:ARG:HH21	1:C:37:ARG:HB3	1.39	0.86
1:J:236:GLN:HB2	1:J:265:LYS:HZ3	1.40	0.86
1:O:273:ARG:HH22	1:O:453:LEU:HD11	1.40	0.86
1:U:165:MSE:HG3	1:U:307:TRP:CE3	2.10	0.86
1:U:46:SER:H	1:U:48:TYR:HE2	1.20	0.86
1:V:273:ARG:HH22	1:V:453:LEU:HD11	1.40	0.86
1:A:41:TRP:HE3	1:A:42:ASP:N	1.70	0.86
1:J:41:TRP:CE3	1:J:42:ASP:HB2	2.09	0.86
1:M:14:ARG:NE	1:M:14:ARG:HA	1.87	0.86
1:M:273:ARG:HH22	1:M:453:LEU:HD11	1.40	0.86
1:O:173:CYS:SG	1:O:298:ILE:HD12	2.15	0.86
1:U:14:ARG:HA	1:U:14:ARG:NE	1.87	0.86
1:X:273:ARG:HH22	1:X:453:LEU:HD11	1.40	0.86
2:Y:23:LEU:HA	2:Y:26:LEU:HG	1.55	0.86
1:G:41:TRP:HE3	1:G:42:ASP:N	1.70	0.86
1:H:41:TRP:HE3	1:H:42:ASP:N	1.70	0.86
1:X:248:LYS:CB	1:X:511:ARG:HH11	1.89	0.86
2:Y:28:VAL:CG2	2:Y:96:LEU:CD1	2.53	0.86
1:G:236:GLN:HB2	1:G:265:LYS:HZ3	1.40	0.86
1:G:40:GLN:O	1:G:41:TRP:HB2	1.75	0.86
1:K:236:GLN:HB2	1:K:265:LYS:HZ3	1.40	0.86
1:A:564:GLY:HA2	1:B:554:LEU:HD21	1.56	0.86
1:H:40:GLN:O	1:H:41:TRP:HB2	1.75	0.86
1:B:236:GLN:HB2	1:B:265:LYS:HZ3	1.40	0.85
1:L:40:GLN:O	1:L:41:TRP:HB2	1.75	0.85
1:U:229:LYS:HA	1:U:272:LYS:HA	1.56	0.85
1:M:229:LYS:HA	1:M:272:LYS:HA	1.56	0.85
1:O:229:LYS:HA	1:O:272:LYS:HA	1.56	0.85
1:R:173:CYS:SG	1:R:298:ILE:HD12	2.16	0.85
2:Z:28:VAL:CG2	2:Z:96:LEU:CD1	2.53	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:14:ARG:NE	1:S:14:ARG:HA	1.86	0.85
1:S:229:LYS:HA	1:S:272:LYS:HA	1.57	0.85
1:T:15:PHE:HZ	1:T:283:CYS:HG	1.23	0.85
1:V:89:ASP:HA	1:W:561:ASP:HB2	1.57	0.85
1:P:173:CYS:SG	1:P:298:ILE:HD12	2.15	0.85
2:Z:28:VAL:HG13	2:Z:97:ALA:CB	2.06	0.85
1:O:14:ARG:HA	1:O:14:ARG:NE	1.88	0.85
1:P:273:ARG:HH22	1:P:453:LEU:HD11	1.41	0.85
1:R:158:TRP:HE3	1:R:173:CYS:SG	2.00	0.85
1:T:273:ARG:HH22	1:T:453:LEU:HD11	1.40	0.85
1:X:165:MSE:HG3	1:X:307:TRP:CE3	2.11	0.85
1:E:40:GLN:O	1:E:41:TRP:HB2	1.75	0.85
1:G:158:TRP:HE3	1:G:173:CYS:SG	2.00	0.85
1:P:165:MSE:HG3	1:P:307:TRP:CE3	2.12	0.85
1:R:248:LYS:CB	1:R:511:ARG:HH11	1.89	0.85
1:U:273:ARG:HH22	1:U:453:LEU:HD11	1.37	0.85
1:S:82:PRO:HD2	1:U:560:LEU:HD13	1.58	0.85
1:C:158:TRP:HE3	1:C:173:CYS:SG	2.00	0.85
1:D:236:GLN:HB2	1:D:265:LYS:HZ3	1.42	0.85
1:H:158:TRP:HE3	1:H:173:CYS:SG	2.00	0.85
1:A:158:TRP:HE3	1:A:173:CYS:SG	2.00	0.85
1:K:40:GLN:O	1:K:41:TRP:HB2	1.75	0.85
1:K:41:TRP:HE3	1:K:42:ASP:N	1.70	0.85
1:U:173:CYS:SG	1:U:298:ILE:HD12	2.17	0.85
1:B:560:LEU:HD13	1:C:82:PRO:HD2	1.59	0.85
1:H:236:GLN:HB2	1:H:265:LYS:HZ3	1.40	0.85
1:N:165:MSE:HG3	1:N:307:TRP:CE3	2.11	0.85
1:X:229:LYS:HA	1:X:272:LYS:HA	1.56	0.85
2:Y:28:VAL:HG13	2:Y:97:ALA:CB	2.07	0.85
2:Z:34:LEU:HD12	2:Z:104:TYR:CD2	2.11	0.85
1:B:158:TRP:HE3	1:B:173:CYS:SG	2.00	0.85
1:D:37:ARG:HB3	1:D:37:ARG:HH21	1.40	0.85
1:R:273:ARG:HH22	1:R:453:LEU:HD11	1.40	0.85
1:S:560:LEU:HD13	1:T:82:PRO:HD2	1.59	0.85
1:I:564:GLY:HA2	1:J:554:LEU:HD21	1.59	0.84
1:J:158:TRP:HE3	1:J:173:CYS:SG	2.00	0.84
1:J:37:ARG:HH21	1:J:37:ARG:HB3	1.40	0.84
1:A:40:GLN:O	1:A:41:TRP:HB2	1.75	0.84
1:L:37:ARG:HB3	1:L:37:ARG:HH21	1.40	0.84
1:Q:158:TRP:HE3	1:Q:173:CYS:SG	1.99	0.84
1:Q:165:MSE:HG3	1:Q:307:TRP:CE3	2.11	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:248:LYS:CB	1:S:511:ARG:HH11	1.90	0.84
1:W:158:TRP:HE3	1:W:173:CYS:SG	1.99	0.84
1:H:37:ARG:HH21	1:H:37:ARG:HB3	1.40	0.84
2:Z:28:VAL:CG2	2:Z:96:LEU:HD13	2.07	0.84
1:B:41:TRP:HE3	1:B:42:ASP:N	1.70	0.84
1:K:158:TRP:HE3	1:K:173:CYS:SG	2.00	0.84
1:L:158:TRP:HE3	1:L:173:CYS:SG	2.00	0.84
1:X:173:CYS:SG	1:X:298:ILE:HD12	2.16	0.84
1:A:212:LEU:HD22	1:B:26:ARG:HG2	1.60	0.84
1:F:158:TRP:HE3	1:F:173:CYS:SG	2.00	0.84
1:S:158:TRP:HE3	1:S:173:CYS:SG	2.00	0.84
1:V:330:ARG:HD2	1:V:409:THR:HG22	1.58	0.84
2:Y:34:LEU:HD12	2:Y:104:TYR:CD2	2.11	0.84
1:A:236:GLN:HB2	1:A:265:LYS:HZ3	1.41	0.84
1:D:158:TRP:HE3	1:D:173:CYS:SG	2.00	0.84
1:X:144:ILE:HG12	1:X:447:TYR:HE1	1.39	0.84
1:A:41:TRP:CE3	1:A:42:ASP:CB	2.61	0.84
1:C:40:GLN:O	1:C:41:TRP:HB2	1.75	0.84
1:F:41:TRP:CE3	1:F:42:ASP:CB	2.61	0.84
1:N:273:ARG:HH22	1:N:453:LEU:HD11	1.41	0.84
1:E:41:TRP:CE3	1:E:42:ASP:CB	2.61	0.84
2:Y:28:VAL:HG13	2:Y:97:ALA:N	1.92	0.84
1:B:41:TRP:CE3	1:B:42:ASP:CB	2.61	0.84
1:I:158:TRP:HE3	1:I:173:CYS:SG	2.00	0.84
1:I:41:TRP:CE3	1:I:42:ASP:CB	2.61	0.84
1:J:40:GLN:O	1:J:41:TRP:HB2	1.75	0.84
1:L:41:TRP:CE3	1:L:42:ASP:CB	2.61	0.84
1:T:14:ARG:NE	1:T:14:ARG:HA	1.87	0.84
1:V:158:TRP:HE3	1:V:173:CYS:SG	2.00	0.84
1:T:330:ARG:HD2	1:T:409:THR:HG22	1.60	0.84
1:W:14:ARG:HA	1:W:14:ARG:NE	1.88	0.84
2:Z:28:VAL:HG13	2:Z:97:ALA:N	1.91	0.84
1:J:41:TRP:CE3	1:J:42:ASP:CB	2.61	0.83
1:K:37:ARG:HH21	1:K:37:ARG:HB3	1.40	0.83
1:K:41:TRP:CE3	1:K:42:ASP:CB	2.61	0.83
1:T:561:ASP:HB2	1:W:89:ASP:HA	1.59	0.83
1:D:40:GLN:O	1:D:41:TRP:HB2	1.75	0.83
1:E:158:TRP:HE3	1:E:173:CYS:SG	2.00	0.83
1:H:41:TRP:CE3	1:H:42:ASP:CB	2.61	0.83
1:I:236:GLN:HB2	1:I:265:LYS:HZ3	1.41	0.83
1:N:158:TRP:HE3	1:N:173:CYS:SG	2.00	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:173:CYS:SG	1:T:298:ILE:HD12	2.18	0.83
1:D:41:TRP:CE3	1:D:42:ASP:CB	2.61	0.83
1:M:82:PRO:HD2	1:N:560:LEU:HD13	1.60	0.83
1:U:15:PHE:HZ	1:U:283:CYS:HG	1.23	0.83
1:X:14:ARG:HA	1:X:14:ARG:NE	1.87	0.83
1:X:158:TRP:HE3	1:X:173:CYS:SG	2.00	0.83
1:X:330:ARG:HD2	1:X:409:THR:HG22	1.61	0.83
1:O:248:LYS:CB	1:O:511:ARG:HH11	1.92	0.83
1:Q:14:ARG:NE	1:Q:14:ARG:HA	1.88	0.83
1:G:41:TRP:CE3	1:G:42:ASP:CB	2.61	0.83
1:M:330:ARG:HD2	1:M:409:THR:HG22	1.61	0.83
1:O:330:ARG:HD2	1:O:409:THR:HG22	1.60	0.83
1:W:330:ARG:HD2	1:W:409:THR:HG22	1.61	0.83
1:P:158:TRP:HE3	1:P:173:CYS:SG	2.00	0.83
1:A:139:SER:CB	1:A:455:THR:HG23	2.09	0.83
2:Y:28:VAL:HG12	2:Y:97:ALA:HA	1.59	0.83
1:T:158:TRP:HE3	1:T:173:CYS:SG	2.01	0.83
1:B:139:SER:CB	1:B:455:THR:HG23	2.09	0.83
1:C:236:GLN:HB2	1:C:265:LYS:HZ3	1.42	0.83
1:H:139:SER:CB	1:H:455:THR:HG23	2.09	0.83
1:K:139:SER:CB	1:K:455:THR:HG23	2.09	0.83
1:O:158:TRP:HE3	1:O:173:CYS:SG	2.01	0.83
1:U:158:TRP:HE3	1:U:173:CYS:SG	2.00	0.83
1:M:158:TRP:HE3	1:M:173:CYS:SG	2.02	0.82
1:N:228:LYS:HA	1:N:228:LYS:HE2	1.61	0.82
1:C:41:TRP:HE3	1:C:42:ASP:N	1.70	0.82
1:J:139:SER:CB	1:J:455:THR:HG23	2.09	0.82
1:Q:560:LEU:HD22	1:R:82:PRO:HG2	1.60	0.82
1:E:236:GLN:HB2	1:E:265:LYS:HZ3	1.43	0.82
1:M:248:LYS:CB	1:M:511:ARG:HH11	1.92	0.82
1:P:14:ARG:HA	1:P:14:ARG:NE	1.88	0.82
1:R:330:ARG:HD2	1:R:409:THR:HG22	1.62	0.82
1:T:35:PHE:HE2	1:T:324:LYS:HZ3	1.26	0.82
1:U:248:LYS:CB	1:U:511:ARG:HH11	1.91	0.82
2:Y:28:VAL:CG2	2:Y:96:LEU:HD13	2.07	0.82
1:P:248:LYS:CB	1:P:511:ARG:HH11	1.91	0.82
1:B:325:ASP:OD2	2:Y:145:SER:HB3	1.79	0.82
1:C:139:SER:CB	1:C:455:THR:HG23	2.09	0.82
1:F:236:GLN:HB2	1:F:265:LYS:HZ3	1.45	0.82
1:T:248:LYS:CB	1:T:511:ARG:HH11	1.91	0.82
1:C:41:TRP:CE3	1:C:42:ASP:CB	2.61	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:139:SER:CB	1:F:455:THR:HG23	2.09	0.82
1:M:173:CYS:SG	1:M:298:ILE:HD12	2.18	0.82
1:S:554:LEU:HD21	1:U:564:GLY:HA2	1.61	0.82
1:L:139:SER:CB	1:L:455:THR:HG23	2.09	0.82
1:H:560:LEU:HD22	1:I:82:PRO:HG2	1.60	0.82
1:R:11:ILE:HD12	1:R:285:ALA:HA	1.62	0.81
1:G:139:SER:CB	1:G:455:THR:HG23	2.09	0.81
1:I:139:SER:CB	1:I:455:THR:HG23	2.09	0.81
1:L:236:GLN:HB2	1:L:265:LYS:HZ3	1.44	0.81
2:Z:28:VAL:HG12	2:Z:97:ALA:HA	1.59	0.81
1:I:212:LEU:HD22	1:J:26:ARG:HG2	1.62	0.81
1:N:248:LYS:CB	1:N:511:ARG:HH11	1.94	0.81
1:S:330:ARG:HD2	1:S:409:THR:HG22	1.60	0.81
1:E:139:SER:CB	1:E:455:THR:HG23	2.09	0.81
1:Q:248:LYS:CB	1:Q:511:ARG:HH11	1.93	0.81
1:N:208:VAL:HG12	1:N:210:PRO:HD3	1.63	0.81
1:R:208:VAL:HG12	1:R:210:PRO:HD3	1.63	0.81
1:D:139:SER:CB	1:D:455:THR:HG23	2.09	0.81
1:Q:228:LYS:HE2	1:Q:228:LYS:HA	1.62	0.81
2:Z:28:VAL:HG13	2:Z:97:ALA:HB2	1.63	0.81
1:D:560:LEU:HD22	1:F:82:PRO:HG2	1.62	0.81
1:F:560:LEU:HD22	1:G:82:PRO:HG2	1.60	0.81
1:Q:15:PHE:HZ	1:Q:283:CYS:HG	1.27	0.81
1:Q:208:VAL:HG12	1:Q:210:PRO:HD3	1.63	0.81
1:R:228:LYS:HA	1:R:228:LYS:HE2	1.63	0.81
1:O:560:LEU:HD13	1:P:82:PRO:HD2	1.61	0.81
1:V:63:VAL:HG21	1:V:416:ALA:HB1	1.63	0.81
1:W:208:VAL:HG12	1:W:210:PRO:HD3	1.62	0.81
1:P:376:ARG:O	1:P:383:ASP:HB3	1.81	0.81
1:U:228:LYS:HE2	1:U:228:LYS:HA	1.63	0.81
1:U:330:ARG:HD2	1:U:409:THR:HG22	1.63	0.81
1:V:208:VAL:HG12	1:V:210:PRO:HD3	1.63	0.81
1:X:208:VAL:HG12	1:X:210:PRO:HD3	1.63	0.81
1:X:228:LYS:HE2	1:X:228:LYS:HA	1.63	0.81
1:V:228:LYS:HA	1:V:228:LYS:HE2	1.62	0.81
1:C:564:GLY:HA2	1:E:554:LEU:HD21	1.62	0.80
1:K:35:PHE:HE2	1:K:324:LYS:HZ3	1.28	0.80
1:S:63:VAL:HG21	1:S:416:ALA:HB1	1.63	0.80
2:Y:28:VAL:CG1	2:Y:97:ALA:N	2.44	0.80
1:M:228:LYS:HE2	1:M:228:LYS:HA	1.62	0.80
1:W:228:LYS:HE2	1:W:228:LYS:HA	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:248:LYS:CB	1:W:511:ARG:HH11	1.92	0.80
1:S:564:GLY:HA2	1:T:554:LEU:HD21	1.64	0.80
1:Q:63:VAL:HG21	1:Q:416:ALA:HB1	1.61	0.80
1:C:58:ASP:O	1:C:59:VAL:CG1	2.30	0.80
1:Q:11:ILE:HD12	1:Q:285:ALA:HA	1.64	0.80
1:S:228:LYS:HE2	1:S:228:LYS:HA	1.64	0.80
1:Q:330:ARG:HD2	1:Q:409:THR:HG22	1.64	0.80
1:W:303:VAL:HA	1:W:439:ASN:OD1	1.82	0.80
1:C:15:PHE:HZ	1:C:283:CYS:HG	1.27	0.80
1:U:35:PHE:HE2	1:U:324:LYS:HZ3	1.28	0.80
1:E:282:THR:HG23	1:E:287:LEU:HD11	1.64	0.80
1:G:282:THR:HG23	1:G:287:LEU:HD11	1.64	0.80
1:F:561:ASP:HB2	1:G:89:ASP:HA	1.63	0.80
1:M:208:VAL:HG12	1:M:210:PRO:HD3	1.63	0.80
1:M:24:GLU:C	1:M:26:ARG:H	1.85	0.80
1:F:282:THR:HG23	1:F:287:LEU:HD11	1.64	0.80
1:I:58:ASP:O	1:I:59:VAL:CG1	2.30	0.80
1:T:208:VAL:HG12	1:T:210:PRO:HD3	1.63	0.80
1:T:228:LYS:HE2	1:T:228:LYS:HA	1.63	0.80
1:A:82:PRO:HG2	1:L:560:LEU:HD22	1.62	0.80
1:J:58:ASP:O	1:J:59:VAL:CG1	2.30	0.80
1:B:282:THR:HG23	1:B:287:LEU:HD11	1.64	0.79
1:H:561:ASP:HB2	1:I:89:ASP:HA	1.62	0.79
1:I:282:THR:HG23	1:I:287:LEU:HD11	1.64	0.79
1:P:208:VAL:HG12	1:P:210:PRO:HD3	1.63	0.79
1:S:208:VAL:HG12	1:S:210:PRO:HD3	1.63	0.79
1:V:303:VAL:HA	1:V:439:ASN:OD1	1.81	0.79
1:A:282:THR:HG23	1:A:287:LEU:HD11	1.64	0.79
1:N:303:VAL:HA	1:N:439:ASN:OD1	1.82	0.79
1:U:11:ILE:HD12	1:U:285:ALA:HA	1.64	0.79
1:C:282:THR:HG23	1:C:287:LEU:HD11	1.64	0.79
1:D:282:THR:HG23	1:D:287:LEU:HD11	1.64	0.79
1:D:58:ASP:O	1:D:59:VAL:CG1	2.30	0.79
1:F:58:ASP:O	1:F:59:VAL:CG1	2.30	0.79
1:N:11:ILE:HD12	1:N:285:ALA:HA	1.63	0.79
1:S:11:ILE:HD12	1:S:285:ALA:HA	1.64	0.79
1:E:58:ASP:O	1:E:59:VAL:CG1	2.30	0.79
1:G:58:ASP:O	1:G:59:VAL:CG1	2.30	0.79
1:H:282:THR:HG23	1:H:287:LEU:HD11	1.64	0.79
1:O:63:VAL:HG21	1:O:416:ALA:HB1	1.64	0.79
1:V:11:ILE:HD12	1:V:285:ALA:HA	1.63	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:248:LYS:HD2	1:E:248:LYS:H	1.48	0.79
1:J:248:LYS:HD2	1:J:248:LYS:H	1.48	0.79
1:O:208:VAL:HG12	1:O:210:PRO:HD3	1.63	0.79
1:O:228:LYS:HE2	1:O:228:LYS:HA	1.63	0.79
1:V:248:LYS:CB	1:V:511:ARG:HH11	1.94	0.79
2:Y:28:VAL:HG13	2:Y:97:ALA:HB2	1.63	0.79
1:A:58:ASP:O	1:A:59:VAL:CG1	2.30	0.79
1:D:248:LYS:H	1:D:248:LYS:HD2	1.48	0.79
1:L:248:LYS:HD2	1:L:248:LYS:H	1.48	0.79
1:N:248:LYS:HD2	1:N:248:LYS:H	1.47	0.79
1:N:330:ARG:HD2	1:N:409:THR:HG22	1.65	0.79
1:P:63:VAL:HG21	1:P:416:ALA:HB1	1.63	0.79
1:Q:35:PHE:HE2	1:Q:324:LYS:HZ3	1.27	0.79
1:W:63:VAL:HG21	1:W:416:ALA:HB1	1.64	0.79
1:X:11:ILE:HD12	1:X:285:ALA:HA	1.65	0.79
1:G:564:GLY:HA2	1:H:554:LEU:HD21	1.64	0.79
1:K:248:LYS:HD2	1:K:248:LYS:H	1.48	0.79
1:P:228:LYS:HA	1:P:228:LYS:HE2	1.64	0.79
1:O:334:MSE:SE	1:P:404:MSE:HE1	2.32	0.79
1:R:24:GLU:C	1:R:26:ARG:H	1.85	0.79
1:W:11:ILE:HD12	1:W:285:ALA:HA	1.63	0.79
1:W:376:ARG:O	1:W:383:ASP:HB3	1.83	0.79
1:H:58:ASP:O	1:H:59:VAL:CG1	2.30	0.79
1:L:282:THR:HG23	1:L:287:LEU:HD11	1.64	0.79
1:P:35:PHE:HE2	1:P:324:LYS:HZ3	1.31	0.79
1:P:303:VAL:HA	1:P:439:ASN:OD1	1.83	0.79
2:Z:143:THR:HB	2:Z:154:GLU:H	1.48	0.79
1:B:212:LEU:HD22	1:C:26:ARG:HG2	1.65	0.79
1:K:58:ASP:O	1:K:59:VAL:CG1	2.30	0.79
1:M:63:VAL:HG21	1:M:416:ALA:HB1	1.64	0.79
1:T:303:VAL:HA	1:T:439:ASN:OD1	1.83	0.79
1:V:35:PHE:HE2	1:V:324:LYS:HZ3	1.30	0.79
1:C:248:LYS:H	1:C:248:LYS:HD2	1.48	0.78
1:P:11:ILE:HD12	1:P:285:ALA:HA	1.64	0.78
1:U:208:VAL:HG12	1:U:210:PRO:HD3	1.62	0.78
1:X:24:GLU:C	1:X:26:ARG:H	1.85	0.78
1:M:554:LEU:HD21	1:N:564:GLY:HA2	1.63	0.78
1:Q:561:ASP:OD2	1:R:92:ASP:HB3	1.81	0.78
1:B:248:LYS:HD2	1:B:248:LYS:H	1.48	0.78
1:N:376:ARG:O	1:N:383:ASP:HB3	1.84	0.78
1:P:144:ILE:HG12	1:P:447:TYR:CE1	2.19	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:236:GLN:HB2	1:Q:265:LYS:HG2	1.65	0.78
1:Q:303:VAL:HA	1:Q:439:ASN:OD1	1.83	0.78
1:N:24:GLU:C	1:N:26:ARG:H	1.85	0.78
1:V:144:ILE:HG12	1:V:447:TYR:CE1	2.18	0.78
1:O:35:PHE:HE2	1:O:324:LYS:HZ3	1.27	0.78
2:Z:28:VAL:CG1	2:Z:97:ALA:N	2.44	0.78
1:A:248:LYS:H	1:A:248:LYS:HD2	1.48	0.78
1:D:334:MSE:HE1	1:F:407:ALA:HB1	1.63	0.78
1:J:282:THR:HG23	1:J:287:LEU:HD11	1.64	0.78
1:J:35:PHE:CZ	1:J:321:ARG:NE	2.52	0.78
1:N:63:VAL:HG21	1:N:416:ALA:HB1	1.65	0.78
1:O:24:GLU:C	1:O:26:ARG:H	1.86	0.78
1:T:11:ILE:HD12	1:T:285:ALA:HA	1.62	0.78
1:T:63:VAL:HG21	1:T:416:ALA:HB1	1.65	0.78
1:S:24:GLU:C	1:S:26:ARG:H	1.86	0.78
1:S:303:VAL:HA	1:S:439:ASN:OD1	1.84	0.78
1:W:236:GLN:HB2	1:W:265:LYS:HG2	1.66	0.78
1:W:24:GLU:C	1:W:26:ARG:H	1.85	0.78
2:Y:28:VAL:CG2	2:Y:96:LEU:HB3	2.14	0.78
1:I:248:LYS:H	1:I:248:LYS:HD2	1.48	0.78
1:L:58:ASP:O	1:L:59:VAL:CG1	2.30	0.78
1:O:236:GLN:HB2	1:O:265:LYS:HG2	1.66	0.78
1:A:35:PHE:CZ	1:A:321:ARG:NE	2.52	0.78
1:B:58:ASP:O	1:B:59:VAL:CG1	2.30	0.78
1:C:35:PHE:CZ	1:C:321:ARG:NE	2.52	0.78
1:D:561:ASP:HB2	1:F:89:ASP:HA	1.64	0.78
1:M:11:ILE:HD12	1:M:285:ALA:HA	1.64	0.78
1:A:334:MSE:HE1	1:B:407:ALA:HB1	1.64	0.78
1:B:35:PHE:CZ	1:B:321:ARG:NE	2.52	0.78
1:H:35:PHE:CZ	1:H:321:ARG:NE	2.52	0.78
1:K:35:PHE:CZ	1:K:321:ARG:NE	2.52	0.78
1:M:144:ILE:HG12	1:M:447:TYR:CE1	2.19	0.78
1:N:35:PHE:HE2	1:N:324:LYS:HZ3	1.30	0.78
1:R:236:GLN:HB2	1:R:265:LYS:HG2	1.66	0.78
1:R:303:VAL:HA	1:R:439:ASN:OD1	1.83	0.78
1:V:376:ARG:O	1:V:383:ASP:HB3	1.84	0.78
1:V:82:PRO:HG2	1:W:560:LEU:HD22	1.66	0.78
1:D:35:PHE:CZ	1:D:321:ARG:NE	2.52	0.77
1:K:282:THR:HG23	1:K:287:LEU:HD11	1.64	0.77
1:M:236:GLN:HB2	1:M:265:LYS:HG2	1.67	0.77
1:O:303:VAL:HA	1:O:439:ASN:OD1	1.83	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:11:ILE:HD12	1:F:285:ALA:HA	1.66	0.77
1:I:35:PHE:CZ	1:I:321:ARG:NE	2.52	0.77
1:O:564:GLY:HA2	1:P:554:LEU:HD21	1.65	0.77
1:X:35:PHE:HE2	1:X:324:LYS:HZ3	1.30	0.77
2:Z:28:VAL:CG2	2:Z:96:LEU:HB3	2.14	0.77
1:G:35:PHE:CZ	1:G:321:ARG:NE	2.52	0.77
1:M:303:VAL:HA	1:M:439:ASN:OD1	1.85	0.77
1:N:236:GLN:HB2	1:N:265:LYS:HG2	1.65	0.77
1:P:236:GLN:HB2	1:P:265:LYS:HG2	1.66	0.77
1:W:248:LYS:HD2	1:W:248:LYS:H	1.48	0.77
1:X:303:VAL:HA	1:X:439:ASN:OD1	1.83	0.77
2:Y:143:THR:HB	2:Y:154:GLU:H	1.48	0.77
1:E:35:PHE:CZ	1:E:321:ARG:NE	2.52	0.77
1:I:334:MSE:HE1	1:J:407:ALA:HB1	1.66	0.77
1:N:144:ILE:HG12	1:N:447:TYR:CE1	2.19	0.77
1:R:376:ARG:O	1:R:383:ASP:HB3	1.84	0.77
1:V:236:GLN:HB2	1:V:265:LYS:HG2	1.67	0.77
1:A:182:ASN:ND2	1:B:171:ARG:HH21	1.81	0.77
1:G:11:ILE:HD12	1:G:285:ALA:HA	1.66	0.77
1:H:11:ILE:HD12	1:H:285:ALA:HA	1.66	0.77
1:L:35:PHE:CZ	1:L:321:ARG:NE	2.52	0.77
1:O:376:ARG:O	1:O:383:ASP:HB3	1.84	0.77
1:Q:376:ARG:O	1:Q:383:ASP:HB3	1.84	0.77
1:T:24:GLU:C	1:T:26:ARG:H	1.86	0.77
1:X:37:ARG:NH2	1:X:37:ARG:HB3	2.00	0.77
2:Y:78:GLU:CG	2:Y:79:GLY:H	1.98	0.77
1:D:11:ILE:HD12	1:D:285:ALA:HA	1.66	0.77
1:L:11:ILE:HD12	1:L:285:ALA:HA	1.66	0.77
1:R:35:PHE:HE2	1:R:324:LYS:HZ3	1.30	0.77
1:R:144:ILE:HG12	1:R:447:TYR:CE1	2.20	0.77
1:H:15:PHE:HZ	1:H:283:CYS:HG	1.27	0.77
1:Q:144:ILE:HG12	1:Q:447:TYR:CE1	2.20	0.77
1:W:35:PHE:HE2	1:W:324:LYS:HZ3	1.31	0.77
1:B:11:ILE:HD12	1:B:285:ALA:HA	1.66	0.77
1:E:273:ARG:HH22	1:E:453:LEU:HD21	1.50	0.77
1:F:248:LYS:H	1:F:248:LYS:HD2	1.48	0.77
1:U:63:VAL:HG21	1:U:416:ALA:HB1	1.65	0.77
1:H:248:LYS:HD2	1:H:248:LYS:H	1.48	0.77
1:M:35:PHE:HE2	1:M:324:LYS:HZ3	1.30	0.77
1:O:248:LYS:HD2	1:O:248:LYS:H	1.50	0.77
1:Q:334:MSE:SE	1:R:404:MSE:HE1	2.35	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:35:PHE:CZ	1:F:321:ARG:NE	2.52	0.77
1:N:82:PRO:HG2	1:V:560:LEU:HD22	1.66	0.77
1:T:376:ARG:O	1:T:383:ASP:HB3	1.82	0.77
1:F:273:ARG:HH22	1:F:453:LEU:HD21	1.50	0.76
1:G:248:LYS:HD2	1:G:248:LYS:H	1.48	0.76
1:H:273:ARG:HH22	1:H:453:LEU:HD21	1.50	0.76
1:I:273:ARG:HH22	1:I:453:LEU:HD21	1.50	0.76
1:M:248:LYS:HD2	1:M:248:LYS:H	1.50	0.76
1:O:144:ILE:HG12	1:O:447:TYR:CE1	2.20	0.76
1:U:24:GLU:C	1:U:26:ARG:H	1.86	0.76
1:X:34:PHE:HZ	1:X:328:ARG:NH2	1.83	0.76
1:K:11:ILE:HD12	1:K:285:ALA:HA	1.66	0.76
1:K:273:ARG:HH22	1:K:453:LEU:HD21	1.50	0.76
1:U:236:GLN:HB2	1:U:265:LYS:HG2	1.66	0.76
1:A:35:PHE:HE2	1:A:324:LYS:HZ3	1.33	0.76
1:A:273:ARG:HH22	1:A:453:LEU:HD21	1.50	0.76
1:G:273:ARG:HH22	1:G:453:LEU:HD21	1.50	0.76
1:Q:24:GLU:C	1:Q:26:ARG:H	1.87	0.76
1:T:236:GLN:HB2	1:T:265:LYS:HG2	1.66	0.76
1:A:11:ILE:HD12	1:A:285:ALA:HA	1.66	0.76
1:C:11:ILE:HD12	1:C:285:ALA:HA	1.66	0.76
1:V:24:GLU:C	1:V:26:ARG:H	1.87	0.76
1:O:34:PHE:HZ	1:O:328:ARG:NH2	1.83	0.76
1:P:24:GLU:C	1:P:26:ARG:H	1.87	0.76
1:P:560:LEU:HD22	1:Q:82:PRO:HG2	1.66	0.76
1:V:248:LYS:H	1:V:248:LYS:HD2	1.50	0.76
1:X:376:ARG:O	1:X:383:ASP:HB3	1.84	0.76
1:O:35:PHE:CZ	1:O:321:ARG:NE	2.54	0.76
1:U:303:VAL:HA	1:U:439:ASN:OD1	1.84	0.76
1:P:44:TRP:O	1:P:45:LEU:HD13	1.86	0.76
1:Q:44:TRP:O	1:Q:45:LEU:HD13	1.86	0.76
2:Z:78:GLU:CG	2:Z:79:GLY:H	1.98	0.76
1:O:11:ILE:HD12	1:O:285:ALA:HA	1.67	0.76
1:S:236:GLN:HB2	1:S:265:LYS:HG2	1.66	0.76
1:U:248:LYS:H	1:U:248:LYS:HD2	1.49	0.76
1:X:63:VAL:HG21	1:X:416:ALA:HB1	1.65	0.76
1:D:273:ARG:HH22	1:D:453:LEU:HD21	1.50	0.76
1:G:49:THR:HG22	1:G:49:THR:O	1.86	0.76
1:I:11:ILE:HD12	1:I:285:ALA:HA	1.66	0.76
1:M:35:PHE:CZ	1:M:321:ARG:NE	2.54	0.76
1:U:376:ARG:O	1:U:383:ASP:HB3	1.84	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:139:SER:HB3	1:V:455:THR:HG23	1.67	0.76
1:Q:35:PHE:CZ	1:Q:321:ARG:NE	2.54	0.76
1:T:248:LYS:HD2	1:T:248:LYS:H	1.50	0.76
1:T:34:PHE:HZ	1:T:328:ARG:NH2	1.84	0.76
1:S:35:PHE:CZ	1:S:321:ARG:NE	2.54	0.75
1:S:376:ARG:O	1:S:383:ASP:HB3	1.84	0.75
1:S:144:ILE:HG12	1:S:447:TYR:CE1	2.20	0.75
1:V:92:ASP:HB3	1:W:561:ASP:OD2	1.86	0.75
1:F:15:PHE:HZ	1:F:283:CYS:HG	1.33	0.75
1:J:273:ARG:HH22	1:J:453:LEU:HD21	1.50	0.75
1:S:35:PHE:HE2	1:S:324:LYS:HZ3	1.32	0.75
1:U:282:THR:HG23	1:U:287:LEU:HD11	1.69	0.75
1:U:93:VAL:HG11	1:U:458:ARG:HG3	1.68	0.75
1:W:511:ARG:HA	1:W:513:ARG:HD2	1.68	0.75
1:P:282:THR:HG23	1:P:287:LEU:HD11	1.68	0.75
1:P:35:PHE:CZ	1:P:321:ARG:NE	2.55	0.75
1:Q:248:LYS:H	1:Q:248:LYS:HD2	1.49	0.75
1:R:63:VAL:HG21	1:R:416:ALA:HB1	1.66	0.75
1:X:93:VAL:HG11	1:X:458:ARG:HG3	1.69	0.75
2:Y:78:GLU:HG3	2:Y:79:GLY:H	1.52	0.75
1:E:11:ILE:HD12	1:E:285:ALA:HA	1.66	0.75
1:F:49:THR:O	1:F:49:THR:HG22	1.86	0.75
1:J:11:ILE:HD12	1:J:285:ALA:HA	1.66	0.75
1:P:232:ALA:HB2	1:P:269:ARG:H	1.51	0.75
1:X:282:THR:HG23	1:X:287:LEU:HD11	1.69	0.75
1:X:34:PHE:CZ	1:X:328:ARG:NH2	2.55	0.75
1:E:49:THR:HG22	1:E:49:THR:O	1.86	0.75
1:E:5:GLU:HG2	1:E:6:ASN:H	1.52	0.75
1:X:236:GLN:HB2	1:X:265:LYS:HG2	1.66	0.75
1:D:49:THR:O	1:D:49:THR:HG22	1.86	0.75
1:L:273:ARG:HH22	1:L:453:LEU:HD21	1.50	0.75
1:N:232:ALA:HB2	1:N:269:ARG:H	1.51	0.75
1:T:44:TRP:O	1:T:45:LEU:HD13	1.87	0.75
1:T:511:ARG:HA	1:T:513:ARG:HD2	1.68	0.75
1:W:144:ILE:HG12	1:W:447:TYR:CE1	2.20	0.75
1:C:273:ARG:HH22	1:C:453:LEU:HD21	1.50	0.75
1:D:5:GLU:HG2	1:D:6:ASN:H	1.52	0.75
1:M:232:ALA:HB2	1:M:269:ARG:H	1.51	0.75
1:P:561:ASP:HB2	1:Q:89:ASP:HA	1.67	0.75
2:Z:34:LEU:HD12	2:Z:104:TYR:HD2	1.51	0.75
1:F:236:GLN:HB2	1:F:265:LYS:HG2	1.68	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:44:TRP:O	1:M:45:LEU:HD13	1.86	0.75
1:S:248:LYS:HD2	1:S:248:LYS:H	1.49	0.75
1:S:44:TRP:O	1:S:45:LEU:HD13	1.86	0.75
1:A:5:GLU:HG2	1:A:6:ASN:H	1.52	0.75
1:G:273:ARG:HH22	1:G:453:LEU:CD2	2.00	0.75
1:K:236:GLN:HB2	1:K:265:LYS:HG2	1.68	0.75
1:P:34:PHE:HZ	1:P:328:ARG:NH2	1.84	0.75
1:F:273:ARG:HH22	1:F:453:LEU:CD2	2.00	0.74
1:K:15:PHE:HZ	1:K:283:CYS:HG	1.33	0.74
1:N:282:THR:HG23	1:N:287:LEU:HD11	1.67	0.74
1:N:93:VAL:HG11	1:N:458:ARG:HG3	1.68	0.74
1:P:330:ARG:HD2	1:P:409:THR:HG22	1.68	0.74
1:Q:511:ARG:HA	1:Q:513:ARG:HD2	1.69	0.74
1:X:330:ARG:HH21	1:X:409:THR:CG2	2.00	0.74
1:A:78:VAL:CG2	1:A:444:LEU:HD11	2.15	0.74
1:D:236:GLN:HB2	1:D:265:LYS:HG2	1.68	0.74
1:G:5:GLU:HG2	1:G:6:ASN:H	1.52	0.74
1:M:34:PHE:HZ	1:M:328:ARG:NH2	1.84	0.74
1:R:93:VAL:HG11	1:R:458:ARG:HG3	1.69	0.74
1:S:93:VAL:HG11	1:S:458:ARG:HG3	1.68	0.74
1:T:34:PHE:CZ	1:T:328:ARG:NH2	2.56	0.74
1:B:273:ARG:HH22	1:B:453:LEU:CD2	2.00	0.74
1:C:49:THR:O	1:C:49:THR:HG22	1.86	0.74
1:E:273:ARG:HH22	1:E:453:LEU:CD2	2.00	0.74
1:F:34:PHE:CZ	1:F:328:ARG:NH2	2.47	0.74
1:J:49:THR:HG22	1:J:49:THR:O	1.86	0.74
1:M:37:ARG:NH2	1:M:37:ARG:HB3	2.03	0.74
1:F:564:GLY:HA2	1:G:554:LEU:HD21	1.70	0.74
1:H:5:GLU:HG2	1:H:6:ASN:H	1.52	0.74
1:I:35:PHE:HE2	1:I:324:LYS:HZ3	1.34	0.74
1:O:34:PHE:CZ	1:O:328:ARG:NH2	2.56	0.74
1:R:248:LYS:H	1:R:248:LYS:HD2	1.51	0.74
1:X:248:LYS:HD2	1:X:248:LYS:H	1.51	0.74
1:A:273:ARG:HH22	1:A:453:LEU:CD2	2.00	0.74
1:A:560:LEU:HD22	1:B:82:PRO:HG2	1.69	0.74
1:C:212:LEU:HD22	1:E:26:ARG:HG2	1.70	0.74
1:E:577:ILE:HG12	1:E:582:LYS:HG2	1.69	0.74
1:K:273:ARG:HH22	1:K:453:LEU:CD2	2.00	0.74
1:K:49:THR:O	1:K:49:THR:HG22	1.86	0.74
1:L:577:ILE:HG12	1:L:582:LYS:HG2	1.69	0.74
1:R:282:THR:HG23	1:R:287:LEU:HD11	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:282:THR:HG23	1:W:287:LEU:HD11	1.69	0.74
1:A:236:GLN:HB2	1:A:265:LYS:HG2	1.68	0.74
1:H:273:ARG:HH22	1:H:453:LEU:CD2	2.00	0.74
1:K:577:ILE:HG12	1:K:582:LYS:HG2	1.69	0.74
1:M:282:THR:HG23	1:M:287:LEU:HD11	1.69	0.74
1:O:93:VAL:HG11	1:O:458:ARG:HG3	1.68	0.74
1:R:34:PHE:HZ	1:R:328:ARG:NH2	1.85	0.74
1:R:139:SER:HB3	1:R:455:THR:HG23	1.69	0.74
1:T:144:ILE:HG12	1:T:447:TYR:CE1	2.21	0.74
1:U:34:PHE:HZ	1:U:328:ARG:NH2	1.85	0.74
1:U:330:ARG:HH21	1:U:409:THR:CG2	2.01	0.74
1:U:144:ILE:HG12	1:U:447:TYR:CE1	2.21	0.74
1:V:44:TRP:O	1:V:45:LEU:HD13	1.88	0.74
2:Z:78:GLU:CA	2:Z:78:GLU:OE1	2.36	0.74
1:A:577:ILE:HG12	1:A:582:LYS:HG2	1.69	0.74
1:B:236:GLN:HB2	1:B:265:LYS:HG2	1.68	0.74
1:G:236:GLN:HB2	1:G:265:LYS:HG2	1.68	0.74
1:H:564:GLY:HA2	1:I:554:LEU:HD21	1.69	0.74
1:J:577:ILE:HG12	1:J:582:LYS:HG2	1.69	0.74
1:L:49:THR:HG22	1:L:49:THR:O	1.86	0.74
1:N:35:PHE:HE1	1:N:321:ARG:HH11	1.36	0.74
1:P:93:VAL:HG11	1:P:458:ARG:HG3	1.69	0.74
1:Q:93:VAL:HG11	1:Q:458:ARG:HG3	1.69	0.74
1:S:35:PHE:HE1	1:S:321:ARG:HH11	1.36	0.74
1:W:232:ALA:HB2	1:W:269:ARG:H	1.53	0.74
1:X:35:PHE:CZ	1:X:321:ARG:NE	2.55	0.74
1:B:273:ARG:HH22	1:B:453:LEU:HD21	1.50	0.74
1:B:577:ILE:HG12	1:B:582:LYS:HG2	1.69	0.74
1:H:236:GLN:HB2	1:H:265:LYS:HG2	1.68	0.74
1:L:236:GLN:HB2	1:L:265:LYS:HG2	1.69	0.74
1:L:273:ARG:HH22	1:L:453:LEU:CD2	2.00	0.74
1:L:78:VAL:CG2	1:L:444:LEU:HD11	2.15	0.74
1:L:5:GLU:HG2	1:L:6:ASN:H	1.52	0.74
1:M:35:PHE:HE1	1:M:321:ARG:HH11	1.35	0.74
1:N:34:PHE:HZ	1:N:328:ARG:NH2	1.86	0.74
1:O:44:TRP:O	1:O:45:LEU:HD13	1.88	0.74
1:Q:34:PHE:HZ	1:Q:328:ARG:NH2	1.86	0.74
1:R:34:PHE:CZ	1:R:328:ARG:NH2	2.56	0.74
1:C:236:GLN:HB2	1:C:265:LYS:HG2	1.68	0.74
1:E:236:GLN:HB2	1:E:265:LYS:HG2	1.68	0.74
1:G:560:LEU:HD22	1:H:82:PRO:HG2	1.69	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:273:ARG:HH22	1:I:453:LEU:CD2	2.00	0.74
1:P:248:LYS:HD2	1:P:248:LYS:H	1.51	0.74
1:T:34:PHE:HZ	1:T:328:ARG:HH22	1.35	0.74
1:U:35:PHE:CZ	1:U:321:ARG:NE	2.55	0.74
1:V:330:ARG:HH21	1:V:409:THR:CG2	2.00	0.74
1:W:44:TRP:O	1:W:45:LEU:HD13	1.87	0.74
1:A:554:LEU:HD21	1:L:564:GLY:HA2	1.70	0.74
1:M:93:VAL:HG11	1:M:458:ARG:HG3	1.68	0.74
1:O:35:PHE:HE1	1:O:321:ARG:HH11	1.36	0.74
1:P:34:PHE:CZ	1:P:328:ARG:NH2	2.56	0.74
1:S:37:ARG:HB3	1:S:37:ARG:NH2	2.03	0.74
1:H:49:THR:O	1:H:49:THR:HG22	1.86	0.73
1:J:35:PHE:HE2	1:J:324:LYS:HZ3	1.34	0.73
1:M:139:SER:HB3	1:M:455:THR:HG23	1.70	0.73
1:S:282:THR:HG23	1:S:287:LEU:HD11	1.70	0.73
1:T:35:PHE:CZ	1:T:321:ARG:NE	2.56	0.73
1:C:5:GLU:HG2	1:C:6:ASN:H	1.52	0.73
1:F:78:VAL:CG2	1:F:444:LEU:HD11	2.15	0.73
1:G:34:PHE:CZ	1:G:328:ARG:NH2	2.48	0.73
1:I:560:LEU:HD22	1:J:82:PRO:HG2	1.70	0.73
1:K:5:GLU:HG2	1:K:6:ASN:H	1.52	0.73
1:M:34:PHE:HZ	1:M:328:ARG:HH22	1.36	0.73
1:N:136:SER:HB3	1:Q:325:ASP:OD2	87.72	0.73
1:R:35:PHE:CZ	1:R:321:ARG:NE	2.56	0.73
1:U:136:SER:HB3	1:V:325:ASP:OD2	87.87	0.73
1:V:34:PHE:CZ	1:V:328:ARG:NH2	2.57	0.73
1:V:93:VAL:HG11	1:V:458:ARG:HG3	1.69	0.73
1:A:74:ASN:CB	1:A:75:PRO:HD3	4.11	0.73
1:C:577:ILE:HG12	1:C:582:LYS:HG2	1.69	0.73
1:J:273:ARG:HH22	1:J:453:LEU:CD2	2.00	0.73
1:W:93:VAL:HG11	1:W:458:ARG:HG3	1.68	0.73
1:B:49:THR:O	1:B:49:THR:HG22	1.86	0.73
1:M:15:PHE:HZ	1:M:283:CYS:HG	1.34	0.73
1:M:376:ARG:O	1:M:383:ASP:HB3	1.87	0.73
1:O:282:THR:HG23	1:O:287:LEU:HD11	1.69	0.73
1:S:34:PHE:HZ	1:S:328:ARG:NH2	1.85	0.73
1:N:92:ASP:HB3	1:V:561:ASP:OD2	1.88	0.73
1:T:560:LEU:HD22	1:W:82:PRO:HG2	1.68	0.73
1:X:144:ILE:HG12	1:X:447:TYR:CE1	2.22	0.73
1:A:49:THR:HG22	1:A:49:THR:O	1.86	0.73
1:F:577:ILE:HG12	1:F:582:LYS:HG2	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:35:PHE:HE2	1:G:324:LYS:HZ3	1.34	0.73
1:G:74:ASN:CB	1:G:75:PRO:HD3	4.11	0.73
1:I:74:ASN:CB	1:I:75:PRO:HD3	4.11	0.73
1:J:236:GLN:HB2	1:J:265:LYS:HG2	1.69	0.73
1:X:34:PHE:HZ	1:X:328:ARG:HH22	1.35	0.73
2:Y:34:LEU:HD12	2:Y:104:TYR:HD2	1.52	0.73
1:D:44:TRP:O	1:D:45:LEU:HD13	1.89	0.73
1:C:560:LEU:HD22	1:E:82:PRO:HG2	1.69	0.73
1:H:74:ASN:CB	1:H:75:PRO:HD3	4.11	0.73
1:I:577:ILE:HG12	1:I:582:LYS:HG2	1.69	0.73
1:J:74:ASN:CB	1:J:75:PRO:HD3	4.11	0.73
1:L:44:TRP:O	1:L:45:LEU:HD13	1.89	0.73
1:S:231:THR:HG21	1:S:249:ARG:HH11	1.53	0.73
1:U:232:ALA:HB2	1:U:269:ARG:H	1.54	0.73
1:U:89:ASP:HA	1:X:561:ASP:HB2	1.69	0.73
2:Y:34:LEU:C	2:Y:35:THR:HG23	2.09	0.73
1:C:74:ASN:CB	1:C:75:PRO:HD3	4.11	0.73
1:D:273:ARG:HH22	1:D:453:LEU:CD2	2.00	0.73
1:G:577:ILE:HG12	1:G:582:LYS:HG2	1.69	0.73
1:I:236:GLN:HB2	1:I:265:LYS:HG2	1.69	0.73
1:I:49:THR:O	1:I:49:THR:HG22	1.86	0.73
1:Q:282:THR:HG23	1:Q:287:LEU:HD11	1.71	0.73
2:Y:78:GLU:OE1	2:Y:78:GLU:CA	2.36	0.73
1:R:511:ARG:HA	1:R:513:ARG:HD2	1.70	0.73
1:R:561:ASP:HB2	1:X:89:ASP:HA	1.70	0.73
1:T:232:ALA:HB2	1:T:269:ARG:H	1.54	0.73
1:V:34:PHE:HZ	1:V:328:ARG:NH2	1.86	0.73
1:T:561:ASP:OD2	1:W:92:ASP:HB3	1.89	0.73
1:E:74:ASN:CB	1:E:75:PRO:HD3	4.11	0.73
1:J:334:MSE:HE1	1:K:407:ALA:HB1	1.69	0.73
1:J:5:GLU:HG2	1:J:6:ASN:H	1.52	0.73
1:O:139:SER:HB3	1:O:455:THR:HG23	1.71	0.73
2:Z:74:ASN:CB	2:Z:75:PRO:HD3	2.18	0.73
1:X:44:TRP:O	1:X:45:LEU:HD13	1.88	0.73
1:C:44:TRP:O	1:C:45:LEU:HD13	1.89	0.72
1:D:577:ILE:HG12	1:D:582:LYS:HG2	1.69	0.72
1:G:44:TRP:O	1:G:45:LEU:HD13	1.89	0.72
1:H:577:ILE:HG12	1:H:582:LYS:HG2	1.69	0.72
1:K:44:TRP:O	1:K:45:LEU:HD13	1.89	0.72
1:M:511:ARG:HA	1:M:513:ARG:HD2	1.70	0.72
1:Q:139:SER:HB3	1:Q:455:THR:HG23	1.69	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:232:ALA:HB2	1:R:269:ARG:H	1.54	0.72
1:S:232:ALA:HB2	1:S:269:ARG:H	1.53	0.72
2:Z:34:LEU:C	2:Z:35:THR:HG23	2.09	0.72
2:Z:78:GLU:HG3	2:Z:79:GLY:H	1.52	0.72
1:C:405:LEU:O	1:C:409:THR:HG23	1.90	0.72
1:E:158:TRP:HB3	1:E:173:CYS:HA	1.71	0.72
1:G:158:TRP:HB3	1:G:173:CYS:HA	1.72	0.72
1:I:44:TRP:O	1:I:45:LEU:HD13	1.89	0.72
1:Q:37:ARG:HB3	1:Q:37:ARG:NH2	2.04	0.72
1:U:511:ARG:HA	1:U:513:ARG:HD2	1.71	0.72
1:B:5:GLU:HG2	1:B:6:ASN:H	1.52	0.72
1:B:74:ASN:CB	1:B:75:PRO:HD3	4.11	0.72
1:D:158:TRP:HB3	1:D:173:CYS:HA	1.72	0.72
1:E:405:LEU:O	1:E:409:THR:HG23	1.90	0.72
1:F:405:LEU:O	1:F:409:THR:HG23	1.90	0.72
1:M:34:PHE:CZ	1:M:328:ARG:NH2	2.56	0.72
1:V:35:PHE:CZ	1:V:321:ARG:NE	2.58	0.72
1:B:34:PHE:CZ	1:B:328:ARG:NH2	2.47	0.72
1:D:74:ASN:CB	1:D:75:PRO:HD3	4.11	0.72
1:F:334:MSE:HE1	1:G:407:ALA:HB1	1.71	0.72
1:H:44:TRP:O	1:H:45:LEU:HD13	1.89	0.72
1:R:44:TRP:O	1:R:45:LEU:HD13	1.89	0.72
1:T:93:VAL:HG11	1:T:458:ARG:HG3	1.70	0.72
1:U:34:PHE:CZ	1:U:328:ARG:NH2	2.56	0.72
1:U:554:LEU:HD21	1:X:564:GLY:HA2	1.72	0.72
1:B:44:TRP:O	1:B:45:LEU:HD13	1.89	0.72
1:F:158:TRP:HB3	1:F:173:CYS:HA	1.71	0.72
1:F:5:GLU:HG2	1:F:6:ASN:H	1.52	0.72
1:J:44:TRP:O	1:J:45:LEU:HD13	1.89	0.72
1:K:158:TRP:HB3	1:K:173:CYS:HA	1.71	0.72
1:L:34:PHE:CZ	1:L:328:ARG:NH2	2.48	0.72
1:N:511:ARG:HA	1:N:513:ARG:HD2	1.70	0.72
1:R:37:ARG:NH2	1:R:37:ARG:HB3	2.04	0.72
1:U:44:TRP:O	1:U:45:LEU:HD13	1.89	0.72
1:V:232:ALA:HB2	1:V:269:ARG:H	1.54	0.72
1:V:511:ARG:HA	1:V:513:ARG:HD2	1.70	0.72
1:W:34:PHE:HZ	1:W:328:ARG:NH2	1.85	0.72
1:A:405:LEU:O	1:A:409:THR:HG23	1.90	0.72
1:B:158:TRP:HB3	1:B:173:CYS:HA	1.71	0.72
1:C:325:ASP:OD2	2:Z:145:SER:HB3	1.89	0.72
1:I:158:TRP:HB3	1:I:173:CYS:HA	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:325:ASP:OD2	1:K:136:SER:HB3	208.06	0.72
1:K:405:LEU:O	1:K:409:THR:HG23	1.90	0.72
1:U:37:ARG:NH2	1:U:37:ARG:HB3	2.04	0.72
2:Y:74:ASN:CB	2:Y:75:PRO:HD3	2.18	0.72
1:A:44:TRP:O	1:A:45:LEU:HD13	1.89	0.72
1:A:457:MSE:O	1:A:457:MSE:HG3	1.90	0.72
1:F:44:TRP:O	1:F:45:LEU:HD13	1.89	0.72
1:A:26:ARG:HG2	1:L:212:LEU:HD22	1.71	0.72
1:O:232:ALA:HB2	1:O:269:ARG:H	1.52	0.72
1:V:577:ILE:HG12	1:V:582:LYS:HG2	1.72	0.72
1:C:273:ARG:HH22	1:C:453:LEU:CD2	2.00	0.72
1:I:5:GLU:HG2	1:I:6:ASN:H	1.52	0.72
1:N:34:PHE:HZ	1:N:328:ARG:HH22	1.38	0.72
1:O:330:ARG:HH21	1:O:409:THR:CG2	2.02	0.72
1:V:282:THR:HG23	1:V:287:LEU:HD11	1.70	0.72
1:G:212:LEU:HD22	1:H:26:ARG:HG2	1.71	0.72
1:J:34:PHE:CZ	1:J:328:ARG:NH2	2.47	0.72
1:N:34:PHE:CZ	1:N:328:ARG:NH2	2.58	0.72
1:O:37:ARG:NH2	1:O:37:ARG:HB3	2.04	0.72
1:S:330:ARG:NH2	1:S:409:THR:HG21	2.05	0.72
1:X:232:ALA:HB2	1:X:269:ARG:H	1.53	0.72
1:D:405:LEU:O	1:D:409:THR:HG23	1.90	0.72
1:C:182:ASN:ND2	1:E:171:ARG:HH21	1.88	0.72
1:L:158:TRP:HB3	1:L:173:CYS:HA	1.71	0.72
1:N:44:TRP:O	1:N:45:LEU:HD13	1.89	0.72
1:N:139:SER:HB3	1:N:455:THR:HG23	1.70	0.72
1:Q:232:ALA:HB2	1:Q:269:ARG:H	1.54	0.72
1:W:34:PHE:HZ	1:W:328:ARG:HH22	1.38	0.72
1:W:450:GLN:O	1:W:450:GLN:HG2	1.90	0.72
1:R:564:GLY:HA2	1:X:554:LEU:HD21	1.70	0.72
1:A:303:VAL:HA	1:A:439:ASN:ND2	2.05	0.71
1:C:246:TYR:HD2	1:C:511:ARG:HB3	1.55	0.71
1:E:246:TYR:HD2	1:E:511:ARG:HB3	1.55	0.71
1:N:35:PHE:CZ	1:N:321:ARG:NE	2.57	0.71
1:X:35:PHE:HE1	1:X:321:ARG:HH11	1.37	0.71
1:C:334:MSE:HE1	1:E:407:ALA:HB1	1.70	0.71
1:I:78:VAL:CG2	1:I:444:LEU:HD11	2.15	0.71
1:P:78:VAL:HG12	1:P:79:LEU:N	2.05	0.71
1:V:246:TYR:HD2	1:V:511:ARG:HB2	1.54	0.71
1:W:35:PHE:HE1	1:W:321:ARG:HH11	1.37	0.71
1:E:44:TRP:O	1:E:45:LEU:HD13	1.89	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:303:VAL:HA	1:G:439:ASN:ND2	2.05	0.71
1:J:303:VAL:HA	1:J:439:ASN:ND2	2.05	0.71
1:J:405:LEU:O	1:J:409:THR:HG23	1.89	0.71
1:S:139:SER:HB3	1:S:455:THR:HG23	1.73	0.71
1:B:457:MSE:HG3	1:B:457:MSE:O	1.90	0.71
1:B:246:TYR:HD2	1:B:511:ARG:HB3	1.55	0.71
1:C:158:TRP:HB3	1:C:173:CYS:HA	1.71	0.71
1:F:212:LEU:HD22	1:G:26:ARG:HG2	1.72	0.71
1:H:405:LEU:O	1:H:409:THR:HG23	1.90	0.71
1:I:405:LEU:O	1:I:409:THR:HG23	1.90	0.71
1:K:457:MSE:HG3	1:K:457:MSE:O	1.90	0.71
1:P:35:PHE:HE1	1:P:321:ARG:HH11	1.38	0.71
1:P:330:ARG:HH21	1:P:409:THR:CG2	2.01	0.71
1:Q:34:PHE:CZ	1:Q:328:ARG:NH2	2.57	0.71
1:P:561:ASP:OD2	1:Q:92:ASP:HB3	1.90	0.71
1:S:136:SER:HB3	1:W:325:ASP:OD2	57.15	0.71
1:X:248:LYS:HB3	1:X:511:ARG:NH1	2.02	0.71
1:B:405:LEU:O	1:B:409:THR:HG23	1.90	0.71
1:L:303:VAL:HA	1:L:439:ASN:ND2	2.05	0.71
1:M:450:GLN:HG2	1:M:450:GLN:O	1.90	0.71
1:M:564:GLY:HA2	1:O:554:LEU:HD21	1.72	0.71
1:W:34:PHE:CZ	1:W:328:ARG:NH2	2.57	0.71
1:C:35:PHE:HE2	1:C:324:LYS:HZ3	1.39	0.71
1:K:303:VAL:HA	1:K:439:ASN:ND2	2.05	0.71
1:P:246:TYR:HD2	1:P:511:ARG:HB2	1.55	0.71
1:S:511:ARG:HA	1:S:513:ARG:HD2	1.73	0.71
1:T:577:ILE:HG12	1:T:582:LYS:HG2	1.73	0.71
1:U:82:PRO:HG2	1:X:560:LEU:HD22	1.71	0.71
1:V:37:ARG:HB3	1:V:37:ARG:NH2	2.05	0.71
1:B:78:VAL:CG2	1:B:444:LEU:HD11	2.15	0.71
1:C:303:VAL:HA	1:C:439:ASN:ND2	2.05	0.71
1:D:34:PHE:CZ	1:D:328:ARG:NH2	2.47	0.71
1:D:78:VAL:CG2	1:D:444:LEU:HD11	2.15	0.71
1:K:78:VAL:CG2	1:K:444:LEU:HD11	2.15	0.71
1:O:511:ARG:HA	1:O:513:ARG:HD2	1.71	0.71
1:Q:330:ARG:HH21	1:Q:409:THR:CG2	2.02	0.71
1:R:330:ARG:HH21	1:R:409:THR:CG2	2.02	0.71
1:W:35:PHE:CZ	1:W:321:ARG:NE	2.59	0.71
1:W:78:VAL:HG12	1:W:79:LEU:N	2.05	0.71
1:A:108:LYS:HD2	1:B:438:LEU:HD11	1.71	0.71
1:D:246:TYR:HD2	1:D:511:ARG:HB3	1.55	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:564:GLY:HA2	1:F:554:LEU:HD21	1.72	0.71
1:H:158:TRP:HB3	1:H:173:CYS:HA	1.71	0.71
1:H:303:VAL:HA	1:H:439:ASN:ND2	2.05	0.71
1:H:35:PHE:HE2	1:H:324:LYS:HZ3	1.38	0.71
1:J:158:TRP:HB3	1:J:173:CYS:HA	1.72	0.71
1:K:99:ARG:HH12	1:K:530:GLN:HE21	1.39	0.71
1:O:34:PHE:HZ	1:O:328:ARG:HH22	1.34	0.71
1:R:15:PHE:HZ	1:R:283:CYS:HG	1.39	0.71
2:Z:46:VAL:CG1	2:Z:77:ALA:HB1	2.19	0.71
1:G:405:LEU:O	1:G:409:THR:HG23	1.90	0.71
1:M:330:ARG:NH2	1:M:409:THR:HG21	2.06	0.71
1:S:330:ARG:HH21	1:S:409:THR:CG2	2.01	0.71
1:S:450:GLN:O	1:S:450:GLN:HG2	1.91	0.71
1:U:450:GLN:HG2	1:U:450:GLN:O	1.90	0.71
1:F:246:TYR:HD2	1:F:511:ARG:HB3	1.55	0.71
1:G:561:ASP:HB2	1:H:89:ASP:HA	1.70	0.71
1:H:78:VAL:CG2	1:H:444:LEU:HD11	2.15	0.71
1:J:246:TYR:HD2	1:J:511:ARG:HB3	1.56	0.71
1:K:246:TYR:HD2	1:K:511:ARG:HB3	1.55	0.71
1:M:330:ARG:HH21	1:M:409:THR:CG2	2.03	0.71
1:O:113:ILE:HD13	1:O:150:HIS:CE1	2.26	0.71
1:S:34:PHE:CZ	1:S:328:ARG:NH2	2.56	0.71
1:T:136:SER:HB3	1:T:325:ASP:OD2	52.59	0.71
1:X:246:TYR:HD2	1:X:511:ARG:HB2	1.56	0.71
1:X:37:ARG:HB3	1:X:37:ARG:HH21	1.56	0.71
1:A:246:TYR:HD2	1:A:511:ARG:HB3	1.55	0.70
1:C:99:ARG:HH12	1:C:530:GLN:HE21	1.39	0.70
1:F:303:VAL:HA	1:F:439:ASN:ND2	2.05	0.70
1:F:74:ASN:CB	1:F:75:PRO:HD3	4.11	0.70
1:G:246:TYR:HD2	1:G:511:ARG:HB3	1.55	0.70
1:I:34:PHE:CZ	1:I:328:ARG:NH2	2.48	0.70
1:J:78:VAL:CG2	1:J:444:LEU:HD11	2.15	0.70
1:J:457:MSE:O	1:J:457:MSE:HG3	1.90	0.70
1:E:41:TRP:CZ3	1:E:42:ASP:HB3	2.26	0.70
1:E:303:VAL:HA	1:E:439:ASN:ND2	2.05	0.70
1:I:303:VAL:HA	1:I:439:ASN:ND2	2.05	0.70
1:I:457:MSE:HG3	1:I:457:MSE:O	1.90	0.70
1:I:99:ARG:HH12	1:I:530:GLN:HE21	1.39	0.70
1:K:34:PHE:CZ	1:K:328:ARG:NH2	2.48	0.70
1:L:405:LEU:O	1:L:409:THR:HG23	1.90	0.70
1:M:238:PRO:HG3	1:M:263:PHE:HB3	1.73	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:113:ILE:HD13	1:N:150:HIS:CE1	2.26	0.70
1:P:334:MSE:SE	1:Q:404:MSE:HE1	2.41	0.70
1:T:575:GLN:O	1:T:579:MSE:HG2	1.92	0.70
1:O:246:TYR:HD2	1:O:511:ARG:HB2	1.55	0.70
1:Q:35:PHE:HE1	1:Q:321:ARG:HH11	1.39	0.70
1:R:577:ILE:HG12	1:R:582:LYS:HG2	1.73	0.70
1:S:577:ILE:HG12	1:S:582:LYS:HG2	1.71	0.70
1:T:238:PRO:HG3	1:T:263:PHE:HB3	1.73	0.70
1:T:37:ARG:HB3	1:T:37:ARG:NH2	2.07	0.70
1:U:35:PHE:HE1	1:U:321:ARG:HH11	1.37	0.70
1:V:330:ARG:NH2	1:V:409:THR:HG21	2.04	0.70
1:X:450:GLN:HG2	1:X:450:GLN:O	1.91	0.70
1:B:41:TRP:CZ3	1:B:42:ASP:HB3	2.26	0.70
1:C:78:VAL:CG2	1:C:444:LEU:HD11	2.15	0.70
1:E:457:MSE:HG3	1:E:457:MSE:O	1.90	0.70
1:F:34:PHE:HE1	1:F:324:LYS:HZ2	1.39	0.70
1:N:577:ILE:HG12	1:N:582:LYS:HG2	1.73	0.70
1:Q:246:TYR:HD2	1:Q:511:ARG:HB2	1.56	0.70
1:Q:450:GLN:O	1:Q:450:GLN:HG2	1.92	0.70
1:R:94:LEU:HA	1:R:97:MSE:HE2	1.74	0.70
1:U:330:ARG:NH2	1:U:409:THR:HG21	2.05	0.70
1:A:158:TRP:HB3	1:A:173:CYS:HA	1.72	0.70
1:D:457:MSE:HG3	1:D:457:MSE:O	1.90	0.70
1:E:99:ARG:HH12	1:E:530:GLN:HE21	1.39	0.70
1:F:457:MSE:O	1:F:457:MSE:HG3	1.90	0.70
1:N:246:TYR:HD2	1:N:511:ARG:HB2	1.56	0.70
1:A:26:ARG:HH21	1:A:30:LYS:HB2	1.57	0.70
1:F:41:TRP:CZ3	1:F:42:ASP:HB3	2.26	0.70
1:I:26:ARG:HH21	1:I:30:LYS:HB2	1.57	0.70
1:J:26:ARG:HH21	1:J:30:LYS:HB2	1.57	0.70
1:K:26:ARG:HH21	1:K:30:LYS:HB2	1.57	0.70
1:T:282:THR:HG23	1:T:287:LEU:HD11	1.73	0.70
1:U:577:ILE:HG12	1:U:582:LYS:HG2	1.73	0.70
1:W:37:ARG:HB3	1:W:37:ARG:NH2	2.07	0.70
1:B:99:ARG:HH12	1:B:530:GLN:HE21	1.39	0.70
1:C:41:TRP:CZ3	1:C:42:ASP:HB3	2.26	0.70
1:D:303:VAL:HA	1:D:439:ASN:ND2	2.05	0.70
1:G:26:ARG:HH21	1:G:30:LYS:HB2	1.57	0.70
1:G:334:MSE:HE1	1:H:407:ALA:HB1	1.72	0.70
1:H:26:ARG:HH21	1:H:30:LYS:HB2	1.57	0.70
1:L:99:ARG:HH12	1:L:530:GLN:HE21	1.39	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:577:ILE:HG12	1:X:582:LYS:HG2	1.73	0.70
1:B:303:VAL:HA	1:B:439:ASN:ND2	2.05	0.70
1:G:78:VAL:CG2	1:G:444:LEU:HD11	2.15	0.70
1:H:246:TYR:HD2	1:H:511:ARG:HB3	1.55	0.70
1:H:212:LEU:HD22	1:I:26:ARG:HG2	1.72	0.70
1:M:246:TYR:HD2	1:M:511:ARG:HB2	1.56	0.70
1:M:404:MSE:HE1	1:N:334:MSE:SE	2.41	0.70
1:P:511:ARG:HA	1:P:513:ARG:HD2	1.72	0.70
1:S:246:TYR:HD2	1:S:511:ARG:HB2	1.56	0.70
1:T:330:ARG:HH21	1:T:409:THR:CG2	2.03	0.70
1:U:248:LYS:HD3	1:U:251:ILE:HB	1.74	0.70
2:Y:46:VAL:CG1	2:Y:77:ALA:HB1	2.19	0.70
1:A:567:MSE:SE	1:B:576:LEU:HD13	2.42	0.70
1:F:26:ARG:HH21	1:F:30:LYS:HB2	1.57	0.70
1:G:457:MSE:O	1:G:457:MSE:HG3	1.90	0.70
1:I:35:PHE:C	1:I:37:ARG:H	1.95	0.70
1:L:246:TYR:HD2	1:L:511:ARG:HB3	1.55	0.70
1:L:457:MSE:O	1:L:457:MSE:HG3	1.90	0.70
1:O:15:PHE:HZ	1:O:283:CYS:HG	1.39	0.70
1:P:238:PRO:HG3	1:P:263:PHE:HB3	1.73	0.70
1:P:37:ARG:HB3	1:P:37:ARG:NH2	2.06	0.70
1:O:556:TYR:OH	1:P:542:THR:HG21	1.92	0.70
1:S:384:LEU:HD22	1:S:384:LEU:H	1.57	0.70
1:T:35:PHE:HE1	1:T:321:ARG:HH11	1.37	0.70
1:A:35:PHE:C	1:A:37:ARG:H	1.95	0.70
1:D:99:ARG:HH12	1:D:530:GLN:HE21	1.39	0.70
1:L:26:ARG:HH21	1:L:30:LYS:HB2	1.57	0.70
1:N:330:ARG:HH21	1:N:409:THR:CG2	2.03	0.70
1:P:384:LEU:H	1:P:384:LEU:HD22	1.57	0.70
1:W:330:ARG:HH21	1:W:409:THR:CG2	2.05	0.70
1:X:511:ARG:HA	1:X:513:ARG:HD2	1.73	0.70
1:B:182:ASN:ND2	1:C:171:ARG:HH21	1.90	0.69
1:G:35:PHE:C	1:G:37:ARG:H	1.95	0.69
1:Q:238:PRO:HG3	1:Q:263:PHE:HB3	1.73	0.69
1:U:139:SER:HB3	1:U:455:THR:HG23	1.73	0.69
1:X:139:SER:HB3	1:X:455:THR:HG23	1.73	0.69
1:F:99:ARG:HH12	1:F:530:GLN:HE21	1.39	0.69
1:I:376:ARG:O	1:I:383:ASP:HB3	1.92	0.69
1:J:99:ARG:HH12	1:J:530:GLN:HE21	1.39	0.69
1:O:248:LYS:HD3	1:O:251:ILE:HB	1.74	0.69
1:U:246:TYR:HD2	1:U:511:ARG:HB2	1.56	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:41:TRP:CZ3	1:G:42:ASP:HB3	2.26	0.69
1:H:457:MSE:HG3	1:H:457:MSE:O	1.90	0.69
1:I:182:ASN:ND2	1:J:171:ARG:HH21	1.90	0.69
1:K:35:PHE:C	1:K:37:ARG:H	1.95	0.69
1:L:41:TRP:CZ3	1:L:42:ASP:HB3	2.26	0.69
1:N:158:TRP:CD1	1:N:158:TRP:N	2.60	0.69
1:O:238:PRO:HG3	1:O:263:PHE:HB3	1.74	0.69
1:P:113:ILE:HD13	1:P:150:HIS:CE1	2.28	0.69
1:P:248:LYS:HB3	1:P:511:ARG:NH1	2.04	0.69
1:T:113:ILE:HD13	1:T:150:HIS:CE1	2.27	0.69
1:V:78:VAL:HG12	1:V:79:LEU:N	2.07	0.69
1:A:376:ARG:O	1:A:383:ASP:HB3	1.93	0.69
1:G:376:ARG:O	1:G:383:ASP:HB3	1.92	0.69
1:J:376:ARG:O	1:J:383:ASP:HB3	1.92	0.69
1:P:450:GLN:O	1:P:450:GLN:HG2	1.92	0.69
1:S:334:MSE:SE	1:T:404:MSE:HE1	2.42	0.69
2:Z:28:VAL:HG21	2:Z:96:LEU:CB	2.22	0.69
1:I:246:TYR:HD2	1:I:511:ARG:HB3	1.55	0.69
1:K:376:ARG:O	1:K:383:ASP:HB3	1.93	0.69
1:L:35:PHE:C	1:L:37:ARG:H	1.95	0.69
1:Q:577:ILE:HG12	1:Q:582:LYS:HG2	1.74	0.69
1:R:248:LYS:HB3	1:R:511:ARG:NH1	2.03	0.69
1:A:99:ARG:HH12	1:A:530:GLN:HE21	1.39	0.69
1:B:26:ARG:HH21	1:B:30:LYS:HB2	1.57	0.69
1:C:26:ARG:HH21	1:C:30:LYS:HB2	1.57	0.69
1:C:457:MSE:O	1:C:457:MSE:HG3	1.90	0.69
1:E:35:PHE:C	1:E:37:ARG:H	1.95	0.69
1:D:554:LEU:HD21	1:E:564:GLY:HA2	1.75	0.69
1:F:35:PHE:C	1:F:37:ARG:H	1.95	0.69
1:F:376:ARG:O	1:F:383:ASP:HB3	1.92	0.69
1:H:99:ARG:HH12	1:H:530:GLN:HE21	1.39	0.69
1:M:248:LYS:HB3	1:M:511:ARG:NH1	2.05	0.69
1:O:577:ILE:HG12	1:O:582:LYS:HG2	1.74	0.69
1:S:248:LYS:HB3	1:S:511:ARG:NH1	2.04	0.69
2:Y:34:LEU:CD1	2:Y:104:TYR:CD2	2.76	0.69
1:B:35:PHE:C	1:B:37:ARG:H	1.95	0.69
1:C:554:LEU:HD12	1:C:557:PHE:HD2	1.58	0.69
1:H:41:TRP:CZ3	1:H:42:ASP:HB3	2.26	0.69
1:L:158:TRP:CD1	1:L:158:TRP:N	2.60	0.69
1:V:35:PHE:HE1	1:V:321:ARG:HH11	1.38	0.69
1:D:26:ARG:HH21	1:D:30:LYS:HB2	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:554:LEU:HD12	1:J:557:PHE:HD2	1.58	0.69
1:K:212:LEU:HD22	1:L:26:ARG:HG2	1.75	0.69
1:U:238:PRO:HG3	1:U:263:PHE:HB3	1.74	0.69
1:W:246:TYR:HD2	1:W:511:ARG:HB2	1.57	0.69
1:W:577:ILE:HG12	1:W:582:LYS:HG2	1.74	0.69
1:B:376:ARG:O	1:B:383:ASP:HB3	1.92	0.69
1:C:561:ASP:HB2	1:E:89:ASP:HA	1.75	0.69
1:D:554:LEU:HD12	1:D:557:PHE:HD2	1.58	0.69
1:E:15:PHE:HZ	1:E:283:CYS:HG	1.40	0.69
1:L:209:PHE:N	1:L:210:PRO:HD3	2.08	0.69
1:N:450:GLN:HG2	1:N:450:GLN:O	1.92	0.69
1:P:577:ILE:HG12	1:P:582:LYS:HG2	1.73	0.69
1:S:534:GLU:O	1:S:538:LEU:HD23	1.92	0.69
1:V:384:LEU:HD22	1:V:384:LEU:H	1.57	0.69
2:Y:28:VAL:CG2	2:Y:96:LEU:HD12	2.22	0.69
2:Y:28:VAL:HG21	2:Y:96:LEU:CB	2.22	0.69
1:D:209:PHE:N	1:D:210:PRO:HD3	2.08	0.69
1:I:209:PHE:N	1:I:210:PRO:HD3	2.08	0.69
1:K:593:LEU:O	1:K:597:GLN:HG2	1.93	0.69
1:M:577:ILE:HG12	1:M:582:LYS:HG2	1.74	0.69
1:N:37:ARG:HB3	1:N:37:ARG:NH2	2.07	0.69
1:R:246:TYR:HD2	1:R:511:ARG:HB2	1.57	0.69
1:E:78:VAL:CG2	1:E:444:LEU:HD11	2.15	0.69
1:G:209:PHE:N	1:G:210:PRO:HD3	2.08	0.69
1:J:209:PHE:N	1:J:210:PRO:HD3	2.08	0.69
1:K:41:TRP:CZ3	1:K:42:ASP:HB3	2.26	0.69
1:R:238:PRO:HG3	1:R:263:PHE:HB3	1.73	0.69
1:S:238:PRO:HG3	1:S:263:PHE:HB3	1.75	0.69
1:S:78:VAL:HG12	1:S:79:LEU:N	2.08	0.69
1:T:384:LEU:H	1:T:384:LEU:HD22	1.58	0.69
1:D:376:ARG:O	1:D:383:ASP:HB3	1.92	0.68
1:G:593:LEU:O	1:G:597:GLN:HG2	1.93	0.68
1:H:158:TRP:CD1	1:H:158:TRP:N	2.60	0.68
1:H:209:PHE:N	1:H:210:PRO:HD3	2.08	0.68
1:J:41:TRP:CZ3	1:J:42:ASP:HB3	2.26	0.68
1:L:593:LEU:O	1:L:597:GLN:HG2	1.93	0.68
1:S:404:MSE:HE1	1:U:334:MSE:SE	2.43	0.68
1:T:139:SER:HB3	1:T:455:THR:HG23	1.75	0.68
1:T:78:VAL:HG12	1:T:79:LEU:N	2.08	0.68
1:W:238:PRO:HG3	1:W:263:PHE:HB3	1.74	0.68
1:A:593:LEU:O	1:A:597:GLN:HG2	1.93	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:158:TRP:N	1:B:158:TRP:CD1	2.60	0.68
1:B:593:LEU:O	1:B:597:GLN:HG2	1.93	0.68
1:F:554:LEU:HD12	1:F:557:PHE:HD2	1.58	0.68
1:K:209:PHE:N	1:K:210:PRO:HD3	2.08	0.68
1:T:450:GLN:HG2	1:T:450:GLN:O	1.93	0.68
1:B:37:ARG:HB3	1:B:37:ARG:NH2	2.09	0.68
1:C:376:ARG:O	1:C:383:ASP:HB3	1.92	0.68
1:D:41:TRP:CZ3	1:D:42:ASP:HB3	2.26	0.68
1:F:158:TRP:N	1:F:158:TRP:CD1	2.60	0.68
1:G:99:ARG:HH12	1:G:530:GLN:HE21	1.39	0.68
1:H:376:ARG:O	1:H:383:ASP:HB3	1.92	0.68
1:J:593:LEU:O	1:J:597:GLN:HG2	1.93	0.68
1:N:238:PRO:HG3	1:N:263:PHE:HB3	1.75	0.68
1:O:330:ARG:NH2	1:O:409:THR:HG21	2.07	0.68
1:M:561:ASP:HB2	1:O:89:ASP:HA	1.75	0.68
1:V:78:VAL:CG2	1:V:444:LEU:HD11	2.20	0.68
1:C:35:PHE:C	1:C:37:ARG:H	1.95	0.68
1:G:554:LEU:HD12	1:G:557:PHE:HD2	1.58	0.68
1:I:158:TRP:CD1	1:I:158:TRP:N	2.60	0.68
1:J:37:ARG:NH2	1:J:37:ARG:HB3	2.09	0.68
1:M:113:ILE:HD13	1:M:150:HIS:CE1	2.28	0.68
1:M:248:LYS:HD3	1:M:251:ILE:HB	1.74	0.68
1:N:248:LYS:HD3	1:N:251:ILE:HB	1.75	0.68
1:Q:78:VAL:HG12	1:Q:79:LEU:N	2.08	0.68
1:R:35:PHE:HE1	1:R:321:ARG:HH11	1.38	0.68
1:T:534:GLU:O	1:T:538:LEU:HD23	1.94	0.68
1:A:209:PHE:N	1:A:210:PRO:HD3	2.08	0.68
1:B:334:MSE:HE1	1:C:407:ALA:HB1	1.75	0.68
1:D:593:LEU:O	1:D:597:GLN:HG2	1.93	0.68
1:L:37:ARG:HB3	1:L:37:ARG:NH2	2.09	0.68
1:O:384:LEU:H	1:O:384:LEU:HD22	1.57	0.68
1:C:108:LYS:HD2	1:E:438:LEU:HD11	1.76	0.68
1:D:212:LEU:HD22	1:F:26:ARG:HG2	1.75	0.68
1:E:34:PHE:CZ	1:E:328:ARG:NH2	2.47	0.68
1:I:593:LEU:O	1:I:597:GLN:HG2	1.93	0.68
1:J:108:LYS:HD2	1:K:438:LEU:HD11	1.75	0.68
1:K:334:MSE:HE1	1:L:407:ALA:HB1	1.73	0.68
1:P:139:SER:HB3	1:P:455:THR:HG23	1.74	0.68
1:Q:575:GLN:O	1:Q:579:MSE:HG2	1.94	0.68
1:B:158:TRP:CH2	1:B:302:PRO:HG3	2.29	0.68
1:B:351:PHE:CD2	1:B:356:ILE:HD11	2.29	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:35:PHE:C	1:D:37:ARG:H	1.95	0.68
1:H:225:VAL:HG22	1:H:276:VAL:HG12	1.76	0.68
1:J:158:TRP:CH2	1:J:302:PRO:HG3	2.29	0.68
1:K:37:ARG:HB3	1:K:37:ARG:NH2	2.09	0.68
1:K:108:LYS:HD2	1:L:438:LEU:HD11	1.75	0.68
1:R:78:VAL:HG12	1:R:79:LEU:N	2.07	0.68
1:C:34:PHE:CZ	1:C:328:ARG:NH2	2.47	0.68
1:E:376:ARG:O	1:E:383:ASP:HB3	1.93	0.68
1:H:158:TRP:CH2	1:H:302:PRO:HG3	2.29	0.68
1:I:108:LYS:HD3	1:I:112:ASN:HD21	1.59	0.68
1:I:41:TRP:CZ3	1:I:42:ASP:HB3	2.26	0.68
1:L:158:TRP:CH2	1:L:302:PRO:HG3	2.29	0.68
1:O:564:GLY:HA3	1:P:535:ILE:HD11	1.76	0.68
1:W:139:SER:HB3	1:W:455:THR:HG23	1.73	0.68
1:W:248:LYS:HB3	1:W:511:ARG:NH1	2.05	0.68
1:F:225:VAL:HG22	1:F:276:VAL:HG12	1.76	0.68
1:I:225:VAL:HG22	1:I:276:VAL:HG12	1.76	0.68
1:K:158:TRP:N	1:K:158:TRP:CD1	2.60	0.68
1:V:450:GLN:HG2	1:V:450:GLN:O	1.92	0.68
2:Z:34:LEU:CD1	2:Z:104:TYR:CD2	2.76	0.68
1:D:158:TRP:CH2	1:D:302:PRO:HG3	2.29	0.68
1:E:158:TRP:N	1:E:158:TRP:CD1	2.60	0.68
1:E:26:ARG:HH21	1:E:30:LYS:HB2	1.57	0.68
1:H:108:LYS:HD3	1:H:112:ASN:HD21	1.59	0.68
1:J:351:PHE:CD2	1:J:356:ILE:HD11	2.29	0.68
1:I:108:LYS:HD2	1:J:438:LEU:HD11	1.76	0.68
1:K:225:VAL:HG22	1:K:276:VAL:HG12	1.76	0.68
1:M:78:VAL:HG12	1:M:79:LEU:N	2.09	0.68
1:P:158:TRP:HB3	1:P:173:CYS:CA	2.24	0.68
1:P:575:GLN:O	1:P:579:MSE:HG2	1.94	0.68
1:Q:384:LEU:HD22	1:Q:384:LEU:H	1.59	0.68
1:O:136:SER:HB3	1:R:325:ASP:OD2	71.98	0.68
1:V:238:PRO:HG3	1:V:263:PHE:HB3	1.75	0.68
1:A:585:GLU:C	1:A:587:PRO:HD3	2.15	0.67
1:E:209:PHE:N	1:E:210:PRO:HD3	2.08	0.67
1:F:158:TRP:CH2	1:F:302:PRO:HG3	2.29	0.67
1:F:209:PHE:N	1:F:210:PRO:HD3	2.08	0.67
1:F:351:PHE:CD2	1:F:356:ILE:HD11	2.29	0.67
1:I:237:ASP:H	1:I:243:PRO:HA	1.60	0.67
1:K:351:PHE:CD2	1:K:356:ILE:HD11	2.29	0.67
1:K:585:GLU:C	1:K:587:PRO:HD3	2.15	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:209:PHE:CZ	1:S:214:GLN:HG2	2.29	0.67
1:U:575:GLN:O	1:U:579:MSE:HG2	1.95	0.67
1:W:534:GLU:O	1:W:538:LEU:HD23	1.94	0.67
1:X:238:PRO:HG3	1:X:263:PHE:HB3	1.74	0.67
1:A:351:PHE:CD2	1:A:356:ILE:HD11	2.29	0.67
1:B:35:PHE:HE2	1:B:324:LYS:HZ3	1.41	0.67
1:B:442:ALA:HB1	3:B:702:HOH:O	1.95	0.67
1:B:554:LEU:HD12	1:B:557:PHE:HD2	1.58	0.67
1:C:593:LEU:O	1:C:597:GLN:HG2	1.93	0.67
1:D:37:ARG:HB3	1:D:37:ARG:NH2	2.09	0.67
1:F:585:GLU:C	1:F:587:PRO:HD3	2.15	0.67
1:G:191:TYR:HE1	1:G:278:LYS:HZ3	1.41	0.67
1:H:585:GLU:C	1:H:587:PRO:HD3	2.15	0.67
1:I:442:ALA:HB1	3:I:702:HOH:O	1.95	0.67
1:I:554:LEU:HD12	1:I:557:PHE:HD2	1.58	0.67
1:I:585:GLU:C	1:I:587:PRO:HD3	2.15	0.67
1:L:351:PHE:CD2	1:L:356:ILE:HD11	2.29	0.67
1:O:158:TRP:N	1:O:158:TRP:CD1	2.62	0.67
1:T:246:TYR:HD2	1:T:511:ARG:HB2	1.59	0.67
1:V:248:LYS:HD3	1:V:251:ILE:HB	1.75	0.67
1:A:108:LYS:HD3	1:A:112:ASN:HD21	1.59	0.67
1:A:442:ALA:HB1	3:A:702:HOH:O	1.95	0.67
1:C:158:TRP:CH2	1:C:302:PRO:HG3	2.29	0.67
1:E:585:GLU:C	1:E:587:PRO:HD3	2.15	0.67
1:G:585:GLU:C	1:G:587:PRO:HD3	2.15	0.67
1:I:158:TRP:CH2	1:I:302:PRO:HG3	2.29	0.67
1:K:237:ASP:H	1:K:243:PRO:HA	1.59	0.67
1:R:248:LYS:HD3	1:R:251:ILE:HB	1.76	0.67
1:X:158:TRP:CD1	1:X:158:TRP:N	2.62	0.67
1:X:384:LEU:HD22	1:X:384:LEU:H	1.59	0.67
1:X:330:ARG:NH2	1:X:409:THR:HG21	2.05	0.67
1:B:585:GLU:C	1:B:587:PRO:HD3	2.15	0.67
1:D:158:TRP:CD1	1:D:158:TRP:N	2.60	0.67
1:E:351:PHE:CD2	1:E:356:ILE:HD11	2.29	0.67
1:G:225:VAL:HG22	1:G:276:VAL:HG12	1.76	0.67
1:H:554:LEU:HD12	1:H:557:PHE:HD2	1.58	0.67
1:H:593:LEU:O	1:H:597:GLN:HG2	1.93	0.67
1:J:158:TRP:N	1:J:158:TRP:CD1	2.60	0.67
1:L:376:ARG:O	1:L:383:ASP:HB3	1.92	0.67
1:N:78:VAL:HG12	1:N:79:LEU:N	2.09	0.67
1:O:209:PHE:CZ	1:O:214:GLN:HG2	2.30	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:450:GLN:O	1:O:450:GLN:HG2	1.94	0.67
1:A:158:TRP:CH2	1:A:302:PRO:HG3	2.29	0.67
1:A:41:TRP:CZ3	1:A:42:ASP:HB3	2.26	0.67
1:C:237:ASP:H	1:C:243:PRO:HA	1.59	0.67
1:G:37:ARG:NH2	1:G:37:ARG:HB3	2.09	0.67
1:I:37:ARG:NH2	1:I:37:ARG:HB3	2.09	0.67
1:J:108:LYS:HD3	1:J:112:ASN:HD21	1.59	0.67
1:J:225:VAL:HG22	1:J:276:VAL:HG12	1.76	0.67
1:K:108:LYS:HD3	1:K:112:ASN:HD21	1.59	0.67
1:K:554:LEU:HD12	1:K:557:PHE:HD2	1.58	0.67
1:O:158:TRP:HB3	1:O:173:CYS:CA	2.24	0.67
1:U:273:ARG:HH22	1:U:453:LEU:CD1	2.08	0.67
1:D:407:ALA:HB1	1:E:334:MSE:HE1	1.77	0.67
1:F:593:LEU:O	1:F:597:GLN:HG2	1.93	0.67
1:G:351:PHE:CD2	1:G:356:ILE:HD11	2.29	0.67
1:H:35:PHE:C	1:H:37:ARG:H	1.95	0.67
1:K:158:TRP:CH2	1:K:302:PRO:HG3	2.29	0.67
1:M:158:TRP:N	1:M:158:TRP:CD1	2.60	0.67
1:O:78:VAL:HG12	1:O:79:LEU:N	2.09	0.67
1:P:209:PHE:CZ	1:P:214:GLN:HG2	2.30	0.67
1:Q:248:LYS:HD3	1:Q:251:ILE:HB	1.77	0.67
1:U:113:ILE:HD13	1:U:150:HIS:CE1	2.29	0.67
1:U:534:GLU:O	1:U:538:LEU:HD23	1.95	0.67
1:A:561:ASP:HB2	1:B:89:ASP:HA	1.77	0.67
1:C:158:TRP:CD1	1:C:158:TRP:N	2.60	0.67
1:E:593:LEU:O	1:E:597:GLN:HG2	1.93	0.67
1:G:108:LYS:HD3	1:G:112:ASN:HD21	1.59	0.67
1:J:237:ASP:H	1:J:243:PRO:HA	1.60	0.67
1:J:442:ALA:HB1	3:J:702:HOH:O	1.95	0.67
1:K:379:GLU:O	1:K:380:ASN:HB2	1.95	0.67
1:Q:248:LYS:HB3	1:Q:511:ARG:NH1	2.06	0.67
1:R:450:GLN:HG2	1:R:450:GLN:O	1.94	0.67
1:S:248:LYS:HD3	1:S:251:ILE:HB	1.75	0.67
1:U:37:ARG:HB3	1:U:37:ARG:HH21	1.60	0.67
1:U:78:VAL:HG12	1:U:79:LEU:N	2.09	0.67
1:W:158:TRP:N	1:W:158:TRP:CD1	2.62	0.67
1:W:248:LYS:HD3	1:W:251:ILE:HB	1.76	0.67
1:A:237:ASP:H	1:A:243:PRO:HA	1.59	0.67
1:C:209:PHE:N	1:C:210:PRO:HD3	2.08	0.67
1:C:442:ALA:HB1	3:C:702:HOH:O	1.95	0.67
1:D:237:ASP:H	1:D:243:PRO:HA	1.59	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:158:TRP:CH2	1:G:302:PRO:HG3	2.29	0.67
1:H:442:ALA:HB1	3:H:702:HOH:O	1.95	0.67
1:I:351:PHE:CD2	1:I:356:ILE:HD11	2.29	0.67
1:L:237:ASP:H	1:L:243:PRO:HA	1.59	0.67
1:M:37:ARG:HB3	1:M:37:ARG:HH21	1.60	0.67
1:N:209:PHE:CZ	1:N:214:GLN:HG2	2.29	0.67
1:N:232:ALA:CB	1:N:269:ARG:H	2.08	0.67
1:Q:209:PHE:CZ	1:Q:214:GLN:HG2	2.30	0.67
1:R:158:TRP:N	1:R:158:TRP:CD1	2.63	0.67
1:B:237:ASP:H	1:B:243:PRO:HA	1.59	0.67
1:D:108:LYS:HD3	1:D:112:ASN:HD21	1.59	0.67
1:D:585:GLU:C	1:D:587:PRO:HD3	2.15	0.67
1:E:554:LEU:HD12	1:E:557:PHE:HD2	1.58	0.67
1:J:561:ASP:OD2	1:K:92:ASP:HB3	1.95	0.67
1:K:561:ASP:OD2	1:L:92:ASP:HB3	1.93	0.67
1:L:379:GLU:O	1:L:380:ASN:HB2	1.95	0.67
1:T:248:LYS:HD3	1:T:251:ILE:HB	1.76	0.67
1:U:384:LEU:HD22	1:U:384:LEU:H	1.59	0.67
1:X:209:PHE:CZ	1:X:214:GLN:HG2	2.30	0.67
1:C:351:PHE:CD2	1:C:356:ILE:HD11	2.29	0.67
1:C:585:GLU:C	1:C:587:PRO:HD3	2.15	0.67
1:D:351:PHE:CD2	1:D:356:ILE:HD11	2.29	0.67
1:G:379:GLU:O	1:G:380:ASN:HB2	1.95	0.67
1:H:165:MSE:HG3	1:H:307:TRP:CE3	2.30	0.67
1:L:165:MSE:HG3	1:L:307:TRP:CE3	2.30	0.67
1:M:534:GLU:O	1:M:538:LEU:HD23	1.95	0.67
1:X:113:ILE:HD13	1:X:150:HIS:CE1	2.31	0.67
1:R:560:LEU:HD22	1:X:82:PRO:HG2	1.75	0.67
1:A:554:LEU:HD12	1:A:557:PHE:HD2	1.58	0.66
1:B:379:GLU:O	1:B:380:ASN:HB2	1.95	0.66
1:D:379:GLU:O	1:D:380:ASN:HB2	1.95	0.66
1:E:165:MSE:HG3	1:E:307:TRP:CE3	2.30	0.66
1:H:351:PHE:CD2	1:H:356:ILE:HD11	2.29	0.66
1:J:35:PHE:C	1:J:37:ARG:H	1.95	0.66
1:M:209:PHE:CZ	1:M:214:GLN:HG2	2.29	0.66
1:M:560:LEU:HD22	1:O:82:PRO:HG2	1.78	0.66
1:R:534:GLU:O	1:R:538:LEU:HD23	1.95	0.66
1:W:384:LEU:H	1:W:384:LEU:HD22	1.59	0.66
1:A:34:PHE:CZ	1:A:328:ARG:NH2	2.47	0.66
1:A:78:VAL:HG22	1:A:444:LEU:HD21	1.78	0.66
1:C:108:LYS:HD3	1:C:112:ASN:HD21	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:225:VAL:HG22	1:C:276:VAL:HG12	1.76	0.66
1:D:34:PHE:HE1	1:D:324:LYS:HZ2	1.39	0.66
1:D:78:VAL:HG22	1:D:444:LEU:HD21	1.78	0.66
1:E:379:GLU:O	1:E:380:ASN:HB2	1.95	0.66
1:E:78:VAL:HG22	1:E:444:LEU:HD21	1.78	0.66
1:H:37:ARG:NH2	1:H:37:ARG:HB3	2.09	0.66
1:J:379:GLU:O	1:J:380:ASN:HB2	1.95	0.66
1:N:330:ARG:NH2	1:N:409:THR:HG21	2.08	0.66
1:O:248:LYS:HB3	1:O:511:ARG:NH1	2.06	0.66
1:A:182:ASN:HD22	1:B:171:ARG:HH21	1.42	0.66
1:B:225:VAL:HG22	1:B:276:VAL:HG12	1.76	0.66
1:G:165:MSE:HG3	1:G:307:TRP:CE3	2.30	0.66
1:H:379:GLU:O	1:H:380:ASN:HB2	1.95	0.66
1:H:78:VAL:HG22	1:H:444:LEU:HD21	1.78	0.66
1:K:227:GLU:HA	1:K:274:ARG:HA	1.78	0.66
1:L:225:VAL:HG22	1:L:276:VAL:HG12	1.76	0.66
1:L:554:LEU:HD12	1:L:557:PHE:HD2	1.58	0.66
1:N:384:LEU:H	1:N:384:LEU:HD22	1.58	0.66
1:N:575:GLN:O	1:N:579:MSE:HG2	1.95	0.66
1:Q:94:LEU:HA	1:Q:97:MSE:HE2	1.77	0.66
1:R:231:THR:HG21	1:R:249:ARG:HH11	1.60	0.66
1:R:78:VAL:CG2	1:R:444:LEU:HD11	2.22	0.66
1:W:209:PHE:CZ	1:W:214:GLN:HG2	2.30	0.66
1:A:227:GLU:HA	1:A:274:ARG:HA	1.78	0.66
1:C:37:ARG:NH2	1:C:37:ARG:HB3	2.09	0.66
1:D:182:ASN:ND2	1:F:171:ARG:HH21	1.94	0.66
1:F:78:VAL:HG22	1:F:444:LEU:HD21	1.78	0.66
1:G:237:ASP:H	1:G:243:PRO:HA	1.60	0.66
1:I:165:MSE:HG3	1:I:307:TRP:CE3	2.30	0.66
1:J:165:MSE:HG3	1:J:307:TRP:CE3	2.30	0.66
1:M:94:LEU:HA	1:M:97:MSE:HE2	1.77	0.66
1:N:248:LYS:HB3	1:N:511:ARG:NH1	2.07	0.66
1:Q:113:ILE:HD13	1:Q:150:HIS:CE1	2.30	0.66
1:Q:158:TRP:N	1:Q:158:TRP:CD1	2.62	0.66
1:Q:534:GLU:O	1:Q:538:LEU:HD23	1.95	0.66
1:S:158:TRP:CD1	1:S:158:TRP:N	2.62	0.66
1:W:113:ILE:HD13	1:W:150:HIS:CE1	2.31	0.66
1:W:231:THR:HG21	1:W:249:ARG:HH11	1.60	0.66
1:C:78:VAL:HG22	1:C:444:LEU:HD21	1.78	0.66
1:E:158:TRP:CH2	1:E:302:PRO:HG3	2.29	0.66
1:F:108:LYS:HD3	1:F:112:ASN:HD21	1.59	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:37:ARG:NH2	1:F:37:ARG:HB3	2.09	0.66
1:G:158:TRP:CD1	1:G:158:TRP:N	2.60	0.66
1:I:41:TRP:HZ3	1:I:42:ASP:HB3	1.61	0.66
1:L:227:GLU:HA	1:L:274:ARG:HA	1.78	0.66
1:L:41:TRP:HZ3	1:L:42:ASP:HB3	1.61	0.66
1:L:585:GLU:C	1:L:587:PRO:HD3	2.15	0.66
1:N:94:LEU:HA	1:N:97:MSE:HE2	1.76	0.66
1:Q:330:ARG:NH2	1:Q:409:THR:HG21	2.06	0.66
1:B:227:GLU:HA	1:B:274:ARG:HA	1.78	0.66
1:B:165:MSE:HG3	1:B:307:TRP:CE3	2.30	0.66
1:C:379:GLU:O	1:C:380:ASN:HB2	1.95	0.66
1:E:225:VAL:HG22	1:E:276:VAL:HG12	1.76	0.66
1:G:442:ALA:HB1	3:G:702:HOH:O	1.95	0.66
1:H:227:GLU:HA	1:H:274:ARG:HA	1.78	0.66
1:K:41:TRP:HZ3	1:K:42:ASP:HB3	1.61	0.66
1:O:534:GLU:O	1:O:538:LEU:HD23	1.96	0.66
1:O:560:LEU:O	1:O:565:VAL:HG21	1.96	0.66
1:P:248:LYS:HD3	1:P:251:ILE:HB	1.77	0.66
1:S:575:GLN:O	1:S:579:MSE:HG2	1.94	0.66
1:T:158:TRP:N	1:T:158:TRP:CD1	2.62	0.66
1:T:209:PHE:CZ	1:T:214:GLN:HG2	2.30	0.66
1:W:94:LEU:HA	1:W:97:MSE:HE2	1.78	0.66
1:F:379:GLU:O	1:F:380:ASN:HB2	1.95	0.66
1:G:110:ALA:O	1:G:113:ILE:HG13	4.33	0.66
1:H:237:ASP:H	1:H:243:PRO:HA	1.60	0.66
1:J:227:GLU:HA	1:J:274:ARG:HA	1.78	0.66
1:K:442:ALA:HB1	3:K:702:HOH:O	1.95	0.66
1:M:575:GLN:O	1:M:579:MSE:HG2	1.96	0.66
1:O:231:THR:HG21	1:O:249:ARG:HH11	1.61	0.66
1:R:209:PHE:CZ	1:R:214:GLN:HG2	2.29	0.66
1:T:158:TRP:HB3	1:T:173:CYS:CA	2.24	0.66
1:U:248:LYS:HB3	1:U:511:ARG:NH1	2.05	0.66
1:W:330:ARG:NH2	1:W:409:THR:HG21	2.09	0.66
2:Z:110:ALA:O	2:Z:113:ILE:HG13	1.96	0.66
1:B:108:LYS:HD3	1:B:112:ASN:HD21	1.59	0.66
1:E:108:LYS:HD3	1:E:112:ASN:HD21	1.59	0.66
1:E:37:ARG:NH2	1:E:37:ARG:HB3	2.09	0.66
1:I:110:ALA:O	1:I:113:ILE:HG13	4.33	0.66
1:J:110:ALA:O	1:J:113:ILE:HG13	4.33	0.66
1:J:41:TRP:HZ3	1:J:42:ASP:HB3	1.61	0.66
1:J:585:GLU:C	1:J:587:PRO:HD3	2.15	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:108:LYS:HD3	1:L:112:ASN:HD21	1.59	0.66
1:L:34:PHE:HE1	1:L:324:LYS:HZ2	1.37	0.66
1:P:232:ALA:CB	1:P:269:ARG:H	2.08	0.66
1:R:330:ARG:NH2	1:R:409:THR:HG21	2.06	0.66
1:S:273:ARG:HH22	1:S:453:LEU:CD1	2.09	0.66
1:A:225:VAL:HG22	1:A:276:VAL:HG12	1.76	0.66
1:A:165:MSE:HG3	1:A:307:TRP:CE3	2.30	0.66
1:B:209:PHE:N	1:B:210:PRO:HD3	2.08	0.66
1:B:561:ASP:HB2	1:C:89:ASP:HA	1.78	0.66
1:F:237:ASP:H	1:F:243:PRO:HA	1.60	0.66
1:K:165:MSE:HG3	1:K:307:TRP:CE3	2.30	0.66
1:K:41:TRP:CE3	1:K:42:ASP:CA	2.79	0.66
1:K:78:VAL:HG22	1:K:444:LEU:HD21	1.78	0.66
1:P:325:ASP:OD2	1:L:136:SER:HB3	165.06	0.66
1:O:232:ALA:CB	1:O:269:ARG:H	2.09	0.66
1:V:248:LYS:HB3	1:V:511:ARG:NH1	2.07	0.66
1:X:248:LYS:HD3	1:X:251:ILE:HB	1.77	0.66
1:B:41:TRP:HZ3	1:B:42:ASP:HB3	1.61	0.66
1:D:442:ALA:HB1	3:D:702:HOH:O	1.95	0.66
1:E:227:GLU:HA	1:E:274:ARG:HA	1.78	0.66
1:E:442:ALA:HB1	3:E:702:HOH:O	1.95	0.66
1:C:556:TYR:OH	1:E:542:THR:HG21	1.96	0.66
1:J:212:LEU:HD22	1:K:26:ARG:HG2	1.78	0.66
1:M:334:MSE:SE	1:O:404:MSE:HE1	2.46	0.66
1:O:94:LEU:HA	1:O:97:MSE:HE2	1.77	0.66
1:P:534:GLU:O	1:P:538:LEU:HD23	1.96	0.66
1:S:94:LEU:HA	1:S:97:MSE:HE2	1.76	0.66
1:V:575:GLN:O	1:V:579:MSE:HG2	1.96	0.66
1:V:94:LEU:HA	1:V:97:MSE:HE2	1.77	0.66
1:W:26:ARG:NH2	1:W:30:LYS:HD3	2.11	0.66
1:C:165:MSE:HG3	1:C:307:TRP:CE3	2.30	0.65
1:D:58:ASP:O	1:D:59:VAL:CB	2.45	0.65
1:E:237:ASP:H	1:E:243:PRO:HA	1.59	0.65
1:E:58:ASP:O	1:E:59:VAL:CB	2.45	0.65
1:F:227:GLU:HA	1:F:274:ARG:HA	1.78	0.65
1:H:41:TRP:CE3	1:H:42:ASP:CA	2.79	0.65
1:P:330:ARG:NH2	1:P:409:THR:HG21	2.07	0.65
1:R:575:GLN:O	1:R:579:MSE:HG2	1.96	0.65
1:W:158:TRP:HB3	1:W:173:CYS:CA	2.23	0.65
1:W:575:GLN:O	1:W:579:MSE:HG2	1.96	0.65
1:A:37:ARG:HB3	1:A:37:ARG:NH2	2.09	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:110:ALA:O	1:F:113:ILE:HG13	4.33	0.65
1:F:442:ALA:HB1	3:F:702:HOH:O	1.95	0.65
1:G:58:ASP:O	1:G:59:VAL:CB	2.45	0.65
1:I:227:GLU:HA	1:I:274:ARG:HA	1.78	0.65
1:I:561:ASP:HB2	1:J:89:ASP:HA	1.78	0.65
1:A:352:TRP:CG	1:L:376:ARG:HB2	2.31	0.65
1:M:232:ALA:CB	1:M:269:ARG:H	2.08	0.65
1:N:26:ARG:NH2	1:N:30:LYS:HD3	2.11	0.65
1:P:78:VAL:CG2	1:P:444:LEU:HD11	2.23	0.65
1:W:15:PHE:HZ	1:W:283:CYS:HG	1.42	0.65
2:Y:32:ALA:O	2:Y:33:THR:HG22	1.92	0.65
1:D:26:ARG:HG2	1:E:212:LEU:HD22	1.77	0.65
1:G:78:VAL:HG22	1:G:444:LEU:HD21	1.78	0.65
1:I:379:GLU:O	1:I:380:ASN:HB2	1.95	0.65
1:J:78:VAL:HG22	1:J:444:LEU:HD21	1.78	0.65
1:R:37:ARG:HB3	1:R:37:ARG:HH21	1.60	0.65
1:S:158:TRP:HB3	1:S:173:CYS:CA	2.25	0.65
1:U:158:TRP:N	1:U:158:TRP:CD1	2.64	0.65
1:U:404:MSE:HE1	1:X:334:MSE:SE	2.47	0.65
2:Z:32:ALA:O	2:Z:33:THR:HG22	1.92	0.65
1:H:58:ASP:O	1:H:59:VAL:CB	2.45	0.65
1:I:556:TYR:OH	1:J:542:THR:HG21	1.95	0.65
1:S:232:ALA:CB	1:S:269:ARG:H	2.10	0.65
2:Y:110:ALA:O	2:Y:113:ILE:HG13	1.96	0.65
1:A:379:GLU:O	1:A:380:ASN:HB2	1.95	0.65
1:B:41:TRP:CE3	1:B:42:ASP:CA	2.79	0.65
1:B:560:LEU:HD22	1:C:82:PRO:HG2	1.78	0.65
1:D:227:GLU:HA	1:D:274:ARG:HA	1.78	0.65
1:F:165:MSE:HG3	1:F:307:TRP:CE3	2.30	0.65
1:O:575:GLN:O	1:O:579:MSE:HG2	1.97	0.65
1:P:158:TRP:N	1:P:158:TRP:CD1	2.63	0.65
1:T:248:LYS:HB3	1:T:511:ARG:NH1	2.04	0.65
1:U:209:PHE:CZ	1:U:214:GLN:HG2	2.30	0.65
1:X:231:THR:HG21	1:X:249:ARG:HH11	1.61	0.65
1:X:78:VAL:CG2	1:X:444:LEU:HD11	2.23	0.65
1:X:560:LEU:O	1:X:565:VAL:HG21	1.97	0.65
1:D:225:VAL:HG22	1:D:276:VAL:HG12	1.76	0.65
1:E:41:TRP:CE3	1:E:42:ASP:CA	2.79	0.65
1:H:41:TRP:HZ3	1:H:42:ASP:HB3	1.61	0.65
1:I:78:VAL:HG22	1:I:444:LEU:HD21	1.78	0.65
1:L:442:ALA:HB1	3:L:702:HOH:O	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:34:PHE:HZ	1:S:328:ARG:HH22	1.38	0.65
1:S:37:ARG:HB3	1:S:37:ARG:HH21	1.61	0.65
1:V:209:PHE:CZ	1:V:214:GLN:HG2	2.30	0.65
1:C:227:GLU:HA	1:C:274:ARG:HA	1.78	0.65
1:F:41:TRP:CE3	1:F:42:ASP:CA	2.79	0.65
1:R:561:ASP:OD2	1:X:92:ASP:HB3	1.97	0.65
1:S:158:TRP:CH2	1:S:302:PRO:HG3	2.31	0.65
1:T:273:ARG:HH22	1:T:453:LEU:CD1	2.09	0.65
1:C:58:ASP:O	1:C:59:VAL:CB	2.45	0.65
1:D:438:LEU:HD11	1:E:108:LYS:HD2	1.79	0.65
1:F:108:LYS:HD2	1:G:438:LEU:HD11	1.79	0.65
1:L:58:ASP:O	1:L:59:VAL:CB	2.45	0.65
1:P:94:LEU:HA	1:P:97:MSE:HE2	1.79	0.65
1:Q:158:TRP:CH2	1:Q:302:PRO:HG3	2.31	0.65
1:Q:231:THR:HG21	1:Q:249:ARG:HH11	1.62	0.65
1:S:431:ALA:O	1:S:435:VAL:HG22	1.96	0.65
2:Z:28:VAL:CG2	2:Z:96:LEU:HD12	2.22	0.65
1:A:158:TRP:CD1	1:A:158:TRP:N	2.60	0.65
1:A:58:ASP:O	1:A:59:VAL:CB	2.45	0.65
1:B:110:ALA:O	1:B:113:ILE:HG13	4.33	0.65
1:C:41:TRP:HZ3	1:C:42:ASP:HB3	1.61	0.65
1:D:41:TRP:CE3	1:D:42:ASP:CA	2.79	0.65
1:F:58:ASP:O	1:F:59:VAL:CB	2.45	0.65
1:G:227:GLU:HA	1:G:274:ARG:HA	1.78	0.65
1:G:41:TRP:HZ3	1:G:42:ASP:HB3	1.61	0.65
1:G:5:GLU:HG2	1:G:6:ASN:N	2.12	0.65
1:H:47:GLN:N	1:H:47:GLN:OE1	2.30	0.65
1:I:47:GLN:OE1	1:I:47:GLN:N	2.30	0.65
1:J:47:GLN:N	1:J:47:GLN:OE1	2.30	0.65
1:K:158:TRP:CE3	1:K:173:CYS:SG	2.88	0.65
1:N:12:LEU:O	1:N:16:ASP:HB2	1.97	0.65
1:R:273:ARG:HH22	1:R:453:LEU:CD1	2.10	0.65
1:S:26:ARG:NH2	1:S:30:LYS:HD3	2.11	0.65
1:T:287:LEU:HD12	1:T:287:LEU:N	2.12	0.65
1:A:41:TRP:HZ3	1:A:42:ASP:HB3	1.61	0.65
1:D:5:GLU:HG2	1:D:6:ASN:N	2.12	0.65
1:E:74:ASN:HB2	1:E:75:PRO:HD3	4.60	0.65
1:G:182:ASN:ND2	1:H:171:ARG:HH21	1.95	0.65
1:G:41:TRP:CE3	1:G:42:ASP:CA	2.79	0.65
1:W:273:ARG:HH22	1:W:453:LEU:CD1	2.09	0.65
1:A:144:ILE:HG12	1:A:447:TYR:HE1	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:5:GLU:HG2	1:B:6:ASN:N	2.12	0.64
1:D:165:MSE:HG3	1:D:307:TRP:CE3	2.30	0.64
1:M:384:LEU:HD22	1:M:384:LEU:H	1.61	0.64
1:N:560:LEU:O	1:N:565:VAL:HG21	1.97	0.64
1:O:212:LEU:HD22	1:P:26:ARG:HG2	1.79	0.64
1:T:330:ARG:NH2	1:T:409:THR:HG21	2.07	0.64
1:A:41:TRP:CE3	1:A:42:ASP:CA	2.79	0.64
1:B:95:MSE:HE1	1:B:99:ARG:CZ	2.27	0.64
1:C:74:ASN:HB2	1:C:75:PRO:HD3	4.59	0.64
1:D:110:ALA:O	1:D:113:ILE:HG13	4.33	0.64
1:H:57:PHE:HD2	1:H:330:ARG:CB	2.10	0.64
1:I:57:PHE:HD2	1:I:330:ARG:CB	2.10	0.64
1:I:41:TRP:CE3	1:I:42:ASP:CA	2.79	0.64
1:J:71:MSE:HE2	1:J:119:ILE:HD11	1.80	0.64
1:J:95:MSE:HE1	1:J:99:ARG:CZ	2.28	0.64
1:K:58:ASP:O	1:K:59:VAL:CB	2.45	0.64
1:K:95:MSE:HE1	1:K:99:ARG:CZ	2.27	0.64
1:L:41:TRP:CE3	1:L:42:ASP:CA	2.79	0.64
1:L:5:GLU:HG2	1:L:6:ASN:N	2.13	0.64
1:R:158:TRP:CE3	1:R:173:CYS:SG	2.86	0.64
1:U:26:ARG:NH2	1:U:30:LYS:HD3	2.13	0.64
1:B:57:PHE:HD2	1:B:330:ARG:CB	2.11	0.64
1:C:41:TRP:CE3	1:C:42:ASP:CA	2.79	0.64
1:D:74:ASN:HB2	1:D:75:PRO:HD3	4.60	0.64
1:E:57:PHE:HD2	1:E:330:ARG:CB	2.10	0.64
1:F:15:PHE:CE1	1:F:283:CYS:HA	2.33	0.64
1:F:57:PHE:HD2	1:F:330:ARG:CB	2.10	0.64
1:H:110:ALA:O	1:H:113:ILE:HG13	4.33	0.64
1:I:58:ASP:O	1:I:59:VAL:CB	2.45	0.64
1:I:5:GLU:HG2	1:I:6:ASN:N	2.12	0.64
1:J:41:TRP:CE3	1:J:42:ASP:CA	2.79	0.64
1:N:128:LEU:HD12	1:N:446:THR:HG23	1.79	0.64
1:N:78:VAL:CG2	1:N:444:LEU:HD11	2.22	0.64
1:O:567:MSE:SE	1:P:576:LEU:HD13	2.47	0.64
1:R:384:LEU:HD22	1:R:384:LEU:H	1.63	0.64
1:V:158:TRP:HB3	1:V:173:CYS:CA	2.23	0.64
1:V:37:ARG:HH21	1:V:37:ARG:HB3	1.62	0.64
1:D:144:ILE:HG12	1:D:447:TYR:HE1	1.63	0.64
1:H:15:PHE:CE1	1:H:283:CYS:HA	2.33	0.64
1:H:35:PHE:HE1	1:H:321:ARG:HH11	1.46	0.64
1:K:71:MSE:HE2	1:K:119:ILE:HD11	1.80	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:78:VAL:HG22	1:L:444:LEU:HD21	1.78	0.64
1:L:528:LYS:NZ	1:L:560:LEU:HD21	2.13	0.64
1:P:15:PHE:CE1	1:P:283:CYS:HA	2.32	0.64
1:Q:136:SER:HB3	1:S:325:ASP:OD2	88.03	0.64
1:T:158:TRP:CH2	1:T:302:PRO:HG3	2.33	0.64
1:V:113:ILE:HD13	1:V:150:HIS:CE1	2.33	0.64
1:V:231:THR:HG21	1:V:249:ARG:HH11	1.62	0.64
1:U:92:ASP:HB3	1:X:561:ASP:OD2	1.97	0.64
1:A:95:MSE:HE1	1:A:99:ARG:CZ	2.28	0.64
1:E:35:PHE:HE1	1:E:321:ARG:HH11	1.46	0.64
1:E:95:MSE:HE1	1:E:99:ARG:CZ	2.28	0.64
1:G:15:PHE:CE1	1:G:283:CYS:HA	2.33	0.64
1:G:95:MSE:HE1	1:G:99:ARG:CZ	2.28	0.64
1:I:15:PHE:CE1	1:I:283:CYS:HA	2.33	0.64
1:I:35:PHE:HE1	1:I:321:ARG:HH11	1.46	0.64
1:I:528:LYS:NZ	1:I:560:LEU:HD21	2.13	0.64
1:N:585:GLU:C	1:N:587:PRO:HD3	2.17	0.64
1:S:113:ILE:HD13	1:S:150:HIS:CE1	2.32	0.64
1:U:585:GLU:C	1:U:587:PRO:HD3	2.18	0.64
1:X:158:TRP:CH2	1:X:302:PRO:HG3	2.33	0.64
1:X:273:ARG:HH22	1:X:453:LEU:CD1	2.09	0.64
1:A:57:PHE:HD2	1:A:330:ARG:CB	2.10	0.64
1:B:528:LYS:NZ	1:B:560:LEU:HD21	2.13	0.64
1:B:78:VAL:HG22	1:B:444:LEU:HD21	1.78	0.64
1:D:15:PHE:CE1	1:D:283:CYS:HA	2.33	0.64
1:E:47:GLN:N	1:E:47:GLN:OE1	2.30	0.64
1:H:236:GLN:HA	1:H:244:VAL:H	1.63	0.64
1:H:95:MSE:HE1	1:H:99:ARG:CZ	2.27	0.64
1:J:5:GLU:HG2	1:J:6:ASN:N	2.12	0.64
1:L:95:MSE:HE1	1:L:99:ARG:CZ	2.28	0.64
1:M:585:GLU:C	1:M:587:PRO:HD3	2.18	0.64
1:N:158:TRP:CH2	1:N:302:PRO:HG3	2.33	0.64
1:N:534:GLU:O	1:N:538:LEU:HD23	1.98	0.64
1:O:585:GLU:C	1:O:587:PRO:HD3	2.18	0.64
1:S:561:ASP:HB2	1:T:89:ASP:HA	1.80	0.64
1:A:71:MSE:HE2	1:A:119:ILE:HD11	1.80	0.64
1:A:236:GLN:HA	1:A:244:VAL:H	1.63	0.64
1:A:528:LYS:NZ	1:A:560:LEU:HD21	2.13	0.64
1:B:236:GLN:HA	1:B:244:VAL:H	1.63	0.64
1:E:15:PHE:CE1	1:E:283:CYS:HA	2.33	0.64
1:E:34:PHE:HE1	1:E:324:LYS:HZ2	1.43	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:144:ILE:HG12	1:E:447:TYR:HE1	1.63	0.64
1:G:546:THR:CG2	1:G:547:PRO:HD3	2.28	0.64
1:H:71:MSE:HE2	1:H:119:ILE:HD11	1.80	0.64
1:H:74:ASN:HB2	1:H:75:PRO:HD3	4.59	0.64
1:J:58:ASP:O	1:J:59:VAL:CB	2.45	0.64
1:N:37:ARG:NH2	1:N:41:TRP:HB3	2.13	0.64
1:O:26:ARG:NH2	1:O:30:LYS:HD3	2.13	0.64
1:O:37:ARG:HH21	1:O:37:ARG:HB3	1.61	0.64
1:Q:273:ARG:HH22	1:Q:453:LEU:CD1	2.09	0.64
1:Q:585:GLU:C	1:Q:587:PRO:HD3	2.18	0.64
1:U:94:LEU:HA	1:U:97:MSE:HE2	1.80	0.64
1:W:232:ALA:CB	1:W:269:ARG:H	2.10	0.64
1:W:585:GLU:C	1:W:587:PRO:HD3	2.18	0.64
1:X:534:GLU:O	1:X:538:LEU:HD23	1.97	0.64
1:X:78:VAL:HG12	1:X:79:LEU:N	2.12	0.64
1:A:47:GLN:OE1	1:A:47:GLN:N	2.30	0.64
1:B:144:ILE:HG12	1:B:447:TYR:HE1	1.62	0.64
1:B:15:PHE:CE1	1:B:283:CYS:HA	2.33	0.64
1:F:47:GLN:N	1:F:47:GLN:OE1	2.30	0.64
1:G:47:GLN:N	1:G:47:GLN:OE1	2.30	0.64
1:G:528:LYS:NZ	1:G:560:LEU:HD21	2.13	0.64
1:I:144:ILE:HG12	1:I:447:TYR:HE1	1.62	0.64
1:K:78:VAL:HG12	1:K:79:LEU:N	2.13	0.64
1:Q:560:LEU:O	1:Q:565:VAL:HG21	1.98	0.64
1:S:585:GLU:C	1:S:587:PRO:HD3	2.18	0.64
1:V:273:ARG:HH22	1:V:453:LEU:CD1	2.10	0.64
2:Y:42:MET:CG	2:Y:42:MET:O	2.30	0.64
1:A:110:ALA:O	1:A:113:ILE:HG13	4.33	0.64
1:A:15:PHE:CE1	1:A:283:CYS:HA	2.33	0.64
1:B:15:PHE:HZ	1:B:283:CYS:HG	1.45	0.64
1:C:236:GLN:HA	1:C:244:VAL:H	1.63	0.64
1:C:528:LYS:NZ	1:C:560:LEU:HD21	2.13	0.64
1:D:528:LYS:NZ	1:D:560:LEU:HD21	2.13	0.64
1:E:110:ALA:O	1:E:113:ILE:HG13	4.33	0.64
1:E:528:LYS:NZ	1:E:560:LEU:HD21	2.13	0.64
1:G:236:GLN:HA	1:G:244:VAL:H	1.63	0.64
1:I:236:GLN:HA	1:I:244:VAL:H	1.63	0.64
1:I:71:MSE:HE2	1:I:119:ILE:HD11	1.80	0.64
1:Q:37:ARG:HH21	1:Q:37:ARG:HB3	1.61	0.64
1:R:113:ILE:HD13	1:R:150:HIS:CE1	2.32	0.64
1:R:273:ARG:NH2	1:R:453:LEU:HD21	2.13	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:560:LEU:O	1:R:565:VAL:HG21	1.98	0.64
1:V:534:GLU:O	1:V:538:LEU:HD23	1.98	0.64
1:V:560:LEU:O	1:V:565:VAL:HG21	1.97	0.64
1:P:136:SER:HB3	1:X:325:ASP:OD2	72.27	0.64
1:C:71:MSE:HE2	1:C:119:ILE:HD11	1.80	0.64
1:E:78:VAL:HG12	1:E:79:LEU:N	2.13	0.64
1:F:71:MSE:HE2	1:F:119:ILE:HD11	1.80	0.64
1:F:78:VAL:HG12	1:F:79:LEU:N	2.13	0.64
1:G:48:TYR:O	1:G:49:THR:HB	1.98	0.64
1:H:144:ILE:HG12	1:H:447:TYR:HE1	1.62	0.64
1:J:15:PHE:CE1	1:J:283:CYS:HA	2.33	0.64
1:J:564:GLY:HA2	1:K:554:LEU:HD21	1.80	0.64
1:K:15:PHE:CE1	1:K:283:CYS:HA	2.33	0.64
1:M:231:THR:HG21	1:M:249:ARG:HH11	1.63	0.64
1:Q:26:ARG:NH2	1:Q:30:LYS:HD3	2.13	0.64
1:U:560:LEU:O	1:U:565:VAL:HG21	1.98	0.64
1:X:585:GLU:C	1:X:587:PRO:HD3	2.18	0.64
1:A:546:THR:CG2	1:A:547:PRO:HD3	2.27	0.63
1:B:71:MSE:HE2	1:B:119:ILE:HD11	1.80	0.63
1:B:58:ASP:O	1:B:59:VAL:CB	2.45	0.63
1:E:41:TRP:HZ3	1:E:42:ASP:HB3	1.61	0.63
1:F:48:TYR:O	1:F:49:THR:HB	1.99	0.63
1:G:158:TRP:CE3	1:G:173:CYS:SG	2.88	0.63
1:G:74:ASN:HB2	1:G:75:PRO:HD3	4.59	0.63
1:H:108:LYS:HD2	1:I:438:LEU:HD11	1.80	0.63
1:H:34:PHE:CZ	1:H:328:ARG:NH2	2.48	0.63
1:J:35:PHE:HE1	1:J:321:ARG:HH11	1.46	0.63
1:J:546:THR:CG2	1:J:547:PRO:HD3	2.28	0.63
1:J:74:ASN:HB2	1:J:75:PRO:HD3	4.59	0.63
1:K:57:PHE:HD2	1:K:330:ARG:CB	2.10	0.63
1:P:231:THR:HG21	1:P:249:ARG:HH11	1.63	0.63
1:P:560:LEU:O	1:P:565:VAL:HG21	1.97	0.63
1:Q:273:ARG:NH2	1:Q:453:LEU:HD11	2.12	0.63
1:T:585:GLU:C	1:T:587:PRO:HD3	2.18	0.63
1:U:232:ALA:CB	1:U:269:ARG:H	2.12	0.63
1:W:128:LEU:HD12	1:W:446:THR:HG23	1.80	0.63
2:Z:42:MET:O	2:Z:42:MET:CG	2.30	0.63
1:C:110:ALA:O	1:C:113:ILE:HG13	4.33	0.63
1:B:556:TYR:OH	1:C:542:THR:HG21	1.99	0.63
1:F:246:TYR:CD2	1:F:511:ARG:HB3	2.34	0.63
1:I:48:TYR:O	1:I:49:THR:HB	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:236:GLN:HA	1:J:244:VAL:H	1.63	0.63
1:J:78:VAL:HG12	1:J:79:LEU:N	2.13	0.63
1:L:57:PHE:HD2	1:L:330:ARG:CB	2.10	0.63
1:N:15:PHE:CE1	1:N:283:CYS:HA	2.33	0.63
1:P:158:TRP:CE3	1:P:173:CYS:SG	2.86	0.63
1:P:585:GLU:C	1:P:587:PRO:HD3	2.18	0.63
1:R:273:ARG:NH2	1:R:453:LEU:HD11	2.12	0.63
1:X:158:TRP:HB3	1:X:173:CYS:CA	2.26	0.63
2:Y:74:ASN:HB2	2:Y:75:PRO:HD3	1.79	0.63
1:D:71:MSE:HE2	1:D:119:ILE:HD11	1.80	0.63
1:D:35:PHE:HE1	1:D:321:ARG:HH11	1.46	0.63
1:D:95:MSE:HE1	1:D:99:ARG:CZ	2.28	0.63
1:F:95:MSE:HE1	1:F:99:ARG:CZ	2.28	0.63
1:G:78:VAL:HG12	1:G:79:LEU:N	2.13	0.63
1:H:5:GLU:HG2	1:H:6:ASN:N	2.12	0.63
1:I:78:VAL:HG12	1:I:79:LEU:N	2.13	0.63
1:K:144:ILE:HG12	1:K:447:TYR:CE1	2.34	0.63
1:M:12:LEU:O	1:M:16:ASP:HB2	1.99	0.63
1:X:12:LEU:O	1:X:16:ASP:HB2	1.98	0.63
1:C:15:PHE:CE1	1:C:283:CYS:HA	2.33	0.63
1:C:144:ILE:HG12	1:C:447:TYR:CE1	2.34	0.63
1:C:5:GLU:HG2	1:C:6:ASN:N	2.12	0.63
1:C:95:MSE:HE1	1:C:99:ARG:CZ	2.28	0.63
1:D:57:PHE:HD2	1:D:330:ARG:CB	2.11	0.63
1:E:236:GLN:HA	1:E:244:VAL:H	1.63	0.63
1:E:5:GLU:HG2	1:E:6:ASN:N	2.12	0.63
1:F:144:ILE:HG12	1:F:447:TYR:CE1	2.34	0.63
1:G:12:LEU:O	1:G:16:ASP:HB2	1.99	0.63
1:G:144:ILE:HG12	1:G:447:TYR:HE1	1.63	0.63
1:H:12:LEU:O	1:H:16:ASP:HB2	1.99	0.63
1:J:528:LYS:NZ	1:J:560:LEU:HD21	2.13	0.63
1:K:12:LEU:O	1:K:16:ASP:HB2	1.99	0.63
1:K:5:GLU:HG2	1:K:6:ASN:N	2.12	0.63
1:L:236:GLN:HA	1:L:244:VAL:H	1.63	0.63
1:N:325:ASP:OD2	1:V:136:SER:HB3	48.62	0.63
1:O:12:LEU:O	1:O:16:ASP:HB2	1.98	0.63
1:P:12:LEU:O	1:P:16:ASP:HB2	1.98	0.63
1:T:12:LEU:O	1:T:16:ASP:HB2	1.98	0.63
1:V:232:ALA:CB	1:V:269:ARG:H	2.11	0.63
1:A:144:ILE:HG12	1:A:447:TYR:CE1	2.34	0.63
1:C:246:TYR:CD2	1:C:511:ARG:HB3	2.34	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:41:TRP:HZ3	1:D:42:ASP:HB3	1.61	0.63
1:E:246:TYR:CD2	1:E:511:ARG:HB3	2.34	0.63
1:E:144:ILE:HG12	1:E:447:TYR:CE1	2.34	0.63
1:E:71:MSE:HE2	1:E:119:ILE:HD11	1.80	0.63
1:F:5:GLU:HG2	1:F:6:ASN:N	2.13	0.63
1:F:74:ASN:HB2	1:F:75:PRO:HD3	4.59	0.63
1:G:57:PHE:HD2	1:G:330:ARG:CB	2.10	0.63
1:I:15:PHE:HZ	1:I:283:CYS:HG	1.45	0.63
1:I:95:MSE:HE1	1:I:99:ARG:CZ	2.28	0.63
1:J:48:TYR:O	1:J:49:THR:HB	1.98	0.63
1:K:144:ILE:HG12	1:K:447:TYR:HE1	1.63	0.63
1:L:78:VAL:HG12	1:L:79:LEU:N	2.13	0.63
1:P:34:PHE:HZ	1:P:328:ARG:HH22	1.36	0.63
1:Q:232:ALA:CB	1:Q:269:ARG:H	2.11	0.63
1:V:585:GLU:C	1:V:587:PRO:HD3	2.19	0.63
1:C:57:PHE:HD2	1:C:330:ARG:CB	2.10	0.63
1:C:48:TYR:O	1:C:49:THR:HB	1.98	0.63
1:D:15:PHE:HZ	1:D:283:CYS:HG	1.46	0.63
1:E:35:PHE:HE2	1:E:324:LYS:HZ3	1.42	0.63
1:F:144:ILE:HG12	1:F:447:TYR:HE1	1.62	0.63
1:F:236:GLN:HA	1:F:244:VAL:H	1.63	0.63
1:G:71:MSE:HE2	1:G:119:ILE:HD11	1.80	0.63
1:H:528:LYS:NZ	1:H:560:LEU:HD21	2.13	0.63
1:J:144:ILE:HG12	1:J:447:TYR:HE1	1.63	0.63
1:K:236:GLN:HA	1:K:244:VAL:H	1.63	0.63
1:L:15:PHE:CE1	1:L:283:CYS:HA	2.33	0.63
1:L:47:GLN:OE1	1:L:47:GLN:N	2.30	0.63
1:N:273:ARG:HH22	1:N:453:LEU:CD1	2.11	0.63
1:R:273:ARG:HH22	1:R:453:LEU:HD21	1.64	0.63
1:R:15:PHE:CE1	1:R:283:CYS:HA	2.34	0.63
1:S:12:LEU:O	1:S:16:ASP:HB2	1.98	0.63
1:T:232:ALA:CB	1:T:269:ARG:H	2.11	0.63
1:T:26:ARG:NH2	1:T:30:LYS:HD3	2.14	0.63
1:V:158:TRP:N	1:V:158:TRP:CD1	2.63	0.63
1:V:158:TRP:CH2	1:V:302:PRO:HG3	2.34	0.63
1:V:398:PRO:HB3	1:W:395:PRO:HD2	1.81	0.63
1:X:575:GLN:O	1:X:579:MSE:HG2	1.99	0.63
1:A:35:PHE:HE1	1:A:321:ARG:HH11	1.46	0.63
1:A:48:TYR:O	1:A:49:THR:HB	1.98	0.63
1:C:99:ARG:O	1:C:103:ARG:HG3	1.99	0.63
1:D:99:ARG:O	1:D:103:ARG:HG3	1.99	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:GLN:N	1:D:47:GLN:OE1	2.30	0.63
1:D:48:TYR:O	1:D:49:THR:HB	1.98	0.63
1:D:546:THR:CG2	1:D:547:PRO:HD3	2.28	0.63
1:F:12:LEU:O	1:F:16:ASP:HB2	1.99	0.63
1:L:158:TRP:CE3	1:L:173:CYS:SG	2.88	0.63
1:M:15:PHE:HZ	1:M:283:CYS:SG	2.21	0.63
1:O:158:TRP:CH2	1:O:302:PRO:HG3	2.34	0.63
1:P:26:ARG:NH2	1:P:30:LYS:HD3	2.14	0.63
2:Z:74:ASN:HB2	2:Z:75:PRO:HD3	1.79	0.63
1:A:5:GLU:HG2	1:A:6:ASN:N	2.12	0.63
1:B:78:VAL:HG12	1:B:79:LEU:N	2.13	0.63
1:D:236:GLN:HA	1:D:244:VAL:H	1.63	0.63
1:G:99:ARG:O	1:G:103:ARG:HG3	1.99	0.63
1:H:334:MSE:HE3	1:I:404:MSE:CE	2.29	0.63
1:I:74:ASN:HB2	1:I:75:PRO:HD3	4.59	0.63
1:J:57:PHE:HD2	1:J:330:ARG:CB	2.10	0.63
1:L:337:ASN:HD21	1:L:401:ASN:HD22	1.47	0.63
1:O:66:LYS:HZ3	1:O:420:VAL:HG11	1.63	0.63
1:S:560:LEU:O	1:S:565:VAL:HG21	1.99	0.63
1:T:128:LEU:HD12	1:T:446:THR:HG23	1.81	0.63
1:V:15:PHE:CE1	1:V:283:CYS:HA	2.34	0.63
1:V:12:LEU:O	1:V:16:ASP:HB2	1.98	0.63
1:W:37:ARG:NH2	1:W:41:TRP:HB3	2.13	0.63
1:B:74:ASN:HB2	1:B:75:PRO:HD3	4.60	0.63
1:E:99:ARG:O	1:E:103:ARG:HG3	1.99	0.63
1:F:528:LYS:NZ	1:F:560:LEU:HD21	2.13	0.63
1:G:144:ILE:HG12	1:G:447:TYR:CE1	2.34	0.63
1:K:528:LYS:NZ	1:K:560:LEU:HD21	2.13	0.63
1:K:564:GLY:HA2	1:L:554:LEU:HD21	1.80	0.63
1:L:99:ARG:O	1:L:103:ARG:HG3	1.99	0.63
1:Q:40:GLN:HG2	1:R:310:VAL:HG22	1.81	0.63
1:U:12:LEU:O	1:U:16:ASP:HB2	1.99	0.63
1:W:12:LEU:O	1:W:16:ASP:HB2	1.98	0.63
1:W:34:PHE:HE2	1:W:45:LEU:HG	1.64	0.63
1:B:246:TYR:CD2	1:B:511:ARG:HB3	2.34	0.62
1:F:35:PHE:HE1	1:F:321:ARG:HH11	1.46	0.62
1:H:144:ILE:HG12	1:H:447:TYR:CE1	2.34	0.62
1:I:246:TYR:CD2	1:I:511:ARG:HB3	2.34	0.62
1:L:12:LEU:O	1:L:16:ASP:HB2	1.99	0.62
1:M:26:ARG:NH2	1:M:30:LYS:HD3	2.13	0.62
1:N:34:PHE:HE2	1:N:45:LEU:HG	1.64	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:560:LEU:HD22	1:P:82:PRO:HG2	1.81	0.62
1:T:15:PHE:CE1	1:T:283:CYS:HA	2.34	0.62
1:T:440:MSE:O	1:T:444:LEU:HD22	1.99	0.62
1:W:15:PHE:CE1	1:W:283:CYS:HA	2.34	0.62
1:W:287:LEU:N	1:W:287:LEU:HD12	2.14	0.62
1:W:431:ALA:O	1:W:435:VAL:HG22	1.98	0.62
1:A:158:TRP:CE3	1:A:173:CYS:SG	2.88	0.62
1:B:35:PHE:HE1	1:B:321:ARG:HH11	1.46	0.62
1:B:144:ILE:HG12	1:B:447:TYR:CE1	2.34	0.62
1:B:47:GLN:N	1:B:47:GLN:OE1	2.30	0.62
1:B:546:THR:CG2	1:B:547:PRO:HD3	2.28	0.62
1:C:12:LEU:O	1:C:16:ASP:HB2	1.99	0.62
1:D:144:ILE:HG12	1:D:447:TYR:CE1	2.34	0.62
1:D:78:VAL:HG12	1:D:79:LEU:N	2.13	0.62
1:E:337:ASN:HD21	1:E:401:ASN:HD22	1.47	0.62
1:F:99:ARG:O	1:F:103:ARG:HG3	1.99	0.62
1:J:99:ARG:O	1:J:103:ARG:HG3	1.99	0.62
1:K:337:ASN:HD21	1:K:401:ASN:HD22	1.47	0.62
1:N:37:ARG:HB3	1:N:37:ARG:HH21	1.64	0.62
1:O:34:PHE:HE2	1:O:45:LEU:HG	1.64	0.62
1:P:37:ARG:HB3	1:P:37:ARG:HH21	1.62	0.62
1:R:585:GLU:C	1:R:587:PRO:HD3	2.18	0.62
1:U:34:PHE:HE2	1:U:45:LEU:HG	1.64	0.62
1:A:78:VAL:HG12	1:A:79:LEU:N	2.13	0.62
1:D:191:TYR:HE1	1:D:278:LYS:HZ3	1.47	0.62
1:E:48:TYR:O	1:E:49:THR:HB	1.98	0.62
1:H:99:ARG:O	1:H:103:ARG:HG3	1.99	0.62
1:I:161:ASN:C	1:I:161:ASN:HD22	2.03	0.62
1:I:144:ILE:HG12	1:I:447:TYR:CE1	2.34	0.62
1:L:144:ILE:HG12	1:L:447:TYR:CE1	2.34	0.62
1:L:546:THR:CG2	1:L:547:PRO:HD3	2.27	0.62
1:O:273:ARG:HH22	1:O:453:LEU:CD1	2.10	0.62
1:Q:15:PHE:HZ	1:Q:283:CYS:SG	2.22	0.62
1:U:158:TRP:HB3	1:U:173:CYS:CA	2.27	0.62
1:W:15:PHE:HZ	1:W:283:CYS:SG	2.22	0.62
1:X:94:LEU:HA	1:X:97:MSE:HE2	1.81	0.62
1:G:246:TYR:CD2	1:G:511:ARG:HB3	2.34	0.62
1:K:99:ARG:O	1:K:103:ARG:HG3	1.99	0.62
1:L:35:PHE:HE1	1:L:321:ARG:HH11	1.46	0.62
1:L:48:TYR:O	1:L:49:THR:HB	1.98	0.62
1:O:37:ARG:NH2	1:O:41:TRP:HB3	2.14	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:15:PHE:CE1	1:Q:283:CYS:HA	2.34	0.62
1:N:89:ASP:HA	1:V:561:ASP:CB	2.26	0.62
1:A:74:ASN:HB2	1:A:75:PRO:HD3	4.59	0.62
1:B:12:LEU:O	1:B:16:ASP:HB2	1.99	0.62
1:C:158:TRP:CE3	1:C:173:CYS:SG	2.88	0.62
1:C:35:PHE:HE1	1:C:321:ARG:HH11	1.46	0.62
1:D:12:LEU:O	1:D:16:ASP:HB2	1.99	0.62
1:D:372:TYR:CE2	1:F:348:LYS:HB2	2.34	0.62
1:H:546:THR:CG2	1:H:547:PRO:HD3	2.27	0.62
1:I:99:ARG:O	1:I:103:ARG:HG3	1.99	0.62
1:L:144:ILE:HG12	1:L:447:TYR:HE1	1.63	0.62
1:P:15:PHE:CZ	1:P:283:CYS:HA	2.35	0.62
1:Q:34:PHE:HE2	1:Q:45:LEU:HG	1.65	0.62
1:T:37:ARG:HB3	1:T:37:ARG:HH21	1.63	0.62
1:U:431:ALA:O	1:U:435:VAL:HG22	2.00	0.62
1:W:560:LEU:O	1:W:565:VAL:HG21	1.97	0.62
1:X:232:ALA:CB	1:X:269:ARG:H	2.12	0.62
1:A:12:LEU:O	1:A:16:ASP:HB2	1.99	0.62
1:C:337:ASN:HD21	1:C:401:ASN:HD22	1.47	0.62
1:C:546:THR:CG2	1:C:547:PRO:HD3	2.27	0.62
1:J:246:TYR:CD2	1:J:511:ARG:HB3	2.34	0.62
1:J:144:ILE:HG12	1:J:447:TYR:CE1	2.34	0.62
1:K:48:TYR:O	1:K:49:THR:HB	1.98	0.62
1:P:47:GLN:HG2	1:P:48:TYR:H	1.64	0.62
1:Q:12:LEU:O	1:Q:16:ASP:HB2	1.99	0.62
1:R:232:ALA:CB	1:R:269:ARG:H	2.12	0.62
1:V:78:VAL:HG22	1:V:444:LEU:HD21	1.81	0.62
1:A:246:TYR:CD2	1:A:511:ARG:HB3	2.34	0.62
1:A:556:TYR:OH	1:B:542:THR:HG21	2.00	0.62
1:E:12:LEU:O	1:E:16:ASP:HB2	1.99	0.62
1:F:161:ASN:C	1:F:161:ASN:HD22	2.03	0.62
1:J:337:ASN:HD21	1:J:401:ASN:HD22	1.47	0.62
1:R:440:MSE:O	1:R:444:LEU:HD22	2.00	0.62
1:V:26:ARG:NH2	1:V:30:LYS:HD3	2.13	0.62
1:W:273:ARG:NH2	1:W:453:LEU:HD11	2.11	0.62
1:D:108:LYS:HD2	1:F:438:LEU:HD11	1.82	0.62
1:D:158:TRP:CE3	1:D:173:CYS:SG	2.88	0.62
1:D:246:TYR:CD2	1:D:511:ARG:HB3	2.34	0.62
1:F:182:ASN:ND2	1:G:171:ARG:HH21	1.98	0.62
1:G:287:LEU:N	1:G:287:LEU:HD12	2.15	0.62
1:H:246:TYR:CD2	1:H:511:ARG:HB3	2.34	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:246:TYR:CD2	1:K:511:ARG:HB3	2.34	0.62
1:L:287:LEU:N	1:L:287:LEU:HD12	2.15	0.62
1:A:407:ALA:HB1	1:L:334:MSE:HE1	1.81	0.62
1:M:34:PHE:HE2	1:M:45:LEU:HG	1.65	0.62
1:R:158:TRP:HB3	1:R:173:CYS:CA	2.27	0.62
1:U:231:THR:HG21	1:U:249:ARG:HH11	1.64	0.62
1:C:144:ILE:HG12	1:C:447:TYR:HE1	1.63	0.62
1:C:161:ASN:HD22	1:C:161:ASN:C	2.03	0.62
1:F:35:PHE:HE2	1:F:324:LYS:HZ3	1.47	0.62
1:J:575:GLN:O	1:J:579:MSE:HG2	2.00	0.62
1:L:71:MSE:HE2	1:L:119:ILE:HD11	1.80	0.62
1:M:431:ALA:O	1:M:435:VAL:HG22	1.99	0.62
1:P:15:PHE:HZ	1:P:283:CYS:SG	2.22	0.62
1:T:231:THR:HG21	1:T:249:ARG:HH11	1.62	0.62
2:Y:34:LEU:O	2:Y:35:THR:HG22	2.00	0.62
2:Z:53:MET:HG2	2:Z:67:TYR:CD1	2.34	0.62
1:A:287:LEU:N	1:A:287:LEU:HD12	2.15	0.62
1:C:287:LEU:N	1:C:287:LEU:HD12	2.15	0.62
1:F:191:TYR:HE1	1:F:278:LYS:HZ3	1.45	0.62
1:F:330:ARG:O	1:F:334:MSE:HB2	2.00	0.62
1:I:12:LEU:O	1:I:16:ASP:HB2	1.99	0.62
1:J:12:LEU:O	1:J:16:ASP:HB2	1.99	0.62
1:N:276:VAL:HG23	1:N:293:ILE:HG23	1.81	0.62
1:V:210:PRO:HD2	1:V:211:TRP:CE3	2.35	0.62
1:V:34:PHE:HE2	1:V:45:LEU:HG	1.64	0.62
1:W:37:ARG:HB3	1:W:37:ARG:HH21	1.65	0.62
1:A:575:GLN:O	1:A:579:MSE:HG2	2.00	0.61
1:D:161:ASN:C	1:D:161:ASN:HD22	2.03	0.61
1:H:287:LEU:N	1:H:287:LEU:HD12	2.15	0.61
1:I:287:LEU:HD12	1:I:287:LEU:N	2.15	0.61
1:L:330:ARG:O	1:L:334:MSE:HB2	2.00	0.61
1:L:575:GLN:O	1:L:579:MSE:HG2	2.00	0.61
1:O:440:MSE:O	1:O:444:LEU:HD22	2.00	0.61
1:Q:138:THR:H	1:Q:143:VAL:HG22	1.63	0.61
1:S:444:LEU:C	1:S:446:THR:N	2.53	0.61
1:W:276:VAL:HG23	1:W:293:ILE:HG23	1.82	0.61
1:W:440:MSE:O	1:W:444:LEU:HD22	2.00	0.61
1:W:5:GLU:HG2	1:W:6:ASN:H	1.65	0.61
1:X:210:PRO:HD2	1:X:211:TRP:CE3	2.35	0.61
1:R:334:MSE:SE	1:X:404:MSE:HE1	2.50	0.61
2:Y:53:MET:HG2	2:Y:67:TYR:CD1	2.34	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Y:53:MET:O	2:Y:69:PHE:HE1	1.83	0.61
2:Z:34:LEU:O	2:Z:35:THR:HG22	2.00	0.61
1:B:287:LEU:HD12	1:B:287:LEU:N	2.15	0.61
1:C:41:TRP:HE3	1:C:42:ASP:CA	2.14	0.61
1:C:47:GLN:OE1	1:C:47:GLN:N	2.30	0.61
1:E:287:LEU:HD12	1:E:287:LEU:N	2.15	0.61
1:H:337:ASN:HD21	1:H:401:ASN:HD22	1.47	0.61
1:H:48:TYR:O	1:H:49:THR:HB	1.98	0.61
1:J:158:TRP:CE3	1:J:173:CYS:SG	2.88	0.61
1:A:398:PRO:HB3	1:L:395:PRO:HD2	1.81	0.61
1:M:560:LEU:O	1:M:565:VAL:HG21	1.98	0.61
1:N:5:GLU:HG2	1:N:6:ASN:H	1.65	0.61
1:Q:287:LEU:HD12	1:Q:287:LEU:N	2.16	0.61
1:Q:34:PHE:HZ	1:Q:328:ARG:HH22	1.40	0.61
3:P:719:HOH:O	1:Q:430:VAL:CG1	2.47	0.61
1:S:15:PHE:CE1	1:S:283:CYS:HA	2.35	0.61
1:T:15:PHE:HZ	1:T:283:CYS:SG	2.23	0.61
1:T:273:ARG:NH2	1:T:453:LEU:HD11	2.13	0.61
1:T:5:GLU:HG2	1:T:6:ASN:H	1.66	0.61
1:T:94:LEU:HA	1:T:97:MSE:HE2	1.81	0.61
1:B:575:GLN:O	1:B:579:MSE:HG2	2.00	0.61
1:B:99:ARG:O	1:B:103:ARG:HG3	1.99	0.61
1:C:330:ARG:O	1:C:334:MSE:HB2	2.00	0.61
1:C:78:VAL:HG12	1:C:79:LEU:N	2.13	0.61
1:E:330:ARG:O	1:E:334:MSE:HB2	2.00	0.61
1:E:546:THR:CG2	1:E:547:PRO:HD3	2.27	0.61
1:M:273:ARG:HH22	1:M:453:LEU:CD1	2.10	0.61
1:M:78:VAL:HG22	1:M:444:LEU:HD21	1.82	0.61
1:N:440:MSE:O	1:N:444:LEU:HD22	1.99	0.61
1:N:444:LEU:C	1:N:446:THR:N	2.53	0.61
1:M:89:ASP:HA	1:N:561:ASP:HB2	1.82	0.61
1:R:5:GLU:HG2	1:R:6:ASN:H	1.65	0.61
1:T:158:TRP:CE3	1:T:173:CYS:SG	2.87	0.61
1:U:210:PRO:HD2	1:U:211:TRP:CE3	2.36	0.61
1:V:128:LEU:HD12	1:V:446:THR:HG23	1.82	0.61
1:F:41:TRP:HZ3	1:F:42:ASP:HB3	1.61	0.61
1:H:78:VAL:HG12	1:H:79:LEU:N	2.13	0.61
1:I:337:ASN:HD21	1:I:401:ASN:HD22	1.47	0.61
1:I:575:GLN:O	1:I:579:MSE:HG2	2.00	0.61
1:L:246:TYR:CD2	1:L:511:ARG:HB3	2.34	0.61
1:N:273:ARG:NH2	1:N:453:LEU:HD11	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:15:PHE:CE1	1:O:283:CYS:HA	2.35	0.61
1:T:34:PHE:HE2	1:T:45:LEU:HG	1.64	0.61
1:U:444:LEU:C	1:U:446:THR:N	2.52	0.61
1:A:337:ASN:HD21	1:A:401:ASN:HD22	1.47	0.61
1:A:99:ARG:O	1:A:103:ARG:HG3	1.99	0.61
1:B:48:TYR:O	1:B:49:THR:HB	1.98	0.61
1:B:586:THR:N	1:B:587:PRO:HD3	2.16	0.61
1:E:586:THR:N	1:E:587:PRO:HD3	2.16	0.61
1:F:337:ASN:HD21	1:F:401:ASN:HD22	1.47	0.61
1:F:586:THR:N	1:F:587:PRO:HD3	2.16	0.61
1:G:161:ASN:HD22	1:G:161:ASN:C	2.03	0.61
1:G:35:PHE:HE1	1:G:321:ARG:HH11	1.46	0.61
1:H:158:TRP:CE3	1:H:173:CYS:SG	2.88	0.61
1:K:35:PHE:HE1	1:K:321:ARG:HH11	1.46	0.61
1:O:138:THR:H	1:O:143:VAL:HG22	1.66	0.61
1:O:78:VAL:HG22	1:O:444:LEU:HD21	1.83	0.61
1:R:37:ARG:NH2	1:R:41:TRP:HB3	2.15	0.61
1:R:34:PHE:HE2	1:R:45:LEU:HG	1.64	0.61
1:S:78:VAL:CG2	1:S:444:LEU:HD11	2.22	0.61
1:T:273:ARG:NH2	1:T:453:LEU:HD21	2.15	0.61
1:U:158:TRP:CH2	1:U:302:PRO:HG3	2.35	0.61
1:U:440:MSE:O	1:U:444:LEU:HD22	2.01	0.61
1:X:26:ARG:NH2	1:X:30:LYS:HD3	2.15	0.61
1:A:191:TYR:HE1	1:A:278:LYS:HZ3	1.48	0.61
1:B:161:ASN:C	1:B:161:ASN:HD22	2.03	0.61
1:B:337:ASN:HD21	1:B:401:ASN:HD22	1.47	0.61
1:C:586:THR:N	1:C:587:PRO:HD3	2.16	0.61
1:D:330:ARG:O	1:D:334:MSE:HB2	2.00	0.61
1:D:586:THR:N	1:D:587:PRO:HD3	2.16	0.61
1:E:575:GLN:O	1:E:579:MSE:HG2	2.00	0.61
1:H:330:ARG:O	1:H:334:MSE:HB2	2.00	0.61
1:I:586:THR:N	1:I:587:PRO:HD3	2.16	0.61
1:K:161:ASN:HD22	1:K:161:ASN:C	2.03	0.61
1:K:395:PRO:HD2	1:L:398:PRO:HB3	1.83	0.61
1:K:575:GLN:O	1:K:579:MSE:HG2	2.00	0.61
1:L:586:THR:N	1:L:587:PRO:HD3	2.16	0.61
1:M:273:ARG:NH2	1:M:453:LEU:HD11	2.14	0.61
1:N:15:PHE:CZ	1:N:283:CYS:HA	2.36	0.61
1:P:440:MSE:O	1:P:444:LEU:HD22	2.00	0.61
1:Q:78:VAL:CG2	1:Q:444:LEU:HD11	2.23	0.61
1:Q:47:GLN:HG2	1:Q:48:TYR:H	1.66	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:12:LEU:O	1:R:16:ASP:HB2	2.00	0.61
1:S:5:GLU:HG2	1:S:6:ASN:H	1.65	0.61
1:V:273:ARG:NH2	1:V:453:LEU:HD11	2.14	0.61
1:W:78:VAL:CG2	1:W:444:LEU:HD11	2.21	0.61
1:F:287:LEU:HD12	1:F:287:LEU:N	2.15	0.61
1:G:586:THR:N	1:G:587:PRO:HD3	2.16	0.61
1:I:330:ARG:O	1:I:334:MSE:HB2	2.00	0.61
1:J:182:ASN:ND2	1:K:171:ARG:HH21	1.98	0.61
1:J:41:TRP:HE3	1:J:42:ASP:CA	2.14	0.61
1:K:287:LEU:HD12	1:K:287:LEU:N	2.15	0.61
1:K:47:GLN:OE1	1:K:47:GLN:N	2.30	0.61
1:M:5:GLU:HG2	1:M:6:ASN:H	1.66	0.61
1:Q:210:PRO:HD2	1:Q:211:TRP:CE3	2.36	0.61
1:R:287:LEU:N	1:R:287:LEU:HD12	2.15	0.61
1:S:210:PRO:HD2	1:S:211:TRP:CE3	2.35	0.61
1:S:287:LEU:N	1:S:287:LEU:HD12	2.15	0.61
1:T:15:PHE:CZ	1:T:283:CYS:HA	2.35	0.61
1:T:560:LEU:O	1:T:565:VAL:HG21	1.99	0.61
1:U:128:LEU:HD12	1:U:446:THR:HG23	1.82	0.61
1:U:5:GLU:HG2	1:U:6:ASN:H	1.65	0.61
1:V:158:TRP:CE3	1:V:173:CYS:SG	2.86	0.61
1:W:210:PRO:HD2	1:W:211:TRP:CE3	2.36	0.61
1:D:337:ASN:HD21	1:D:401:ASN:HD22	1.47	0.61
1:E:161:ASN:HD22	1:E:161:ASN:C	2.03	0.61
1:H:41:TRP:HE3	1:H:42:ASP:CA	2.14	0.61
1:L:161:ASN:C	1:L:161:ASN:HD22	2.03	0.61
1:N:15:PHE:HZ	1:N:283:CYS:SG	2.18	0.61
1:N:41:TRP:CE3	1:N:42:ASP:HB3	2.36	0.61
1:O:5:GLU:HG2	1:O:6:ASN:H	1.65	0.61
1:P:564:GLY:HA2	1:Q:554:LEU:HD21	1.81	0.61
1:R:158:TRP:CH2	1:R:302:PRO:HG3	2.36	0.61
1:V:273:ARG:NH2	1:V:453:LEU:HD21	2.16	0.61
1:X:273:ARG:NH2	1:X:453:LEU:HD11	2.13	0.61
1:D:287:LEU:N	1:D:287:LEU:HD12	2.15	0.61
1:D:35:PHE:HE2	1:D:324:LYS:HZ3	1.48	0.61
1:E:233:PHE:CE2	1:E:249:ARG:HD3	2.36	0.61
1:H:233:PHE:CE2	1:H:249:ARG:HD3	2.36	0.61
1:J:233:PHE:CE2	1:J:249:ARG:HD3	2.36	0.61
1:J:287:LEU:N	1:J:287:LEU:HD12	2.15	0.61
1:M:246:TYR:CD2	1:M:511:ARG:HB2	2.36	0.61
1:M:15:PHE:CE1	1:M:283:CYS:HA	2.35	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:78:VAL:HG22	1:N:444:LEU:HD21	1.83	0.61
1:O:128:LEU:HD12	1:O:446:THR:HG23	1.83	0.61
1:P:5:GLU:HG2	1:P:6:ASN:H	1.65	0.61
1:Q:444:LEU:C	1:Q:446:THR:N	2.53	0.61
1:T:47:GLN:HG2	1:T:48:TYR:H	1.65	0.61
1:V:440:MSE:O	1:V:444:LEU:HD22	2.00	0.61
1:X:5:GLU:HG2	1:X:6:ASN:H	1.65	0.61
1:A:330:ARG:O	1:A:334:MSE:HB2	2.00	0.61
1:G:330:ARG:O	1:G:334:MSE:HB2	2.00	0.61
1:N:47:GLN:HG2	1:N:48:TYR:H	1.66	0.61
1:P:41:TRP:CE3	1:P:42:ASP:HB3	2.36	0.61
1:R:15:PHE:CZ	1:R:283:CYS:HA	2.36	0.61
1:S:379:GLU:O	1:S:380:ASN:HB2	2.01	0.61
1:U:15:PHE:CE1	1:U:283:CYS:HA	2.36	0.61
1:V:15:PHE:CZ	1:V:283:CYS:HA	2.36	0.61
1:W:444:LEU:C	1:W:446:THR:N	2.54	0.61
1:X:34:PHE:HE2	1:X:45:LEU:HG	1.64	0.61
1:H:575:GLN:O	1:H:579:MSE:HG2	2.00	0.60
1:M:210:PRO:HD2	1:M:211:TRP:CE3	2.36	0.60
1:M:128:LEU:HD12	1:M:446:THR:HG23	1.82	0.60
1:M:47:GLN:HG2	1:M:48:TYR:H	1.65	0.60
1:R:78:VAL:HG22	1:R:444:LEU:HD21	1.82	0.60
1:T:334:MSE:SE	1:W:404:MSE:HE1	2.51	0.60
1:U:41:TRP:CE3	1:U:42:ASP:HB3	2.36	0.60
1:N:390:ALA:CB	1:V:387:GLN:HB3	2.30	0.60
1:X:287:LEU:N	1:X:287:LEU:HD12	2.16	0.60
1:A:234:ILE:CG1	1:A:267:ALA:HB3	2.32	0.60
1:B:234:ILE:CG1	1:B:267:ALA:HB3	2.31	0.60
1:C:233:PHE:CE2	1:C:249:ARG:HD3	2.36	0.60
1:H:586:THR:N	1:H:587:PRO:HD3	2.16	0.60
1:I:233:PHE:CE2	1:I:249:ARG:HD3	2.36	0.60
1:I:372:TYR:CE2	1:J:348:LYS:HB2	2.35	0.60
1:K:586:THR:N	1:K:587:PRO:HD3	2.16	0.60
1:L:234:ILE:CG1	1:L:267:ALA:HB3	2.32	0.60
1:L:233:PHE:CE2	1:L:249:ARG:HD3	2.36	0.60
1:M:542:THR:HG21	1:N:556:TYR:OH	2.01	0.60
1:O:237:ASP:H	1:O:243:PRO:HA	1.65	0.60
1:O:276:VAL:HG23	1:O:293:ILE:HG23	1.83	0.60
1:P:210:PRO:HD2	1:P:211:TRP:CE3	2.36	0.60
1:P:287:LEU:N	1:P:287:LEU:HD12	2.15	0.60
1:P:34:PHE:HE2	1:P:45:LEU:HG	1.65	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:210:PRO:HD2	1:R:211:TRP:CE3	2.36	0.60
1:T:37:ARG:NH2	1:T:41:TRP:HB3	2.15	0.60
1:T:41:TRP:CE3	1:T:42:ASP:HB3	2.37	0.60
1:T:564:GLY:HA2	1:W:554:LEU:HD21	1.82	0.60
1:S:542:THR:HG21	1:U:556:TYR:OH	2.01	0.60
1:V:165:MSE:HE3	1:V:304:PHE:HB2	1.82	0.60
1:V:287:LEU:HD12	1:V:287:LEU:N	2.16	0.60
1:B:330:ARG:O	1:B:334:MSE:HB2	2.00	0.60
1:J:234:ILE:CG1	1:J:267:ALA:HB3	2.31	0.60
1:J:586:THR:N	1:J:587:PRO:HD3	2.16	0.60
1:K:561:ASP:CB	1:L:89:ASP:HA	2.28	0.60
1:M:37:ARG:NH2	1:M:41:TRP:HB3	2.16	0.60
1:O:287:LEU:N	1:O:287:LEU:HD12	2.16	0.60
1:O:246:TYR:CD2	1:O:511:ARG:HB2	2.36	0.60
1:P:246:TYR:CD2	1:P:511:ARG:HB2	2.36	0.60
1:Q:37:ARG:NH2	1:Q:41:TRP:HB3	2.17	0.60
1:S:276:VAL:HG23	1:S:293:ILE:HG23	1.83	0.60
1:V:276:VAL:HG23	1:V:293:ILE:HG23	1.83	0.60
1:W:273:ARG:NH2	1:W:453:LEU:HD21	2.16	0.60
1:C:154:SER:O	1:C:204:PRO:HB3	2.02	0.60
1:O:15:PHE:CZ	1:O:283:CYS:HA	2.36	0.60
1:P:273:ARG:NH2	1:P:453:LEU:HD11	2.14	0.60
1:Q:15:PHE:CZ	1:Q:283:CYS:HA	2.37	0.60
1:R:158:TRP:O	1:R:160:SER:N	2.34	0.60
1:T:78:VAL:CG2	1:T:444:LEU:HD11	2.22	0.60
1:T:577:ILE:HA	1:T:582:LYS:HB3	1.83	0.60
1:V:246:TYR:CD2	1:V:511:ARG:HB2	2.35	0.60
1:A:586:THR:N	1:A:587:PRO:HD3	2.16	0.60
1:B:233:PHE:CE2	1:B:249:ARG:HD3	2.36	0.60
1:D:575:GLN:O	1:D:579:MSE:HG2	2.00	0.60
1:E:199:PRO:HB3	1:E:282:THR:HG22	1.84	0.60
1:F:154:SER:O	1:F:204:PRO:HB3	2.02	0.60
1:F:575:GLN:O	1:F:579:MSE:HG2	2.00	0.60
1:G:154:SER:O	1:G:204:PRO:HB3	2.02	0.60
1:I:41:TRP:HE3	1:I:42:ASP:CA	2.14	0.60
1:K:330:ARG:O	1:K:334:MSE:HB2	2.00	0.60
1:L:154:SER:O	1:L:204:PRO:HB3	2.02	0.60
1:M:276:VAL:HG23	1:M:293:ILE:HG23	1.82	0.60
1:M:440:MSE:O	1:M:444:LEU:HD22	2.01	0.60
1:P:273:ARG:HH22	1:P:453:LEU:CD1	2.11	0.60
1:R:78:VAL:HG11	1:R:444:LEU:HG	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:37:ARG:NH2	1:V:41:TRP:HB3	2.15	0.60
1:W:41:TRP:CE3	1:W:42:ASP:HB3	2.37	0.60
1:A:395:PRO:HD2	1:B:398:PRO:HB3	1.84	0.60
1:B:154:SER:O	1:B:204:PRO:HB3	2.02	0.60
1:C:575:GLN:O	1:C:579:MSE:HG2	2.00	0.60
1:D:233:PHE:CE2	1:D:249:ARG:HD3	2.36	0.60
1:E:158:TRP:CE3	1:E:173:CYS:SG	2.88	0.60
1:C:567:MSE:SE	1:E:576:LEU:HD13	2.52	0.60
1:H:161:ASN:HD22	1:H:161:ASN:C	2.03	0.60
1:H:154:SER:O	1:H:204:PRO:HB3	2.02	0.60
1:J:598:GLN:HB2	1:J:601:GLN:HB2	1.84	0.60
1:N:379:GLU:O	1:N:380:ASN:HB2	2.02	0.60
1:O:5:GLU:HG2	1:O:6:ASN:N	2.16	0.60
1:Q:128:LEU:HD12	1:Q:446:THR:HG23	1.83	0.60
1:Q:236:GLN:CB	1:Q:265:LYS:HG2	2.32	0.60
1:R:15:PHE:HZ	1:R:283:CYS:SG	2.24	0.60
1:S:246:TYR:CD2	1:S:511:ARG:HB2	2.36	0.60
1:S:47:GLN:HG2	1:S:48:TYR:H	1.66	0.60
1:T:210:PRO:HD2	1:T:211:TRP:CE3	2.36	0.60
1:T:236:GLN:CB	1:T:265:LYS:HG2	2.32	0.60
1:T:78:VAL:HG22	1:T:444:LEU:HD21	1.84	0.60
1:U:577:ILE:HA	1:U:582:LYS:HB3	1.84	0.60
1:W:47:GLN:HG2	1:W:48:TYR:H	1.67	0.60
1:X:37:ARG:NH2	1:X:41:TRP:HB3	2.17	0.60
1:X:440:MSE:O	1:X:444:LEU:HD22	2.02	0.60
2:Z:53:MET:O	2:Z:69:PHE:HE1	1.83	0.60
1:A:154:SER:O	1:A:204:PRO:HB3	2.02	0.60
1:A:233:PHE:CE2	1:A:249:ARG:HD3	2.36	0.60
1:A:41:TRP:HE3	1:A:42:ASP:CA	2.14	0.60
1:C:598:GLN:HB2	1:C:601:GLN:HB2	1.84	0.60
1:F:199:PRO:HB3	1:F:282:THR:HG22	1.84	0.60
1:F:234:ILE:CG1	1:F:267:ALA:HB3	2.32	0.60
1:G:108:LYS:HD2	1:H:438:LEU:HD11	1.82	0.60
1:G:41:TRP:HE3	1:G:42:ASP:CA	2.14	0.60
1:G:598:GLN:HB2	1:G:601:GLN:HB2	1.84	0.60
1:I:154:SER:O	1:I:204:PRO:HB3	2.02	0.60
1:J:161:ASN:C	1:J:161:ASN:HD22	2.03	0.60
1:N:210:PRO:HD2	1:N:211:TRP:CE3	2.35	0.60
1:S:236:GLN:CB	1:S:265:LYS:HG2	2.32	0.60
1:S:34:PHE:HE2	1:S:45:LEU:HG	1.65	0.60
1:N:398:PRO:HB3	1:V:395:PRO:HD2	1.84	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:15:PHE:CE1	1:X:283:CYS:HA	2.36	0.60
1:X:431:ALA:O	1:X:435:VAL:HG22	2.02	0.60
1:C:577:ILE:HA	1:C:582:LYS:HB3	1.84	0.60
1:D:154:SER:O	1:D:204:PRO:HB3	2.02	0.60
1:N:236:GLN:CB	1:N:265:LYS:HG2	2.32	0.60
1:O:210:PRO:HD2	1:O:211:TRP:CE3	2.36	0.60
1:S:577:ILE:HA	1:S:582:LYS:HB3	1.84	0.60
1:U:5:GLU:HG2	1:U:6:ASN:N	2.17	0.60
1:X:237:ASP:H	1:X:243:PRO:HA	1.67	0.60
1:A:89:ASP:HA	1:L:561:ASP:CB	2.25	0.60
1:G:337:ASN:HD21	1:G:401:ASN:HD22	1.47	0.60
1:G:575:GLN:O	1:G:579:MSE:HG2	2.00	0.60
1:J:199:PRO:HB3	1:J:282:THR:HG22	1.84	0.60
1:K:154:SER:O	1:K:204:PRO:HB3	2.02	0.60
1:N:390:ALA:HB2	1:V:387:GLN:HB2	1.84	0.60
1:N:246:TYR:CD2	1:N:511:ARG:HB2	2.37	0.60
1:P:165:MSE:HE3	1:P:304:PHE:HB2	1.84	0.60
1:P:37:ARG:NH2	1:P:41:TRP:HB3	2.17	0.60
1:P:273:ARG:NH2	1:P:453:LEU:HD21	2.16	0.60
1:R:26:ARG:NH2	1:R:30:LYS:HD3	2.16	0.60
1:S:158:TRP:CE3	1:S:173:CYS:SG	2.87	0.60
1:U:236:GLN:CB	1:U:265:LYS:HG2	2.32	0.60
1:U:276:VAL:HG23	1:U:293:ILE:HG23	1.83	0.60
1:V:47:GLN:HG2	1:V:48:TYR:H	1.67	0.60
1:W:5:GLU:HG2	1:W:6:ASN:N	2.17	0.60
1:X:154:SER:O	1:X:204:PRO:HB3	2.02	0.60
1:X:444:LEU:C	1:X:446:THR:N	2.53	0.60
1:B:54:ARG:HB2	2:Z:146:GLY:HA3	1.83	0.60
1:F:233:PHE:CE2	1:F:249:ARG:HD3	2.36	0.60
1:I:199:PRO:HB3	1:I:282:THR:HG22	1.84	0.60
1:K:598:GLN:HB2	1:K:601:GLN:HB2	1.84	0.60
1:M:287:LEU:N	1:M:287:LEU:HD12	2.16	0.60
1:O:158:TRP:CE3	1:O:173:CYS:SG	2.87	0.60
1:O:41:TRP:CE3	1:O:42:ASP:HB3	2.37	0.60
1:O:47:GLN:HG2	1:O:48:TYR:H	1.67	0.60
1:Q:41:TRP:CE3	1:Q:42:ASP:HB3	2.37	0.60
1:R:24:GLU:C	1:R:26:ARG:N	2.55	0.60
1:S:41:TRP:CE3	1:S:42:ASP:HB3	2.36	0.60
1:U:246:TYR:CD2	1:U:511:ARG:HB2	2.36	0.60
1:V:5:GLU:HG2	1:V:6:ASN:N	2.17	0.60
2:Y:137:TYR:CD1	2:Y:141:MET:HG2	2.37	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:161:ASN:C	1:A:161:ASN:HD22	2.03	0.59
1:B:444:LEU:O	1:B:448:VAL:HG23	2.02	0.59
1:B:598:GLN:HB2	1:B:601:GLN:HB2	1.84	0.59
1:C:199:PRO:HB3	1:C:282:THR:HG22	1.84	0.59
1:D:234:ILE:CG1	1:D:267:ALA:HB3	2.32	0.59
1:E:598:GLN:HB2	1:E:601:GLN:HB2	1.84	0.59
1:G:233:PHE:CE2	1:G:249:ARG:HD3	2.36	0.59
1:J:330:ARG:O	1:J:334:MSE:HB2	2.00	0.59
1:K:199:PRO:HB3	1:K:282:THR:HG22	1.84	0.59
1:L:41:TRP:HE3	1:L:42:ASP:CA	2.14	0.59
1:L:598:GLN:HB2	1:L:601:GLN:HB2	1.84	0.59
1:M:15:PHE:CZ	1:M:283:CYS:HA	2.37	0.59
1:N:158:TRP:CE3	1:N:173:CYS:SG	2.86	0.59
1:P:15:PHE:HZ	1:P:283:CYS:HG	1.49	0.59
1:P:237:ASP:H	1:P:243:PRO:HA	1.65	0.59
1:P:554:LEU:HD12	1:P:557:PHE:HD2	1.66	0.59
1:P:5:GLU:HG2	1:P:6:ASN:N	2.17	0.59
1:S:37:ARG:NH2	1:S:41:TRP:HB3	2.16	0.59
1:S:560:LEU:HD22	1:T:82:PRO:HG2	1.84	0.59
1:V:138:THR:H	1:V:143:VAL:HG22	1.67	0.59
1:V:273:ARG:HH22	1:V:453:LEU:HD21	1.67	0.59
1:B:26:ARG:NH2	1:B:30:LYS:HD3	2.17	0.59
1:E:154:SER:O	1:E:204:PRO:HB3	2.02	0.59
1:I:234:ILE:CG1	1:I:267:ALA:HB3	2.32	0.59
1:K:233:PHE:CE2	1:K:249:ARG:HD3	2.36	0.59
1:L:199:PRO:HB3	1:L:282:THR:HG22	1.84	0.59
1:N:24:GLU:C	1:N:26:ARG:N	2.56	0.59
1:O:15:PHE:HZ	1:O:283:CYS:SG	2.25	0.59
1:Q:5:GLU:HG2	1:Q:6:ASN:H	1.65	0.59
1:S:78:VAL:HG22	1:S:444:LEU:HD21	1.84	0.59
1:T:5:GLU:HG2	1:T:6:ASN:N	2.17	0.59
1:U:237:ASP:H	1:U:243:PRO:HA	1.66	0.59
1:W:15:PHE:CZ	1:W:283:CYS:HA	2.36	0.59
1:X:5:GLU:HG2	1:X:6:ASN:N	2.17	0.59
1:X:78:VAL:HG11	1:X:444:LEU:HG	1.83	0.59
1:H:234:ILE:CG1	1:H:267:ALA:HB3	2.32	0.59
1:J:154:SER:O	1:J:204:PRO:HB3	2.02	0.59
1:M:165:MSE:HE3	1:M:304:PHE:HB2	1.84	0.59
1:O:236:GLN:CB	1:O:265:LYS:HG2	2.32	0.59
1:Q:5:GLU:HG2	1:Q:6:ASN:N	2.17	0.59
1:S:5:GLU:HG2	1:S:6:ASN:N	2.17	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:287:LEU:HD12	1:U:287:LEU:N	2.16	0.59
1:X:128:LEU:HD12	1:X:446:THR:HG23	1.83	0.59
2:Y:28:VAL:HG22	2:Y:93:PHE:O	2.02	0.59
1:C:234:ILE:CG1	1:C:267:ALA:HB3	2.32	0.59
1:E:234:ILE:CG1	1:E:267:ALA:HB3	2.32	0.59
1:E:236:GLN:CB	1:E:265:LYS:HZ3	2.15	0.59
1:E:577:ILE:HA	1:E:582:LYS:HB3	1.84	0.59
1:F:41:TRP:HE3	1:F:42:ASP:CA	2.14	0.59
1:G:234:ILE:CG1	1:G:267:ALA:HB3	2.32	0.59
1:I:444:LEU:O	1:I:448:VAL:HG23	2.03	0.59
1:N:5:GLU:HG2	1:N:6:ASN:N	2.17	0.59
1:P:78:VAL:HG22	1:P:444:LEU:HD21	1.85	0.59
1:S:15:PHE:CZ	1:S:283:CYS:HA	2.38	0.59
1:U:273:ARG:NH2	1:U:453:LEU:HD11	2.11	0.59
1:N:390:ALA:HB2	1:V:387:GLN:CB	2.32	0.59
1:W:158:TRP:CH2	1:W:302:PRO:HG3	2.36	0.59
1:W:78:VAL:HG22	1:W:444:LEU:HD21	1.84	0.59
2:Z:28:VAL:HG22	2:Z:93:PHE:O	2.02	0.59
1:A:26:ARG:NH2	1:A:30:LYS:HD3	2.17	0.59
1:D:26:ARG:NH2	1:D:30:LYS:HD3	2.17	0.59
1:H:264:ILE:O	1:H:265:LYS:HD3	2.03	0.59
1:J:26:ARG:NH2	1:J:30:LYS:HD3	2.18	0.59
1:J:444:LEU:O	1:J:448:VAL:HG23	2.02	0.59
1:K:26:ARG:NH2	1:K:30:LYS:HD3	2.17	0.59
1:M:138:THR:H	1:M:143:VAL:HG22	1.67	0.59
1:M:158:TRP:CE3	1:M:173:CYS:SG	2.87	0.59
1:O:273:ARG:NH2	1:O:453:LEU:HD11	2.14	0.59
1:O:431:ALA:O	1:O:435:VAL:HG22	2.01	0.59
1:O:564:GLY:O	1:P:554:LEU:HD21	2.02	0.59
1:R:5:GLU:HG2	1:R:6:ASN:N	2.17	0.59
1:S:440:MSE:O	1:S:444:LEU:HD22	2.02	0.59
1:S:273:ARG:NH2	1:S:453:LEU:HD11	2.13	0.59
1:T:379:GLU:O	1:T:380:ASN:HB2	2.03	0.59
1:V:554:LEU:HD21	1:W:564:GLY:HA2	1.84	0.59
1:W:237:ASP:H	1:W:243:PRO:HA	1.67	0.59
1:W:273:ARG:HH22	1:W:453:LEU:HD21	1.68	0.59
1:W:78:VAL:HG12	1:W:79:LEU:H	1.67	0.59
1:C:26:ARG:NH2	1:C:30:LYS:HD3	2.17	0.59
1:C:444:LEU:O	1:C:448:VAL:HG23	2.03	0.59
1:E:444:LEU:O	1:E:448:VAL:HG23	2.03	0.59
1:F:577:ILE:HA	1:F:582:LYS:HB3	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:577:ILE:HA	1:H:582:LYS:HB3	1.84	0.59
1:H:598:GLN:HB2	1:H:601:GLN:HB2	1.84	0.59
1:L:384:LEU:O	1:L:386:THR:N	2.36	0.59
1:M:158:TRP:CH2	1:M:302:PRO:HG3	2.38	0.59
1:N:287:LEU:HD12	1:N:287:LEU:N	2.16	0.59
1:Q:273:ARG:NH2	1:Q:453:LEU:HD21	2.18	0.59
1:Q:99:ARG:O	1:Q:103:ARG:HG3	2.02	0.59
1:U:138:THR:H	1:U:143:VAL:HG22	1.68	0.59
1:U:15:PHE:CZ	1:U:283:CYS:HA	2.38	0.59
2:Z:137:TYR:CD1	2:Z:141:MET:HG2	2.37	0.59
1:A:577:ILE:HA	1:A:582:LYS:HB3	1.84	0.59
1:B:158:TRP:CE3	1:B:173:CYS:SG	2.88	0.59
1:B:264:ILE:O	1:B:265:LYS:HD3	2.03	0.59
1:D:199:PRO:HB3	1:D:282:THR:HG22	1.84	0.59
1:D:236:GLN:CB	1:D:265:LYS:HZ3	2.15	0.59
1:D:444:LEU:O	1:D:448:VAL:HG23	2.03	0.59
1:E:191:TYR:HE1	1:E:278:LYS:HZ3	1.50	0.59
1:E:384:LEU:H	1:E:384:LEU:HD22	1.68	0.59
1:F:384:LEU:H	1:F:384:LEU:HD22	1.68	0.59
1:I:26:ARG:NH2	1:I:30:LYS:HD3	2.17	0.59
1:K:234:ILE:CG1	1:K:267:ALA:HB3	2.32	0.59
1:M:5:GLU:HG2	1:M:6:ASN:N	2.17	0.59
1:N:390:ALA:CB	1:V:387:GLN:CB	2.80	0.59
1:N:273:ARG:NH2	1:N:453:LEU:HD21	2.18	0.59
1:P:236:GLN:CB	1:P:265:LYS:HG2	2.32	0.59
1:P:86:ALA:HB2	1:P:515:GLU:HG3	1.85	0.59
1:S:237:ASP:H	1:S:243:PRO:HA	1.66	0.59
1:T:138:THR:H	1:T:143:VAL:HG22	1.67	0.59
1:U:158:TRP:CE3	1:U:173:CYS:SG	2.86	0.59
1:D:158:TRP:O	1:D:160:SER:N	2.36	0.59
1:E:34:PHE:HZ	1:E:328:ARG:HH22	0.80	0.59
1:G:556:TYR:OH	1:H:542:THR:HG21	2.03	0.59
1:H:158:TRP:O	1:H:160:SER:N	2.36	0.59
1:H:26:ARG:NH2	1:H:30:LYS:HD3	2.17	0.59
1:H:334:MSE:SE	1:I:404:MSE:HE1	2.53	0.59
1:J:384:LEU:O	1:J:386:THR:N	2.36	0.59
1:K:264:ILE:O	1:K:265:LYS:HD3	2.03	0.59
1:K:384:LEU:O	1:K:386:THR:N	2.36	0.59
1:M:158:TRP:HB3	1:M:173:CYS:CA	2.28	0.59
1:N:431:ALA:O	1:N:435:VAL:HG22	2.03	0.59
1:O:24:GLU:C	1:O:26:ARG:N	2.56	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:273:ARG:NH2	1:O:453:LEU:HD21	2.17	0.59
1:R:41:TRP:CE3	1:R:42:ASP:HB3	2.37	0.59
1:R:554:LEU:HD12	1:R:557:PHE:HD2	1.68	0.59
1:S:89:ASP:HA	1:U:561:ASP:HB2	1.85	0.59
1:U:15:PHE:HZ	1:U:283:CYS:SG	2.25	0.59
1:U:78:VAL:HG22	1:U:444:LEU:HD21	1.84	0.59
1:V:5:GLU:HG2	1:V:6:ASN:H	1.65	0.59
1:X:236:GLN:CB	1:X:265:LYS:HG2	2.32	0.59
1:X:41:TRP:CE3	1:X:42:ASP:HB3	2.36	0.59
2:Y:42:MET:HE3	2:Y:78:GLU:OE1	2.03	0.59
1:B:34:PHE:HE1	1:B:324:LYS:HZ2	1.44	0.59
1:D:384:LEU:O	1:D:386:THR:N	2.36	0.59
1:K:49:THR:CG2	1:K:49:THR:O	2.51	0.59
1:L:384:LEU:HD22	1:L:384:LEU:H	1.68	0.59
1:M:561:ASP:OD2	1:O:92:ASP:HB3	2.02	0.59
1:M:82:PRO:HG2	1:N:560:LEU:HD22	1.84	0.59
1:N:165:MSE:HE3	1:N:304:PHE:HB2	1.85	0.59
1:P:379:GLU:O	1:P:380:ASN:HB2	2.03	0.59
1:Q:237:ASP:H	1:Q:243:PRO:HA	1.67	0.59
1:V:236:GLN:CB	1:V:265:LYS:HG2	2.32	0.59
1:W:246:TYR:CD2	1:W:511:ARG:HB2	2.38	0.59
1:A:384:LEU:O	1:A:386:THR:N	2.36	0.59
1:A:49:THR:O	1:A:49:THR:CG2	2.51	0.59
1:C:158:TRP:O	1:C:160:SER:N	2.36	0.59
1:D:598:GLN:HB2	1:D:601:GLN:HB2	1.84	0.59
1:E:173:CYS:SG	1:E:298:ILE:HD13	2.43	0.59
1:D:92:ASP:HB3	1:E:561:ASP:OD2	2.03	0.59
1:F:115:VAL:HA	1:F:118:GLN:HB3	1.85	0.59
1:G:26:ARG:NH2	1:G:30:LYS:HD3	2.17	0.59
1:G:384:LEU:O	1:G:386:THR:N	2.36	0.59
1:H:384:LEU:O	1:H:386:THR:N	2.36	0.59
1:I:158:TRP:O	1:I:160:SER:N	2.36	0.59
1:J:49:THR:CG2	1:J:49:THR:O	2.51	0.59
1:K:50:THR:HG21	1:K:54:ARG:NH2	2.18	0.59
1:M:236:GLN:CB	1:M:265:LYS:HG2	2.32	0.59
3:O:719:HOH:O	1:P:430:VAL:CG1	2.51	0.59
1:Q:246:TYR:CD2	1:Q:511:ARG:HB2	2.36	0.59
1:R:128:LEU:HD12	1:R:446:THR:HG23	1.85	0.59
1:U:24:GLU:C	1:U:26:ARG:N	2.56	0.59
1:U:379:GLU:O	1:U:380:ASN:HB2	2.03	0.59
1:V:41:TRP:CE3	1:V:42:ASP:HB3	2.38	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:390:ALA:HB2	1:W:387:GLN:HB2	1.83	0.59
1:D:577:ILE:HA	1:D:582:LYS:HB3	1.84	0.58
1:E:26:ARG:NH2	1:E:30:LYS:HD3	2.17	0.58
1:F:264:ILE:O	1:F:265:LYS:HD3	2.03	0.58
1:G:173:CYS:SG	1:G:298:ILE:HD13	2.43	0.58
1:H:444:LEU:O	1:H:448:VAL:HG23	2.03	0.58
1:J:50:THR:HG21	1:J:54:ARG:NH2	2.18	0.58
1:K:384:LEU:HD22	1:K:384:LEU:H	1.68	0.58
1:L:264:ILE:O	1:L:265:LYS:HD3	2.03	0.58
1:M:199:PRO:HB3	1:M:282:THR:HG22	1.85	0.58
1:O:78:VAL:CG2	1:O:444:LEU:HD11	2.23	0.58
1:S:554:LEU:HD12	1:S:557:PHE:HD2	1.68	0.58
1:T:444:LEU:C	1:T:446:THR:N	2.55	0.58
1:W:24:GLU:C	1:W:26:ARG:N	2.56	0.58
1:X:246:TYR:CD2	1:X:511:ARG:HB2	2.36	0.58
1:A:563:LYS:HD3	1:B:557:PHE:CE2	2.38	0.58
1:A:598:GLN:HB2	1:A:601:GLN:HB2	1.84	0.58
1:B:158:TRP:O	1:B:160:SER:N	2.36	0.58
1:B:577:ILE:HA	1:B:582:LYS:HB3	1.84	0.58
1:F:158:TRP:O	1:F:160:SER:N	2.36	0.58
1:F:444:LEU:O	1:F:448:VAL:HG23	2.03	0.58
1:G:158:TRP:O	1:G:160:SER:N	2.36	0.58
1:I:384:LEU:H	1:I:384:LEU:HD22	1.68	0.58
1:I:384:LEU:O	1:I:386:THR:N	2.36	0.58
1:I:598:GLN:HB2	1:I:601:GLN:HB2	1.84	0.58
1:J:115:VAL:HA	1:J:118:GLN:HB3	1.85	0.58
1:J:158:TRP:O	1:J:160:SER:N	2.36	0.58
1:A:438:LEU:HD11	1:L:108:LYS:HD2	1.85	0.58
1:L:26:ARG:NH2	1:L:30:LYS:HD3	2.17	0.58
1:N:586:THR:N	1:N:587:PRO:HD3	2.18	0.58
1:O:379:GLU:O	1:O:380:ASN:HB2	2.03	0.58
1:O:444:LEU:C	1:O:446:THR:N	2.55	0.58
1:P:273:ARG:HH22	1:P:453:LEU:HD21	1.66	0.58
1:P:276:VAL:HG23	1:P:293:ILE:HG23	1.85	0.58
1:Q:440:MSE:O	1:Q:444:LEU:HD22	2.03	0.58
1:T:273:ARG:HH22	1:T:453:LEU:HD21	1.66	0.58
1:A:158:TRP:O	1:A:160:SER:N	2.36	0.58
1:B:199:PRO:HB3	1:B:282:THR:HG22	1.84	0.58
1:D:264:ILE:O	1:D:265:LYS:HD3	2.03	0.58
1:E:384:LEU:O	1:E:386:THR:N	2.36	0.58
1:F:26:ARG:NH2	1:F:30:LYS:HD3	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:598:GLN:HB2	1:F:601:GLN:HB2	1.84	0.58
1:G:389:LEU:H	1:G:389:LEU:HD12	1.68	0.58
1:I:49:THR:O	1:I:49:THR:CG2	2.51	0.58
1:J:384:LEU:HD22	1:J:384:LEU:H	1.68	0.58
1:K:158:TRP:O	1:K:160:SER:N	2.36	0.58
1:K:41:TRP:HE3	1:K:42:ASP:CA	2.14	0.58
1:P:99:ARG:O	1:P:103:ARG:HG3	2.04	0.58
1:R:136:SER:HB3	1:U:325:ASP:OD2	57.05	0.58
1:T:554:LEU:HD12	1:T:557:PHE:HD2	1.69	0.58
1:U:430:VAL:CG1	3:X:719:HOH:O	2.51	0.58
1:V:158:TRP:O	1:V:160:SER:N	2.36	0.58
1:X:24:GLU:C	1:X:26:ARG:N	2.55	0.58
1:X:78:VAL:HG22	1:X:444:LEU:HD21	1.85	0.58
1:C:276:VAL:HG23	1:C:293:ILE:CG2	2.34	0.58
1:D:173:CYS:SG	1:D:298:ILE:HD13	2.43	0.58
1:E:50:THR:HG21	1:E:54:ARG:NH2	2.18	0.58
1:G:577:ILE:HA	1:G:582:LYS:HB3	1.84	0.58
1:H:384:LEU:HD22	1:H:384:LEU:H	1.68	0.58
1:I:389:LEU:HD12	1:I:389:LEU:H	1.68	0.58
1:J:276:VAL:HG23	1:J:293:ILE:CG2	2.34	0.58
1:K:276:VAL:HG23	1:K:293:ILE:CG2	2.34	0.58
1:L:158:TRP:O	1:L:160:SER:N	2.36	0.58
1:L:389:LEU:H	1:L:389:LEU:HD12	1.68	0.58
1:L:444:LEU:O	1:L:448:VAL:HG23	2.03	0.58
1:M:237:ASP:H	1:M:243:PRO:HA	1.68	0.58
1:M:41:TRP:CE3	1:M:42:ASP:HB3	2.38	0.58
1:M:86:ALA:HB2	1:M:515:GLU:HG3	1.85	0.58
1:O:577:ILE:HA	1:O:582:LYS:HB3	1.85	0.58
1:Q:78:VAL:HG11	1:Q:444:LEU:HG	1.84	0.58
1:Q:554:LEU:HD12	1:Q:557:PHE:HD2	1.69	0.58
1:R:237:ASP:H	1:R:243:PRO:HA	1.68	0.58
1:T:276:VAL:HG23	1:T:293:ILE:HG23	1.85	0.58
1:T:431:ALA:O	1:T:435:VAL:HG22	2.03	0.58
1:X:47:GLN:HG2	1:X:48:TYR:H	1.67	0.58
1:A:276:VAL:HG23	1:A:293:ILE:CG2	2.34	0.58
1:D:50:THR:HG21	1:D:54:ARG:NH2	2.18	0.58
1:E:276:VAL:HG23	1:E:293:ILE:CG2	2.34	0.58
1:F:384:LEU:O	1:F:386:THR:N	2.36	0.58
1:G:384:LEU:H	1:G:384:LEU:HD22	1.68	0.58
1:H:199:PRO:HB3	1:H:282:THR:HG22	1.84	0.58
1:J:577:ILE:HA	1:J:582:LYS:HB3	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:115:VAL:HA	1:L:118:GLN:HB3	1.86	0.58
1:L:276:VAL:HG23	1:L:293:ILE:CG2	2.34	0.58
1:L:49:THR:CG2	1:L:49:THR:O	2.51	0.58
1:P:138:THR:H	1:P:143:VAL:HG22	1.67	0.58
1:R:94:LEU:HA	1:R:97:MSE:CE	2.34	0.58
1:S:128:LEU:HD12	1:S:446:THR:HG23	1.84	0.58
1:S:586:THR:N	1:S:587:PRO:HD3	2.19	0.58
1:A:444:LEU:O	1:A:448:VAL:HG23	2.02	0.58
1:B:173:CYS:SG	1:B:298:ILE:HD13	2.43	0.58
1:B:384:LEU:HD22	1:B:384:LEU:H	1.68	0.58
1:B:50:THR:HG21	1:B:54:ARG:NH2	2.18	0.58
1:C:334:MSE:SE	1:E:404:MSE:HE1	2.53	0.58
1:C:47:GLN:CD	1:C:47:GLN:O	2.42	0.58
1:E:115:VAL:HA	1:E:118:GLN:HB3	1.86	0.58
1:F:158:TRP:CE3	1:F:173:CYS:SG	2.88	0.58
1:F:389:LEU:H	1:F:389:LEU:HD12	1.68	0.58
1:G:14:ARG:HH11	1:G:17:ALA:CB	2.17	0.58
1:G:444:LEU:O	1:G:448:VAL:HG23	2.02	0.58
1:G:49:THR:CG2	1:G:49:THR:O	2.51	0.58
1:H:276:VAL:HG23	1:H:293:ILE:CG2	2.34	0.58
1:I:158:TRP:CE3	1:I:173:CYS:SG	2.88	0.58
1:J:173:CYS:SG	1:J:298:ILE:HD13	2.43	0.58
1:M:577:ILE:HA	1:M:582:LYS:HB3	1.85	0.58
1:N:273:ARG:HH22	1:N:453:LEU:HD21	1.68	0.58
1:R:99:ARG:O	1:R:103:ARG:HG3	2.03	0.58
1:R:246:TYR:CD2	1:R:511:ARG:HB2	2.38	0.58
1:S:273:ARG:NH2	1:S:453:LEU:HD21	2.19	0.58
1:T:237:ASP:H	1:T:243:PRO:HA	1.68	0.58
1:S:556:TYR:OH	1:T:542:THR:HG21	2.03	0.58
1:V:199:PRO:HB3	1:V:282:THR:HG22	1.85	0.58
1:W:577:ILE:HA	1:W:582:LYS:HB3	1.84	0.58
2:Y:28:VAL:HG11	2:Y:97:ALA:N	2.19	0.58
1:A:264:ILE:O	1:A:265:LYS:HD3	2.03	0.58
1:C:115:VAL:HA	1:C:118:GLN:HB3	1.86	0.58
1:E:118:GLN:NE2	1:E:303:VAL:HB	2.19	0.58
1:F:173:CYS:SG	1:F:298:ILE:HD13	2.43	0.58
1:G:264:ILE:O	1:G:265:LYS:HD3	2.03	0.58
1:I:173:CYS:SG	1:I:298:ILE:HD13	2.43	0.58
1:I:14:ARG:HH11	1:I:17:ALA:CB	2.17	0.58
1:I:264:ILE:O	1:I:265:LYS:HD3	2.03	0.58
1:J:248:LYS:NZ	1:J:513:ARG:HH12	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:264:ILE:O	1:J:265:LYS:HD3	2.03	0.58
1:K:173:CYS:SG	1:K:298:ILE:HD13	2.43	0.58
1:N:237:ASP:H	1:N:243:PRO:HA	1.67	0.58
1:P:66:LYS:HZ3	1:P:420:VAL:HG11	1.67	0.58
3:Q:719:HOH:O	1:R:430:VAL:CG1	2.50	0.58
1:V:577:ILE:HA	1:V:582:LYS:HB3	1.85	0.58
1:W:138:THR:H	1:W:143:VAL:HG22	1.69	0.58
1:V:404:MSE:HE1	1:W:334:MSE:SE	2.52	0.58
1:X:554:LEU:HD12	1:X:557:PHE:HD2	1.68	0.58
1:B:276:VAL:HG23	1:B:293:ILE:CG2	2.34	0.58
1:C:118:GLN:NE2	1:C:303:VAL:HB	2.19	0.58
1:B:182:ASN:HD22	1:C:171:ARG:HH21	1.50	0.58
1:C:384:LEU:HD22	1:C:384:LEU:H	1.68	0.58
1:C:384:LEU:O	1:C:386:THR:N	2.36	0.58
1:D:248:LYS:NZ	1:D:513:ARG:HH12	2.02	0.58
1:E:47:GLN:O	1:E:47:GLN:CD	2.42	0.58
1:F:276:VAL:HG23	1:F:293:ILE:CG2	2.34	0.58
1:G:276:VAL:HG23	1:G:293:ILE:CG2	2.34	0.58
1:I:577:ILE:HA	1:I:582:LYS:HB3	1.84	0.58
1:K:389:LEU:H	1:K:389:LEU:HD12	1.68	0.58
1:K:444:LEU:O	1:K:448:VAL:HG23	2.02	0.58
1:K:577:ILE:HA	1:K:582:LYS:HB3	1.84	0.58
1:K:372:TYR:CE2	1:L:348:LYS:HB2	2.39	0.58
1:L:577:ILE:HA	1:L:582:LYS:HB3	1.84	0.58
1:N:231:THR:HG21	1:N:249:ARG:HH11	1.69	0.58
1:O:199:PRO:HB3	1:O:282:THR:HG22	1.86	0.58
1:Q:199:PRO:HB3	1:Q:282:THR:HG22	1.86	0.58
1:Q:24:GLU:C	1:Q:26:ARG:N	2.57	0.58
1:Q:586:THR:N	1:Q:587:PRO:HD3	2.19	0.58
1:U:554:LEU:HD12	1:U:557:PHE:HD2	1.69	0.58
1:V:237:ASP:H	1:V:243:PRO:HA	1.68	0.58
1:V:444:LEU:C	1:V:446:THR:N	2.55	0.58
1:X:586:THR:N	1:X:587:PRO:HD3	2.19	0.58
1:A:118:GLN:NE2	1:A:303:VAL:HB	2.19	0.58
1:A:348:LYS:HB2	1:L:372:TYR:CE2	2.39	0.58
1:A:47:GLN:CD	1:A:47:GLN:O	2.42	0.58
1:A:54:ARG:HB2	2:Y:146:GLY:HA3	1.84	0.58
1:A:50:THR:HG21	1:A:54:ARG:NH2	2.18	0.58
1:C:182:ASN:HD22	1:E:171:ARG:HH21	1.51	0.58
1:C:248:LYS:NZ	1:C:513:ARG:HH12	2.02	0.58
1:D:118:GLN:NE2	1:D:303:VAL:HB	2.19	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:389:LEU:HD12	1:D:389:LEU:H	1.68	0.58
1:D:41:TRP:HE3	1:D:42:ASP:CA	2.14	0.58
1:E:248:LYS:NZ	1:E:513:ARG:HH12	2.02	0.58
1:F:50:THR:HG21	1:F:54:ARG:NH2	2.18	0.58
1:G:334:MSE:HE3	1:H:404:MSE:CE	2.34	0.58
1:G:47:GLN:O	1:G:47:GLN:CD	2.42	0.58
1:H:173:CYS:SG	1:H:298:ILE:HD13	2.43	0.58
1:J:158:TRP:HD1	1:J:158:TRP:H	1.52	0.58
1:K:47:GLN:O	1:K:47:GLN:CD	2.42	0.58
1:A:89:ASP:CA	1:L:561:ASP:HB2	2.30	0.58
1:M:379:GLU:O	1:M:380:ASN:HB2	2.04	0.58
1:M:586:THR:N	1:M:587:PRO:HD3	2.19	0.58
1:M:95:MSE:HB3	1:M:527:MSE:HE1	1.85	0.58
1:N:554:LEU:HD12	1:N:557:PHE:HD2	1.69	0.58
1:Q:273:ARG:HH22	1:Q:453:LEU:HD21	1.69	0.58
1:Q:379:GLU:O	1:Q:380:ASN:HB2	2.03	0.58
1:S:24:GLU:C	1:S:26:ARG:N	2.56	0.58
1:T:586:THR:N	1:T:587:PRO:HD3	2.19	0.58
1:V:154:SER:O	1:V:204:PRO:HB3	2.03	0.58
1:X:158:TRP:O	1:X:160:SER:N	2.37	0.58
1:A:173:CYS:SG	1:A:298:ILE:HD13	2.43	0.58
1:A:14:ARG:HH11	1:A:17:ALA:CB	2.17	0.58
1:A:199:PRO:HB3	1:A:282:THR:HG22	1.84	0.58
1:A:34:PHE:HZ	1:A:328:ARG:HH22	0.80	0.58
1:A:363:TYR:HE1	1:B:350:PHE:HE1	1.52	0.58
1:B:158:TRP:HD1	1:B:158:TRP:H	1.52	0.58
1:B:384:LEU:O	1:B:386:THR:N	2.36	0.58
1:C:49:THR:O	1:C:49:THR:CG2	2.51	0.58
1:D:238:PRO:HG3	1:D:263:PHE:HB3	1.86	0.58
1:D:598:GLN:HB2	1:D:601:GLN:CB	2.34	0.58
1:E:158:TRP:O	1:E:160:SER:N	2.36	0.58
1:F:14:ARG:HH11	1:F:17:ALA:CB	2.17	0.58
1:F:158:TRP:H	1:F:158:TRP:HD1	1.52	0.58
1:F:47:GLN:CD	1:F:47:GLN:O	2.42	0.58
1:F:49:THR:CG2	1:F:49:THR:O	2.51	0.58
1:H:14:ARG:HH11	1:H:17:ALA:CB	2.17	0.58
1:H:598:GLN:HB2	1:H:601:GLN:CB	2.34	0.58
1:H:334:MSE:HE1	1:I:407:ALA:HB1	1.86	0.58
1:I:50:THR:HG21	1:I:54:ARG:NH2	2.18	0.58
1:K:598:GLN:HB2	1:K:601:GLN:CB	2.34	0.58
1:L:173:CYS:SG	1:L:298:ILE:HD13	2.43	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:50:THR:HG21	1:L:54:ARG:NH2	2.18	0.58
1:M:444:LEU:C	1:M:446:THR:N	2.54	0.58
1:N:86:ALA:HB2	1:N:515:GLU:HG3	1.85	0.58
1:M:136:SER:HB3	1:O:325:ASP:OD2	48.52	0.58
1:O:86:ALA:HB2	1:O:515:GLU:HG3	1.84	0.58
1:S:15:PHE:HZ	1:S:283:CYS:SG	2.26	0.58
1:S:66:LYS:HZ3	1:S:420:VAL:HG11	1.69	0.58
1:V:598:GLN:HB2	1:V:601:GLN:CB	2.34	0.58
1:W:379:GLU:O	1:W:380:ASN:HB2	2.04	0.58
1:A:238:PRO:HG3	1:A:263:PHE:HB3	1.86	0.57
1:A:384:LEU:HD22	1:A:384:LEU:H	1.68	0.57
1:B:118:GLN:NE2	1:B:303:VAL:HB	2.19	0.57
1:B:47:GLN:CD	1:B:47:GLN:O	2.42	0.57
1:B:598:GLN:HB2	1:B:601:GLN:CB	2.34	0.57
1:C:173:CYS:SG	1:C:298:ILE:HD13	2.43	0.57
1:C:238:PRO:HG3	1:C:263:PHE:HB3	1.86	0.57
1:E:41:TRP:HE3	1:E:42:ASP:CA	2.14	0.57
1:J:389:LEU:H	1:J:389:LEU:HD12	1.68	0.57
1:J:47:GLN:CD	1:J:47:GLN:O	2.42	0.57
1:K:560:LEU:HD13	1:L:82:PRO:CD	2.20	0.57
1:N:352:TRP:CG	1:V:376:ARG:HB2	2.40	0.57
1:Q:158:TRP:CE3	1:Q:173:CYS:SG	2.85	0.57
1:R:236:GLN:CB	1:R:265:LYS:HG2	2.33	0.57
1:R:276:VAL:HG23	1:R:293:ILE:HG23	1.85	0.57
1:U:586:THR:N	1:U:587:PRO:HD3	2.19	0.57
1:V:99:ARG:O	1:V:103:ARG:HG3	2.03	0.57
1:V:15:PHE:HZ	1:V:283:CYS:SG	2.22	0.57
1:T:395:PRO:HD2	1:W:398:PRO:HB3	1.86	0.57
1:X:15:PHE:CZ	1:X:283:CYS:HA	2.38	0.57
1:A:158:TRP:HD1	1:A:158:TRP:H	1.52	0.57
1:C:144:ILE:HD12	1:C:145:ARG:N	2.20	0.57
1:C:264:ILE:O	1:C:265:LYS:HD3	2.03	0.57
1:E:264:ILE:O	1:E:265:LYS:HD3	2.03	0.57
1:F:238:PRO:HG3	1:F:263:PHE:HB3	1.86	0.57
1:G:248:LYS:NZ	1:G:513:ARG:HH12	2.02	0.57
1:H:118:GLN:NE2	1:H:303:VAL:HB	2.19	0.57
1:H:50:THR:HG21	1:H:54:ARG:NH2	2.18	0.57
1:I:546:THR:CG2	1:I:547:PRO:HD3	2.27	0.57
1:M:26:ARG:HG2	1:N:212:LEU:HD22	1.86	0.57
1:M:554:LEU:HD12	1:M:557:PHE:HD2	1.69	0.57
1:N:78:VAL:HG11	1:N:444:LEU:HG	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:586:THR:N	1:O:587:PRO:HD3	2.18	0.57
1:P:128:LEU:HD12	1:P:446:THR:HG23	1.84	0.57
1:S:563:LYS:HD3	1:T:557:PHE:CE2	2.38	0.57
1:S:86:ALA:HB2	1:S:515:GLU:HG3	1.86	0.57
1:T:46:SER:N	1:T:48:TYR:HE2	1.97	0.57
1:T:86:ALA:HB2	1:T:515:GLU:HG3	1.86	0.57
1:U:47:GLN:HG2	1:U:48:TYR:H	1.69	0.57
1:U:510:ILE:HG12	1:U:511:ARG:N	2.19	0.57
1:V:431:ALA:O	1:V:435:VAL:HG22	2.04	0.57
1:V:510:ILE:HG12	1:V:511:ARG:N	2.19	0.57
2:Y:43:GLN:C	2:Y:45:ALA:H	2.07	0.57
1:B:49:THR:O	1:B:49:THR:CG2	2.51	0.57
1:C:236:GLN:CB	1:C:265:LYS:HZ3	2.15	0.57
1:C:389:LEU:HD12	1:C:389:LEU:H	1.68	0.57
1:D:384:LEU:H	1:D:384:LEU:HD22	1.68	0.57
1:D:541:LYS:HD3	1:D:542:THR:HG23	1.87	0.57
1:E:598:GLN:HB2	1:E:601:GLN:CB	2.34	0.57
1:F:248:LYS:NZ	1:F:513:ARG:HH12	2.02	0.57
1:G:144:ILE:HD12	1:G:145:ARG:N	2.20	0.57
1:G:199:PRO:HB3	1:G:282:THR:HG22	1.84	0.57
1:G:598:GLN:HB2	1:G:601:GLN:CB	2.34	0.57
1:H:144:ILE:HD12	1:H:145:ARG:N	2.20	0.57
1:H:34:PHE:HE1	1:H:324:LYS:HZ2	1.47	0.57
1:H:389:LEU:H	1:H:389:LEU:HD12	1.68	0.57
1:I:210:PRO:HD2	1:I:211:TRP:CZ3	2.39	0.57
1:I:182:ASN:HD22	1:J:171:ARG:HH21	1.51	0.57
1:J:210:PRO:HD2	1:J:211:TRP:CZ3	2.39	0.57
1:K:210:PRO:HD2	1:K:211:TRP:CZ3	2.39	0.57
1:K:238:PRO:HG3	1:K:263:PHE:HB3	1.86	0.57
1:N:138:THR:H	1:N:143:VAL:HG22	1.67	0.57
3:M:719:HOH:O	1:O:430:VAL:CG1	2.52	0.57
1:Q:78:VAL:HG22	1:Q:444:LEU:HD21	1.87	0.57
1:R:47:GLN:HG2	1:R:48:TYR:H	1.67	0.57
1:R:510:ILE:HG12	1:R:511:ARG:N	2.20	0.57
1:R:577:ILE:HA	1:R:582:LYS:HB3	1.86	0.57
1:T:24:GLU:C	1:T:26:ARG:N	2.57	0.57
1:S:82:PRO:HG2	1:U:560:LEU:HD22	1.86	0.57
1:V:71:MSE:HE2	1:V:119:ILE:HD11	1.85	0.57
1:W:86:ALA:HB2	1:W:515:GLU:HG3	1.86	0.57
1:X:138:THR:H	1:X:143:VAL:HG22	1.69	0.57
1:X:276:VAL:HG23	1:X:293:ILE:HG23	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:379:GLU:O	1:X:380:ASN:HB2	2.04	0.57
2:Y:51:ALA:O	2:Y:54:ALA:HB3	2.04	0.57
2:Y:92:VAL:O	2:Y:96:LEU:HB2	2.04	0.57
2:Z:43:GLN:C	2:Z:45:ALA:H	2.07	0.57
1:A:144:ILE:HD12	1:A:145:ARG:N	2.20	0.57
1:A:210:PRO:HD2	1:A:211:TRP:CZ3	2.39	0.57
1:A:598:GLN:HB2	1:A:601:GLN:CB	2.34	0.57
1:B:14:ARG:HH11	1:B:17:ALA:CB	2.17	0.57
1:B:166:ASP:OD2	1:B:168:SER:HB3	2.05	0.57
1:B:248:LYS:NZ	1:B:513:ARG:HH12	2.02	0.57
1:B:541:LYS:HD3	1:B:542:THR:HG23	1.87	0.57
1:C:14:ARG:HH11	1:C:17:ALA:CB	2.17	0.57
1:D:14:ARG:HH11	1:D:17:ALA:CB	2.17	0.57
1:D:395:PRO:HD2	1:F:398:PRO:HB3	1.86	0.57
1:E:210:PRO:HD2	1:E:211:TRP:CZ3	2.39	0.57
1:E:389:LEU:HD12	1:E:389:LEU:H	1.68	0.57
1:G:210:PRO:HD2	1:G:211:TRP:CZ3	2.39	0.57
1:G:50:THR:HG21	1:G:54:ARG:NH2	2.18	0.57
1:H:210:PRO:HD2	1:H:211:TRP:CZ3	2.39	0.57
1:I:166:ASP:OD2	1:I:168:SER:HB3	2.05	0.57
1:N:510:ILE:HG12	1:N:511:ARG:N	2.19	0.57
1:O:273:ARG:HH22	1:O:453:LEU:HD21	1.68	0.57
1:P:444:LEU:C	1:P:446:THR:N	2.53	0.57
1:P:577:ILE:HA	1:P:582:LYS:HB3	1.85	0.57
1:Q:577:ILE:HA	1:Q:582:LYS:HB3	1.86	0.57
1:R:431:ALA:O	1:R:435:VAL:HG22	2.04	0.57
1:T:598:GLN:HB2	1:T:601:GLN:CB	2.34	0.57
1:V:379:GLU:O	1:V:380:ASN:HB2	2.04	0.57
1:V:78:VAL:HG11	1:V:444:LEU:HG	1.86	0.57
1:W:586:THR:N	1:W:587:PRO:HD3	2.19	0.57
1:X:86:ALA:HB2	1:X:515:GLU:HG3	1.85	0.57
1:A:166:ASP:OD2	1:A:168:SER:HB3	2.05	0.57
1:B:144:ILE:HD12	1:B:145:ARG:N	2.19	0.57
1:B:238:PRO:HG3	1:B:263:PHE:HB3	1.86	0.57
1:B:41:TRP:HE3	1:B:42:ASP:CA	2.14	0.57
1:B:108:LYS:HD2	1:C:438:LEU:HD11	1.86	0.57
1:D:363:TYR:HE1	1:F:350:PHE:HE1	1.50	0.57
1:D:47:GLN:CD	1:D:47:GLN:O	2.42	0.57
1:F:210:PRO:HD2	1:F:211:TRP:CZ3	2.39	0.57
1:F:118:GLN:NE2	1:F:303:VAL:HB	2.19	0.57
1:G:238:PRO:HG3	1:G:263:PHE:HB3	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:191:TYR:HE1	1:H:278:LYS:HZ3	1.51	0.57
1:H:49:THR:CG2	1:H:49:THR:O	2.51	0.57
1:J:144:ILE:HD12	1:J:145:ARG:N	2.20	0.57
1:J:14:ARG:HH11	1:J:17:ALA:CB	2.17	0.57
1:K:546:THR:CG2	1:K:547:PRO:HD3	2.27	0.57
1:L:118:GLN:NE2	1:L:303:VAL:HB	2.19	0.57
1:L:210:PRO:HD2	1:L:211:TRP:CZ3	2.39	0.57
1:S:138:THR:H	1:S:143:VAL:HG22	1.68	0.57
1:X:199:PRO:HB3	1:X:282:THR:HG22	1.86	0.57
1:X:99:ARG:O	1:X:103:ARG:HG3	2.04	0.57
2:Z:28:VAL:HG11	2:Z:97:ALA:N	2.19	0.57
1:C:166:ASP:OD2	1:C:168:SER:HB3	2.05	0.57
1:C:34:PHE:HZ	1:C:328:ARG:HH22	0.80	0.57
1:D:158:TRP:H	1:D:158:TRP:HD1	1.52	0.57
1:D:166:ASP:OD2	1:D:168:SER:HB3	2.05	0.57
1:D:276:VAL:HG23	1:D:293:ILE:CG2	2.34	0.57
1:E:14:ARG:HH11	1:E:17:ALA:CB	2.17	0.57
1:F:144:ILE:HD12	1:F:145:ARG:N	2.19	0.57
1:G:118:GLN:NE2	1:G:303:VAL:HB	2.19	0.57
1:I:158:TRP:H	1:I:158:TRP:HD1	1.52	0.57
1:I:238:PRO:HG3	1:I:263:PHE:HB3	1.86	0.57
1:I:248:LYS:NZ	1:I:513:ARG:HH12	2.02	0.57
1:J:118:GLN:NE2	1:J:303:VAL:HB	2.19	0.57
1:I:334:MSE:SE	1:J:404:MSE:HE1	2.55	0.57
1:K:115:VAL:HA	1:K:118:GLN:HB3	1.86	0.57
1:K:14:ARG:HH11	1:K:17:ALA:CB	2.17	0.57
1:J:334:MSE:SE	1:K:404:MSE:HE1	2.55	0.57
1:K:541:LYS:HD3	1:K:542:THR:HG23	1.87	0.57
1:L:236:GLN:CB	1:L:265:LYS:HZ3	2.15	0.57
1:L:35:PHE:HE2	1:L:324:LYS:HZ3	1.50	0.57
1:L:598:GLN:HB2	1:L:601:GLN:CB	2.34	0.57
1:N:99:ARG:O	1:N:103:ARG:HG3	2.05	0.57
1:O:554:LEU:HD12	1:O:557:PHE:HD2	1.69	0.57
1:P:199:PRO:HB3	1:P:282:THR:HG22	1.87	0.57
1:R:586:THR:N	1:R:587:PRO:HD3	2.19	0.57
1:V:86:ALA:HB2	1:V:515:GLU:HG3	1.86	0.57
1:W:554:LEU:HD12	1:W:557:PHE:HD2	1.68	0.57
1:X:577:ILE:HA	1:X:582:LYS:HB3	1.85	0.57
2:Z:78:GLU:CG	2:Z:79:GLY:N	2.63	0.57
1:A:115:VAL:HA	1:A:118:GLN:HB3	1.86	0.57
1:B:563:LYS:HD3	1:C:557:PHE:CE2	2.40	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:50:THR:HG21	1:C:54:ARG:NH2	2.18	0.57
1:D:210:PRO:HD2	1:D:211:TRP:CZ3	2.39	0.57
1:E:49:THR:CG2	1:E:49:THR:O	2.51	0.57
1:F:166:ASP:OD2	1:F:168:SER:HB3	2.05	0.57
1:H:37:ARG:HH21	1:H:37:ARG:CB	2.16	0.57
1:I:144:ILE:HD12	1:I:145:ARG:N	2.20	0.57
1:I:598:GLN:HB2	1:I:601:GLN:CB	2.34	0.57
1:K:440:MSE:O	1:K:444:LEU:HD22	2.05	0.57
1:L:14:ARG:HH11	1:L:17:ALA:CB	2.17	0.57
1:L:238:PRO:HG3	1:L:263:PHE:HB3	1.86	0.57
1:N:158:TRP:HB3	1:N:173:CYS:CA	2.27	0.57
1:P:154:SER:O	1:P:204:PRO:HB3	2.03	0.57
1:O:564:GLY:CA	1:P:554:LEU:HD21	2.34	0.57
1:Q:276:VAL:HG23	1:Q:293:ILE:HG23	1.85	0.57
1:Q:598:GLN:HB2	1:Q:601:GLN:CB	2.35	0.57
1:R:165:MSE:HE3	1:R:304:PHE:HB2	1.87	0.57
1:N:310:VAL:HG22	1:V:40:GLN:HG2	1.86	0.57
1:V:390:ALA:CB	1:W:387:GLN:CB	2.83	0.57
1:B:389:LEU:HD12	1:B:389:LEU:H	1.68	0.57
1:B:597:GLN:HA	1:B:597:GLN:HE21	1.70	0.57
1:C:37:ARG:CB	1:C:37:ARG:HH21	2.16	0.57
1:C:597:GLN:HE21	1:C:597:GLN:HA	1.70	0.57
1:D:49:THR:O	1:D:49:THR:CG2	2.51	0.57
1:E:144:ILE:HD12	1:E:145:ARG:N	2.20	0.57
1:D:171:ARG:HH21	1:E:182:ASN:ND2	2.02	0.57
1:F:598:GLN:HB2	1:F:601:GLN:CB	2.34	0.57
1:G:115:VAL:HA	1:G:118:GLN:HB3	1.86	0.57
1:F:372:TYR:CE2	1:G:348:LYS:HB2	2.40	0.57
1:H:166:ASP:OD2	1:H:168:SER:HB3	2.05	0.57
1:H:47:GLN:O	1:H:47:GLN:CD	2.42	0.57
1:I:276:VAL:HG23	1:I:293:ILE:CG2	2.34	0.57
1:K:376:ARG:HB2	1:L:352:TRP:CG	2.40	0.57
1:M:154:SER:O	1:M:204:PRO:HB3	2.04	0.57
1:M:273:ARG:NH2	1:M:453:LEU:HD21	2.19	0.57
1:O:165:MSE:HE3	1:O:304:PHE:HB2	1.85	0.57
1:R:379:GLU:O	1:R:380:ASN:HB2	2.04	0.57
1:S:199:PRO:HB3	1:S:282:THR:HG22	1.85	0.57
1:U:273:ARG:NH2	1:U:453:LEU:HD21	2.19	0.57
1:U:95:MSE:HB3	1:U:527:MSE:HE1	1.87	0.57
1:V:586:THR:N	1:V:587:PRO:HD3	2.19	0.57
1:W:598:GLN:HB2	1:W:601:GLN:CB	2.35	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:51:ALA:O	2:Z:54:ALA:HB3	2.04	0.57
2:Z:92:VAL:O	2:Z:96:LEU:HB2	2.04	0.57
1:A:389:LEU:HD12	1:A:389:LEU:H	1.68	0.57
1:A:248:LYS:NZ	1:A:513:ARG:HH12	2.02	0.57
1:B:210:PRO:HD2	1:B:211:TRP:CZ3	2.39	0.57
1:B:440:MSE:O	1:B:444:LEU:HD22	2.05	0.57
1:C:541:LYS:HD3	1:C:542:THR:HG23	1.87	0.57
1:C:598:GLN:HB2	1:C:601:GLN:CB	2.34	0.57
1:E:440:MSE:O	1:E:444:LEU:HD22	2.05	0.57
1:E:541:LYS:HD3	1:E:542:THR:HG23	1.87	0.57
1:H:440:MSE:O	1:H:444:LEU:HD22	2.05	0.57
1:I:47:GLN:CD	1:I:47:GLN:O	2.42	0.57
1:L:47:GLN:O	1:L:47:GLN:CD	2.42	0.57
1:L:597:GLN:HA	1:L:597:GLN:HE21	1.70	0.57
1:O:561:ASP:OD2	1:P:92:ASP:HB3	2.04	0.57
1:O:99:ARG:O	1:O:103:ARG:HG3	2.05	0.57
1:P:586:THR:N	1:P:587:PRO:HD3	2.19	0.57
1:R:138:THR:H	1:R:143:VAL:HG22	1.69	0.57
1:T:78:VAL:HG11	1:T:444:LEU:HG	1.86	0.57
1:V:210:PRO:HD2	1:V:211:TRP:CD2	2.40	0.57
1:V:390:ALA:CB	1:W:387:GLN:HB3	2.35	0.57
1:W:236:GLN:CB	1:W:265:LYS:HG2	2.32	0.57
1:W:78:VAL:HG11	1:W:444:LEU:HG	1.87	0.57
1:B:248:LYS:HG3	1:B:511:ARG:HH11	1.70	0.57
1:D:248:LYS:HG3	1:D:511:ARG:HH11	1.70	0.57
1:E:238:PRO:HG3	1:E:263:PHE:HB3	1.86	0.57
1:C:334:MSE:HE3	1:E:404:MSE:CE	2.34	0.57
1:E:597:GLN:HE21	1:E:597:GLN:HA	1.70	0.57
1:H:115:VAL:HA	1:H:118:GLN:HB3	1.86	0.57
1:H:597:GLN:HE21	1:H:597:GLN:HA	1.70	0.57
1:I:115:VAL:HA	1:I:118:GLN:HB3	1.86	0.57
1:J:597:GLN:HE21	1:J:597:GLN:HA	1.70	0.57
1:J:598:GLN:HB2	1:J:601:GLN:CB	2.34	0.57
1:K:248:LYS:NZ	1:K:513:ARG:HH12	2.02	0.57
1:O:598:GLN:HB2	1:O:601:GLN:CB	2.35	0.57
1:P:431:ALA:O	1:P:435:VAL:HG22	2.05	0.57
1:R:598:GLN:HB2	1:R:601:GLN:CB	2.35	0.57
1:T:165:MSE:HE3	1:T:304:PHE:HB2	1.87	0.57
3:S:719:HOH:O	1:T:430:VAL:CG1	2.53	0.57
1:X:598:GLN:HB2	1:X:601:GLN:CB	2.35	0.57
2:Z:78:GLU:HG3	2:Z:79:GLY:N	2.20	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:VAL:HA	1:D:118:GLN:HB3	1.86	0.56
1:D:144:ILE:HD12	1:D:145:ARG:N	2.19	0.56
1:D:597:GLN:HA	1:D:597:GLN:HE21	1.70	0.56
1:E:166:ASP:OD2	1:E:168:SER:HB3	2.05	0.56
1:F:34:PHE:HZ	1:F:328:ARG:HH22	0.80	0.56
1:H:334:MSE:HE3	1:I:404:MSE:HE3	1.86	0.56
1:L:248:LYS:NZ	1:L:513:ARG:HH12	2.02	0.56
1:M:158:TRP:O	1:M:160:SER:N	2.38	0.56
1:P:46:SER:N	1:P:48:TYR:HE2	1.97	0.56
1:S:561:ASP:OD2	1:T:92:ASP:HB3	2.03	0.56
1:T:209:PHE:HZ	1:T:214:GLN:HG2	1.70	0.56
1:U:37:ARG:NH2	1:U:41:TRP:HB3	2.20	0.56
1:U:78:VAL:HG11	1:U:444:LEU:HG	1.86	0.56
1:U:94:LEU:HA	1:U:97:MSE:CE	2.34	0.56
2:Y:78:GLU:CG	2:Y:79:GLY:N	2.63	0.56
1:B:115:VAL:HA	1:B:118:GLN:HB3	1.86	0.56
1:A:372:TYR:CE2	1:B:348:LYS:HB2	2.39	0.56
1:G:440:MSE:O	1:G:444:LEU:HD22	2.05	0.56
1:I:440:MSE:O	1:I:444:LEU:HD22	2.05	0.56
1:K:118:GLN:NE2	1:K:303:VAL:HB	2.19	0.56
1:K:248:LYS:CG	1:K:511:ARG:HH11	2.19	0.56
1:L:440:MSE:O	1:L:444:LEU:HD22	2.05	0.56
1:L:541:LYS:HD3	1:L:542:THR:HG23	1.87	0.56
1:M:598:GLN:HB2	1:M:601:GLN:CB	2.35	0.56
1:O:158:TRP:O	1:O:160:SER:N	2.37	0.56
1:P:158:TRP:CH2	1:P:302:PRO:HG3	2.39	0.56
1:P:158:TRP:O	1:P:160:SER:N	2.38	0.56
1:Q:94:LEU:HA	1:Q:97:MSE:CE	2.35	0.56
1:U:86:ALA:HB2	1:U:515:GLU:HG3	1.86	0.56
1:V:273:ARG:NH1	1:V:275:ARG:HE	2.03	0.56
1:G:166:ASP:OD2	1:G:168:SER:HB3	2.05	0.56
1:G:236:GLN:CB	1:G:265:LYS:HZ3	2.16	0.56
1:G:34:PHE:HE1	1:G:324:LYS:HZ2	1.50	0.56
1:I:334:MSE:HE3	1:J:404:MSE:CE	2.35	0.56
1:I:597:GLN:HE21	1:I:597:GLN:HA	1.70	0.56
1:M:430:VAL:CG1	3:N:719:HOH:O	2.53	0.56
1:M:71:MSE:HE2	1:M:119:ILE:HD11	1.86	0.56
1:S:165:MSE:HE3	1:S:304:PHE:HB2	1.86	0.56
1:S:598:GLN:HB2	1:S:601:GLN:CB	2.35	0.56
1:U:273:ARG:HH22	1:U:453:LEU:HD21	1.70	0.56
1:V:578:GLN:HG2	1:V:596:ALA:HB2	1.87	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:210:PRO:HD2	1:X:211:TRP:CD2	2.40	0.56
1:X:456:ALA:HB1	1:X:509:ASP:OD1	2.05	0.56
1:F:248:LYS:HG3	1:F:511:ARG:HH11	1.70	0.56
1:I:118:GLN:NE2	1:I:303:VAL:HB	2.19	0.56
1:J:166:ASP:OD2	1:J:168:SER:HB3	2.05	0.56
1:J:440:MSE:O	1:J:444:LEU:HD22	2.05	0.56
1:J:248:LYS:HG3	1:J:511:ARG:HH11	1.70	0.56
1:I:567:MSE:SE	1:J:576:LEU:HD13	2.55	0.56
1:K:248:LYS:HG3	1:K:511:ARG:HH11	1.70	0.56
1:L:248:LYS:HG3	1:L:511:ARG:HH11	1.70	0.56
1:M:78:VAL:CG2	1:M:444:LEU:HD11	2.23	0.56
1:M:578:GLN:HG2	1:M:596:ALA:HB2	1.87	0.56
1:N:577:ILE:HA	1:N:582:LYS:HB3	1.85	0.56
1:V:78:VAL:HG12	1:V:79:LEU:H	1.70	0.56
1:W:158:TRP:O	1:W:160:SER:N	2.38	0.56
1:A:72:ARG:HD2	1:B:434:THR:HG21	1.87	0.56
1:C:210:PRO:HD2	1:C:211:TRP:CZ3	2.39	0.56
1:G:37:ARG:HH21	1:G:37:ARG:CB	2.16	0.56
1:H:158:TRP:H	1:H:158:TRP:HD1	1.52	0.56
1:H:248:LYS:CG	1:H:511:ARG:HH11	2.19	0.56
1:I:210:PRO:HD2	1:I:211:TRP:CE3	2.41	0.56
1:J:210:PRO:HD2	1:J:211:TRP:CE3	2.41	0.56
1:K:166:ASP:OD2	1:K:168:SER:HB3	2.05	0.56
1:K:273:ARG:NH2	1:K:453:LEU:HD21	2.21	0.56
1:L:144:ILE:HD12	1:L:145:ARG:N	2.20	0.56
1:M:210:PRO:HD2	1:M:211:TRP:CD2	2.41	0.56
1:N:598:GLN:HB2	1:N:601:GLN:CB	2.35	0.56
1:N:71:MSE:HE2	1:N:119:ILE:HD11	1.85	0.56
1:O:144:ILE:HD12	1:O:145:ARG:N	2.20	0.56
1:P:510:ILE:HG12	1:P:511:ARG:N	2.20	0.56
1:P:598:GLN:HB2	1:P:601:GLN:CB	2.35	0.56
1:Q:158:TRP:O	1:Q:160:SER:N	2.39	0.56
1:Q:210:PRO:HD2	1:Q:211:TRP:CD2	2.40	0.56
1:Q:46:SER:N	1:Q:48:TYR:HE2	1.98	0.56
1:R:165:MSE:HE1	1:R:435:VAL:HB	1.87	0.56
1:Q:564:GLY:HA2	1:R:554:LEU:HD21	1.87	0.56
1:S:209:PHE:N	1:S:210:PRO:HD3	2.21	0.56
1:U:210:PRO:HD2	1:U:211:TRP:CD2	2.40	0.56
1:U:199:PRO:HB3	1:U:282:THR:HG22	1.87	0.56
1:U:99:ARG:O	1:U:103:ARG:HG3	2.05	0.56
1:V:209:PHE:HZ	1:V:214:GLN:HG2	1.70	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:440:MSE:O	1:A:444:LEU:HD22	2.05	0.56
1:A:597:GLN:HE21	1:A:597:GLN:HA	1.70	0.56
1:B:161:ASN:C	1:B:161:ASN:ND2	2.59	0.56
1:D:248:LYS:CG	1:D:511:ARG:HH11	2.19	0.56
1:E:158:TRP:H	1:E:158:TRP:HD1	1.52	0.56
1:E:210:PRO:HD2	1:E:211:TRP:CE3	2.41	0.56
1:E:248:LYS:CG	1:E:511:ARG:HH11	2.19	0.56
1:G:248:LYS:HG3	1:G:511:ARG:HH11	1.70	0.56
1:I:161:ASN:C	1:I:161:ASN:ND2	2.59	0.56
1:J:236:GLN:CB	1:J:265:LYS:HZ3	2.16	0.56
1:K:144:ILE:HD12	1:K:145:ARG:N	2.20	0.56
1:N:210:PRO:HD2	1:N:211:TRP:CD2	2.41	0.56
1:N:554:LEU:HD21	1:V:564:GLY:HA2	1.86	0.56
1:O:210:PRO:HD2	1:O:211:TRP:CD2	2.41	0.56
1:R:199:PRO:HB3	1:R:282:THR:HG22	1.86	0.56
1:S:510:ILE:HG12	1:S:511:ARG:N	2.20	0.56
1:U:598:GLN:HB2	1:U:601:GLN:CB	2.35	0.56
1:X:158:TRP:CE3	1:X:173:CYS:SG	2.85	0.56
1:A:236:GLN:CB	1:A:265:LYS:HZ3	2.16	0.56
1:A:541:LYS:HD3	1:A:542:THR:HG23	1.87	0.56
1:D:337:ASN:ND2	1:D:401:ASN:HD22	2.04	0.56
1:F:210:PRO:HD2	1:F:211:TRP:CE3	2.41	0.56
1:F:363:TYR:HE1	1:G:350:PHE:HE1	1.53	0.56
1:H:210:PRO:HD2	1:H:211:TRP:CE3	2.41	0.56
1:I:248:LYS:CG	1:I:511:ARG:HH11	2.19	0.56
1:I:248:LYS:HG3	1:I:511:ARG:HH11	1.70	0.56
1:J:238:PRO:HG3	1:J:263:PHE:HB3	1.86	0.56
1:J:248:LYS:CG	1:J:511:ARG:HH11	2.19	0.56
1:R:578:GLN:HG2	1:R:596:ALA:HB2	1.88	0.56
1:S:273:ARG:HH22	1:S:453:LEU:HD21	1.70	0.56
1:S:78:VAL:HG11	1:S:444:LEU:HG	1.86	0.56
1:T:158:TRP:O	1:T:160:SER:N	2.39	0.56
1:U:158:TRP:O	1:U:160:SER:N	2.39	0.56
1:U:165:MSE:HE3	1:U:304:PHE:HB2	1.87	0.56
1:V:209:PHE:N	1:V:210:PRO:HD3	2.21	0.56
1:W:158:TRP:CE3	1:W:173:CYS:SG	2.85	0.56
1:X:510:ILE:HG12	1:X:511:ARG:N	2.19	0.56
2:Z:78:GLU:O	2:Z:80:ASP:OD2	2.24	0.56
1:A:210:PRO:HD2	1:A:211:TRP:CE3	2.41	0.56
1:A:352:TRP:CD2	1:L:376:ARG:HB2	2.41	0.56
1:C:158:TRP:HD1	1:C:158:TRP:H	1.52	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:337:ASN:ND2	1:E:401:ASN:HD22	2.04	0.56
1:F:597:GLN:HA	1:F:597:GLN:HE21	1.70	0.56
1:G:158:TRP:HD1	1:G:158:TRP:H	1.52	0.56
1:G:597:GLN:HE21	1:G:597:GLN:HA	1.70	0.56
1:H:248:LYS:NZ	1:H:513:ARG:HH12	2.02	0.56
1:G:334:MSE:SE	1:H:404:MSE:HE1	2.55	0.56
1:K:597:GLN:HE21	1:K:597:GLN:HA	1.70	0.56
1:O:273:ARG:NH1	1:O:275:ARG:HE	2.04	0.56
1:S:158:TRP:O	1:S:160:SER:N	2.39	0.56
1:T:66:LYS:HZ3	1:T:420:VAL:HG11	1.71	0.56
1:T:456:ALA:HB1	1:T:509:ASP:OD1	2.05	0.56
1:V:95:MSE:HB3	1:V:527:MSE:HE1	1.88	0.56
1:W:165:MSE:HE3	1:W:304:PHE:HB2	1.86	0.56
1:X:273:ARG:NH1	1:X:275:ARG:HE	2.04	0.56
1:X:273:ARG:NH2	1:X:453:LEU:HD21	2.21	0.56
1:A:248:LYS:CG	1:A:511:ARG:HH11	2.19	0.56
1:C:248:LYS:CG	1:C:511:ARG:HH11	2.19	0.56
1:D:161:ASN:ND2	1:D:161:ASN:C	2.59	0.56
1:F:546:THR:CG2	1:F:547:PRO:HD3	2.27	0.56
1:I:541:LYS:HD3	1:I:542:THR:HG23	1.87	0.56
1:K:182:ASN:ND2	1:L:171:ARG:HH21	2.03	0.56
1:N:158:TRP:O	1:N:160:SER:N	2.38	0.56
1:O:209:PHE:N	1:O:210:PRO:HD3	2.21	0.56
1:O:35:PHE:CE1	1:O:321:ARG:NE	2.73	0.56
1:S:210:PRO:HD2	1:S:211:TRP:CD2	2.40	0.56
1:S:430:VAL:CG1	3:U:719:HOH:O	2.52	0.56
1:T:578:GLN:HG2	1:T:596:ALA:HB2	1.86	0.56
2:Y:78:GLU:O	2:Y:80:ASP:OD2	2.24	0.56
1:B:236:GLN:CB	1:B:265:LYS:HZ3	2.16	0.56
1:C:210:PRO:HD2	1:C:211:TRP:CE3	2.41	0.56
1:C:440:MSE:O	1:C:444:LEU:HD22	2.05	0.56
1:G:248:LYS:CG	1:G:511:ARG:HH11	2.19	0.56
1:H:337:ASN:ND2	1:H:401:ASN:HD22	2.04	0.56
1:I:337:ASN:ND2	1:I:401:ASN:HD22	2.04	0.56
1:J:273:ARG:NH2	1:J:453:LEU:HD21	2.21	0.56
1:K:158:TRP:HD1	1:K:158:TRP:H	1.52	0.56
1:K:158:TRP:HB3	1:K:173:CYS:CA	2.36	0.56
1:L:161:ASN:ND2	1:L:161:ASN:C	2.59	0.56
1:N:199:PRO:HB3	1:N:282:THR:HG22	1.87	0.56
1:N:209:PHE:HZ	1:N:214:GLN:HG2	1.70	0.56
1:N:94:LEU:HA	1:N:97:MSE:CE	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:158:TRP:HB3	1:Q:173:CYS:CA	2.27	0.56
1:Q:431:ALA:O	1:Q:435:VAL:HG22	2.05	0.56
1:Q:510:ILE:HG12	1:Q:511:ARG:N	2.20	0.56
1:Q:578:GLN:HG2	1:Q:596:ALA:HB2	1.86	0.56
1:Q:86:ALA:HB2	1:Q:515:GLU:HG3	1.87	0.56
1:S:578:GLN:HG2	1:S:596:ALA:HB2	1.87	0.56
1:T:209:PHE:N	1:T:210:PRO:HD3	2.21	0.56
1:S:212:LEU:HD22	1:T:26:ARG:HG2	1.86	0.56
1:U:434:THR:O	1:U:437:GLN:HG2	2.06	0.56
3:T:719:HOH:O	1:W:430:VAL:CG1	2.53	0.56
1:B:27:ARG:HB2	1:B:313:LYS:HE3	1.88	0.56
1:E:380:ASN:O	1:E:381:SER:HB3	2.06	0.56
1:F:248:LYS:CG	1:F:511:ARG:HH11	2.19	0.56
1:G:34:PHE:HZ	1:G:328:ARG:HH22	0.80	0.56
1:J:161:ASN:ND2	1:J:161:ASN:C	2.59	0.56
1:O:578:GLN:HG2	1:O:596:ALA:HB2	1.88	0.56
1:P:144:ILE:HD12	1:P:145:ARG:N	2.21	0.56
1:P:296:GLU:HG2	1:P:449:PHE:HB3	1.88	0.56
1:Q:101:ASP:HB2	1:Q:144:ILE:O	2.06	0.56
1:Q:209:PHE:N	1:Q:210:PRO:HD3	2.21	0.56
1:Q:41:TRP:HE1	1:R:27:ARG:HH21	1.54	0.56
1:R:210:PRO:HD2	1:R:211:TRP:CD2	2.41	0.56
1:S:564:GLY:CA	1:T:554:LEU:HD21	2.36	0.56
1:V:430:VAL:CG1	3:W:719:HOH:O	2.54	0.56
1:W:209:PHE:HZ	1:W:214:GLN:HG2	1.70	0.56
1:W:209:PHE:N	1:W:210:PRO:HD3	2.21	0.56
1:W:199:PRO:HB3	1:W:282:THR:HG22	1.87	0.56
1:A:158:TRP:HB3	1:A:173:CYS:CA	2.36	0.55
1:B:158:TRP:HB3	1:B:173:CYS:CA	2.36	0.55
1:B:210:PRO:HD2	1:B:211:TRP:CE3	2.41	0.55
1:D:440:MSE:O	1:D:444:LEU:HD22	2.05	0.55
1:D:404:MSE:CE	1:E:334:MSE:HE3	2.36	0.55
1:E:248:LYS:HG3	1:E:511:ARG:HH11	1.70	0.55
1:F:541:LYS:HD3	1:F:542:THR:HG23	1.87	0.55
1:G:541:LYS:HD3	1:G:542:THR:HG23	1.87	0.55
1:H:248:LYS:HG3	1:H:511:ARG:HH11	1.70	0.55
1:I:380:ASN:O	1:I:381:SER:HB3	2.07	0.55
1:L:158:TRP:H	1:L:158:TRP:HD1	1.52	0.55
1:L:248:LYS:CG	1:L:511:ARG:HH11	2.19	0.55
1:M:78:VAL:HG11	1:M:444:LEU:HG	1.87	0.55
1:P:94:LEU:HA	1:P:97:MSE:CE	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:273:ARG:NH1	1:Q:275:ARG:HE	2.04	0.55
1:R:209:PHE:N	1:R:210:PRO:HD3	2.21	0.55
1:R:420:VAL:HG22	1:R:428:GLY:HA3	1.88	0.55
1:R:71:MSE:HE2	1:R:119:ILE:HD11	1.86	0.55
1:V:94:LEU:HA	1:V:97:MSE:CE	2.36	0.55
1:W:593:LEU:O	1:W:597:GLN:HG2	2.06	0.55
1:X:101:ASP:HB2	1:X:144:ILE:O	2.07	0.55
1:U:390:ALA:CB	1:X:387:GLN:HB3	2.36	0.55
1:F:47:GLN:CD	1:F:47:GLN:H	2.10	0.55
1:G:210:PRO:HD2	1:G:211:TRP:CE3	2.41	0.55
1:G:27:ARG:HB2	1:G:313:LYS:HE3	1.89	0.55
1:G:380:ASN:O	1:G:381:SER:HB3	2.07	0.55
1:H:238:PRO:HG3	1:H:263:PHE:HB3	1.87	0.55
1:J:395:PRO:HD2	1:K:398:PRO:HB3	1.87	0.55
1:K:34:PHE:CE1	1:K:324:LYS:NZ	2.72	0.55
1:L:337:ASN:ND2	1:L:401:ASN:HD22	2.04	0.55
1:L:589:GLU:HA	1:L:592:TRP:HB2	1.88	0.55
1:N:546:THR:CG2	1:N:547:PRO:HD3	2.29	0.55
1:O:44:TRP:CE2	1:O:54:ARG:HB3	2.41	0.55
1:Q:296:GLU:HG2	1:Q:449:PHE:HB3	1.87	0.55
1:R:296:GLU:HG2	1:R:449:PHE:HB3	1.88	0.55
1:S:99:ARG:O	1:S:103:ARG:HG3	2.05	0.55
1:T:210:PRO:HD2	1:T:211:TRP:CD2	2.41	0.55
1:T:99:ARG:O	1:T:103:ARG:HG3	2.04	0.55
1:U:71:MSE:HE2	1:U:119:ILE:HD11	1.88	0.55
1:U:35:PHE:CE1	1:U:321:ARG:NE	2.74	0.55
1:X:273:ARG:HH22	1:X:453:LEU:HD21	1.71	0.55
1:X:81:ARG:HB2	1:X:517:TYR:CZ	2.41	0.55
1:X:578:GLN:HG2	1:X:596:ALA:HB2	1.87	0.55
1:D:47:GLN:CD	1:D:47:GLN:H	2.10	0.55
1:D:589:GLU:HA	1:D:592:TRP:HB2	1.89	0.55
1:F:161:ASN:C	1:F:161:ASN:ND2	2.59	0.55
1:F:440:MSE:O	1:F:444:LEU:HD22	2.05	0.55
1:J:380:ASN:O	1:J:381:SER:HB3	2.07	0.55
1:K:210:PRO:HD2	1:K:211:TRP:CE3	2.41	0.55
1:L:380:ASN:O	1:L:381:SER:HB3	2.06	0.55
1:M:92:ASP:HB3	1:N:561:ASP:OD2	2.06	0.55
1:O:94:LEU:HA	1:O:97:MSE:CE	2.36	0.55
1:Q:165:MSE:HE3	1:Q:304:PHE:HB2	1.87	0.55
1:Q:456:ALA:HB1	1:Q:509:ASP:OD1	2.06	0.55
1:R:273:ARG:NH1	1:R:275:ARG:HE	2.05	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:71:MSE:HE2	1:S:119:ILE:HD11	1.87	0.55
1:S:296:GLU:HG2	1:S:449:PHE:HB3	1.87	0.55
1:T:246:TYR:CD2	1:T:511:ARG:HB2	2.39	0.55
1:W:99:ARG:O	1:W:103:ARG:HG3	2.05	0.55
1:X:15:PHE:HZ	1:X:283:CYS:SG	2.26	0.55
1:X:296:GLU:HG2	1:X:449:PHE:HB3	1.88	0.55
1:B:589:GLU:HA	1:B:592:TRP:HB2	1.88	0.55
1:E:161:ASN:C	1:E:161:ASN:ND2	2.59	0.55
1:D:404:MSE:HE1	1:E:334:MSE:SE	2.57	0.55
1:H:161:ASN:ND2	1:H:161:ASN:C	2.59	0.55
1:H:589:GLU:HA	1:H:592:TRP:HB2	1.89	0.55
1:J:589:GLU:HA	1:J:592:TRP:HB2	1.89	0.55
1:L:166:ASP:OD2	1:L:168:SER:HB3	2.05	0.55
1:L:158:TRP:HB3	1:L:173:CYS:CA	2.36	0.55
1:L:210:PRO:HD2	1:L:211:TRP:CE3	2.41	0.55
1:L:27:ARG:HB2	1:L:313:LYS:HE3	1.89	0.55
1:A:557:PHE:CE2	1:L:563:LYS:HD3	2.41	0.55
1:N:413:LYS:HA	1:N:416:ALA:HB3	1.88	0.55
1:P:578:GLN:HG2	1:P:596:ALA:HB2	1.87	0.55
1:R:209:PHE:HZ	1:R:214:GLN:HG2	1.70	0.55
1:T:71:MSE:HE2	1:T:119:ILE:HD11	1.87	0.55
1:N:404:MSE:HE1	1:V:334:MSE:SE	2.56	0.55
1:W:546:THR:CG2	1:W:547:PRO:HD3	2.29	0.55
1:A:248:LYS:HG3	1:A:511:ARG:HH11	1.70	0.55
1:C:380:ASN:O	1:C:381:SER:HB3	2.07	0.55
1:D:210:PRO:HD2	1:D:211:TRP:CE3	2.41	0.55
1:G:337:ASN:ND2	1:G:401:ASN:HD22	2.04	0.55
1:G:47:GLN:H	1:G:47:GLN:CD	2.10	0.55
1:K:108:LYS:HD3	1:K:112:ASN:ND2	2.21	0.55
1:K:236:GLN:CB	1:K:265:LYS:HZ3	2.17	0.55
1:N:209:PHE:N	1:N:210:PRO:HD3	2.21	0.55
1:N:296:GLU:HG2	1:N:449:PHE:HB3	1.89	0.55
1:Q:44:TRP:C	1:Q:45:LEU:HD22	2.26	0.55
1:R:444:LEU:C	1:R:446:THR:N	2.54	0.55
1:R:546:THR:CG2	1:R:547:PRO:HD3	2.29	0.55
1:S:557:PHE:CE2	1:U:563:LYS:HD3	2.42	0.55
1:V:456:ALA:HB1	1:V:509:ASP:OD1	2.06	0.55
1:X:94:LEU:HA	1:X:97:MSE:CE	2.36	0.55
1:A:27:ARG:HB2	1:A:313:LYS:HE3	1.89	0.55
1:B:380:ASN:O	1:B:381:SER:HB3	2.06	0.55
1:F:80:TYR:CE2	1:F:94:LEU:HD22	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:235:TYR:HA	1:G:265:LYS:HB3	1.89	0.55
1:H:541:LYS:HD3	1:H:542:THR:HG23	1.87	0.55
1:J:541:LYS:HD3	1:J:542:THR:HG23	1.87	0.55
1:L:273:ARG:NH2	1:L:453:LEU:HD21	2.21	0.55
1:M:273:ARG:HH22	1:M:453:LEU:HD21	1.71	0.55
1:S:78:VAL:HG12	1:S:79:LEU:H	1.71	0.55
1:U:35:PHE:HE1	1:U:321:ARG:NH1	2.05	0.55
1:V:546:THR:CG2	1:V:547:PRO:HD3	2.29	0.55
1:W:210:PRO:HD2	1:W:211:TRP:CD2	2.41	0.55
1:W:95:MSE:HB3	1:W:527:MSE:HE1	1.87	0.55
1:X:46:SER:N	1:X:48:TYR:HE2	1.98	0.55
2:Y:19:VAL:O	2:Y:82:HIS:CD2	2.60	0.55
2:Z:19:VAL:O	2:Z:82:HIS:CD2	2.60	0.55
1:B:108:LYS:HD3	1:B:112:ASN:ND2	2.21	0.55
1:D:27:ARG:HB2	1:D:313:LYS:HE3	1.89	0.55
1:E:235:TYR:HA	1:E:265:LYS:HB3	1.89	0.55
1:F:235:TYR:HA	1:F:265:LYS:HB3	1.89	0.55
1:F:273:ARG:NH2	1:F:453:LEU:HD21	2.21	0.55
1:G:311:GLU:O	1:G:312:ASP:HB2	2.07	0.55
1:J:47:GLN:CD	1:J:47:GLN:H	2.10	0.55
1:K:276:VAL:HG23	1:K:293:ILE:HG23	1.89	0.55
1:J:372:TYR:CE2	1:K:348:LYS:HB2	2.41	0.55
1:M:99:ARG:O	1:M:103:ARG:HG3	2.07	0.55
1:O:71:MSE:HE2	1:O:119:ILE:HD11	1.87	0.55
1:O:510:ILE:HG12	1:O:511:ARG:N	2.21	0.55
1:R:351:PHE:CD2	1:R:356:ILE:HD12	2.41	0.55
1:X:93:VAL:CG1	1:X:458:ARG:HG3	2.37	0.55
1:A:171:ARG:HH21	1:L:182:ASN:ND2	2.05	0.55
1:B:235:TYR:HA	1:B:265:LYS:HB3	1.89	0.55
1:C:248:LYS:HG3	1:C:511:ARG:HH11	1.70	0.55
1:C:235:TYR:HA	1:C:265:LYS:HB3	1.89	0.55
1:C:276:VAL:HG23	1:C:293:ILE:HG23	1.89	0.55
1:C:589:GLU:HA	1:C:592:TRP:HB2	1.89	0.55
1:D:158:TRP:HB3	1:D:173:CYS:CA	2.36	0.55
1:D:306:GLU:O	1:D:316:TYR:HA	2.07	0.55
1:E:27:ARG:HB2	1:E:313:LYS:HE3	1.88	0.55
1:E:80:TYR:CE2	1:E:94:LEU:HD22	2.42	0.55
1:F:108:LYS:HD3	1:F:112:ASN:ND2	2.21	0.55
1:H:108:LYS:HD3	1:H:112:ASN:ND2	2.21	0.55
1:H:47:GLN:H	1:H:47:GLN:CD	2.10	0.55
1:I:108:LYS:HD3	1:I:112:ASN:ND2	2.21	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:161:ASN:ND2	1:K:161:ASN:C	2.59	0.55
1:K:236:GLN:CB	1:K:265:LYS:HG2	2.37	0.55
1:P:24:GLU:C	1:P:26:ARG:N	2.57	0.55
1:S:273:ARG:NH1	1:S:275:ARG:HE	2.05	0.55
1:S:420:VAL:HG22	1:S:428:GLY:HA3	1.88	0.55
1:U:165:MSE:HE1	1:U:435:VAL:HB	1.89	0.55
1:W:296:GLU:HG2	1:W:449:PHE:HB3	1.89	0.55
1:A:108:LYS:HD3	1:A:112:ASN:ND2	2.21	0.55
1:A:306:GLU:O	1:A:316:TYR:HA	2.07	0.55
1:A:589:GLU:HA	1:A:592:TRP:HB2	1.89	0.55
1:C:108:LYS:HD3	1:C:112:ASN:ND2	2.21	0.55
1:D:108:LYS:HD3	1:D:112:ASN:ND2	2.21	0.55
1:D:276:VAL:HG23	1:D:293:ILE:HG23	1.89	0.55
1:E:589:GLU:HA	1:E:592:TRP:HB2	1.89	0.55
1:F:158:TRP:HB3	1:F:173:CYS:CA	2.36	0.55
1:F:306:GLU:O	1:F:316:TYR:HA	2.07	0.55
1:I:235:TYR:HA	1:I:265:LYS:HB3	1.89	0.55
1:K:337:ASN:ND2	1:K:401:ASN:HD22	2.04	0.55
1:K:80:TYR:CE2	1:K:94:LEU:HD22	2.42	0.55
1:L:108:LYS:HD3	1:L:112:ASN:ND2	2.21	0.55
1:M:209:PHE:N	1:M:210:PRO:HD3	2.21	0.55
1:M:296:GLU:HG2	1:M:449:PHE:HB3	1.89	0.55
1:Q:47:GLN:HG2	1:Q:48:TYR:N	2.22	0.55
1:U:578:GLN:HG2	1:U:596:ALA:HB2	1.88	0.55
1:V:554:LEU:HD12	1:V:557:PHE:HD2	1.70	0.55
2:Y:34:LEU:C	2:Y:35:THR:CG2	2.73	0.55
1:C:158:TRP:HB3	1:C:173:CYS:CA	2.36	0.55
1:C:337:ASN:ND2	1:C:401:ASN:HD22	2.04	0.55
1:D:311:GLU:O	1:D:312:ASP:HB2	2.07	0.55
1:D:380:ASN:O	1:D:381:SER:HB3	2.07	0.55
1:E:276:VAL:HG23	1:E:293:ILE:HG23	1.89	0.55
1:F:334:MSE:HE3	1:G:404:MSE:CE	2.37	0.55
1:F:380:ASN:O	1:F:381:SER:HB3	2.06	0.55
1:H:380:ASN:O	1:H:381:SER:HB3	2.06	0.55
1:I:589:GLU:HA	1:I:592:TRP:HB2	1.89	0.55
1:L:34:PHE:HZ	1:L:328:ARG:HH22	0.80	0.55
1:P:44:TRP:C	1:P:45:LEU:HD22	2.27	0.55
1:P:47:GLN:HG2	1:P:48:TYR:N	2.20	0.55
1:P:584:PRO:HG2	1:P:593:LEU:HD12	1.89	0.55
1:P:593:LEU:O	1:P:597:GLN:HG2	2.07	0.55
1:R:86:ALA:HB2	1:R:515:GLU:HG3	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:302:PRO:O	1:V:439:ASN:ND2	2.40	0.55
1:W:510:ILE:HG12	1:W:511:ARG:N	2.20	0.55
3:R:719:HOH:O	1:X:430:VAL:CG1	2.55	0.55
2:Y:27:GLY:HA2	2:Y:30:SER:HB3	1.88	0.55
1:A:380:ASN:O	1:A:381:SER:HB3	2.07	0.54
1:B:337:ASN:ND2	1:B:401:ASN:HD22	2.04	0.54
1:E:236:GLN:CB	1:E:265:LYS:HG2	2.37	0.54
1:G:161:ASN:C	1:G:161:ASN:ND2	2.59	0.54
1:H:158:TRP:HB3	1:H:173:CYS:CA	2.36	0.54
1:I:276:VAL:HG23	1:I:293:ILE:HG23	1.89	0.54
1:J:108:LYS:HD3	1:J:112:ASN:ND2	2.21	0.54
1:K:380:ASN:O	1:K:381:SER:HB3	2.06	0.54
1:L:306:GLU:O	1:L:316:TYR:HA	2.07	0.54
1:L:311:GLU:O	1:L:312:ASP:HB2	2.07	0.54
1:L:37:ARG:CB	1:L:37:ARG:HH21	2.16	0.54
1:M:35:PHE:HE1	1:M:321:ARG:NH1	2.04	0.54
1:N:93:VAL:CG1	1:N:458:ARG:HG3	2.38	0.54
1:N:78:VAL:HG12	1:N:79:LEU:H	1.72	0.54
1:P:210:PRO:HD2	1:P:211:TRP:CD2	2.41	0.54
1:P:389:LEU:HD12	1:P:389:LEU:H	1.73	0.54
1:Q:154:SER:O	1:Q:204:PRO:HB3	2.07	0.54
1:Q:35:PHE:CE1	1:Q:321:ARG:NE	2.75	0.54
1:S:44:TRP:C	1:S:45:LEU:HD22	2.27	0.54
1:S:593:LEU:O	1:S:597:GLN:HG2	2.06	0.54
1:T:199:PRO:HB3	1:T:282:THR:HG22	1.87	0.54
1:X:44:TRP:CE2	1:X:54:ARG:HB3	2.42	0.54
1:A:235:TYR:HA	1:A:265:LYS:HB3	1.89	0.54
1:B:248:LYS:CG	1:B:511:ARG:HH11	2.19	0.54
1:C:236:GLN:HE21	1:C:265:LYS:NZ	2.06	0.54
1:C:80:TYR:CE2	1:C:94:LEU:HD22	2.42	0.54
1:E:108:LYS:HD3	1:E:112:ASN:ND2	2.21	0.54
1:F:27:ARG:HB2	1:F:313:LYS:HE3	1.88	0.54
1:G:80:TYR:CE2	1:G:94:LEU:HD22	2.42	0.54
1:H:236:GLN:CB	1:H:265:LYS:HZ3	2.16	0.54
1:H:80:TYR:CE2	1:H:94:LEU:HD22	2.42	0.54
1:J:276:VAL:HG23	1:J:293:ILE:HG23	1.89	0.54
1:J:306:GLU:O	1:J:316:TYR:HA	2.07	0.54
1:J:337:ASN:ND2	1:J:401:ASN:HD22	2.04	0.54
1:K:34:PHE:HZ	1:K:328:ARG:HH22	0.80	0.54
1:J:72:ARG:HD2	1:K:434:THR:HG21	1.89	0.54
1:M:456:ALA:HB1	1:M:509:ASP:OD1	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:593:LEU:O	1:M:597:GLN:HG2	2.07	0.54
1:N:158:TRP:HD1	1:N:158:TRP:N	2.06	0.54
1:M:557:PHE:CE2	1:N:563:LYS:HD3	2.42	0.54
1:N:578:GLN:HG2	1:N:596:ALA:HB2	1.89	0.54
1:O:35:PHE:HE1	1:O:321:ARG:NH1	2.05	0.54
1:S:35:PHE:CE1	1:S:321:ARG:NE	2.75	0.54
1:S:546:THR:CG2	1:S:547:PRO:HD3	2.30	0.54
1:T:47:GLN:HG2	1:T:48:TYR:N	2.22	0.54
1:U:209:PHE:N	1:U:210:PRO:HD3	2.21	0.54
1:X:165:MSE:HE3	1:X:304:PHE:HB2	1.88	0.54
1:A:80:TYR:CE2	1:A:94:LEU:HD22	2.42	0.54
1:B:80:TYR:CE2	1:B:94:LEU:HD22	2.42	0.54
1:C:311:GLU:O	1:C:312:ASP:HB2	2.07	0.54
1:C:444:LEU:C	1:C:446:THR:N	2.61	0.54
1:E:236:GLN:HE21	1:E:265:LYS:NZ	2.06	0.54
1:E:306:GLU:O	1:E:316:TYR:HA	2.07	0.54
1:F:123:VAL:HG22	1:F:316:TYR:CE2	2.43	0.54
1:F:337:ASN:ND2	1:F:401:ASN:HD22	2.04	0.54
1:G:138:THR:H	1:G:143:VAL:HG22	1.73	0.54
1:I:158:TRP:HB3	1:I:173:CYS:CA	2.36	0.54
1:K:589:GLU:HA	1:K:592:TRP:HB2	1.89	0.54
1:M:101:ASP:HB2	1:M:144:ILE:O	2.07	0.54
1:P:209:PHE:N	1:P:210:PRO:HD3	2.21	0.54
1:P:35:PHE:CE1	1:P:321:ARG:NE	2.76	0.54
1:P:78:VAL:CG1	1:P:79:LEU:N	2.70	0.54
1:T:510:ILE:HG12	1:T:511:ARG:N	2.22	0.54
1:T:94:LEU:HA	1:T:97:MSE:CE	2.36	0.54
1:U:209:PHE:HZ	1:U:214:GLN:HG2	1.71	0.54
1:U:93:VAL:CG1	1:U:458:ARG:HG3	2.36	0.54
1:A:123:VAL:HG22	1:A:316:TYR:CE2	2.43	0.54
1:A:337:ASN:ND2	1:A:401:ASN:HD22	2.04	0.54
1:B:123:VAL:HG22	1:B:316:TYR:CE2	2.43	0.54
1:B:37:ARG:CB	1:B:37:ARG:HH21	2.16	0.54
1:C:236:GLN:CB	1:C:265:LYS:HG2	2.37	0.54
1:C:306:GLU:O	1:C:316:TYR:HA	2.07	0.54
1:C:72:ARG:HD2	1:E:434:THR:HG21	1.90	0.54
1:D:444:LEU:C	1:D:446:THR:N	2.61	0.54
1:F:236:GLN:HE21	1:F:265:LYS:NZ	2.06	0.54
1:F:561:ASP:OD2	1:G:92:ASP:HB3	2.07	0.54
1:G:15:PHE:HZ	1:G:283:CYS:SG	2.31	0.54
1:J:123:VAL:HG22	1:J:316:TYR:CE2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:80:TYR:CE2	1:J:94:LEU:HD22	2.42	0.54
1:M:158:TRP:HD1	1:M:158:TRP:N	2.04	0.54
1:M:273:ARG:NH1	1:M:275:ARG:HE	2.05	0.54
1:M:302:PRO:O	1:M:439:ASN:ND2	2.41	0.54
1:S:154:SER:O	1:S:204:PRO:HB3	2.07	0.54
1:S:209:PHE:HZ	1:S:214:GLN:HG2	1.70	0.54
1:S:94:LEU:HA	1:S:97:MSE:CE	2.37	0.54
1:T:584:PRO:HG2	1:T:593:LEU:HD12	1.90	0.54
1:U:26:ARG:HG2	1:X:212:LEU:HD22	1.88	0.54
1:V:390:ALA:HB2	1:W:387:GLN:CB	2.38	0.54
1:W:578:GLN:HG2	1:W:596:ALA:HB2	1.87	0.54
1:X:209:PHE:HZ	1:X:214:GLN:HG2	1.70	0.54
1:X:35:PHE:CE1	1:X:321:ARG:NE	2.75	0.54
1:A:161:ASN:C	1:A:161:ASN:ND2	2.59	0.54
1:A:15:PHE:HZ	1:A:283:CYS:SG	2.31	0.54
1:C:273:ARG:NH2	1:C:453:LEU:HD21	2.21	0.54
1:D:235:TYR:HA	1:D:265:LYS:HB3	1.89	0.54
1:D:15:PHE:HZ	1:D:283:CYS:SG	2.31	0.54
1:F:236:GLN:CB	1:F:265:LYS:HZ3	2.16	0.54
1:F:311:GLU:O	1:F:312:ASP:HB2	2.07	0.54
1:F:589:GLU:HA	1:F:592:TRP:HB2	1.89	0.54
1:H:138:THR:H	1:H:143:VAL:HG22	1.73	0.54
1:H:235:TYR:HA	1:H:265:LYS:HB3	1.89	0.54
1:I:236:GLN:CB	1:I:265:LYS:HG2	2.37	0.54
1:I:311:GLU:O	1:I:312:ASP:HB2	2.07	0.54
1:I:47:GLN:CD	1:I:47:GLN:H	2.10	0.54
1:K:236:GLN:HE21	1:K:265:LYS:NZ	2.06	0.54
1:L:15:PHE:HZ	1:L:283:CYS:SG	2.31	0.54
1:L:47:GLN:CD	1:L:47:GLN:H	2.10	0.54
1:M:47:GLN:HG2	1:M:48:TYR:N	2.22	0.54
1:M:584:PRO:HG2	1:M:593:LEU:HD12	1.90	0.54
1:O:101:ASP:HB2	1:O:144:ILE:O	2.07	0.54
1:P:35:PHE:C	1:P:37:ARG:H	2.11	0.54
1:R:66:LYS:NZ	1:R:420:VAL:HG11	2.22	0.54
1:Q:561:ASP:CB	1:R:89:ASP:HA	2.31	0.54
1:T:66:LYS:NZ	1:T:420:VAL:HG11	2.23	0.54
1:U:144:ILE:HD12	1:U:145:ARG:N	2.22	0.54
1:V:93:VAL:CG1	1:V:458:ARG:HG3	2.37	0.54
1:T:387:GLN:HB2	1:W:390:ALA:HB2	1.90	0.54
1:X:209:PHE:N	1:X:210:PRO:HD3	2.21	0.54
2:Z:42:MET:HE3	2:Z:78:GLU:OE1	2.08	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:273:ARG:NH2	1:A:453:LEU:HD21	2.21	0.54
1:E:44:TRP:C	1:E:45:LEU:HD22	2.28	0.54
1:G:306:GLU:O	1:G:316:TYR:HA	2.07	0.54
1:H:311:GLU:O	1:H:312:ASP:HB2	2.07	0.54
1:G:372:TYR:CE2	1:H:348:LYS:HB2	2.42	0.54
1:H:444:LEU:C	1:H:446:THR:N	2.61	0.54
1:H:44:TRP:C	1:H:45:LEU:HD22	2.28	0.54
1:I:306:GLU:O	1:I:316:TYR:HA	2.07	0.54
1:J:138:THR:H	1:J:143:VAL:HG22	1.73	0.54
1:J:34:PHE:HZ	1:J:328:ARG:HH22	0.80	0.54
1:K:311:GLU:O	1:K:312:ASP:HB2	2.07	0.54
1:K:27:ARG:HB2	1:K:313:LYS:HE3	1.89	0.54
1:K:306:GLU:O	1:K:316:TYR:HA	2.07	0.54
1:K:37:ARG:CB	1:K:37:ARG:HH21	2.16	0.54
1:M:510:ILE:HG12	1:M:511:ARG:N	2.22	0.54
1:N:95:MSE:HB3	1:N:527:MSE:HE1	1.88	0.54
1:P:273:ARG:NH1	1:P:275:ARG:HE	2.06	0.54
1:P:302:PRO:O	1:P:439:ASN:ND2	2.41	0.54
1:Q:593:LEU:O	1:Q:597:GLN:HG2	2.08	0.54
1:Q:78:VAL:HG12	1:Q:79:LEU:H	1.70	0.54
1:R:573:ASN:O	1:R:577:ILE:HG13	2.08	0.54
1:S:46:SER:N	1:S:48:TYR:HE2	1.99	0.54
1:T:420:VAL:HG22	1:T:428:GLY:HA3	1.90	0.54
1:V:144:ILE:HD12	1:V:145:ARG:N	2.22	0.54
1:W:456:ALA:HB1	1:W:509:ASP:OD1	2.08	0.54
1:X:420:VAL:HG22	1:X:428:GLY:HA3	1.90	0.54
2:Z:27:GLY:HA2	2:Z:30:SER:HB3	1.88	0.54
1:A:47:GLN:H	1:A:47:GLN:CD	2.10	0.54
1:C:138:THR:H	1:C:143:VAL:HG22	1.73	0.54
1:D:236:GLN:HE21	1:D:265:LYS:NZ	2.06	0.54
1:D:384:LEU:N	1:D:384:LEU:HD22	2.23	0.54
1:D:561:ASP:OD2	1:F:92:ASP:HB3	2.07	0.54
1:G:236:GLN:CB	1:G:265:LYS:HG2	2.37	0.54
1:H:236:GLN:HE21	1:H:265:LYS:NZ	2.06	0.54
1:H:27:ARG:HB2	1:H:313:LYS:HE3	1.89	0.54
1:L:235:TYR:HA	1:L:265:LYS:HB3	1.89	0.54
1:O:81:ARG:HB2	1:O:517:TYR:CZ	2.42	0.54
1:R:154:SER:O	1:R:204:PRO:HB3	2.08	0.54
1:S:40:GLN:HG2	1:T:310:VAL:HG22	1.90	0.54
1:S:456:ALA:HB1	1:S:509:ASP:OD1	2.07	0.54
1:T:296:GLU:HG2	1:T:449:PHE:HB3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:444:LEU:C	1:U:446:THR:H	2.11	0.54
1:W:46:SER:N	1:W:48:TYR:HE2	1.97	0.54
1:W:66:LYS:NZ	1:W:420:VAL:HG11	2.23	0.54
1:X:71:MSE:HE2	1:X:119:ILE:HD11	1.88	0.54
2:Z:71:ASP:O	2:Z:72:ASP:HB3	2.08	0.54
1:B:306:GLU:O	1:B:316:TYR:HA	2.07	0.54
1:C:44:TRP:C	1:C:45:LEU:HD22	2.28	0.54
1:E:123:VAL:HG22	1:E:316:TYR:CE2	2.43	0.54
1:G:236:GLN:HE21	1:G:265:LYS:NZ	2.06	0.54
1:I:14:ARG:CA	1:I:14:ARG:NE	2.67	0.54
1:J:44:TRP:C	1:J:45:LEU:HD22	2.28	0.54
1:J:47:GLN:O	1:J:47:GLN:NE2	2.41	0.54
1:K:15:PHE:HZ	1:K:283:CYS:SG	2.31	0.54
1:K:44:TRP:C	1:K:45:LEU:HD22	2.28	0.54
1:K:47:GLN:O	1:K:47:GLN:NE2	2.41	0.54
1:M:78:VAL:HG12	1:M:79:LEU:H	1.73	0.54
1:O:593:LEU:O	1:O:597:GLN:HG2	2.07	0.54
1:S:47:GLN:HG2	1:S:48:TYR:N	2.22	0.54
1:V:101:ASP:HB2	1:V:144:ILE:O	2.08	0.54
1:V:80:TYR:CE1	1:V:448:VAL:HG22	2.43	0.54
1:X:66:LYS:HZ3	1:X:420:VAL:HG11	1.73	0.54
2:Y:58:GLN:H	2:Y:62:GLY:HA3	1.73	0.54
1:B:236:GLN:HE21	1:B:265:LYS:NZ	2.06	0.54
1:B:234:ILE:HG13	1:B:267:ALA:HB3	1.90	0.54
1:B:311:GLU:O	1:B:312:ASP:HB2	2.07	0.54
1:C:27:ARG:HB2	1:C:313:LYS:HE3	1.89	0.54
1:D:35:PHE:C	1:D:37:ARG:N	2.62	0.54
1:D:47:GLN:O	1:D:47:GLN:NE2	2.41	0.54
1:D:80:TYR:CE2	1:D:94:LEU:HD22	2.42	0.54
1:E:37:ARG:HH21	1:E:37:ARG:CB	2.16	0.54
1:E:384:LEU:N	1:E:384:LEU:HD22	2.23	0.54
1:F:234:ILE:HG13	1:F:267:ALA:HB3	1.90	0.54
1:G:108:LYS:HD3	1:G:112:ASN:ND2	2.21	0.54
1:G:35:PHE:C	1:G:37:ARG:N	2.62	0.54
1:G:80:TYR:CE1	1:G:448:VAL:HG22	2.43	0.54
1:H:123:VAL:HG22	1:H:316:TYR:CE2	2.43	0.54
1:I:15:PHE:HZ	1:I:283:CYS:SG	2.31	0.54
1:I:47:GLN:NE2	1:I:47:GLN:O	2.41	0.54
1:J:235:TYR:HA	1:J:265:LYS:HB3	1.89	0.54
1:J:236:GLN:CB	1:J:265:LYS:HG2	2.37	0.54
1:K:80:TYR:CE1	1:K:448:VAL:HG22	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:80:TYR:CE2	1:L:94:LEU:HD22	2.42	0.54
1:M:209:PHE:HZ	1:M:214:GLN:HG2	1.70	0.54
1:M:93:VAL:CG1	1:M:458:ARG:HG3	2.37	0.54
1:O:236:GLN:HA	1:O:244:VAL:H	1.73	0.54
1:O:584:PRO:HG2	1:O:593:LEU:HD12	1.90	0.54
1:Q:209:PHE:HZ	1:Q:214:GLN:HG2	1.70	0.54
1:Q:405:LEU:O	1:Q:409:THR:HG23	2.08	0.54
1:U:420:VAL:HG22	1:U:428:GLY:HA3	1.89	0.54
1:W:81:ARG:HB2	1:W:517:TYR:CZ	2.43	0.54
1:W:584:PRO:HG2	1:W:593:LEU:HD12	1.89	0.54
2:Y:78:GLU:CD	2:Y:79:GLY:H	2.11	0.54
1:A:528:LYS:HZ2	1:A:560:LEU:HD21	1.72	0.54
1:D:123:VAL:HG22	1:D:316:TYR:CE2	2.43	0.54
1:E:138:THR:H	1:E:143:VAL:HG22	1.73	0.54
1:F:560:LEU:O	1:F:561:ASP:O	2.26	0.54
1:F:80:TYR:CE1	1:F:448:VAL:HG22	2.43	0.54
1:G:158:TRP:HB3	1:G:173:CYS:CA	2.36	0.54
1:G:266:ILE:HG23	1:G:267:ALA:N	2.23	0.54
1:G:44:TRP:C	1:G:45:LEU:HD22	2.28	0.54
1:G:589:GLU:HA	1:G:592:TRP:HB2	1.89	0.54
1:J:15:PHE:HZ	1:J:283:CYS:SG	2.31	0.54
1:J:560:LEU:O	1:J:561:ASP:O	2.26	0.54
1:J:579:MSE:HB2	1:J:581:VAL:HG12	1.90	0.54
1:K:14:ARG:NE	1:K:14:ARG:CA	2.67	0.54
1:K:47:GLN:H	1:K:47:GLN:CD	2.10	0.54
1:L:123:VAL:HG22	1:L:316:TYR:CE2	2.43	0.54
1:N:101:ASP:HB2	1:N:144:ILE:O	2.08	0.54
1:N:47:GLN:HG2	1:N:48:TYR:N	2.22	0.54
1:O:563:LYS:HD3	1:P:557:PHE:CE2	2.42	0.54
1:Q:344:THR:HG23	1:Q:344:THR:O	2.07	0.54
1:Q:584:PRO:HG2	1:Q:593:LEU:HD12	1.90	0.54
1:S:444:LEU:C	1:S:446:THR:H	2.11	0.54
1:S:66:LYS:NZ	1:S:420:VAL:HG11	2.22	0.54
1:T:123:VAL:HG22	1:T:316:TYR:CE2	2.42	0.54
1:U:191:TYR:HE1	1:U:278:LYS:HZ3	1.56	0.54
1:U:390:ALA:HB2	1:X:387:GLN:HB2	1.89	0.54
1:X:66:LYS:NZ	1:X:420:VAL:HG11	2.23	0.54
2:Z:78:GLU:CD	2:Z:79:GLY:H	2.11	0.54
1:B:35:PHE:C	1:B:37:ARG:N	2.61	0.53
1:C:161:ASN:ND2	1:C:161:ASN:C	2.59	0.53
1:C:80:TYR:CE1	1:C:448:VAL:HG22	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:234:ILE:HG13	1:E:267:ALA:HB3	1.91	0.53
1:E:47:GLN:H	1:E:47:GLN:CD	2.10	0.53
1:F:266:ILE:HG23	1:F:267:ALA:N	2.23	0.53
1:F:384:LEU:HD22	1:F:384:LEU:N	2.23	0.53
1:G:384:LEU:N	1:G:384:LEU:HD22	2.23	0.53
1:H:266:ILE:HG23	1:H:267:ALA:N	2.23	0.53
1:H:47:GLN:NE2	1:H:47:GLN:O	2.41	0.53
1:H:78:VAL:HG11	1:H:444:LEU:HG	1.90	0.53
1:K:234:ILE:HG13	1:K:267:ALA:HB3	1.90	0.53
1:K:123:VAL:HG22	1:K:316:TYR:CE2	2.43	0.53
1:K:35:PHE:C	1:K:37:ARG:N	2.61	0.53
1:K:560:LEU:O	1:K:561:ASP:O	2.26	0.53
1:M:389:LEU:H	1:M:389:LEU:HD12	1.72	0.53
1:M:444:LEU:O	1:M:448:VAL:HG23	2.08	0.53
1:M:81:ARG:HB2	1:M:517:TYR:CZ	2.43	0.53
1:N:273:ARG:NH1	1:N:275:ARG:HE	2.05	0.53
1:N:389:LEU:HD12	1:N:389:LEU:H	1.72	0.53
1:N:535:ILE:HD13	1:N:554:LEU:HG	1.89	0.53
1:O:296:GLU:HG2	1:O:449:PHE:HB3	1.89	0.53
1:P:101:ASP:HB2	1:P:144:ILE:O	2.08	0.53
1:P:209:PHE:HZ	1:P:214:GLN:HG2	1.70	0.53
1:P:444:LEU:C	1:P:446:THR:H	2.11	0.53
1:U:58:ASP:HA	1:U:327:GLN:NE2	2.23	0.53
1:U:78:VAL:CG2	1:U:444:LEU:HD11	2.22	0.53
1:V:389:LEU:H	1:V:389:LEU:HD12	1.72	0.53
1:W:94:LEU:HA	1:W:97:MSE:CE	2.37	0.53
1:U:390:ALA:HB2	1:X:387:GLN:CB	2.38	0.53
2:Y:78:GLU:HG3	2:Y:79:GLY:N	2.20	0.53
1:A:236:GLN:CB	1:A:265:LYS:HG2	2.37	0.53
1:A:236:GLN:HE21	1:A:265:LYS:NZ	2.06	0.53
1:A:37:ARG:HH21	1:A:37:ARG:CB	2.16	0.53
1:B:273:ARG:NH2	1:B:453:LEU:HD21	2.21	0.53
1:B:47:GLN:NE2	1:B:47:GLN:O	2.41	0.53
1:C:35:PHE:C	1:C:37:ARG:N	2.62	0.53
1:C:47:GLN:H	1:C:47:GLN:CD	2.10	0.53
1:C:47:GLN:NE2	1:C:47:GLN:O	2.41	0.53
1:E:311:GLU:O	1:E:312:ASP:HB2	2.07	0.53
1:E:80:TYR:CE1	1:E:448:VAL:HG22	2.43	0.53
1:G:177:HIS:O	1:G:218:GLN:HA	2.08	0.53
1:G:444:LEU:C	1:G:446:THR:N	2.61	0.53
1:G:560:LEU:O	1:G:561:ASP:O	2.26	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:78:VAL:HG11	1:G:444:LEU:HG	1.90	0.53
1:H:306:GLU:O	1:H:316:TYR:HA	2.07	0.53
1:I:236:GLN:HE21	1:I:265:LYS:NZ	2.06	0.53
1:I:78:VAL:HG11	1:I:444:LEU:HG	1.90	0.53
1:I:560:LEU:O	1:I:561:ASP:O	2.26	0.53
1:I:80:TYR:CE1	1:I:448:VAL:HG22	2.43	0.53
1:J:191:TYR:HE1	1:J:278:LYS:HZ3	1.54	0.53
1:J:35:PHE:C	1:J:37:ARG:N	2.61	0.53
1:J:78:VAL:HG11	1:J:444:LEU:HG	1.90	0.53
1:L:177:HIS:O	1:L:218:GLN:HA	2.09	0.53
1:L:234:ILE:HG13	1:L:267:ALA:HB3	1.90	0.53
1:M:398:PRO:HB3	1:N:395:PRO:HD2	1.90	0.53
1:N:456:ALA:HB1	1:N:509:ASP:OD1	2.08	0.53
1:N:46:SER:N	1:N:48:TYR:HE2	1.98	0.53
1:O:344:THR:O	1:O:344:THR:HG23	2.08	0.53
1:O:434:THR:HA	1:O:437:GLN:HG2	1.90	0.53
1:P:405:LEU:O	1:P:409:THR:HG23	2.08	0.53
1:Q:66:LYS:NZ	1:Q:420:VAL:HG11	2.23	0.53
1:S:584:PRO:HG2	1:S:593:LEU:HD12	1.89	0.53
1:U:35:PHE:C	1:U:37:ARG:H	2.11	0.53
1:W:154:SER:O	1:W:204:PRO:HB3	2.08	0.53
1:W:434:THR:O	1:W:437:GLN:HG2	2.08	0.53
1:X:37:ARG:CB	1:X:37:ARG:HH21	2.20	0.53
1:B:328:ARG:HB3	2:Y:142:PRO:HG3	1.90	0.53
1:A:266:ILE:HG23	1:A:267:ALA:N	2.23	0.53
1:B:384:LEU:HD22	1:B:384:LEU:N	2.23	0.53
1:C:123:VAL:HG22	1:C:316:TYR:CE2	2.43	0.53
1:C:384:LEU:HD22	1:C:384:LEU:N	2.23	0.53
1:D:266:ILE:HG23	1:D:267:ALA:N	2.23	0.53
1:E:35:PHE:C	1:E:37:ARG:N	2.62	0.53
1:F:138:THR:H	1:F:143:VAL:HG22	1.73	0.53
1:F:78:VAL:HG11	1:F:444:LEU:HG	1.90	0.53
1:G:123:VAL:HG22	1:G:316:TYR:CE2	2.43	0.53
1:H:276:VAL:HG23	1:H:293:ILE:HG23	1.89	0.53
1:I:80:TYR:CE2	1:I:94:LEU:HD22	2.42	0.53
1:J:266:ILE:HG23	1:J:267:ALA:N	2.23	0.53
1:J:311:GLU:O	1:J:312:ASP:HB2	2.07	0.53
1:K:78:VAL:HG11	1:K:444:LEU:HG	1.91	0.53
1:L:276:VAL:HG23	1:L:293:ILE:HG23	1.89	0.53
1:N:236:GLN:HA	1:N:244:VAL:H	1.74	0.53
1:N:81:ARG:HB2	1:N:517:TYR:CZ	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:154:SER:O	1:O:204:PRO:HB3	2.07	0.53
1:P:66:LYS:NZ	1:P:420:VAL:HG11	2.24	0.53
1:R:47:GLN:HG2	1:R:48:TYR:N	2.23	0.53
1:S:35:PHE:C	1:S:37:ARG:H	2.12	0.53
1:S:80:TYR:CE1	1:S:448:VAL:HG22	2.43	0.53
1:T:593:LEU:O	1:T:597:GLN:HG2	2.08	0.53
1:S:26:ARG:HG2	1:U:212:LEU:HD22	1.90	0.53
1:V:66:LYS:NZ	1:V:420:VAL:HG11	2.22	0.53
1:W:273:ARG:NH1	1:W:275:ARG:HE	2.06	0.53
1:W:344:THR:O	1:W:344:THR:HG23	2.08	0.53
1:X:593:LEU:O	1:X:597:GLN:HG2	2.08	0.53
1:A:384:LEU:N	1:A:384:LEU:HD22	2.23	0.53
1:A:560:LEU:O	1:A:561:ASP:O	2.26	0.53
1:B:138:THR:H	1:B:143:VAL:HG22	1.73	0.53
1:B:177:HIS:O	1:B:218:GLN:HA	2.09	0.53
1:B:15:PHE:HZ	1:B:283:CYS:SG	2.31	0.53
1:B:47:GLN:H	1:B:47:GLN:CD	2.10	0.53
1:D:78:VAL:HG11	1:D:444:LEU:HG	1.90	0.53
1:D:44:TRP:C	1:D:45:LEU:HD22	2.28	0.53
1:E:266:ILE:HG23	1:E:267:ALA:N	2.23	0.53
1:C:334:MSE:HE3	1:E:404:MSE:HE3	1.90	0.53
1:E:47:GLN:O	1:E:47:GLN:NE2	2.41	0.53
1:F:177:HIS:O	1:F:218:GLN:HA	2.09	0.53
1:F:276:VAL:HG23	1:F:293:ILE:HG23	1.89	0.53
1:G:276:VAL:HG23	1:G:293:ILE:HG23	1.89	0.53
1:G:273:ARG:NH2	1:G:453:LEU:HD21	2.21	0.53
1:H:236:GLN:CB	1:H:265:LYS:HG2	2.37	0.53
1:H:560:LEU:O	1:H:561:ASP:O	2.26	0.53
1:I:27:ARG:HB2	1:I:313:LYS:HE3	1.89	0.53
1:I:44:TRP:C	1:I:45:LEU:HD22	2.28	0.53
1:K:138:THR:H	1:K:143:VAL:HG22	1.73	0.53
1:K:235:TYR:HA	1:K:265:LYS:HB3	1.89	0.53
1:K:266:ILE:HG23	1:K:267:ALA:N	2.23	0.53
1:K:579:MSE:HB2	1:K:581:VAL:HG12	1.91	0.53
1:L:78:VAL:HG11	1:L:444:LEU:HG	1.90	0.53
1:L:80:TYR:CE1	1:L:448:VAL:HG22	2.43	0.53
1:M:44:TRP:CE2	1:M:54:ARG:HB3	2.43	0.53
1:N:44:TRP:CE2	1:N:54:ARG:HB3	2.43	0.53
1:N:584:PRO:HG2	1:N:593:LEU:HD12	1.91	0.53
1:O:427:GLY:C	1:O:429:GLN:H	2.12	0.53
1:O:444:LEU:O	1:O:448:VAL:HG23	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:236:GLN:HA	1:P:244:VAL:H	1.72	0.53
1:P:58:ASP:HA	1:P:327:GLN:NE2	2.24	0.53
1:Q:236:GLN:HA	1:Q:244:VAL:H	1.74	0.53
1:R:395:PRO:HD2	1:X:398:PRO:HB3	1.90	0.53
3:Q:718:HOH:O	1:R:438:LEU:HD22	2.08	0.53
1:T:158:TRP:HD1	1:T:158:TRP:N	2.07	0.53
1:T:44:TRP:C	1:T:45:LEU:HD22	2.29	0.53
1:V:420:VAL:HG22	1:V:428:GLY:HA3	1.90	0.53
1:V:584:PRO:HG2	1:V:593:LEU:HD12	1.90	0.53
1:W:35:PHE:HE1	1:W:321:ARG:NH1	2.05	0.53
1:W:44:TRP:C	1:W:45:LEU:HD22	2.28	0.53
1:W:78:VAL:CG1	1:W:79:LEU:N	2.71	0.53
1:A:80:TYR:CE1	1:A:448:VAL:HG22	2.43	0.53
1:C:78:VAL:HG11	1:C:444:LEU:HG	1.90	0.53
1:E:15:PHE:HZ	1:E:283:CYS:SG	2.31	0.53
1:F:15:PHE:HZ	1:F:283:CYS:SG	2.31	0.53
1:F:78:VAL:CG1	1:F:79:LEU:N	2.72	0.53
1:G:229:LYS:HA	1:G:272:LYS:HA	1.90	0.53
1:H:177:HIS:O	1:H:218:GLN:HA	2.09	0.53
1:L:266:ILE:HG23	1:L:267:ALA:N	2.23	0.53
1:L:44:TRP:C	1:L:45:LEU:HD22	2.28	0.53
1:N:593:LEU:O	1:N:597:GLN:HG2	2.08	0.53
1:O:66:LYS:NZ	1:O:420:VAL:HG11	2.23	0.53
1:P:78:VAL:HG12	1:P:79:LEU:H	1.69	0.53
1:Q:444:LEU:C	1:Q:446:THR:H	2.12	0.53
1:S:44:TRP:CE2	1:S:54:ARG:HB3	2.44	0.53
1:T:344:THR:HG23	1:T:344:THR:O	2.06	0.53
1:T:444:LEU:O	1:T:448:VAL:HG23	2.09	0.53
1:T:78:VAL:HG12	1:T:79:LEU:H	1.72	0.53
1:U:380:ASN:O	1:U:381:SER:HB3	2.08	0.53
1:W:123:VAL:HG22	1:W:316:TYR:CE2	2.43	0.53
1:A:35:PHE:C	1:A:37:ARG:N	2.62	0.53
1:A:44:TRP:C	1:A:45:LEU:HD22	2.28	0.53
1:A:78:VAL:CG1	1:A:79:LEU:N	2.72	0.53
1:B:276:VAL:HG23	1:B:293:ILE:HG23	1.89	0.53
1:B:444:LEU:C	1:B:446:THR:N	2.61	0.53
1:C:511:ARG:HA	1:C:513:ARG:HD2	1.91	0.53
1:D:138:THR:H	1:D:143:VAL:HG22	1.73	0.53
1:E:158:TRP:HB3	1:E:173:CYS:CA	2.36	0.53
1:F:236:GLN:CB	1:F:265:LYS:HG2	2.37	0.53
1:F:579:MSE:HB2	1:F:581:VAL:HG12	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:35:PHE:C	1:H:37:ARG:N	2.62	0.53
1:H:78:VAL:CG1	1:H:79:LEU:N	2.72	0.53
1:I:384:LEU:N	1:I:384:LEU:HD22	2.23	0.53
1:I:511:ARG:HA	1:I:513:ARG:HD2	1.91	0.53
1:I:579:MSE:HB2	1:I:581:VAL:HG12	1.90	0.53
1:J:177:HIS:O	1:J:218:GLN:HA	2.09	0.53
1:J:229:LYS:HA	1:J:272:LYS:HA	1.90	0.53
1:J:236:GLN:HE21	1:J:265:LYS:NZ	2.06	0.53
1:J:27:ARG:HB2	1:J:313:LYS:HE3	1.89	0.53
1:J:444:LEU:C	1:J:446:THR:N	2.61	0.53
1:M:236:GLN:HA	1:M:244:VAL:H	1.74	0.53
1:M:94:LEU:HA	1:M:97:MSE:CE	2.38	0.53
1:O:47:GLN:HG2	1:O:48:TYR:N	2.23	0.53
1:Q:44:TRP:CE2	1:Q:54:ARG:HB3	2.44	0.53
1:R:101:ASP:HB2	1:R:144:ILE:O	2.08	0.53
1:R:380:ASN:O	1:R:381:SER:HB3	2.09	0.53
1:S:236:GLN:HA	1:S:244:VAL:H	1.74	0.53
1:T:380:ASN:O	1:T:381:SER:HB3	2.09	0.53
1:U:101:ASP:HB2	1:U:144:ILE:O	2.09	0.53
1:U:81:ARG:HB2	1:U:517:TYR:CZ	2.44	0.53
1:V:593:LEU:O	1:V:597:GLN:HG2	2.08	0.53
1:W:144:ILE:HD12	1:W:145:ARG:N	2.24	0.53
1:X:47:GLN:HG2	1:X:48:TYR:N	2.24	0.53
1:X:584:PRO:HG2	1:X:593:LEU:HD12	1.90	0.53
1:B:329:LEU:HD22	2:Y:142:PRO:HG2	1.89	0.53
1:A:311:GLU:O	1:A:312:ASP:HB2	2.07	0.53
1:B:80:TYR:CE1	1:B:448:VAL:HG22	2.43	0.53
1:C:177:HIS:O	1:C:218:GLN:HA	2.09	0.53
1:C:234:ILE:HG13	1:C:267:ALA:HB3	1.91	0.53
1:E:32:ASP:HA	1:E:35:PHE:CE1	2.44	0.53
1:E:78:VAL:HG11	1:E:444:LEU:HG	1.91	0.53
1:G:78:VAL:CG1	1:G:79:LEU:N	2.72	0.53
1:I:123:VAL:HG22	1:I:316:TYR:CE2	2.43	0.53
1:I:177:HIS:O	1:I:218:GLN:HA	2.09	0.53
1:J:511:ARG:HA	1:J:513:ARG:HD2	1.91	0.53
1:J:80:TYR:CE1	1:J:448:VAL:HG22	2.43	0.53
1:K:511:ARG:HA	1:K:513:ARG:HD2	1.91	0.53
1:L:236:GLN:HE21	1:L:265:LYS:NZ	2.06	0.53
1:N:66:LYS:NZ	1:N:420:VAL:HG11	2.23	0.53
1:Q:35:PHE:C	1:Q:37:ARG:H	2.12	0.53
1:Q:165:MSE:HE1	1:Q:435:VAL:HB	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:78:VAL:HG12	1:R:79:LEU:H	1.72	0.53
1:S:123:VAL:HG22	1:S:316:TYR:CE2	2.44	0.53
1:T:58:ASP:HA	1:T:327:GLN:NE2	2.24	0.53
1:T:80:TYR:CE1	1:T:448:VAL:HG22	2.44	0.53
1:U:236:GLN:HA	1:U:244:VAL:H	1.73	0.53
1:U:389:LEU:HD12	1:U:389:LEU:H	1.73	0.53
1:V:81:ARG:HB2	1:V:517:TYR:CZ	2.44	0.53
1:V:598:GLN:HB2	1:V:601:GLN:HB2	1.91	0.53
1:W:35:PHE:C	1:W:37:ARG:H	2.10	0.53
1:W:44:TRP:CE2	1:W:54:ARG:HB3	2.44	0.53
1:W:47:GLN:HG2	1:W:48:TYR:N	2.23	0.53
1:U:348:LYS:HB2	1:X:372:TYR:CE2	2.43	0.53
1:X:380:ASN:O	1:X:381:SER:HB3	2.07	0.53
1:A:177:HIS:O	1:A:218:GLN:HA	2.09	0.53
1:A:234:ILE:HG13	1:A:267:ALA:HB3	1.90	0.53
1:A:276:VAL:HG23	1:A:293:ILE:HG23	1.89	0.53
1:A:511:ARG:HA	1:A:513:ARG:HD2	1.91	0.53
1:B:32:ASP:HA	1:B:35:PHE:CE1	2.44	0.53
1:B:44:TRP:C	1:B:45:LEU:HD22	2.28	0.53
1:D:177:HIS:O	1:D:218:GLN:HA	2.09	0.53
1:E:177:HIS:O	1:E:218:GLN:HA	2.09	0.53
1:F:32:ASP:HA	1:F:35:PHE:CE1	2.44	0.53
1:F:511:ARG:HA	1:F:513:ARG:HD2	1.91	0.53
1:F:395:PRO:HD2	1:G:398:PRO:HB3	1.91	0.53
1:H:229:LYS:HA	1:H:272:LYS:HA	1.90	0.53
1:H:32:ASP:HA	1:H:35:PHE:CE1	2.44	0.53
1:H:384:LEU:HD22	1:H:384:LEU:N	2.23	0.53
1:I:229:LYS:HA	1:I:272:LYS:HA	1.90	0.53
1:L:47:GLN:NE2	1:L:47:GLN:O	2.41	0.53
1:M:35:PHE:CE1	1:M:321:ARG:NE	2.75	0.53
1:M:344:THR:O	1:M:344:THR:HG23	2.07	0.53
1:P:456:ALA:HB1	1:P:509:ASP:OD1	2.09	0.53
1:Q:41:TRP:HE1	1:R:27:ARG:NH2	2.07	0.53
1:R:35:PHE:C	1:R:37:ARG:H	2.11	0.53
1:R:456:ALA:HB1	1:R:509:ASP:OD1	2.08	0.53
1:R:593:LEU:O	1:R:597:GLN:HG2	2.08	0.53
1:U:593:LEU:O	1:U:597:GLN:HG2	2.08	0.53
1:U:66:LYS:NZ	1:U:420:VAL:HG11	2.23	0.53
1:V:351:PHE:CD2	1:V:356:ILE:HD12	2.44	0.53
1:V:35:PHE:HE1	1:V:321:ARG:NH1	2.06	0.53
1:U:352:TRP:CG	1:X:376:ARG:HB2	2.44	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:44:TRP:C	1:X:45:LEU:HD22	2.29	0.53
2:Y:71:ASP:O	2:Y:72:ASP:HB3	2.08	0.53
2:Z:58:GLN:H	2:Z:62:GLY:HA3	1.73	0.53
1:A:138:THR:H	1:A:143:VAL:HG22	1.73	0.53
1:A:47:GLN:NE2	1:A:47:GLN:O	2.41	0.53
1:C:560:LEU:O	1:C:561:ASP:O	2.26	0.53
1:D:560:LEU:O	1:D:561:ASP:O	2.26	0.53
1:E:229:LYS:HA	1:E:272:LYS:HA	1.90	0.53
1:E:511:ARG:HA	1:E:513:ARG:HD2	1.91	0.53
1:H:511:ARG:HA	1:H:513:ARG:HD2	1.91	0.53
1:H:80:TYR:CE1	1:H:448:VAL:HG22	2.43	0.53
1:L:229:LYS:HA	1:L:272:LYS:HA	1.90	0.53
1:L:35:PHE:C	1:L:37:ARG:N	2.61	0.53
1:M:351:PHE:CD2	1:M:356:ILE:HD12	2.43	0.53
1:M:444:LEU:C	1:M:446:THR:H	2.13	0.53
1:N:302:PRO:O	1:N:439:ASN:ND2	2.41	0.53
1:N:35:PHE:HE1	1:N:321:ARG:NH1	2.05	0.53
1:N:434:THR:HA	1:N:437:GLN:HG2	1.90	0.53
1:N:434:THR:O	1:N:437:GLN:HG2	2.09	0.53
1:P:55:GLY:HA3	1:P:57:PHE:CE1	2.44	0.53
1:Q:420:VAL:HG22	1:Q:428:GLY:HA3	1.91	0.53
1:Q:427:GLY:C	1:Q:429:GLN:H	2.12	0.53
1:Q:81:ARG:HB2	1:Q:517:TYR:CZ	2.44	0.53
1:V:158:TRP:HD1	1:V:158:TRP:N	2.07	0.53
1:B:560:LEU:O	1:B:561:ASP:O	2.26	0.53
1:B:334:MSE:HE3	1:C:404:MSE:CE	2.39	0.53
1:D:34:PHE:HZ	1:D:328:ARG:HH22	0.80	0.53
1:D:511:ARG:HA	1:D:513:ARG:HD2	1.91	0.53
1:D:80:TYR:CE1	1:D:448:VAL:HG22	2.43	0.53
1:E:35:PHE:HE2	1:E:324:LYS:NZ	2.07	0.53
1:H:15:PHE:HZ	1:H:283:CYS:SG	2.31	0.53
1:I:266:ILE:HG23	1:I:267:ALA:N	2.23	0.53
1:L:511:ARG:HA	1:L:513:ARG:HD2	1.91	0.53
1:M:380:ASN:O	1:M:381:SER:HB3	2.09	0.53
1:P:71:MSE:HE2	1:P:119:ILE:HD11	1.90	0.53
1:Q:71:MSE:HE2	1:Q:119:ILE:HD11	1.91	0.53
1:S:101:ASP:HB2	1:S:144:ILE:O	2.09	0.53
1:T:35:PHE:CE1	1:T:321:ARG:NE	2.76	0.53
1:V:236:GLN:HA	1:V:244:VAL:H	1.73	0.53
1:V:325:ASP:O	1:V:329:LEU:HD23	2.09	0.53
1:V:35:PHE:C	1:V:37:ARG:H	2.11	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:302:PRO:O	1:W:439:ASN:ND2	2.42	0.53
1:W:80:TYR:CE1	1:W:448:VAL:HG22	2.44	0.53
1:X:325:ASP:O	1:X:329:LEU:HD23	2.09	0.53
1:X:389:LEU:H	1:X:389:LEU:HD12	1.74	0.53
1:X:80:TYR:CE1	1:X:448:VAL:HG22	2.44	0.53
1:B:511:ARG:HA	1:B:513:ARG:HD2	1.91	0.52
1:B:78:VAL:HG11	1:B:444:LEU:HG	1.90	0.52
1:D:273:ARG:NH2	1:D:453:LEU:HD21	2.21	0.52
1:F:35:PHE:C	1:F:37:ARG:N	2.62	0.52
1:F:47:GLN:NE2	1:F:47:GLN:O	2.41	0.52
1:G:32:ASP:HA	1:G:35:PHE:CE1	2.44	0.52
1:I:138:THR:H	1:I:143:VAL:HG22	1.73	0.52
1:I:15:PHE:CZ	1:I:283:CYS:HA	2.45	0.52
1:I:563:LYS:HD3	1:J:557:PHE:CE2	2.44	0.52
1:I:72:ARG:HD2	1:J:434:THR:HG21	1.91	0.52
1:J:234:ILE:HG13	1:J:267:ALA:HB3	1.90	0.52
1:K:32:ASP:HA	1:K:35:PHE:CE1	2.44	0.52
1:N:154:SER:O	1:N:204:PRO:HB3	2.09	0.52
1:N:444:LEU:C	1:N:446:THR:H	2.13	0.52
1:O:78:VAL:HG11	1:O:444:LEU:HG	1.90	0.52
1:R:164:LEU:HD22	1:R:169:ASP:CG	2.29	0.52
1:R:302:PRO:O	1:R:439:ASN:ND2	2.42	0.52
1:R:344:THR:O	1:R:344:THR:HG23	2.08	0.52
1:R:46:SER:N	1:R:48:TYR:HE2	1.98	0.52
1:V:34:PHE:HZ	1:V:328:ARG:HH22	1.40	0.52
1:X:434:THR:HA	1:X:437:GLN:HG2	1.91	0.52
1:B:78:VAL:CG1	1:B:79:LEU:N	2.72	0.52
1:C:229:LYS:HA	1:C:272:LYS:HA	1.90	0.52
1:C:15:PHE:CZ	1:C:283:CYS:HA	2.45	0.52
1:D:229:LYS:HA	1:D:272:LYS:HA	1.90	0.52
1:D:556:TYR:OH	1:F:542:THR:HG21	2.09	0.52
1:F:15:PHE:CZ	1:F:283:CYS:HA	2.45	0.52
1:G:265:LYS:O	1:G:266:ILE:HG12	2.10	0.52
1:G:579:MSE:HB2	1:G:581:VAL:HG12	1.91	0.52
1:J:158:TRP:HB3	1:J:173:CYS:CA	2.36	0.52
1:K:229:LYS:HA	1:K:272:LYS:HA	1.90	0.52
1:K:384:LEU:HD22	1:K:384:LEU:N	2.23	0.52
1:K:78:VAL:CG1	1:K:79:LEU:N	2.72	0.52
1:L:138:THR:H	1:L:143:VAL:HG22	1.73	0.52
1:L:209:PHE:HA	1:L:211:TRP:NE1	2.24	0.52
1:L:236:GLN:CB	1:L:265:LYS:HG2	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:265:LYS:O	1:L:266:ILE:HG12	2.10	0.52
1:L:384:LEU:HD22	1:L:384:LEU:N	2.23	0.52
1:M:123:VAL:HG22	1:M:316:TYR:CE2	2.45	0.52
1:M:66:LYS:NZ	1:M:420:VAL:HG11	2.24	0.52
1:O:420:VAL:HG22	1:O:428:GLY:HA3	1.90	0.52
1:R:427:GLY:C	1:R:429:GLN:H	2.12	0.52
1:R:93:VAL:CG1	1:R:458:ARG:HG3	2.38	0.52
1:R:81:ARG:HB2	1:R:517:TYR:CZ	2.45	0.52
1:R:584:PRO:HG2	1:R:593:LEU:HD12	1.90	0.52
1:S:380:ASN:O	1:S:381:SER:HB3	2.10	0.52
1:S:434:THR:HA	1:S:437:GLN:HG2	1.91	0.52
1:T:81:ARG:HB2	1:T:517:TYR:CZ	2.44	0.52
1:T:546:THR:CG2	1:T:547:PRO:HD3	2.28	0.52
1:T:573:ASN:O	1:T:577:ILE:HG13	2.09	0.52
1:V:47:GLN:HG2	1:V:48:TYR:N	2.23	0.52
1:X:427:GLY:C	1:X:429:GLN:H	2.12	0.52
1:A:78:VAL:HG11	1:A:444:LEU:HG	1.90	0.52
1:A:579:MSE:HB2	1:A:581:VAL:HG12	1.91	0.52
1:B:229:LYS:HA	1:B:272:LYS:HA	1.90	0.52
1:E:560:LEU:O	1:E:561:ASP:O	2.26	0.52
1:D:376:ARG:HB2	1:F:352:TRP:CG	2.44	0.52
1:G:47:GLN:NE2	1:G:47:GLN:O	2.41	0.52
1:H:429:GLN:HG2	1:H:429:GLN:O	2.10	0.52
1:I:457:MSE:O	1:I:458:ARG:HD2	2.10	0.52
1:L:32:ASP:HA	1:L:35:PHE:CE1	2.44	0.52
1:L:579:MSE:HB2	1:L:581:VAL:HG12	1.90	0.52
1:N:380:ASN:O	1:N:381:SER:HB3	2.09	0.52
1:Q:380:ASN:O	1:Q:381:SER:HB3	2.10	0.52
1:S:165:MSE:HE1	1:S:435:VAL:HB	1.91	0.52
1:S:95:MSE:HB3	1:S:527:MSE:HE1	1.90	0.52
1:T:144:ILE:HD12	1:T:145:ARG:N	2.25	0.52
1:T:35:PHE:HE1	1:T:321:ARG:NH1	2.06	0.52
1:U:398:PRO:HB3	1:X:395:PRO:HD2	1.90	0.52
1:U:296:GLU:HG2	1:U:449:PHE:HB3	1.90	0.52
1:D:209:PHE:HA	1:D:211:TRP:NE1	2.24	0.52
1:D:234:ILE:HG13	1:D:267:ALA:HB3	1.90	0.52
1:D:379:GLU:O	1:D:380:ASN:CB	2.58	0.52
1:F:265:LYS:O	1:F:266:ILE:HG12	2.10	0.52
1:I:310:VAL:C	1:I:312:ASP:H	2.13	0.52
1:J:334:MSE:HE3	1:K:404:MSE:CE	2.40	0.52
1:L:78:VAL:CG1	1:L:79:LEU:N	2.72	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:434:THR:HA	1:R:437:GLN:HG2	1.90	0.52
1:S:93:VAL:CG1	1:S:458:ARG:HG3	2.37	0.52
1:T:434:THR:HA	1:T:437:GLN:HG2	1.91	0.52
1:T:93:VAL:CG1	1:T:458:ARG:HG3	2.39	0.52
2:Y:57:TYR:O	2:Y:57:TYR:CD2	2.62	0.52
1:C:457:MSE:O	1:C:458:ARG:HD2	2.10	0.52
1:E:444:LEU:C	1:E:446:THR:N	2.61	0.52
1:F:229:LYS:HA	1:F:272:LYS:HA	1.90	0.52
1:F:379:GLU:O	1:F:380:ASN:CB	2.58	0.52
1:F:44:TRP:C	1:F:45:LEU:HD22	2.28	0.52
1:G:209:PHE:HA	1:G:211:TRP:NE1	2.24	0.52
1:G:310:VAL:C	1:G:312:ASP:H	2.13	0.52
1:F:334:MSE:SE	1:G:404:MSE:HE1	2.60	0.52
1:H:273:ARG:NH2	1:H:453:LEU:HD21	2.21	0.52
1:J:310:VAL:C	1:J:312:ASP:H	2.13	0.52
1:J:457:MSE:O	1:J:458:ARG:HD2	2.10	0.52
1:K:209:PHE:HA	1:K:211:TRP:NE1	2.24	0.52
1:K:444:LEU:C	1:K:446:THR:N	2.61	0.52
1:L:48:TYR:HD2	1:L:48:TYR:O	4.89	0.52
1:M:40:GLN:HG2	1:O:310:VAL:HG22	1.90	0.52
1:M:556:TYR:OH	1:O:542:THR:HG21	2.10	0.52
1:P:93:VAL:CG1	1:P:458:ARG:HG3	2.38	0.52
1:Q:66:LYS:HZ3	1:Q:420:VAL:HG11	1.74	0.52
1:R:236:GLN:HA	1:R:244:VAL:H	1.74	0.52
1:S:144:ILE:HD12	1:S:145:ARG:N	2.24	0.52
1:S:81:ARG:HB2	1:S:517:TYR:CZ	2.44	0.52
1:T:35:PHE:C	1:T:37:ARG:H	2.11	0.52
1:U:344:THR:O	1:U:344:THR:HG23	2.10	0.52
1:U:302:PRO:O	1:U:439:ASN:ND2	2.42	0.52
1:U:456:ALA:HB1	1:U:509:ASP:OD1	2.09	0.52
1:V:352:TRP:CG	1:W:376:ARG:HB2	2.45	0.52
1:V:296:GLU:HG2	1:V:449:PHE:HB3	1.91	0.52
1:W:93:VAL:CG1	1:W:458:ARG:HG3	2.37	0.52
1:W:598:GLN:HB2	1:W:601:GLN:HB2	1.92	0.52
1:A:209:PHE:HA	1:A:211:TRP:NE1	2.24	0.52
1:A:15:PHE:CZ	1:A:283:CYS:HA	2.45	0.52
1:A:350:PHE:HE1	1:L:363:TYR:HE1	1.57	0.52
1:A:379:GLU:O	1:A:380:ASN:CB	2.58	0.52
1:B:266:ILE:HG23	1:B:267:ALA:N	2.23	0.52
1:B:363:TYR:HE1	1:C:350:PHE:HE1	1.56	0.52
1:C:113:ILE:HD13	1:C:150:HIS:CE1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:266:ILE:HG23	1:C:267:ALA:N	2.23	0.52
1:C:32:ASP:HA	1:C:35:PHE:CE1	2.44	0.52
1:D:221:GLU:OE2	1:D:278:LYS:HD2	2.10	0.52
1:D:32:ASP:HA	1:D:35:PHE:CE1	2.44	0.52
1:E:113:ILE:HD13	1:E:150:HIS:CE1	2.45	0.52
1:E:265:LYS:O	1:E:266:ILE:HG12	2.10	0.52
1:G:234:ILE:HG13	1:G:267:ALA:HB3	1.91	0.52
1:H:15:PHE:CZ	1:H:283:CYS:HA	2.45	0.52
1:H:234:ILE:HG13	1:H:267:ALA:HB3	1.90	0.52
1:I:209:PHE:HA	1:I:211:TRP:NE1	2.24	0.52
1:I:221:GLU:OE2	1:I:278:LYS:HD2	2.10	0.52
1:I:78:VAL:CG1	1:I:79:LEU:N	2.72	0.52
1:J:209:PHE:HA	1:J:211:TRP:NE1	2.24	0.52
1:J:384:LEU:N	1:J:384:LEU:HD22	2.23	0.52
1:J:78:VAL:CG1	1:J:79:LEU:N	2.72	0.52
1:K:113:ILE:HD13	1:K:150:HIS:CE1	2.45	0.52
1:K:177:HIS:O	1:K:218:GLN:HA	2.09	0.52
1:M:165:MSE:HE1	1:M:435:VAL:HB	1.92	0.52
1:N:44:TRP:C	1:N:45:LEU:HD22	2.30	0.52
1:P:380:ASN:O	1:P:381:SER:HB3	2.09	0.52
1:P:165:MSE:HE1	1:P:435:VAL:HB	1.91	0.52
1:P:44:TRP:CE2	1:P:54:ARG:HB3	2.44	0.52
1:T:434:THR:O	1:T:437:GLN:HG2	2.10	0.52
1:U:434:THR:HA	1:U:437:GLN:HG2	1.91	0.52
1:U:44:TRP:CE2	1:U:54:ARG:HB3	2.45	0.52
1:V:24:GLU:C	1:V:26:ARG:N	2.57	0.52
1:V:329:LEU:HD21	1:W:53:TYR:OH	2.10	0.52
1:V:444:LEU:O	1:V:448:VAL:HG23	2.10	0.52
1:W:165:MSE:HG3	1:W:307:TRP:CD2	2.44	0.52
1:W:380:ASN:O	1:W:381:SER:HB3	2.10	0.52
1:W:165:MSE:HE1	1:W:435:VAL:HB	1.91	0.52
1:A:32:ASP:HA	1:A:35:PHE:CE1	2.44	0.52
1:A:438:LEU:HD22	3:L:719:HOH:O	2.09	0.52
1:C:209:PHE:HA	1:C:211:TRP:NE1	2.24	0.52
1:D:265:LYS:O	1:D:266:ILE:HG12	2.10	0.52
1:F:444:LEU:C	1:F:446:THR:N	2.61	0.52
1:G:457:MSE:O	1:G:458:ARG:HD2	2.10	0.52
1:I:32:ASP:HA	1:I:35:PHE:CE1	2.44	0.52
1:I:363:TYR:HE1	1:J:350:PHE:HE1	1.56	0.52
1:J:113:ILE:HD13	1:J:150:HIS:CE1	2.45	0.52
1:L:113:ILE:HD13	1:L:150:HIS:CE1	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:139:SER:CB	1:L:455:THR:CG2	2.80	0.52
1:L:457:MSE:O	1:L:458:ARG:HD2	2.10	0.52
1:N:352:TRP:CD1	1:V:376:ARG:HB2	2.45	0.52
1:N:165:MSE:HE1	1:N:435:VAL:HB	1.92	0.52
1:O:53:TYR:OH	1:P:329:LEU:HD21	2.07	0.52
1:Q:144:ILE:HD12	1:Q:145:ARG:N	2.25	0.52
1:Q:55:GLY:HA3	1:Q:57:PHE:CE1	2.45	0.52
1:R:80:TYR:CE1	1:R:448:VAL:HG22	2.43	0.52
1:S:389:LEU:HD12	1:S:389:LEU:H	1.75	0.52
1:S:434:THR:O	1:S:437:GLN:HG2	2.09	0.52
1:T:236:GLN:HA	1:T:244:VAL:H	1.74	0.52
1:T:427:GLY:C	1:T:429:GLN:H	2.13	0.52
1:U:273:ARG:NH1	1:U:275:ARG:HE	2.07	0.52
1:W:35:PHE:CE1	1:W:321:ARG:NE	2.78	0.52
1:B:113:ILE:HD13	1:B:150:HIS:CE1	2.45	0.52
1:B:310:VAL:C	1:B:312:ASP:H	2.13	0.52
1:B:379:GLU:O	1:B:380:ASN:CB	2.58	0.52
1:B:579:MSE:HB2	1:B:581:VAL:HG12	1.91	0.52
1:D:139:SER:CB	1:D:455:THR:CG2	2.80	0.52
1:E:457:MSE:O	1:E:458:ARG:HD2	2.10	0.52
1:E:579:MSE:HB2	1:E:581:VAL:HG12	1.91	0.52
1:F:310:VAL:C	1:F:312:ASP:H	2.13	0.52
1:H:556:TYR:OH	1:I:542:THR:HG21	2.09	0.52
1:J:32:ASP:HA	1:J:35:PHE:CE1	2.44	0.52
1:J:379:GLU:O	1:J:380:ASN:CB	2.58	0.52
1:K:457:MSE:O	1:K:458:ARG:HD2	2.10	0.52
1:M:48:TYR:O	1:M:48:TYR:HD2	5.13	0.52
1:M:598:GLN:HB2	1:M:601:GLN:HB2	1.92	0.52
1:N:598:GLN:HB2	1:N:601:GLN:HB2	1.92	0.52
1:O:209:PHE:HZ	1:O:214:GLN:HG2	1.70	0.52
1:O:546:THR:CG2	1:O:547:PRO:HD3	2.29	0.52
1:P:344:THR:HG23	1:P:344:THR:O	2.08	0.52
1:P:95:MSE:HB3	1:P:527:MSE:HE1	1.90	0.52
1:Q:58:ASP:HA	1:Q:327:GLN:NE2	2.24	0.52
1:R:35:PHE:HE1	1:R:321:ARG:NH1	2.07	0.52
1:T:273:ARG:NH1	1:T:275:ARG:HE	2.08	0.52
1:T:598:GLN:HB2	1:T:601:GLN:HB2	1.91	0.52
1:A:221:GLU:OE2	1:A:278:LYS:HD2	2.10	0.52
1:A:457:MSE:O	1:A:458:ARG:HD2	2.10	0.52
1:A:573:ASN:O	1:A:577:ILE:HG13	2.10	0.52
1:B:209:PHE:HA	1:B:211:TRP:NE1	2.24	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:310:VAL:C	1:C:312:ASP:H	2.13	0.52
1:D:35:PHE:HE2	1:D:324:LYS:NZ	2.07	0.52
1:D:579:MSE:HB2	1:D:581:VAL:HG12	1.90	0.52
1:E:15:PHE:CZ	1:E:283:CYS:HA	2.45	0.52
1:E:273:ARG:NH2	1:E:453:LEU:HD21	2.21	0.52
1:F:113:ILE:HD13	1:F:150:HIS:CE1	2.45	0.52
1:G:113:ILE:HD13	1:G:150:HIS:CE1	2.45	0.52
1:H:579:MSE:HB2	1:H:581:VAL:HG12	1.90	0.52
1:I:113:ILE:HD13	1:I:150:HIS:CE1	2.45	0.52
1:I:395:PRO:HD2	1:J:398:PRO:HB3	1.92	0.52
1:J:15:PHE:CZ	1:J:283:CYS:HA	2.45	0.52
1:L:560:LEU:O	1:L:561:ASP:O	2.26	0.52
1:M:325:ASP:O	1:M:329:LEU:HD23	2.10	0.52
1:O:93:VAL:CG1	1:O:458:ARG:HG3	2.38	0.52
1:P:420:VAL:HG22	1:P:428:GLY:HA3	1.91	0.52
1:Q:389:LEU:H	1:Q:389:LEU:HD12	1.74	0.52
1:R:325:ASP:O	1:R:329:LEU:HD23	2.09	0.52
1:V:427:GLY:C	1:V:429:GLN:H	2.13	0.52
1:W:236:GLN:HA	1:W:244:VAL:H	1.74	0.52
1:A:229:LYS:HA	1:A:272:LYS:HA	1.90	0.52
1:A:561:ASP:OD2	1:B:92:ASP:HB3	2.10	0.52
1:B:15:PHE:CZ	1:B:283:CYS:HA	2.45	0.52
1:B:35:PHE:CE2	1:B:321:ARG:HG3	2.45	0.52
1:C:221:GLU:OE2	1:C:278:LYS:HD2	2.10	0.52
1:C:379:GLU:O	1:C:380:ASN:CB	2.58	0.52
1:C:573:ASN:O	1:C:577:ILE:HG13	2.10	0.52
1:D:310:VAL:C	1:D:312:ASP:H	2.13	0.52
1:D:78:VAL:CG1	1:D:79:LEU:N	2.72	0.52
1:E:14:ARG:NE	1:E:14:ARG:CA	2.67	0.52
1:E:78:VAL:CG1	1:E:79:LEU:N	2.72	0.52
1:F:35:PHE:CE2	1:F:321:ARG:HG3	2.45	0.52
1:G:35:PHE:HE2	1:G:324:LYS:NZ	2.07	0.52
1:G:334:MSE:HE3	1:H:404:MSE:HE3	1.92	0.52
1:H:457:MSE:O	1:H:458:ARG:HD2	2.10	0.52
1:I:265:LYS:O	1:I:266:ILE:HG12	2.10	0.52
1:J:14:ARG:CA	1:J:14:ARG:NE	2.67	0.52
1:J:248:LYS:HZ1	1:J:513:ARG:HH12	1.58	0.52
1:K:310:VAL:C	1:K:312:ASP:H	2.13	0.52
1:K:573:ASN:O	1:K:577:ILE:HG13	2.11	0.52
1:L:15:PHE:CZ	1:L:283:CYS:HA	2.45	0.52
3:K:719:HOH:O	1:L:438:LEU:HD22	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:P:719:HOH:O	1:Q:430:VAL:HG11	2.10	0.52
1:R:387:GLN:HB3	1:X:390:ALA:CB	2.40	0.52
1:U:325:ASP:O	1:U:329:LEU:HD23	2.10	0.52
1:U:34:PHE:CE2	1:U:45:LEU:HG	2.45	0.52
1:W:444:LEU:O	1:W:448:VAL:HG23	2.10	0.52
1:X:535:ILE:HD13	1:X:554:LEU:HG	1.92	0.52
2:Y:77:ALA:O	2:Y:78:GLU:HB3	2.10	0.52
2:Z:57:TYR:CD2	2:Z:57:TYR:O	2.62	0.52
2:Z:57:TYR:O	2:Z:57:TYR:HD2	1.92	0.52
2:Z:53:MET:O	2:Z:69:PHE:CE1	2.63	0.52
1:A:35:PHE:CE2	1:A:321:ARG:HG3	2.45	0.51
1:B:302:PRO:O	1:B:439:ASN:CG	2.49	0.51
1:B:443:ASP:C	1:B:444:LEU:HD13	2.31	0.51
1:B:457:MSE:O	1:B:458:ARG:HD2	2.10	0.51
1:C:14:ARG:NE	1:C:14:ARG:CA	2.67	0.51
1:C:265:LYS:O	1:C:266:ILE:HG12	2.10	0.51
1:C:35:PHE:CE2	1:C:321:ARG:HG3	2.45	0.51
1:C:429:GLN:O	1:C:429:GLN:HG2	2.10	0.51
1:D:113:ILE:HD13	1:D:150:HIS:CE1	2.45	0.51
1:F:160:SER:O	1:F:161:ASN:ND2	2.43	0.51
1:F:209:PHE:HA	1:F:211:TRP:NE1	2.24	0.51
1:G:160:SER:O	1:G:161:ASN:ND2	2.44	0.51
1:G:511:ARG:HA	1:G:513:ARG:HD2	1.91	0.51
1:J:35:PHE:CE2	1:J:321:ARG:HG3	2.45	0.51
1:J:37:ARG:HH21	1:J:37:ARG:CB	2.16	0.51
1:L:35:PHE:CE2	1:L:321:ARG:HG3	2.45	0.51
1:O:164:LEU:HD22	1:O:169:ASP:CG	2.31	0.51
1:O:434:THR:O	1:O:437:GLN:HG2	2.10	0.51
1:O:456:ALA:HB1	1:O:509:ASP:OD1	2.09	0.51
1:O:78:VAL:HG12	1:O:79:LEU:H	1.74	0.51
1:O:334:MSE:HE1	1:P:407:ALA:HB1	1.91	0.51
1:P:427:GLY:C	1:P:429:GLN:H	2.13	0.51
3:O:719:HOH:O	1:P:430:VAL:HG11	2.10	0.51
1:P:573:ASN:O	1:P:577:ILE:HG13	2.10	0.51
1:P:78:VAL:HG11	1:P:444:LEU:HG	1.91	0.51
1:R:434:THR:O	1:R:437:GLN:HG2	2.10	0.51
1:V:164:LEU:HD22	1:V:169:ASP:CG	2.30	0.51
1:V:380:ASN:O	1:V:381:SER:HB3	2.10	0.51
1:X:236:GLN:HA	1:X:244:VAL:H	1.74	0.51
1:X:35:PHE:C	1:X:37:ARG:H	2.12	0.51
1:X:444:LEU:C	1:X:446:THR:H	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:77:ALA:O	2:Z:78:GLU:HB3	2.10	0.51
1:B:221:GLU:OE2	1:B:278:LYS:HD2	2.10	0.51
1:B:372:TYR:CE2	1:C:348:LYS:HB2	2.45	0.51
1:D:15:PHE:CZ	1:D:283:CYS:HA	2.45	0.51
1:D:160:SER:O	1:D:161:ASN:ND2	2.44	0.51
1:D:334:MSE:HE3	1:F:404:MSE:CE	2.40	0.51
1:D:573:ASN:O	1:D:577:ILE:HG13	2.10	0.51
1:E:379:GLU:O	1:E:380:ASN:CB	2.58	0.51
1:E:443:ASP:C	1:E:444:LEU:HD13	2.31	0.51
1:C:563:LYS:HD3	1:E:557:PHE:CE2	2.45	0.51
1:F:556:TYR:OH	1:G:542:THR:HG21	2.09	0.51
1:H:182:ASN:ND2	1:I:171:ARG:HH21	2.08	0.51
1:I:443:ASP:C	1:I:444:LEU:HD13	2.31	0.51
1:K:265:LYS:O	1:K:266:ILE:HG12	2.10	0.51
1:K:443:ASP:C	1:K:444:LEU:HD13	2.31	0.51
1:M:37:ARG:HH21	1:M:37:ARG:CB	2.23	0.51
1:M:95:MSE:HE1	1:M:99:ARG:CZ	2.41	0.51
1:N:427:GLY:C	1:N:429:GLN:H	2.13	0.51
1:N:34:PHE:CE2	1:N:45:LEU:HG	2.46	0.51
1:N:80:TYR:CE1	1:N:448:VAL:HG22	2.45	0.51
1:Q:598:GLN:HB2	1:Q:601:GLN:HB2	1.92	0.51
1:R:389:LEU:H	1:R:389:LEU:HD12	1.74	0.51
1:U:154:SER:O	1:U:204:PRO:HB3	2.10	0.51
1:U:44:TRP:C	1:U:45:LEU:HD22	2.30	0.51
1:V:123:VAL:HG22	1:V:316:TYR:CE2	2.45	0.51
1:W:389:LEU:HD12	1:W:389:LEU:H	1.75	0.51
1:X:123:VAL:HG22	1:X:316:TYR:CE2	2.45	0.51
1:A:302:PRO:O	1:A:439:ASN:CG	2.49	0.51
1:A:443:ASP:C	1:A:444:LEU:HD13	2.31	0.51
1:C:302:PRO:O	1:C:439:ASN:CG	2.49	0.51
1:B:395:PRO:HD2	1:C:398:PRO:HB3	1.92	0.51
1:C:63:VAL:HG21	1:C:416:ALA:HB1	1.93	0.51
1:C:579:MSE:HB2	1:C:581:VAL:HG12	1.91	0.51
1:D:37:ARG:HH21	1:D:37:ARG:CB	2.16	0.51
1:D:63:VAL:HG21	1:D:416:ALA:HB1	1.93	0.51
1:E:221:GLU:OE2	1:E:278:LYS:HD2	2.10	0.51
1:F:63:VAL:HG21	1:F:416:ALA:HB1	1.93	0.51
1:G:221:GLU:OE2	1:G:278:LYS:HD2	2.10	0.51
1:H:113:ILE:HD13	1:H:150:HIS:CE1	2.45	0.51
1:H:265:LYS:O	1:H:266:ILE:HG12	2.10	0.51
1:H:139:SER:CB	1:H:455:THR:CG2	2.80	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:160:SER:O	1:I:161:ASN:ND2	2.44	0.51
1:I:236:GLN:CB	1:I:265:LYS:HZ3	2.16	0.51
1:I:35:PHE:C	1:I:37:ARG:N	2.62	0.51
1:I:35:PHE:HE2	1:I:324:LYS:NZ	2.08	0.51
1:I:573:ASN:O	1:I:577:ILE:HG13	2.10	0.51
1:J:265:LYS:O	1:J:266:ILE:HG12	2.10	0.51
1:J:443:ASP:C	1:J:444:LEU:HD13	2.31	0.51
1:L:310:VAL:C	1:L:312:ASP:H	2.13	0.51
1:M:322:LEU:HD22	1:M:322:LEU:N	2.25	0.51
1:N:351:PHE:CD2	1:N:356:ILE:HD12	2.46	0.51
1:O:58:ASP:HA	1:O:327:GLN:NE2	2.26	0.51
1:O:598:GLN:HB2	1:O:601:GLN:HB2	1.92	0.51
1:P:164:LEU:HD22	1:P:169:ASP:CG	2.31	0.51
1:Q:158:TRP:HD1	1:Q:158:TRP:N	2.07	0.51
1:Q:164:LEU:HD22	1:Q:169:ASP:CG	2.31	0.51
1:Q:434:THR:HA	1:Q:437:GLN:HG2	1.92	0.51
1:S:35:PHE:HE1	1:S:321:ARG:NH1	2.06	0.51
1:S:379:GLU:O	1:S:380:ASN:CB	2.58	0.51
1:U:390:ALA:CB	1:X:387:GLN:CB	2.88	0.51
1:X:158:TRP:HD1	1:X:158:TRP:N	2.07	0.51
2:Y:57:TYR:O	2:Y:57:TYR:HD2	1.92	0.51
1:A:348:LYS:HB3	1:L:371:TYR:HA	1.92	0.51
1:A:63:VAL:HG21	1:A:416:ALA:HB1	1.93	0.51
1:C:78:VAL:CG1	1:C:79:LEU:N	2.72	0.51
1:D:111:VAL:O	1:D:115:VAL:HG13	2.11	0.51
1:D:302:PRO:O	1:D:439:ASN:CG	2.49	0.51
1:D:457:MSE:O	1:D:458:ARG:HD2	2.10	0.51
1:E:302:PRO:O	1:E:439:ASN:CG	2.49	0.51
1:E:573:ASN:O	1:E:577:ILE:HG13	2.11	0.51
1:F:111:VAL:O	1:F:115:VAL:HG13	2.11	0.51
1:F:573:ASN:O	1:F:577:ILE:HG13	2.11	0.51
1:G:429:GLN:O	1:G:429:GLN:HG2	2.10	0.51
1:H:35:PHE:CE2	1:H:321:ARG:HG3	2.45	0.51
1:I:35:PHE:CE2	1:I:321:ARG:HG3	2.45	0.51
1:I:379:GLU:O	1:I:380:ASN:CB	2.58	0.51
1:J:63:VAL:HG21	1:J:416:ALA:HB1	1.93	0.51
1:K:379:GLU:O	1:K:380:ASN:CB	2.58	0.51
1:K:363:TYR:HE1	1:L:350:PHE:HE1	1.57	0.51
1:L:443:ASP:C	1:L:444:LEU:HD13	2.31	0.51
1:L:573:ASN:O	1:L:577:ILE:HG13	2.10	0.51
1:M:434:THR:O	1:M:437:GLN:HG2	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:35:PHE:C	1:N:37:ARG:H	2.14	0.51
1:N:66:LYS:HZ3	1:N:420:VAL:HG11	1.75	0.51
1:O:302:PRO:O	1:O:439:ASN:ND2	2.43	0.51
1:O:46:SER:N	1:O:48:TYR:HE2	1.98	0.51
1:P:434:THR:HA	1:P:437:GLN:HG2	1.92	0.51
1:P:81:ARG:HB2	1:P:517:TYR:CZ	2.45	0.51
1:P:395:PRO:HD2	1:Q:398:PRO:HB3	1.91	0.51
1:Q:302:PRO:O	1:Q:439:ASN:ND2	2.44	0.51
1:Q:546:THR:CG2	1:Q:547:PRO:HD3	2.29	0.51
1:R:34:PHE:CE2	1:R:45:LEU:HG	2.44	0.51
1:T:101:ASP:HB2	1:T:144:ILE:O	2.11	0.51
1:T:154:SER:O	1:T:204:PRO:HB3	2.09	0.51
1:T:95:MSE:HB3	1:T:527:MSE:HE1	1.91	0.51
1:U:351:PHE:CD2	1:U:356:ILE:HD12	2.44	0.51
1:U:598:GLN:HB2	1:U:601:GLN:HB2	1.92	0.51
1:V:348:LYS:HB2	1:W:372:TYR:CE2	2.46	0.51
1:V:44:TRP:CE2	1:V:54:ARG:HB3	2.46	0.51
1:V:44:TRP:C	1:V:45:LEU:HD22	2.31	0.51
1:W:535:ILE:HD13	1:W:554:LEU:HG	1.93	0.51
1:X:144:ILE:HD12	1:X:145:ARG:N	2.25	0.51
1:A:101:ASP:HB3	1:A:138:THR:HG21	1.93	0.51
1:A:160:SER:O	1:A:161:ASN:ND2	2.44	0.51
1:A:310:VAL:C	1:A:312:ASP:H	2.13	0.51
1:A:444:LEU:C	1:A:446:THR:N	2.61	0.51
1:B:34:PHE:HZ	1:B:328:ARG:HH22	0.80	0.51
1:B:573:ASN:O	1:B:577:ILE:HG13	2.11	0.51
1:C:111:VAL:O	1:C:115:VAL:HG13	2.11	0.51
1:E:14:ARG:HH11	1:E:17:ALA:HB2	1.76	0.51
1:F:14:ARG:NE	1:F:14:ARG:CA	2.67	0.51
1:F:429:GLN:HG2	1:F:429:GLN:O	2.10	0.51
1:G:14:ARG:HH11	1:G:17:ALA:HB2	1.76	0.51
1:H:443:ASP:C	1:H:444:LEU:HD13	2.31	0.51
1:I:234:ILE:HG13	1:I:267:ALA:HB3	1.90	0.51
1:H:561:ASP:OD2	1:I:92:ASP:HB3	2.10	0.51
1:J:101:ASP:HB3	1:J:138:THR:HG21	1.93	0.51
1:K:63:VAL:HG21	1:K:416:ALA:HB1	1.93	0.51
1:L:528:LYS:HZ2	1:L:560:LEU:HD21	1.75	0.51
1:M:420:VAL:HG22	1:M:428:GLY:HA3	1.92	0.51
1:N:344:THR:HG23	1:N:344:THR:O	2.09	0.51
1:N:430:VAL:CG1	3:V:719:HOH:O	2.59	0.51
1:N:438:LEU:HD22	3:V:718:HOH:O	2.09	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:598:GLN:HB2	1:P:601:GLN:HB2	1.92	0.51
1:R:44:TRP:C	1:R:45:LEU:HD22	2.30	0.51
1:U:123:VAL:HG22	1:U:316:TYR:CE2	2.46	0.51
1:U:584:PRO:HG2	1:U:593:LEU:HD12	1.91	0.51
1:X:344:THR:HG23	1:X:344:THR:O	2.09	0.51
1:X:434:THR:O	1:X:437:GLN:HG2	2.10	0.51
1:B:35:PHE:HE2	1:B:324:LYS:NZ	2.07	0.51
1:E:209:PHE:HA	1:E:211:TRP:NE1	2.24	0.51
1:E:63:VAL:HG21	1:E:416:ALA:HB1	1.93	0.51
1:F:14:ARG:HH11	1:F:17:ALA:HB2	1.76	0.51
1:G:15:PHE:CZ	1:G:283:CYS:HA	2.45	0.51
1:H:101:ASP:HB3	1:H:138:THR:HG21	1.93	0.51
1:H:160:SER:O	1:H:161:ASN:ND2	2.44	0.51
1:H:209:PHE:HA	1:H:211:TRP:NE1	2.24	0.51
1:H:221:GLU:OE2	1:H:278:LYS:HD2	2.10	0.51
1:H:573:ASN:O	1:H:577:ILE:HG13	2.10	0.51
1:J:111:VAL:O	1:J:115:VAL:HG13	2.11	0.51
1:J:160:SER:O	1:J:161:ASN:ND2	2.44	0.51
1:J:302:PRO:O	1:J:439:ASN:CG	2.49	0.51
1:K:15:PHE:CZ	1:K:283:CYS:HA	2.45	0.51
1:K:221:GLU:OE2	1:K:278:LYS:HD2	2.10	0.51
1:M:48:TYR:O	1:M:48:TYR:CD2	5.16	0.51
1:N:164:LEU:HD22	1:N:169:ASP:CG	2.30	0.51
1:O:35:PHE:C	1:O:37:ARG:H	2.12	0.51
1:O:456:ALA:O	1:O:457:MSE:HB2	2.11	0.51
1:Q:37:ARG:HH21	1:Q:37:ARG:CB	2.24	0.51
1:R:598:GLN:HB2	1:R:601:GLN:HB2	1.92	0.51
1:S:351:PHE:CD2	1:S:356:ILE:HD12	2.45	0.51
1:S:48:TYR:O	1:S:48:TYR:CD2	5.17	0.51
1:S:48:TYR:O	1:S:48:TYR:HD2	5.14	0.51
1:V:58:ASP:HA	1:V:327:GLN:NE2	2.25	0.51
1:V:344:THR:HG23	1:V:344:THR:O	2.09	0.51
1:W:434:THR:HA	1:W:437:GLN:HG2	1.92	0.51
1:X:302:PRO:O	1:X:439:ASN:ND2	2.43	0.51
2:Y:53:MET:O	2:Y:69:PHE:CE1	2.63	0.51
1:A:111:VAL:O	1:A:115:VAL:HG13	2.11	0.51
1:A:113:ILE:HD13	1:A:150:HIS:CE1	2.45	0.51
1:A:564:GLY:CA	1:B:554:LEU:HD21	2.35	0.51
1:C:528:LYS:HZ2	1:C:560:LEU:HD21	1.76	0.51
1:D:14:ARG:CA	1:D:14:ARG:NE	2.67	0.51
1:F:37:ARG:HH21	1:F:37:ARG:CB	2.16	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:457:MSE:O	1:F:458:ARG:HD2	2.10	0.51
1:G:35:PHE:CE2	1:G:321:ARG:HG3	2.45	0.51
1:G:379:GLU:O	1:G:380:ASN:CB	2.58	0.51
1:H:251:ILE:O	1:H:507:LEU:HD13	2.11	0.51
1:K:302:PRO:O	1:K:439:ASN:CG	2.49	0.51
1:L:160:SER:O	1:L:161:ASN:ND2	2.44	0.51
1:L:35:PHE:HE2	1:L:324:LYS:NZ	2.07	0.51
1:L:444:LEU:C	1:L:446:THR:N	2.61	0.51
1:O:380:ASN:O	1:O:381:SER:HB3	2.11	0.51
1:O:389:LEU:HD12	1:O:389:LEU:H	1.75	0.51
1:P:546:THR:CG2	1:P:547:PRO:HD3	2.31	0.51
1:P:80:TYR:CE1	1:P:448:VAL:HG22	2.45	0.51
1:R:443:ASP:C	1:R:446:THR:HG22	2.31	0.51
1:R:44:TRP:CE2	1:R:54:ARG:HB3	2.46	0.51
1:R:78:VAL:CG1	1:R:79:LEU:N	2.73	0.51
1:S:58:ASP:HA	1:S:327:GLN:NE2	2.25	0.51
1:T:34:PHE:CE2	1:T:45:LEU:HG	2.45	0.51
1:V:35:PHE:CE1	1:V:321:ARG:NE	2.76	0.51
1:X:351:PHE:CD2	1:X:356:ILE:HD12	2.45	0.51
1:X:573:ASN:O	1:X:577:ILE:HG13	2.10	0.51
1:A:427:GLY:C	1:A:429:GLN:H	2.15	0.51
1:B:111:VAL:O	1:B:115:VAL:HG13	2.11	0.51
1:B:37:ARG:HH22	1:B:45:LEU:CD1	2.24	0.51
1:C:248:LYS:HD3	1:C:251:ILE:HB	1.93	0.51
1:F:101:ASP:HB3	1:F:138:THR:HG21	1.93	0.51
1:D:376:ARG:HB2	1:F:352:TRP:CD2	2.46	0.51
1:F:251:ILE:O	1:F:507:LEU:HD13	2.11	0.51
1:H:379:GLU:O	1:H:380:ASN:CB	2.58	0.51
1:H:302:PRO:O	1:H:439:ASN:CG	2.49	0.51
1:I:273:ARG:NH2	1:I:453:LEU:HD21	2.21	0.51
1:I:37:ARG:HH22	1:I:45:LEU:CD1	2.24	0.51
1:I:302:PRO:O	1:I:439:ASN:CG	2.49	0.51
1:J:221:GLU:OE2	1:J:278:LYS:HD2	2.10	0.51
1:J:573:ASN:O	1:J:577:ILE:HG13	2.10	0.51
1:L:111:VAL:O	1:L:115:VAL:HG13	2.11	0.51
1:L:379:GLU:O	1:L:380:ASN:CB	2.58	0.51
1:L:37:ARG:HH22	1:L:45:LEU:CD1	2.24	0.51
1:M:144:ILE:HD12	1:M:145:ARG:N	2.26	0.51
1:M:430:VAL:HG11	3:N:719:HOH:O	2.11	0.51
1:N:325:ASP:O	1:N:329:LEU:HD23	2.10	0.51
1:N:456:ALA:O	1:N:457:MSE:HB2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:165:MSE:HE1	1:O:435:VAL:HB	1.93	0.51
1:O:78:VAL:CG1	1:O:79:LEU:N	2.74	0.51
1:Q:80:TYR:CE1	1:Q:448:VAL:HG22	2.46	0.51
1:R:123:VAL:HG22	1:R:316:TYR:CE2	2.45	0.51
1:R:456:ALA:O	1:R:457:MSE:HB2	2.11	0.51
1:R:58:ASP:HA	1:R:327:GLN:NE2	2.26	0.51
1:R:95:MSE:HB3	1:R:527:MSE:HE1	1.93	0.51
1:S:37:ARG:CB	1:S:37:ARG:HH21	2.24	0.51
1:U:535:ILE:HD13	1:U:554:LEU:HG	1.93	0.51
1:U:66:LYS:HZ3	1:U:420:VAL:HG11	1.74	0.51
1:U:78:VAL:HG12	1:U:79:LEU:H	1.75	0.51
1:W:34:PHE:CE2	1:W:45:LEU:HG	2.45	0.51
1:V:399:GLN:OE1	1:W:396:GLU:O	2.29	0.51
1:X:405:LEU:O	1:X:409:THR:HG23	2.10	0.51
1:X:34:PHE:CE2	1:X:45:LEU:HG	2.45	0.51
1:X:95:MSE:HB3	1:X:527:MSE:HE1	1.92	0.51
1:A:265:LYS:O	1:A:266:ILE:HG12	2.10	0.51
1:C:160:SER:O	1:C:161:ASN:ND2	2.44	0.51
1:C:35:PHE:HE2	1:C:324:LYS:NZ	2.08	0.51
1:D:14:ARG:HH11	1:D:17:ALA:HB2	1.76	0.51
1:E:429:GLN:O	1:E:429:GLN:HG2	2.10	0.51
1:F:221:GLU:OE2	1:F:278:LYS:HD2	2.10	0.51
1:G:443:ASP:C	1:G:444:LEU:HD13	2.31	0.51
1:I:444:LEU:C	1:I:446:THR:N	2.61	0.51
1:J:14:ARG:HH11	1:J:17:ALA:HB2	1.76	0.51
1:L:101:ASP:HB3	1:L:138:THR:HG21	1.93	0.51
1:L:14:ARG:CA	1:L:14:ARG:NE	2.67	0.51
1:L:221:GLU:OE2	1:L:278:LYS:HD2	2.10	0.51
1:L:191:TYR:HE1	1:L:278:LYS:HZ3	1.57	0.51
1:L:48:TYR:O	1:L:48:TYR:CD2	5.23	0.51
1:N:144:ILE:HD12	1:N:145:ARG:N	2.26	0.51
1:N:420:VAL:HG22	1:N:428:GLY:HA3	1.92	0.51
1:R:535:ILE:HD13	1:R:554:LEU:HG	1.92	0.51
1:S:55:GLY:HA3	1:S:57:PHE:CE1	2.46	0.51
1:T:302:PRO:O	1:T:439:ASN:ND2	2.44	0.51
1:T:44:TRP:CE2	1:T:54:ARG:HB3	2.46	0.51
1:W:456:ALA:O	1:W:457:MSE:HB2	2.11	0.51
1:B:160:SER:O	1:B:161:ASN:ND2	2.44	0.51
1:B:429:GLN:HG2	1:B:429:GLN:O	2.10	0.51
1:B:251:ILE:O	1:B:507:LEU:HD13	2.11	0.51
1:B:63:VAL:HG21	1:B:416:ALA:HB1	1.93	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:101:ASP:HB3	1:C:138:THR:HG21	1.93	0.51
1:D:236:GLN:CB	1:D:265:LYS:HG2	2.37	0.51
1:E:160:SER:O	1:E:161:ASN:ND2	2.44	0.51
1:E:310:VAL:C	1:E:312:ASP:H	2.13	0.51
1:F:248:LYS:HD3	1:F:251:ILE:HB	1.93	0.51
1:F:560:LEU:O	1:F:565:VAL:HG21	2.11	0.51
1:G:560:LEU:O	1:G:565:VAL:HG21	2.11	0.51
1:H:310:VAL:C	1:H:312:ASP:H	2.13	0.51
1:H:560:LEU:O	1:H:565:VAL:HG21	2.11	0.51
1:I:429:GLN:O	1:I:429:GLN:HG2	2.10	0.51
1:K:72:ARG:HD2	1:L:434:THR:HG21	1.93	0.51
1:M:429:GLN:HG2	1:M:429:GLN:O	2.11	0.51
1:M:434:THR:HA	1:M:437:GLN:HG2	1.92	0.51
1:M:456:ALA:O	1:M:457:MSE:HB2	2.11	0.51
1:O:158:TRP:N	1:O:158:TRP:HD1	2.07	0.51
3:M:719:HOH:O	1:O:430:VAL:HG11	2.11	0.51
1:O:444:LEU:C	1:O:446:THR:H	2.13	0.51
1:R:212:LEU:HD22	1:X:26:ARG:HG2	1.93	0.51
1:S:456:ALA:O	1:S:457:MSE:HB2	2.10	0.51
1:T:78:VAL:CG1	1:T:79:LEU:N	2.74	0.51
1:U:80:TYR:CE1	1:U:448:VAL:HG22	2.45	0.51
1:W:413:LYS:HA	1:W:416:ALA:HB3	1.93	0.51
1:A:248:LYS:HD3	1:A:251:ILE:HB	1.93	0.50
1:A:37:ARG:HH22	1:A:45:LEU:CD1	2.24	0.50
1:B:265:LYS:O	1:B:266:ILE:HG12	2.10	0.50
1:D:35:PHE:CE2	1:D:321:ARG:HG3	2.45	0.50
1:E:35:PHE:CE2	1:E:321:ARG:HG3	2.45	0.50
1:G:111:VAL:O	1:G:115:VAL:HG13	2.11	0.50
1:G:63:VAL:HG21	1:G:416:ALA:HB1	1.93	0.50
1:H:35:PHE:HE2	1:H:324:LYS:NZ	2.08	0.50
1:H:63:VAL:HG21	1:H:416:ALA:HB1	1.93	0.50
1:I:111:VAL:O	1:I:115:VAL:HG13	2.11	0.50
1:I:427:GLY:C	1:I:429:GLN:H	2.14	0.50
1:I:513:ARG:H	1:I:513:ARG:HD3	1.77	0.50
1:I:63:VAL:HG21	1:I:416:ALA:HB1	1.93	0.50
1:J:560:LEU:O	1:J:565:VAL:HG21	2.11	0.50
1:K:101:ASP:HB3	1:K:138:THR:HG21	1.93	0.50
1:K:160:SER:O	1:K:161:ASN:ND2	2.44	0.50
1:K:35:PHE:CE2	1:K:321:ARG:HG3	2.45	0.50
1:K:427:GLY:C	1:K:429:GLN:H	2.15	0.50
1:K:81:ARG:HB2	1:K:517:TYR:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:376:ARG:HB2	1:L:352:TRP:CD2	2.46	0.50
1:L:81:ARG:HB2	1:L:517:TYR:CE2	2.46	0.50
1:N:35:PHE:CE1	1:N:321:ARG:NE	2.78	0.50
1:N:58:ASP:HA	1:N:327:GLN:NE2	2.26	0.50
1:O:171:ARG:O	1:O:224:GLU:HA	2.11	0.50
1:O:80:TYR:CE1	1:O:448:VAL:HG22	2.46	0.50
1:Q:78:VAL:CG1	1:Q:79:LEU:N	2.74	0.50
1:R:35:PHE:CE1	1:R:321:ARG:NE	2.77	0.50
1:T:389:LEU:HD12	1:T:389:LEU:H	1.76	0.50
1:V:46:SER:N	1:V:48:TYR:HE2	1.96	0.50
1:W:444:LEU:C	1:W:446:THR:H	2.13	0.50
1:X:413:LYS:HA	1:X:416:ALA:HB3	1.92	0.50
2:Z:38:GLU:N	2:Z:39:PRO:HD3	2.26	0.50
1:A:429:GLN:O	1:A:429:GLN:HG2	2.10	0.50
1:A:251:ILE:O	1:A:507:LEU:HD13	2.11	0.50
1:A:92:ASP:HB3	1:L:561:ASP:OD2	2.10	0.50
1:B:248:LYS:HD3	1:B:251:ILE:HB	1.93	0.50
1:B:560:LEU:O	1:B:565:VAL:HG21	2.11	0.50
1:C:443:ASP:C	1:C:444:LEU:HD13	2.31	0.50
1:C:513:ARG:HD3	1:C:513:ARG:H	1.77	0.50
1:D:429:GLN:O	1:D:429:GLN:HG2	2.10	0.50
1:F:418:LEU:HB2	1:F:428:GLY:O	2.12	0.50
1:F:586:THR:N	1:F:587:PRO:CD	2.74	0.50
1:G:427:GLY:C	1:G:429:GLN:H	2.15	0.50
1:H:111:VAL:O	1:H:115:VAL:HG13	2.11	0.50
1:I:418:LEU:HB2	1:I:428:GLY:O	2.12	0.50
1:J:246:TYR:HE2	1:J:512:GLY:N	2.10	0.50
1:J:586:THR:N	1:J:587:PRO:CD	2.75	0.50
1:J:81:ARG:HB2	1:J:517:TYR:CE2	2.46	0.50
1:L:429:GLN:HG2	1:L:429:GLN:O	2.10	0.50
1:M:405:LEU:O	1:M:409:THR:HG23	2.12	0.50
1:Q:325:ASP:O	1:Q:329:LEU:HD23	2.11	0.50
1:R:405:LEU:O	1:R:409:THR:HG23	2.12	0.50
1:S:427:GLY:C	1:S:429:GLN:H	2.14	0.50
1:T:456:ALA:O	1:T:457:MSE:HB2	2.11	0.50
1:U:427:GLY:C	1:U:429:GLN:H	2.15	0.50
2:Z:70:SER:HB2	2:Z:75:PRO:O	2.12	0.50
1:B:101:ASP:HB3	1:B:138:THR:HG21	1.93	0.50
1:B:246:TYR:HE2	1:B:512:GLY:N	2.10	0.50
1:C:418:LEU:HB2	1:C:428:GLY:O	2.12	0.50
1:C:81:ARG:HB2	1:C:517:TYR:CE2	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:37:ARG:HH22	1:D:45:LEU:CD1	2.24	0.50
1:D:404:MSE:HE3	1:E:334:MSE:HE3	1.93	0.50
1:D:560:LEU:O	1:D:565:VAL:HG21	2.11	0.50
1:E:513:ARG:HD3	1:E:513:ARG:H	1.76	0.50
1:E:586:THR:N	1:E:587:PRO:CD	2.75	0.50
1:F:302:PRO:O	1:F:439:ASN:CG	2.49	0.50
1:G:302:PRO:O	1:G:439:ASN:CG	2.49	0.50
1:G:37:ARG:HH22	1:G:45:LEU:CD1	2.24	0.50
1:G:81:ARG:HB2	1:G:517:TYR:CE2	2.46	0.50
1:G:573:ASN:O	1:G:577:ILE:HG13	2.10	0.50
1:G:563:LYS:HD3	1:H:557:PHE:CE2	2.47	0.50
1:I:101:ASP:HB3	1:I:138:THR:HG21	1.93	0.50
1:I:191:TYR:HE1	1:I:278:LYS:HZ3	1.57	0.50
1:I:34:PHE:HE1	1:I:324:LYS:HZ2	1.50	0.50
1:I:586:THR:N	1:I:587:PRO:CD	2.75	0.50
1:J:251:ILE:O	1:J:507:LEU:HD13	2.11	0.50
1:K:418:LEU:HB2	1:K:428:GLY:O	2.12	0.50
1:L:113:ILE:HD12	1:L:148:PRO:HB3	1.94	0.50
1:L:251:ILE:O	1:L:507:LEU:HD13	2.11	0.50
1:N:174:THR:N	3:N:705:HOH:O	2.44	0.50
1:O:135:GLN:NE2	1:P:514:TYR:HE2	2.09	0.50
1:P:325:ASP:O	1:P:329:LEU:HD23	2.11	0.50
1:R:158:TRP:N	1:R:158:TRP:HD1	2.08	0.50
1:U:546:THR:CG2	1:U:547:PRO:HD3	2.31	0.50
1:V:9:GLU:HG3	1:V:12:LEU:H	1.77	0.50
1:T:396:GLU:O	1:W:399:GLN:OE1	2.29	0.50
1:W:420:VAL:HG22	1:W:428:GLY:HA3	1.91	0.50
1:A:126:TRP:CD1	1:A:146:ARG:HG3	2.46	0.50
1:A:14:ARG:NE	1:A:14:ARG:CA	2.67	0.50
1:A:81:ARG:HB2	1:A:517:TYR:CE2	2.46	0.50
1:B:409:THR:O	1:B:413:LYS:HG2	2.12	0.50
1:C:584:PRO:HG2	1:C:593:LEU:HD12	1.94	0.50
1:D:443:ASP:C	1:D:444:LEU:HD13	2.31	0.50
1:E:535:ILE:HD11	1:E:554:LEU:HG	1.94	0.50
1:G:15:PHE:HZ	1:G:283:CYS:HG	1.60	0.50
1:G:198:ILE:HG22	1:G:198:ILE:O	2.12	0.50
1:H:126:TRP:CD1	1:H:146:ARG:HG3	2.46	0.50
1:H:14:ARG:HH11	1:H:17:ALA:HB2	1.76	0.50
1:I:126:TRP:CD1	1:I:146:ARG:HG3	2.46	0.50
1:I:14:ARG:HH11	1:I:17:ALA:HB2	1.76	0.50
1:K:246:TYR:HE2	1:K:512:GLY:N	2.10	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:429:GLN:O	1:K:429:GLN:HG2	2.10	0.50
1:K:251:ILE:O	1:K:507:LEU:HD13	2.11	0.50
1:K:510:ILE:O	1:K:513:ARG:HD2	2.12	0.50
1:L:246:TYR:HE2	1:L:512:GLY:N	2.10	0.50
1:L:248:LYS:HD3	1:L:251:ILE:HB	1.93	0.50
1:L:409:THR:O	1:L:413:LYS:HG2	2.12	0.50
1:L:535:ILE:HD11	1:L:554:LEU:HG	1.94	0.50
1:M:535:ILE:HD13	1:M:554:LEU:HG	1.93	0.50
1:Q:266:ILE:HG23	1:Q:267:ALA:N	2.26	0.50
1:Q:34:PHE:CE2	1:Q:45:LEU:HG	2.46	0.50
1:R:37:ARG:CB	1:R:37:ARG:HH21	2.24	0.50
1:S:235:TYR:HA	1:S:265:LYS:HB3	1.94	0.50
1:S:302:PRO:O	1:S:439:ASN:ND2	2.44	0.50
1:T:235:TYR:HA	1:T:265:LYS:HB3	1.94	0.50
1:V:266:ILE:HG23	1:V:267:ALA:N	2.26	0.50
1:V:26:ARG:HG2	1:W:212:LEU:HD22	1.94	0.50
1:X:164:LEU:HD22	1:X:169:ASP:CG	2.32	0.50
1:X:598:GLN:HB2	1:X:601:GLN:HB2	1.92	0.50
2:Z:104:TYR:HB2	2:Z:106:LEU:HD12	1.93	0.50
1:A:246:TYR:HE2	1:A:512:GLY:N	2.10	0.50
1:C:409:THR:O	1:C:413:LYS:HG2	2.12	0.50
1:C:535:ILE:HD11	1:C:554:LEU:HG	1.94	0.50
1:D:248:LYS:HD3	1:D:251:ILE:HB	1.93	0.50
1:D:251:ILE:O	1:D:507:LEU:HD13	2.11	0.50
1:D:81:ARG:HB2	1:D:517:TYR:CE2	2.46	0.50
1:D:535:ILE:HD11	1:D:554:LEU:HG	1.94	0.50
1:E:113:ILE:HD12	1:E:148:PRO:HB3	1.94	0.50
1:E:37:ARG:HH22	1:E:45:LEU:CD1	2.24	0.50
1:E:81:ARG:HB2	1:E:517:TYR:CE2	2.46	0.50
1:E:94:LEU:HA	1:E:97:MSE:CE	2.37	0.50
1:F:113:ILE:HD12	1:F:148:PRO:HB3	1.94	0.50
1:F:246:TYR:HE2	1:F:512:GLY:N	2.10	0.50
1:F:35:PHE:HE2	1:F:324:LYS:NZ	2.08	0.50
1:F:443:ASP:C	1:F:444:LEU:HD13	2.31	0.50
1:G:586:THR:N	1:G:587:PRO:CD	2.75	0.50
1:H:37:ARG:HH22	1:H:45:LEU:CD1	2.24	0.50
1:H:510:ILE:O	1:H:513:ARG:HD2	2.12	0.50
1:H:81:ARG:HB2	1:H:517:TYR:CE2	2.46	0.50
1:K:126:TRP:CD1	1:K:146:ARG:HG3	2.46	0.50
1:K:14:ARG:HH11	1:K:17:ALA:HB2	1.76	0.50
1:K:560:LEU:O	1:K:565:VAL:HG21	2.11	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:302:PRO:O	1:L:439:ASN:CG	2.49	0.50
1:L:57:PHE:CD2	1:L:330:ARG:CB	2.95	0.50
1:N:379:GLU:O	1:N:380:ASN:CB	2.59	0.50
1:P:158:TRP:N	1:P:158:TRP:HD1	2.07	0.50
1:Q:573:ASN:O	1:Q:577:ILE:HG13	2.12	0.50
1:R:48:TYR:CD2	1:R:48:TYR:O	5.16	0.50
1:S:344:THR:O	1:S:344:THR:HG23	2.11	0.50
1:S:598:GLN:HB2	1:S:601:GLN:HB2	1.92	0.50
1:T:535:ILE:HD13	1:T:554:LEU:HG	1.93	0.50
1:U:37:ARG:CB	1:U:37:ARG:HH21	2.24	0.50
1:U:443:ASP:C	1:U:446:THR:HG22	2.32	0.50
1:U:55:GLY:HA3	1:U:57:PHE:CE1	2.46	0.50
1:V:34:PHE:CE2	1:V:45:LEU:HG	2.46	0.50
1:W:351:PHE:CD2	1:W:356:ILE:HD12	2.46	0.50
1:W:434:THR:HG23	1:W:435:VAL:N	2.26	0.50
2:Y:89:VAL:C	2:Y:91:ALA:H	2.15	0.50
1:A:513:ARG:HD3	1:A:513:ARG:H	1.76	0.50
1:A:510:ILE:O	1:A:513:ARG:HD2	2.12	0.50
1:B:113:ILE:HD12	1:B:148:PRO:HB3	1.94	0.50
1:B:14:ARG:HH11	1:B:17:ALA:HB2	1.76	0.50
1:B:513:ARG:H	1:B:513:ARG:HD3	1.77	0.50
1:B:81:ARG:HB2	1:B:517:TYR:CE2	2.46	0.50
1:C:34:PHE:HE1	1:C:324:LYS:HZ2	1.46	0.50
1:C:251:ILE:O	1:C:507:LEU:HD13	2.11	0.50
1:D:101:ASP:HB3	1:D:138:THR:HG21	1.93	0.50
1:D:136:SER:N	1:D:137:PRO:HD3	2.27	0.50
1:D:126:TRP:CD1	1:D:146:ARG:HG3	2.46	0.50
1:D:409:THR:O	1:D:413:LYS:HG2	2.12	0.50
1:D:418:LEU:HB2	1:D:428:GLY:O	2.12	0.50
1:D:246:TYR:HE2	1:D:512:GLY:N	2.10	0.50
1:D:510:ILE:O	1:D:513:ARG:HD2	2.12	0.50
1:E:251:ILE:O	1:E:507:LEU:HD13	2.11	0.50
1:E:560:LEU:O	1:E:565:VAL:HG21	2.11	0.50
1:F:57:PHE:CD2	1:F:330:ARG:CB	2.95	0.50
1:H:248:LYS:HD3	1:H:251:ILE:HB	1.93	0.50
1:H:427:GLY:C	1:H:429:GLN:H	2.15	0.50
1:I:535:ILE:HD11	1:I:554:LEU:HG	1.94	0.50
1:J:126:TRP:CD1	1:J:146:ARG:HG3	2.46	0.50
1:K:113:ILE:HD12	1:K:148:PRO:HB3	1.94	0.50
1:K:409:THR:O	1:K:413:LYS:HG2	2.12	0.50
1:K:513:ARG:HD3	1:K:513:ARG:H	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:560:LEU:O	1:L:565:VAL:HG21	2.11	0.50
1:M:322:LEU:HD22	1:M:322:LEU:H	1.77	0.50
1:N:586:THR:N	1:N:587:PRO:CD	2.75	0.50
1:Q:9:GLU:HG3	1:Q:12:LEU:H	1.77	0.50
1:S:573:ASN:O	1:S:577:ILE:HG13	2.12	0.50
1:U:235:TYR:HA	1:U:265:LYS:HB3	1.94	0.50
1:V:165:MSE:HE1	1:V:435:VAL:HB	1.94	0.50
2:Y:70:SER:HB2	2:Y:75:PRO:O	2.12	0.50
2:Y:72:ASP:O	2:Y:72:ASP:OD1	2.30	0.50
2:Z:72:ASP:OD1	2:Z:72:ASP:O	2.30	0.50
1:A:136:SER:N	1:A:137:PRO:HD3	2.27	0.50
1:A:160:SER:HB3	1:A:171:ARG:NH2	2.27	0.50
1:A:352:TRP:CD1	1:L:376:ARG:HB2	2.47	0.50
1:C:136:SER:N	1:C:137:PRO:HD3	2.27	0.50
1:C:37:ARG:HH22	1:C:45:LEU:CD1	2.24	0.50
1:D:513:ARG:HD3	1:D:513:ARG:H	1.77	0.50
1:D:586:THR:N	1:D:587:PRO:CD	2.75	0.50
1:E:126:TRP:CD1	1:E:146:ARG:HG3	2.46	0.50
1:E:409:THR:O	1:E:413:LYS:HG2	2.12	0.50
1:E:418:LEU:HB2	1:E:428:GLY:O	2.12	0.50
1:C:561:ASP:OD2	1:E:92:ASP:HB3	2.12	0.50
1:G:126:TRP:CD1	1:G:146:ARG:HG3	2.46	0.50
1:G:409:THR:O	1:G:413:LYS:HG2	2.12	0.50
1:G:418:LEU:HB2	1:G:428:GLY:O	2.12	0.50
1:I:334:MSE:HE3	1:J:404:MSE:HE3	1.93	0.50
1:I:560:LEU:O	1:I:565:VAL:HG21	2.11	0.50
1:J:128:LEU:HD12	1:J:446:THR:HG23	1.94	0.50
1:L:586:THR:N	1:L:587:PRO:CD	2.75	0.50
1:P:34:PHE:CE2	1:P:45:LEU:HG	2.46	0.50
1:R:235:TYR:HA	1:R:265:LYS:HB3	1.94	0.50
1:R:444:LEU:O	1:R:448:VAL:HG23	2.11	0.50
1:S:14:ARG:NE	1:S:14:ARG:CA	2.69	0.50
1:S:9:GLU:HG3	1:S:12:LEU:H	1.77	0.50
1:U:379:GLU:O	1:U:380:ASN:CB	2.59	0.50
1:U:47:GLN:HG2	1:U:48:TYR:N	2.26	0.50
1:U:78:VAL:CG1	1:U:79:LEU:N	2.74	0.50
1:V:322:LEU:N	1:V:322:LEU:HD22	2.27	0.50
1:V:343:ARG:O	1:V:344:THR:HB	2.12	0.50
1:N:27:ARG:NH2	1:V:41:TRP:HE1	2.10	0.50
2:Z:28:VAL:HG21	2:Z:96:LEU:CG	2.40	0.50
1:B:57:PHE:CD2	1:B:330:ARG:CB	2.95	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:586:THR:N	1:C:587:PRO:CD	2.75	0.50
1:E:111:VAL:O	1:E:115:VAL:HG13	2.11	0.50
1:E:160:SER:HB3	1:E:171:ARG:NH2	2.27	0.50
1:E:198:ILE:O	1:E:198:ILE:HG22	2.12	0.50
1:E:427:GLY:C	1:E:429:GLN:H	2.15	0.50
1:F:160:SER:HB3	1:F:171:ARG:NH2	2.27	0.50
1:F:409:THR:O	1:F:413:LYS:HG2	2.12	0.50
1:G:251:ILE:O	1:G:507:LEU:HD13	2.11	0.50
1:H:535:ILE:HD11	1:H:554:LEU:HG	1.94	0.50
1:I:160:SER:HB3	1:I:171:ARG:NH2	2.27	0.50
1:I:248:LYS:HD3	1:I:251:ILE:HB	1.93	0.50
1:I:81:ARG:HB2	1:I:517:TYR:CE2	2.46	0.50
1:J:409:THR:O	1:J:413:LYS:HG2	2.12	0.50
1:L:126:TRP:CD1	1:L:146:ARG:HG3	2.46	0.50
1:L:14:ARG:HH11	1:L:17:ALA:HB2	1.76	0.50
1:L:513:ARG:HD3	1:L:513:ARG:H	1.77	0.50
1:M:413:LYS:HA	1:M:416:ALA:HB3	1.93	0.50
1:M:427:GLY:C	1:M:429:GLN:H	2.15	0.50
1:O:48:TYR:O	1:O:48:TYR:HD2	5.13	0.50
1:Q:434:THR:O	1:Q:437:GLN:HG2	2.11	0.50
1:Q:444:LEU:O	1:Q:448:VAL:HG23	2.11	0.50
1:Q:535:ILE:HD13	1:Q:554:LEU:HG	1.94	0.50
1:R:27:ARG:HB2	1:R:313:LYS:HE3	1.94	0.50
1:S:434:THR:HG23	1:S:435:VAL:N	2.26	0.50
1:T:387:GLN:CB	1:W:390:ALA:CB	2.89	0.50
1:V:248:LYS:HG3	1:V:511:ARG:HE	1.77	0.50
1:X:35:PHE:HE1	1:X:321:ARG:NH1	2.06	0.50
1:X:78:VAL:CG1	1:X:444:LEU:HG	2.42	0.50
1:A:128:LEU:HD12	1:A:446:THR:HG23	1.94	0.50
1:A:14:ARG:HH11	1:A:17:ALA:HB2	1.76	0.50
1:A:280:ILE:HG22	1:A:287:LEU:HD13	1.94	0.50
1:A:418:LEU:HB2	1:A:428:GLY:O	2.12	0.50
1:B:160:SER:HB3	1:B:171:ARG:NH2	2.27	0.50
1:B:586:THR:N	1:B:587:PRO:CD	2.75	0.50
1:B:584:PRO:HG2	1:B:593:LEU:HD12	1.94	0.50
1:C:113:ILE:HD12	1:C:148:PRO:HB3	1.94	0.50
1:C:126:TRP:CD1	1:C:146:ARG:HG3	2.46	0.50
1:D:160:SER:HB3	1:D:171:ARG:NH2	2.27	0.50
1:D:280:ILE:HG22	1:D:287:LEU:HD13	1.94	0.50
1:D:584:PRO:CG	1:D:593:LEU:HD12	2.42	0.50
1:E:248:LYS:HD3	1:E:251:ILE:HB	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:280:ILE:HG22	1:E:287:LEU:HD13	1.94	0.50
1:F:126:TRP:CD1	1:F:146:ARG:HG3	2.46	0.50
1:G:160:SER:HB3	1:G:171:ARG:NH2	2.27	0.50
1:G:510:ILE:O	1:G:513:ARG:HD2	2.12	0.50
1:G:513:ARG:HD3	1:G:513:ARG:H	1.77	0.50
1:G:584:PRO:HG2	1:G:593:LEU:HD12	1.94	0.50
1:H:119:ILE:HA	1:H:432:PHE:HE2	1.77	0.50
1:H:418:LEU:HB2	1:H:428:GLY:O	2.12	0.50
1:I:57:PHE:CD2	1:I:330:ARG:CB	2.95	0.50
1:I:584:PRO:HG2	1:I:593:LEU:HD12	1.94	0.50
1:J:15:PHE:HZ	1:J:283:CYS:HG	1.60	0.50
1:J:57:PHE:CD2	1:J:330:ARG:CB	2.95	0.50
1:J:451:ASP:O	1:J:456:ALA:N	2.41	0.50
1:J:37:ARG:HH22	1:J:45:LEU:CD1	2.24	0.50
1:K:160:SER:HB3	1:K:171:ARG:NH2	2.27	0.50
1:K:198:ILE:O	1:K:198:ILE:HG22	2.12	0.50
1:K:586:THR:N	1:K:587:PRO:CD	2.75	0.50
1:L:280:ILE:HG22	1:L:287:LEU:HD13	1.94	0.50
1:L:427:GLY:C	1:L:429:GLN:H	2.15	0.50
1:O:95:MSE:HE1	1:O:99:ARG:CZ	2.41	0.50
1:P:95:MSE:HE1	1:P:99:ARG:CZ	2.42	0.50
1:S:34:PHE:CE2	1:S:45:LEU:HG	2.46	0.50
1:T:27:ARG:HB2	1:T:313:LYS:HE3	1.94	0.50
1:V:444:LEU:C	1:V:446:THR:H	2.16	0.50
1:V:89:ASP:HA	1:W:561:ASP:CB	2.37	0.50
1:X:78:VAL:HG12	1:X:79:LEU:H	1.74	0.50
1:A:535:ILE:HD11	1:A:554:LEU:HG	1.94	0.49
1:B:44:TRP:CE2	1:B:54:ARG:HB3	2.48	0.49
1:C:14:ARG:HH11	1:C:17:ALA:HB2	1.76	0.49
1:C:427:GLY:C	1:C:429:GLN:H	2.15	0.49
1:D:334:MSE:SE	1:F:404:MSE:HE1	2.61	0.49
1:F:81:ARG:HB2	1:F:517:TYR:CE2	2.46	0.49
1:H:160:SER:HB3	1:H:171:ARG:NH2	2.27	0.49
1:H:409:THR:O	1:H:413:LYS:HG2	2.12	0.49
1:H:584:PRO:HG2	1:H:593:LEU:HD12	1.94	0.49
1:I:248:LYS:HZ1	1:I:513:ARG:HH12	1.59	0.49
1:K:111:VAL:O	1:K:115:VAL:HG13	2.11	0.49
1:L:128:LEU:HD12	1:L:446:THR:HG23	1.94	0.49
1:L:255:ILE:O	1:L:257:ASP:N	2.45	0.49
1:L:584:PRO:HG2	1:L:593:LEU:HD12	1.94	0.49
1:M:379:GLU:O	1:M:380:ASN:CB	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:248:LYS:CD	1:O:248:LYS:H	2.17	0.49
1:Q:456:ALA:O	1:Q:457:MSE:HB2	2.12	0.49
1:Q:48:TYR:CD2	1:Q:48:TYR:O	5.17	0.49
1:T:9:GLU:HG3	1:T:12:LEU:H	1.76	0.49
1:U:27:ARG:HB2	1:U:313:LYS:HE3	1.94	0.49
1:V:322:LEU:HD22	1:V:322:LEU:H	1.77	0.49
1:W:164:LEU:HD22	1:W:169:ASP:CG	2.33	0.49
1:W:58:ASP:HA	1:W:327:GLN:NE2	2.27	0.49
1:X:343:ARG:O	1:X:344:THR:HB	2.12	0.49
2:Y:28:VAL:HG11	2:Y:96:LEU:C	2.33	0.49
1:A:44:TRP:CE2	1:A:54:ARG:HB3	2.48	0.49
1:A:586:THR:N	1:A:587:PRO:CD	2.75	0.49
1:B:427:GLY:C	1:B:429:GLN:H	2.15	0.49
1:C:128:LEU:HD12	1:C:446:THR:HG23	1.94	0.49
1:C:246:TYR:HE2	1:C:512:GLY:N	2.10	0.49
1:C:584:PRO:CG	1:C:593:LEU:HD12	2.42	0.49
1:D:584:PRO:HG2	1:D:593:LEU:HD12	1.94	0.49
1:E:584:PRO:HG2	1:E:593:LEU:HD12	1.94	0.49
1:E:80:TYR:CE1	1:E:444:LEU:HB3	2.48	0.49
1:F:119:ILE:HA	1:F:432:PHE:HE2	1.78	0.49
1:G:182:ASN:HD22	1:H:171:ARG:HH21	1.58	0.49
1:H:280:ILE:HG22	1:H:287:LEU:HD13	1.94	0.49
1:H:578:GLN:HG2	1:H:596:ALA:HB2	1.94	0.49
1:I:136:SER:N	1:I:137:PRO:HD3	2.27	0.49
1:I:255:ILE:O	1:I:257:ASP:N	2.45	0.49
1:I:280:ILE:HG22	1:I:287:LEU:HD13	1.94	0.49
1:I:510:ILE:O	1:I:513:ARG:HD2	2.12	0.49
1:J:160:SER:HB3	1:J:171:ARG:NH2	2.27	0.49
1:J:248:LYS:HD3	1:J:251:ILE:HB	1.93	0.49
1:J:429:GLN:O	1:J:429:GLN:HG2	2.10	0.49
1:J:510:ILE:O	1:J:513:ARG:HD2	2.12	0.49
1:J:584:PRO:CG	1:J:593:LEU:HD12	2.42	0.49
1:K:128:LEU:HD12	1:K:446:THR:HG23	1.94	0.49
1:L:418:LEU:HB2	1:L:428:GLY:O	2.12	0.49
1:L:584:PRO:CG	1:L:593:LEU:HD12	2.42	0.49
1:M:164:LEU:HA	1:M:307:TRP:HH2	1.77	0.49
1:M:573:ASN:O	1:M:577:ILE:HG13	2.12	0.49
1:N:405:LEU:O	1:N:409:THR:HG23	2.11	0.49
1:P:95:MSE:HE1	1:P:99:ARG:NH2	2.26	0.49
1:Q:387:GLN:CB	1:R:390:ALA:CB	2.90	0.49
1:T:40:GLN:HG2	1:W:310:VAL:HG22	1.93	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:444:LEU:C	1:T:446:THR:H	2.14	0.49
1:U:164:LEU:HD22	1:U:169:ASP:CG	2.32	0.49
1:U:46:SER:N	1:U:48:TYR:HE2	1.99	0.49
1:V:434:THR:HA	1:V:437:GLN:HG2	1.93	0.49
1:N:82:PRO:CD	1:V:560:LEU:HD13	2.27	0.49
1:W:66:LYS:HZ3	1:W:420:VAL:HG11	1.77	0.49
1:W:443:ASP:C	1:W:446:THR:HG22	2.32	0.49
1:W:586:THR:N	1:W:587:PRO:CD	2.75	0.49
2:Y:104:TYR:HB2	2:Y:106:LEU:HD12	1.93	0.49
2:Y:28:VAL:HG21	2:Y:96:LEU:CG	2.40	0.49
2:Y:38:GLU:N	2:Y:39:PRO:HD3	2.26	0.49
1:A:255:ILE:O	1:A:257:ASP:N	2.45	0.49
1:A:409:THR:O	1:A:413:LYS:HG2	2.12	0.49
1:A:456:ALA:HB1	1:A:509:ASP:OD2	2.13	0.49
1:B:126:TRP:CD1	1:B:146:ARG:HG3	2.46	0.49
1:B:584:PRO:CG	1:B:593:LEU:HD12	2.42	0.49
1:C:328:ARG:HB3	2:Z:142:PRO:HG3	1.94	0.49
1:C:456:ALA:HB1	1:C:509:ASP:OD2	2.13	0.49
1:D:119:ILE:HA	1:D:432:PHE:HE2	1.78	0.49
1:D:427:GLY:C	1:D:429:GLN:H	2.14	0.49
1:G:119:ILE:HA	1:G:432:PHE:HE2	1.77	0.49
1:G:280:ILE:HG22	1:G:287:LEU:HD13	1.94	0.49
1:G:584:PRO:CG	1:G:593:LEU:HD12	2.42	0.49
1:H:584:PRO:CG	1:H:593:LEU:HD12	2.42	0.49
1:H:586:THR:N	1:H:587:PRO:CD	2.75	0.49
1:J:535:ILE:HD11	1:J:554:LEU:HG	1.94	0.49
1:K:37:ARG:HH22	1:K:45:LEU:CD1	2.24	0.49
1:K:535:ILE:HD11	1:K:554:LEU:HG	1.94	0.49
1:L:160:SER:HB3	1:L:171:ARG:NH2	2.27	0.49
1:L:386:THR:O	1:L:387:GLN:O	2.31	0.49
1:N:443:ASP:C	1:N:446:THR:HG22	2.33	0.49
1:Q:93:VAL:CG1	1:Q:458:ARG:HG3	2.38	0.49
1:S:78:VAL:CG1	1:S:79:LEU:N	2.74	0.49
1:X:235:TYR:HA	1:X:265:LYS:HB3	1.94	0.49
1:X:58:ASP:HA	1:X:327:GLN:NE2	2.27	0.49
1:X:95:MSE:HE1	1:X:99:ARG:CZ	2.42	0.49
1:L:359:PHE:HD1	2:Z:129:ILE:HD11	1.76	0.49
1:A:560:LEU:O	1:A:565:VAL:HG21	2.11	0.49
1:B:119:ILE:HA	1:B:432:PHE:HE2	1.77	0.49
1:B:280:ILE:HG22	1:B:287:LEU:HD13	1.94	0.49
1:C:34:PHE:O	1:C:34:PHE:CG	2.66	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:386:THR:O	1:D:387:GLN:O	2.31	0.49
1:D:456:ALA:HB1	1:D:509:ASP:OD2	2.13	0.49
1:E:101:ASP:HB3	1:E:138:THR:HG21	1.93	0.49
1:E:136:SER:N	1:E:137:PRO:HD3	2.27	0.49
1:E:451:ASP:O	1:E:456:ALA:N	2.41	0.49
1:F:456:ALA:HB1	1:F:509:ASP:OD2	2.13	0.49
1:G:101:ASP:HB3	1:G:138:THR:HG21	1.93	0.49
1:G:456:ALA:HB1	1:G:509:ASP:OD2	2.13	0.49
1:G:535:ILE:HD11	1:G:554:LEU:HG	1.94	0.49
1:G:47:GLN:HG3	1:G:54:ARG:NH1	2.28	0.49
1:H:128:LEU:HD12	1:H:446:THR:HG23	1.94	0.49
1:H:198:ILE:O	1:H:198:ILE:HG22	2.12	0.49
1:H:246:TYR:HE2	1:H:512:GLY:N	2.10	0.49
1:H:513:ARG:H	1:H:513:ARG:HD3	1.77	0.49
1:I:246:TYR:HE2	1:I:512:GLY:N	2.10	0.49
1:I:34:PHE:HZ	1:I:328:ARG:HH22	0.80	0.49
1:J:113:ILE:HD12	1:J:148:PRO:HB3	1.94	0.49
1:J:280:ILE:HG22	1:J:287:LEU:HD13	1.94	0.49
1:J:427:GLY:C	1:J:429:GLN:H	2.15	0.49
1:J:456:ALA:HB1	1:J:509:ASP:OD2	2.13	0.49
1:J:578:GLN:HG2	1:J:596:ALA:HB2	1.94	0.49
1:J:584:PRO:HG2	1:J:593:LEU:HD12	1.94	0.49
1:K:136:SER:N	1:K:137:PRO:HD3	2.27	0.49
1:K:280:ILE:HG22	1:K:287:LEU:HD13	1.95	0.49
1:K:386:THR:O	1:K:387:GLN:O	2.31	0.49
1:K:456:ALA:HB1	1:K:509:ASP:OD2	2.13	0.49
1:K:44:TRP:CE2	1:K:54:ARG:HB3	2.47	0.49
1:L:119:ILE:HA	1:L:432:PHE:HE2	1.77	0.49
1:L:63:VAL:HG21	1:L:416:ALA:HB1	1.93	0.49
1:L:44:TRP:CE2	1:L:54:ARG:HB3	2.48	0.49
1:M:266:ILE:HG23	1:M:267:ALA:N	2.27	0.49
1:M:46:SER:N	1:M:48:TYR:HE2	1.98	0.49
1:M:80:TYR:CE1	1:M:448:VAL:HG22	2.48	0.49
1:O:384:LEU:HD22	1:O:384:LEU:N	2.27	0.49
1:O:48:TYR:O	1:O:48:TYR:CD2	5.16	0.49
1:O:95:MSE:HB3	1:O:527:MSE:HE1	1.93	0.49
1:O:586:THR:N	1:O:587:PRO:CD	2.75	0.49
1:P:235:TYR:HA	1:P:265:LYS:HB3	1.95	0.49
1:P:266:ILE:HG23	1:P:267:ALA:N	2.27	0.49
1:Q:379:GLU:O	1:Q:380:ASN:CB	2.60	0.49
1:Q:409:THR:O	1:Q:413:LYS:HG2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:191:TYR:HE1	1:R:278:LYS:HZ3	1.60	0.49
1:U:123:VAL:CG1	1:U:304:PHE:CE1	2.95	0.49
1:V:434:THR:O	1:V:437:GLN:HG2	2.11	0.49
1:V:586:THR:N	1:V:587:PRO:CD	2.76	0.49
1:V:95:MSE:HE1	1:V:99:ARG:CZ	2.42	0.49
1:X:95:MSE:HE1	1:X:99:ARG:NH2	2.28	0.49
1:A:113:ILE:HD12	1:A:148:PRO:HB3	1.94	0.49
1:A:198:ILE:O	1:A:198:ILE:HG22	2.12	0.49
1:B:34:PHE:O	1:B:34:PHE:CG	2.66	0.49
1:B:418:LEU:HB2	1:B:428:GLY:O	2.12	0.49
1:C:160:SER:HB3	1:C:171:ARG:NH2	2.27	0.49
1:C:198:ILE:HG22	1:C:198:ILE:O	2.12	0.49
1:D:255:ILE:O	1:D:257:ASP:N	2.45	0.49
1:D:348:LYS:HB2	1:E:372:TYR:CE2	2.47	0.49
1:F:37:ARG:HH22	1:F:45:LEU:CD1	2.24	0.49
1:F:513:ARG:H	1:F:513:ARG:HD3	1.76	0.49
1:F:535:ILE:HD11	1:F:554:LEU:HG	1.94	0.49
1:I:251:ILE:O	1:I:507:LEU:HD13	2.11	0.49
1:J:255:ILE:O	1:J:257:ASP:N	2.45	0.49
1:J:418:LEU:HB2	1:J:428:GLY:O	2.12	0.49
1:J:44:TRP:CE2	1:J:54:ARG:HB3	2.47	0.49
1:J:334:MSE:HE3	1:K:404:MSE:HE3	1.94	0.49
1:M:443:ASP:C	1:M:446:THR:HG22	2.32	0.49
1:M:390:ALA:HB2	1:N:387:GLN:HB2	1.95	0.49
1:O:379:GLU:O	1:O:380:ASN:CB	2.60	0.49
1:O:443:ASP:C	1:O:444:LEU:HD13	2.32	0.49
1:P:456:ALA:O	1:P:457:MSE:HB2	2.11	0.49
1:P:48:TYR:O	1:P:48:TYR:CD2	5.17	0.49
1:P:586:THR:N	1:P:587:PRO:CD	2.76	0.49
1:Q:235:TYR:HA	1:Q:265:LYS:HB3	1.94	0.49
1:Q:586:THR:N	1:Q:587:PRO:CD	2.76	0.49
1:R:48:TYR:HD2	1:R:48:TYR:O	5.13	0.49
1:S:586:THR:N	1:S:587:PRO:CD	2.76	0.49
1:T:48:TYR:O	1:T:48:TYR:CD2	5.17	0.49
1:S:407:ALA:HB1	1:U:334:MSE:HE1	1.94	0.49
1:V:386:THR:O	1:V:387:GLN:C	2.51	0.49
1:W:101:ASP:HB2	1:W:144:ILE:O	2.11	0.49
1:A:584:PRO:CG	1:A:593:LEU:HD12	2.42	0.49
1:B:136:SER:N	1:B:137:PRO:HD3	2.27	0.49
1:B:255:ILE:O	1:B:257:ASP:N	2.45	0.49
1:B:236:GLN:CB	1:B:265:LYS:HG2	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:535:ILE:HD11	1:B:554:LEU:HG	1.94	0.49
1:C:44:TRP:CE2	1:C:54:ARG:HB3	2.47	0.49
1:C:560:LEU:O	1:C:565:VAL:HG21	2.11	0.49
1:D:398:PRO:HB3	1:E:395:PRO:HD2	1.93	0.49
1:D:578:GLN:HG2	1:D:596:ALA:HB2	1.94	0.49
1:E:255:ILE:O	1:E:257:ASP:N	2.45	0.49
1:E:386:THR:O	1:E:387:GLN:O	2.31	0.49
1:E:44:TRP:CE2	1:E:54:ARG:HB3	2.47	0.49
1:E:528:LYS:HZ3	1:E:560:LEU:HD21	1.77	0.49
1:F:34:PHE:O	1:F:34:PHE:CG	2.65	0.49
1:G:113:ILE:HD12	1:G:148:PRO:HB3	1.94	0.49
1:I:119:ILE:HA	1:I:432:PHE:HE2	1.77	0.49
1:I:226:VAL:O	1:I:274:ARG:HA	2.13	0.49
1:I:37:ARG:HH21	1:I:37:ARG:CB	2.16	0.49
1:I:47:GLN:HG3	1:I:54:ARG:NH1	2.28	0.49
1:L:47:GLN:HG3	1:L:54:ARG:NH1	2.28	0.49
1:L:80:TYR:CE1	1:L:444:LEU:HB3	2.48	0.49
1:M:95:MSE:HE1	1:M:99:ARG:NH2	2.28	0.49
1:N:48:TYR:HD2	1:N:48:TYR:O	5.13	0.49
1:O:34:PHE:CE2	1:O:45:LEU:HG	2.45	0.49
1:O:405:LEU:O	1:O:409:THR:HG23	2.12	0.49
1:P:191:TYR:HE1	1:P:278:LYS:HZ3	1.61	0.49
1:O:372:TYR:CE2	1:P:348:LYS:HB2	2.47	0.49
1:P:418:LEU:HB2	1:P:428:GLY:O	2.13	0.49
1:Q:95:MSE:HB3	1:Q:527:MSE:HE1	1.93	0.49
1:R:165:MSE:HG3	1:R:307:TRP:CD2	2.47	0.49
1:V:78:VAL:CG1	1:V:79:LEU:N	2.73	0.49
1:X:33:LEU:HD12	1:X:34:PHE:N	2.28	0.49
1:B:510:ILE:O	1:B:513:ARG:HD2	2.12	0.49
1:C:94:LEU:HA	1:C:97:MSE:CE	2.37	0.49
1:E:128:LEU:HD12	1:E:446:THR:HG23	1.94	0.49
1:E:34:PHE:O	1:E:34:PHE:CG	2.66	0.49
1:E:456:ALA:HB1	1:E:509:ASP:OD2	2.13	0.49
1:F:427:GLY:C	1:F:429:GLN:H	2.15	0.49
1:G:226:VAL:O	1:G:274:ARG:HA	2.13	0.49
1:G:80:TYR:CE1	1:G:444:LEU:HB3	2.48	0.49
1:H:255:ILE:O	1:H:257:ASP:N	2.45	0.49
1:I:44:TRP:CE2	1:I:54:ARG:HB3	2.48	0.49
1:I:578:GLN:HG2	1:I:596:ALA:HB2	1.94	0.49
1:J:198:ILE:HG22	1:J:198:ILE:O	2.12	0.49
1:K:561:ASP:HB2	1:L:89:ASP:CA	2.32	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:510:ILE:O	1:L:513:ARG:HD2	2.12	0.49
1:M:24:GLU:C	1:M:26:ARG:N	2.55	0.49
1:N:95:MSE:HE1	1:N:99:ARG:NH2	2.27	0.49
1:O:27:ARG:HB2	1:O:313:LYS:HE3	1.94	0.49
1:O:418:LEU:HB2	1:O:428:GLY:O	2.13	0.49
1:O:95:MSE:HE1	1:O:99:ARG:NH2	2.28	0.49
1:P:379:GLU:O	1:P:380:ASN:CB	2.60	0.49
1:P:248:LYS:HG3	1:P:511:ARG:HE	1.77	0.49
1:Q:123:VAL:HG22	1:Q:316:TYR:CE2	2.48	0.49
1:R:379:GLU:O	1:R:380:ASN:CB	2.61	0.49
1:R:586:THR:N	1:R:587:PRO:CD	2.76	0.49
1:S:430:VAL:HG11	3:U:719:HOH:O	2.10	0.49
1:S:92:ASP:HB3	1:U:561:ASP:OD2	2.13	0.49
1:T:351:PHE:CD2	1:T:356:ILE:HD12	2.47	0.49
1:U:248:LYS:HG3	1:U:511:ARG:HE	1.78	0.49
1:V:235:TYR:HA	1:V:265:LYS:HB3	1.93	0.49
1:X:14:ARG:NE	1:X:14:ARG:CA	2.71	0.49
2:Z:23:LEU:HD23	2:Z:26:LEU:HD11	1.94	0.49
1:C:15:PHE:CE2	1:C:19:TRP:NE1	2.81	0.49
1:C:577:ILE:HG12	1:C:582:LYS:CG	2.41	0.49
1:D:113:ILE:HD12	1:D:148:PRO:HB3	1.94	0.49
1:E:246:TYR:HE2	1:E:512:GLY:N	2.10	0.49
1:F:386:THR:O	1:F:387:GLN:O	2.31	0.49
1:F:80:TYR:CE1	1:F:444:LEU:HB3	2.48	0.49
1:G:136:SER:N	1:G:137:PRO:HD3	2.27	0.49
1:G:577:ILE:HG12	1:G:582:LYS:CG	2.41	0.49
1:H:47:GLN:HG3	1:H:54:ARG:NH1	2.28	0.49
1:I:386:THR:O	1:I:387:GLN:O	2.31	0.49
1:I:409:THR:O	1:I:413:LYS:HG2	2.12	0.49
3:H:719:HOH:O	1:I:438:LEU:HD22	2.12	0.49
1:I:80:TYR:CE1	1:I:444:LEU:HB3	2.48	0.49
1:J:80:TYR:CE1	1:J:444:LEU:HB3	2.47	0.49
1:K:119:ILE:HA	1:K:432:PHE:HE2	1.78	0.49
1:K:48:TYR:HD2	1:K:48:TYR:O	4.89	0.49
1:K:584:PRO:CG	1:K:593:LEU:HD12	2.42	0.49
1:L:226:VAL:O	1:L:274:ARG:HA	2.13	0.49
1:M:171:ARG:O	1:M:224:GLU:HA	2.13	0.49
1:O:535:ILE:HD13	1:O:554:LEU:HG	1.95	0.49
1:P:37:ARG:HH21	1:P:37:ARG:CB	2.26	0.49
1:R:66:LYS:HZ3	1:R:420:VAL:HG21	1.77	0.49
1:T:37:ARG:C	1:T:39:SER:N	2.66	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:451:ASP:C	1:T:453:LEU:H	2.15	0.49
1:U:9:GLU:HG3	1:U:12:LEU:H	1.78	0.49
1:V:535:ILE:HD13	1:V:554:LEU:HG	1.94	0.49
1:V:55:GLY:HA3	1:V:57:PHE:CE1	2.48	0.49
1:V:598:GLN:HB2	1:V:601:GLN:HB3	1.94	0.49
1:W:427:GLY:C	1:W:429:GLN:H	2.14	0.49
1:W:9:GLU:HG3	1:W:12:LEU:H	1.78	0.49
3:R:719:HOH:O	1:X:430:VAL:HG11	2.13	0.49
1:B:386:THR:O	1:B:387:GLN:O	2.31	0.49
1:B:80:TYR:CE1	1:B:444:LEU:HB3	2.48	0.49
1:B:456:ALA:HB1	1:B:509:ASP:OD2	2.13	0.49
1:C:15:PHE:HZ	1:C:283:CYS:SG	2.31	0.49
1:C:47:GLN:HG3	1:C:54:ARG:NH1	2.28	0.49
1:C:510:ILE:O	1:C:513:ARG:HD2	2.12	0.49
1:C:578:GLN:HG2	1:C:596:ALA:HB2	1.94	0.49
1:E:15:PHE:CE2	1:E:19:TRP:NE1	2.81	0.49
1:F:280:ILE:HG22	1:F:287:LEU:HD13	1.94	0.49
1:F:510:ILE:O	1:F:513:ARG:HD2	2.12	0.49
1:F:578:GLN:HG2	1:F:596:ALA:HB2	1.94	0.49
1:G:246:TYR:HE2	1:G:512:GLY:N	2.10	0.49
1:H:113:ILE:HD12	1:H:148:PRO:HB3	1.94	0.49
1:H:386:THR:O	1:H:387:GLN:O	2.31	0.49
1:H:80:TYR:CE1	1:H:444:LEU:HB3	2.47	0.49
1:I:34:PHE:CG	1:I:34:PHE:O	2.66	0.49
1:J:513:ARG:H	1:J:513:ARG:HD3	1.77	0.49
1:J:47:GLN:HG3	1:J:54:ARG:NH1	2.28	0.49
1:K:248:LYS:HD3	1:K:251:ILE:HB	1.93	0.49
1:K:80:TYR:CE1	1:K:444:LEU:HB3	2.48	0.49
1:K:48:TYR:CD2	1:K:48:TYR:O	5.23	0.49
1:L:198:ILE:O	1:L:198:ILE:HG22	2.12	0.49
1:K:334:MSE:SE	1:L:404:MSE:HE1	2.62	0.49
1:L:578:GLN:HG2	1:L:596:ALA:HB2	1.94	0.49
1:M:44:TRP:C	1:M:45:LEU:HD22	2.33	0.49
1:M:554:LEU:HD21	1:N:564:GLY:CA	2.38	0.49
1:P:443:ASP:C	1:P:446:THR:HG22	2.33	0.49
1:Q:27:ARG:HB2	1:Q:313:LYS:HE3	1.94	0.49
1:S:405:LEU:O	1:S:409:THR:HG23	2.12	0.49
1:T:443:ASP:C	1:T:446:THR:HG22	2.34	0.49
1:T:586:THR:N	1:T:587:PRO:CD	2.75	0.49
1:W:71:MSE:HE2	1:W:119:ILE:HD11	1.94	0.49
1:X:266:ILE:HG23	1:X:267:ALA:N	2.26	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:14:ARG:NE	1:B:14:ARG:CA	2.67	0.49
1:D:47:GLN:HG3	1:D:54:ARG:NH1	2.28	0.49
1:E:510:ILE:O	1:E:513:ARG:HD2	2.12	0.49
1:F:136:SER:N	1:F:137:PRO:HD3	2.27	0.49
1:G:255:ILE:O	1:G:257:ASP:N	2.45	0.49
1:H:136:SER:N	1:H:137:PRO:HD3	2.27	0.49
1:H:456:ALA:HB1	1:H:509:ASP:OD2	2.13	0.49
1:K:255:ILE:O	1:K:257:ASP:N	2.45	0.49
1:M:78:VAL:CG1	1:M:79:LEU:N	2.75	0.49
1:N:14:ARG:CA	1:N:14:ARG:NE	2.70	0.49
1:N:235:TYR:OH	1:N:252:LYS:NZ	2.45	0.49
1:O:55:GLY:HA3	1:O:57:PHE:CE1	2.48	0.49
1:P:443:ASP:C	1:P:444:LEU:HD13	2.34	0.49
1:P:535:ILE:HD13	1:P:554:LEU:HG	1.95	0.49
1:Q:443:ASP:C	1:Q:446:THR:HG22	2.34	0.49
1:Q:95:MSE:HE1	1:Q:99:ARG:NH2	2.28	0.49
1:R:164:LEU:HA	1:R:307:TRP:HH2	1.78	0.49
1:R:78:VAL:CG1	1:R:444:LEU:HG	2.43	0.49
1:S:413:LYS:HA	1:S:416:ALA:HB3	1.94	0.49
1:S:535:ILE:HD13	1:S:554:LEU:HG	1.95	0.49
1:T:386:THR:O	1:T:387:GLN:C	2.51	0.49
1:V:31:ASN:O	1:V:34:PHE:HB3	2.12	0.49
1:V:456:ALA:O	1:V:457:MSE:HB2	2.13	0.49
1:R:387:GLN:HB2	1:X:390:ALA:HB2	1.94	0.49
1:A:34:PHE:CG	1:A:34:PHE:O	2.66	0.48
1:A:578:GLN:HG2	1:A:596:ALA:HB2	1.94	0.48
1:C:226:VAL:O	1:C:274:ARG:HA	2.13	0.48
1:C:329:LEU:HD22	2:Z:142:PRO:HG2	1.94	0.48
1:C:80:TYR:CE1	1:C:444:LEU:HB3	2.48	0.48
1:E:47:GLN:HG3	1:E:54:ARG:NH1	2.28	0.48
1:F:236:GLN:HE21	1:F:265:LYS:HZ3	1.61	0.48
1:F:44:TRP:CE2	1:F:54:ARG:HB3	2.47	0.48
1:G:142:GLN:O	1:G:143:VAL:HG23	2.13	0.48
1:G:15:PHE:CE2	1:G:19:TRP:NE1	2.81	0.48
1:G:248:LYS:HD3	1:G:251:ILE:HB	1.93	0.48
1:G:57:PHE:CD2	1:G:330:ARG:CB	2.95	0.48
1:I:15:PHE:CE2	1:I:19:TRP:NE1	2.81	0.48
1:I:456:ALA:HB1	1:I:509:ASP:OD2	2.13	0.48
1:I:584:PRO:CG	1:I:593:LEU:HD12	2.42	0.48
1:K:226:VAL:O	1:K:274:ARG:HA	2.13	0.48
1:L:15:PHE:CE2	1:L:19:TRP:NE1	2.81	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:235:TYR:OH	1:M:252:LYS:NZ	2.45	0.48
1:M:31:ASN:O	1:M:34:PHE:HB3	2.12	0.48
1:M:35:PHE:C	1:M:37:ARG:H	2.16	0.48
1:N:343:ARG:O	1:N:344:THR:HB	2.13	0.48
1:N:384:LEU:N	1:N:384:LEU:HD22	2.28	0.48
1:P:434:THR:O	1:P:437:GLN:HG2	2.12	0.48
1:Q:235:TYR:OH	1:Q:252:LYS:NZ	2.46	0.48
1:R:444:LEU:C	1:R:446:THR:H	2.15	0.48
1:S:598:GLN:HB2	1:S:601:GLN:HB3	1.95	0.48
1:T:48:TYR:O	1:T:48:TYR:HD2	5.14	0.48
1:T:598:GLN:HB2	1:T:601:GLN:HB3	1.95	0.48
1:V:379:GLU:O	1:V:380:ASN:CB	2.61	0.48
1:V:573:ASN:O	1:V:577:ILE:HG13	2.13	0.48
1:W:37:ARG:C	1:W:39:SER:N	2.67	0.48
1:W:598:GLN:HB2	1:W:601:GLN:HB3	1.95	0.48
1:W:95:MSE:HE1	1:W:99:ARG:CZ	2.43	0.48
1:X:293:ILE:HD13	1:X:294:ALA:N	2.28	0.48
1:X:456:ALA:O	1:X:457:MSE:HB2	2.12	0.48
1:X:586:THR:N	1:X:587:PRO:CD	2.76	0.48
1:A:15:PHE:CE2	1:A:19:TRP:NE1	2.81	0.48
1:B:198:ILE:HG22	1:B:198:ILE:O	2.12	0.48
1:C:11:ILE:O	1:C:15:PHE:HB2	2.13	0.48
1:D:198:ILE:O	1:D:198:ILE:HG22	2.12	0.48
1:E:11:ILE:O	1:E:15:PHE:HB2	2.13	0.48
1:E:584:PRO:CG	1:E:593:LEU:HD12	2.42	0.48
1:F:255:ILE:O	1:F:257:ASP:N	2.45	0.48
1:F:376:ARG:HB2	1:G:352:TRP:CG	2.48	0.48
1:G:34:PHE:O	1:G:34:PHE:CG	2.66	0.48
1:H:44:TRP:CE2	1:H:54:ARG:HB3	2.47	0.48
1:J:34:PHE:CG	1:J:34:PHE:O	2.65	0.48
1:J:386:THR:O	1:J:387:GLN:O	2.31	0.48
1:I:567:MSE:HE2	1:J:554:LEU:HD22	1.94	0.48
1:K:142:GLN:O	1:K:143:VAL:HG23	2.13	0.48
1:K:47:GLN:HG3	1:K:54:ARG:NH1	2.28	0.48
1:M:9:GLU:HG3	1:M:12:LEU:H	1.77	0.48
1:M:164:LEU:HD22	1:M:169:ASP:CG	2.33	0.48
1:M:212:LEU:HD22	1:O:26:ARG:HG2	1.95	0.48
1:N:429:GLN:HG2	1:N:429:GLN:O	2.13	0.48
1:N:95:MSE:HE1	1:N:99:ARG:CZ	2.44	0.48
1:O:325:ASP:O	1:O:329:LEU:HD23	2.12	0.48
1:R:387:GLN:CB	1:X:390:ALA:CB	2.91	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:398:PRO:HB3	1:U:395:PRO:HD2	1.95	0.48
1:U:322:LEU:N	1:U:322:LEU:HD22	2.29	0.48
1:U:378:ASP:O	1:U:381:SER:O	2.31	0.48
1:U:560:LEU:O	1:U:561:ASP:O	2.32	0.48
1:U:586:THR:N	1:U:587:PRO:CD	2.76	0.48
1:V:293:ILE:HD13	1:V:294:ALA:N	2.27	0.48
1:W:405:LEU:O	1:W:409:THR:HG23	2.13	0.48
1:T:561:ASP:CB	1:W:89:ASP:HA	2.38	0.48
1:X:164:LEU:HA	1:X:307:TRP:CH2	2.48	0.48
2:Z:89:VAL:C	2:Z:91:ALA:H	2.15	0.48
1:A:119:ILE:HA	1:A:432:PHE:HE2	1.77	0.48
1:A:386:THR:O	1:A:387:GLN:O	2.31	0.48
1:A:584:PRO:HG2	1:A:593:LEU:HD12	1.94	0.48
1:B:128:LEU:HD12	1:B:446:THR:HG23	1.94	0.48
1:B:11:ILE:O	1:B:15:PHE:HB2	2.13	0.48
1:B:567:MSE:SE	1:C:576:LEU:HD13	2.63	0.48
1:D:208:VAL:HG12	1:D:210:PRO:HD3	1.96	0.48
1:D:72:ARG:HD2	1:F:434:THR:HG21	1.96	0.48
1:D:89:ASP:HA	1:E:561:ASP:CB	2.36	0.48
1:F:47:GLN:HG3	1:F:54:ARG:NH1	2.28	0.48
1:F:584:PRO:CG	1:F:593:LEU:HD12	2.42	0.48
1:G:128:LEU:HD12	1:G:446:THR:HG23	1.94	0.48
1:G:395:PRO:HD2	1:H:398:PRO:HB3	1.94	0.48
1:F:72:ARG:HD2	1:G:434:THR:HG21	1.95	0.48
1:H:248:LYS:CD	1:H:248:LYS:H	2.16	0.48
1:I:208:VAL:HG12	1:I:210:PRO:HD3	1.95	0.48
1:H:563:LYS:HD3	1:I:557:PHE:CE2	2.48	0.48
1:J:208:VAL:HG12	1:J:210:PRO:HD3	1.96	0.48
1:K:94:LEU:HA	1:K:97:MSE:CE	2.37	0.48
1:L:208:VAL:HG12	1:L:210:PRO:HD3	1.95	0.48
1:M:164:LEU:HA	1:M:307:TRP:CH2	2.48	0.48
1:M:563:LYS:HD3	1:O:557:PHE:CE2	2.48	0.48
1:N:123:VAL:CG1	1:N:304:PHE:CE1	2.96	0.48
1:N:266:ILE:HG23	1:N:267:ALA:N	2.29	0.48
1:N:27:ARG:HH21	1:V:41:TRP:HE1	1.61	0.48
1:O:443:ASP:C	1:O:446:THR:HG22	2.34	0.48
1:P:123:VAL:HG22	1:P:316:TYR:CE2	2.48	0.48
1:P:351:PHE:CD2	1:P:356:ILE:HD12	2.48	0.48
1:P:444:LEU:O	1:P:448:VAL:HG23	2.13	0.48
3:Q:719:HOH:O	1:R:430:VAL:HG13	2.12	0.48
1:R:451:ASP:C	1:R:453:LEU:H	2.17	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:266:ILE:HG23	1:S:267:ALA:N	2.28	0.48
1:S:443:ASP:C	1:S:444:LEU:HD13	2.34	0.48
1:T:164:LEU:HD22	1:T:169:ASP:CG	2.33	0.48
1:T:293:ILE:HD13	1:T:294:ALA:N	2.29	0.48
1:U:266:ILE:HG23	1:U:267:ALA:N	2.28	0.48
1:U:48:TYR:CD2	1:U:48:TYR:O	5.17	0.48
1:V:37:ARG:HH21	1:V:37:ARG:CB	2.25	0.48
1:V:95:MSE:HE1	1:V:99:ARG:NH2	2.29	0.48
1:W:158:TRP:N	1:W:158:TRP:HD1	2.07	0.48
1:W:235:TYR:OH	1:W:252:LYS:NZ	2.45	0.48
1:W:164:LEU:HA	1:W:307:TRP:HH2	1.79	0.48
1:W:248:LYS:HG3	1:W:511:ARG:HE	1.78	0.48
1:A:80:TYR:CE1	1:A:444:LEU:HB3	2.47	0.48
1:B:226:VAL:O	1:B:274:ARG:HA	2.13	0.48
1:C:280:ILE:HG22	1:C:287:LEU:HD13	1.94	0.48
1:D:15:PHE:CE2	1:D:19:TRP:NE1	2.81	0.48
1:D:34:PHE:CG	1:D:34:PHE:O	2.66	0.48
1:D:334:MSE:SE	1:D:405:LEU:HD11	2.64	0.48
1:D:80:TYR:CE1	1:D:444:LEU:HB3	2.48	0.48
1:E:119:ILE:HA	1:E:432:PHE:HE2	1.77	0.48
1:F:142:GLN:O	1:F:143:VAL:HG23	2.13	0.48
1:F:198:ILE:O	1:F:198:ILE:HG22	2.12	0.48
1:H:15:PHE:CE2	1:H:19:TRP:NE1	2.81	0.48
1:I:198:ILE:O	1:I:198:ILE:HG22	2.12	0.48
1:J:119:ILE:HA	1:J:432:PHE:HE2	1.77	0.48
1:J:136:SER:N	1:J:137:PRO:HD3	2.27	0.48
1:K:191:TYR:HE1	1:K:278:LYS:HZ3	1.60	0.48
1:K:584:PRO:HG2	1:K:593:LEU:HD12	1.94	0.48
1:L:142:GLN:O	1:L:143:VAL:HG23	2.13	0.48
1:M:586:THR:N	1:M:587:PRO:CD	2.76	0.48
1:O:293:ILE:HD13	1:O:294:ALA:N	2.28	0.48
1:O:322:LEU:N	1:O:322:LEU:HD22	2.28	0.48
1:P:47:GLN:H	1:P:48:TYR:HD2	1.61	0.48
1:Q:95:MSE:HE1	1:Q:99:ARG:CZ	2.43	0.48
1:S:41:TRP:HE1	1:T:27:ARG:HH21	1.62	0.48
1:T:379:GLU:O	1:T:380:ASN:CB	2.60	0.48
1:T:418:LEU:HB2	1:T:428:GLY:O	2.13	0.48
1:U:407:ALA:HB1	1:X:334:MSE:HE1	1.96	0.48
1:U:434:THR:HG23	1:U:435:VAL:N	2.28	0.48
1:V:66:LYS:HZ3	1:V:420:VAL:HG21	1.77	0.48
1:R:387:GLN:CB	1:X:390:ALA:HB2	2.44	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:28:VAL:HG11	2:Z:96:LEU:C	2.33	0.48
1:B:208:VAL:HG12	1:B:210:PRO:HD3	1.95	0.48
1:B:47:GLN:HG3	1:B:54:ARG:NH1	2.28	0.48
1:B:578:GLN:HG2	1:B:596:ALA:HB2	1.94	0.48
1:C:386:THR:CG2	1:C:389:LEU:HD21	2.44	0.48
1:D:44:TRP:CE2	1:D:54:ARG:HB3	2.48	0.48
1:D:577:ILE:HG12	1:D:582:LYS:CG	2.41	0.48
1:D:434:THR:HG21	1:E:72:ARG:HD2	1.96	0.48
1:F:208:VAL:HG12	1:F:210:PRO:HD3	1.95	0.48
1:G:334:MSE:SE	1:G:405:LEU:HD11	2.64	0.48
1:G:386:THR:O	1:G:387:GLN:O	2.31	0.48
1:I:128:LEU:HD12	1:I:446:THR:HG23	1.94	0.48
1:J:226:VAL:O	1:J:274:ARG:HA	2.13	0.48
1:J:376:ARG:HB2	1:K:352:TRP:CG	2.48	0.48
1:J:386:THR:O	1:J:387:GLN:C	2.52	0.48
1:K:15:PHE:CE2	1:K:19:TRP:NE1	2.81	0.48
1:M:37:ARG:C	1:M:39:SER:N	2.67	0.48
1:M:248:LYS:HG3	1:M:511:ARG:HE	1.79	0.48
1:O:37:ARG:CB	1:O:37:ARG:HH21	2.24	0.48
1:O:413:LYS:HA	1:O:416:ALA:HB3	1.95	0.48
1:P:48:TYR:O	1:P:48:TYR:HD2	5.14	0.48
1:O:561:ASP:HB2	1:P:89:ASP:HA	1.95	0.48
1:Q:293:ILE:HD13	1:Q:294:ALA:N	2.29	0.48
1:Q:164:LEU:HA	1:Q:307:TRP:HH2	1.79	0.48
1:Q:35:PHE:HE1	1:Q:321:ARG:NH1	2.08	0.48
1:Q:37:ARG:C	1:Q:39:SER:H	2.16	0.48
1:Q:386:THR:O	1:Q:387:GLN:C	2.52	0.48
1:S:325:ASP:O	1:S:329:LEU:HD23	2.13	0.48
1:S:418:LEU:HB2	1:S:428:GLY:O	2.13	0.48
1:S:444:LEU:O	1:S:446:THR:N	2.46	0.48
1:T:266:ILE:HG23	1:T:267:ALA:N	2.29	0.48
1:U:444:LEU:O	1:U:446:THR:N	2.46	0.48
1:U:95:MSE:HE1	1:U:99:ARG:NH2	2.28	0.48
1:V:164:LEU:HA	1:V:307:TRP:CH2	2.49	0.48
1:W:78:VAL:CG1	1:W:79:LEU:H	2.26	0.48
1:X:9:GLU:HG3	1:X:12:LEU:H	1.79	0.48
1:X:379:GLU:O	1:X:380:ASN:CB	2.61	0.48
1:X:37:ARG:C	1:X:39:SER:N	2.66	0.48
1:B:343:ARG:NH1	2:Z:135:ALA:O	2.41	0.48
1:A:57:PHE:CD2	1:A:330:ARG:CB	2.95	0.48
1:A:94:LEU:HA	1:A:97:MSE:CE	2.37	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:15:PHE:CE2	1:B:19:TRP:NE1	2.81	0.48
1:B:386:THR:O	1:B:387:GLN:C	2.52	0.48
1:C:255:ILE:O	1:C:257:ASP:N	2.45	0.48
1:E:142:GLN:O	1:E:143:VAL:HG23	2.13	0.48
1:E:139:SER:CB	1:E:455:THR:CG2	2.80	0.48
1:E:578:GLN:HG2	1:E:596:ALA:HB2	1.94	0.48
1:F:227:GLU:HA	1:F:274:ARG:CA	2.44	0.48
1:F:226:VAL:O	1:F:274:ARG:HA	2.13	0.48
1:F:334:MSE:SE	1:F:405:LEU:HD11	2.64	0.48
1:F:584:PRO:HG2	1:F:593:LEU:HD12	1.94	0.48
1:G:578:GLN:HG2	1:G:596:ALA:HB2	1.94	0.48
1:H:208:VAL:HG12	1:H:210:PRO:HD3	1.96	0.48
1:H:34:PHE:O	1:H:34:PHE:CG	2.66	0.48
1:K:34:PHE:CG	1:K:34:PHE:O	2.66	0.48
1:K:386:THR:O	1:K:387:GLN:C	2.52	0.48
1:L:34:PHE:O	1:L:34:PHE:CG	2.66	0.48
1:M:58:ASP:HA	1:M:327:GLN:NE2	2.28	0.48
1:M:386:THR:O	1:M:387:GLN:C	2.51	0.48
1:N:273:ARG:CZ	1:N:275:ARG:HE	2.27	0.48
1:N:322:LEU:HD22	1:N:322:LEU:H	1.78	0.48
1:O:573:ASN:O	1:O:577:ILE:HG13	2.13	0.48
1:P:71:MSE:CE	1:P:115:VAL:HB	2.44	0.48
1:P:560:LEU:O	1:P:561:ASP:O	2.32	0.48
1:Q:164:LEU:HA	1:Q:307:TRP:CH2	2.49	0.48
1:Q:351:PHE:CD2	1:Q:356:ILE:HD12	2.49	0.48
1:Q:82:PRO:O	1:Q:516:CYS:HA	2.13	0.48
1:R:273:ARG:HH22	1:R:453:LEU:CD2	2.27	0.48
1:U:164:LEU:HA	1:U:307:TRP:HH2	1.79	0.48
1:U:48:TYR:O	1:U:48:TYR:HD2	5.14	0.48
1:V:118:GLN:OE1	1:V:303:VAL:HB	2.13	0.48
1:V:413:LYS:HA	1:V:416:ALA:HB3	1.95	0.48
1:W:379:GLU:O	1:W:380:ASN:CB	2.61	0.48
1:W:418:LEU:HB2	1:W:428:GLY:O	2.13	0.48
1:X:164:LEU:HA	1:X:307:TRP:HH2	1.78	0.48
1:X:598:GLN:HB2	1:X:601:GLN:HB3	1.95	0.48
2:Y:23:LEU:HD23	2:Y:26:LEU:HD11	1.94	0.48
1:A:11:ILE:O	1:A:15:PHE:HB2	2.13	0.48
1:A:577:ILE:HG12	1:A:582:LYS:CG	2.41	0.48
1:C:142:GLN:O	1:C:143:VAL:HG23	2.13	0.48
1:C:208:VAL:HG12	1:C:210:PRO:HD3	1.95	0.48
1:D:11:ILE:O	1:D:15:PHE:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:208:VAL:HG12	1:E:210:PRO:HD3	1.96	0.48
1:H:11:ILE:O	1:H:15:PHE:HB2	2.13	0.48
1:H:142:GLN:O	1:H:143:VAL:HG23	2.13	0.48
1:H:334:MSE:SE	1:H:405:LEU:HD11	2.64	0.48
1:H:577:ILE:HG12	1:H:582:LYS:CG	2.41	0.48
1:I:142:GLN:O	1:I:143:VAL:HG23	2.13	0.48
1:J:15:PHE:CE2	1:J:19:TRP:NE1	2.81	0.48
1:J:334:MSE:SE	1:J:405:LEU:HD11	2.64	0.48
1:K:248:LYS:CD	1:K:248:LYS:H	2.16	0.48
1:K:386:THR:CG2	1:K:389:LEU:HD21	2.44	0.48
1:N:158:TRP:HD1	1:N:158:TRP:H	1.62	0.48
1:N:322:LEU:N	1:N:322:LEU:HD22	2.29	0.48
1:N:443:ASP:C	1:N:444:LEU:HD13	2.34	0.48
1:N:48:TYR:O	1:N:48:TYR:CD2	5.16	0.48
1:O:266:ILE:HG23	1:O:267:ALA:N	2.27	0.48
1:O:248:LYS:HG3	1:O:511:ARG:HE	1.79	0.48
1:P:386:THR:O	1:P:387:GLN:C	2.51	0.48
1:Q:48:TYR:HD2	1:Q:48:TYR:O	5.14	0.48
1:R:164:LEU:HA	1:R:307:TRP:CH2	2.48	0.48
1:R:235:TYR:OH	1:R:252:LYS:NZ	2.46	0.48
1:R:322:LEU:N	1:R:322:LEU:HD22	2.29	0.48
1:R:371:TYR:HE2	1:R:373:LEU:HD21	1.79	0.48
1:S:235:TYR:OH	1:S:252:LYS:NZ	2.47	0.48
1:S:322:LEU:HD22	1:S:322:LEU:N	2.28	0.48
1:S:384:LEU:HD22	1:S:384:LEU:N	2.28	0.48
1:T:387:GLN:HB3	1:W:390:ALA:CB	2.44	0.48
1:T:434:THR:HG23	1:T:435:VAL:N	2.28	0.48
1:U:310:VAL:HG22	1:X:40:GLN:HG2	1.96	0.48
1:U:456:ALA:O	1:U:457:MSE:HB2	2.12	0.48
1:W:235:TYR:HA	1:W:265:LYS:HB3	1.96	0.48
1:W:266:ILE:HG23	1:W:267:ALA:N	2.28	0.48
1:W:386:THR:O	1:W:387:GLN:C	2.52	0.48
1:X:165:MSE:HE1	1:X:435:VAL:HB	1.95	0.48
1:B:42:ASP:OD2	2:Z:145:SER:O	2.31	0.48
1:A:165:MSE:HG3	1:A:307:TRP:CD2	2.49	0.48
1:A:376:ARG:HB2	1:B:352:TRP:CG	2.49	0.48
1:A:386:THR:CG2	1:A:389:LEU:HD21	2.44	0.48
1:A:47:GLN:HG3	1:A:54:ARG:NH1	2.28	0.48
1:C:165:MSE:HG3	1:C:307:TRP:CD2	2.49	0.48
1:C:372:TYR:CE2	1:E:348:LYS:HB2	2.49	0.48
1:C:386:THR:O	1:C:387:GLN:C	2.52	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:386:THR:CG2	1:D:389:LEU:HD21	2.44	0.48
1:E:227:GLU:HA	1:E:274:ARG:CA	2.44	0.48
1:E:226:VAL:O	1:E:274:ARG:HA	2.13	0.48
1:F:11:ILE:O	1:F:15:PHE:HB2	2.13	0.48
1:G:11:ILE:O	1:G:15:PHE:HB2	2.13	0.48
1:G:14:ARG:NE	1:G:14:ARG:CA	2.67	0.48
1:G:44:TRP:CE2	1:G:54:ARG:HB3	2.48	0.48
1:H:165:MSE:HG3	1:H:307:TRP:CD2	2.49	0.48
1:H:34:PHE:HZ	1:H:328:ARG:HH22	0.80	0.48
1:I:11:ILE:O	1:I:15:PHE:HB2	2.13	0.48
1:I:34:PHE:CE1	1:I:324:LYS:NZ	2.72	0.48
1:J:386:THR:CG2	1:J:389:LEU:HD21	2.44	0.48
1:K:578:GLN:HG2	1:K:596:ALA:HB2	1.94	0.48
1:K:334:MSE:HE3	1:L:404:MSE:CE	2.44	0.48
1:N:9:GLU:HG3	1:N:12:LEU:H	1.77	0.48
1:N:248:LYS:HG3	1:N:511:ARG:HE	1.79	0.48
1:N:598:GLN:HB2	1:N:601:GLN:HB3	1.96	0.48
1:P:35:PHE:HE1	1:P:321:ARG:NH1	2.08	0.48
1:Q:37:ARG:C	1:Q:39:SER:N	2.66	0.48
1:Q:395:PRO:HD2	1:R:398:PRO:HB3	1.95	0.48
1:S:27:ARG:HB2	1:S:313:LYS:HE3	1.95	0.48
1:S:560:LEU:O	1:S:561:ASP:O	2.31	0.48
1:U:164:LEU:HA	1:U:307:TRP:CH2	2.49	0.48
1:U:329:LEU:HD21	1:X:53:TYR:OH	2.13	0.48
1:V:248:LYS:CD	1:V:248:LYS:H	2.18	0.48
1:V:27:ARG:HB2	1:V:313:LYS:HE3	1.96	0.48
1:V:384:LEU:HD22	1:V:384:LEU:N	2.27	0.48
1:V:443:ASP:C	1:V:446:THR:HG22	2.34	0.48
1:V:48:TYR:CD2	1:V:48:TYR:O	5.17	0.48
1:N:89:ASP:CA	1:V:561:ASP:HB2	2.31	0.48
1:W:123:VAL:HG22	1:W:316:TYR:HE2	1.79	0.48
1:B:165:MSE:HG3	1:B:307:TRP:CD2	2.49	0.48
1:B:386:THR:CG2	1:B:389:LEU:HD21	2.44	0.48
1:C:386:THR:O	1:C:387:GLN:O	2.31	0.48
1:B:334:MSE:SE	1:C:404:MSE:HE1	2.64	0.48
1:E:334:MSE:SE	1:E:405:LEU:HD11	2.64	0.48
1:D:182:ASN:HD22	1:F:171:ARG:HH21	1.62	0.48
1:F:165:MSE:HG3	1:F:307:TRP:CD2	2.49	0.48
1:F:386:THR:CG2	1:F:389:LEU:HD21	2.44	0.48
1:J:165:MSE:HG3	1:J:307:TRP:CD2	2.49	0.48
1:K:11:ILE:O	1:K:15:PHE:HB2	2.13	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:165:MSE:HG3	1:K:307:TRP:CD2	2.49	0.48
1:K:577:ILE:HG12	1:K:582:LYS:CG	2.41	0.48
1:L:227:GLU:HA	1:L:274:ARG:CA	2.44	0.48
1:L:386:THR:CG2	1:L:389:LEU:HD21	2.44	0.48
1:M:47:GLN:H	1:M:48:TYR:HD2	1.62	0.48
1:N:123:VAL:HG22	1:N:316:TYR:CE2	2.49	0.48
1:O:155:HIS:CE1	1:O:204:PRO:HB2	2.49	0.48
1:O:123:VAL:HG22	1:O:316:TYR:CE2	2.49	0.48
1:P:78:VAL:CG1	1:P:79:LEU:H	2.27	0.48
1:P:9:GLU:HG3	1:P:12:LEU:H	1.77	0.48
1:Q:443:ASP:C	1:Q:444:LEU:HD13	2.34	0.48
1:S:158:TRP:HD1	1:S:158:TRP:N	2.07	0.48
1:S:164:LEU:HD22	1:S:169:ASP:CG	2.34	0.48
1:S:248:LYS:CD	1:S:248:LYS:H	2.17	0.48
1:S:293:ILE:HD13	1:S:294:ALA:N	2.28	0.48
1:S:47:GLN:CG	1:S:48:TYR:H	2.27	0.48
1:S:95:MSE:HE1	1:S:99:ARG:NH2	2.29	0.48
1:T:14:ARG:NE	1:T:14:ARG:CA	2.70	0.48
1:T:33:LEU:HD12	1:T:34:PHE:N	2.29	0.48
1:T:384:LEU:HD22	1:T:384:LEU:N	2.28	0.48
1:T:95:MSE:HE1	1:T:99:ARG:CZ	2.44	0.48
1:U:386:THR:O	1:U:387:GLN:C	2.52	0.48
1:W:31:ASN:O	1:W:34:PHE:HB3	2.14	0.48
1:X:127:ARG:HG2	1:X:147:GLU:HB2	1.96	0.48
1:X:248:LYS:HG3	1:X:511:ARG:HE	1.77	0.48
1:X:78:VAL:CG1	1:X:79:LEU:N	2.77	0.48
1:A:234:ILE:HG12	1:A:267:ALA:HB3	1.96	0.48
1:A:334:MSE:SE	1:A:405:LEU:HD11	2.64	0.48
1:C:119:ILE:HA	1:C:432:PHE:HE2	1.77	0.48
1:C:227:GLU:HA	1:C:274:ARG:CA	2.44	0.48
1:D:128:LEU:HD12	1:D:446:THR:HG23	1.94	0.48
1:D:227:GLU:HA	1:D:274:ARG:CA	2.44	0.48
1:D:40:GLN:O	1:D:41:TRP:CB	2.54	0.48
1:D:539:LEU:HD21	1:D:551:LEU:HB3	1.96	0.48
1:F:128:LEU:HD12	1:F:446:THR:HG23	1.94	0.48
1:F:15:PHE:CE2	1:F:19:TRP:NE1	2.81	0.48
1:H:386:THR:CG2	1:H:389:LEU:HD21	2.44	0.48
1:K:227:GLU:HA	1:K:274:ARG:CA	2.44	0.48
1:K:248:LYS:HZ1	1:K:513:ARG:HH12	1.60	0.48
1:J:561:ASP:CB	1:K:89:ASP:HA	2.33	0.48
1:L:101:ASP:HB2	1:L:144:ILE:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:136:SER:N	1:L:137:PRO:HD3	2.27	0.48
1:L:164:LEU:HA	1:L:307:TRP:HH2	1.79	0.48
1:L:386:THR:O	1:L:387:GLN:C	2.52	0.48
1:L:334:MSE:SE	1:L:405:LEU:HD11	2.64	0.48
1:M:235:TYR:HA	1:M:265:LYS:HB3	1.94	0.48
1:M:329:LEU:HD21	1:N:53:TYR:OH	2.13	0.48
1:N:47:GLN:CG	1:N:48:TYR:H	2.27	0.48
1:P:238:PRO:HD3	1:P:263:PHE:HB2	1.95	0.48
1:P:444:LEU:O	1:P:446:THR:N	2.46	0.48
1:P:82:PRO:O	1:P:516:CYS:HA	2.13	0.48
1:Q:322:LEU:N	1:Q:322:LEU:HD22	2.29	0.48
1:R:266:ILE:HG23	1:R:267:ALA:N	2.28	0.48
1:R:37:ARG:C	1:R:39:SER:N	2.66	0.48
1:R:55:GLY:HA3	1:R:57:PHE:CE1	2.48	0.48
1:T:38:VAL:HG21	1:T:324:LYS:HD2	1.96	0.48
1:T:165:MSE:HE1	1:T:435:VAL:HB	1.95	0.48
1:U:444:LEU:O	1:U:448:VAL:HG23	2.14	0.48
1:V:48:TYR:O	1:V:48:TYR:HD2	5.14	0.48
1:W:164:LEU:HA	1:W:307:TRP:CH2	2.49	0.48
1:W:451:ASP:C	1:W:453:LEU:H	2.18	0.48
1:X:386:THR:O	1:X:387:GLN:C	2.52	0.48
1:X:444:LEU:O	1:X:446:THR:N	2.47	0.48
1:A:226:VAL:O	1:A:274:ARG:HA	2.13	0.47
1:A:434:THR:HA	1:A:437:GLN:CD	2.35	0.47
1:B:234:ILE:HG12	1:B:267:ALA:HB3	1.96	0.47
1:B:577:ILE:HG12	1:B:582:LYS:CG	2.41	0.47
1:D:226:VAL:O	1:D:274:ARG:HA	2.13	0.47
1:F:230:GLU:HG2	1:F:273:ARG:HB2	1.96	0.47
1:G:165:MSE:HG3	1:G:307:TRP:CD2	2.49	0.47
1:G:26:ARG:NH2	1:G:30:LYS:HB2	2.28	0.47
1:G:58:ASP:O	1:G:59:VAL:HB	2.14	0.47
1:H:226:VAL:O	1:H:274:ARG:HA	2.13	0.47
1:I:165:MSE:HG3	1:I:307:TRP:CD2	2.49	0.47
1:I:334:MSE:SE	1:I:405:LEU:HD11	2.64	0.47
1:J:142:GLN:O	1:J:143:VAL:HG23	2.13	0.47
1:J:101:ASP:HB2	1:J:144:ILE:O	2.14	0.47
1:J:539:LEU:HD21	1:J:551:LEU:CB	2.44	0.47
1:K:208:VAL:HG12	1:K:210:PRO:HD3	1.96	0.47
1:K:334:MSE:SE	1:K:405:LEU:HD11	2.64	0.47
1:K:58:ASP:O	1:K:59:VAL:HB	2.14	0.47
1:L:230:GLU:HG2	1:L:273:ARG:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:456:ALA:HB1	1:L:509:ASP:OD2	2.13	0.47
1:L:539:LEU:HD21	1:L:551:LEU:HB3	1.96	0.47
1:L:86:ALA:HB2	1:L:515:GLU:HG3	1.96	0.47
1:M:66:LYS:HZ3	1:M:420:VAL:HG11	1.79	0.47
1:O:14:ARG:NE	1:O:14:ARG:CA	2.71	0.47
1:O:434:THR:HG23	1:O:435:VAL:N	2.28	0.47
1:P:71:MSE:HE3	1:P:115:VAL:HB	1.95	0.47
1:Q:165:MSE:HG3	1:Q:307:TRP:CD2	2.48	0.47
1:Q:387:GLN:HB2	1:R:390:ALA:HB2	1.94	0.47
1:Q:387:GLN:HB3	1:R:390:ALA:CB	2.44	0.47
1:R:9:GLU:HG3	1:R:12:LEU:H	1.78	0.47
1:S:123:VAL:CG1	1:S:304:PHE:CE1	2.97	0.47
1:S:127:ARG:HG2	1:S:147:GLU:HB2	1.96	0.47
1:T:248:LYS:HG3	1:T:511:ARG:HE	1.79	0.47
1:V:330:ARG:HD2	1:V:409:THR:CG2	2.38	0.47
1:X:86:ALA:CB	1:X:515:GLU:HG3	2.44	0.47
2:Z:75:PRO:HA	2:Z:76:PRO:HD3	1.42	0.47
1:B:86:ALA:HB2	1:B:515:GLU:HG3	1.96	0.47
1:C:81:ARG:HB2	1:C:517:TYR:CZ	2.50	0.47
1:D:230:GLU:HG2	1:D:273:ARG:HB2	1.96	0.47
1:E:535:ILE:CD1	1:E:554:LEU:HG	2.44	0.47
1:H:101:ASP:HB2	1:H:144:ILE:O	2.14	0.47
1:I:113:ILE:HD12	1:I:148:PRO:HB3	1.94	0.47
1:I:227:GLU:HA	1:I:274:ARG:CA	2.44	0.47
1:I:86:ALA:HB2	1:I:515:GLU:HG3	1.96	0.47
1:K:101:ASP:HB2	1:K:144:ILE:O	2.14	0.47
1:K:539:LEU:HD21	1:K:551:LEU:HB3	1.96	0.47
1:L:11:ILE:O	1:L:15:PHE:HB2	2.13	0.47
1:M:434:THR:HG23	1:M:435:VAL:N	2.29	0.47
1:N:573:ASN:O	1:N:577:ILE:HG13	2.14	0.47
1:O:123:VAL:CG1	1:O:304:PHE:CE1	2.97	0.47
1:O:451:ASP:C	1:O:453:LEU:H	2.17	0.47
1:P:434:THR:HG23	1:P:435:VAL:N	2.29	0.47
1:S:35:PHE:HZ	1:S:321:ARG:NE	2.11	0.47
1:T:193:LEU:HD22	1:T:287:LEU:HB3	1.96	0.47
1:U:127:ARG:HG2	1:U:147:GLU:HB2	1.96	0.47
1:U:31:ASN:O	1:U:34:PHE:HB3	2.14	0.47
1:U:598:GLN:HB2	1:U:601:GLN:HB3	1.95	0.47
1:W:27:ARG:HB2	1:W:313:LYS:HE3	1.96	0.47
1:W:95:MSE:HE1	1:W:99:ARG:NH2	2.29	0.47
1:X:443:ASP:C	1:X:444:LEU:HD13	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:X:444:LEU:O	1:X:448:VAL:HG23	2.13	0.47
1:A:198:ILE:HA	1:A:199:PRO:HD3	1.64	0.47
1:A:334:MSE:SE	1:B:404:MSE:HE1	2.64	0.47
1:A:535:ILE:CD1	1:A:554:LEU:HG	2.44	0.47
1:B:273:ARG:HH22	1:B:453:LEU:CD1	2.28	0.47
1:D:142:GLN:O	1:D:143:VAL:HG23	2.13	0.47
1:E:162:SER:HB2	1:E:170:ALA:HB2	1.97	0.47
1:E:386:THR:CG2	1:E:389:LEU:HD21	2.44	0.47
1:E:86:ALA:HB2	1:E:515:GLU:HG3	1.96	0.47
1:H:40:GLN:O	1:H:41:TRP:CB	2.55	0.47
1:G:567:MSE:HE2	1:H:554:LEU:HD22	1.96	0.47
1:I:101:ASP:HB2	1:I:144:ILE:O	2.14	0.47
1:I:535:ILE:CD1	1:I:554:LEU:HG	2.44	0.47
1:K:273:ARG:HH22	1:K:453:LEU:CD1	2.28	0.47
1:K:539:LEU:HD21	1:K:551:LEU:CB	2.44	0.47
1:M:27:ARG:HB2	1:M:313:LYS:HE3	1.94	0.47
1:N:293:ILE:HD13	1:N:294:ALA:N	2.29	0.47
1:N:78:VAL:CG1	1:N:444:LEU:HG	2.44	0.47
1:O:227:GLU:O	1:O:227:GLU:CG	2.63	0.47
1:Q:35:PHE:HZ	1:Q:321:ARG:NE	2.10	0.47
1:R:378:ASP:O	1:R:381:SER:O	2.33	0.47
1:R:386:THR:O	1:R:387:GLN:C	2.51	0.47
1:S:95:MSE:HE1	1:S:99:ARG:CZ	2.45	0.47
1:T:325:ASP:O	1:T:329:LEU:HD23	2.14	0.47
1:T:409:THR:O	1:T:413:LYS:HG2	2.15	0.47
1:S:564:GLY:HA3	1:T:535:ILE:HD11	1.96	0.47
1:U:430:VAL:HG11	3:X:719:HOH:O	2.13	0.47
1:X:238:PRO:HD3	1:X:263:PHE:HB2	1.96	0.47
1:X:27:ARG:HB2	1:X:313:LYS:HE3	1.95	0.47
1:X:47:GLN:H	1:X:48:TYR:HD2	1.61	0.47
1:B:35:PHE:HE1	1:B:321:ARG:NH1	2.13	0.47
1:D:164:LEU:HA	1:D:307:TRP:HH2	1.79	0.47
1:E:34:PHE:O	1:E:34:PHE:CD2	2.68	0.47
1:E:539:LEU:HD21	1:E:551:LEU:CB	2.45	0.47
1:C:567:MSE:HE2	1:E:554:LEU:HD22	1.95	0.47
1:F:434:THR:HA	1:F:437:GLN:CD	2.35	0.47
1:G:101:ASP:HB2	1:G:144:ILE:O	2.14	0.47
1:G:386:THR:O	1:G:387:GLN:C	2.52	0.47
1:H:130:THR:HG22	1:H:144:ILE:HA	1.97	0.47
1:H:57:PHE:CD2	1:H:330:ARG:CB	2.95	0.47
1:H:58:ASP:O	1:H:59:VAL:HB	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:115:VAL:O	1:I:119:ILE:HG13	2.15	0.47
1:I:230:GLU:HG2	1:I:273:ARG:HB2	1.96	0.47
1:I:386:THR:O	1:I:387:GLN:C	2.52	0.47
1:I:58:ASP:O	1:I:59:VAL:HB	2.14	0.47
1:J:164:LEU:HA	1:J:307:TRP:HH2	1.79	0.47
1:J:35:PHE:HE2	1:J:324:LYS:NZ	2.08	0.47
1:K:535:ILE:CD1	1:K:554:LEU:HG	2.44	0.47
1:K:86:ALA:HB2	1:K:515:GLU:HG3	1.96	0.47
1:L:165:MSE:HG3	1:L:307:TRP:CD2	2.49	0.47
1:L:451:ASP:O	1:L:456:ALA:N	2.41	0.47
1:L:81:ARG:HB2	1:L:517:TYR:CZ	2.50	0.47
1:N:118:GLN:OE1	1:N:303:VAL:HB	2.14	0.47
1:N:38:VAL:HG21	1:N:324:LYS:HD2	1.96	0.47
1:O:164:LEU:HA	1:O:307:TRP:CH2	2.50	0.47
1:O:37:ARG:C	1:O:39:SER:N	2.67	0.47
1:O:568:MSE:HG3	1:P:551:LEU:CD2	2.44	0.47
1:P:35:PHE:HZ	1:P:321:ARG:NE	2.11	0.47
1:Q:158:TRP:HD1	1:Q:158:TRP:H	1.62	0.47
1:Q:560:LEU:O	1:Q:561:ASP:O	2.33	0.47
1:R:376:ARG:HB2	1:X:352:TRP:CG	2.49	0.47
1:R:418:LEU:HB2	1:R:428:GLY:O	2.14	0.47
1:S:227:GLU:CG	1:S:227:GLU:O	2.62	0.47
1:T:95:MSE:HE1	1:T:99:ARG:NH2	2.29	0.47
1:U:413:LYS:HA	1:U:416:ALA:HB3	1.96	0.47
1:V:33:LEU:HD12	1:V:34:PHE:N	2.30	0.47
1:W:293:ILE:HD13	1:W:294:ALA:N	2.29	0.47
1:X:123:VAL:CG1	1:X:304:PHE:CE1	2.97	0.47
1:R:563:LYS:HD3	1:X:557:PHE:CE2	2.49	0.47
1:A:130:THR:HG22	1:A:144:ILE:HA	1.97	0.47
1:A:208:VAL:HG12	1:A:210:PRO:HD3	1.96	0.47
1:A:86:ALA:HB2	1:A:515:GLU:HG3	1.96	0.47
1:B:101:ASP:HB2	1:B:144:ILE:O	2.14	0.47
1:B:434:THR:HA	1:B:437:GLN:CD	2.35	0.47
1:B:539:LEU:HD21	1:B:551:LEU:HB3	1.96	0.47
1:C:101:ASP:HB2	1:C:144:ILE:O	2.14	0.47
1:F:81:ARG:HB2	1:F:517:TYR:CZ	2.50	0.47
1:F:535:ILE:CD1	1:F:554:LEU:HG	2.44	0.47
1:F:86:ALA:HB2	1:F:515:GLU:HG3	1.96	0.47
1:G:29:ALA:O	1:G:33:LEU:HG	2.15	0.47
1:G:81:ARG:HB2	1:G:517:TYR:CZ	2.50	0.47
1:H:34:PHE:CD2	1:H:34:PHE:O	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:539:LEU:HD21	1:H:551:LEU:CB	2.44	0.47
1:J:81:ARG:HB2	1:J:517:TYR:CZ	2.50	0.47
1:L:434:THR:HA	1:L:437:GLN:CD	2.35	0.47
1:L:535:ILE:CD1	1:L:554:LEU:HG	2.44	0.47
1:L:539:LEU:HD21	1:L:551:LEU:CB	2.45	0.47
1:M:238:PRO:HD3	1:M:263:PHE:HB2	1.97	0.47
1:M:443:ASP:C	1:M:444:LEU:HD13	2.35	0.47
1:N:235:TYR:HA	1:N:265:LYS:HB3	1.95	0.47
1:N:386:THR:O	1:N:387:GLN:C	2.52	0.47
1:N:444:LEU:O	1:N:446:THR:N	2.48	0.47
1:P:260:ASP:HA	1:P:264:ILE:HB	1.97	0.47
1:P:316:TYR:O	1:P:321:ARG:NH1	2.48	0.47
1:P:86:ALA:CB	1:P:515:GLU:HG3	2.44	0.47
1:Q:260:ASP:HA	1:Q:264:ILE:HB	1.97	0.47
1:Q:34:PHE:O	1:Q:37:ARG:HB2	2.14	0.47
1:Q:78:VAL:CG1	1:Q:444:LEU:HG	2.44	0.47
1:R:434:THR:HG23	1:R:435:VAL:N	2.28	0.47
1:S:443:ASP:C	1:S:446:THR:HG22	2.34	0.47
1:U:451:ASP:C	1:U:453:LEU:H	2.18	0.47
1:W:325:ASP:O	1:W:329:LEU:HD23	2.13	0.47
1:A:34:PHE:CD2	1:A:34:PHE:O	2.68	0.47
1:A:386:THR:O	1:A:387:GLN:C	2.52	0.47
1:A:42:ASP:OD2	2:Y:145:SER:O	2.32	0.47
1:B:142:GLN:O	1:B:143:VAL:HG23	2.13	0.47
1:B:164:LEU:HA	1:B:307:TRP:HH2	1.80	0.47
1:B:334:MSE:SE	1:B:405:LEU:HD11	2.64	0.47
1:C:197:ASP:O	1:C:198:ILE:HB	2.15	0.47
1:C:334:MSE:SE	1:C:405:LEU:HD11	2.64	0.47
1:C:434:THR:HA	1:C:437:GLN:CD	2.35	0.47
1:D:386:THR:O	1:D:387:GLN:C	2.52	0.47
1:D:58:ASP:O	1:D:59:VAL:HB	2.14	0.47
1:E:165:MSE:HG3	1:E:307:TRP:CD2	2.49	0.47
1:F:130:THR:HG22	1:F:144:ILE:HA	1.97	0.47
1:F:101:ASP:HB2	1:F:144:ILE:O	2.14	0.47
1:F:164:LEU:HA	1:F:307:TRP:HH2	1.80	0.47
1:F:29:ALA:O	1:F:33:LEU:HG	2.15	0.47
1:F:563:LYS:HD3	1:G:557:PHE:CE2	2.49	0.47
1:G:539:LEU:HD21	1:G:551:LEU:CB	2.44	0.47
1:H:386:THR:O	1:H:387:GLN:C	2.52	0.47
1:J:71:MSE:CE	1:J:115:VAL:HB	2.45	0.47
1:J:230:GLU:HG2	1:J:273:ARG:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:26:ARG:NH2	1:J:30:LYS:HB2	2.28	0.47
1:J:34:PHE:CD2	1:J:34:PHE:O	2.68	0.47
1:L:130:THR:HG22	1:L:144:ILE:HA	1.97	0.47
1:L:197:ASP:O	1:L:198:ILE:HB	2.15	0.47
1:L:35:PHE:HE1	1:L:321:ARG:NH1	2.13	0.47
1:M:371:TYR:HE2	1:M:373:LEU:HD21	1.79	0.47
1:N:37:ARG:CB	1:N:37:ARG:HH21	2.28	0.47
1:N:444:LEU:O	1:N:447:TYR:N	2.47	0.47
1:N:444:LEU:O	1:N:448:VAL:HG23	2.14	0.47
1:O:260:ASP:HA	1:O:264:ILE:HB	1.97	0.47
1:O:235:TYR:HA	1:O:265:LYS:HB3	1.95	0.47
1:O:330:ARG:HD2	1:O:409:THR:CG2	2.40	0.47
1:O:44:TRP:C	1:O:45:LEU:HD22	2.35	0.47
1:P:235:TYR:OH	1:P:252:LYS:NZ	2.48	0.47
1:P:413:LYS:HA	1:P:416:ALA:HB3	1.97	0.47
1:P:212:LEU:HD22	1:Q:26:ARG:HG2	1.96	0.47
1:P:40:GLN:HG2	1:Q:310:VAL:HG22	1.95	0.47
1:Q:451:ASP:C	1:Q:453:LEU:H	2.17	0.47
1:R:164:LEU:HD22	1:R:169:ASP:OD1	2.15	0.47
1:R:556:TYR:OH	1:X:542:THR:HG21	2.13	0.47
1:R:598:GLN:HB2	1:R:601:GLN:HB3	1.95	0.47
1:S:248:LYS:HG3	1:S:511:ARG:HE	1.78	0.47
1:S:420:VAL:HA	1:S:428:GLY:HA2	1.96	0.47
1:T:405:LEU:O	1:T:409:THR:HG23	2.14	0.47
1:T:454:ALA:O	1:T:455:THR:C	2.53	0.47
1:U:14:ARG:NE	1:U:14:ARG:CA	2.70	0.47
1:V:235:TYR:OH	1:V:252:LYS:NZ	2.47	0.47
1:V:260:ASP:HA	1:V:264:ILE:HB	1.96	0.47
1:V:434:THR:HG23	1:V:435:VAL:N	2.29	0.47
1:W:171:ARG:O	1:W:224:GLU:HA	2.15	0.47
1:W:238:PRO:HD3	1:W:263:PHE:HB2	1.96	0.47
1:X:47:GLN:N	1:X:48:TYR:HD2	2.13	0.47
1:X:82:PRO:O	1:X:516:CYS:HA	2.14	0.47
1:B:197:ASP:O	1:B:198:ILE:HB	2.15	0.47
1:B:535:ILE:CD1	1:B:554:LEU:HG	2.44	0.47
1:D:101:ASP:HB2	1:D:144:ILE:O	2.14	0.47
1:D:162:SER:HB2	1:D:170:ALA:HB2	1.97	0.47
1:D:29:ALA:O	1:D:33:LEU:HG	2.15	0.47
1:D:81:ARG:HB2	1:D:517:TYR:CZ	2.50	0.47
1:D:57:PHE:CD2	1:D:330:ARG:CB	2.95	0.47
1:E:230:GLU:HG2	1:E:273:ARG:HB2	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:539:LEU:HD21	1:E:551:LEU:HB3	1.96	0.47
1:F:577:ILE:HG12	1:F:582:LYS:CG	2.41	0.47
1:G:115:VAL:O	1:G:119:ILE:HG13	2.15	0.47
1:G:208:VAL:HG12	1:G:210:PRO:HD3	1.95	0.47
1:G:86:ALA:HB2	1:G:515:GLU:HG3	1.96	0.47
1:I:130:THR:HG22	1:I:144:ILE:HA	1.97	0.47
1:J:11:ILE:O	1:J:15:PHE:HB2	2.13	0.47
1:J:535:ILE:CD1	1:J:554:LEU:HG	2.44	0.47
1:K:34:PHE:CD2	1:K:34:PHE:O	2.68	0.47
1:M:248:LYS:CD	1:M:248:LYS:H	2.17	0.47
1:M:418:LEU:HB2	1:M:428:GLY:O	2.15	0.47
1:N:164:LEU:HA	1:N:307:TRP:CH2	2.50	0.47
1:N:27:ARG:HB2	1:N:313:LYS:HE3	1.96	0.47
1:O:164:LEU:HA	1:O:307:TRP:HH2	1.80	0.47
1:O:158:TRP:HH2	1:O:302:PRO:HG3	1.80	0.47
1:O:31:ASN:O	1:O:34:PHE:HB3	2.14	0.47
1:O:47:GLN:H	1:O:48:TYR:HD2	1.63	0.47
1:Q:14:ARG:NE	1:Q:14:ARG:CA	2.71	0.47
1:Q:238:PRO:HD3	1:Q:263:PHE:HB2	1.95	0.47
1:Q:561:ASP:HB2	1:R:89:ASP:CA	2.35	0.47
1:R:248:LYS:HG3	1:R:511:ARG:HE	1.78	0.47
1:S:322:LEU:H	1:S:322:LEU:HD22	1.79	0.47
1:U:66:LYS:HZ3	1:U:420:VAL:HG21	1.79	0.47
1:U:573:ASN:O	1:U:577:ILE:HG13	2.13	0.47
1:V:29:ALA:O	1:V:33:LEU:HG	2.15	0.47
1:W:47:GLN:CG	1:W:48:TYR:H	2.28	0.47
1:W:528:LYS:CD	1:W:560:LEU:HD21	2.45	0.47
1:X:155:HIS:CE1	1:X:204:PRO:HB2	2.50	0.47
1:A:273:ARG:HH22	1:A:453:LEU:CD1	2.28	0.47
1:A:81:ARG:HB2	1:A:517:TYR:CZ	2.50	0.47
1:B:162:SER:HB2	1:B:170:ALA:HB2	1.97	0.47
1:B:451:ASP:O	1:B:456:ALA:N	2.41	0.47
1:B:58:ASP:O	1:B:59:VAL:HB	2.14	0.47
1:C:115:VAL:O	1:C:119:ILE:HG13	2.15	0.47
1:C:57:PHE:CD2	1:C:330:ARG:CB	2.95	0.47
1:E:71:MSE:CE	1:E:115:VAL:HB	2.45	0.47
1:E:115:VAL:O	1:E:119:ILE:HG13	2.15	0.47
1:E:130:THR:HG22	1:E:144:ILE:HA	1.97	0.47
1:F:115:VAL:O	1:F:119:ILE:HG13	2.15	0.47
1:F:34:PHE:CD2	1:F:34:PHE:O	2.68	0.47
1:G:162:SER:HB2	1:G:170:ALA:HB2	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:230:GLU:HG2	1:G:273:ARG:HB2	1.96	0.47
1:F:334:MSE:HE3	1:G:404:MSE:HE3	1.96	0.47
1:G:565:VAL:O	1:G:569:ARG:HB3	2.15	0.47
1:I:162:SER:HB2	1:I:170:ALA:HB2	1.96	0.47
1:J:130:THR:HG22	1:J:144:ILE:HA	1.97	0.47
1:K:130:THR:HG22	1:K:144:ILE:HA	1.97	0.47
1:K:563:LYS:HD3	1:L:557:PHE:CE2	2.50	0.47
1:M:451:ASP:C	1:M:453:LEU:H	2.17	0.47
1:N:348:LYS:HB2	1:V:372:TYR:CE2	2.50	0.47
1:N:47:GLN:H	1:N:48:TYR:HD2	1.62	0.47
1:O:386:THR:O	1:O:387:GLN:C	2.52	0.47
1:P:136:SER:N	1:P:137:PRO:HD3	2.30	0.47
1:P:554:LEU:O	1:P:557:PHE:HB3	2.14	0.47
1:R:238:PRO:HD3	1:R:263:PHE:HB2	1.97	0.47
1:T:123:VAL:HG22	1:T:316:TYR:HE2	1.79	0.47
1:U:418:LEU:HB2	1:U:428:GLY:O	2.14	0.47
1:V:438:LEU:HD22	3:W:718:HOH:O	2.13	0.47
1:V:454:ALA:O	1:V:455:THR:C	2.53	0.47
1:W:293:ILE:HG12	1:W:294:ALA:H	1.80	0.47
1:X:260:ASP:HA	1:X:264:ILE:HB	1.96	0.47
1:X:31:ASN:O	1:X:34:PHE:HB3	2.15	0.47
1:X:37:ARG:C	1:X:39:SER:H	2.18	0.47
1:X:560:LEU:O	1:X:561:ASP:O	2.33	0.47
1:A:142:GLN:O	1:A:143:VAL:HG23	2.13	0.47
1:B:130:THR:HG22	1:B:144:ILE:HA	1.97	0.47
1:C:207:TRP:O	1:C:208:VAL:C	2.54	0.47
1:C:535:ILE:CD1	1:C:554:LEU:HG	2.44	0.47
1:C:92:ASP:OD2	1:C:92:ASP:N	2.48	0.47
1:D:197:ASP:O	1:D:198:ILE:HB	2.15	0.47
1:D:26:ARG:NH2	1:D:30:LYS:HB2	2.28	0.47
1:E:197:ASP:O	1:E:198:ILE:HB	2.15	0.47
1:E:81:ARG:HB2	1:E:517:TYR:CZ	2.50	0.47
1:G:234:ILE:HG12	1:G:267:ALA:HB3	1.96	0.47
1:H:29:ALA:O	1:H:33:LEU:HG	2.15	0.47
1:H:273:ARG:HH22	1:H:453:LEU:CD1	2.28	0.47
1:H:81:ARG:HB2	1:H:517:TYR:CZ	2.50	0.47
1:I:273:ARG:HH22	1:I:453:LEU:CD1	2.28	0.47
1:I:29:ALA:O	1:I:33:LEU:HG	2.15	0.47
1:I:34:PHE:CD2	1:I:34:PHE:O	2.68	0.47
1:I:386:THR:CG2	1:I:389:LEU:HD21	2.44	0.47
1:J:234:ILE:HG12	1:J:267:ALA:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:565:VAL:O	1:J:569:ARG:HB3	2.15	0.47
1:J:577:ILE:HG12	1:J:582:LYS:CG	2.41	0.47
1:L:207:TRP:O	1:L:208:VAL:C	2.53	0.47
1:M:343:ARG:O	1:M:344:THR:HB	2.15	0.47
1:M:47:GLN:CG	1:M:48:TYR:H	2.27	0.47
1:M:511:ARG:HA	1:M:513:ARG:CD	2.44	0.47
1:M:546:THR:CG2	1:M:547:PRO:HD3	2.31	0.47
1:M:66:LYS:HZ3	1:M:420:VAL:HG21	1.78	0.47
1:P:293:ILE:HD13	1:P:294:ALA:N	2.30	0.47
1:Q:434:THR:HG23	1:Q:435:VAL:N	2.29	0.47
1:Q:47:GLN:H	1:Q:48:TYR:HD2	1.62	0.47
1:Q:598:GLN:HB2	1:Q:601:GLN:HB3	1.95	0.47
1:S:386:THR:O	1:S:387:GLN:C	2.52	0.47
1:T:191:TYR:HE1	1:T:278:LYS:HZ3	1.63	0.47
1:T:413:LYS:HA	1:T:416:ALA:HB3	1.96	0.47
1:T:554:LEU:O	1:T:557:PHE:HB3	2.15	0.47
1:V:245:SER:HG	1:V:247:PHE:HE1	1.62	0.47
1:V:273:ARG:CZ	1:V:275:ARG:HE	2.28	0.47
1:V:47:GLN:N	1:V:48:TYR:HD2	2.13	0.47
1:A:101:ASP:HB2	1:A:144:ILE:O	2.14	0.47
1:A:248:LYS:HZ1	1:A:513:ARG:HH12	1.62	0.47
1:B:115:VAL:O	1:B:119:ILE:HG13	2.15	0.47
1:B:248:LYS:HB3	1:B:511:ARG:NH1	2.30	0.47
1:C:230:GLU:HG2	1:C:273:ARG:HB2	1.96	0.47
1:D:535:ILE:CD1	1:D:554:LEU:HG	2.44	0.47
1:D:528:LYS:HZ3	1:D:560:LEU:HD21	1.78	0.47
1:F:539:LEU:HD21	1:F:551:LEU:CB	2.44	0.47
1:G:197:ASP:O	1:G:198:ILE:HB	2.15	0.47
1:G:539:LEU:HD21	1:G:551:LEU:HB3	1.96	0.47
1:H:164:LEU:HA	1:H:307:TRP:HH2	1.80	0.47
1:H:535:ILE:CD1	1:H:554:LEU:HG	2.44	0.47
1:J:207:TRP:O	1:J:208:VAL:C	2.53	0.47
1:K:162:SER:HB2	1:K:170:ALA:HB2	1.97	0.47
1:K:201:PHE:HE2	1:K:281:ILE:HG22	1.80	0.47
1:K:434:THR:HA	1:K:437:GLN:CD	2.35	0.47
1:L:227:GLU:OE2	1:L:227:GLU:N	2.47	0.47
1:L:34:PHE:CD2	1:L:34:PHE:O	2.68	0.47
1:M:232:ALA:HB2	1:M:269:ARG:O	2.15	0.47
1:M:273:ARG:CZ	1:M:275:ARG:HE	2.27	0.47
1:M:38:VAL:HG21	1:M:324:LYS:HD2	1.97	0.47
1:M:598:GLN:HB2	1:M:601:GLN:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:71:MSE:HE3	1:N:115:VAL:HB	1.97	0.47
1:O:160:SER:O	1:O:161:ASN:ND2	2.44	0.47
1:O:9:GLU:HG3	1:O:12:LEU:H	1.78	0.47
1:P:155:HIS:CE1	1:P:204:PRO:HB2	2.50	0.47
1:P:37:ARG:C	1:P:39:SER:N	2.68	0.47
1:O:568:MSE:SE	1:P:550:GLN:HB3	2.65	0.47
3:P:719:HOH:O	1:Q:430:VAL:HG13	2.13	0.47
1:Q:444:LEU:O	1:Q:446:THR:N	2.47	0.47
1:R:171:ARG:O	1:R:224:GLU:HA	2.14	0.47
1:R:227:GLU:CG	1:R:227:GLU:O	2.63	0.47
1:R:293:ILE:HG12	1:R:294:ALA:H	1.80	0.47
1:S:444:LEU:O	1:S:448:VAL:HG23	2.15	0.47
1:S:528:LYS:CD	1:S:560:LEU:HD21	2.45	0.47
1:S:554:LEU:O	1:S:557:PHE:HB3	2.14	0.47
1:T:158:TRP:HH2	1:T:302:PRO:HG3	1.80	0.47
1:U:273:ARG:CZ	1:U:275:ARG:HE	2.28	0.47
1:U:123:VAL:HG13	1:U:304:PHE:CE1	2.50	0.47
1:U:37:ARG:C	1:U:39:SER:N	2.68	0.47
1:U:76:ILE:HD12	1:U:433:ASP:OD1	2.15	0.47
1:U:78:VAL:CG1	1:U:444:LEU:HG	2.44	0.47
1:W:322:LEU:HD22	1:W:322:LEU:N	2.30	0.47
1:W:66:LYS:HZ3	1:W:420:VAL:HG21	1.80	0.47
1:A:197:ASP:O	1:A:198:ILE:HB	2.15	0.47
1:A:248:LYS:HB3	1:A:511:ARG:NH1	2.30	0.47
1:B:227:GLU:OE2	1:B:227:GLU:N	2.47	0.47
1:B:81:ARG:HB2	1:B:517:TYR:CZ	2.50	0.47
1:B:565:VAL:O	1:B:569:ARG:HB3	2.15	0.47
1:C:35:PHE:HE1	1:C:321:ARG:NH1	2.13	0.47
1:C:451:ASP:O	1:C:456:ALA:N	2.41	0.47
1:C:539:LEU:HD21	1:C:551:LEU:HB3	1.96	0.47
1:D:130:THR:HG22	1:D:144:ILE:HA	1.97	0.47
1:D:165:MSE:HG3	1:D:307:TRP:CD2	2.49	0.47
1:D:542:THR:HG21	1:E:556:TYR:OH	2.15	0.47
1:E:207:TRP:O	1:E:208:VAL:C	2.53	0.47
1:E:386:THR:O	1:E:387:GLN:C	2.52	0.47
1:E:434:THR:HA	1:E:437:GLN:CD	2.35	0.47
1:E:248:LYS:HB3	1:E:511:ARG:NH1	2.30	0.47
1:E:57:PHE:CD2	1:E:330:ARG:CB	2.95	0.47
1:E:58:ASP:O	1:E:59:VAL:HB	2.14	0.47
1:F:386:THR:O	1:F:387:GLN:C	2.52	0.47
1:F:273:ARG:HH22	1:F:453:LEU:CD1	2.28	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:539:LEU:HD21	1:F:551:LEU:HB3	1.96	0.47
1:F:92:ASP:N	1:F:92:ASP:OD2	2.48	0.47
1:G:434:THR:HA	1:G:437:GLN:CD	2.35	0.47
1:H:201:PHE:HE2	1:H:281:ILE:HG22	1.80	0.47
1:H:434:THR:HA	1:H:437:GLN:CD	2.35	0.47
1:I:164:LEU:HA	1:I:307:TRP:HH2	1.80	0.47
1:I:434:THR:HA	1:I:437:GLN:CD	2.35	0.47
1:J:28:GLU:HG3	1:J:32:ASP:OD2	2.15	0.47
1:J:29:ALA:O	1:J:33:LEU:HG	2.15	0.47
1:J:86:ALA:HB2	1:J:515:GLU:HG3	1.96	0.47
1:K:115:VAL:O	1:K:119:ILE:HG13	2.15	0.47
1:M:55:GLY:HA3	1:M:57:PHE:CE1	2.49	0.47
1:N:78:VAL:CG1	1:N:79:LEU:N	2.75	0.47
1:Q:245:SER:HG	1:Q:247:PHE:HE1	1.62	0.47
1:Q:444:LEU:N	1:Q:444:LEU:HD13	2.30	0.47
1:R:293:ILE:HD13	1:R:294:ALA:N	2.29	0.47
1:R:560:LEU:O	1:R:561:ASP:O	2.32	0.47
1:S:238:PRO:HD3	1:S:263:PHE:HB2	1.97	0.47
1:S:38:VAL:HG21	1:S:324:LYS:HD2	1.97	0.47
1:S:41:TRP:HE1	1:T:27:ARG:NH2	2.13	0.47
1:S:86:ALA:CB	1:S:515:GLU:HG3	2.45	0.47
1:S:577:ILE:HG12	1:S:582:LYS:CG	2.43	0.47
1:T:235:TYR:OH	1:T:252:LYS:NZ	2.48	0.47
1:T:266:ILE:O	1:T:267:ALA:HB2	2.16	0.47
1:T:37:ARG:CB	1:T:37:ARG:HH21	2.28	0.47
1:U:235:TYR:OH	1:U:252:LYS:NZ	2.48	0.47
1:U:384:LEU:N	1:U:384:LEU:HD22	2.29	0.47
1:V:409:THR:O	1:V:413:LYS:HG2	2.15	0.47
1:W:118:GLN:OE1	1:W:303:VAL:HB	2.14	0.47
1:W:193:LEU:HD22	1:W:287:LEU:HB3	1.97	0.47
1:W:343:ARG:O	1:W:344:THR:HB	2.15	0.47
1:X:227:GLU:CG	1:X:227:GLU:O	2.63	0.47
1:U:557:PHE:CE2	1:X:563:LYS:HD3	2.49	0.47
1:A:29:ALA:O	1:A:33:LEU:HG	2.15	0.46
1:B:376:ARG:HB2	1:C:352:TRP:CG	2.50	0.46
1:B:94:LEU:HA	1:B:97:MSE:CE	2.37	0.46
1:C:395:PRO:HD2	1:E:398:PRO:HB3	1.96	0.46
1:D:71:MSE:CE	1:D:115:VAL:HB	2.45	0.46
1:D:115:VAL:O	1:D:119:ILE:HG13	2.15	0.46
1:D:86:ALA:HB2	1:D:515:GLU:HG3	1.96	0.46
1:D:92:ASP:OD2	1:D:92:ASP:N	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:197:ASP:O	1:F:198:ILE:HB	2.15	0.46
1:F:207:TRP:O	1:F:208:VAL:C	2.54	0.46
1:G:386:THR:CG2	1:G:389:LEU:HD21	2.44	0.46
1:H:248:LYS:HB3	1:H:511:ARG:NH1	2.30	0.46
1:H:539:LEU:HD21	1:H:551:LEU:HB3	1.96	0.46
1:H:86:ALA:HB2	1:H:515:GLU:HG3	1.96	0.46
1:H:92:ASP:N	1:H:92:ASP:OD2	2.48	0.46
1:I:539:LEU:HD21	1:I:551:LEU:HB3	1.96	0.46
1:I:565:VAL:O	1:I:569:ARG:HB3	2.15	0.46
1:J:58:ASP:O	1:J:59:VAL:HB	2.14	0.46
1:J:92:ASP:N	1:J:92:ASP:OD2	2.48	0.46
1:K:230:GLU:HG2	1:K:273:ARG:HB2	1.96	0.46
1:L:201:PHE:HE2	1:L:281:ILE:HG22	1.80	0.46
1:L:444:LEU:C	1:L:446:THR:H	2.19	0.46
1:L:577:ILE:HG12	1:L:582:LYS:CG	2.41	0.46
1:M:198:ILE:HG22	1:M:198:ILE:O	2.14	0.46
1:M:260:ASP:HA	1:M:264:ILE:HB	1.98	0.46
1:M:78:VAL:CG1	1:M:444:LEU:HG	2.45	0.46
1:N:165:MSE:HG3	1:N:307:TRP:CD2	2.49	0.46
1:N:198:ILE:HG22	1:N:198:ILE:O	2.15	0.46
1:N:348:LYS:HE2	1:V:369:TYR:O	2.15	0.46
1:O:598:GLN:HB2	1:O:601:GLN:HB3	1.95	0.46
1:P:27:ARG:HB2	1:P:313:LYS:HE3	1.96	0.46
1:P:343:ARG:O	1:P:344:THR:HB	2.14	0.46
1:P:47:GLN:N	1:P:48:TYR:HD2	2.13	0.46
1:R:273:ARG:CZ	1:R:275:ARG:HE	2.28	0.46
1:R:343:ARG:O	1:R:344:THR:HB	2.15	0.46
1:R:47:GLN:N	1:R:48:TYR:HD2	2.13	0.46
1:S:78:VAL:CG1	1:S:444:LEU:HG	2.45	0.46
1:T:260:ASP:HA	1:T:264:ILE:HB	1.96	0.46
1:U:405:LEU:O	1:U:409:THR:HG23	2.15	0.46
1:U:80:TYR:OH	1:U:444:LEU:HD12	2.15	0.46
1:U:82:PRO:O	1:U:516:CYS:HA	2.15	0.46
1:U:86:ALA:CB	1:U:515:GLU:HG3	2.45	0.46
1:U:95:MSE:HE1	1:U:99:ARG:CZ	2.44	0.46
1:W:123:VAL:CG1	1:W:304:PHE:CE1	2.98	0.46
1:A:201:PHE:HE2	1:A:281:ILE:HG22	1.80	0.46
1:A:207:TRP:O	1:A:208:VAL:C	2.53	0.46
1:A:539:LEU:HD21	1:A:551:LEU:CB	2.44	0.46
1:B:230:GLU:HG2	1:B:273:ARG:HB2	1.96	0.46
1:C:162:SER:HB2	1:C:170:ALA:HB2	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:86:ALA:HB2	1:C:515:GLU:HG3	1.96	0.46
1:D:207:TRP:O	1:D:208:VAL:C	2.54	0.46
1:D:317:GLU:HB3	1:D:321:ARG:CZ	2.46	0.46
1:D:34:PHE:O	1:D:34:PHE:CD2	2.68	0.46
1:D:438:LEU:HD22	3:E:719:HOH:O	2.15	0.46
1:D:539:LEU:HD21	1:D:551:LEU:CB	2.44	0.46
1:E:444:LEU:C	1:E:446:THR:H	2.19	0.46
1:E:565:VAL:O	1:E:569:ARG:HB3	2.15	0.46
1:F:376:ARG:HB2	1:G:352:TRP:CD2	2.50	0.46
1:G:164:LEU:HA	1:G:307:TRP:HH2	1.80	0.46
1:G:317:GLU:HB3	1:G:321:ARG:CZ	2.46	0.46
1:G:34:PHE:O	1:G:34:PHE:CD2	2.68	0.46
1:G:413:LYS:HB3	1:G:413:LYS:HE2	1.74	0.46
1:G:273:ARG:HH22	1:G:453:LEU:CD1	2.28	0.46
1:H:565:VAL:O	1:H:569:ARG:HB3	2.15	0.46
1:I:343:ARG:HG2	1:I:343:ARG:H	1.52	0.46
1:I:444:LEU:C	1:I:446:THR:H	2.19	0.46
1:I:539:LEU:HD21	1:I:551:LEU:CB	2.44	0.46
1:H:567:MSE:HE2	1:I:554:LEU:HD22	1.96	0.46
1:J:227:GLU:HA	1:J:274:ARG:CA	2.44	0.46
1:J:317:GLU:HB3	1:J:321:ARG:CZ	2.46	0.46
1:J:343:ARG:H	1:J:343:ARG:HG2	1.52	0.46
1:K:434:THR:HA	1:K:437:GLN:HG2	1.97	0.46
1:M:127:ARG:HG2	1:M:147:GLU:HB2	1.96	0.46
1:M:193:LEU:HD22	1:M:287:LEU:HB3	1.97	0.46
1:M:293:ILE:HD13	1:M:294:ALA:N	2.31	0.46
1:M:560:LEU:O	1:M:561:ASP:O	2.33	0.46
1:N:171:ARG:O	1:N:224:GLU:HA	2.15	0.46
1:N:37:ARG:C	1:N:39:SER:N	2.67	0.46
1:O:322:LEU:HD22	1:O:322:LEU:H	1.79	0.46
1:O:395:PRO:HD2	1:P:398:PRO:HB3	1.96	0.46
1:O:560:LEU:O	1:O:561:ASP:O	2.33	0.46
1:P:598:GLN:HB2	1:P:601:GLN:HB3	1.95	0.46
1:R:413:LYS:HA	1:R:416:ALA:HB3	1.96	0.46
1:R:420:VAL:HA	1:R:428:GLY:HA2	1.98	0.46
1:R:47:GLN:H	1:R:48:TYR:HD2	1.62	0.46
1:R:82:PRO:O	1:R:516:CYS:HA	2.15	0.46
1:R:564:GLY:CA	1:X:554:LEU:HD21	2.42	0.46
1:S:37:ARG:C	1:S:39:SER:N	2.68	0.46
1:T:451:ASP:C	1:T:453:LEU:N	2.69	0.46
1:T:47:GLN:CG	1:T:48:TYR:H	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:47:GLN:H	1:T:48:TYR:HD2	1.64	0.46
1:U:542:THR:HG21	1:X:556:TYR:OH	2.14	0.46
1:U:71:MSE:HE3	1:U:115:VAL:HB	1.96	0.46
1:X:165:MSE:HG3	1:X:307:TRP:CD2	2.49	0.46
1:X:378:ASP:O	1:X:381:SER:O	2.33	0.46
1:X:434:THR:HG23	1:X:435:VAL:N	2.30	0.46
1:A:162:SER:HB2	1:A:170:ALA:HB2	1.96	0.46
1:A:164:LEU:HA	1:A:307:TRP:HH2	1.80	0.46
1:A:227:GLU:HA	1:A:274:ARG:CA	2.44	0.46
1:B:139:SER:CB	1:B:455:THR:CG2	2.80	0.46
1:B:539:LEU:HD21	1:B:551:LEU:CB	2.44	0.46
1:C:28:GLU:HG3	1:C:32:ASP:OD2	2.15	0.46
1:C:29:ALA:O	1:C:33:LEU:HG	2.15	0.46
1:C:34:PHE:CD2	1:C:34:PHE:O	2.68	0.46
1:C:539:LEU:HD21	1:C:551:LEU:CB	2.44	0.46
1:D:444:LEU:N	1:D:444:LEU:HD13	2.31	0.46
1:E:273:ARG:HH22	1:E:453:LEU:CD1	2.28	0.46
1:E:410:SER:O	1:E:414:GLU:HG2	2.16	0.46
1:F:162:SER:HB2	1:F:170:ALA:HB2	1.96	0.46
1:F:565:VAL:O	1:F:569:ARG:HB3	2.15	0.46
1:H:28:GLU:HG3	1:H:32:ASP:OD2	2.15	0.46
1:H:444:LEU:HD13	1:H:444:LEU:N	2.31	0.46
1:I:410:SER:O	1:I:414:GLU:HG2	2.16	0.46
1:I:71:MSE:CE	1:I:115:VAL:HB	2.45	0.46
1:J:197:ASP:O	1:J:198:ILE:HB	2.15	0.46
1:J:376:ARG:HB2	1:J:352:TRP:CG	2.51	0.46
1:J:410:SER:O	1:J:414:GLU:HG2	2.16	0.46
1:J:434:THR:HA	1:J:437:GLN:CD	2.35	0.46
1:J:273:ARG:HH22	1:J:453:LEU:CD1	2.28	0.46
1:J:539:LEU:HD21	1:J:551:LEU:HB3	1.96	0.46
1:K:234:ILE:HG12	1:K:267:ALA:HB3	1.96	0.46
1:K:28:GLU:HG3	1:K:32:ASP:OD2	2.15	0.46
1:K:29:ALA:O	1:K:33:LEU:HG	2.15	0.46
1:K:81:ARG:HB2	1:K:517:TYR:CZ	2.50	0.46
1:K:92:ASP:N	1:K:92:ASP:OD2	2.48	0.46
1:M:158:TRP:H	1:M:158:TRP:HD1	1.61	0.46
1:M:510:ILE:O	1:M:513:ARG:HD2	2.15	0.46
1:N:238:PRO:HD3	1:N:263:PHE:HB2	1.97	0.46
1:O:127:ARG:HG2	1:O:147:GLU:HB2	1.96	0.46
1:O:238:PRO:HD3	1:O:263:PHE:HB2	1.96	0.46
1:P:322:LEU:N	1:P:322:LEU:HD22	2.29	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:127:ARG:HG2	1:Q:147:GLU:HB2	1.96	0.46
1:Q:174:THR:N	3:Q:705:HOH:O	2.47	0.46
1:Q:454:ALA:O	1:Q:455:THR:C	2.53	0.46
1:Q:560:LEU:HD13	1:R:82:PRO:CD	2.22	0.46
1:R:510:ILE:O	1:R:513:ARG:HD2	2.15	0.46
1:R:95:MSE:HE1	1:R:99:ARG:NH2	2.31	0.46
1:T:164:LEU:HA	1:T:307:TRP:CH2	2.51	0.46
1:T:165:MSE:HG3	1:T:307:TRP:CD2	2.49	0.46
1:T:387:GLN:HG2	1:T:387:GLN:H	1.57	0.46
1:T:429:GLN:O	1:T:429:GLN:HG2	2.15	0.46
1:U:165:MSE:HG3	1:U:307:TRP:CD2	2.50	0.46
1:U:260:ASP:HA	1:U:264:ILE:HB	1.97	0.46
1:U:33:LEU:HD12	1:U:34:PHE:N	2.30	0.46
1:N:26:ARG:HG2	1:V:212:LEU:HD22	1.98	0.46
1:V:280:ILE:HG22	1:V:287:LEU:HD13	1.97	0.46
1:V:378:ASP:O	1:V:381:SER:O	2.34	0.46
1:V:418:LEU:HB2	1:V:428:GLY:O	2.15	0.46
1:V:443:ASP:C	1:V:444:LEU:HD13	2.35	0.46
1:V:78:VAL:CG1	1:V:444:LEU:HG	2.45	0.46
1:W:227:GLU:O	1:W:227:GLU:CG	2.63	0.46
1:X:273:ARG:CZ	1:X:275:ARG:HE	2.28	0.46
1:X:41:TRP:HE3	1:X:42:ASP:HB3	1.81	0.46
1:X:546:THR:CG2	1:X:547:PRO:HD3	2.30	0.46
2:Z:140:ARG:O	2:Z:141:MET:HB3	2.16	0.46
1:A:230:GLU:HG2	1:A:273:ARG:HB2	1.96	0.46
1:A:238:PRO:HG3	1:A:263:PHE:CB	2.46	0.46
1:A:539:LEU:HD21	1:A:551:LEU:HB3	1.96	0.46
1:A:565:VAL:O	1:A:569:ARG:HB3	2.15	0.46
1:B:207:TRP:O	1:B:208:VAL:C	2.53	0.46
1:B:227:GLU:HA	1:B:274:ARG:CA	2.44	0.46
1:B:48:TYR:O	1:B:49:THR:CB	2.64	0.46
1:C:273:ARG:HH22	1:C:453:LEU:CD1	2.28	0.46
1:C:26:ARG:NH2	1:C:30:LYS:HB2	2.28	0.46
1:D:248:LYS:HB3	1:D:511:ARG:NH1	2.30	0.46
1:E:101:ASP:HB2	1:E:144:ILE:O	2.14	0.46
1:E:28:GLU:HG3	1:E:32:ASP:OD2	2.15	0.46
1:E:434:THR:HA	1:E:437:GLN:HG2	1.98	0.46
1:E:444:LEU:N	1:E:444:LEU:HD13	2.31	0.46
1:F:219:ILE:HD12	1:F:281:ILE:O	2.16	0.46
1:G:410:SER:O	1:G:414:GLU:HG2	2.16	0.46
1:G:71:MSE:CE	1:G:115:VAL:HB	2.45	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:115:VAL:O	1:H:119:ILE:HG13	2.15	0.46
1:H:230:GLU:HG2	1:H:273:ARG:HB2	1.96	0.46
1:H:71:MSE:CE	1:H:115:VAL:HB	2.45	0.46
1:I:207:TRP:O	1:I:208:VAL:C	2.53	0.46
1:I:317:GLU:HB3	1:I:321:ARG:CZ	2.46	0.46
1:I:77:ASP:HB2	1:I:523:SER:HB2	1.98	0.46
1:J:78:VAL:CG2	1:J:444:LEU:HD21	2.46	0.46
1:K:248:LYS:HB3	1:K:511:ARG:NH1	2.30	0.46
1:L:162:SER:HB2	1:L:170:ALA:HB2	1.96	0.46
1:L:248:LYS:HB3	1:L:511:ARG:NH1	2.30	0.46
1:L:273:ARG:HH22	1:L:453:LEU:CD1	2.28	0.46
1:L:565:VAL:O	1:L:569:ARG:HB3	2.15	0.46
1:O:164:LEU:HD22	1:O:169:ASP:OD1	2.15	0.46
1:P:164:LEU:HA	1:P:307:TRP:CH2	2.51	0.46
1:P:409:THR:O	1:P:413:LYS:HG2	2.15	0.46
1:Q:316:TYR:O	1:Q:321:ARG:NH1	2.49	0.46
1:S:33:LEU:HD12	1:S:34:PHE:N	2.31	0.46
1:T:227:GLU:O	1:T:227:GLU:CG	2.63	0.46
1:T:330:ARG:O	1:T:334:MSE:HB2	2.16	0.46
1:T:37:ARG:C	1:T:39:SER:H	2.18	0.46
3:S:719:HOH:O	1:T:430:VAL:HG11	2.15	0.46
1:T:80:TYR:OH	1:T:444:LEU:HD12	2.16	0.46
1:T:86:ALA:CB	1:T:515:GLU:HG3	2.45	0.46
1:T:577:ILE:HG12	1:T:582:LYS:CG	2.45	0.46
1:U:238:PRO:HD3	1:U:263:PHE:HB2	1.98	0.46
1:U:322:LEU:H	1:U:322:LEU:HD22	1.80	0.46
1:V:47:GLN:CG	1:V:48:TYR:H	2.28	0.46
1:V:560:LEU:O	1:V:561:ASP:O	2.33	0.46
1:W:198:ILE:O	1:W:198:ILE:HG22	2.14	0.46
1:W:409:THR:O	1:W:413:LYS:HG2	2.16	0.46
3:T:718:HOH:O	1:W:438:LEU:HD22	2.15	0.46
1:W:443:ASP:C	1:W:444:LEU:HD13	2.36	0.46
1:W:47:GLN:N	1:W:48:TYR:HD2	2.14	0.46
1:X:193:LEU:HD22	1:X:287:LEU:HB3	1.97	0.46
1:A:219:ILE:HD12	1:A:281:ILE:O	2.16	0.46
1:A:34:PHE:HE1	1:A:324:LYS:HZ2	1.52	0.46
1:A:35:PHE:HE1	1:A:321:ARG:NH1	2.13	0.46
1:B:71:MSE:CE	1:B:115:VAL:HB	2.45	0.46
1:B:201:PHE:HE2	1:B:281:ILE:HG22	1.80	0.46
1:B:28:GLU:HG3	1:B:32:ASP:OD2	2.15	0.46
1:B:92:ASP:N	1:B:92:ASP:OD2	2.48	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:248:LYS:HB3	1:C:511:ARG:NH1	2.30	0.46
1:D:219:ILE:HD12	1:D:281:ILE:O	2.16	0.46
1:D:557:PHE:CE2	1:E:563:LYS:HD3	2.50	0.46
1:E:92:ASP:N	1:E:92:ASP:OD2	2.48	0.46
1:F:71:MSE:CE	1:F:115:VAL:HB	2.45	0.46
1:F:234:ILE:HG12	1:F:267:ALA:HB3	1.96	0.46
1:F:444:LEU:C	1:F:446:THR:H	2.19	0.46
1:G:535:ILE:CD1	1:G:554:LEU:HG	2.44	0.46
1:H:234:ILE:HG22	1:H:246:TYR:HB3	1.98	0.46
1:I:81:ARG:HB2	1:I:517:TYR:CZ	2.50	0.46
1:J:115:VAL:O	1:J:119:ILE:HG13	2.15	0.46
1:J:162:SER:HB2	1:J:170:ALA:HB2	1.97	0.46
1:J:273:ARG:O	1:J:274:ARG:CB	2.64	0.46
1:J:77:ASP:HB2	1:J:523:SER:HB2	1.98	0.46
1:K:164:LEU:HA	1:K:307:TRP:HH2	1.80	0.46
1:L:28:GLU:HG3	1:L:32:ASP:OD2	2.15	0.46
1:M:80:TYR:OH	1:M:444:LEU:HD12	2.16	0.46
1:N:193:LEU:HD22	1:N:287:LEU:HB3	1.97	0.46
1:N:262:GLY:O	1:N:263:PHE:HB3	2.14	0.46
1:N:29:ALA:O	1:N:33:LEU:HG	2.16	0.46
1:N:47:GLN:N	1:N:48:TYR:HD2	2.14	0.46
1:N:86:ALA:CB	1:N:515:GLU:HG3	2.44	0.46
1:N:560:LEU:O	1:N:561:ASP:O	2.33	0.46
1:O:191:TYR:HE1	1:O:278:LYS:HZ3	1.62	0.46
1:O:198:ILE:HG22	1:O:198:ILE:O	2.14	0.46
1:P:165:MSE:HG3	1:P:307:TRP:CD2	2.50	0.46
1:P:387:GLN:HB2	1:Q:390:ALA:HB2	1.98	0.46
1:O:108:LYS:HD2	1:P:438:LEU:HD11	1.97	0.46
1:P:556:TYR:OH	1:Q:542:THR:HG21	2.15	0.46
1:R:144:ILE:HD12	1:R:145:ARG:N	2.30	0.46
1:R:422:THR:HG22	1:R:423:GLU:N	2.31	0.46
1:S:31:ASN:O	1:S:34:PHE:HB3	2.15	0.46
1:S:348:LYS:HB2	1:U:372:TYR:CE2	2.50	0.46
1:T:238:PRO:HD3	1:T:263:PHE:HB2	1.96	0.46
1:T:82:PRO:O	1:T:516:CYS:HA	2.15	0.46
1:T:78:VAL:CG1	1:T:444:LEU:HG	2.45	0.46
1:U:293:ILE:HD13	1:U:294:ALA:N	2.30	0.46
1:U:438:LEU:HD22	3:X:718:HOH:O	2.15	0.46
1:U:554:LEU:O	1:U:557:PHE:HB3	2.15	0.46
1:V:193:LEU:HD22	1:V:287:LEU:HB3	1.98	0.46
1:V:66:LYS:HZ3	1:V:420:VAL:HG11	1.80	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:100:THR:HG22	1:W:138:THR:HG22	1.96	0.46
1:W:232:ALA:HB2	1:W:269:ARG:O	2.15	0.46
1:T:387:GLN:CB	1:W:390:ALA:HB2	2.46	0.46
1:W:422:THR:HG22	1:W:423:GLU:N	2.31	0.46
1:W:47:GLN:H	1:W:48:TYR:HD2	1.63	0.46
1:W:554:LEU:O	1:W:557:PHE:HB3	2.16	0.46
1:W:560:LEU:O	1:W:561:ASP:O	2.32	0.46
1:X:293:ILE:HG12	1:X:294:ALA:H	1.81	0.46
2:Y:28:VAL:CB	2:Y:96:LEU:HD13	2.45	0.46
2:Z:28:VAL:CB	2:Z:96:LEU:HD13	2.45	0.46
1:A:227:GLU:OE2	1:A:227:GLU:N	2.47	0.46
1:D:434:THR:HA	1:D:437:GLN:CD	2.35	0.46
1:E:164:LEU:HA	1:E:307:TRP:CH2	2.51	0.46
1:E:317:GLU:HB3	1:E:321:ARG:CZ	2.46	0.46
1:F:201:PHE:HE2	1:F:281:ILE:HG22	1.80	0.46
1:F:273:ARG:O	1:F:274:ARG:CB	2.64	0.46
1:F:28:GLU:HG3	1:F:32:ASP:OD2	2.15	0.46
1:G:248:LYS:HB3	1:G:511:ARG:NH1	2.30	0.46
1:H:162:SER:HB2	1:H:170:ALA:HB2	1.97	0.46
1:H:198:ILE:HA	1:H:199:PRO:HD3	1.64	0.46
1:I:234:ILE:HG12	1:I:267:ALA:HB3	1.96	0.46
1:I:26:ARG:NH2	1:I:30:LYS:HB2	2.28	0.46
1:I:248:LYS:HB3	1:I:511:ARG:NH1	2.30	0.46
1:J:434:THR:HA	1:J:437:GLN:HG2	1.98	0.46
1:K:219:ILE:HD12	1:K:281:ILE:O	2.16	0.46
1:K:77:ASP:HB2	1:K:523:SER:HB2	1.98	0.46
1:L:234:ILE:HG12	1:L:267:ALA:HB3	1.96	0.46
1:L:219:ILE:HD12	1:L:281:ILE:O	2.16	0.46
1:M:378:ASP:O	1:M:381:SER:O	2.34	0.46
1:M:409:THR:O	1:M:413:LYS:HG2	2.16	0.46
1:M:34:PHE:CE2	1:M:45:LEU:HG	2.46	0.46
1:M:528:LYS:CD	1:M:560:LEU:HD21	2.46	0.46
1:N:71:MSE:CE	1:N:115:VAL:HB	2.46	0.46
1:O:29:ALA:O	1:O:33:LEU:HG	2.16	0.46
1:O:37:ARG:C	1:O:39:SER:H	2.19	0.46
1:O:528:LYS:CD	1:O:560:LEU:HD21	2.46	0.46
1:P:47:GLN:CG	1:P:48:TYR:H	2.26	0.46
1:Q:293:ILE:HG12	1:Q:294:ALA:H	1.81	0.46
1:Q:71:MSE:CE	1:Q:115:VAL:HB	2.46	0.46
1:S:429:GLN:HG2	1:S:429:GLN:O	2.16	0.46
1:S:41:TRP:HE3	1:S:42:ASP:HB3	1.81	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:390:ALA:HB2	1:U:387:GLN:HB2	1.98	0.46
1:V:164:LEU:HA	1:V:307:TRP:HH2	1.79	0.46
1:V:82:PRO:O	1:V:516:CYS:HA	2.16	0.46
1:W:266:ILE:O	1:W:267:ALA:HB2	2.15	0.46
1:W:429:GLN:HG2	1:W:429:GLN:O	2.16	0.46
1:W:454:ALA:O	1:W:455:THR:C	2.52	0.46
1:W:573:ASN:O	1:W:577:ILE:HG13	2.16	0.46
1:W:577:ILE:HG12	1:W:582:LYS:CG	2.44	0.46
1:X:123:VAL:HG22	1:X:316:TYR:HE2	1.81	0.46
1:X:528:LYS:CD	1:X:560:LEU:HD21	2.46	0.46
1:A:48:TYR:O	1:A:49:THR:CB	2.64	0.46
1:B:34:PHE:CD2	1:B:34:PHE:O	2.68	0.46
1:B:248:LYS:HZ1	1:B:513:ARG:HH12	1.63	0.46
1:C:164:LEU:HA	1:C:307:TRP:HH2	1.80	0.46
1:D:234:ILE:HG12	1:D:267:ALA:HB3	1.96	0.46
1:D:28:GLU:HG3	1:D:32:ASP:OD2	2.15	0.46
1:D:434:THR:HA	1:D:437:GLN:HG2	1.98	0.46
1:D:444:LEU:C	1:D:446:THR:H	2.19	0.46
1:E:164:LEU:HA	1:E:307:TRP:HH2	1.79	0.46
1:E:238:PRO:HG3	1:E:263:PHE:CB	2.46	0.46
1:E:29:ALA:O	1:E:33:LEU:HG	2.15	0.46
1:F:248:LYS:HB3	1:F:511:ARG:NH1	2.30	0.46
1:G:130:THR:HG22	1:G:144:ILE:HA	1.97	0.46
1:G:72:ARG:HD2	1:H:434:THR:HG21	1.98	0.46
1:I:219:ILE:HD12	1:I:281:ILE:O	2.16	0.46
1:J:164:LEU:HA	1:J:307:TRP:CH2	2.51	0.46
1:J:542:THR:HA	1:J:543:PRO:HD3	1.82	0.46
1:J:82:PRO:HB2	1:J:83:LYS:H	1.58	0.46
1:K:273:ARG:O	1:K:274:ARG:CB	2.64	0.46
1:L:115:VAL:O	1:L:119:ILE:HG13	2.15	0.46
1:L:317:GLU:HB3	1:L:321:ARG:CZ	2.46	0.46
1:L:343:ARG:HG2	1:L:343:ARG:H	1.52	0.46
1:L:413:LYS:HE2	1:L:413:LYS:HB3	1.74	0.46
1:L:78:VAL:CG2	1:L:444:LEU:HD21	2.46	0.46
1:M:47:GLN:N	1:M:48:TYR:HD2	2.14	0.46
1:M:535:ILE:HD11	1:N:564:GLY:HA3	1.98	0.46
1:M:554:LEU:O	1:M:557:PHE:HB3	2.15	0.46
1:M:86:ALA:CB	1:M:515:GLU:HG3	2.45	0.46
1:N:434:THR:HG23	1:N:435:VAL:N	2.30	0.46
1:O:47:GLN:CG	1:O:48:TYR:H	2.28	0.46
1:P:387:GLN:CB	1:Q:390:ALA:CB	2.94	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:528:LYS:CD	1:Q:560:LEU:HD21	2.46	0.46
1:Q:71:MSE:HE3	1:Q:115:VAL:HB	1.97	0.46
1:R:280:ILE:HD12	1:R:280:ILE:N	2.31	0.46
1:S:174:THR:N	3:S:705:HOH:O	2.49	0.46
1:S:171:ARG:O	1:S:224:GLU:HA	2.15	0.46
1:T:155:HIS:CE1	1:T:204:PRO:HB2	2.51	0.46
1:T:123:VAL:CG1	1:T:304:PHE:CE1	2.99	0.46
1:T:322:LEU:HD22	1:T:322:LEU:N	2.31	0.46
1:V:227:GLU:O	1:V:227:GLU:CG	2.64	0.46
1:V:37:ARG:C	1:V:39:SER:N	2.68	0.46
1:V:405:LEU:O	1:V:409:THR:HG23	2.16	0.46
1:V:420:VAL:HA	1:V:428:GLY:HA2	1.98	0.46
1:V:422:THR:HG22	1:V:423:GLU:N	2.31	0.46
1:W:378:ASP:O	1:W:381:SER:O	2.34	0.46
1:X:77:ASP:HB2	1:X:523:SER:HB2	1.98	0.46
1:A:115:VAL:O	1:A:119:ILE:HG13	2.15	0.46
1:A:28:GLU:HG3	1:A:32:ASP:OD2	2.15	0.46
1:B:219:ILE:HD12	1:B:281:ILE:O	2.16	0.46
1:B:413:LYS:HB3	1:B:413:LYS:HE2	1.73	0.46
1:D:565:VAL:O	1:D:569:ARG:HB3	2.15	0.46
1:F:410:SER:O	1:F:414:GLU:HG2	2.16	0.46
1:F:139:SER:CB	1:F:455:THR:CG2	2.80	0.46
1:F:567:MSE:HE2	1:G:554:LEU:HD22	1.97	0.46
1:F:58:ASP:O	1:F:59:VAL:HB	2.14	0.46
1:F:94:LEU:HA	1:F:97:MSE:CE	2.37	0.46
1:G:201:PHE:HE2	1:G:281:ILE:HG22	1.80	0.46
1:G:219:ILE:HD12	1:G:281:ILE:O	2.16	0.46
1:G:92:ASP:OD2	1:G:92:ASP:N	2.48	0.46
1:G:363:TYR:HE1	1:H:350:PHE:HE1	1.64	0.46
1:I:197:ASP:O	1:I:198:ILE:HB	2.15	0.46
1:I:561:ASP:OD2	1:J:92:ASP:HB3	2.16	0.46
1:J:219:ILE:HD12	1:J:281:ILE:O	2.16	0.46
1:J:248:LYS:HB3	1:J:511:ARG:NH1	2.30	0.46
1:K:197:ASP:O	1:K:198:ILE:HB	2.15	0.46
1:K:444:LEU:C	1:K:446:THR:H	2.19	0.46
1:K:528:LYS:HZ3	1:K:560:LEU:HD21	1.80	0.46
1:N:155:HIS:CE1	1:N:204:PRO:HB2	2.50	0.46
1:N:82:PRO:O	1:N:516:CYS:HA	2.16	0.46
1:O:273:ARG:CZ	1:O:275:ARG:HE	2.29	0.46
1:O:76:ILE:HD12	1:O:433:ASP:OD1	2.16	0.46
1:P:160:SER:O	1:P:161:ASN:ND2	2.44	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:123:VAL:CG1	1:P:304:PHE:CE1	2.99	0.46
1:Q:31:ASN:O	1:Q:34:PHE:HB3	2.15	0.46
1:R:260:ASP:HA	1:R:264:ILE:HB	1.97	0.46
1:R:274:ARG:O	1:R:275:ARG:HD2	2.15	0.46
1:R:343:ARG:H	1:R:343:ARG:HG2	1.56	0.46
1:Q:376:ARG:HB2	1:R:352:TRP:CG	2.50	0.46
1:R:47:GLN:CG	1:R:48:TYR:H	2.28	0.46
1:R:95:MSE:HE1	1:R:99:ARG:CZ	2.46	0.46
1:S:118:GLN:OE1	1:S:303:VAL:HB	2.15	0.46
1:S:260:ASP:HA	1:S:264:ILE:HB	1.96	0.46
1:S:340:ILE:O	1:S:344:THR:HG21	2.16	0.46
1:S:396:GLU:O	1:T:399:GLN:OE1	2.34	0.46
1:T:164:LEU:HA	1:T:307:TRP:HH2	1.81	0.46
1:T:330:ARG:HD2	1:T:409:THR:CG2	2.39	0.46
1:V:451:ASP:C	1:V:453:LEU:H	2.19	0.46
1:W:260:ASP:HA	1:W:264:ILE:HB	1.97	0.46
1:W:444:LEU:O	1:W:446:THR:N	2.49	0.46
1:W:55:GLY:HA3	1:W:57:PHE:CE1	2.50	0.46
1:X:55:GLY:HA3	1:X:57:PHE:CE1	2.50	0.46
1:A:171:ARG:HH21	1:L:182:ASN:HD22	1.64	0.46
1:A:410:SER:O	1:A:414:GLU:HG2	2.16	0.46
1:B:164:LEU:HA	1:B:307:TRP:CH2	2.51	0.46
1:B:317:GLU:HB3	1:B:321:ARG:CZ	2.46	0.46
1:B:77:ASP:HB2	1:B:523:SER:HB2	1.98	0.46
1:C:234:ILE:HG22	1:C:246:TYR:HB3	1.98	0.46
1:D:273:ARG:O	1:D:274:ARG:CB	2.64	0.46
1:D:567:MSE:HE2	1:F:554:LEU:HD22	1.97	0.46
1:E:219:ILE:HD12	1:E:281:ILE:O	2.16	0.46
1:F:234:ILE:HG22	1:F:246:TYR:HB3	1.98	0.46
1:G:207:TRP:O	1:G:208:VAL:C	2.53	0.46
1:G:273:ARG:O	1:G:274:ARG:CB	2.64	0.46
1:G:35:PHE:HE1	1:G:321:ARG:NH1	2.13	0.46
1:H:197:ASP:O	1:H:198:ILE:HB	2.15	0.46
1:H:234:ILE:HG12	1:H:267:ALA:HB3	1.96	0.46
1:I:35:PHE:CE1	1:I:321:ARG:NH1	2.84	0.46
1:K:293:ILE:HD13	1:K:294:ALA:N	2.31	0.46
1:K:565:VAL:O	1:K:569:ARG:HB3	2.15	0.46
1:L:29:ALA:O	1:L:33:LEU:HG	2.15	0.46
1:L:410:SER:O	1:L:414:GLU:HG2	2.16	0.46
1:M:227:GLU:CG	1:M:227:GLU:O	2.64	0.46
1:M:444:LEU:N	1:M:444:LEU:HD13	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:77:ASP:HB2	1:N:523:SER:HB2	1.98	0.46
1:O:24:GLU:O	1:O:26:ARG:N	2.49	0.46
1:O:371:TYR:HE2	1:O:373:LEU:HD21	1.81	0.46
1:O:82:PRO:O	1:O:516:CYS:HA	2.16	0.46
1:P:273:ARG:HH22	1:P:453:LEU:CD2	2.29	0.46
1:Q:198:ILE:O	1:Q:198:ILE:HG22	2.16	0.46
1:Q:378:ASP:O	1:Q:381:SER:O	2.34	0.46
1:R:451:ASP:C	1:R:453:LEU:N	2.69	0.46
1:S:158:TRP:HD1	1:S:158:TRP:H	1.63	0.46
1:S:451:ASP:C	1:S:453:LEU:H	2.19	0.46
1:T:575:GLN:O	1:T:579:MSE:CG	2.63	0.46
1:T:66:LYS:HZ3	1:T:420:VAL:HG21	1.81	0.46
1:U:26:ARG:HG3	1:U:27:ARG:N	2.31	0.46
1:U:437:GLN:HA	1:U:440:MSE:HB2	1.98	0.46
1:V:238:PRO:HD3	1:V:263:PHE:HB2	1.98	0.46
1:W:322:LEU:H	1:W:322:LEU:HD22	1.80	0.46
1:W:35:PHE:C	1:W:37:ARG:N	2.69	0.46
1:W:86:ALA:CB	1:W:515:GLU:HG3	2.45	0.46
1:A:273:ARG:O	1:A:274:ARG:CB	2.64	0.46
1:A:317:GLU:HB3	1:A:321:ARG:CZ	2.46	0.46
1:A:376:ARG:HB2	1:B:352:TRP:CD2	2.51	0.46
1:A:334:MSE:HE3	1:B:404:MSE:CE	2.46	0.46
1:C:219:ILE:HD12	1:C:281:ILE:O	2.16	0.46
1:C:71:MSE:CE	1:C:115:VAL:HB	2.45	0.46
1:D:78:VAL:HG21	1:D:444:LEU:CD1	2.21	0.46
1:F:48:TYR:O	1:F:49:THR:CB	2.64	0.46
1:G:35:PHE:CE1	1:G:321:ARG:NH1	2.84	0.46
1:H:234:ILE:CG2	1:H:246:TYR:HB3	2.46	0.46
1:I:234:ILE:HG22	1:I:246:TYR:HB3	1.98	0.46
1:I:28:GLU:HG3	1:I:32:ASP:OD2	2.15	0.46
1:I:92:ASP:N	1:I:92:ASP:OD2	2.48	0.46
1:J:293:ILE:HD13	1:J:294:ALA:N	2.31	0.46
1:K:71:MSE:CE	1:K:115:VAL:HB	2.45	0.46
1:K:238:PRO:HG3	1:K:263:PHE:CB	2.46	0.46
1:K:78:VAL:CG2	1:K:444:LEU:HD21	2.46	0.46
1:M:14:ARG:NE	1:M:14:ARG:CA	2.70	0.46
1:M:165:MSE:HG3	1:M:307:TRP:CD2	2.51	0.46
1:M:270:GLN:HA	1:M:270:GLN:OE1	2.16	0.46
1:M:35:PHE:CE1	1:M:321:ARG:NH1	2.83	0.46
1:M:349:PRO:HG3	1:M:391:TYR:CE1	2.51	0.46
1:M:390:ALA:CB	1:N:387:GLN:CB	2.94	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:227:GLU:CG	1:N:227:GLU:O	2.64	0.46
1:N:35:PHE:CE1	1:N:321:ARG:NH1	2.84	0.46
1:N:554:LEU:O	1:N:557:PHE:HB3	2.15	0.46
1:O:232:ALA:HB2	1:O:269:ARG:O	2.16	0.46
1:O:33:LEU:HD12	1:O:34:PHE:N	2.31	0.46
1:P:171:ARG:O	1:P:224:GLU:HA	2.15	0.46
1:P:422:THR:HG22	1:P:423:GLU:N	2.31	0.46
1:P:528:LYS:CD	1:P:560:LEU:HD21	2.46	0.46
1:Q:38:VAL:HG21	1:Q:324:LYS:HD2	1.98	0.46
1:Q:78:VAL:CG1	1:Q:79:LEU:H	2.29	0.46
1:Q:80:TYR:OH	1:Q:444:LEU:HD12	2.16	0.46
1:R:316:TYR:O	1:R:321:ARG:NH1	2.49	0.46
1:R:429:GLN:HG2	1:R:429:GLN:O	2.16	0.46
1:R:454:ALA:O	1:R:455:THR:C	2.54	0.46
1:S:236:GLN:HG3	1:S:265:LYS:HG2	1.98	0.46
1:S:37:ARG:C	1:S:39:SER:H	2.20	0.46
1:S:71:MSE:HE3	1:S:115:VAL:HB	1.97	0.46
1:T:171:ARG:O	1:T:224:GLU:HA	2.16	0.46
1:T:55:GLY:HA3	1:T:57:PHE:CE1	2.51	0.46
1:T:560:LEU:O	1:T:561:ASP:O	2.33	0.46
1:V:71:MSE:HE3	1:V:115:VAL:HB	1.98	0.46
1:V:86:ALA:CB	1:V:515:GLU:HG3	2.45	0.46
1:W:37:ARG:CB	1:W:37:ARG:HH21	2.28	0.46
1:W:37:ARG:C	1:W:39:SER:H	2.19	0.46
1:V:310:VAL:HG22	1:W:40:GLN:HG2	1.98	0.46
1:W:78:VAL:CG1	1:W:444:LEU:HG	2.45	0.46
1:X:248:LYS:CD	1:X:248:LYS:H	2.17	0.46
1:X:422:THR:HG22	1:X:423:GLU:N	2.31	0.46
1:X:437:GLN:HA	1:X:440:MSE:HB2	1.98	0.46
1:A:71:MSE:CE	1:A:115:VAL:HB	2.45	0.45
1:A:434:THR:HA	1:A:437:GLN:HG2	1.98	0.45
1:A:444:LEU:HD13	1:A:444:LEU:N	2.31	0.45
1:A:92:ASP:OD2	1:A:92:ASP:N	2.48	0.45
1:B:238:PRO:HG3	1:B:263:PHE:CB	2.46	0.45
1:C:130:THR:HG22	1:C:144:ILE:HA	1.97	0.45
1:C:246:TYR:HD2	1:C:511:ARG:CB	2.28	0.45
1:C:565:VAL:O	1:C:569:ARG:HB3	2.15	0.45
1:D:234:ILE:CG2	1:D:246:TYR:HB3	2.47	0.45
1:D:273:ARG:HH22	1:D:453:LEU:CD1	2.28	0.45
1:D:48:TYR:O	1:D:49:THR:CB	2.64	0.45
1:D:528:LYS:HD2	1:D:560:LEU:HD21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:201:PHE:HE2	1:E:281:ILE:HG22	1.80	0.45
1:E:234:ILE:HG12	1:E:267:ALA:HB3	1.96	0.45
1:F:238:PRO:HG3	1:F:263:PHE:CB	2.46	0.45
1:F:444:LEU:N	1:F:444:LEU:HD13	2.31	0.45
1:D:563:LYS:HD3	1:F:557:PHE:CE2	2.51	0.45
1:G:164:LEU:HA	1:G:307:TRP:CH2	2.51	0.45
1:H:590:GLN:O	1:H:594:VAL:HG23	2.16	0.45
1:I:293:ILE:HD13	1:I:294:ALA:N	2.31	0.45
1:I:590:GLN:O	1:I:594:VAL:HG23	2.16	0.45
1:J:234:ILE:CG2	1:J:246:TYR:HB3	2.46	0.45
1:K:234:ILE:HG22	1:K:246:TYR:HB3	1.98	0.45
1:K:273:ARG:O	1:K:274:ARG:HB3	2.17	0.45
1:K:40:GLN:O	1:K:41:TRP:CB	2.54	0.45
1:K:590:GLN:O	1:K:594:VAL:HG23	2.16	0.45
1:L:164:LEU:HA	1:L:307:TRP:CH2	2.51	0.45
1:N:160:SER:O	1:N:161:ASN:ND2	2.46	0.45
1:N:418:LEU:HB2	1:N:428:GLY:O	2.15	0.45
1:O:34:PHE:O	1:O:37:ARG:HB2	2.16	0.45
1:P:429:GLN:HG2	1:P:429:GLN:O	2.17	0.45
1:Q:47:GLN:CG	1:Q:48:TYR:H	2.28	0.45
1:Q:248:LYS:HG3	1:Q:511:ARG:HE	1.81	0.45
1:R:26:ARG:HG3	1:R:27:ARG:N	2.31	0.45
1:R:409:THR:O	1:R:413:LYS:HG2	2.16	0.45
1:R:443:ASP:C	1:R:444:LEU:HD13	2.36	0.45
1:S:231:THR:CG2	1:S:249:ARG:HH11	2.23	0.45
1:S:343:ARG:O	1:S:344:THR:HB	2.16	0.45
1:S:378:ASP:O	1:S:381:SER:O	2.34	0.45
1:T:293:ILE:HG12	1:T:294:ALA:H	1.81	0.45
1:U:37:ARG:C	1:U:39:SER:H	2.19	0.45
1:U:41:TRP:HE3	1:U:42:ASP:HB3	1.81	0.45
1:V:160:SER:O	1:V:161:ASN:ND2	2.46	0.45
1:V:38:VAL:HG21	1:V:324:LYS:HD2	1.98	0.45
1:V:47:GLN:H	1:V:48:TYR:HD2	1.62	0.45
1:V:554:LEU:O	1:V:557:PHE:HB3	2.16	0.45
1:X:24:GLU:O	1:X:26:ARG:N	2.48	0.45
1:A:35:PHE:CE1	1:A:321:ARG:NH1	2.84	0.45
1:B:234:ILE:HG22	1:B:246:TYR:HB3	1.98	0.45
1:B:234:ILE:CG2	1:B:246:TYR:HB3	2.47	0.45
1:B:29:ALA:O	1:B:33:LEU:HG	2.15	0.45
1:B:434:THR:HA	1:B:437:GLN:HG2	1.97	0.45
1:C:413:LYS:HE2	1:C:413:LYS:HB3	1.74	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:77:ASP:HB2	1:E:523:SER:HB2	1.98	0.45
1:G:227:GLU:HA	1:G:274:ARG:CA	2.44	0.45
1:G:234:ILE:HG22	1:G:246:TYR:HB3	1.98	0.45
1:G:451:ASP:O	1:G:456:ALA:N	2.40	0.45
1:G:78:VAL:HG21	1:G:444:LEU:CD1	2.21	0.45
1:G:82:PRO:HB2	1:G:83:LYS:H	1.58	0.45
1:H:273:ARG:O	1:H:274:ARG:HB3	2.17	0.45
1:H:219:ILE:HD12	1:H:281:ILE:O	2.16	0.45
1:I:238:PRO:HG3	1:I:263:PHE:CB	2.46	0.45
1:I:427:GLY:C	1:I:429:GLN:N	2.70	0.45
1:J:444:LEU:N	1:J:444:LEU:HD13	2.31	0.45
1:K:35:PHE:CE1	1:K:321:ARG:NH1	2.84	0.45
1:L:236:GLN:HE21	1:L:265:LYS:HZ3	1.63	0.45
1:M:155:HIS:CE1	1:M:204:PRO:HB2	2.52	0.45
1:M:37:ARG:C	1:M:39:SER:H	2.19	0.45
1:N:444:LEU:HD13	1:N:444:LEU:N	2.31	0.45
1:O:136:SER:N	1:O:137:PRO:HD3	2.31	0.45
1:O:101:ASP:HB3	1:O:138:THR:HG21	1.98	0.45
1:O:422:THR:HG22	1:O:423:GLU:N	2.31	0.45
1:P:127:ARG:HG2	1:P:147:GLU:HB2	1.97	0.45
1:Q:227:GLU:O	1:Q:227:GLU:CG	2.64	0.45
1:Q:47:GLN:N	1:Q:48:TYR:HD2	2.14	0.45
1:Q:86:ALA:CB	1:Q:515:GLU:HG3	2.45	0.45
1:R:136:SER:N	1:R:137:PRO:HD3	2.31	0.45
1:R:444:LEU:HD13	1:R:444:LEU:N	2.31	0.45
1:R:86:ALA:CB	1:R:515:GLU:HG3	2.46	0.45
1:S:158:TRP:HH2	1:S:302:PRO:HG3	1.78	0.45
1:S:316:TYR:O	1:S:321:ARG:NH1	2.50	0.45
1:S:40:GLN:HE21	1:S:40:GLN:HB2	1.58	0.45
1:T:118:GLN:OE1	1:T:303:VAL:HB	2.16	0.45
1:T:26:ARG:HG3	1:T:27:ARG:N	2.30	0.45
1:S:395:PRO:HD2	1:T:398:PRO:HB3	1.99	0.45
1:U:193:LEU:HD22	1:U:287:LEU:HB3	1.98	0.45
1:V:171:ARG:O	1:V:224:GLU:HA	2.15	0.45
1:W:136:SER:N	1:W:137:PRO:HD3	2.31	0.45
1:W:273:ARG:CZ	1:W:275:ARG:HE	2.29	0.45
1:W:38:VAL:HG21	1:W:324:LYS:HD2	1.99	0.45
2:Y:140:ARG:O	2:Y:141:MET:HB3	2.16	0.45
1:A:234:ILE:HG22	1:A:246:TYR:HB3	1.98	0.45
1:A:273:ARG:O	1:A:274:ARG:HB3	2.17	0.45
1:A:293:ILE:HD13	1:A:294:ALA:N	2.31	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:78:VAL:CG2	1:A:444:LEU:HD21	2.46	0.45
1:C:232:ALA:N	1:C:269:ARG:O	2.50	0.45
1:C:317:GLU:HB3	1:C:321:ARG:CZ	2.46	0.45
1:C:444:LEU:HD13	1:C:444:LEU:N	2.31	0.45
1:D:164:LEU:HA	1:D:307:TRP:CH2	2.51	0.45
1:D:251:ILE:HG23	1:D:507:LEU:HD22	1.98	0.45
1:E:45:LEU:HD21	1:E:328:ARG:HH21	1.82	0.45
1:F:246:TYR:HD2	1:F:511:ARG:CB	2.28	0.45
1:F:35:PHE:CE1	1:F:321:ARG:NH1	2.84	0.45
1:G:234:ILE:CG2	1:G:246:TYR:HB3	2.47	0.45
1:G:444:LEU:N	1:G:444:LEU:HD13	2.31	0.45
1:H:232:ALA:N	1:H:269:ARG:O	2.50	0.45
1:H:317:GLU:HB3	1:H:321:ARG:CZ	2.46	0.45
1:I:273:ARG:O	1:I:274:ARG:CB	2.64	0.45
1:I:577:ILE:HG12	1:I:582:LYS:CG	2.41	0.45
1:J:234:ILE:HG22	1:J:246:TYR:HB3	1.98	0.45
1:K:262:GLY:O	1:K:263:PHE:HB3	2.17	0.45
1:K:317:GLU:HB3	1:K:321:ARG:CZ	2.46	0.45
1:K:444:LEU:HD13	1:K:444:LEU:N	2.31	0.45
1:K:139:SER:CB	1:K:455:THR:CG2	2.80	0.45
1:M:123:VAL:HG22	1:M:316:TYR:HE2	1.82	0.45
1:N:31:ASN:O	1:N:34:PHE:HB3	2.15	0.45
1:N:371:TYR:HE2	1:N:373:LEU:HD21	1.82	0.45
1:N:66:LYS:HZ3	1:N:420:VAL:HG21	1.81	0.45
1:O:118:GLN:OE1	1:O:303:VAL:HB	2.15	0.45
1:O:351:PHE:CD2	1:O:356:ILE:HD12	2.51	0.45
1:O:86:ALA:CB	1:O:515:GLU:HG3	2.44	0.45
1:O:71:MSE:HE3	1:O:115:VAL:HB	1.98	0.45
1:P:232:ALA:HB2	1:P:269:ARG:O	2.16	0.45
1:P:282:THR:HG23	1:P:287:LEU:CD1	2.44	0.45
1:P:564:GLY:HA3	1:Q:535:ILE:HD11	1.99	0.45
1:Q:273:ARG:CZ	1:Q:275:ARG:HE	2.30	0.45
1:Q:413:LYS:HA	1:Q:416:ALA:HB3	1.99	0.45
1:R:334:MSE:HE1	1:X:407:ALA:HB1	1.99	0.45
1:U:409:THR:O	1:U:413:LYS:HG2	2.16	0.45
1:U:528:LYS:CD	1:U:560:LEU:HD21	2.46	0.45
1:U:71:MSE:CE	1:U:115:VAL:HB	2.46	0.45
1:W:71:MSE:HE3	1:W:115:VAL:HB	1.98	0.45
1:X:66:LYS:HZ3	1:X:420:VAL:HG21	1.82	0.45
2:Y:43:GLN:C	2:Y:45:ALA:N	2.70	0.45
1:A:9:GLU:HG3	1:A:12:LEU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:262:GLY:O	1:A:263:PHE:HB3	2.17	0.45
1:A:35:PHE:HE2	1:A:324:LYS:NZ	2.08	0.45
1:B:262:GLY:O	1:B:263:PHE:HB3	2.17	0.45
1:B:273:ARG:O	1:B:274:ARG:HB3	2.17	0.45
1:B:26:ARG:NH2	1:B:30:LYS:HB2	2.28	0.45
1:C:164:LEU:HA	1:C:307:TRP:CH2	2.51	0.45
1:C:273:ARG:O	1:C:274:ARG:CB	2.64	0.45
1:D:410:SER:O	1:D:414:GLU:HG2	2.16	0.45
1:D:86:ALA:CB	1:D:515:GLU:HG3	2.47	0.45
1:E:262:GLY:O	1:E:263:PHE:HB3	2.17	0.45
1:E:590:GLN:O	1:E:594:VAL:HG23	2.16	0.45
1:F:164:LEU:HA	1:F:307:TRP:CH2	2.51	0.45
1:F:9:GLU:HG3	1:F:12:LEU:H	1.82	0.45
1:G:28:GLU:HG3	1:G:32:ASP:OD2	2.15	0.45
1:G:427:GLY:C	1:G:429:GLN:N	2.70	0.45
1:G:528:LYS:HD2	1:G:560:LEU:HD21	1.99	0.45
1:G:561:ASP:OD2	1:H:92:ASP:HB3	2.16	0.45
1:H:262:GLY:O	1:H:263:PHE:HB3	2.17	0.45
1:H:293:ILE:HD13	1:H:294:ALA:N	2.31	0.45
1:H:164:LEU:HA	1:H:307:TRP:CH2	2.51	0.45
1:H:78:VAL:CG2	1:H:444:LEU:HD21	2.46	0.45
1:J:201:PHE:HE2	1:J:281:ILE:HG22	1.80	0.45
1:J:182:ASN:HD22	1:K:171:ARG:HH21	1.65	0.45
1:K:207:TRP:O	1:K:208:VAL:C	2.53	0.45
1:L:273:ARG:O	1:L:274:ARG:HB3	2.17	0.45
1:L:293:ILE:HD13	1:L:294:ALA:N	2.31	0.45
1:L:92:ASP:OD2	1:L:92:ASP:N	2.48	0.45
1:M:29:ALA:O	1:M:33:LEU:HG	2.16	0.45
1:M:34:PHE:O	1:M:37:ARG:HB2	2.17	0.45
1:O:343:ARG:O	1:O:344:THR:HB	2.16	0.45
1:P:14:ARG:CA	1:P:14:ARG:NE	2.71	0.45
1:P:396:GLU:O	1:Q:399:GLN:OE1	2.34	0.45
1:P:76:ILE:HD12	1:P:433:ASP:OD1	2.16	0.45
1:R:66:LYS:HZ3	1:R:420:VAL:HG11	1.79	0.45
3:Q:719:HOH:O	1:R:430:VAL:HG11	2.15	0.45
1:R:443:ASP:O	1:R:446:THR:HG22	2.17	0.45
1:S:164:LEU:HA	1:S:307:TRP:CH2	2.51	0.45
1:T:41:TRP:HE3	1:T:42:ASP:HB3	1.82	0.45
1:U:174:THR:N	3:U:705:HOH:O	2.50	0.45
1:U:34:PHE:O	1:U:37:ARG:HB2	2.16	0.45
1:V:127:ARG:HG2	1:V:147:GLU:HB2	1.98	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:26:ARG:HG3	1:V:27:ARG:N	2.31	0.45
1:V:316:TYR:O	1:V:321:ARG:NH1	2.50	0.45
1:V:528:LYS:CD	1:V:560:LEU:HD21	2.46	0.45
1:W:198:ILE:HA	1:W:199:PRO:HD3	1.71	0.45
1:W:24:GLU:HG3	1:W:313:LYS:HE2	1.98	0.45
1:W:444:LEU:HD13	1:W:444:LEU:N	2.32	0.45
1:W:82:PRO:O	1:W:516:CYS:HA	2.17	0.45
1:X:136:SER:N	1:X:137:PRO:HD3	2.32	0.45
1:X:409:THR:O	1:X:413:LYS:HG2	2.16	0.45
1:X:429:GLN:O	1:X:429:GLN:HG2	2.16	0.45
1:A:26:ARG:NH2	1:A:30:LYS:HB2	2.28	0.45
1:A:77:ASP:HB2	1:A:523:SER:HB2	1.98	0.45
1:A:86:ALA:CB	1:A:515:GLU:HG3	2.47	0.45
1:B:410:SER:O	1:B:414:GLU:HG2	2.16	0.45
1:B:444:LEU:N	1:B:444:LEU:HD13	2.31	0.45
1:C:234:ILE:HG12	1:C:267:ALA:HB3	1.96	0.45
1:C:410:SER:O	1:C:414:GLU:HG2	2.16	0.45
1:C:251:ILE:HG23	1:C:507:LEU:HD22	1.98	0.45
1:C:77:ASP:HB2	1:C:523:SER:HB2	1.98	0.45
1:D:293:ILE:HD13	1:D:294:ALA:N	2.31	0.45
1:D:427:GLY:C	1:D:429:GLN:N	2.70	0.45
1:E:293:ILE:HD13	1:E:294:ALA:N	2.31	0.45
1:E:427:GLY:C	1:E:429:GLN:N	2.70	0.45
1:E:251:ILE:HG23	1:E:507:LEU:HD22	1.98	0.45
1:F:232:ALA:N	1:F:269:ARG:O	2.50	0.45
1:F:234:ILE:CG2	1:F:246:TYR:HB3	2.47	0.45
1:F:434:THR:HA	1:F:437:GLN:HG2	1.97	0.45
1:F:251:ILE:HG23	1:F:507:LEU:HD22	1.98	0.45
1:F:528:LYS:HD2	1:F:560:LEU:HD21	1.99	0.45
1:F:567:MSE:SE	1:G:576:LEU:HD13	2.66	0.45
1:F:182:ASN:HD22	1:G:171:ARG:HH21	1.61	0.45
1:G:232:ALA:N	1:G:269:ARG:O	2.50	0.45
1:G:590:GLN:O	1:G:594:VAL:HG23	2.16	0.45
1:G:77:ASP:HB2	1:G:523:SER:HB2	1.98	0.45
1:K:57:PHE:CD2	1:K:330:ARG:CB	2.95	0.45
1:L:71:MSE:CE	1:L:115:VAL:HB	2.45	0.45
1:L:232:ALA:N	1:L:269:ARG:O	2.50	0.45
1:N:343:ARG:H	1:N:343:ARG:HG2	1.53	0.45
1:N:378:ASP:O	1:N:381:SER:O	2.34	0.45
1:N:528:LYS:CD	1:N:560:LEU:HD21	2.46	0.45
1:O:165:MSE:HG3	1:O:307:TRP:CD2	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:26:ARG:HG3	1:O:27:ARG:N	2.32	0.45
1:P:53:TYR:OH	1:Q:329:LEU:HD21	2.16	0.45
1:Q:322:LEU:H	1:Q:322:LEU:HD22	1.82	0.45
1:Q:66:LYS:HZ3	1:Q:420:VAL:HG21	1.82	0.45
1:R:24:GLU:O	1:R:26:ARG:N	2.50	0.45
1:Q:396:GLU:O	1:R:399:GLN:OE1	2.34	0.45
1:S:273:ARG:CZ	1:S:275:ARG:HE	2.29	0.45
1:S:193:LEU:HD22	1:S:287:LEU:HB3	1.97	0.45
1:T:31:ASN:O	1:T:34:PHE:HB3	2.16	0.45
1:T:528:LYS:CD	1:T:560:LEU:HD21	2.47	0.45
1:U:198:ILE:HA	1:U:199:PRO:HD3	1.71	0.45
1:U:227:GLU:O	1:U:227:GLU:CG	2.64	0.45
1:V:136:SER:N	1:V:137:PRO:HD3	2.31	0.45
1:W:420:VAL:HA	1:W:428:GLY:HA2	1.98	0.45
1:R:53:TYR:OH	1:X:329:LEU:HD21	2.16	0.45
1:X:384:LEU:HD22	1:X:384:LEU:N	2.29	0.45
1:A:232:ALA:N	1:A:269:ARG:O	2.50	0.45
1:A:47:GLN:CG	1:A:47:GLN:O	2.65	0.45
1:B:444:LEU:C	1:B:446:THR:H	2.19	0.45
1:B:590:GLN:O	1:B:594:VAL:HG23	2.17	0.45
1:C:273:ARG:O	1:C:274:ARG:HB3	2.17	0.45
1:C:58:ASP:O	1:C:59:VAL:HB	2.15	0.45
1:D:238:PRO:HG3	1:D:263:PHE:CB	2.46	0.45
1:D:262:GLY:O	1:D:263:PHE:HB3	2.17	0.45
1:E:234:ILE:HG22	1:E:246:TYR:HB3	1.98	0.45
1:E:35:PHE:CE1	1:E:321:ARG:NH1	2.84	0.45
1:F:45:LEU:HD21	1:F:328:ARG:HH21	1.82	0.45
1:F:427:GLY:C	1:F:429:GLN:N	2.70	0.45
1:F:590:GLN:O	1:F:594:VAL:HG23	2.16	0.45
1:G:9:GLU:HG3	1:G:12:LEU:H	1.82	0.45
1:G:48:TYR:O	1:G:49:THR:CB	2.64	0.45
1:H:207:TRP:O	1:H:208:VAL:C	2.54	0.45
1:H:273:ARG:O	1:H:274:ARG:CB	2.64	0.45
1:I:201:PHE:HE2	1:I:281:ILE:HG22	1.80	0.45
1:I:227:GLU:OE2	1:I:227:GLU:N	2.47	0.45
1:J:86:ALA:CB	1:J:515:GLU:HG3	2.47	0.45
1:K:410:SER:O	1:K:414:GLU:HG2	2.16	0.45
1:K:47:GLN:O	1:K:47:GLN:CG	2.65	0.45
1:K:9:GLU:HG3	1:K:12:LEU:H	1.82	0.45
1:L:427:GLY:C	1:L:429:GLN:N	2.70	0.45
1:N:422:THR:HG22	1:N:423:GLU:N	2.32	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:193:LEU:HD22	1:O:287:LEU:HB3	1.98	0.45
1:O:554:LEU:O	1:O:557:PHE:HB3	2.16	0.45
1:Q:510:ILE:O	1:Q:513:ARG:HD2	2.17	0.45
1:R:127:ARG:HG2	1:R:147:GLU:HB2	1.97	0.45
1:R:31:ASN:O	1:R:34:PHE:HB3	2.16	0.45
1:R:35:PHE:C	1:R:37:ARG:N	2.70	0.45
1:R:37:ARG:C	1:R:39:SER:H	2.18	0.45
1:R:40:GLN:HG2	1:X:310:VAL:HG22	1.98	0.45
1:T:160:SER:O	1:T:161:ASN:ND2	2.43	0.45
1:T:270:GLN:OE1	1:T:270:GLN:HA	2.17	0.45
1:T:334:MSE:HE1	1:W:407:ALA:HB1	1.98	0.45
1:T:443:ASP:C	1:T:444:LEU:HD13	2.36	0.45
1:T:47:GLN:N	1:T:48:TYR:HD2	2.15	0.45
1:T:511:ARG:HA	1:T:513:ARG:CD	2.44	0.45
1:U:136:SER:N	1:U:137:PRO:HD3	2.31	0.45
1:U:35:PHE:C	1:U:37:ARG:N	2.69	0.45
1:U:443:ASP:C	1:U:444:LEU:HD13	2.37	0.45
1:V:165:MSE:HG3	1:V:307:TRP:CD2	2.49	0.45
1:V:343:ARG:HG2	1:V:343:ARG:H	1.55	0.45
1:X:171:ARG:O	1:X:224:GLU:HA	2.17	0.45
1:X:158:TRP:HH2	1:X:302:PRO:HG3	1.80	0.45
2:Y:71:ASP:O	2:Y:72:ASP:CB	2.65	0.45
2:Y:75:PRO:HA	2:Y:76:PRO:HD3	1.42	0.45
1:A:234:ILE:CG2	1:A:246:TYR:HB3	2.46	0.45
1:B:293:ILE:HD13	1:B:294:ALA:N	2.31	0.45
1:B:456:ALA:CB	1:B:509:ASP:OD2	2.65	0.45
1:B:86:ALA:CB	1:B:515:GLU:HG3	2.47	0.45
1:C:201:PHE:HE2	1:C:281:ILE:HG22	1.80	0.45
1:C:238:PRO:HG3	1:C:263:PHE:CB	2.46	0.45
1:E:177:HIS:HE1	1:E:221:GLU:OE1	2.00	0.45
1:E:234:ILE:CG2	1:E:246:TYR:HB3	2.47	0.45
1:E:273:ARG:O	1:E:274:ARG:CB	2.64	0.45
1:E:273:ARG:O	1:E:274:ARG:HB3	2.17	0.45
1:E:47:GLN:O	1:E:47:GLN:CG	2.65	0.45
1:E:248:LYS:HZ1	1:E:513:ARG:HH12	1.64	0.45
1:F:293:ILE:HD13	1:F:294:ALA:N	2.31	0.45
1:G:273:ARG:O	1:G:274:ARG:HB3	2.16	0.45
1:G:534:GLU:O	1:G:538:LEU:HD23	2.17	0.45
1:H:410:SER:O	1:H:414:GLU:HG2	2.16	0.45
1:I:232:ALA:N	1:I:269:ARG:O	2.50	0.45
1:H:72:ARG:HD2	1:I:434:THR:HG21	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:528:LYS:HZ3	1:I:560:LEU:HD21	1.80	0.45
1:I:94:LEU:HA	1:I:97:MSE:CE	2.37	0.45
1:J:48:TYR:O	1:J:49:THR:CB	2.64	0.45
1:J:590:GLN:O	1:J:594:VAL:HG23	2.17	0.45
3:J:719:HOH:O	1:K:438:LEU:HD22	2.16	0.45
1:K:451:ASP:O	1:K:456:ALA:N	2.41	0.45
1:L:262:GLY:O	1:L:263:PHE:HB3	2.17	0.45
1:L:273:ARG:O	1:L:274:ARG:CB	2.64	0.45
1:L:444:LEU:N	1:L:444:LEU:HD13	2.31	0.45
1:L:456:ALA:CB	1:L:509:ASP:OD2	2.65	0.45
1:M:24:GLU:O	1:M:26:ARG:N	2.49	0.45
1:M:276:VAL:CG2	1:M:293:ILE:HG23	2.47	0.45
1:M:298:ILE:HA	1:M:299:PRO:HD3	1.79	0.45
1:M:422:THR:HG22	1:M:423:GLU:N	2.32	0.45
1:N:55:GLY:HA3	1:N:57:PHE:CE1	2.51	0.45
1:M:41:TRP:HE1	1:O:27:ARG:NH2	2.14	0.45
1:O:316:TYR:O	1:O:321:ARG:NH1	2.49	0.45
1:O:35:PHE:CE1	1:O:321:ARG:NH1	2.84	0.45
1:O:510:ILE:O	1:O:513:ARG:HD2	2.17	0.45
1:P:227:GLU:CG	1:P:227:GLU:O	2.64	0.45
1:P:334:MSE:HE1	1:Q:407:ALA:HB1	1.99	0.45
1:P:378:ASP:O	1:P:381:SER:O	2.35	0.45
1:Q:171:ARG:O	1:Q:224:GLU:HA	2.17	0.45
1:Q:343:ARG:O	1:Q:344:THR:HB	2.16	0.45
1:R:444:LEU:O	1:R:446:THR:N	2.49	0.45
1:T:316:TYR:O	1:T:321:ARG:NH1	2.50	0.45
1:T:451:ASP:O	1:T:453:LEU:N	2.49	0.45
1:U:371:TYR:HE2	1:U:373:LEU:HD21	1.81	0.45
1:S:310:VAL:HG22	1:U:40:GLN:HG2	1.99	0.45
1:U:420:VAL:HA	1:U:428:GLY:HA2	1.98	0.45
1:U:422:THR:HG22	1:U:423:GLU:N	2.31	0.45
1:V:123:VAL:CG1	1:V:304:PHE:CE1	3.00	0.45
1:V:35:PHE:C	1:V:37:ARG:N	2.70	0.45
1:X:235:TYR:OH	1:X:252:LYS:NZ	2.48	0.45
1:X:232:ALA:HB2	1:X:269:ARG:O	2.17	0.45
1:X:26:ARG:HG3	1:X:27:ARG:N	2.31	0.45
1:X:444:LEU:HD13	1:X:444:LEU:N	2.30	0.45
2:Z:71:ASP:O	2:Z:72:ASP:CB	2.65	0.45
1:A:404:MSE:CE	1:L:334:MSE:HE3	2.47	0.45
1:A:427:GLY:C	1:A:429:GLN:N	2.70	0.45
1:A:45:LEU:HD21	1:A:328:ARG:HH21	1.82	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:246:TYR:HD2	1:B:511:ARG:CB	2.28	0.45
1:B:273:ARG:O	1:B:274:ARG:CB	2.64	0.45
1:B:47:GLN:CG	1:B:47:GLN:O	2.65	0.45
1:C:35:PHE:CE1	1:C:321:ARG:NH1	2.84	0.45
1:D:177:HIS:HE1	1:D:221:GLU:OE1	2.00	0.45
1:D:590:GLN:O	1:D:594:VAL:HG23	2.17	0.45
1:E:577:ILE:HG12	1:E:582:LYS:CG	2.41	0.45
1:E:9:GLU:HG3	1:E:12:LEU:H	1.82	0.45
1:F:317:GLU:HB3	1:F:321:ARG:CZ	2.46	0.45
1:G:293:ILE:HD13	1:G:294:ALA:N	2.31	0.45
1:G:434:THR:HA	1:G:437:GLN:HG2	1.98	0.45
1:H:177:HIS:HE1	1:H:221:GLU:OE1	2.00	0.45
1:H:413:LYS:HE2	1:H:413:LYS:HB3	1.74	0.45
1:H:77:ASP:HB2	1:H:523:SER:HB2	1.98	0.45
1:I:251:ILE:HG23	1:I:507:LEU:HD22	1.98	0.45
1:I:48:TYR:O	1:I:49:THR:CB	2.64	0.45
1:I:528:LYS:HD2	1:I:560:LEU:HD21	1.99	0.45
1:J:528:LYS:HZ3	1:J:560:LEU:HD21	1.80	0.45
1:J:78:VAL:HG21	1:J:444:LEU:CD1	2.21	0.45
1:K:234:ILE:CG2	1:K:246:TYR:HB3	2.47	0.45
1:K:534:GLU:O	1:K:538:LEU:HD23	2.17	0.45
1:L:35:PHE:CE1	1:L:321:ARG:NH1	2.84	0.45
1:L:251:ILE:HG23	1:L:507:LEU:HD22	1.99	0.45
1:M:100:THR:HG22	1:M:138:THR:HG22	1.97	0.45
1:M:82:PRO:O	1:M:516:CYS:HA	2.17	0.45
1:N:164:LEU:HA	1:N:307:TRP:HH2	1.81	0.45
1:N:191:TYR:HE1	1:N:278:LYS:HZ3	1.63	0.45
1:M:348:LYS:HB2	1:N:372:TYR:CE2	2.52	0.45
1:N:41:TRP:HE3	1:N:42:ASP:HB3	1.80	0.45
1:O:190:LYS:HE3	1:O:190:LYS:HA	1.99	0.45
1:O:409:THR:O	1:O:413:LYS:HG2	2.16	0.45
1:O:420:VAL:HA	1:O:428:GLY:HA2	1.98	0.45
1:O:444:LEU:O	1:O:446:THR:N	2.50	0.45
1:P:31:ASN:O	1:P:34:PHE:HB3	2.15	0.45
1:P:37:ARG:C	1:P:39:SER:H	2.20	0.45
1:Q:26:ARG:HG3	1:Q:27:ARG:N	2.31	0.45
1:Q:422:THR:HG22	1:Q:423:GLU:N	2.32	0.45
1:Q:41:TRP:HE3	1:Q:42:ASP:HB3	1.82	0.45
1:Q:451:ASP:C	1:Q:453:LEU:N	2.70	0.45
1:R:301:VAL:HA	1:R:302:PRO:HD3	1.79	0.45
1:R:322:LEU:HD22	1:R:322:LEU:H	1.81	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:77:ASP:HB2	1:R:523:SER:HB2	1.98	0.45
1:S:301:VAL:HA	1:S:302:PRO:HD3	1.80	0.45
1:S:123:VAL:HG22	1:S:316:TYR:HE2	1.80	0.45
1:T:273:ARG:HH22	1:T:453:LEU:CD2	2.28	0.45
1:T:76:ILE:HD12	1:T:433:ASP:OD1	2.16	0.45
1:U:454:ALA:O	1:U:455:THR:C	2.54	0.45
1:U:47:GLN:H	1:U:48:TYR:HD2	1.65	0.45
1:W:443:ASP:O	1:W:446:THR:HG22	2.17	0.45
1:W:511:ARG:HA	1:W:513:ARG:CD	2.44	0.45
1:X:118:GLN:OE1	1:X:303:VAL:HB	2.17	0.45
1:X:164:LEU:HD22	1:X:169:ASP:OD1	2.17	0.45
1:A:177:HIS:HE1	1:A:221:GLU:OE1	2.00	0.45
1:A:444:LEU:C	1:A:446:THR:H	2.19	0.45
1:A:534:GLU:O	1:A:538:LEU:HD23	2.17	0.45
1:B:232:ALA:N	1:B:269:ARG:O	2.50	0.45
1:C:444:LEU:C	1:C:446:THR:H	2.19	0.45
1:C:456:ALA:CB	1:C:509:ASP:OD2	2.65	0.45
1:D:456:ALA:CB	1:D:509:ASP:OD2	2.65	0.45
1:E:48:TYR:O	1:E:49:THR:CB	2.64	0.45
1:F:456:ALA:CB	1:F:509:ASP:OD2	2.65	0.45
1:G:86:ALA:CB	1:G:515:GLU:HG3	2.47	0.45
1:G:567:MSE:SE	1:H:576:LEU:HD13	2.67	0.45
1:H:47:GLN:O	1:H:47:GLN:CG	2.65	0.45
1:H:534:GLU:O	1:H:538:LEU:HD23	2.17	0.45
1:I:177:HIS:HE1	1:I:221:GLU:OE1	2.00	0.45
1:I:273:ARG:O	1:I:274:ARG:HB3	2.16	0.45
1:I:164:LEU:HA	1:I:307:TRP:CH2	2.51	0.45
1:I:434:THR:HA	1:I:437:GLN:HG2	1.98	0.45
1:I:451:ASP:O	1:I:456:ALA:N	2.41	0.45
1:J:563:LYS:HD3	1:K:557:PHE:CE2	2.52	0.45
1:L:234:ILE:HG22	1:L:246:TYR:HB3	1.98	0.45
1:L:434:THR:HA	1:L:437:GLN:HG2	1.98	0.45
1:L:534:GLU:O	1:L:538:LEU:HD23	2.17	0.45
1:N:260:ASP:HA	1:N:264:ILE:HB	1.97	0.45
1:O:444:LEU:N	1:O:444:LEU:HD13	2.31	0.45
1:P:193:LEU:HD22	1:P:287:LEU:HB3	1.98	0.45
1:P:26:ARG:HG3	1:P:27:ARG:N	2.31	0.45
1:S:266:ILE:O	1:S:267:ALA:HB2	2.17	0.45
1:S:123:VAL:HG13	1:S:304:PHE:CE1	2.52	0.45
1:S:78:VAL:CG1	1:S:79:LEU:H	2.30	0.45
1:U:232:ALA:HB1	1:U:233:PHE:H	1.57	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:429:GLN:O	1:U:429:GLN:HG2	2.16	0.45
1:W:127:ARG:HG2	1:W:147:GLU:HB2	1.98	0.45
1:W:77:ASP:HB2	1:W:523:SER:HB2	1.99	0.45
1:X:35:PHE:C	1:X:37:ARG:N	2.70	0.45
1:X:76:ILE:HD12	1:X:433:ASP:OD1	2.17	0.45
1:A:348:LYS:HB2	1:L:372:TYR:CD2	2.50	0.45
1:B:9:GLU:HG3	1:B:12:LEU:H	1.81	0.45
1:C:234:ILE:CG2	1:C:246:TYR:HB3	2.47	0.45
1:B:334:MSE:HE3	1:C:404:MSE:HE3	1.99	0.45
1:C:434:THR:HA	1:C:437:GLN:HG2	1.98	0.45
1:C:139:SER:CB	1:C:455:THR:CG2	2.80	0.45
1:D:201:PHE:HE2	1:D:281:ILE:HG22	1.80	0.45
1:D:45:LEU:HD21	1:D:328:ARG:HH21	1.82	0.45
1:D:534:GLU:O	1:D:538:LEU:HD23	2.17	0.45
1:D:554:LEU:HD22	1:E:567:MSE:HE2	1.99	0.45
1:E:86:ALA:CB	1:E:515:GLU:HG3	2.47	0.45
1:F:31:ASN:HD22	1:F:31:ASN:HA	1.62	0.45
1:F:86:ALA:CB	1:F:515:GLU:HG3	2.47	0.45
1:G:238:PRO:HG3	1:G:263:PHE:CB	2.46	0.45
1:H:227:GLU:HA	1:H:274:ARG:CA	2.44	0.45
1:G:376:ARG:HB2	1:H:352:TRP:CG	2.52	0.45
1:H:434:THR:HA	1:H:437:GLN:HG2	1.97	0.45
1:H:542:THR:HA	1:H:543:PRO:HD3	1.82	0.45
1:H:372:TYR:CE2	1:I:348:LYS:HB2	2.51	0.45
1:I:45:LEU:HD22	1:I:45:LEU:N	2.32	0.45
1:J:427:GLY:C	1:J:429:GLN:N	2.70	0.45
1:K:164:LEU:HA	1:K:307:TRP:CH2	2.51	0.45
1:K:26:ARG:NH2	1:K:30:LYS:HB2	2.28	0.45
1:L:246:TYR:HD2	1:L:511:ARG:CB	2.28	0.45
1:L:47:GLN:CG	1:L:47:GLN:O	2.65	0.45
1:M:26:ARG:HG3	1:M:27:ARG:N	2.31	0.45
1:N:198:ILE:HA	1:N:199:PRO:HD3	1.70	0.45
1:N:451:ASP:C	1:N:453:LEU:H	2.19	0.45
1:O:35:PHE:HZ	1:O:321:ARG:NE	2.11	0.45
1:O:35:PHE:C	1:O:37:ARG:N	2.70	0.45
1:P:273:ARG:CZ	1:P:275:ARG:HE	2.30	0.45
1:P:444:LEU:HD13	1:P:444:LEU:N	2.30	0.45
1:P:80:TYR:OH	1:P:444:LEU:HD12	2.17	0.45
1:Q:136:SER:N	1:Q:137:PRO:HD3	2.33	0.45
1:S:15:PHE:CE2	1:S:19:TRP:NE1	2.85	0.45
1:T:232:ALA:HB2	1:T:269:ARG:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:378:ASP:O	1:T:381:SER:O	2.35	0.45
1:U:330:ARG:O	1:U:334:MSE:HB2	2.17	0.45
1:U:343:ARG:O	1:U:344:THR:HB	2.16	0.45
1:V:198:ILE:O	1:V:198:ILE:HG22	2.17	0.45
1:W:280:ILE:HD12	1:W:280:ILE:N	2.32	0.45
1:W:330:ARG:HD2	1:W:409:THR:CG2	2.40	0.45
1:W:33:LEU:HD12	1:W:34:PHE:N	2.31	0.45
1:X:158:TRP:H	1:X:158:TRP:HD1	1.65	0.45
1:X:418:LEU:HB2	1:X:428:GLY:O	2.16	0.45
1:A:45:LEU:HD22	1:A:45:LEU:N	2.32	0.44
1:B:35:PHE:CE1	1:B:321:ARG:NH1	2.84	0.44
1:B:78:VAL:HG21	1:B:444:LEU:CD1	2.21	0.44
1:C:427:GLY:C	1:C:429:GLN:N	2.70	0.44
1:C:78:VAL:HG21	1:C:444:LEU:CD1	2.21	0.44
1:D:232:ALA:N	1:D:269:ARG:O	2.50	0.44
1:E:434:THR:O	1:E:437:GLN:HG2	2.17	0.44
1:E:528:LYS:HD2	1:E:560:LEU:HD21	1.99	0.44
1:F:177:HIS:HE1	1:F:221:GLU:OE1	2.00	0.44
1:F:47:GLN:CG	1:F:47:GLN:O	2.65	0.44
1:F:534:GLU:O	1:F:538:LEU:HD23	2.17	0.44
1:G:262:GLY:O	1:G:263:PHE:HB3	2.17	0.44
1:G:434:THR:O	1:G:437:GLN:HG2	2.17	0.44
1:G:444:LEU:C	1:G:446:THR:H	2.19	0.44
1:H:9:GLU:HG3	1:H:12:LEU:H	1.81	0.44
1:J:9:GLU:HG3	1:J:12:LEU:H	1.81	0.44
1:J:238:PRO:HG3	1:J:263:PHE:CB	2.46	0.44
1:J:273:ARG:NH2	1:J:453:LEU:HD11	2.32	0.44
1:J:444:LEU:C	1:J:446:THR:H	2.19	0.44
1:J:45:LEU:N	1:J:45:LEU:HD22	2.32	0.44
1:J:528:LYS:HD2	1:J:560:LEU:HD21	1.99	0.44
1:K:232:ALA:N	1:K:269:ARG:O	2.50	0.44
1:K:273:ARG:NH2	1:K:453:LEU:HD11	2.33	0.44
1:K:86:ALA:CB	1:K:515:GLU:HG3	2.47	0.44
1:L:45:LEU:HD21	1:L:328:ARG:HH21	1.82	0.44
1:L:77:ASP:HB2	1:L:523:SER:HB2	1.98	0.44
1:M:274:ARG:O	1:M:275:ARG:HD2	2.18	0.44
1:M:118:GLN:OE1	1:M:303:VAL:HB	2.17	0.44
1:M:41:TRP:HE1	1:O:27:ARG:HH21	1.63	0.44
1:M:437:GLN:HA	1:M:440:MSE:HB2	1.97	0.44
1:N:136:SER:N	1:N:137:PRO:HD3	2.31	0.44
1:N:236:GLN:H	1:N:265:LYS:HB2	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:37:ARG:C	1:N:39:SER:H	2.19	0.44
1:N:577:ILE:HG12	1:N:582:LYS:CG	2.45	0.44
1:Q:193:LEU:HD22	1:Q:287:LEU:HB3	1.97	0.44
1:Q:273:ARG:HH22	1:Q:453:LEU:CD2	2.30	0.44
1:Q:280:ILE:N	1:Q:280:ILE:HD12	2.33	0.44
1:Q:429:GLN:O	1:Q:429:GLN:HG2	2.17	0.44
1:Q:57:PHE:N	1:Q:57:PHE:CD1	2.84	0.44
1:R:71:MSE:HE3	1:R:115:VAL:HB	1.98	0.44
1:R:123:VAL:CG1	1:R:304:PHE:CE1	3.00	0.44
1:R:236:GLN:H	1:R:265:LYS:HB2	1.82	0.44
1:R:511:ARG:HA	1:R:513:ARG:CD	2.45	0.44
1:S:82:PRO:O	1:S:516:CYS:HA	2.17	0.44
1:T:158:TRP:HD1	1:T:158:TRP:H	1.64	0.44
1:T:420:VAL:HA	1:T:428:GLY:HA2	1.98	0.44
1:U:100:THR:HG22	1:U:138:THR:HG22	1.98	0.44
1:U:147:GLU:HA	1:U:148:PRO:HD3	1.81	0.44
1:U:316:TYR:O	1:U:321:ARG:NH1	2.50	0.44
1:V:444:LEU:HD13	1:V:444:LEU:N	2.32	0.44
1:X:34:PHE:O	1:X:37:ARG:HB2	2.17	0.44
2:Z:39:PRO:HB2	2:Z:40:GLN:H	1.51	0.44
1:A:590:GLN:O	1:A:594:VAL:HG23	2.16	0.44
1:B:343:ARG:H	1:B:343:ARG:HG2	1.52	0.44
1:B:251:ILE:HG23	1:B:507:LEU:HD22	1.98	0.44
1:C:590:GLN:O	1:C:594:VAL:HG23	2.16	0.44
1:D:77:ASP:HB2	1:D:523:SER:HB2	1.98	0.44
1:E:246:TYR:HD2	1:E:511:ARG:CB	2.28	0.44
1:E:78:VAL:CG2	1:E:444:LEU:HD21	2.46	0.44
1:F:227:GLU:N	1:F:227:GLU:OE2	2.47	0.44
1:F:273:ARG:O	1:F:274:ARG:HB3	2.17	0.44
1:F:451:ASP:O	1:F:456:ALA:N	2.41	0.44
1:F:45:LEU:N	1:F:45:LEU:HD22	2.32	0.44
1:G:456:ALA:CB	1:G:509:ASP:OD2	2.65	0.44
1:G:47:GLN:CG	1:G:47:GLN:O	2.65	0.44
1:H:251:ILE:HG23	1:H:507:LEU:HD22	1.99	0.44
1:H:45:LEU:HD21	1:H:328:ARG:HH21	1.82	0.44
1:I:234:ILE:CG2	1:I:246:TYR:HB3	2.47	0.44
1:J:177:HIS:HE1	1:J:221:GLU:OE1	2.00	0.44
1:K:45:LEU:N	1:K:45:LEU:HD22	2.32	0.44
1:K:538:LEU:HB3	1:K:551:LEU:HD13	2.00	0.44
1:L:177:HIS:HE1	1:L:221:GLU:OE1	2.00	0.44
1:L:234:ILE:CG2	1:L:246:TYR:HB3	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:26:ARG:NH2	1:L:30:LYS:HB2	2.28	0.44
1:L:9:GLU:HG3	1:L:12:LEU:H	1.81	0.44
1:M:136:SER:N	1:M:137:PRO:HD3	2.32	0.44
1:M:236:GLN:H	1:M:265:LYS:HB2	1.83	0.44
1:O:78:VAL:CG1	1:O:444:LEU:HG	2.47	0.44
1:O:47:GLN:N	1:O:48:TYR:HD2	2.15	0.44
1:P:164:LEU:HA	1:P:307:TRP:HH2	1.81	0.44
1:P:198:ILE:O	1:P:198:ILE:HG22	2.16	0.44
1:P:322:LEU:H	1:P:322:LEU:HD22	1.81	0.44
1:P:57:PHE:N	1:P:57:PHE:CD1	2.86	0.44
1:Q:383:ASP:C	1:Q:385:PRO:HD3	2.38	0.44
1:Q:418:LEU:HB2	1:Q:428:GLY:O	2.16	0.44
1:R:118:GLN:OE1	1:R:303:VAL:HB	2.16	0.44
1:R:528:LYS:CD	1:R:560:LEU:HD21	2.47	0.44
1:S:155:HIS:CE1	1:S:204:PRO:HB2	2.52	0.44
1:S:236:GLN:H	1:S:265:LYS:HB2	1.82	0.44
1:S:564:GLY:O	1:T:554:LEU:HD21	2.17	0.44
1:T:71:MSE:HE3	1:T:115:VAL:HB	1.98	0.44
1:V:190:LYS:HE3	1:V:190:LYS:HA	2.00	0.44
1:V:387:GLN:HG2	1:V:387:GLN:H	1.57	0.44
1:W:236:GLN:HG3	1:W:265:LYS:HG2	1.99	0.44
1:W:24:GLU:O	1:W:26:ARG:N	2.49	0.44
1:X:322:LEU:N	1:X:322:LEU:HD22	2.32	0.44
1:X:340:ILE:O	1:X:344:THR:HG21	2.16	0.44
1:X:38:VAL:HG21	1:X:324:LYS:HD2	1.99	0.44
1:X:443:ASP:C	1:X:446:THR:HG22	2.36	0.44
1:X:71:MSE:HE3	1:X:115:VAL:HB	1.99	0.44
2:Z:37:VAL:C	2:Z:39:PRO:HD3	2.38	0.44
1:B:427:GLY:C	1:B:429:GLN:N	2.70	0.44
1:C:262:GLY:O	1:C:263:PHE:HB3	2.17	0.44
1:C:343:ARG:HG2	1:C:343:ARG:H	1.52	0.44
1:C:48:TYR:O	1:C:49:THR:CB	2.64	0.44
1:D:273:ARG:NH2	1:D:453:LEU:HD11	2.32	0.44
1:D:451:ASP:O	1:D:456:ALA:N	2.41	0.44
1:D:45:LEU:HD22	1:D:45:LEU:N	2.32	0.44
1:E:26:ARG:NH2	1:E:30:LYS:HB2	2.28	0.44
1:E:456:ALA:CB	1:E:509:ASP:OD2	2.65	0.44
1:F:15:PHE:HE2	1:F:19:TRP:HE1	1.66	0.44
1:F:528:LYS:HZ2	1:F:560:LEU:HD21	1.79	0.44
1:G:251:ILE:HG23	1:G:507:LEU:HD22	1.99	0.44
1:H:334:MSE:HE3	1:I:404:MSE:HE1	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:86:ALA:CB	1:H:515:GLU:HG3	2.47	0.44
1:I:25:ALA:O	1:I:29:ALA:CB	2.58	0.44
1:I:444:LEU:N	1:I:444:LEU:HD13	2.31	0.44
1:I:456:ALA:CB	1:I:509:ASP:OD2	2.65	0.44
1:I:86:ALA:CB	1:I:515:GLU:HG3	2.47	0.44
1:J:232:ALA:N	1:J:269:ARG:O	2.50	0.44
1:J:273:ARG:O	1:J:274:ARG:HB3	2.17	0.44
1:J:34:PHE:CE1	1:J:324:LYS:NZ	2.72	0.44
1:K:177:HIS:HE1	1:K:221:GLU:OE1	2.00	0.44
1:A:400:ALA:HB3	1:L:395:PRO:HB2	1.99	0.44
1:N:232:ALA:HB2	1:N:269:ARG:O	2.18	0.44
1:N:454:ALA:O	1:N:455:THR:C	2.54	0.44
1:O:236:GLN:HG3	1:O:265:LYS:HG2	2.00	0.44
1:O:273:ARG:HH22	1:O:453:LEU:CD2	2.30	0.44
1:P:118:GLN:OE1	1:P:303:VAL:HB	2.17	0.44
1:P:35:PHE:C	1:P:37:ARG:N	2.70	0.44
1:P:451:ASP:C	1:P:453:LEU:H	2.18	0.44
1:Q:236:GLN:H	1:Q:265:LYS:HB2	1.82	0.44
1:Q:420:VAL:HA	1:Q:428:GLY:HA2	1.99	0.44
1:S:26:ARG:HG3	1:S:27:ARG:N	2.31	0.44
1:S:422:THR:HG22	1:S:423:GLU:N	2.32	0.44
1:S:444:LEU:HD13	1:S:444:LEU:N	2.32	0.44
1:S:454:ALA:O	1:S:455:THR:C	2.54	0.44
1:T:136:SER:N	1:T:137:PRO:HD3	2.32	0.44
1:T:422:THR:HG22	1:T:423:GLU:N	2.31	0.44
1:U:164:LEU:HD22	1:U:169:ASP:OD1	2.17	0.44
1:V:77:ASP:HB2	1:V:523:SER:HB2	1.98	0.44
1:W:26:ARG:HG3	1:W:27:ARG:N	2.32	0.44
1:W:316:TYR:O	1:W:321:ARG:NH1	2.50	0.44
1:W:34:PHE:O	1:W:37:ARG:HB2	2.18	0.44
1:X:191:TYR:HE1	1:X:278:LYS:HZ3	1.66	0.44
1:X:316:TYR:O	1:X:321:ARG:NH1	2.50	0.44
2:Y:39:PRO:HB2	2:Y:40:GLN:H	1.51	0.44
2:Y:57:TYR:H	2:Y:63:ILE:H	1.65	0.44
1:B:538:LEU:HB3	1:B:551:LEU:HD13	2.00	0.44
1:C:47:GLN:CG	1:C:47:GLN:O	2.65	0.44
1:C:538:LEU:HB3	1:C:551:LEU:HD13	2.00	0.44
1:D:219:ILE:HD13	1:D:282:THR:HG22	2.00	0.44
1:D:66:LYS:O	1:D:70:GLU:HG3	2.18	0.44
1:E:45:LEU:N	1:E:45:LEU:HD22	2.32	0.44
1:F:262:GLY:O	1:F:263:PHE:HB3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:77:ASP:HB2	1:F:523:SER:HB2	1.98	0.44
1:G:45:LEU:N	1:G:45:LEU:HD22	2.32	0.44
1:H:182:ASN:HD22	1:I:171:ARG:HH21	1.65	0.44
1:H:456:ALA:CB	1:H:509:ASP:OD2	2.65	0.44
1:I:434:THR:O	1:I:437:GLN:HG2	2.18	0.44
1:I:538:LEU:HB3	1:I:551:LEU:HD13	2.00	0.44
1:J:251:ILE:HG23	1:J:507:LEU:HD22	1.98	0.44
1:K:45:LEU:HD21	1:K:328:ARG:HH21	1.82	0.44
1:L:273:ARG:NH2	1:L:453:LEU:HD11	2.33	0.44
1:L:434:THR:O	1:L:437:GLN:HG2	2.18	0.44
1:L:86:ALA:CB	1:L:515:GLU:HG3	2.47	0.44
1:M:191:TYR:HE1	1:M:278:LYS:HZ3	1.64	0.44
1:M:443:ASP:O	1:M:446:THR:HG22	2.18	0.44
1:N:276:VAL:CG2	1:N:293:ILE:HG23	2.47	0.44
1:O:429:GLN:HG2	1:O:429:GLN:O	2.18	0.44
1:P:274:ARG:O	1:P:275:ARG:HD2	2.18	0.44
1:P:38:VAL:HG21	1:P:324:LYS:HD2	1.98	0.44
1:P:33:LEU:HD12	1:P:34:PHE:N	2.32	0.44
1:P:437:GLN:HA	1:P:440:MSE:HB2	2.00	0.44
1:P:510:ILE:O	1:P:513:ARG:HD2	2.16	0.44
1:P:78:VAL:CG1	1:P:444:LEU:HG	2.47	0.44
1:Q:118:GLN:OE1	1:Q:303:VAL:HB	2.17	0.44
1:Q:190:LYS:HA	1:Q:190:LYS:HE3	2.00	0.44
1:Q:40:GLN:HB2	1:Q:40:GLN:HE21	1.58	0.44
1:R:100:THR:HG22	1:R:138:THR:HG22	1.98	0.44
1:R:174:THR:N	3:R:705:HOH:O	2.50	0.44
1:S:437:GLN:HA	1:S:440:MSE:HB2	1.99	0.44
1:S:80:TYR:OH	1:S:444:LEU:HD12	2.18	0.44
1:T:236:GLN:H	1:T:265:LYS:HB2	1.82	0.44
1:U:29:ALA:O	1:U:33:LEU:HG	2.18	0.44
1:V:34:PHE:O	1:V:37:ARG:HB2	2.17	0.44
1:W:71:MSE:CE	1:W:115:VAL:HB	2.47	0.44
1:W:276:VAL:CG2	1:W:293:ILE:HG23	2.47	0.44
1:W:35:PHE:CE1	1:W:321:ARG:NH1	2.85	0.44
1:X:190:LYS:HA	1:X:190:LYS:HE3	2.00	0.44
1:X:236:GLN:H	1:X:265:LYS:HB2	1.83	0.44
2:Y:104:TYR:CD1	2:Y:104:TYR:N	2.85	0.44
2:Z:143:THR:N	2:Z:154:GLU:HA	2.32	0.44
1:A:164:LEU:HA	1:A:307:TRP:CH2	2.51	0.44
1:A:443:ASP:C	1:A:446:THR:HG22	2.38	0.44
1:A:251:ILE:HG23	1:A:507:LEU:HD22	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:456:ALA:CB	1:A:509:ASP:OD2	2.65	0.44
1:C:9:GLU:HG3	1:C:12:LEU:H	1.81	0.44
1:C:78:VAL:CG2	1:C:444:LEU:HD21	2.46	0.44
1:C:86:ALA:CB	1:C:515:GLU:HG3	2.47	0.44
1:D:234:ILE:HG22	1:D:246:TYR:HB3	1.98	0.44
1:D:434:THR:O	1:D:437:GLN:HG2	2.18	0.44
1:D:78:VAL:CG2	1:D:444:LEU:HD21	2.46	0.44
1:D:538:LEU:HB3	1:D:551:LEU:HD13	2.00	0.44
1:E:444:LEU:HD23	1:E:518:THR:OG1	2.18	0.44
1:F:383:ASP:C	1:F:385:PRO:CD	2.86	0.44
1:F:40:GLN:O	1:F:41:TRP:CB	2.55	0.44
1:F:444:LEU:HD23	1:F:518:THR:OG1	2.18	0.44
1:G:45:LEU:HD21	1:G:328:ARG:HH21	1.82	0.44
1:G:444:LEU:HD23	1:G:518:THR:OG1	2.18	0.44
1:H:238:PRO:HG3	1:H:263:PHE:CB	2.46	0.44
1:H:427:GLY:C	1:H:429:GLN:N	2.70	0.44
1:H:434:THR:O	1:H:437:GLN:HG2	2.18	0.44
1:H:443:ASP:C	1:H:446:THR:HG22	2.38	0.44
1:H:528:LYS:HD2	1:H:560:LEU:HD21	1.99	0.44
1:I:444:LEU:HD23	1:I:518:THR:OG1	2.18	0.44
1:J:227:GLU:OE2	1:J:227:GLU:N	2.47	0.44
1:J:35:PHE:CE1	1:J:321:ARG:NH1	2.84	0.44
1:J:434:THR:O	1:J:437:GLN:HG2	2.18	0.44
1:J:534:GLU:O	1:J:538:LEU:HD23	2.17	0.44
1:K:456:ALA:CB	1:K:509:ASP:OD2	2.65	0.44
1:L:590:GLN:O	1:L:594:VAL:HG23	2.17	0.44
1:L:94:LEU:HA	1:L:97:MSE:CE	2.37	0.44
1:M:310:VAL:HG22	1:N:40:GLN:HG2	1.98	0.44
1:M:387:GLN:H	1:M:387:GLN:HG2	1.58	0.44
1:M:444:LEU:O	1:M:446:THR:N	2.50	0.44
1:O:266:ILE:O	1:O:267:ALA:HB2	2.17	0.44
1:P:454:ALA:O	1:P:455:THR:C	2.56	0.44
1:Q:155:HIS:CE1	1:Q:204:PRO:HB2	2.53	0.44
1:Q:35:PHE:C	1:Q:37:ARG:N	2.71	0.44
1:S:198:ILE:HG22	1:S:198:ILE:O	2.16	0.44
1:S:444:LEU:O	1:S:447:TYR:N	2.50	0.44
1:T:343:ARG:O	1:T:344:THR:HB	2.18	0.44
1:U:266:ILE:O	1:U:267:ALA:HB2	2.18	0.44
1:U:301:VAL:HG23	1:U:439:ASN:HB3	2.00	0.44
1:U:301:VAL:HA	1:U:302:PRO:HD3	1.79	0.44
1:U:35:PHE:CE1	1:U:321:ARG:NH1	2.85	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:77:ASP:HB2	1:U:523:SER:HB2	1.99	0.44
1:V:232:ALA:HB2	1:V:269:ARG:O	2.17	0.44
1:V:57:PHE:N	1:V:57:PHE:CD1	2.85	0.44
1:W:76:ILE:HD12	1:W:433:ASP:OD1	2.18	0.44
1:W:80:TYR:OH	1:W:444:LEU:HD12	2.18	0.44
1:X:107:ALA:HA	1:X:146:ARG:HB3	2.00	0.44
1:X:160:SER:O	1:X:161:ASN:ND2	2.46	0.44
1:X:383:ASP:C	1:X:385:PRO:HD3	2.38	0.44
1:U:399:GLN:OE1	1:X:396:GLU:O	2.35	0.44
1:X:577:ILE:HG12	1:X:582:LYS:CG	2.45	0.44
2:Z:43:GLN:C	2:Z:45:ALA:N	2.70	0.44
1:A:451:ASP:O	1:A:456:ALA:N	2.41	0.44
1:A:58:ASP:O	1:A:59:VAL:HB	2.14	0.44
1:B:434:THR:O	1:B:437:GLN:HG2	2.18	0.44
1:B:45:LEU:N	1:B:45:LEU:HD22	2.32	0.44
1:B:95:MSE:HE1	1:B:99:ARG:NH2	2.33	0.44
1:C:293:ILE:HD13	1:C:294:ALA:N	2.31	0.44
1:C:273:ARG:NH2	1:C:453:LEU:HD11	2.33	0.44
1:D:155:HIS:CE1	1:D:204:PRO:HB2	2.53	0.44
1:D:9:GLU:HG3	1:D:12:LEU:H	1.81	0.44
1:D:352:TRP:CG	1:E:376:ARG:HB2	2.53	0.44
1:E:534:GLU:O	1:E:538:LEU:HD23	2.17	0.44
1:F:298:ILE:HA	1:F:299:PRO:HD3	1.82	0.44
1:G:383:ASP:C	1:G:385:PRO:CD	2.86	0.44
1:H:219:ILE:HD13	1:H:282:THR:HG22	2.00	0.44
1:I:9:GLU:HG3	1:I:12:LEU:H	1.81	0.44
1:I:45:LEU:HD21	1:I:328:ARG:HH21	1.82	0.44
1:J:219:ILE:HD13	1:J:282:THR:HG22	2.00	0.44
1:J:456:ALA:CB	1:J:509:ASP:OD2	2.65	0.44
1:L:35:PHE:CE2	1:L:324:LYS:NZ	2.80	0.44
1:A:348:LYS:HE2	1:L:369:TYR:O	2.18	0.44
1:L:248:LYS:HZ1	1:L:513:ARG:HH12	1.64	0.44
1:L:528:LYS:HD2	1:L:560:LEU:HD21	1.99	0.44
1:M:236:GLN:HG3	1:M:265:LYS:HG2	1.99	0.44
1:M:528:LYS:NZ	1:M:560:LEU:HD21	2.32	0.44
1:M:577:ILE:HG12	1:M:582:LYS:CG	2.45	0.44
1:M:78:VAL:CG1	1:M:79:LEU:H	2.31	0.44
1:N:420:VAL:HA	1:N:428:GLY:HA2	2.00	0.44
1:O:38:VAL:HG21	1:O:324:LYS:HD2	1.99	0.44
1:O:451:ASP:C	1:O:453:LEU:N	2.70	0.44
1:O:451:ASP:O	1:O:453:LEU:N	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:451:ASP:C	1:P:453:LEU:N	2.71	0.44
1:R:155:HIS:CE1	1:R:204:PRO:HB2	2.52	0.44
1:S:164:LEU:HA	1:S:307:TRP:HH2	1.83	0.44
1:S:165:MSE:HG3	1:S:307:TRP:CD2	2.51	0.44
1:U:444:LEU:O	1:U:447:TYR:N	2.49	0.44
1:U:451:ASP:C	1:U:453:LEU:N	2.70	0.44
1:U:47:GLN:CG	1:U:48:TYR:H	2.30	0.44
1:V:155:HIS:CE1	1:V:204:PRO:HB2	2.52	0.44
1:V:293:ILE:HG12	1:V:294:ALA:H	1.82	0.44
1:V:387:GLN:O	1:V:389:LEU:HG	2.18	0.44
1:V:407:ALA:HB1	1:W:334:MSE:HE1	1.99	0.44
1:W:155:HIS:CE1	1:W:204:PRO:HB2	2.52	0.44
1:X:236:GLN:HG3	1:X:265:LYS:HG2	2.00	0.44
1:X:454:ALA:O	1:X:455:THR:C	2.56	0.44
1:X:554:LEU:O	1:X:557:PHE:HB3	2.18	0.44
2:Y:37:VAL:C	2:Y:39:PRO:HD3	2.38	0.44
1:A:444:LEU:HD23	1:A:518:THR:OG1	2.18	0.44
1:C:45:LEU:HD22	1:C:45:LEU:N	2.32	0.44
1:D:47:GLN:CG	1:D:47:GLN:O	2.65	0.44
1:D:94:LEU:HA	1:D:97:MSE:CE	2.37	0.44
1:E:232:ALA:N	1:E:269:ARG:O	2.50	0.44
1:E:413:LYS:HB3	1:E:413:LYS:HE2	1.74	0.44
1:E:95:MSE:HE1	1:E:99:ARG:NH2	2.33	0.44
1:F:413:LYS:HB3	1:F:413:LYS:HE2	1.74	0.44
1:F:95:MSE:HE1	1:F:99:ARG:NH2	2.33	0.44
1:G:282:THR:HG23	1:G:287:LEU:CD1	2.43	0.44
1:G:443:ASP:C	1:G:446:THR:HG22	2.38	0.44
1:G:95:MSE:HE1	1:G:99:ARG:NH2	2.33	0.44
1:H:444:LEU:C	1:H:446:THR:H	2.19	0.44
1:I:443:ASP:C	1:I:446:THR:HG22	2.38	0.44
1:I:534:GLU:O	1:I:538:LEU:HD23	2.17	0.44
1:J:383:ASP:C	1:J:385:PRO:CD	2.86	0.44
1:J:47:GLN:CG	1:J:47:GLN:O	2.65	0.44
1:J:444:LEU:HD23	1:J:518:THR:OG1	2.18	0.44
1:K:434:THR:O	1:K:437:GLN:HG2	2.18	0.44
1:L:15:PHE:HE2	1:L:19:TRP:HE1	1.66	0.44
1:M:190:LYS:HA	1:M:190:LYS:HE3	2.00	0.44
1:M:248:LYS:HE2	1:M:513:ARG:HH12	1.83	0.44
1:N:127:ARG:HG2	1:N:147:GLU:HB2	2.00	0.44
1:N:33:LEU:HD12	1:N:34:PHE:N	2.33	0.44
1:N:34:PHE:O	1:N:37:ARG:HB2	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:158:TRP:HD1	1:O:158:TRP:H	1.64	0.44
1:O:80:TYR:OH	1:O:444:LEU:HD12	2.18	0.44
1:P:236:GLN:HG3	1:P:265:LYS:HG2	2.00	0.44
1:P:24:GLU:HG3	1:P:313:LYS:HE2	2.00	0.44
1:Q:135:GLN:OE1	1:R:273:ARG:HG2	2.18	0.44
1:Q:236:GLN:HG3	1:Q:265:LYS:HG2	2.00	0.44
3:P:718:HOH:O	1:Q:438:LEU:HD22	2.15	0.44
1:R:71:MSE:CE	1:R:115:VAL:HB	2.48	0.44
1:S:330:ARG:O	1:S:334:MSE:HB2	2.17	0.44
1:S:352:TRP:O	1:S:355:GLN:HG2	2.18	0.44
1:S:510:ILE:O	1:S:513:ARG:HD2	2.18	0.44
1:S:66:LYS:HZ3	1:S:420:VAL:HG21	1.82	0.44
1:U:158:TRP:HD1	1:U:158:TRP:H	1.66	0.44
1:V:100:THR:HG22	1:V:138:THR:HG22	2.00	0.44
1:V:236:GLN:HG3	1:V:265:LYS:HG2	1.99	0.44
1:V:71:MSE:CE	1:V:115:VAL:HB	2.48	0.44
1:W:273:ARG:HH22	1:W:453:LEU:CD2	2.30	0.44
1:R:372:TYR:CE2	1:X:348:LYS:HB2	2.53	0.44
2:Y:143:THR:N	2:Y:154:GLU:HA	2.32	0.44
2:Z:28:VAL:HG11	2:Z:97:ALA:HA	1.88	0.44
1:B:177:HIS:HE1	1:B:221:GLU:OE1	2.00	0.44
1:B:45:LEU:HD21	1:B:328:ARG:HH21	1.82	0.44
1:B:66:LYS:O	1:B:70:GLU:HG3	2.18	0.44
1:C:248:LYS:HZ1	1:C:513:ARG:HH12	1.64	0.44
1:D:334:MSE:HE3	1:F:404:MSE:HE3	1.99	0.44
1:D:444:LEU:HD23	1:D:518:THR:OG1	2.18	0.44
1:D:542:THR:HA	1:D:543:PRO:HD3	1.82	0.44
1:E:35:PHE:HZ	1:E:321:ARG:NE	2.12	0.44
1:E:35:PHE:HE1	1:E:321:ARG:NH1	2.13	0.44
1:F:78:VAL:CG2	1:F:444:LEU:HD21	2.46	0.44
1:H:35:PHE:CE1	1:H:321:ARG:NH1	2.84	0.44
1:H:383:ASP:C	1:H:385:PRO:CD	2.86	0.44
1:H:45:LEU:N	1:H:45:LEU:HD22	2.32	0.44
1:I:273:ARG:NH2	1:I:453:LEU:HD11	2.32	0.44
1:I:49:THR:O	1:I:50:THR:C	2.56	0.44
1:J:443:ASP:C	1:J:446:THR:HG22	2.38	0.44
1:K:155:HIS:CE1	1:K:204:PRO:HB2	2.53	0.44
1:K:334:MSE:HE3	1:L:404:MSE:HE3	2.00	0.44
1:L:45:LEU:N	1:L:45:LEU:HD22	2.32	0.44
1:M:589:GLU:HA	1:M:592:TRP:HB2	1.99	0.44
1:N:101:ASP:HB3	1:N:138:THR:HG21	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:236:GLN:HG3	1:N:265:LYS:HG2	2.00	0.44
1:M:390:ALA:CB	1:N:387:GLN:HB3	2.47	0.44
1:N:399:GLN:OE1	1:V:396:GLU:O	2.36	0.44
1:O:236:GLN:H	1:O:265:LYS:HB2	1.83	0.44
1:P:198:ILE:HA	1:P:199:PRO:HD3	1.70	0.44
1:P:34:PHE:O	1:P:37:ARG:HB2	2.17	0.44
1:Q:33:LEU:HD12	1:Q:34:PHE:N	2.32	0.44
1:Q:584:PRO:CG	1:Q:593:LEU:HD12	2.48	0.44
1:R:236:GLN:HG3	1:R:265:LYS:HG2	2.00	0.44
1:R:26:ARG:O	1:R:27:ARG:C	2.56	0.44
1:R:76:ILE:HD12	1:R:433:ASP:OD1	2.17	0.44
1:R:57:PHE:CD1	1:R:57:PHE:N	2.86	0.44
1:S:399:GLN:OE1	1:U:396:GLU:O	2.36	0.44
1:S:77:ASP:HB2	1:S:523:SER:HB2	2.00	0.44
1:T:35:PHE:CE1	1:T:321:ARG:NH1	2.85	0.44
1:U:158:TRP:N	1:U:158:TRP:HD1	2.11	0.44
1:U:293:ILE:HG12	1:U:294:ALA:H	1.83	0.44
1:U:589:GLU:HA	1:U:592:TRP:HB2	1.99	0.44
1:U:78:VAL:CG1	1:U:79:LEU:H	2.31	0.44
1:V:37:ARG:C	1:V:39:SER:H	2.20	0.44
1:V:82:PRO:HB2	1:V:83:LYS:H	1.62	0.44
1:W:451:ASP:C	1:W:453:LEU:N	2.70	0.44
1:X:266:ILE:O	1:X:267:ALA:HB2	2.17	0.44
1:X:71:MSE:CE	1:X:115:VAL:HB	2.48	0.44
1:A:79:LEU:N	1:A:519:ASP:O	2.51	0.44
1:B:155:HIS:CE1	1:B:204:PRO:HB2	2.53	0.44
1:D:15:PHE:HE2	1:D:19:TRP:HE1	1.66	0.44
1:E:15:PHE:HE2	1:E:19:TRP:HE1	1.66	0.44
1:E:49:THR:O	1:E:50:THR:C	2.56	0.44
1:E:79:LEU:N	1:E:519:ASP:O	2.51	0.44
1:F:434:THR:O	1:F:437:GLN:HG2	2.17	0.44
1:G:177:HIS:HE1	1:G:221:GLU:OE1	2.00	0.44
1:G:66:LYS:O	1:G:70:GLU:HG3	2.18	0.44
1:H:94:LEU:HA	1:H:97:MSE:CE	2.37	0.44
1:H:561:ASP:CB	1:I:89:ASP:HA	2.41	0.44
1:K:251:ILE:HG23	1:K:507:LEU:HD22	1.98	0.44
1:K:528:LYS:HD2	1:K:560:LEU:HD21	1.99	0.44
1:L:238:PRO:HG3	1:L:263:PHE:CB	2.46	0.44
1:L:383:ASP:C	1:L:385:PRO:CD	2.86	0.44
1:L:443:ASP:C	1:L:446:THR:HG22	2.38	0.44
1:L:79:LEU:N	1:L:519:ASP:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:58:ASP:O	1:L:59:VAL:HB	2.14	0.44
1:M:316:TYR:O	1:M:321:ARG:NH1	2.51	0.44
1:M:344:THR:CG2	1:M:344:THR:O	2.66	0.44
1:M:420:VAL:HA	1:M:428:GLY:HA2	2.00	0.44
1:N:437:GLN:HA	1:N:440:MSE:HB2	1.99	0.44
1:P:101:ASP:HB3	1:P:138:THR:HG21	1.99	0.44
1:P:265:LYS:O	1:P:266:ILE:HG12	2.18	0.44
1:P:301:VAL:HA	1:P:302:PRO:HD3	1.79	0.44
1:P:344:THR:O	1:P:344:THR:CG2	2.66	0.44
1:Q:101:ASP:HB3	1:Q:138:THR:HG21	2.00	0.44
1:Q:344:THR:O	1:Q:344:THR:CG2	2.66	0.44
1:Q:334:MSE:SE	1:Q:405:LEU:HD11	2.67	0.44
1:R:107:ALA:HA	1:R:146:ARG:HB3	1.99	0.44
1:R:245:SER:HG	1:R:247:PHE:HE1	1.61	0.44
1:S:29:ALA:O	1:S:33:LEU:HG	2.18	0.44
1:S:409:THR:O	1:S:413:LYS:HG2	2.18	0.44
1:S:47:GLN:N	1:S:48:TYR:HD2	2.15	0.44
1:T:127:ARG:HG2	1:T:147:GLU:HB2	1.98	0.44
1:T:198:ILE:O	1:T:198:ILE:HG22	2.16	0.44
1:T:344:THR:CG2	1:T:344:THR:O	2.66	0.44
1:U:248:LYS:H	1:U:248:LYS:CD	2.17	0.44
1:U:38:VAL:HG21	1:U:324:LYS:HD2	1.98	0.44
1:U:387:GLN:O	1:U:389:LEU:HG	2.18	0.44
1:U:575:GLN:O	1:U:579:MSE:CG	2.65	0.44
1:V:451:ASP:C	1:V:453:LEU:N	2.71	0.44
1:V:511:ARG:HA	1:V:513:ARG:CD	2.45	0.44
1:V:577:ILE:HG12	1:V:582:LYS:CG	2.44	0.44
1:X:100:THR:HG22	1:X:138:THR:HG22	1.99	0.44
1:X:265:LYS:O	1:X:266:ILE:HG12	2.17	0.44
1:X:322:LEU:H	1:X:322:LEU:HD22	1.83	0.44
1:X:371:TYR:HE2	1:X:373:LEU:HD21	1.82	0.44
1:X:589:GLU:HA	1:X:592:TRP:HB2	1.99	0.44
1:A:71:MSE:HE3	1:A:115:VAL:HB	2.00	0.43
1:A:127:ARG:HA	1:A:299:PRO:O	2.18	0.43
1:B:71:MSE:HE3	1:B:115:VAL:HB	2.00	0.43
1:C:434:THR:O	1:C:437:GLN:HG2	2.18	0.43
1:D:273:ARG:O	1:D:274:ARG:HB3	2.17	0.43
1:D:99:ARG:NH1	1:D:530:GLN:HE21	2.13	0.43
1:E:383:ASP:C	1:E:385:PRO:CD	2.86	0.43
1:E:538:LEU:HB3	1:E:551:LEU:HD13	2.00	0.43
1:E:78:VAL:HG21	1:E:444:LEU:CD1	2.21	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:24:GLU:CD	1:G:24:GLU:N	2.71	0.43
1:H:15:PHE:HE2	1:H:19:TRP:HE1	1.66	0.43
1:H:273:ARG:NH2	1:H:453:LEU:HD11	2.33	0.43
1:H:26:ARG:NH2	1:H:30:LYS:HB2	2.28	0.43
1:J:79:LEU:N	1:J:519:ASP:O	2.51	0.43
1:J:95:MSE:HE1	1:J:99:ARG:NH2	2.33	0.43
1:L:66:LYS:O	1:L:70:GLU:HG3	2.18	0.43
1:M:33:LEU:HD12	1:M:34:PHE:N	2.33	0.43
1:M:451:ASP:C	1:M:453:LEU:N	2.71	0.43
1:N:190:LYS:HE3	1:N:190:LYS:HA	2.00	0.43
1:N:35:PHE:C	1:N:37:ARG:N	2.71	0.43
1:O:235:TYR:OH	1:O:252:LYS:NZ	2.50	0.43
1:P:458:ARG:HD3	1:P:458:ARG:HA	1.83	0.43
1:P:248:LYS:HE2	1:P:513:ARG:HH12	1.83	0.43
1:P:575:GLN:O	1:P:579:MSE:CG	2.64	0.43
1:Q:349:PRO:HG3	1:Q:391:TYR:CE1	2.53	0.43
1:P:567:MSE:HE2	1:Q:554:LEU:HD22	2.00	0.43
1:Q:575:GLN:O	1:Q:579:MSE:CG	2.65	0.43
1:R:34:PHE:O	1:R:37:ARG:HB2	2.18	0.43
1:S:245:SER:HG	1:S:247:PHE:HE1	1.65	0.43
1:T:35:PHE:HZ	1:T:321:ARG:NE	2.14	0.43
3:S:718:HOH:O	1:T:438:LEU:HD22	2.17	0.43
1:S:390:ALA:CB	1:U:387:GLN:CB	2.96	0.43
1:U:47:GLN:N	1:U:48:TYR:HD2	2.15	0.43
1:V:179:MSE:O	1:V:217:ILE:HD12	2.18	0.43
1:W:158:TRP:H	1:W:158:TRP:HD1	1.65	0.43
1:W:123:VAL:HG13	1:W:304:PHE:CE1	2.53	0.43
1:X:343:ARG:HG2	1:X:343:ARG:H	1.53	0.43
1:X:47:GLN:CG	1:X:48:TYR:H	2.28	0.43
1:A:404:MSE:HE1	1:L:334:MSE:SE	2.67	0.43
1:B:198:ILE:HA	1:B:199:PRO:HD3	1.64	0.43
1:B:273:ARG:NH2	1:B:453:LEU:HD11	2.32	0.43
1:B:534:GLU:O	1:B:538:LEU:HD23	2.17	0.43
1:C:177:HIS:HE1	1:C:221:GLU:OE1	2.00	0.43
1:C:155:HIS:CE1	1:C:204:PRO:HB2	2.53	0.43
1:C:266:ILE:O	1:C:267:ALA:HB2	2.19	0.43
1:C:45:LEU:HD21	1:C:328:ARG:HH21	1.82	0.43
1:C:528:LYS:HD2	1:C:560:LEU:HD21	1.99	0.43
1:C:534:GLU:O	1:C:538:LEU:HD23	2.17	0.43
1:D:35:PHE:CE1	1:D:321:ARG:NH1	2.84	0.43
1:D:443:ASP:C	1:D:446:THR:HG22	2.38	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:LEU:N	1:D:519:ASP:O	2.51	0.43
1:E:155:HIS:CE1	1:E:204:PRO:HB2	2.53	0.43
1:E:273:ARG:NH2	1:E:453:LEU:HD11	2.33	0.43
1:F:266:ILE:O	1:F:267:ALA:HB2	2.19	0.43
1:F:383:ASP:C	1:F:385:PRO:HD3	2.39	0.43
1:F:443:ASP:C	1:F:446:THR:HG22	2.38	0.43
1:F:542:THR:HA	1:F:543:PRO:HD3	1.82	0.43
1:F:82:PRO:HB2	1:F:83:LYS:H	1.58	0.43
1:G:155:HIS:CE1	1:G:204:PRO:HB2	2.53	0.43
1:G:94:LEU:HA	1:G:97:MSE:CE	2.37	0.43
1:H:155:HIS:CE1	1:H:204:PRO:HB2	2.53	0.43
1:H:391:TYR:CD2	1:H:391:TYR:N	2.87	0.43
1:H:49:THR:O	1:H:50:THR:C	2.56	0.43
1:H:82:PRO:HB2	1:H:83:LYS:H	1.58	0.43
1:I:219:ILE:HD13	1:I:282:THR:HG22	2.00	0.43
1:I:383:ASP:C	1:I:385:PRO:CD	2.86	0.43
1:I:95:MSE:HE1	1:I:99:ARG:NH2	2.33	0.43
1:J:262:GLY:O	1:J:263:PHE:HB3	2.17	0.43
1:J:79:LEU:HD23	1:J:521:GLY:HA3	2.00	0.43
1:K:219:ILE:HD13	1:K:282:THR:HG22	2.00	0.43
1:K:282:THR:HG23	1:K:287:LEU:CD1	2.43	0.43
1:K:383:ASP:C	1:K:385:PRO:HD3	2.39	0.43
1:K:444:LEU:HD23	1:K:518:THR:OG1	2.18	0.43
1:K:79:LEU:N	1:K:519:ASP:O	2.51	0.43
1:K:66:LYS:O	1:K:70:GLU:HG3	2.18	0.43
1:L:155:HIS:CE1	1:L:204:PRO:HB2	2.53	0.43
1:L:266:ILE:O	1:L:267:ALA:HB2	2.18	0.43
1:L:298:ILE:HA	1:L:299:PRO:HD3	1.82	0.43
1:L:444:LEU:HD23	1:L:518:THR:OG1	2.18	0.43
1:L:79:LEU:HD23	1:L:521:GLY:HA3	2.00	0.43
1:L:538:LEU:HB3	1:L:551:LEU:HD13	2.00	0.43
1:L:583:LYS:HA	1:L:584:PRO:HD3	1.85	0.43
1:M:265:LYS:O	1:M:266:ILE:HG12	2.18	0.43
1:N:228:LYS:CE	1:N:228:LYS:HA	2.42	0.43
1:N:76:ILE:HD12	1:N:433:ASP:OD1	2.18	0.43
1:O:276:VAL:CG2	1:O:293:ILE:HG23	2.47	0.43
1:O:378:ASP:O	1:O:381:SER:O	2.36	0.43
1:O:454:ALA:O	1:O:455:THR:C	2.56	0.43
1:P:584:PRO:CG	1:P:593:LEU:HD12	2.47	0.43
1:Q:266:ILE:O	1:Q:267:ALA:HB2	2.18	0.43
1:S:35:PHE:CE1	1:S:321:ARG:NH1	2.85	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:198:ILE:O	1:U:198:ILE:HG22	2.17	0.43
1:U:276:VAL:CG2	1:U:293:ILE:HG23	2.47	0.43
1:V:274:ARG:O	1:V:275:ARG:HD2	2.18	0.43
1:V:429:GLN:HG2	1:V:429:GLN:O	2.18	0.43
1:V:78:VAL:CG1	1:V:79:LEU:H	2.29	0.43
1:W:265:LYS:O	1:W:266:ILE:HG12	2.18	0.43
1:W:584:PRO:CG	1:W:593:LEU:HD12	2.48	0.43
1:X:80:TYR:OH	1:X:444:LEU:HD12	2.18	0.43
1:X:451:ASP:C	1:X:453:LEU:N	2.71	0.43
1:A:528:LYS:HD2	1:A:560:LEU:HD21	1.99	0.43
1:B:383:ASP:C	1:B:385:PRO:CD	2.86	0.43
1:C:383:ASP:C	1:C:385:PRO:HD3	2.39	0.43
1:C:71:MSE:HE3	1:C:115:VAL:HB	2.01	0.43
1:D:266:ILE:O	1:D:267:ALA:HB2	2.19	0.43
1:I:155:HIS:CE1	1:I:204:PRO:HB2	2.53	0.43
1:I:262:GLY:O	1:I:263:PHE:HB3	2.17	0.43
1:I:139:SER:CB	1:I:455:THR:CG2	2.80	0.43
1:I:47:GLN:CG	1:I:47:GLN:O	2.65	0.43
1:J:15:PHE:HE2	1:J:19:TRP:HE1	1.66	0.43
1:J:383:ASP:C	1:J:385:PRO:HD3	2.39	0.43
1:K:266:ILE:O	1:K:267:ALA:HB2	2.19	0.43
1:K:71:MSE:HE3	1:K:115:VAL:HB	2.01	0.43
1:L:127:ARG:HA	1:L:299:PRO:O	2.18	0.43
1:M:174:THR:N	3:M:705:HOH:O	2.50	0.43
1:M:340:ILE:O	1:M:344:THR:HG21	2.19	0.43
1:M:71:MSE:HE3	1:M:115:VAL:HB	1.99	0.43
1:N:24:GLU:O	1:N:26:ARG:N	2.50	0.43
1:O:387:GLN:O	1:O:389:LEU:HG	2.19	0.43
1:P:174:THR:N	3:P:705:HOH:O	2.51	0.43
1:Q:53:TYR:OH	1:R:329:LEU:HD21	2.18	0.43
1:Q:92:ASP:N	1:Q:92:ASP:OD2	2.52	0.43
1:R:198:ILE:HG22	1:R:198:ILE:O	2.17	0.43
1:R:92:ASP:N	1:R:92:ASP:OD2	2.51	0.43
1:S:232:ALA:HB2	1:S:269:ARG:O	2.18	0.43
1:S:34:PHE:O	1:S:37:ARG:HB2	2.19	0.43
1:T:123:VAL:HG13	1:T:304:PHE:CE1	2.52	0.43
1:T:236:GLN:HG3	1:T:265:LYS:HG2	2.00	0.43
1:T:589:GLU:HA	1:T:592:TRP:HB2	2.00	0.43
1:T:77:ASP:HB2	1:T:523:SER:HB2	1.99	0.43
1:U:155:HIS:CE1	1:U:204:PRO:HB2	2.53	0.43
1:U:273:ARG:HH22	1:U:453:LEU:CD2	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:236:GLN:H	1:V:265:LYS:HB2	1.83	0.43
1:V:273:ARG:HH22	1:V:453:LEU:CD2	2.29	0.43
1:W:344:THR:CG2	1:W:344:THR:O	2.66	0.43
1:X:24:GLU:HG3	1:X:313:LYS:HE2	2.01	0.43
1:A:155:HIS:CE1	1:A:204:PRO:HB2	2.53	0.43
1:A:343:ARG:NH2	2:Y:134:ARG:HD3	2.33	0.43
1:A:99:ARG:NH1	1:A:530:GLN:HE21	2.13	0.43
1:A:95:MSE:HE1	1:A:99:ARG:NH2	2.33	0.43
1:B:383:ASP:C	1:B:385:PRO:HD3	2.39	0.43
1:B:79:LEU:N	1:B:519:ASP:O	2.51	0.43
1:C:227:GLU:OE2	1:C:227:GLU:N	2.47	0.43
1:C:437:GLN:HA	1:C:440:MSE:HB2	2.01	0.43
1:D:24:GLU:N	1:D:24:GLU:CD	2.71	0.43
1:D:383:ASP:C	1:D:385:PRO:CD	2.86	0.43
1:D:79:LEU:HD23	1:D:521:GLY:HA3	2.00	0.43
1:E:236:GLN:HE21	1:E:265:LYS:HZ3	1.65	0.43
1:F:24:GLU:CD	1:F:24:GLU:N	2.71	0.43
1:F:127:ARG:HA	1:F:299:PRO:O	2.18	0.43
1:F:273:ARG:NH2	1:F:453:LEU:HD11	2.32	0.43
1:G:34:PHE:CE1	1:G:324:LYS:NZ	2.72	0.43
1:G:383:ASP:C	1:G:385:PRO:HD3	2.39	0.43
1:H:444:LEU:HD23	1:H:518:THR:OG1	2.18	0.43
1:H:79:LEU:HD23	1:H:521:GLY:HA3	2.00	0.43
1:I:229:LYS:HD2	1:I:270:GLN:HG3	2.01	0.43
1:I:266:ILE:O	1:I:267:ALA:HB2	2.19	0.43
1:I:391:TYR:N	1:I:391:TYR:CD2	2.87	0.43
1:I:437:GLN:HA	1:I:440:MSE:HB2	2.00	0.43
1:I:79:LEU:N	1:I:519:ASP:O	2.51	0.43
1:J:538:LEU:HB3	1:J:551:LEU:HD13	2.00	0.43
1:K:343:ARG:H	1:K:343:ARG:HG2	1.52	0.43
1:K:35:PHE:HE2	1:K:324:LYS:NZ	2.08	0.43
1:K:383:ASP:C	1:K:385:PRO:CD	2.86	0.43
1:L:229:LYS:HD2	1:L:270:GLN:HG3	2.01	0.43
1:L:35:PHE:CZ	1:L:321:ARG:CZ	3.02	0.43
1:L:391:TYR:CD2	1:L:391:TYR:N	2.86	0.43
1:O:71:MSE:CE	1:O:115:VAL:HB	2.48	0.43
1:O:228:LYS:CE	1:O:228:LYS:HA	2.43	0.43
1:O:245:SER:HG	1:O:247:PHE:HE1	1.62	0.43
1:P:190:LYS:HE3	1:P:190:LYS:HA	2.00	0.43
1:P:420:VAL:HA	1:P:428:GLY:HA2	2.00	0.43
1:Q:164:LEU:HD22	1:Q:169:ASP:OD1	2.17	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:387:GLN:CB	1:R:390:ALA:HB2	2.49	0.43
1:R:344:THR:O	1:R:344:THR:CG2	2.67	0.43
1:R:376:ARG:HB2	1:X:352:TRP:CD1	2.54	0.43
1:R:383:ASP:C	1:R:385:PRO:HD3	2.39	0.43
1:S:293:ILE:HG12	1:S:294:ALA:H	1.83	0.43
1:S:329:LEU:HD21	1:U:53:TYR:OH	2.17	0.43
1:S:35:PHE:C	1:S:37:ARG:N	2.71	0.43
1:S:451:ASP:C	1:S:453:LEU:N	2.72	0.43
1:V:266:ILE:O	1:V:267:ALA:HB2	2.18	0.43
1:V:387:GLN:HA	1:V:388:PRO:HD3	1.92	0.43
1:V:352:TRP:CD1	1:W:376:ARG:HB2	2.53	0.43
1:A:252:LYS:O	1:A:252:LYS:HE3	2.19	0.43
1:A:391:TYR:N	1:A:391:TYR:CD2	2.87	0.43
1:A:437:GLN:HA	1:A:440:MSE:HB2	2.01	0.43
1:A:273:ARG:NH2	1:A:453:LEU:HD11	2.33	0.43
1:A:66:LYS:O	1:A:70:GLU:HG3	2.18	0.43
1:B:528:LYS:HD2	1:B:560:LEU:HD21	1.99	0.43
1:B:79:LEU:HD23	1:B:521:GLY:HA3	2.00	0.43
1:C:66:LYS:O	1:C:70:GLU:HG3	2.18	0.43
1:C:82:PRO:HB2	1:C:83:LYS:H	1.58	0.43
1:D:71:MSE:HE3	1:D:115:VAL:HB	2.00	0.43
1:D:383:ASP:C	1:D:385:PRO:HD3	2.39	0.43
1:E:127:ARG:HA	1:E:299:PRO:O	2.18	0.43
1:E:391:TYR:N	1:E:391:TYR:CD2	2.87	0.43
1:E:43:ASP:OD2	1:E:43:ASP:N	2.52	0.43
1:E:82:PRO:HB2	1:E:83:LYS:H	1.58	0.43
1:G:273:ARG:NH2	1:G:453:LEU:HD11	2.33	0.43
1:H:246:TYR:HD2	1:H:511:ARG:CB	2.28	0.43
1:H:248:LYS:HZ2	1:H:251:ILE:HD12	1.84	0.43
1:H:343:ARG:HG2	1:H:343:ARG:H	1.52	0.43
1:I:378:ASP:O	1:I:381:SER:O	2.37	0.43
1:I:43:ASP:N	1:I:43:ASP:OD2	2.52	0.43
1:I:78:VAL:CG2	1:I:444:LEU:HD21	2.46	0.43
1:J:155:HIS:CE1	1:J:204:PRO:HB2	2.53	0.43
1:K:427:GLY:C	1:K:429:GLN:N	2.70	0.43
1:L:95:MSE:HE1	1:L:99:ARG:NH2	2.33	0.43
1:M:280:ILE:HG22	1:M:287:LEU:HD13	2.00	0.43
1:M:123:VAL:CG1	1:M:304:PHE:CE1	3.00	0.43
1:M:576:LEU:HD13	1:N:567:MSE:SE	2.68	0.43
1:N:15:PHE:CE2	1:N:19:TRP:NE1	2.87	0.43
1:N:266:ILE:O	1:N:267:ALA:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:451:ASP:C	1:N:453:LEU:N	2.71	0.43
1:N:458:ARG:HD3	1:N:458:ARG:HA	1.82	0.43
1:O:369:TYR:HA	1:O:370:PRO:HD3	1.83	0.43
1:O:40:GLN:HB2	1:O:40:GLN:HE21	1.57	0.43
1:O:334:MSE:CG	1:P:404:MSE:HE1	2.48	0.43
1:P:92:ASP:N	1:P:92:ASP:OD2	2.51	0.43
1:Q:15:PHE:CE2	1:Q:19:TRP:NE1	2.86	0.43
1:Q:343:ARG:H	1:Q:343:ARG:HG2	1.53	0.43
1:R:190:LYS:HE3	1:R:190:LYS:HA	1.99	0.43
1:R:270:GLN:HA	1:R:270:GLN:OE1	2.18	0.43
1:S:371:TYR:HE2	1:S:373:LEU:HD21	1.83	0.43
1:T:343:ARG:H	1:T:343:ARG:HG2	1.58	0.43
1:T:444:LEU:O	1:T:446:THR:N	2.50	0.43
1:U:236:GLN:H	1:U:265:LYS:HB2	1.83	0.43
1:U:232:ALA:HB2	1:U:269:ARG:O	2.18	0.43
1:U:26:ARG:O	1:U:27:ARG:C	2.56	0.43
1:V:340:ILE:O	1:V:344:THR:HG21	2.18	0.43
1:V:437:GLN:HA	1:V:440:MSE:HB2	2.00	0.43
1:V:444:LEU:O	1:V:446:THR:N	2.51	0.43
1:V:80:TYR:OH	1:V:444:LEU:HD12	2.18	0.43
1:V:92:ASP:N	1:V:92:ASP:OD2	2.51	0.43
1:W:384:LEU:HD22	1:W:384:LEU:N	2.29	0.43
1:W:413:LYS:HE2	1:W:413:LYS:HB3	1.87	0.43
1:W:589:GLU:HA	1:W:592:TRP:HB2	2.00	0.43
1:X:123:VAL:HG13	1:X:304:PHE:CE1	2.53	0.43
1:X:198:ILE:HG22	1:X:198:ILE:O	2.18	0.43
1:X:35:PHE:CE1	1:X:321:ARG:NH1	2.85	0.43
1:X:440:MSE:O	1:X:443:ASP:HB3	2.18	0.43
1:X:510:ILE:O	1:X:513:ARG:HD2	2.18	0.43
1:A:24:GLU:CD	1:A:24:GLU:N	2.71	0.43
1:A:383:ASP:C	1:A:385:PRO:HD3	2.39	0.43
1:A:434:THR:O	1:A:437:GLN:HG2	2.18	0.43
1:A:49:THR:O	1:A:50:THR:C	2.56	0.43
1:B:219:ILE:HD13	1:B:282:THR:HG22	2.00	0.43
1:B:78:VAL:CG2	1:B:444:LEU:HD21	2.46	0.43
1:B:49:THR:O	1:B:50:THR:C	2.56	0.43
1:C:443:ASP:C	1:C:446:THR:HG22	2.38	0.43
1:D:127:ARG:HA	1:D:299:PRO:O	2.18	0.43
1:D:598:GLN:O	1:D:601:GLN:HB2	2.19	0.43
1:D:95:MSE:HE1	1:D:99:ARG:NH2	2.33	0.43
1:D:350:PHE:HE1	1:E:363:TYR:HE1	1.67	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:443:ASP:C	1:E:446:THR:HG22	2.38	0.43
1:F:155:HIS:CE1	1:F:204:PRO:HB2	2.53	0.43
1:F:219:ILE:HD13	1:F:282:THR:HG22	2.00	0.43
1:F:35:PHE:CZ	1:F:321:ARG:CZ	3.02	0.43
1:D:567:MSE:SE	1:F:576:LEU:HD13	2.68	0.43
1:G:266:ILE:O	1:G:267:ALA:HB2	2.19	0.43
1:H:538:LEU:HB3	1:H:551:LEU:HD13	2.00	0.43
1:I:198:ILE:HA	1:I:199:PRO:HD3	1.64	0.43
1:I:24:GLU:CD	1:I:24:GLU:N	2.71	0.43
1:I:127:ARG:HA	1:I:299:PRO:O	2.18	0.43
1:I:71:MSE:HE3	1:I:115:VAL:HB	2.00	0.43
1:J:47:GLN:CD	1:J:47:GLN:N	2.72	0.43
1:K:24:GLU:N	1:K:24:GLU:CD	2.71	0.43
1:K:391:TYR:CD2	1:K:391:TYR:N	2.87	0.43
1:L:71:MSE:HE3	1:L:115:VAL:HB	2.00	0.43
1:M:345:PRO:HB2	1:M:392:TYR:CE1	2.54	0.43
1:N:26:ARG:HG3	1:N:27:ARG:N	2.32	0.43
1:P:293:ILE:HG12	1:P:294:ALA:H	1.82	0.43
1:P:380:ASN:O	1:P:381:SER:CB	2.66	0.43
1:P:542:THR:HA	1:P:543:PRO:HD3	1.88	0.43
1:Q:265:LYS:O	1:Q:266:ILE:HG12	2.18	0.43
1:R:265:LYS:O	1:R:266:ILE:HG12	2.18	0.43
1:R:334:MSE:SE	1:R:405:LEU:HD11	2.69	0.43
1:S:47:GLN:H	1:S:48:TYR:HD2	1.65	0.43
1:S:57:PHE:N	1:S:57:PHE:CD1	2.87	0.43
1:T:100:THR:HG22	1:T:138:THR:HG22	2.00	0.43
1:T:24:GLU:O	1:T:26:ARG:N	2.50	0.43
1:T:413:LYS:HE2	1:T:413:LYS:HB3	1.85	0.43
1:T:510:ILE:O	1:T:513:ARG:HD2	2.18	0.43
1:T:78:VAL:CG1	1:T:79:LEU:H	2.30	0.43
1:U:24:GLU:O	1:U:26:ARG:N	2.50	0.43
1:N:352:TRP:CD2	1:V:376:ARG:HB2	2.53	0.43
1:V:510:ILE:O	1:V:513:ARG:HD2	2.19	0.43
1:V:589:GLU:HA	1:V:592:TRP:HB2	2.00	0.43
1:X:420:VAL:HA	1:X:428:GLY:HA2	2.00	0.43
1:X:301:VAL:HG23	1:X:439:ASN:HB3	2.01	0.43
1:A:15:PHE:HE2	1:A:19:TRP:HE1	1.66	0.43
1:A:35:PHE:CZ	1:A:321:ARG:CZ	3.02	0.43
1:A:383:ASP:C	1:A:385:PRO:CD	2.86	0.43
1:A:43:ASP:OD2	1:A:43:ASP:N	2.52	0.43
1:B:212:LEU:HD12	1:B:212:LEU:N	2.34	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:LYS:HD2	1:B:270:GLN:HG3	2.01	0.43
1:B:37:ARG:HA	1:B:37:ARG:HD2	1.79	0.43
1:B:391:TYR:N	1:B:391:TYR:CD2	2.87	0.43
1:B:437:GLN:HA	1:B:440:MSE:HB2	2.00	0.43
1:C:38:VAL:HG21	1:C:324:LYS:HD2	2.01	0.43
1:C:49:THR:O	1:C:50:THR:C	2.56	0.43
1:D:246:TYR:HD2	1:D:511:ARG:CB	2.28	0.43
1:D:35:PHE:CZ	1:D:321:ARG:CZ	3.02	0.43
1:D:43:ASP:N	1:D:43:ASP:OD2	2.52	0.43
1:E:598:GLN:O	1:E:601:GLN:HB2	2.19	0.43
1:F:25:ALA:O	1:F:29:ALA:CB	2.58	0.43
1:F:437:GLN:HA	1:F:440:MSE:HB2	2.00	0.43
1:F:538:LEU:HB3	1:F:551:LEU:HD13	2.00	0.43
1:F:66:LYS:O	1:F:70:GLU:HG3	2.18	0.43
1:G:219:ILE:HD13	1:G:282:THR:HG22	2.00	0.43
1:G:391:TYR:CD2	1:G:391:TYR:N	2.86	0.43
1:G:79:LEU:N	1:G:519:ASP:O	2.51	0.43
1:H:95:MSE:HE1	1:H:99:ARG:NH2	2.33	0.43
1:I:413:LYS:HB3	1:I:413:LYS:HE2	1.73	0.43
1:I:80:TYR:CZ	1:I:448:VAL:HG22	2.54	0.43
1:I:79:LEU:HD23	1:I:521:GLY:HA3	2.00	0.43
1:J:266:ILE:O	1:J:267:ALA:HB2	2.19	0.43
1:J:45:LEU:HD21	1:J:328:ARG:HH21	1.82	0.43
1:J:391:TYR:CD2	1:J:391:TYR:N	2.87	0.43
1:K:15:PHE:HE2	1:K:19:TRP:HE1	1.66	0.43
1:K:378:ASP:O	1:K:381:SER:O	2.37	0.43
1:K:80:TYR:CZ	1:K:448:VAL:HG22	2.54	0.43
1:K:95:MSE:HE1	1:K:99:ARG:NH2	2.33	0.43
1:L:378:ASP:O	1:L:381:SER:O	2.37	0.43
1:M:330:ARG:O	1:M:334:MSE:HB2	2.18	0.43
1:N:212:LEU:HD12	1:N:212:LEU:N	2.34	0.43
1:P:384:LEU:N	1:P:384:LEU:HD22	2.27	0.43
1:Q:274:ARG:O	1:Q:275:ARG:HD2	2.19	0.43
1:Q:542:THR:HA	1:Q:543:PRO:HD3	1.88	0.43
1:R:38:VAL:HG21	1:R:324:LYS:HD2	1.99	0.43
1:R:78:VAL:CG1	1:R:79:LEU:H	2.30	0.43
1:S:101:ASP:HB3	1:S:138:THR:HG21	2.01	0.43
1:S:431:ALA:HA	1:S:434:THR:HG22	2.01	0.43
1:T:212:LEU:HD12	1:T:212:LEU:N	2.33	0.43
1:U:584:PRO:CG	1:U:593:LEU:HD12	2.49	0.43
1:V:191:TYR:HE1	1:V:278:LYS:HZ3	1.65	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:190:LYS:HA	1:W:190:LYS:HE3	2.00	0.43
1:A:266:ILE:O	1:A:267:ALA:HB2	2.19	0.43
1:A:80:TYR:CZ	1:A:448:VAL:HG22	2.54	0.43
1:A:94:LEU:HD23	1:A:94:LEU:O	2.19	0.43
1:B:252:LYS:HE3	1:B:252:LYS:O	2.19	0.43
1:B:35:PHE:CZ	1:B:321:ARG:CZ	3.02	0.43
1:B:444:LEU:O	1:B:447:TYR:N	2.52	0.43
1:C:15:PHE:HE2	1:C:19:TRP:HE1	1.66	0.43
1:B:371:TYR:HA	1:C:348:LYS:HB3	2.01	0.43
1:C:79:LEU:N	1:C:519:ASP:O	2.51	0.43
1:C:95:MSE:HE1	1:C:99:ARG:NH2	2.33	0.43
1:D:35:PHE:HZ	1:D:321:ARG:NE	2.12	0.43
1:D:378:ASP:O	1:D:381:SER:O	2.37	0.43
1:E:282:THR:HG23	1:E:287:LEU:CD1	2.44	0.43
1:F:378:ASP:O	1:F:381:SER:O	2.37	0.43
1:F:43:ASP:OD2	1:F:43:ASP:N	2.52	0.43
1:H:212:LEU:N	1:H:212:LEU:HD12	2.34	0.43
1:H:24:GLU:N	1:H:24:GLU:CD	2.71	0.43
1:H:444:LEU:O	1:H:447:TYR:N	2.52	0.43
1:H:66:LYS:O	1:H:70:GLU:HG3	2.18	0.43
1:I:212:LEU:N	1:I:212:LEU:HD12	2.34	0.43
1:I:123:VAL:HG13	1:I:304:PHE:CE1	2.54	0.43
1:I:99:ARG:NH1	1:I:530:GLN:HE21	2.13	0.43
1:I:94:LEU:O	1:I:94:LEU:HD23	2.19	0.43
1:J:35:PHE:CZ	1:J:321:ARG:CZ	3.02	0.43
1:J:560:LEU:HD13	1:K:82:PRO:CD	2.25	0.43
1:J:583:LYS:HA	1:J:584:PRO:HD3	1.85	0.43
1:L:274:ARG:HD3	1:L:296:GLU:O	2.19	0.43
1:L:219:ILE:HD13	1:L:282:THR:HG22	2.00	0.43
1:L:383:ASP:C	1:L:385:PRO:HD3	2.39	0.43
1:M:387:GLN:O	1:M:389:LEU:HG	2.18	0.43
1:M:395:PRO:HD2	1:O:398:PRO:HB3	2.00	0.43
1:N:179:MSE:O	1:N:217:ILE:HD12	2.19	0.43
1:N:26:ARG:O	1:N:27:ARG:C	2.57	0.43
1:N:270:GLN:HA	1:N:270:GLN:OE1	2.19	0.43
1:N:298:ILE:HA	1:N:299:PRO:HD3	1.78	0.43
1:N:316:TYR:O	1:N:321:ARG:NH1	2.52	0.43
1:O:589:GLU:HA	1:O:592:TRP:HB2	2.00	0.43
1:O:78:VAL:CG1	1:O:79:LEU:H	2.31	0.43
1:O:180:SER:OG	1:P:161:ASN:HB3	2.19	0.43
1:Q:35:PHE:CE1	1:Q:321:ARG:NH1	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:589:GLU:HA	1:Q:592:TRP:HB2	2.00	0.43
1:R:158:TRP:H	1:R:158:TRP:HD1	1.65	0.43
1:R:437:GLN:HA	1:R:440:MSE:HB2	1.99	0.43
1:S:71:MSE:CE	1:S:115:VAL:HB	2.48	0.43
1:T:340:ILE:O	1:T:344:THR:HG21	2.19	0.43
1:T:443:ASP:O	1:T:446:THR:HG22	2.19	0.43
1:T:71:MSE:CE	1:T:115:VAL:HB	2.49	0.43
1:U:179:MSE:O	1:U:217:ILE:HD12	2.19	0.43
1:U:340:ILE:O	1:U:344:THR:HG21	2.19	0.43
1:U:383:ASP:C	1:U:385:PRO:HD3	2.39	0.43
1:U:451:ASP:O	1:U:453:LEU:N	2.52	0.43
1:V:248:LYS:HE2	1:V:513:ARG:HH12	1.83	0.43
1:X:15:PHE:CE2	1:X:19:TRP:NE1	2.87	0.43
1:X:431:ALA:HA	1:X:434:THR:HG22	2.01	0.43
3:R:718:HOH:O	1:X:438:LEU:HD22	2.19	0.43
1:X:444:LEU:O	1:X:447:TYR:N	2.52	0.43
1:A:49:THR:O	1:A:50:THR:O	2.37	0.43
1:C:219:ILE:HD13	1:C:282:THR:HG22	2.00	0.43
1:C:444:LEU:HD23	1:C:518:THR:OG1	2.18	0.43
1:E:66:LYS:O	1:E:70:GLU:HG3	2.18	0.43
1:F:229:LYS:HD2	1:F:270:GLN:HG3	2.01	0.43
1:F:598:GLN:O	1:F:601:GLN:HB2	2.19	0.43
1:G:252:LYS:HE3	1:G:252:LYS:O	2.19	0.43
1:G:71:MSE:HE3	1:G:115:VAL:HB	2.00	0.43
1:H:127:ARG:HA	1:H:299:PRO:O	2.18	0.43
1:H:383:ASP:C	1:H:385:PRO:HD3	2.39	0.43
1:H:38:VAL:HG21	1:H:324:LYS:HD2	2.01	0.43
1:I:35:PHE:CZ	1:I:321:ARG:CZ	3.02	0.43
1:J:80:TYR:CZ	1:J:448:VAL:HG22	2.54	0.43
1:J:49:THR:O	1:J:50:THR:O	2.37	0.43
1:J:66:LYS:O	1:J:70:GLU:HG3	2.18	0.43
1:J:94:LEU:HD23	1:J:94:LEU:O	2.19	0.43
1:K:274:ARG:HD3	1:K:296:GLU:O	2.19	0.43
1:K:35:PHE:CZ	1:K:321:ARG:CZ	3.02	0.43
1:K:182:ASN:HD22	1:L:171:ARG:HH21	1.65	0.43
1:N:164:LEU:HD22	1:N:169:ASP:OD1	2.19	0.43
1:N:191:TYR:O	1:N:288:LYS:HE2	2.19	0.43
1:N:248:LYS:CD	1:N:248:LYS:H	2.15	0.43
1:N:273:ARG:HH22	1:N:453:LEU:CD2	2.30	0.43
1:N:340:ILE:O	1:N:344:THR:HG21	2.19	0.43
1:O:248:LYS:HE2	1:O:513:ARG:HH12	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:236:GLN:H	1:P:265:LYS:HB2	1.83	0.43
1:Q:380:ASN:O	1:Q:381:SER:CB	2.67	0.43
1:R:35:PHE:CE1	1:R:321:ARG:NH1	2.86	0.43
1:R:248:LYS:HE2	1:R:513:ARG:HH12	1.84	0.43
1:R:575:GLN:O	1:R:579:MSE:CG	2.67	0.43
1:S:136:SER:N	1:S:137:PRO:HD3	2.33	0.43
1:T:245:SER:HG	1:T:247:PHE:HE1	1.65	0.43
1:T:35:PHE:C	1:T:37:ARG:N	2.70	0.43
1:T:372:TYR:CE2	1:W:348:LYS:HB2	2.53	0.43
1:T:387:GLN:HA	1:T:388:PRO:HD3	1.93	0.43
1:T:53:TYR:OH	1:W:329:LEU:HD21	2.19	0.43
1:V:164:LEU:HD22	1:V:169:ASP:OD1	2.18	0.43
1:V:174:THR:N	3:V:705:HOH:O	2.51	0.43
1:W:160:SER:O	1:W:161:ASN:ND2	2.45	0.43
1:W:174:THR:N	3:W:705:HOH:O	2.51	0.43
1:W:212:LEU:HD12	1:W:212:LEU:N	2.34	0.43
1:W:510:ILE:O	1:W:513:ARG:HD2	2.19	0.43
1:W:92:ASP:OD2	1:W:92:ASP:N	2.51	0.43
1:X:273:ARG:HH22	1:X:453:LEU:CD2	2.32	0.43
1:A:282:THR:HG23	1:A:287:LEU:CD1	2.43	0.43
1:A:35:PHE:HZ	1:A:321:ARG:NE	2.12	0.43
1:A:38:VAL:HG21	1:A:324:LYS:HD2	2.01	0.43
1:A:139:SER:CB	1:A:455:THR:CG2	2.80	0.43
1:C:198:ILE:HA	1:C:199:PRO:HD3	1.64	0.43
1:C:79:LEU:HD23	1:C:521:GLY:HA3	2.00	0.43
1:C:80:TYR:CZ	1:C:448:VAL:HG22	2.54	0.43
1:D:31:ASN:HD22	1:D:31:ASN:HA	1.62	0.43
1:D:391:TYR:N	1:D:391:TYR:CD2	2.87	0.43
1:E:79:LEU:HD23	1:E:521:GLY:HA3	2.00	0.43
1:E:94:LEU:O	1:E:94:LEU:HD23	2.19	0.43
1:F:252:LYS:HE3	1:F:252:LYS:O	2.19	0.43
1:F:391:TYR:N	1:F:391:TYR:CD2	2.87	0.43
1:F:79:LEU:N	1:F:519:ASP:O	2.51	0.43
1:G:251:ILE:HD11	1:G:275:ARG:NH2	2.34	0.43
1:G:378:ASP:O	1:G:381:SER:O	2.37	0.43
1:G:94:LEU:HD23	1:G:94:LEU:O	2.19	0.43
1:H:49:THR:O	1:H:50:THR:O	2.37	0.43
1:H:583:LYS:HA	1:H:584:PRO:HD3	1.85	0.43
1:I:49:THR:O	1:I:50:THR:O	2.37	0.43
1:I:583:LYS:HA	1:I:584:PRO:HD3	1.85	0.43
1:J:127:ARG:HA	1:J:299:PRO:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:274:ARG:HD3	1:J:296:GLU:O	2.19	0.43
1:J:34:PHE:HE1	1:J:324:LYS:HZ2	1.50	0.43
1:J:444:LEU:O	1:J:447:TYR:N	2.52	0.43
1:K:94:LEU:O	1:K:94:LEU:HD23	2.19	0.43
1:L:252:LYS:HE3	1:L:252:LYS:O	2.19	0.43
1:L:43:ASP:OD2	1:L:43:ASP:N	2.52	0.43
1:L:49:THR:O	1:L:50:THR:O	2.37	0.43
1:L:78:VAL:HG21	1:L:444:LEU:CD1	2.21	0.43
1:M:387:GLN:CB	1:O:390:ALA:CB	2.97	0.43
1:N:387:GLN:O	1:N:389:LEU:HG	2.19	0.43
1:N:510:ILE:O	1:N:513:ARG:HD2	2.19	0.43
1:N:528:LYS:NZ	1:N:560:LEU:HD21	2.33	0.43
1:M:387:GLN:HB3	1:O:390:ALA:CB	2.49	0.43
1:O:437:GLN:HA	1:O:440:MSE:HB2	2.01	0.43
1:O:528:LYS:HD2	1:O:560:LEU:HD21	2.01	0.43
1:P:158:TRP:H	1:P:158:TRP:HD1	1.66	0.43
1:P:164:LEU:HD22	1:P:169:ASP:OD1	2.18	0.43
1:Q:123:VAL:CG1	1:Q:304:PHE:CE1	3.02	0.43
1:Q:437:GLN:HA	1:Q:440:MSE:HB2	2.01	0.43
1:R:179:MSE:O	1:R:217:ILE:HD12	2.19	0.43
1:R:231:THR:CG2	1:R:249:ARG:HH11	2.31	0.43
1:S:190:LYS:HA	1:S:190:LYS:HE3	2.00	0.43
1:S:270:GLN:HA	1:S:270:GLN:OE1	2.18	0.43
1:S:92:ASP:N	1:S:92:ASP:OD2	2.52	0.43
1:T:236:GLN:H	1:T:265:LYS:CB	2.32	0.43
1:T:262:GLY:O	1:T:263:PHE:HB3	2.19	0.43
1:S:567:MSE:SE	1:T:576:LEU:HD13	2.67	0.43
1:U:171:ARG:O	1:U:224:GLU:HA	2.18	0.43
1:U:280:ILE:HD12	1:U:280:ILE:N	2.33	0.43
1:U:306:GLU:O	1:U:316:TYR:HA	2.19	0.43
1:U:430:VAL:HG13	3:X:719:HOH:O	2.17	0.43
1:W:298:ILE:HA	1:W:299:PRO:HD3	1.80	0.43
1:A:219:ILE:HD13	1:A:282:THR:HG22	2.00	0.42
1:A:34:PHE:CE1	1:A:324:LYS:NZ	2.72	0.42
1:A:79:LEU:HD23	1:A:521:GLY:HA3	2.00	0.42
1:A:538:LEU:HB3	1:A:551:LEU:HD13	2.00	0.42
1:A:579:MSE:CB	1:A:581:VAL:HG12	2.49	0.42
1:A:598:GLN:O	1:A:601:GLN:HB2	2.19	0.42
1:B:274:ARG:HD3	1:B:296:GLU:O	2.19	0.42
1:B:127:ARG:HA	1:B:299:PRO:O	2.18	0.42
1:C:123:VAL:HG13	1:C:304:PHE:CE1	2.54	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:212:LEU:N	1:C:212:LEU:HD12	2.34	0.42
1:C:252:LYS:HE3	1:C:252:LYS:O	2.19	0.42
1:D:229:LYS:HD2	1:D:270:GLN:HG3	2.01	0.42
1:D:123:VAL:HG13	1:D:304:PHE:CE1	2.54	0.42
1:D:38:VAL:HG21	1:D:324:LYS:HD2	2.01	0.42
1:D:80:TYR:CZ	1:D:448:VAL:HG22	2.54	0.42
1:E:219:ILE:HD13	1:E:282:THR:HG22	2.00	0.42
1:E:227:GLU:OE2	1:E:227:GLU:N	2.47	0.42
1:E:232:ALA:HB1	1:E:233:PHE:H	1.71	0.42
1:E:266:ILE:O	1:E:267:ALA:HB2	2.19	0.42
1:F:274:ARG:HD3	1:F:296:GLU:O	2.19	0.42
1:F:123:VAL:HG13	1:F:304:PHE:CE1	2.54	0.42
1:F:49:THR:O	1:F:50:THR:O	2.37	0.42
1:G:227:GLU:N	1:G:227:GLU:OE2	2.47	0.42
1:G:229:LYS:HD2	1:G:270:GLN:HG3	2.01	0.42
1:G:127:ARG:HA	1:G:299:PRO:O	2.18	0.42
1:G:49:THR:O	1:G:50:THR:C	2.56	0.42
1:G:538:LEU:HB3	1:G:551:LEU:HD13	2.00	0.42
1:H:71:MSE:HE3	1:H:115:VAL:HB	2.00	0.42
1:H:14:ARG:CA	1:H:14:ARG:NE	2.67	0.42
1:H:266:ILE:O	1:H:267:ALA:HB2	2.19	0.42
1:H:35:PHE:CZ	1:H:321:ARG:CZ	3.02	0.42
1:H:437:GLN:HA	1:H:440:MSE:HB2	2.01	0.42
1:I:15:PHE:HE2	1:I:19:TRP:HE1	1.66	0.42
1:J:212:LEU:N	1:J:212:LEU:HD12	2.34	0.42
1:J:123:VAL:HG13	1:J:304:PHE:CE1	2.54	0.42
1:K:212:LEU:HD12	1:K:212:LEU:N	2.34	0.42
1:K:229:LYS:HD2	1:K:270:GLN:HG3	2.01	0.42
1:K:123:VAL:HG13	1:K:304:PHE:CE1	2.54	0.42
1:K:79:LEU:HD23	1:K:521:GLY:HA3	2.00	0.42
1:K:99:ARG:NH1	1:K:530:GLN:HE21	2.13	0.42
1:L:24:GLU:CD	1:L:24:GLU:N	2.71	0.42
1:O:107:ALA:HA	1:O:146:ARG:HB3	2.00	0.42
1:O:147:GLU:HA	1:O:148:PRO:HD3	1.81	0.42
1:O:179:MSE:O	1:O:217:ILE:HD12	2.19	0.42
1:O:212:LEU:HD12	1:O:212:LEU:N	2.34	0.42
1:O:274:ARG:O	1:O:275:ARG:HD2	2.19	0.42
1:P:29:ALA:O	1:P:33:LEU:HG	2.19	0.42
1:Q:232:ALA:HB2	1:Q:269:ARG:O	2.19	0.42
1:Q:76:ILE:HD12	1:Q:433:ASP:OD1	2.18	0.42
1:R:282:THR:HG23	1:R:287:LEU:CD1	2.46	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:306:GLU:O	1:R:316:TYR:HA	2.19	0.42
1:R:330:ARG:O	1:R:334:MSE:HB2	2.19	0.42
1:S:276:VAL:CG2	1:S:293:ILE:HG23	2.48	0.42
1:T:444:LEU:HD13	1:T:444:LEU:N	2.34	0.42
1:U:118:GLN:OE1	1:U:303:VAL:HB	2.19	0.42
1:U:15:PHE:CE2	1:U:19:TRP:NE1	2.87	0.42
1:V:386:THR:CG2	1:V:389:LEU:HD21	2.49	0.42
1:W:245:SER:HG	1:W:247:PHE:HE1	1.65	0.42
1:W:575:GLN:O	1:W:579:MSE:CG	2.66	0.42
1:X:179:MSE:O	1:X:217:ILE:HD12	2.19	0.42
1:B:15:PHE:HE2	1:B:19:TRP:HE1	1.66	0.42
1:B:251:ILE:HD11	1:B:275:ARG:NH2	2.34	0.42
1:B:123:VAL:HG13	1:B:304:PHE:CE1	2.54	0.42
1:B:273:ARG:HH22	1:B:453:LEU:HD11	1.85	0.42
1:B:598:GLN:O	1:B:601:GLN:HB2	2.19	0.42
1:C:383:ASP:C	1:C:385:PRO:CD	2.86	0.42
1:C:43:ASP:OD2	1:C:43:ASP:N	2.52	0.42
1:C:94:LEU:HD23	1:C:94:LEU:O	2.19	0.42
1:D:212:LEU:HD12	1:D:212:LEU:N	2.34	0.42
1:D:252:LYS:O	1:D:252:LYS:HE3	2.19	0.42
1:D:444:LEU:O	1:D:447:TYR:N	2.52	0.42
1:D:94:LEU:O	1:D:94:LEU:HD23	2.19	0.42
1:E:24:GLU:CD	1:E:24:GLU:N	2.71	0.42
1:E:252:LYS:O	1:E:252:LYS:HE3	2.19	0.42
1:E:273:ARG:HD2	1:E:275:ARG:HD2	2.02	0.42
1:E:38:VAL:HG21	1:E:324:LYS:HD2	2.01	0.42
1:F:251:ILE:HD11	1:F:275:ARG:NH2	2.34	0.42
1:F:79:LEU:HD23	1:F:521:GLY:HA3	2.00	0.42
1:H:123:VAL:HG13	1:H:304:PHE:CE1	2.54	0.42
1:I:66:LYS:O	1:I:70:GLU:HG3	2.18	0.42
1:J:378:ASP:O	1:J:381:SER:O	2.37	0.42
1:J:43:ASP:N	1:J:43:ASP:OD2	2.52	0.42
1:K:443:ASP:C	1:K:446:THR:HG22	2.38	0.42
1:K:49:THR:O	1:K:50:THR:O	2.37	0.42
1:K:598:GLN:O	1:K:601:GLN:HB2	2.19	0.42
1:A:390:ALA:HB2	1:L:387:GLN:HG3	1.99	0.42
1:L:598:GLN:O	1:L:601:GLN:HB2	2.19	0.42
1:M:444:LEU:O	1:M:447:TYR:N	2.52	0.42
1:M:77:ASP:HB2	1:M:523:SER:HB2	2.02	0.42
1:N:92:ASP:N	1:N:92:ASP:OD2	2.53	0.42
1:O:344:THR:O	1:O:344:THR:CG2	2.67	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:383:ASP:C	1:O:385:PRO:HD3	2.39	0.42
1:P:387:GLN:HB3	1:Q:390:ALA:CB	2.49	0.42
1:Q:371:TYR:HE2	1:Q:373:LEU:HD21	1.84	0.42
1:R:266:ILE:O	1:R:267:ALA:HB2	2.19	0.42
1:R:29:ALA:O	1:R:33:LEU:HG	2.19	0.42
1:R:349:PRO:HG3	1:R:391:TYR:CE1	2.54	0.42
1:S:100:THR:HG22	1:S:138:THR:HG22	2.00	0.42
1:S:24:GLU:O	1:S:26:ARG:N	2.50	0.42
1:S:589:GLU:HA	1:S:592:TRP:HB2	2.00	0.42
1:T:179:MSE:O	1:T:217:ILE:HD12	2.20	0.42
1:T:273:ARG:CZ	1:T:275:ARG:HE	2.31	0.42
1:T:29:ALA:O	1:T:33:LEU:HG	2.18	0.42
1:T:376:ARG:HB2	1:W:352:TRP:CG	2.54	0.42
1:T:584:PRO:CG	1:T:593:LEU:HD12	2.49	0.42
1:U:57:PHE:CD1	1:U:57:PHE:N	2.87	0.42
1:V:265:LYS:O	1:V:266:ILE:HG12	2.19	0.42
1:V:344:THR:O	1:V:344:THR:CG2	2.66	0.42
1:W:236:GLN:H	1:W:265:LYS:HB2	1.83	0.42
1:W:29:ALA:O	1:W:33:LEU:HG	2.19	0.42
1:X:528:LYS:NZ	1:X:560:LEU:HD21	2.34	0.42
1:X:584:PRO:CG	1:X:593:LEU:HD12	2.49	0.42
2:Z:57:TYR:H	2:Z:63:ILE:H	1.65	0.42
1:A:25:ALA:O	1:A:29:ALA:CB	2.58	0.42
1:B:248:LYS:CD	1:B:248:LYS:H	2.16	0.42
1:B:528:LYS:HZ3	1:B:560:LEU:HD21	1.83	0.42
1:C:273:ARG:HD2	1:C:275:ARG:HD2	2.02	0.42
1:C:378:ASP:O	1:C:381:SER:O	2.37	0.42
1:D:171:ARG:HH21	1:E:182:ASN:HD22	1.65	0.42
1:D:273:ARG:HD2	1:D:275:ARG:HD2	2.01	0.42
1:D:35:PHE:HE1	1:D:321:ARG:NH1	2.13	0.42
1:E:383:ASP:C	1:E:385:PRO:HD3	2.39	0.42
1:F:26:ARG:NH2	1:F:30:LYS:HB2	2.28	0.42
1:F:38:VAL:HG21	1:F:324:LYS:HD2	2.01	0.42
1:F:273:ARG:HH22	1:F:453:LEU:HD11	1.85	0.42
1:G:15:PHE:HE2	1:G:19:TRP:HE1	1.66	0.42
1:G:246:TYR:HD2	1:G:511:ARG:CB	2.28	0.42
1:G:35:PHE:CZ	1:G:321:ARG:CZ	3.02	0.42
1:H:79:LEU:N	1:H:519:ASP:O	2.51	0.42
1:I:35:PHE:HE1	1:I:321:ARG:NH1	2.13	0.42
1:J:229:LYS:HD2	1:J:270:GLN:HG3	2.01	0.42
1:J:49:THR:O	1:J:50:THR:C	2.56	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:43:ASP:OD2	1:K:43:ASP:N	2.52	0.42
1:K:444:LEU:O	1:K:447:TYR:N	2.52	0.42
1:K:48:TYR:O	1:K:49:THR:CB	2.64	0.42
1:L:251:ILE:HD11	1:L:275:ARG:NH2	2.35	0.42
1:L:49:THR:O	1:L:50:THR:C	2.56	0.42
1:L:542:THR:HA	1:L:543:PRO:HD3	1.82	0.42
1:L:82:PRO:HB2	1:L:83:LYS:H	1.58	0.42
1:M:24:GLU:N	1:M:24:GLU:CD	2.73	0.42
1:M:407:ALA:HB1	1:N:334:MSE:HE1	2.00	0.42
1:O:280:ILE:HG22	1:O:287:LEU:HD13	2.02	0.42
1:O:584:PRO:CG	1:O:593:LEU:HD12	2.49	0.42
1:P:589:GLU:HA	1:P:592:TRP:HB2	2.01	0.42
1:Q:198:ILE:HA	1:Q:199:PRO:HD3	1.72	0.42
1:Q:431:ALA:HA	1:Q:434:THR:HG22	2.01	0.42
1:S:280:ILE:HG22	1:S:287:LEU:HD13	2.01	0.42
1:S:584:PRO:CG	1:S:593:LEU:HD12	2.49	0.42
1:T:101:ASP:HB3	1:T:138:THR:HG21	2.01	0.42
1:T:322:LEU:HD22	1:T:322:LEU:H	1.83	0.42
1:T:578:GLN:HG2	1:T:596:ALA:CB	2.49	0.42
1:V:15:PHE:CE2	1:V:19:TRP:NE1	2.88	0.42
1:W:191:TYR:O	1:W:288:LYS:HE2	2.20	0.42
1:X:191:TYR:O	1:X:288:LYS:HE2	2.19	0.42
1:A:274:ARG:HD3	1:A:296:GLU:O	2.19	0.42
1:A:528:LYS:CD	1:A:560:LEU:HD21	2.50	0.42
1:B:378:ASP:O	1:B:381:SER:O	2.37	0.42
1:B:444:LEU:HD23	1:B:518:THR:OG1	2.18	0.42
1:C:127:ARG:HA	1:C:299:PRO:O	2.18	0.42
1:C:35:PHE:CZ	1:C:321:ARG:CZ	3.02	0.42
1:C:47:GLN:CD	1:C:47:GLN:N	2.72	0.42
1:C:579:MSE:CB	1:C:581:VAL:HG12	2.49	0.42
1:E:369:TYR:HA	1:E:370:PRO:HD3	1.84	0.42
1:E:444:LEU:O	1:E:447:TYR:N	2.52	0.42
1:G:123:VAL:HG13	1:G:304:PHE:CE1	2.54	0.42
1:G:208:VAL:HB	1:G:209:PHE:H	1.69	0.42
1:G:78:VAL:CG2	1:G:444:LEU:HD21	2.46	0.42
1:G:552:LEU:O	1:G:556:TYR:HD2	2.03	0.42
1:G:598:GLN:O	1:G:601:GLN:HB2	2.19	0.42
1:H:251:ILE:HD11	1:H:275:ARG:NH2	2.34	0.42
1:H:528:LYS:CD	1:H:560:LEU:HD21	2.50	0.42
1:H:598:GLN:O	1:H:601:GLN:HB2	2.19	0.42
1:J:251:ILE:HD11	1:J:275:ARG:NH2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:598:GLN:O	1:J:601:GLN:HB2	2.19	0.42
1:J:71:MSE:HE3	1:J:115:VAL:HB	2.01	0.42
1:K:434:THR:HG23	1:K:435:VAL:N	2.35	0.42
1:K:49:THR:O	1:K:50:THR:C	2.56	0.42
1:J:556:TYR:OH	1:K:542:THR:HG21	2.20	0.42
1:L:579:MSE:CB	1:L:581:VAL:HG12	2.50	0.42
1:N:24:GLU:HG3	1:N:313:LYS:HE2	2.00	0.42
1:N:158:TRP:HH2	1:N:302:PRO:HG3	1.80	0.42
1:N:589:GLU:HA	1:N:592:TRP:HB2	2.01	0.42
1:O:123:VAL:HG13	1:O:304:PHE:CE1	2.54	0.42
1:P:444:LEU:O	1:P:447:TYR:N	2.52	0.42
1:Q:301:VAL:HA	1:Q:302:PRO:HD3	1.79	0.42
1:R:584:PRO:CG	1:R:593:LEU:HD12	2.50	0.42
1:T:437:GLN:HA	1:T:440:MSE:HB2	2.02	0.42
1:T:528:LYS:NZ	1:T:560:LEU:HD21	2.35	0.42
1:U:190:LYS:HA	1:U:190:LYS:HE3	2.00	0.42
1:V:575:GLN:O	1:V:579:MSE:CG	2.66	0.42
1:W:554:LEU:HD12	1:W:557:PHE:CD2	2.53	0.42
1:X:227:GLU:HG2	1:X:227:GLU:O	2.20	0.42
1:X:26:ARG:O	1:X:27:ARG:C	2.56	0.42
1:A:444:LEU:O	1:A:447:TYR:N	2.52	0.42
1:B:266:ILE:O	1:B:267:ALA:HB2	2.19	0.42
1:B:579:MSE:CB	1:B:581:VAL:HG12	2.50	0.42
1:B:94:LEU:HD23	1:B:94:LEU:O	2.19	0.42
1:C:391:TYR:N	1:C:391:TYR:CD2	2.87	0.42
1:D:363:TYR:HE1	1:F:350:PHE:CE1	2.35	0.42
1:E:49:THR:O	1:E:50:THR:O	2.37	0.42
1:G:80:TYR:CZ	1:G:448:VAL:HG22	2.54	0.42
1:G:93:VAL:O	1:G:97:MSE:HG3	2.20	0.42
1:H:229:LYS:HD2	1:H:270:GLN:HG3	2.01	0.42
1:H:552:LEU:O	1:H:556:TYR:HD2	2.03	0.42
1:H:68:VAL:HG22	1:H:119:ILE:HD12	2.02	0.42
1:H:94:LEU:O	1:H:94:LEU:HD23	2.19	0.42
1:I:246:TYR:HD2	1:I:511:ARG:CB	2.28	0.42
1:I:383:ASP:C	1:I:385:PRO:HD3	2.39	0.42
1:I:47:GLN:N	1:I:47:GLN:CD	2.72	0.42
1:I:552:LEU:O	1:I:556:TYR:HD2	2.03	0.42
1:J:24:GLU:N	1:J:24:GLU:CD	2.71	0.42
1:J:99:ARG:NH1	1:J:530:GLN:HE21	2.13	0.42
1:J:528:LYS:CD	1:J:560:LEU:HD21	2.50	0.42
1:L:434:THR:HG23	1:L:435:VAL:N	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:437:GLN:HA	1:L:440:MSE:HB2	2.01	0.42
1:L:94:LEU:O	1:L:94:LEU:HD23	2.19	0.42
1:M:212:LEU:N	1:M:212:LEU:HD12	2.34	0.42
1:M:35:PHE:HZ	1:M:321:ARG:NE	2.12	0.42
1:M:35:PHE:C	1:M:37:ARG:N	2.73	0.42
1:O:265:LYS:O	1:O:266:ILE:HG12	2.19	0.42
3:M:718:HOH:O	1:O:438:LEU:HD22	2.19	0.42
1:Q:160:SER:O	1:Q:161:ASN:ND2	2.44	0.42
1:Q:24:GLU:O	1:Q:26:ARG:N	2.50	0.42
1:Q:528:LYS:NZ	1:Q:560:LEU:HD21	2.34	0.42
1:R:33:LEU:HD12	1:R:34:PHE:N	2.34	0.42
1:T:34:PHE:O	1:T:37:ARG:HB2	2.19	0.42
1:T:79:LEU:N	1:T:519:ASP:O	2.53	0.42
1:U:101:ASP:HB3	1:U:138:THR:HG21	2.02	0.42
1:U:236:GLN:HG3	1:U:265:LYS:HG2	2.00	0.42
1:U:443:ASP:O	1:U:446:THR:HG22	2.20	0.42
1:U:61:ARG:CB	1:U:62:PRO:HD3	2.49	0.42
1:V:158:TRP:HH2	1:V:302:PRO:HG3	1.81	0.42
1:V:306:GLU:O	1:V:316:TYR:HA	2.19	0.42
1:W:179:MSE:O	1:W:217:ILE:HD12	2.19	0.42
1:W:306:GLU:O	1:W:316:TYR:HA	2.20	0.42
1:W:343:ARG:HG2	1:W:343:ARG:H	1.56	0.42
1:X:280:ILE:HD12	1:X:280:ILE:N	2.34	0.42
1:A:229:LYS:HD2	1:A:270:GLN:HG3	2.01	0.42
1:B:43:ASP:OD2	1:B:43:ASP:N	2.52	0.42
1:B:443:ASP:C	1:B:446:THR:HG22	2.38	0.42
1:B:49:THR:O	1:B:50:THR:O	2.37	0.42
1:C:24:GLU:C	1:C:26:ARG:N	2.73	0.42
1:C:444:LEU:O	1:C:447:TYR:N	2.52	0.42
1:D:93:VAL:O	1:D:97:MSE:HG3	2.20	0.42
1:E:123:VAL:HG13	1:E:304:PHE:CE1	2.54	0.42
1:E:71:MSE:HE3	1:E:115:VAL:HB	2.01	0.42
1:F:80:TYR:CZ	1:F:448:VAL:HG22	2.54	0.42
1:F:93:VAL:O	1:F:97:MSE:HG3	2.20	0.42
1:G:444:LEU:O	1:G:447:TYR:N	2.52	0.42
1:H:93:VAL:O	1:H:97:MSE:HG3	2.20	0.42
1:I:434:THR:HG23	1:I:435:VAL:N	2.35	0.42
1:J:273:ARG:HD2	1:J:275:ARG:HD2	2.02	0.42
1:K:127:ARG:HA	1:K:299:PRO:O	2.19	0.42
1:M:383:ASP:C	1:M:385:PRO:HD3	2.40	0.42
1:M:40:GLN:HE21	1:M:40:GLN:HB2	1.57	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:280:ILE:HG22	1:N:287:LEU:HD13	2.02	0.42
1:N:301:VAL:HG23	1:N:439:ASN:HB3	2.01	0.42
1:O:92:ASP:N	1:O:92:ASP:OD2	2.52	0.42
1:P:528:LYS:NZ	1:P:560:LEU:HD21	2.34	0.42
1:Q:334:MSE:HE1	1:R:407:ALA:HB1	2.01	0.42
1:S:212:LEU:HD12	1:S:212:LEU:N	2.34	0.42
1:S:248:LYS:HE2	1:S:513:ARG:HH12	1.85	0.42
1:S:248:LYS:CG	1:S:511:ARG:HH11	2.31	0.42
1:S:554:LEU:HD21	1:U:564:GLY:CA	2.39	0.42
1:S:575:GLN:O	1:S:579:MSE:CG	2.66	0.42
1:T:503:GLU:HB3	1:T:508:ASN:HB3	2.02	0.42
1:T:92:ASP:N	1:T:92:ASP:OD2	2.52	0.42
1:U:115:VAL:HA	1:U:118:GLN:HB3	2.02	0.42
1:U:212:LEU:N	1:U:212:LEU:HD12	2.34	0.42
1:U:344:THR:CG2	1:U:344:THR:O	2.68	0.42
1:U:369:TYR:HA	1:U:370:PRO:HD3	1.83	0.42
1:V:123:VAL:HG22	1:V:316:TYR:HE2	1.83	0.42
1:V:24:GLU:HG3	1:V:313:LYS:HE2	2.00	0.42
1:V:528:LYS:NZ	1:V:560:LEU:HD21	2.34	0.42
1:W:41:TRP:HE3	1:W:42:ASP:HB3	1.82	0.42
1:X:270:GLN:OE1	1:X:270:GLN:HA	2.19	0.42
1:X:92:ASP:N	1:X:92:ASP:OD2	2.52	0.42
1:A:248:LYS:H	1:A:248:LYS:CD	2.16	0.42
1:A:251:ILE:HD11	1:A:275:ARG:NH2	2.35	0.42
1:A:123:VAL:HG13	1:A:304:PHE:CE1	2.54	0.42
1:B:332:MSE:SE	2:Y:141:MET:HA	2.69	0.42
1:B:430:VAL:HG12	1:B:431:ALA:N	2.35	0.42
1:B:528:LYS:CD	1:B:560:LEU:HD21	2.50	0.42
1:B:567:MSE:HE2	1:C:554:LEU:HD22	2.00	0.42
1:C:229:LYS:HD2	1:C:270:GLN:HG3	2.01	0.42
1:C:301:VAL:HG23	1:C:439:ASN:HB3	2.02	0.42
1:C:457:MSE:O	1:C:457:MSE:CG	2.63	0.42
1:C:598:GLN:O	1:C:601:GLN:HB2	2.19	0.42
1:D:24:GLU:C	1:D:26:ARG:N	2.73	0.42
1:E:34:PHE:CE1	1:E:324:LYS:NZ	2.72	0.42
1:E:579:MSE:CB	1:E:581:VAL:HG12	2.50	0.42
1:E:583:LYS:HA	1:E:584:PRO:HD3	1.85	0.42
1:E:80:TYR:CZ	1:E:448:VAL:HG22	2.54	0.42
1:F:248:LYS:HZ2	1:F:251:ILE:HD12	1.85	0.42
1:F:24:GLU:C	1:F:26:ARG:N	2.73	0.42
1:F:528:LYS:CD	1:F:560:LEU:HD21	2.50	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:561:ASP:CB	1:F:89:ASP:HA	2.43	0.42
1:G:68:VAL:HG22	1:G:119:ILE:HD12	2.02	0.42
1:H:227:GLU:OE2	1:H:227:GLU:N	2.47	0.42
1:H:80:TYR:CZ	1:H:448:VAL:HG22	2.54	0.42
1:I:598:GLN:O	1:I:601:GLN:HB2	2.19	0.42
1:J:437:GLN:HA	1:J:440:MSE:HB2	2.00	0.42
1:K:252:LYS:O	1:K:252:LYS:HE3	2.19	0.42
1:K:35:PHE:HZ	1:K:321:ARG:NE	2.12	0.42
1:K:68:VAL:HG22	1:K:119:ILE:HD12	2.02	0.42
1:L:123:VAL:HG13	1:L:304:PHE:CE1	2.54	0.42
1:L:48:TYR:O	1:L:49:THR:CB	2.64	0.42
1:M:179:MSE:O	1:M:217:ILE:HD12	2.20	0.42
1:N:409:THR:O	1:N:413:LYS:HG2	2.20	0.42
1:O:293:ILE:HG12	1:O:294:ALA:H	1.84	0.42
1:P:262:GLY:O	1:P:263:PHE:HB3	2.20	0.42
1:P:383:ASP:C	1:P:385:PRO:HD3	2.40	0.42
1:P:77:ASP:HB2	1:P:523:SER:HB2	2.02	0.42
1:Q:376:ARG:HB2	1:R:352:TRP:CD1	2.55	0.42
1:Q:451:ASP:O	1:Q:453:LEU:N	2.53	0.42
1:R:212:LEU:HD12	1:R:212:LEU:N	2.35	0.42
1:R:394:ASN:HA	1:R:395:PRO:HD3	1.93	0.42
1:R:528:LYS:HD2	1:R:560:LEU:HD21	2.02	0.42
1:R:589:GLU:HA	1:R:592:TRP:HB2	2.00	0.42
1:R:80:TYR:OH	1:R:444:LEU:HD12	2.19	0.42
1:S:227:GLU:HG2	1:S:227:GLU:O	2.18	0.42
1:S:383:ASP:C	1:S:385:PRO:HD3	2.40	0.42
1:T:306:GLU:O	1:T:316:TYR:HA	2.19	0.42
1:T:301:VAL:HG23	1:T:439:ASN:HB3	2.01	0.42
1:U:191:TYR:O	1:U:288:LYS:HE2	2.19	0.42
1:U:234:ILE:HG12	1:U:267:ALA:O	2.20	0.42
1:U:444:LEU:N	1:U:444:LEU:HD13	2.34	0.42
1:V:584:PRO:CG	1:V:593:LEU:HD12	2.50	0.42
1:W:248:LYS:HE2	1:W:513:ARG:HH12	1.84	0.42
1:W:340:ILE:O	1:W:344:THR:HG21	2.20	0.42
1:W:451:ASP:O	1:W:453:LEU:N	2.52	0.42
1:X:101:ASP:HB3	1:X:138:THR:HG21	2.01	0.42
1:X:306:GLU:O	1:X:316:TYR:HA	2.20	0.42
1:X:451:ASP:C	1:X:453:LEU:H	2.20	0.42
1:X:248:LYS:HE2	1:X:513:ARG:HH12	1.85	0.42
1:R:564:GLY:HA3	1:X:535:ILE:HD11	2.00	0.42
1:X:61:ARG:CB	1:X:62:PRO:HD3	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Z:104:TYR:CD1	2:Z:104:TYR:N	2.85	0.42
1:A:37:ARG:HA	1:A:37:ARG:HD2	1.79	0.42
1:C:147:GLU:HA	1:C:148:PRO:HD3	1.86	0.42
1:D:528:LYS:CD	1:D:560:LEU:HD21	2.50	0.42
1:E:212:LEU:HD12	1:E:212:LEU:N	2.34	0.42
1:F:209:PHE:N	1:F:210:PRO:CD	2.82	0.42
1:F:552:LEU:O	1:F:556:TYR:HD2	2.03	0.42
1:F:71:MSE:HE3	1:F:115:VAL:HB	2.00	0.42
1:G:212:LEU:N	1:G:212:LEU:HD12	2.34	0.42
1:G:165:MSE:HE1	1:G:435:VAL:HB	2.02	0.42
1:G:79:LEU:HD23	1:G:521:GLY:HA3	2.00	0.42
1:H:252:LYS:O	1:H:252:LYS:HE3	2.19	0.42
1:H:386:THR:HG21	1:H:389:LEU:HD21	2.02	0.42
1:I:252:LYS:HE3	1:I:252:LYS:O	2.19	0.42
1:I:229:LYS:HG2	1:I:272:LYS:CG	2.50	0.42
1:I:35:PHE:HZ	1:I:321:ARG:NE	2.12	0.42
1:I:369:TYR:HA	1:I:370:PRO:HD3	1.84	0.42
1:I:386:THR:HG21	1:I:389:LEU:HD21	2.02	0.42
1:I:444:LEU:O	1:I:447:TYR:N	2.52	0.42
1:J:386:THR:HG21	1:J:389:LEU:HD21	2.02	0.42
1:J:434:THR:HG23	1:J:435:VAL:N	2.35	0.42
1:K:426:ASN:O	1:K:427:GLY:C	2.58	0.42
1:L:198:ILE:HA	1:L:199:PRO:HD3	1.64	0.42
1:M:15:PHE:CE2	1:M:19:TRP:NE1	2.88	0.42
1:M:262:GLY:O	1:M:263:PHE:HB3	2.20	0.42
1:M:578:GLN:HG2	1:M:596:ALA:CB	2.50	0.42
1:N:431:ALA:HA	1:N:434:THR:HG22	2.01	0.42
1:O:227:GLU:HG2	1:O:227:GLU:O	2.20	0.42
1:O:41:TRP:HE3	1:O:42:ASP:HB3	1.83	0.42
1:O:431:ALA:HA	1:O:434:THR:HG22	2.02	0.42
1:P:212:LEU:N	1:P:212:LEU:HD12	2.34	0.42
1:P:387:GLN:O	1:P:389:LEU:HG	2.20	0.42
1:P:443:ASP:O	1:P:446:THR:HG22	2.20	0.42
1:Q:384:LEU:HD22	1:Q:384:LEU:N	2.29	0.42
1:Q:528:LYS:HD2	1:Q:560:LEU:HD21	2.02	0.42
1:R:24:GLU:HG3	1:R:313:LYS:HE2	2.01	0.42
1:R:158:TRP:HH2	1:R:302:PRO:HG3	1.84	0.42
1:Q:372:TYR:CE2	1:R:348:LYS:HB2	2.55	0.42
1:S:265:LYS:O	1:S:266:ILE:HG12	2.20	0.42
1:S:27:ARG:HH21	1:U:41:TRP:HE1	1.67	0.42
1:S:451:ASP:O	1:S:453:LEU:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:528:LYS:NZ	1:S:560:LEU:HD21	2.35	0.42
1:T:15:PHE:CE2	1:T:19:TRP:NE1	2.88	0.42
1:T:265:LYS:O	1:T:266:ILE:HG12	2.19	0.42
1:T:431:ALA:HA	1:T:434:THR:HG22	2.01	0.42
1:T:458:ARG:HA	1:T:458:ARG:HD3	1.84	0.42
1:U:503:GLU:HB3	1:U:508:ASN:HB3	2.02	0.42
1:U:528:LYS:HD2	1:U:560:LEU:HD21	2.02	0.42
1:V:158:TRP:HD1	1:V:158:TRP:H	1.66	0.42
1:V:270:GLN:OE1	1:V:270:GLN:HA	2.20	0.42
1:V:438:LEU:HD12	1:V:441:ARG:NH1	2.35	0.42
1:V:443:ASP:O	1:V:446:THR:HG22	2.20	0.42
1:V:542:THR:HA	1:V:543:PRO:HD3	1.87	0.42
1:W:437:GLN:HA	1:W:440:MSE:HB2	2.01	0.42
1:X:115:VAL:HA	1:X:118:GLN:HB3	2.02	0.42
1:X:510:ILE:HG12	1:X:511:ARG:H	1.84	0.42
1:A:212:LEU:N	1:A:212:LEU:HD12	2.34	0.42
1:B:24:GLU:C	1:B:26:ARG:N	2.73	0.42
1:C:386:THR:HG21	1:C:389:LEU:HD21	2.02	0.42
1:C:434:THR:HG23	1:C:435:VAL:N	2.35	0.42
1:C:552:LEU:O	1:C:556:TYR:HD2	2.03	0.42
1:D:282:THR:HG23	1:D:287:LEU:CD1	2.43	0.42
1:D:165:MSE:HE1	1:D:435:VAL:HB	2.02	0.42
1:D:47:GLN:CD	1:D:47:GLN:N	2.72	0.42
1:D:49:THR:O	1:D:50:THR:O	2.37	0.42
1:E:68:VAL:HG22	1:E:119:ILE:HD12	2.02	0.42
1:E:229:LYS:HD2	1:E:270:GLN:HG3	2.01	0.42
1:E:273:ARG:HH22	1:E:453:LEU:HD11	1.85	0.42
1:E:35:PHE:CZ	1:E:321:ARG:CZ	3.02	0.42
1:E:378:ASP:O	1:E:381:SER:O	2.37	0.42
1:E:552:LEU:O	1:E:556:TYR:HD2	2.03	0.42
1:F:130:THR:HG23	1:F:450:GLN:NE2	2.35	0.42
1:G:528:LYS:CD	1:G:560:LEU:HD21	2.50	0.42
1:H:130:THR:HG23	1:H:450:GLN:NE2	2.35	0.42
1:H:165:MSE:HE1	1:H:435:VAL:HB	2.02	0.42
1:I:273:ARG:HH22	1:I:453:LEU:HD11	1.85	0.42
1:I:93:VAL:O	1:I:97:MSE:HG3	2.20	0.42
1:K:209:PHE:N	1:K:210:PRO:CD	2.82	0.42
1:K:229:LYS:HG2	1:K:272:LYS:CG	2.50	0.42
1:K:38:VAL:HG21	1:K:324:LYS:HD2	2.01	0.42
1:L:212:LEU:N	1:L:212:LEU:HD12	2.34	0.42
1:M:306:GLU:O	1:M:316:TYR:HA	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:301:VAL:HG23	1:M:439:ASN:HB3	2.00	0.42
1:M:92:ASP:N	1:M:92:ASP:OD2	2.53	0.42
1:N:228:LYS:O	1:N:229:LYS:HB3	2.20	0.42
1:N:301:VAL:HA	1:N:302:PRO:HD3	1.77	0.42
1:N:457:MSE:O	1:N:458:ARG:CD	2.68	0.42
1:O:511:ARG:HA	1:O:513:ARG:CD	2.45	0.42
1:P:24:GLU:O	1:P:26:ARG:N	2.51	0.42
1:P:554:LEU:HD12	1:P:557:PHE:CD2	2.52	0.42
1:Q:443:ASP:O	1:Q:446:THR:HG22	2.19	0.42
1:Q:248:LYS:HE2	1:Q:513:ARG:HH12	1.84	0.42
1:R:160:SER:O	1:R:161:ASN:ND2	2.46	0.42
1:R:15:PHE:CE2	1:R:19:TRP:NE1	2.88	0.42
1:S:61:ARG:CB	1:S:62:PRO:HD3	2.49	0.42
1:T:40:GLN:HB2	1:T:40:GLN:HE21	1.58	0.42
1:T:591:GLN:HA	1:T:594:VAL:CG2	2.50	0.42
1:V:123:VAL:HG13	1:V:304:PHE:CE1	2.55	0.42
1:V:35:PHE:CE1	1:V:321:ARG:NH1	2.86	0.42
1:V:301:VAL:HG23	1:V:439:ASN:HB3	2.01	0.42
1:V:578:GLN:HG2	1:V:596:ALA:CB	2.50	0.42
1:W:107:ALA:HA	1:W:146:ARG:HB3	2.01	0.42
3:T:719:HOH:O	1:W:430:VAL:HG13	2.18	0.42
1:X:311:GLU:O	1:X:312:ASP:HB2	2.20	0.42
1:X:344:THR:CG2	1:X:344:THR:O	2.68	0.42
2:Y:101:ALA:N	2:Y:102:PRO:CD	2.82	0.42
1:A:130:THR:HG23	1:A:450:GLN:NE2	2.35	0.42
1:A:430:VAL:HG12	1:A:431:ALA:N	2.35	0.42
1:A:68:VAL:HG22	1:A:119:ILE:HD12	2.02	0.42
1:A:93:VAL:O	1:A:97:MSE:HG3	2.20	0.42
1:B:282:THR:HG23	1:B:287:LEU:CD1	2.43	0.42
1:C:229:LYS:HG2	1:C:272:LYS:CG	2.50	0.42
1:C:274:ARG:HD3	1:C:296:GLU:O	2.19	0.42
1:C:68:VAL:HG22	1:C:119:ILE:HD12	2.02	0.42
1:D:130:THR:HG23	1:D:450:GLN:NE2	2.35	0.42
1:D:274:ARG:HD3	1:D:296:GLU:O	2.19	0.42
1:D:301:VAL:HG23	1:D:439:ASN:HB3	2.02	0.42
1:D:248:LYS:HZ1	1:D:513:ARG:HH12	1.66	0.42
1:E:251:ILE:HD11	1:E:275:ARG:NH2	2.34	0.42
1:E:274:ARG:HD3	1:E:296:GLU:O	2.19	0.42
1:F:229:LYS:HG2	1:F:272:LYS:CG	2.50	0.42
1:F:386:THR:HG21	1:F:389:LEU:HD21	2.02	0.42
1:G:130:THR:HG23	1:G:450:GLN:NE2	2.35	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:265:LYS:HD2	1:G:265:LYS:HA	1.96	0.42
1:G:437:GLN:HA	1:G:440:MSE:HB2	2.01	0.42
1:H:274:ARG:HD3	1:H:296:GLU:O	2.19	0.42
1:H:434:THR:HG23	1:H:435:VAL:N	2.35	0.42
1:H:451:ASP:O	1:H:456:ALA:N	2.41	0.42
1:H:48:TYR:O	1:H:49:THR:CB	2.64	0.42
1:I:376:ARG:HB2	1:J:352:TRP:CD2	2.55	0.42
1:I:528:LYS:CD	1:I:560:LEU:HD21	2.50	0.42
1:J:35:PHE:HE1	1:J:321:ARG:NH1	2.13	0.42
1:J:301:VAL:HG23	1:J:439:ASN:HB3	2.02	0.42
1:J:567:MSE:SE	1:K:576:LEU:HD13	2.69	0.42
1:L:368:ASP:O	2:Z:134:ARG:HG3	2.20	0.42
1:L:426:ASN:O	1:L:427:GLY:C	2.58	0.42
1:L:528:LYS:CD	1:L:560:LEU:HD21	2.50	0.42
1:L:93:VAL:O	1:L:97:MSE:HG3	2.20	0.42
1:M:160:SER:O	1:M:161:ASN:ND2	2.45	0.42
1:M:431:ALA:HA	1:M:434:THR:HG22	2.02	0.42
1:M:76:ILE:HD12	1:M:433:ASP:OD1	2.20	0.42
1:N:265:LYS:O	1:N:266:ILE:HG12	2.20	0.42
1:N:280:ILE:HD12	1:N:280:ILE:N	2.35	0.42
1:N:344:THR:CG2	1:N:344:THR:O	2.67	0.42
1:O:270:GLN:HA	1:O:270:GLN:OE1	2.20	0.42
1:M:387:GLN:HB2	1:O:390:ALA:HB2	2.01	0.42
1:P:115:VAL:HA	1:P:118:GLN:HB3	2.02	0.42
1:P:266:ILE:O	1:P:267:ALA:HB2	2.18	0.42
1:P:591:GLN:HA	1:P:594:VAL:CG2	2.50	0.42
1:Q:266:ILE:HD13	1:Q:266:ILE:HA	1.89	0.42
1:Q:330:ARG:O	1:Q:334:MSE:HB2	2.20	0.42
1:R:232:ALA:HB2	1:R:269:ARG:O	2.19	0.42
1:S:219:ILE:HG13	1:S:220:ALA:N	2.35	0.42
1:S:306:GLU:O	1:S:316:TYR:HA	2.20	0.42
1:S:330:ARG:HD2	1:S:409:THR:CG2	2.41	0.42
1:T:190:LYS:HE3	1:T:190:LYS:HA	2.00	0.42
1:T:191:TYR:O	1:T:288:LYS:HE2	2.20	0.42
1:T:383:ASP:C	1:T:385:PRO:HD3	2.40	0.42
1:U:24:GLU:CD	1:U:24:GLU:N	2.73	0.42
1:U:270:GLN:HA	1:U:270:GLN:OE1	2.19	0.42
1:V:212:LEU:HD12	1:V:212:LEU:N	2.35	0.42
1:V:236:GLN:H	1:V:265:LYS:CB	2.33	0.42
1:V:503:GLU:HB3	1:V:508:ASN:HB3	2.02	0.42
1:V:76:ILE:HD12	1:V:433:ASP:OD1	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:280:ILE:HG22	1:W:287:LEU:HD13	2.01	0.42
1:W:528:LYS:HD2	1:W:560:LEU:HD21	2.01	0.42
1:W:542:THR:HA	1:W:543:PRO:HD3	1.87	0.42
1:X:252:LYS:HZ1	1:X:256:ASP:HB3	1.83	0.42
1:X:380:ASN:O	1:X:381:SER:CB	2.68	0.42
1:X:78:VAL:CG1	1:X:79:LEU:H	2.33	0.42
2:Z:101:ALA:N	2:Z:102:PRO:CD	2.82	0.42
1:A:598:GLN:HB2	1:A:601:GLN:HB3	2.02	0.41
1:B:130:THR:HG23	1:B:450:GLN:NE2	2.35	0.41
1:B:80:TYR:CZ	1:B:448:VAL:HG22	2.54	0.41
1:C:35:PHE:HZ	1:C:321:ARG:NE	2.12	0.41
1:C:49:THR:O	1:C:50:THR:O	2.37	0.41
1:D:68:VAL:HG22	1:D:119:ILE:HD12	2.02	0.41
1:D:229:LYS:HG2	1:D:272:LYS:CG	2.50	0.41
1:D:426:ASN:O	1:D:427:GLY:C	2.58	0.41
1:D:437:GLN:HA	1:D:440:MSE:HB2	2.01	0.41
1:E:430:VAL:HG12	1:E:431:ALA:N	2.35	0.41
1:E:434:THR:HG23	1:E:435:VAL:N	2.35	0.41
1:C:568:MSE:HG3	1:E:551:LEU:CD2	2.50	0.41
1:F:198:ILE:HA	1:F:199:PRO:HD3	1.64	0.41
1:F:273:ARG:HD2	1:F:275:ARG:HD2	2.01	0.41
1:G:209:PHE:N	1:G:210:PRO:CD	2.82	0.41
1:G:229:LYS:HG2	1:G:272:LYS:CG	2.50	0.41
1:G:38:VAL:HG21	1:G:324:LYS:HD2	2.01	0.41
1:G:434:THR:HG23	1:G:435:VAL:N	2.35	0.41
1:G:43:ASP:OD2	1:G:43:ASP:N	2.52	0.41
1:H:273:ARG:HH22	1:H:453:LEU:HD11	1.85	0.41
1:I:15:PHE:HE2	1:I:19:TRP:NE1	2.18	0.41
1:I:251:ILE:HD11	1:I:275:ARG:NH2	2.35	0.41
1:I:274:ARG:HD3	1:I:296:GLU:O	2.19	0.41
1:I:78:VAL:HG21	1:I:444:LEU:CD1	2.21	0.41
1:I:99:ARG:HH12	1:I:530:GLN:NE2	2.14	0.41
1:J:252:LYS:O	1:J:252:LYS:HE3	2.19	0.41
1:J:165:MSE:HE1	1:J:435:VAL:HB	2.02	0.41
1:J:93:VAL:O	1:J:97:MSE:HG3	2.20	0.41
1:K:127:ARG:HG2	1:K:147:GLU:HB2	2.02	0.41
1:K:130:THR:HG23	1:K:450:GLN:NE2	2.35	0.41
1:K:430:VAL:HG12	1:K:431:ALA:N	2.35	0.41
1:K:437:GLN:HA	1:K:440:MSE:HB2	2.00	0.41
1:K:528:LYS:CD	1:K:560:LEU:HD21	2.50	0.41
1:L:127:ARG:HG2	1:L:147:GLU:HB2	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:165:MSE:HE1	1:L:435:VAL:HB	2.02	0.41
1:L:229:LYS:HG2	1:L:272:LYS:CG	2.50	0.41
1:L:273:ARG:HD2	1:L:275:ARG:HD2	2.02	0.41
1:L:282:THR:HG23	1:L:287:LEU:CD1	2.43	0.41
1:M:266:ILE:O	1:M:267:ALA:HB2	2.19	0.41
1:M:26:ARG:O	1:M:27:ARG:C	2.58	0.41
1:M:458:ARG:HA	1:M:458:ARG:HD3	1.83	0.41
1:M:575:GLN:O	1:M:579:MSE:CG	2.66	0.41
1:N:236:GLN:H	1:N:265:LYS:CB	2.33	0.41
1:N:57:PHE:N	1:N:57:PHE:CD1	2.88	0.41
1:O:24:GLU:HG3	1:O:313:LYS:HE2	2.01	0.41
1:O:298:ILE:HA	1:O:299:PRO:HD3	1.79	0.41
1:O:528:LYS:NZ	1:O:560:LEU:HD21	2.35	0.41
1:P:15:PHE:CE2	1:P:19:TRP:NE1	2.88	0.41
1:Q:115:VAL:HA	1:Q:118:GLN:HB3	2.02	0.41
1:Q:147:GLU:HA	1:Q:148:PRO:HD3	1.81	0.41
1:Q:554:LEU:O	1:Q:557:PHE:HB3	2.20	0.41
1:R:101:ASP:HB3	1:R:138:THR:HG21	2.01	0.41
1:R:301:VAL:HG23	1:R:439:ASN:HB3	2.02	0.41
1:R:35:PHE:HZ	1:R:321:ARG:NE	2.13	0.41
1:R:380:ASN:O	1:R:381:SER:CB	2.68	0.41
1:R:384:LEU:HD22	1:R:384:LEU:N	2.33	0.41
1:S:24:GLU:HG3	1:S:313:LYS:HE2	2.02	0.41
1:S:443:ASP:O	1:S:446:THR:HG22	2.20	0.41
1:T:280:ILE:HD12	1:T:280:ILE:N	2.35	0.41
1:S:334:MSE:HE1	1:T:407:ALA:HB1	2.02	0.41
1:S:27:ARG:NH2	1:U:41:TRP:HE1	2.18	0.41
1:U:511:ARG:HA	1:U:513:ARG:CD	2.47	0.41
1:U:528:LYS:NZ	1:U:560:LEU:HD21	2.34	0.41
1:U:554:LEU:HD21	1:X:564:GLY:CA	2.46	0.41
1:U:579:MSE:HB2	1:U:581:VAL:HG12	2.02	0.41
1:U:92:ASP:N	1:U:92:ASP:OD2	2.53	0.41
1:V:191:TYR:O	1:V:288:LYS:HE2	2.19	0.41
1:V:430:VAL:HG11	3:W:719:HOH:O	2.16	0.41
1:V:557:PHE:CE2	1:W:563:LYS:HD3	2.55	0.41
1:V:528:LYS:HD2	1:V:560:LEU:HD21	2.01	0.41
1:W:101:ASP:HB3	1:W:138:THR:HG21	2.01	0.41
1:W:262:GLY:O	1:W:263:PHE:HB3	2.21	0.41
1:W:387:GLN:HG2	1:W:387:GLN:H	1.58	0.41
1:A:229:LYS:HG2	1:A:272:LYS:CG	2.50	0.41
1:B:123:VAL:HG21	1:B:153:CYS:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:229:LYS:HG2	1:B:272:LYS:CG	2.50	0.41
1:B:434:THR:HG23	1:B:435:VAL:N	2.35	0.41
1:B:93:VAL:O	1:B:97:MSE:HG3	2.20	0.41
1:B:376:ARG:HB2	1:C:352:TRP:CD2	2.55	0.41
1:D:440:MSE:O	1:D:444:LEU:CD2	2.69	0.41
1:D:49:THR:O	1:D:50:THR:C	2.56	0.41
1:D:552:LEU:O	1:D:556:TYR:HD2	2.03	0.41
1:F:212:LEU:N	1:F:212:LEU:HD12	2.34	0.41
1:F:440:MSE:O	1:F:444:LEU:CD2	2.69	0.41
1:F:94:LEU:HD23	1:F:94:LEU:O	2.19	0.41
1:G:24:GLU:C	1:G:26:ARG:N	2.73	0.41
1:G:528:LYS:HZ2	1:G:560:LEU:HD21	1.82	0.41
1:G:579:MSE:CB	1:G:581:VAL:HG12	2.50	0.41
1:H:378:ASP:O	1:H:381:SER:O	2.37	0.41
1:I:130:THR:HG23	1:I:450:GLN:NE2	2.35	0.41
1:H:395:PRO:HD2	1:I:398:PRO:HB3	2.02	0.41
1:I:68:VAL:HG22	1:I:119:ILE:HD12	2.02	0.41
1:J:130:THR:HG23	1:J:450:GLN:NE2	2.35	0.41
1:J:316:TYR:O	1:J:321:ARG:NH1	2.54	0.41
1:K:251:ILE:HD11	1:K:275:ARG:NH2	2.35	0.41
1:L:397:VAL:HG12	1:L:397:VAL:O	2.20	0.41
1:L:68:VAL:HG22	1:L:119:ILE:HD12	2.02	0.41
1:N:430:VAL:HG11	3:V:719:HOH:O	2.19	0.41
1:P:245:SER:HG	1:P:247:PHE:HE1	1.62	0.41
1:P:280:ILE:N	1:P:280:ILE:HD12	2.35	0.41
1:P:310:VAL:HB	1:P:311:GLU:H	1.64	0.41
1:Q:301:VAL:HG23	1:Q:439:ASN:HB3	2.02	0.41
1:R:193:LEU:HD22	1:R:287:LEU:HB3	2.01	0.41
1:R:236:GLN:H	1:R:265:LYS:CB	2.33	0.41
1:R:340:ILE:O	1:R:344:THR:HG21	2.20	0.41
1:R:41:TRP:HE3	1:R:42:ASP:HB3	1.82	0.41
1:R:444:LEU:O	1:R:445:GLU:C	2.58	0.41
1:S:236:GLN:H	1:S:265:LYS:CB	2.33	0.41
1:S:273:ARG:HH22	1:S:453:LEU:CD2	2.31	0.41
1:S:457:MSE:O	1:S:458:ARG:CD	2.69	0.41
1:T:349:PRO:HB2	1:T:351:PHE:CE2	2.55	0.41
1:T:380:ASN:O	1:T:381:SER:CB	2.68	0.41
1:U:236:GLN:H	1:U:265:LYS:CB	2.33	0.41
1:U:583:LYS:HA	1:U:584:PRO:HD3	1.92	0.41
1:V:280:ILE:N	1:V:280:ILE:HD12	2.34	0.41
1:V:276:VAL:CG2	1:V:293:ILE:HG23	2.49	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:W:380:ASN:O	1:W:381:SER:CB	2.68	0.41
1:X:11:ILE:O	1:X:15:PHE:HB2	2.20	0.41
2:Z:156:HIS:C	2:Z:158:PHE:H	2.23	0.41
1:A:157:ILE:CG1	1:A:157:ILE:O	2.69	0.41
1:A:246:TYR:HD2	1:A:511:ARG:CB	2.28	0.41
1:A:255:ILE:O	1:A:258:LEU:N	2.53	0.41
1:A:273:ARG:HD2	1:A:275:ARG:HD2	2.02	0.41
1:A:434:THR:HG23	1:A:435:VAL:N	2.35	0.41
1:A:568:MSE:HG3	1:B:551:LEU:CD2	2.50	0.41
1:B:157:ILE:O	1:B:157:ILE:CG1	2.69	0.41
1:B:273:ARG:HD2	1:B:275:ARG:HD2	2.02	0.41
1:B:397:VAL:O	1:B:397:VAL:HG12	2.20	0.41
1:B:552:LEU:O	1:B:556:TYR:HD2	2.03	0.41
1:C:130:THR:HG23	1:C:450:GLN:NE2	2.35	0.41
1:C:15:PHE:HE2	1:C:19:TRP:NE1	2.18	0.41
1:C:251:ILE:HD11	1:C:275:ARG:NH2	2.35	0.41
1:C:426:ASN:O	1:C:427:GLY:C	2.58	0.41
1:C:528:LYS:CD	1:C:560:LEU:HD21	2.50	0.41
1:D:434:THR:HG23	1:D:435:VAL:N	2.35	0.41
1:E:130:THR:HG23	1:E:450:GLN:NE2	2.35	0.41
1:E:426:ASN:O	1:E:427:GLY:C	2.59	0.41
1:E:437:GLN:HA	1:E:440:MSE:HB2	2.00	0.41
1:F:434:THR:HG23	1:F:435:VAL:N	2.35	0.41
1:F:444:LEU:O	1:F:447:TYR:N	2.52	0.41
1:G:274:ARG:HD3	1:G:296:GLU:O	2.19	0.41
1:G:426:ASN:O	1:G:427:GLY:C	2.59	0.41
1:G:49:THR:O	1:G:50:THR:O	2.37	0.41
1:G:248:LYS:HZ1	1:G:513:ARG:HH12	1.67	0.41
1:I:157:ILE:O	1:I:157:ILE:CG1	2.69	0.41
1:I:38:VAL:HG21	1:I:324:LYS:HD2	2.01	0.41
1:I:568:MSE:HG3	1:J:551:LEU:CD2	2.50	0.41
1:J:229:LYS:HG2	1:J:272:LYS:CG	2.50	0.41
1:J:579:MSE:CB	1:J:581:VAL:HG12	2.49	0.41
1:J:68:VAL:HG22	1:J:119:ILE:HD12	2.02	0.41
1:K:227:GLU:OE2	1:K:227:GLU:N	2.47	0.41
1:K:579:MSE:CB	1:K:581:VAL:HG12	2.50	0.41
1:K:93:VAL:O	1:K:97:MSE:HG3	2.20	0.41
1:L:209:PHE:N	1:L:210:PRO:CD	2.82	0.41
1:L:444:LEU:O	1:L:447:TYR:N	2.52	0.41
1:L:47:GLN:CD	1:L:47:GLN:N	2.72	0.41
1:M:454:ALA:O	1:M:455:THR:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:591:GLN:HA	1:M:594:VAL:CG2	2.50	0.41
1:N:123:VAL:HG22	1:N:316:TYR:HE2	1.84	0.41
1:N:528:LYS:HD2	1:N:560:LEU:HD21	2.03	0.41
1:O:174:THR:N	3:O:705:HOH:O	2.53	0.41
1:O:177:HIS:O	1:O:218:GLN:HA	2.21	0.41
1:O:301:VAL:HG23	1:O:439:ASN:HB3	2.02	0.41
1:P:147:GLU:HA	1:P:148:PRO:HD3	1.82	0.41
1:P:41:TRP:HE1	1:Q:27:ARG:HH21	1.67	0.41
1:P:66:LYS:HZ3	1:P:420:VAL:HG21	1.85	0.41
1:Q:212:LEU:HD22	1:R:26:ARG:HG2	2.03	0.41
1:Q:591:GLN:HA	1:Q:594:VAL:CG2	2.50	0.41
1:R:227:GLU:HG2	1:R:227:GLU:O	2.20	0.41
1:R:298:ILE:HA	1:R:299:PRO:HD3	1.78	0.41
1:R:583:LYS:HA	1:R:584:PRO:HD3	1.91	0.41
1:R:61:ARG:CB	1:R:62:PRO:HD3	2.51	0.41
1:S:24:GLU:CD	1:S:24:GLU:N	2.74	0.41
1:S:282:THR:HG23	1:S:287:LEU:CD1	2.47	0.41
1:S:511:ARG:HA	1:S:513:ARG:CD	2.47	0.41
1:S:554:LEU:HD12	1:S:557:PHE:CD2	2.53	0.41
1:T:24:GLU:HG3	1:T:313:LYS:HE2	2.02	0.41
1:T:371:TYR:HE2	1:T:373:LEU:HD21	1.85	0.41
1:T:248:LYS:HE2	1:T:513:ARG:HH12	1.85	0.41
1:U:265:LYS:O	1:U:266:ILE:HG12	2.19	0.41
1:U:413:LYS:HB3	1:U:413:LYS:HE2	1.84	0.41
1:U:79:LEU:N	1:U:519:ASP:O	2.53	0.41
1:W:227:GLU:O	1:W:227:GLU:HG2	2.20	0.41
1:W:431:ALA:HA	1:W:434:THR:HG22	2.01	0.41
1:W:457:MSE:O	1:W:458:ARG:CD	2.68	0.41
1:X:29:ALA:O	1:X:33:LEU:HG	2.19	0.41
1:X:528:LYS:HD2	1:X:560:LEU:HD21	2.02	0.41
2:Y:63:ILE:CG2	2:Y:123:LEU:HB3	2.51	0.41
2:Y:28:VAL:HG11	2:Y:97:ALA:HA	1.88	0.41
2:Z:124:TYR:O	2:Z:124:TYR:CG	2.73	0.41
1:A:165:MSE:HE1	1:A:435:VAL:HB	2.02	0.41
1:A:209:PHE:N	1:A:210:PRO:CD	2.82	0.41
1:A:24:GLU:C	1:A:26:ARG:N	2.73	0.41
1:A:313:LYS:HD3	1:A:314:GLU:N	2.36	0.41
1:A:316:TYR:O	1:A:321:ARG:NH1	2.54	0.41
1:B:24:GLU:CD	1:B:24:GLU:N	2.71	0.41
1:B:316:TYR:O	1:B:321:ARG:NH1	2.53	0.41
1:B:352:TRP:HB2	1:B:355:GLN:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:165:MSE:HE1	1:B:435:VAL:HB	2.02	0.41
1:D:316:TYR:O	1:D:321:ARG:NH1	2.54	0.41
1:D:352:TRP:HB2	1:D:355:GLN:HG2	2.03	0.41
1:D:579:MSE:CB	1:D:581:VAL:HG12	2.49	0.41
1:E:157:ILE:CG1	1:E:157:ILE:O	2.68	0.41
1:E:15:PHE:HE2	1:E:19:TRP:NE1	2.18	0.41
1:E:209:PHE:CE2	1:E:214:GLN:HG2	2.56	0.41
1:E:24:GLU:C	1:E:26:ARG:N	2.73	0.41
1:F:118:GLN:HB2	1:F:118:GLN:HE21	1.77	0.41
1:F:32:ASP:CG	1:F:316:TYR:CE2	2.94	0.41
1:F:598:GLN:HB2	1:F:601:GLN:HB3	2.03	0.41
1:G:123:VAL:HG21	1:G:153:CYS:HB3	2.02	0.41
1:G:209:PHE:CE2	1:G:214:GLN:HG2	2.56	0.41
1:G:273:ARG:HH22	1:G:453:LEU:HD11	1.85	0.41
1:G:316:TYR:O	1:G:321:ARG:NH1	2.54	0.41
1:I:273:ARG:HD2	1:I:275:ARG:HD2	2.01	0.41
1:J:32:ASP:CG	1:J:316:TYR:CE2	2.94	0.41
1:K:236:GLN:HE21	1:K:265:LYS:HZ1	1.68	0.41
1:K:255:ILE:O	1:K:258:LEU:N	2.53	0.41
1:L:301:VAL:HG23	1:L:439:ASN:HB3	2.02	0.41
1:L:80:TYR:CZ	1:L:448:VAL:HG22	2.54	0.41
1:M:24:GLU:N	1:M:24:GLU:OE1	2.54	0.41
1:M:293:ILE:HG12	1:M:294:ALA:H	1.85	0.41
1:M:438:LEU:HD12	1:M:441:ARG:NH1	2.35	0.41
1:M:528:LYS:HD2	1:M:560:LEU:HD21	2.02	0.41
1:N:310:VAL:HB	1:N:311:GLU:H	1.67	0.41
1:M:399:GLN:OE1	1:N:396:GLU:O	2.38	0.41
1:O:191:TYR:O	1:O:288:LYS:HE2	2.21	0.41
1:O:444:LEU:O	1:O:447:TYR:N	2.53	0.41
1:P:270:GLN:HA	1:P:270:GLN:OE1	2.19	0.41
1:P:191:TYR:O	1:P:288:LYS:HE2	2.20	0.41
1:P:371:TYR:HE2	1:P:373:LEU:HD21	1.85	0.41
1:Q:100:THR:HG22	1:Q:138:THR:HG22	2.02	0.41
1:Q:24:GLU:CD	1:Q:24:GLU:N	2.74	0.41
1:P:372:TYR:CE2	1:Q:348:LYS:HB2	2.56	0.41
1:Q:72:ARG:HG2	1:R:434:THR:HG21	2.03	0.41
1:R:387:GLN:O	1:R:389:LEU:HG	2.20	0.41
1:R:451:ASP:O	1:R:453:LEU:N	2.53	0.41
1:R:78:VAL:HG11	1:R:444:LEU:CG	2.50	0.41
1:S:262:GLY:O	1:S:263:PHE:HB3	2.20	0.41
1:S:343:ARG:HG2	1:S:343:ARG:H	1.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:444:LEU:O	1:S:445:GLU:C	2.57	0.41
1:S:76:ILE:HD12	1:S:433:ASP:OD1	2.19	0.41
1:T:310:VAL:HB	1:T:311:GLU:H	1.70	0.41
1:T:457:MSE:O	1:T:458:ARG:CD	2.68	0.41
1:V:101:ASP:HB3	1:V:138:THR:HG21	2.01	0.41
1:W:164:LEU:HD22	1:W:169:ASP:OD1	2.20	0.41
1:W:371:TYR:HE2	1:W:373:LEU:HD21	1.86	0.41
1:W:458:ARG:HA	1:W:458:ARG:HD3	1.83	0.41
1:X:349:PRO:HG3	1:X:391:TYR:CE1	2.55	0.41
1:X:575:GLN:O	1:X:579:MSE:CG	2.68	0.41
2:Y:156:HIS:C	2:Y:158:PHE:H	2.23	0.41
2:Z:56:TRP:N	2:Z:56:TRP:CD1	2.89	0.41
1:A:15:PHE:HE2	1:A:19:TRP:NE1	2.18	0.41
1:A:378:ASP:O	1:A:381:SER:O	2.37	0.41
1:A:426:ASN:O	1:A:427:GLY:C	2.58	0.41
1:B:15:PHE:HE2	1:B:19:TRP:NE1	2.18	0.41
1:B:273:ARG:NH1	1:B:275:ARG:HE	2.19	0.41
1:B:276:VAL:HG23	1:B:293:ILE:HG22	2.03	0.41
1:C:598:GLN:HB2	1:C:601:GLN:HB3	2.03	0.41
1:C:99:ARG:HH12	1:C:530:GLN:NE2	2.14	0.41
1:D:386:THR:HG21	1:D:389:LEU:HD21	2.02	0.41
1:D:397:VAL:HG12	1:D:397:VAL:O	2.20	0.41
1:E:165:MSE:HE1	1:E:435:VAL:HB	2.02	0.41
1:E:313:LYS:HD3	1:E:314:GLU:N	2.36	0.41
1:E:93:VAL:O	1:E:97:MSE:HG3	2.20	0.41
1:F:35:PHE:HZ	1:F:321:ARG:NE	2.12	0.41
1:G:313:LYS:HD3	1:G:314:GLU:N	2.36	0.41
1:G:598:GLN:HB2	1:G:601:GLN:HB3	2.02	0.41
1:H:273:ARG:NH1	1:H:275:ARG:HE	2.19	0.41
1:H:301:VAL:HG23	1:H:439:ASN:HB3	2.02	0.41
1:H:310:VAL:HB	1:H:311:GLU:H	1.78	0.41
1:H:80:TYR:HB2	1:H:95:MSE:HG2	2.03	0.41
1:I:165:MSE:HE1	1:I:435:VAL:HB	2.02	0.41
1:J:198:ILE:HA	1:J:199:PRO:HD3	1.64	0.41
1:K:273:ARG:HH22	1:K:453:LEU:HD11	1.85	0.41
1:K:313:LYS:HD3	1:K:314:GLU:N	2.36	0.41
1:K:316:TYR:O	1:K:321:ARG:NH1	2.54	0.41
1:K:542:THR:HA	1:K:543:PRO:HD3	1.82	0.41
1:K:598:GLN:HB2	1:K:601:GLN:HB3	2.02	0.41
1:L:209:PHE:CE2	1:L:214:GLN:HG2	2.56	0.41
1:L:313:LYS:HD3	1:L:314:GLU:N	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:316:TYR:O	1:L:321:ARG:NH1	2.54	0.41
1:L:38:VAL:HG21	1:L:324:LYS:HD2	2.01	0.41
1:L:40:GLN:O	1:L:41:TRP:CB	2.55	0.41
1:L:80:TYR:HB2	1:L:95:MSE:HG2	2.03	0.41
1:M:164:LEU:HD22	1:M:169:ASP:OD1	2.20	0.41
1:M:301:VAL:HA	1:M:302:PRO:HD3	1.75	0.41
1:M:390:ALA:HB2	1:N:387:GLN:CB	2.50	0.41
1:M:59:VAL:CG2	1:M:59:VAL:O	2.69	0.41
1:M:71:MSE:CE	1:M:115:VAL:HB	2.50	0.41
1:N:440:MSE:O	1:N:443:ASP:HB3	2.20	0.41
1:N:80:TYR:OH	1:N:444:LEU:HD12	2.20	0.41
1:O:380:ASN:O	1:O:381:SER:CB	2.69	0.41
1:O:77:ASP:HB2	1:O:523:SER:HB2	2.02	0.41
1:P:179:MSE:O	1:P:217:ILE:HD12	2.21	0.41
1:P:577:ILE:HG12	1:P:582:LYS:CG	2.45	0.41
1:Q:270:GLN:OE1	1:Q:270:GLN:HA	2.20	0.41
1:Q:394:ASN:HA	1:Q:395:PRO:HD3	1.93	0.41
1:Q:444:LEU:O	1:Q:445:GLU:C	2.58	0.41
1:P:563:LYS:HD3	1:Q:557:PHE:CE2	2.55	0.41
1:R:24:GLU:CD	1:R:24:GLU:N	2.74	0.41
1:R:431:ALA:HA	1:R:434:THR:HG22	2.01	0.41
1:R:458:ARG:HD3	1:R:458:ARG:HA	1.83	0.41
1:S:191:TYR:O	1:S:288:LYS:HE2	2.20	0.41
1:T:387:GLN:O	1:T:389:LEU:HG	2.20	0.41
1:U:274:ARG:O	1:U:275:ARG:HD2	2.20	0.41
1:U:510:ILE:O	1:U:513:ARG:HD2	2.20	0.41
1:V:591:GLN:HA	1:V:594:VAL:CG2	2.51	0.41
1:W:270:GLN:HA	1:W:270:GLN:OE1	2.20	0.41
1:W:301:VAL:HG23	1:W:439:ASN:HB3	2.02	0.41
1:W:528:LYS:NZ	1:W:560:LEU:HD21	2.35	0.41
1:X:443:ASP:O	1:X:446:THR:HG22	2.21	0.41
2:Z:78:GLU:O	2:Z:79:GLY:C	2.59	0.41
1:B:209:PHE:CE2	1:B:214:GLN:HG2	2.56	0.41
1:B:313:LYS:HD3	1:B:314:GLU:N	2.36	0.41
1:B:38:VAL:HG21	1:B:324:LYS:HD2	2.01	0.41
1:B:68:VAL:HG22	1:B:119:ILE:HD12	2.02	0.41
1:C:265:LYS:HA	1:C:265:LYS:HD2	1.96	0.41
1:C:273:ARG:NH1	1:C:275:ARG:HE	2.19	0.41
1:C:276:VAL:HG23	1:C:293:ILE:HG22	2.03	0.41
1:C:583:LYS:HA	1:C:584:PRO:HD3	1.85	0.41
1:C:93:VAL:O	1:C:97:MSE:HG3	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:TYR:HB2	1:C:95:MSE:HG2	2.03	0.41
1:D:123:VAL:HG21	1:D:153:CYS:HB3	2.02	0.41
1:D:251:ILE:HD11	1:D:275:ARG:NH2	2.35	0.41
1:E:528:LYS:CD	1:E:560:LEU:HD21	2.50	0.41
1:F:313:LYS:HD3	1:F:314:GLU:N	2.36	0.41
1:D:372:TYR:CD2	1:F:348:LYS:HB2	2.56	0.41
1:F:165:MSE:HE1	1:F:435:VAL:HB	2.02	0.41
1:F:80:TYR:HB2	1:F:95:MSE:HG2	2.03	0.41
1:G:276:VAL:HG23	1:G:293:ILE:HG22	2.03	0.41
1:H:579:MSE:CB	1:H:581:VAL:HG12	2.49	0.41
1:I:127:ARG:HG2	1:I:147:GLU:HB2	2.02	0.41
1:I:209:PHE:CE2	1:I:214:GLN:HG2	2.56	0.41
1:I:301:VAL:HA	1:I:302:PRO:HD3	1.84	0.41
1:I:316:TYR:O	1:I:321:ARG:NH1	2.54	0.41
1:I:426:ASN:O	1:I:427:GLY:C	2.58	0.41
1:J:157:ILE:O	1:J:157:ILE:CG1	2.68	0.41
1:J:236:GLN:CG	1:J:243:PRO:HB2	2.51	0.41
1:L:528:LYS:HD2	1:L:560:LEU:HD11	2.03	0.41
1:M:198:ILE:HA	1:M:199:PRO:HD3	1.70	0.41
1:M:273:ARG:HH22	1:M:453:LEU:CD2	2.31	0.41
1:M:384:LEU:HD22	1:M:384:LEU:N	2.31	0.41
1:M:451:ASP:O	1:M:453:LEU:N	2.53	0.41
1:M:82:PRO:HB2	1:M:83:LYS:H	1.63	0.41
1:N:115:VAL:HA	1:N:118:GLN:HB3	2.03	0.41
1:N:123:VAL:HG13	1:N:304:PHE:CE1	2.56	0.41
1:N:413:LYS:HB3	1:N:413:LYS:HE2	1.87	0.41
1:N:451:ASP:O	1:N:453:LEU:N	2.54	0.41
1:N:78:VAL:CG1	1:N:79:LEU:H	2.31	0.41
1:P:228:LYS:O	1:P:229:LYS:HB3	2.21	0.41
1:P:298:ILE:HA	1:P:299:PRO:HD3	1.77	0.41
1:P:330:ARG:O	1:P:334:MSE:HB2	2.20	0.41
1:P:528:LYS:HD2	1:P:560:LEU:HD21	2.02	0.41
1:Q:212:LEU:HD12	1:Q:212:LEU:N	2.35	0.41
1:Q:236:GLN:H	1:Q:265:LYS:CB	2.33	0.41
1:Q:29:ALA:O	1:Q:33:LEU:HG	2.20	0.41
1:Q:369:TYR:HA	1:Q:370:PRO:HD3	1.84	0.41
1:Q:65:ARG:HG2	1:R:306:GLU:OE2	2.21	0.41
1:R:156:VAL:O	1:R:156:VAL:CG2	2.69	0.41
1:T:126:TRP:NE1	1:T:301:VAL:HG13	2.36	0.41
1:T:24:GLU:N	1:T:24:GLU:CD	2.74	0.41
1:T:61:ARG:CB	1:T:62:PRO:HD3	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:U:107:ALA:HA	1:U:146:ARG:HB3	2.02	0.41
1:V:232:ALA:HB1	1:V:233:PHE:H	1.58	0.41
1:V:35:PHE:O	1:V:37:ARG:N	2.46	0.41
1:V:431:ALA:HA	1:V:434:THR:HG22	2.02	0.41
1:V:444:LEU:O	1:V:447:TYR:N	2.53	0.41
1:W:15:PHE:CE2	1:W:19:TRP:NE1	2.88	0.41
1:W:249:ARG:HH21	1:W:249:ARG:HD2	1.52	0.41
1:W:57:PHE:CD1	1:W:57:PHE:N	2.88	0.41
1:W:591:GLN:HA	1:W:594:VAL:CG2	2.50	0.41
1:X:444:LEU:O	1:X:445:GLU:C	2.58	0.41
2:Y:78:GLU:O	2:Y:79:GLY:C	2.59	0.41
2:Z:63:ILE:CG2	2:Z:123:LEU:HB3	2.51	0.41
1:A:32:ASP:CG	1:A:316:TYR:CE2	2.94	0.41
1:A:301:VAL:HG23	1:A:439:ASN:HB3	2.02	0.41
1:B:127:ARG:HG2	1:B:147:GLU:HB2	2.03	0.41
1:C:397:VAL:HG12	1:C:397:VAL:O	2.20	0.41
1:D:227:GLU:OE2	1:D:227:GLU:N	2.47	0.41
1:D:32:ASP:CG	1:D:316:TYR:CE2	2.94	0.41
1:E:301:VAL:HG23	1:E:439:ASN:HB3	2.02	0.41
1:F:343:ARG:HG2	1:F:343:ARG:H	1.52	0.41
1:F:579:MSE:CB	1:F:581:VAL:HG12	2.49	0.41
1:G:236:GLN:CG	1:G:243:PRO:HB2	2.51	0.41
1:G:273:ARG:HD2	1:G:275:ARG:HD2	2.02	0.41
1:G:430:VAL:HG12	1:G:431:ALA:N	2.35	0.41
1:H:236:GLN:CG	1:H:243:PRO:HB2	2.51	0.41
1:H:313:LYS:HD3	1:H:314:GLU:N	2.36	0.41
1:I:273:ARG:NH1	1:I:275:ARG:HE	2.19	0.41
1:I:397:VAL:HG12	1:I:397:VAL:O	2.20	0.41
1:J:15:PHE:HE2	1:J:19:TRP:NE1	2.18	0.41
1:J:567:MSE:HE2	1:K:554:LEU:HD22	2.02	0.41
1:L:301:VAL:HA	1:L:302:PRO:HD3	1.85	0.41
1:M:584:PRO:CG	1:M:593:LEU:HD12	2.48	0.41
1:N:107:ALA:HA	1:N:146:ARG:HB3	2.02	0.41
1:N:306:GLU:O	1:N:316:TYR:HA	2.21	0.41
1:N:387:GLN:HA	1:N:388:PRO:HD3	1.93	0.41
1:N:443:ASP:O	1:N:446:THR:HG22	2.20	0.41
1:O:159:ASP:OD2	1:O:161:ASN:N	2.51	0.41
1:O:387:GLN:HB2	1:P:390:ALA:HB2	2.03	0.41
1:O:396:GLU:O	1:P:399:GLN:OE1	2.38	0.41
1:P:156:VAL:O	1:P:156:VAL:CG2	2.69	0.41
1:P:276:VAL:CG2	1:P:293:ILE:HG23	2.50	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:107:ALA:HA	1:Q:146:ARG:HB3	2.03	0.41
1:P:564:GLY:O	1:Q:554:LEU:HD21	2.19	0.41
1:R:14:ARG:CA	1:R:14:ARG:NE	2.70	0.41
1:R:231:THR:HG23	1:R:249:ARG:HE	1.85	0.41
1:R:577:ILE:HG12	1:R:582:LYS:CG	2.45	0.41
1:T:174:THR:N	3:T:705:HOH:O	2.53	0.41
1:T:369:TYR:HA	1:T:370:PRO:HD3	1.83	0.41
1:S:108:LYS:HD2	1:T:438:LEU:HD11	2.01	0.41
1:U:123:VAL:HG22	1:U:316:TYR:HE2	1.83	0.41
1:U:352:TRP:O	1:U:355:GLN:HG2	2.20	0.41
1:U:404:MSE:HE1	1:X:334:MSE:HG3	2.02	0.41
1:W:311:GLU:H	1:W:311:GLU:HG3	1.76	0.41
1:W:352:TRP:HB2	1:W:355:GLN:HG2	2.03	0.41
1:W:61:ARG:CB	1:W:62:PRO:HD3	2.50	0.41
1:X:387:GLN:O	1:X:389:LEU:HG	2.20	0.41
1:X:427:GLY:C	1:X:429:GLN:N	2.74	0.41
2:Y:119:GLY:O	2:Y:123:LEU:HD13	2.21	0.41
2:Z:135:ALA:HA	2:Z:136:PRO:HD3	1.92	0.41
1:A:127:ARG:HG2	1:A:147:GLU:HB2	2.02	0.41
1:A:273:ARG:HH22	1:A:453:LEU:HD11	1.85	0.41
1:A:552:LEU:O	1:A:556:TYR:HD2	2.03	0.41
1:B:236:GLN:CG	1:B:243:PRO:HB2	2.51	0.41
1:B:298:ILE:HA	1:B:299:PRO:HD3	1.82	0.41
1:C:24:GLU:CD	1:C:24:GLU:N	2.71	0.41
1:C:322:LEU:N	1:C:322:LEU:HD22	2.36	0.41
1:C:165:MSE:HE1	1:C:435:VAL:HB	2.02	0.41
1:D:273:ARG:HH22	1:D:453:LEU:HD11	1.85	0.41
1:F:157:ILE:O	1:F:157:ILE:CG1	2.68	0.41
1:F:301:VAL:HG23	1:F:439:ASN:HB3	2.02	0.41
1:F:316:TYR:O	1:F:321:ARG:NH1	2.53	0.41
1:F:426:ASN:O	1:F:427:GLY:C	2.58	0.41
1:G:32:ASP:CG	1:G:316:TYR:CE2	2.94	0.41
1:G:386:THR:HG21	1:G:389:LEU:HD21	2.02	0.41
1:I:147:GLU:HA	1:I:148:PRO:HD3	1.86	0.41
1:I:313:LYS:HD3	1:I:314:GLU:N	2.36	0.41
1:J:127:ARG:HG2	1:J:147:GLU:HB2	2.03	0.41
1:J:430:VAL:HG12	1:J:431:ALA:N	2.35	0.41
1:J:528:LYS:HD2	1:J:560:LEU:HD11	2.03	0.41
1:J:80:TYR:HB2	1:J:95:MSE:HG2	2.03	0.41
1:K:236:GLN:CG	1:K:243:PRO:HB2	2.51	0.41
1:K:322:LEU:N	1:K:322:LEU:HD22	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:376:ARG:NE	1:K:354:GLU:OE2	2.51	0.41
1:L:130:THR:HG23	1:L:450:GLN:NE2	2.35	0.41
1:L:386:THR:HG21	1:L:389:LEU:HD21	2.02	0.41
1:M:248:LYS:HZ1	1:M:513:ARG:HH12	1.69	0.41
1:N:584:PRO:CG	1:N:593:LEU:HD12	2.49	0.41
1:O:93:VAL:O	1:O:97:MSE:HG3	2.21	0.41
1:P:123:VAL:HG13	1:P:304:PHE:CE1	2.56	0.41
1:Q:156:VAL:O	1:Q:156:VAL:CG2	2.69	0.41
1:Q:262:GLY:O	1:Q:263:PHE:HB3	2.20	0.41
1:Q:158:TRP:HH2	1:Q:302:PRO:HG3	1.80	0.41
1:Q:340:ILE:O	1:Q:344:THR:HG21	2.21	0.41
1:Q:444:LEU:O	1:Q:447:TYR:N	2.54	0.41
1:Q:77:ASP:HB2	1:Q:523:SER:HB2	2.03	0.41
1:R:276:VAL:CG2	1:R:293:ILE:HG23	2.49	0.41
1:R:438:LEU:HD12	1:R:441:ARG:NH1	2.36	0.41
1:S:280:ILE:HD12	1:S:280:ILE:N	2.35	0.41
1:S:349:PRO:HG3	1:S:391:TYR:CE1	2.55	0.41
1:T:266:ILE:HD13	1:T:266:ILE:HA	1.90	0.41
1:T:276:VAL:CG2	1:T:293:ILE:HG23	2.49	0.41
1:T:248:LYS:HZ1	1:T:513:ARG:HH12	1.68	0.41
1:U:248:LYS:HE2	1:U:513:ARG:HH12	1.84	0.41
1:U:349:PRO:HG3	1:U:391:TYR:CE1	2.55	0.41
1:U:40:GLN:HB2	1:U:40:GLN:HE21	1.58	0.41
1:V:107:ALA:HA	1:V:146:ARG:HB3	2.03	0.41
1:V:115:VAL:HA	1:V:118:GLN:HB3	2.02	0.41
1:W:387:GLN:O	1:W:389:LEU:HG	2.20	0.41
1:W:40:GLN:HB2	1:W:40:GLN:HE21	1.61	0.41
1:X:274:ARG:O	1:X:275:ARG:HD2	2.19	0.41
1:U:27:ARG:HH21	1:X:41:TRP:HE1	1.68	0.41
1:X:457:MSE:O	1:X:458:ARG:CD	2.69	0.41
1:X:591:GLN:HA	1:X:594:VAL:CG2	2.50	0.41
1:A:236:GLN:CG	1:A:243:PRO:HB2	2.51	0.41
1:B:386:THR:HG21	1:B:389:LEU:HD21	2.02	0.41
1:B:426:ASN:O	1:B:427:GLY:C	2.59	0.41
1:B:301:VAL:HG23	1:B:439:ASN:HB3	2.02	0.41
1:B:598:GLN:HB2	1:B:601:GLN:HB3	2.03	0.41
1:C:352:TRP:HB2	1:C:355:GLN:HG2	2.03	0.41
1:C:61:ARG:N	1:C:62:PRO:CD	2.84	0.41
1:D:313:LYS:HD3	1:D:314:GLU:N	2.36	0.41
1:E:298:ILE:HA	1:E:299:PRO:HD3	1.82	0.41
1:E:301:VAL:HA	1:E:302:PRO:HD3	1.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:123:VAL:HG21	1:F:153:CYS:HB3	2.02	0.41
1:F:68:VAL:HG22	1:F:119:ILE:HD12	2.02	0.41
1:G:157:ILE:O	1:G:157:ILE:CG1	2.69	0.41
1:H:164:LEU:HD22	1:H:169:ASP:CG	2.42	0.41
1:H:229:LYS:HG2	1:H:272:LYS:CG	2.50	0.41
1:H:273:ARG:HD2	1:H:275:ARG:HD2	2.02	0.41
1:H:426:ASN:O	1:H:427:GLY:C	2.58	0.41
1:H:43:ASP:N	1:H:43:ASP:OD2	2.52	0.41
1:I:80:TYR:HB2	1:I:95:MSE:HG2	2.03	0.41
1:J:164:LEU:HD22	1:J:169:ASP:CG	2.42	0.41
1:J:298:ILE:HA	1:J:299:PRO:HD3	1.82	0.41
1:J:322:LEU:HD22	1:J:322:LEU:N	2.36	0.41
1:J:426:ASN:O	1:J:427:GLY:C	2.58	0.41
1:J:552:LEU:O	1:J:556:TYR:HD2	2.03	0.41
1:K:165:MSE:HE1	1:K:435:VAL:HB	2.02	0.41
1:K:209:PHE:CE2	1:K:214:GLN:HG2	2.56	0.41
1:K:24:GLU:C	1:K:26:ARG:N	2.73	0.41
1:M:227:GLU:HG2	1:M:227:GLU:O	2.21	0.41
1:M:554:LEU:HD12	1:M:557:PHE:CD2	2.54	0.41
1:N:311:GLU:O	1:N:312:ASP:HB2	2.21	0.41
1:N:383:ASP:C	1:N:385:PRO:HD3	2.40	0.41
1:O:330:ARG:O	1:O:334:MSE:HB2	2.20	0.41
1:M:564:GLY:CA	1:O:554:LEU:HD21	2.48	0.41
1:O:591:GLN:HA	1:O:594:VAL:CG2	2.51	0.41
1:P:227:GLU:HG2	1:P:227:GLU:O	2.21	0.41
1:P:349:PRO:HG3	1:P:391:TYR:CE1	2.55	0.41
1:P:376:ARG:HB2	1:Q:352:TRP:CG	2.56	0.41
1:P:41:TRP:HE3	1:P:42:ASP:HB3	1.80	0.41
1:P:451:ASP:O	1:P:453:LEU:N	2.54	0.41
1:O:103:ARG:NH1	1:P:517:TYR:HB2	2.36	0.41
1:P:578:GLN:HG2	1:P:596:ALA:CB	2.50	0.41
1:Q:228:LYS:O	1:Q:229:LYS:HB3	2.21	0.41
1:Q:236:GLN:CG	1:Q:243:PRO:HB2	2.51	0.41
1:Q:387:GLN:O	1:Q:389:LEU:HG	2.21	0.41
1:Q:440:MSE:O	1:Q:443:ASP:HB3	2.21	0.41
1:R:177:HIS:O	1:R:218:GLN:HA	2.21	0.41
1:R:79:LEU:N	1:R:519:ASP:O	2.53	0.41
1:T:298:ILE:HA	1:T:299:PRO:HD3	1.80	0.41
1:V:227:GLU:O	1:V:227:GLU:HG2	2.21	0.41
1:V:262:GLY:O	1:V:263:PHE:HB3	2.20	0.41
1:V:26:ARG:O	1:V:27:ARG:C	2.58	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:V:298:ILE:HA	1:V:299:PRO:HD3	1.79	0.41
1:W:236:GLN:H	1:W:265:LYS:CB	2.34	0.41
1:W:349:PRO:HG3	1:W:391:TYR:CE1	2.56	0.41
1:W:35:PHE:O	1:W:37:ARG:N	2.46	0.41
1:X:236:GLN:H	1:X:265:LYS:CB	2.34	0.41
1:X:438:LEU:HD12	1:X:441:ARG:NH1	2.35	0.41
1:B:265:LYS:HD2	1:B:265:LYS:HA	1.96	0.41
1:B:32:ASP:CG	1:B:316:TYR:CE2	2.94	0.41
1:C:123:VAL:HG21	1:C:153:CYS:HB3	2.02	0.41
1:C:236:GLN:CG	1:C:243:PRO:HB2	2.51	0.41
1:C:369:TYR:HA	1:C:370:PRO:HD3	1.84	0.41
1:C:383:ASP:CB	1:C:385:PRO:HD3	2.51	0.41
1:C:273:ARG:HH22	1:C:453:LEU:HD11	1.85	0.41
1:C:528:LYS:HD2	1:C:560:LEU:HD11	2.03	0.41
1:D:236:GLN:CG	1:D:243:PRO:HB2	2.51	0.41
1:E:276:VAL:HG23	1:E:293:ILE:HG22	2.03	0.41
1:E:32:ASP:CG	1:E:316:TYR:CE2	2.94	0.41
1:E:386:THR:HG21	1:E:389:LEU:HD21	2.02	0.41
1:E:80:TYR:HB2	1:E:95:MSE:HG2	2.03	0.41
1:F:383:ASP:CB	1:F:385:PRO:HD3	2.51	0.41
1:F:430:VAL:HG12	1:F:431:ALA:N	2.35	0.41
1:F:528:LYS:HD2	1:F:560:LEU:HD11	2.03	0.41
1:G:164:LEU:HD22	1:G:169:ASP:CG	2.42	0.41
1:I:236:GLN:CG	1:I:243:PRO:HB2	2.51	0.41
1:I:598:GLN:HB2	1:I:601:GLN:HB3	2.03	0.41
1:J:313:LYS:HD3	1:J:314:GLU:N	2.36	0.41
1:J:38:VAL:HG21	1:J:324:LYS:HD2	2.01	0.41
1:J:397:VAL:O	1:J:397:VAL:HG12	2.20	0.41
1:J:440:MSE:O	1:J:444:LEU:CD2	2.69	0.41
1:J:61:ARG:N	1:J:62:PRO:CD	2.84	0.41
1:J:94:LEU:HA	1:J:97:MSE:CE	2.37	0.41
1:K:273:ARG:NH1	1:K:275:ARG:HE	2.19	0.41
1:K:32:ASP:CG	1:K:316:TYR:CE2	2.94	0.41
1:K:359:PHE:HD1	2:Y:129:ILE:HD11	1.86	0.41
1:K:35:PHE:HE1	1:K:321:ARG:NH1	2.13	0.41
1:K:413:LYS:HE2	1:K:413:LYS:HB3	1.74	0.41
1:K:440:MSE:O	1:K:444:LEU:CD2	2.69	0.41
1:K:552:LEU:O	1:K:556:TYR:HD2	2.03	0.41
1:L:24:GLU:C	1:L:26:ARG:N	2.73	0.41
1:M:101:ASP:HB3	1:M:138:THR:HG21	2.02	0.41
1:M:115:VAL:HA	1:M:118:GLN:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:11:ILE:O	1:M:15:PHE:HB2	2.21	0.41
1:M:191:TYR:O	1:M:288:LYS:HE2	2.21	0.41
1:M:236:GLN:H	1:M:265:LYS:CB	2.34	0.41
1:M:440:MSE:O	1:M:443:ASP:HB3	2.21	0.41
1:N:123:VAL:HG23	3:N:709:HOH:O	2.21	0.41
1:N:293:ILE:HG12	1:N:294:ALA:H	1.85	0.41
1:N:330:ARG:O	1:N:334:MSE:HB2	2.21	0.41
1:N:349:PRO:HG3	1:N:391:TYR:CE1	2.56	0.41
1:O:503:GLU:HB3	1:O:508:ASN:HB3	2.03	0.41
1:O:564:GLY:HA2	1:P:554:LEU:CD2	2.43	0.41
1:P:219:ILE:HG13	1:P:220:ALA:N	2.36	0.41
1:P:35:PHE:CE1	1:P:321:ARG:NH1	2.87	0.41
1:Q:61:ARG:CB	1:Q:62:PRO:HD3	2.50	0.41
1:R:123:VAL:HG22	1:R:316:TYR:HE2	1.84	0.41
1:R:191:TYR:O	1:R:288:LYS:HE2	2.20	0.41
1:S:387:GLN:O	1:S:389:LEU:HG	2.21	0.41
1:T:394:ASN:HA	1:T:395:PRO:HD3	1.91	0.41
1:U:24:GLU:HG3	1:U:313:LYS:HE2	2.03	0.41
1:U:282:THR:HG23	1:U:287:LEU:CD1	2.46	0.41
1:U:35:PHE:HZ	1:U:321:ARG:NE	2.13	0.41
1:U:577:ILE:HG12	1:U:582:LYS:CG	2.46	0.41
1:U:591:GLN:HA	1:U:594:VAL:CG2	2.51	0.41
1:V:228:LYS:O	1:V:229:LYS:HB3	2.21	0.41
1:V:334:MSE:SE	1:V:405:LEU:HD11	2.71	0.41
1:W:24:GLU:CD	1:W:24:GLU:N	2.74	0.41
1:W:274:ARG:O	1:W:275:ARG:HD2	2.21	0.41
1:W:444:LEU:O	1:W:447:TYR:N	2.53	0.41
1:W:503:GLU:HB3	1:W:508:ASN:HB3	2.02	0.41
1:X:78:VAL:HG11	1:X:444:LEU:CG	2.48	0.41
1:B:78:VAL:CG1	1:B:444:LEU:HG	2.51	0.41
1:B:80:TYR:HB2	1:B:95:MSE:HG2	2.03	0.41
1:C:118:GLN:HB2	1:C:118:GLN:HE21	1.77	0.41
1:C:316:TYR:O	1:C:321:ARG:NH1	2.53	0.41
1:C:440:MSE:O	1:C:444:LEU:CD2	2.69	0.41
1:D:157:ILE:CG1	1:D:157:ILE:O	2.68	0.41
1:D:273:ARG:NH1	1:D:275:ARG:HE	2.19	0.41
1:E:383:ASP:CB	1:E:385:PRO:HD3	2.51	0.41
1:G:301:VAL:HG23	1:G:439:ASN:HB3	2.02	0.41
1:H:316:TYR:O	1:H:321:ARG:NH1	2.54	0.41
1:H:322:LEU:HD22	1:H:322:LEU:N	2.36	0.41
1:H:352:TRP:HB2	1:H:355:GLN:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:383:ASP:CB	1:H:385:PRO:HD3	2.51	0.41
1:H:430:VAL:HG12	1:H:431:ALA:N	2.35	0.41
1:H:459:ARG:HD2	1:H:459:ARG:C	2.42	0.41
1:I:24:GLU:C	1:I:26:ARG:N	2.73	0.41
1:I:322:LEU:N	1:I:322:LEU:HD22	2.36	0.41
1:I:383:ASP:CB	1:I:385:PRO:HD3	2.51	0.41
1:I:301:VAL:HG23	1:I:439:ASN:HB3	2.02	0.41
1:I:93:VAL:HG11	1:I:458:ARG:HG2	2.03	0.41
1:J:273:ARG:HH22	1:J:453:LEU:HD11	1.85	0.41
1:K:198:ILE:HA	1:K:199:PRO:HD3	1.64	0.41
1:K:47:GLN:N	1:K:47:GLN:CD	2.72	0.41
1:L:273:ARG:HH22	1:L:453:LEU:HD11	1.85	0.41
1:N:61:ARG:CB	1:N:62:PRO:HD3	2.51	0.41
1:O:349:PRO:HG3	1:O:391:TYR:CE1	2.56	0.41
1:P:340:ILE:O	1:P:344:THR:HG21	2.20	0.41
1:Q:191:TYR:O	1:Q:288:LYS:HE2	2.21	0.41
1:Q:231:THR:CG2	1:Q:249:ARG:HH11	2.32	0.41
1:Q:306:GLU:O	1:Q:316:TYR:HA	2.21	0.41
1:Q:457:MSE:O	1:Q:458:ARG:CD	2.69	0.41
1:R:198:ILE:HA	1:R:199:PRO:HD3	1.71	0.41
1:R:262:GLY:O	1:R:263:PHE:HB3	2.21	0.41
1:R:578:GLN:HG2	1:R:596:ALA:CB	2.51	0.41
1:S:107:ALA:HA	1:S:146:ARG:HB3	2.02	0.41
1:S:177:HIS:O	1:S:218:GLN:HA	2.21	0.41
1:S:210:PRO:HD2	1:S:211:TRP:CZ3	2.56	0.41
1:S:579:MSE:HB2	1:S:581:VAL:HG12	2.03	0.41
1:T:202:GLN:O	1:T:203:ASN:HB3	2.21	0.41
1:U:262:GLY:O	1:U:263:PHE:HB3	2.21	0.41
1:V:383:ASP:C	1:V:385:PRO:HD3	2.41	0.41
1:W:24:GLU:N	1:W:24:GLU:OE1	2.54	0.41
1:X:212:LEU:N	1:X:212:LEU:HD12	2.35	0.41
2:Z:119:GLY:O	2:Z:123:LEU:HD13	2.21	0.41
1:A:209:PHE:CE2	1:A:214:GLN:HG2	2.56	0.40
1:A:459:ARG:HD2	1:A:459:ARG:C	2.42	0.40
1:B:440:MSE:O	1:B:444:LEU:CD2	2.69	0.40
1:C:164:LEU:HD22	1:C:169:ASP:CG	2.42	0.40
1:C:232:ALA:HB1	1:C:233:PHE:H	1.71	0.40
1:D:209:PHE:CE2	1:D:214:GLN:HG2	2.56	0.40
1:D:322:LEU:N	1:D:322:LEU:HD22	2.36	0.40
1:D:528:LYS:HD2	1:D:560:LEU:HD11	2.03	0.40
1:D:576:LEU:HD13	1:E:567:MSE:SE	2.71	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:229:LYS:HG2	1:E:272:LYS:CG	2.50	0.40
1:E:322:LEU:HD22	1:E:322:LEU:N	2.36	0.40
1:E:397:VAL:O	1:E:397:VAL:HG12	2.20	0.40
1:E:440:MSE:O	1:E:444:LEU:CD2	2.69	0.40
1:E:99:ARG:NH1	1:E:530:GLN:HE21	2.13	0.40
1:F:15:PHE:HE2	1:F:19:TRP:NE1	2.18	0.40
1:F:351:PHE:CD2	1:F:356:ILE:CD1	3.04	0.40
1:F:61:ARG:N	1:F:62:PRO:CD	2.84	0.40
1:G:127:ARG:HG2	1:G:147:GLU:HB2	2.03	0.40
1:G:248:LYS:HZ2	1:G:251:ILE:HD12	1.86	0.40
1:G:273:ARG:NH1	1:G:275:ARG:HE	2.19	0.40
1:G:31:ASN:HA	1:G:31:ASN:HD22	1.62	0.40
1:G:352:TRP:HB2	1:G:355:GLN:HG2	2.03	0.40
1:H:127:ARG:HG2	1:H:147:GLU:HB2	2.02	0.40
1:H:15:PHE:HE2	1:H:19:TRP:NE1	2.18	0.40
1:H:397:VAL:HG12	1:H:397:VAL:O	2.20	0.40
1:H:440:MSE:O	1:H:444:LEU:CD2	2.69	0.40
1:I:123:VAL:HG21	1:I:153:CYS:HB3	2.02	0.40
1:I:352:TRP:HB2	1:I:355:GLN:HG2	2.03	0.40
1:J:255:ILE:O	1:J:258:LEU:N	2.53	0.40
1:J:35:PHE:HZ	1:J:321:ARG:NE	2.12	0.40
1:K:273:ARG:HD2	1:K:275:ARG:HD2	2.02	0.40
1:K:383:ASP:CB	1:K:385:PRO:HD3	2.51	0.40
1:K:386:THR:HG21	1:K:389:LEU:HD21	2.02	0.40
1:K:80:TYR:HB2	1:K:95:MSE:HG2	2.03	0.40
1:L:108:LYS:HE2	1:L:108:LYS:HB3	4.41	0.40
1:L:35:PHE:HZ	1:L:321:ARG:NE	2.12	0.40
1:L:552:LEU:O	1:L:556:TYR:HD2	2.03	0.40
1:L:598:GLN:HB2	1:L:601:GLN:HB3	2.02	0.40
1:M:123:VAL:HG13	1:M:304:PHE:CE1	2.56	0.40
1:N:227:GLU:HG2	1:N:227:GLU:O	2.21	0.40
1:N:386:THR:CG2	1:N:389:LEU:HD21	2.51	0.40
1:N:444:LEU:O	1:N:445:GLU:C	2.60	0.40
1:N:591:GLN:HA	1:N:594:VAL:CG2	2.51	0.40
1:N:82:PRO:HB2	1:N:83:LYS:H	1.63	0.40
1:O:340:ILE:O	1:O:344:THR:HG21	2.22	0.40
1:P:248:LYS:H	1:P:248:LYS:CD	2.18	0.40
1:P:236:GLN:H	1:P:265:LYS:CB	2.34	0.40
1:P:511:ARG:HA	1:P:513:ARG:CD	2.46	0.40
1:Q:79:LEU:N	1:Q:519:ASP:O	2.54	0.40
1:R:310:VAL:HB	1:R:311:GLU:H	1.66	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:330:ARG:HD2	1:R:409:THR:CG2	2.42	0.40
1:S:179:MSE:O	1:S:217:ILE:HD12	2.21	0.40
1:S:503:GLU:HB3	1:S:508:ASN:HB3	2.03	0.40
1:S:80:TYR:CE1	1:S:448:VAL:CG2	3.05	0.40
1:T:26:ARG:O	1:T:27:ARG:C	2.59	0.40
1:T:528:LYS:HD2	1:T:560:LEU:HD21	2.02	0.40
1:U:380:ASN:O	1:U:381:SER:CB	2.69	0.40
1:U:394:ASN:HA	1:U:395:PRO:HD3	1.93	0.40
1:U:334:MSE:SE	1:U:405:LEU:HD11	2.71	0.40
1:U:457:MSE:O	1:U:458:ARG:CD	2.69	0.40
1:U:458:ARG:HD3	1:U:458:ARG:HA	1.84	0.40
1:V:251:ILE:HD11	1:V:275:ARG:HH21	1.86	0.40
1:V:451:ASP:O	1:V:453:LEU:N	2.54	0.40
1:V:438:LEU:HD11	1:W:108:LYS:HD2	2.02	0.40
1:W:219:ILE:HG13	1:W:220:ALA:N	2.36	0.40
1:X:370:PRO:HB2	1:X:371:TYR:CD1	2.56	0.40
1:A:383:ASP:CB	1:A:385:PRO:HD3	2.51	0.40
1:A:397:VAL:O	1:A:397:VAL:HG12	2.20	0.40
1:A:528:LYS:HD2	1:A:560:LEU:HD11	2.03	0.40
1:A:567:MSE:HE2	1:B:554:LEU:HD22	2.03	0.40
1:A:61:ARG:N	1:A:62:PRO:CD	2.84	0.40
1:B:351:PHE:CD2	1:B:356:ILE:CD1	3.04	0.40
1:B:459:ARG:C	1:B:459:ARG:HD2	2.42	0.40
1:B:93:VAL:HG11	1:B:458:ARG:HG2	2.03	0.40
1:C:157:ILE:O	1:C:157:ILE:CG1	2.69	0.40
1:C:191:TYR:HE1	1:C:278:LYS:HZ3	1.66	0.40
1:C:32:ASP:CG	1:C:316:TYR:CE2	2.94	0.40
1:C:351:PHE:CD2	1:C:356:ILE:CD1	3.04	0.40
1:D:61:ARG:N	1:D:62:PRO:CD	2.84	0.40
1:E:164:LEU:HD22	1:E:169:ASP:CG	2.42	0.40
1:E:236:GLN:CG	1:E:243:PRO:HB2	2.51	0.40
1:E:352:TRP:HB2	1:E:355:GLN:HG2	2.02	0.40
1:F:276:VAL:HG23	1:F:293:ILE:HG22	2.03	0.40
1:G:459:ARG:C	1:G:459:ARG:HD2	2.42	0.40
1:H:123:VAL:HG21	1:H:153:CYS:HB3	2.02	0.40
1:H:209:PHE:CE2	1:H:214:GLN:HG2	2.56	0.40
1:H:528:LYS:HD2	1:H:560:LEU:HD11	2.03	0.40
1:I:293:ILE:HD13	1:I:294:ALA:H	1.86	0.40
1:J:352:TRP:HB2	1:J:355:GLN:HG2	2.03	0.40
1:L:123:VAL:HG21	1:L:153:CYS:HB3	2.02	0.40
1:L:322:LEU:HD22	1:L:322:LEU:N	2.36	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:32:ASP:CG	1:L:316:TYR:CE2	2.94	0.40
1:K:372:TYR:CD2	1:L:348:LYS:HB2	2.55	0.40
1:K:376:ARG:HB2	1:L:352:TRP:CD1	2.56	0.40
1:L:352:TRP:HB2	1:L:355:GLN:HG2	2.03	0.40
1:L:383:ASP:CB	1:L:385:PRO:HD3	2.51	0.40
1:M:24:GLU:HG3	1:M:313:LYS:HE2	2.03	0.40
1:M:386:THR:CG2	1:M:389:LEU:HD21	2.51	0.40
1:M:457:MSE:O	1:M:458:ARG:CD	2.70	0.40
1:N:216:THR:HB	1:N:218:GLN:OE1	2.21	0.40
1:N:229:LYS:CG	1:N:229:LYS:O	2.69	0.40
1:N:503:GLU:HB3	1:N:508:ASN:HB3	2.03	0.40
1:N:248:LYS:HE2	1:N:513:ARG:HH12	1.85	0.40
1:N:583:LYS:HA	1:N:584:PRO:HD3	1.91	0.40
1:O:198:ILE:HA	1:O:199:PRO:HD3	1.69	0.40
1:O:24:GLU:N	1:O:24:GLU:CD	2.74	0.40
1:O:538:LEU:HB3	1:O:551:LEU:HD13	2.02	0.40
1:P:301:VAL:HG23	1:P:439:ASN:HB3	2.02	0.40
1:P:457:MSE:O	1:P:458:ARG:CD	2.69	0.40
1:Q:210:PRO:HD2	1:Q:211:TRP:CZ3	2.56	0.40
1:Q:282:THR:HG23	1:Q:287:LEU:CD1	2.47	0.40
1:R:147:GLU:HA	1:R:148:PRO:HD3	1.80	0.40
1:R:311:GLU:O	1:R:312:ASP:HB2	2.21	0.40
1:T:228:LYS:O	1:T:229:LYS:HB3	2.22	0.40
1:S:390:ALA:CB	1:U:387:GLN:HB3	2.51	0.40
1:U:444:LEU:O	1:U:445:GLU:C	2.58	0.40
1:V:457:MSE:O	1:V:458:ARG:CD	2.69	0.40
1:W:310:VAL:HB	1:W:311:GLU:H	1.68	0.40
1:W:578:GLN:HG2	1:W:596:ALA:CB	2.50	0.40
1:X:177:HIS:O	1:X:218:GLN:HA	2.21	0.40
1:X:236:GLN:CG	1:X:243:PRO:HB2	2.51	0.40
1:X:231:THR:HG23	1:X:249:ARG:HE	1.86	0.40
1:X:24:GLU:CD	1:X:24:GLU:N	2.75	0.40
1:X:387:GLN:HA	1:X:388:PRO:HD3	1.93	0.40
2:Y:124:TYR:O	2:Y:124:TYR:CG	2.73	0.40
1:A:273:ARG:NH1	1:A:275:ARG:HE	2.19	0.40
1:B:35:PHE:HZ	1:B:321:ARG:NE	2.12	0.40
1:C:209:PHE:CE2	1:C:214:GLN:HG2	2.56	0.40
1:C:313:LYS:HD3	1:C:314:GLU:N	2.36	0.40
1:D:430:VAL:HG12	1:D:431:ALA:N	2.35	0.40
1:D:80:TYR:HB2	1:D:95:MSE:HG2	2.03	0.40
1:E:316:TYR:O	1:E:321:ARG:NH1	2.53	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:528:LYS:HD2	1:E:560:LEU:HD11	2.03	0.40
1:E:598:GLN:HB2	1:E:601:GLN:HB3	2.02	0.40
1:E:61:ARG:N	1:E:62:PRO:CD	2.84	0.40
1:G:40:GLN:NE2	1:G:120:GLU:OE1	2.46	0.40
1:G:383:ASP:CB	1:G:385:PRO:HD3	2.51	0.40
1:H:71:MSE:HG2	1:H:429:GLN:HG3	2.03	0.40
1:H:99:ARG:NH1	1:H:530:GLN:HE21	2.13	0.40
1:I:32:ASP:CG	1:I:316:TYR:CE2	2.94	0.40
1:I:71:MSE:HG2	1:I:429:GLN:HG3	2.04	0.40
1:I:45:LEU:O	1:I:46:SER:HB3	2.22	0.40
1:I:542:THR:HA	1:I:543:PRO:HD3	1.82	0.40
1:I:579:MSE:CB	1:I:581:VAL:HG12	2.49	0.40
1:J:147:GLU:HA	1:J:148:PRO:HD3	1.86	0.40
1:J:71:MSE:HG2	1:J:429:GLN:HG3	2.03	0.40
1:J:598:GLN:HB2	1:J:601:GLN:HB3	2.02	0.40
1:K:93:VAL:HG11	1:K:458:ARG:HG2	2.03	0.40
1:L:255:ILE:O	1:L:256:ASP:C	2.60	0.40
1:L:293:ILE:HD13	1:L:294:ALA:H	1.87	0.40
1:L:364:ASP:CG	2:Y:135:ALA:HB2	2.42	0.40
1:L:430:VAL:HG12	1:L:431:ALA:N	2.35	0.40
1:M:219:ILE:HG13	1:M:220:ALA:N	2.35	0.40
1:M:245:SER:HG	1:M:247:PHE:HE1	1.64	0.40
1:O:228:LYS:O	1:O:229:LYS:HB3	2.20	0.40
1:O:236:GLN:H	1:O:265:LYS:CB	2.34	0.40
1:O:440:MSE:O	1:O:443:ASP:HB3	2.22	0.40
1:O:458:ARG:HD3	1:O:458:ARG:HA	1.83	0.40
1:O:57:PHE:N	1:O:57:PHE:CD1	2.88	0.40
1:Q:510:ILE:HG12	1:Q:511:ARG:H	1.86	0.40
1:R:123:VAL:HG13	1:R:304:PHE:CE1	2.57	0.40
1:R:202:GLN:O	1:R:203:ASN:HB3	2.22	0.40
1:R:236:GLN:CG	1:R:243:PRO:HB2	2.51	0.40
1:R:457:MSE:O	1:R:458:ARG:CD	2.69	0.40
1:R:503:GLU:HB3	1:R:508:ASN:HB3	2.03	0.40
1:S:311:GLU:O	1:S:312:ASP:HB2	2.22	0.40
1:U:160:SER:O	1:U:161:ASN:ND2	2.46	0.40
1:U:298:ILE:HA	1:U:299:PRO:HD3	1.77	0.40
1:X:578:GLN:HG2	1:X:596:ALA:CB	2.50	0.40
2:Y:20:ARG:C	2:Y:22:ALA:N	2.74	0.40
1:A:123:VAL:HG21	1:A:153:CYS:HB3	2.02	0.40
1:A:386:THR:HG21	1:A:389:LEU:HD21	2.02	0.40
1:A:40:GLN:O	1:A:41:TRP:CB	2.55	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:252:LYS:HZ1	1:B:256:ASP:HB3	1.86	0.40
1:B:528:LYS:HZ2	1:B:560:LEU:HD21	1.87	0.40
1:B:583:LYS:HA	1:B:584:PRO:HD3	1.85	0.40
1:C:71:MSE:HG2	1:C:429:GLN:HG3	2.03	0.40
1:D:298:ILE:HA	1:D:299:PRO:HD3	1.82	0.40
1:E:123:VAL:HG21	1:E:153:CYS:HB3	2.02	0.40
1:E:255:ILE:O	1:E:258:LEU:N	2.53	0.40
1:E:273:ARG:NH1	1:E:275:ARG:HE	2.19	0.40
1:E:459:ARG:C	1:E:459:ARG:HD2	2.42	0.40
1:F:255:ILE:O	1:F:256:ASP:C	2.60	0.40
1:F:322:LEU:HD22	1:F:322:LEU:N	2.36	0.40
1:F:459:ARG:C	1:F:459:ARG:HD2	2.42	0.40
1:F:71:MSE:HG2	1:F:429:GLN:HG3	2.03	0.40
1:G:255:ILE:O	1:G:256:ASP:C	2.60	0.40
1:G:322:LEU:HD22	1:G:322:LEU:N	2.36	0.40
3:F:719:HOH:O	1:G:438:LEU:HD22	2.20	0.40
1:G:45:LEU:O	1:G:46:SER:HB3	2.22	0.40
1:G:528:LYS:HD2	1:G:560:LEU:HD11	2.03	0.40
1:H:102:MSE:CE	1:H:144:ILE:HD11	2.52	0.40
1:H:24:GLU:C	1:H:26:ARG:N	2.73	0.40
1:H:37:ARG:HA	1:H:37:ARG:HD2	1.79	0.40
1:H:61:ARG:N	1:H:62:PRO:CD	2.84	0.40
1:I:248:LYS:H	1:I:248:LYS:CD	2.16	0.40
1:I:430:VAL:HG12	1:I:431:ALA:N	2.35	0.40
1:I:528:LYS:HD2	1:I:560:LEU:HD11	2.03	0.40
1:J:139:SER:CB	1:J:455:THR:CG2	2.80	0.40
1:J:45:LEU:O	1:J:46:SER:HB3	2.22	0.40
1:K:371:TYR:HA	1:L:348:LYS:HB3	2.03	0.40
1:K:78:VAL:CG1	1:K:444:LEU:HG	2.51	0.40
1:K:45:LEU:O	1:K:46:SER:HB3	2.22	0.40
1:K:528:LYS:HD2	1:K:560:LEU:HD11	2.03	0.40
1:L:380:ASN:O	1:L:381:SER:CB	2.70	0.40
1:M:371:TYR:CE2	1:M:373:LEU:HD21	2.56	0.40
1:N:11:ILE:O	1:N:15:PHE:HB2	2.22	0.40
1:O:232:ALA:HB1	1:O:233:PHE:H	1.58	0.40
1:O:236:GLN:CG	1:O:243:PRO:HB2	2.51	0.40
1:M:387:GLN:CB	1:O:390:ALA:HB2	2.52	0.40
1:O:578:GLN:HG2	1:O:596:ALA:CB	2.51	0.40
1:P:24:GLU:N	1:P:24:GLU:CD	2.74	0.40
1:P:306:GLU:O	1:P:316:TYR:HA	2.22	0.40
1:P:61:ARG:CB	1:P:62:PRO:HD3	2.52	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:115:VAL:HA	1:R:118:GLN:HB3	2.04	0.40
1:R:280:ILE:HG22	1:R:287:LEU:HD13	2.03	0.40
1:R:444:LEU:O	1:R:447:TYR:N	2.54	0.40
1:S:160:SER:O	1:S:161:ASN:ND2	2.46	0.40
1:S:198:ILE:HA	1:S:199:PRO:HD3	1.71	0.40
1:S:232:ALA:HB1	1:S:233:PHE:H	1.56	0.40
1:T:164:LEU:HD22	1:T:169:ASP:OD1	2.22	0.40
1:T:227:GLU:HG2	1:T:227:GLU:O	2.20	0.40
1:T:252:LYS:HE3	1:T:252:LYS:O	2.22	0.40
1:T:311:GLU:O	1:T:312:ASP:HB2	2.21	0.40
1:T:386:THR:CG2	1:T:389:LEU:HD21	2.51	0.40
1:T:440:MSE:O	1:T:443:ASP:HB3	2.21	0.40
1:U:310:VAL:HB	1:U:311:GLU:H	1.66	0.40
1:V:14:ARG:CA	1:V:14:ARG:NE	2.69	0.40
1:V:177:HIS:O	1:V:218:GLN:HA	2.22	0.40
1:W:156:VAL:O	1:W:156:VAL:CG2	2.68	0.40
1:W:383:ASP:C	1:W:385:PRO:HD3	2.40	0.40
2:Y:28:VAL:HG22	2:Y:93:PHE:CA	2.52	0.40
1:A:352:TRP:HB2	1:A:355:GLN:HG2	2.03	0.40
1:B:164:LEU:HD22	1:B:169:ASP:CG	2.42	0.40
1:B:47:GLN:N	1:B:47:GLN:CD	2.72	0.40
1:B:61:ARG:N	1:B:62:PRO:CD	2.84	0.40
1:C:47:GLN:C	1:C:48:TYR:CD2	2.95	0.40
1:E:127:ARG:HG2	1:E:147:GLU:HB2	2.02	0.40
1:E:37:ARG:HA	1:E:37:ARG:HD2	1.79	0.40
1:F:127:ARG:HG2	1:F:147:GLU:HB2	2.02	0.40
1:G:35:PHE:HZ	1:G:321:ARG:NE	2.12	0.40
1:G:71:MSE:HG2	1:G:429:GLN:HG3	2.03	0.40
1:G:440:MSE:O	1:G:444:LEU:CD2	2.69	0.40
1:G:139:SER:CB	1:G:455:THR:CG2	2.80	0.40
1:G:47:GLN:C	1:G:48:TYR:CD2	2.95	0.40
1:G:99:ARG:NH1	1:G:530:GLN:HE21	2.13	0.40
1:H:298:ILE:HA	1:H:299:PRO:HD3	1.82	0.40
1:H:380:ASN:O	1:H:381:SER:CB	2.70	0.40
1:H:248:LYS:HZ1	1:H:513:ARG:HH12	1.70	0.40
1:I:78:VAL:CG1	1:I:444:LEU:HG	2.51	0.40
1:J:123:VAL:HG21	1:J:153:CYS:HB3	2.02	0.40
1:J:246:TYR:HD2	1:J:511:ARG:CB	2.28	0.40
1:J:380:ASN:O	1:J:381:SER:CB	2.70	0.40
1:J:99:ARG:HH12	1:J:530:GLN:NE2	2.14	0.40
1:K:123:VAL:HG21	1:K:153:CYS:HB3	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:255:ILE:O	1:K:256:ASP:C	2.60	0.40
1:K:276:VAL:HG23	1:K:293:ILE:HG22	2.03	0.40
1:L:102:MSE:CE	1:L:144:ILE:HD11	2.52	0.40
1:L:147:GLU:HA	1:L:148:PRO:HD3	1.86	0.40
1:L:164:LEU:HD22	1:L:169:ASP:CG	2.41	0.40
1:L:45:LEU:O	1:L:46:SER:HB3	2.22	0.40
1:M:251:ILE:HD11	1:M:275:ARG:HH21	1.86	0.40
1:N:210:PRO:HD2	1:N:211:TRP:CZ3	2.56	0.40
1:N:232:ALA:N	1:N:269:ARG:O	2.54	0.40
1:N:438:LEU:HD12	1:N:441:ARG:NH1	2.37	0.40
1:O:219:ILE:HG13	1:O:220:ALA:N	2.37	0.40
1:P:107:ALA:HA	1:P:146:ARG:HB3	2.03	0.40
1:P:216:THR:HB	1:P:218:GLN:OE1	2.22	0.40
1:P:26:ARG:O	1:P:27:ARG:C	2.59	0.40
1:Q:577:ILE:HG12	1:Q:582:LYS:CG	2.45	0.40
1:R:591:GLN:HA	1:R:594:VAL:CG2	2.51	0.40
1:S:301:VAL:HG23	1:S:439:ASN:HB3	2.02	0.40
1:S:514:TYR:HE2	1:U:135:GLN:NE2	2.19	0.40
1:U:236:GLN:CG	1:U:243:PRO:HB2	2.52	0.40
1:V:349:PRO:HG3	1:V:391:TYR:CE1	2.56	0.40
1:W:334:MSE:SE	1:W:405:LEU:HD11	2.71	0.40
3:T:719:HOH:O	1:W:430:VAL:HG11	2.17	0.40
1:X:210:PRO:HD2	1:X:211:TRP:CZ3	2.56	0.40
1:X:260:ASP:CA	1:X:264:ILE:HB	2.52	0.40
1:R:396:GLU:O	1:X:399:GLN:OE1	2.39	0.40
2:Y:57:TYR:O	2:Y:59:ASP:N	2.54	0.40

All (13) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:230:GLU:OE2	2:c:74:ASN:ND2[2_546]	1.06	1.14
1:N:230:GLU:N	2:r:64:GLU:OE2[2_455]	1.79	0.41
1:N:260:ASP:OD2	1:B:601:GLN:NE2[2_555]	1.79	0.41
1:C:250:ASP:OD2	2:c:74:ASN:OD1[2_546]	1.83	0.37
1:N:228:LYS:CG	2:r:64:GLU:OE1[2_455]	1.89	0.31
1:N:229:LYS:C	2:r:64:GLU:OE2[2_455]	1.92	0.28
1:S:249:ARG:NH1	2:v:65:ASN:CB[2_445]	1.94	0.26
1:S:249:ARG:NH2	2:v:65:ASN:ND2[2_445]	1.99	0.21
1:C:277:TYR:OH	2:c:73:GLU:CG[2_546]	2.05	0.15

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:262:GLY:O	1:B:594:VAL:CG1[2_555]	2.08	0.12
1:C:230:GLU:CD	2:c:74:ASN:ND2[2_546]	2.08	0.12
1:S:249:ARG:NH1	2:v:65:ASN:ND2[2_445]	2.09	0.11
1:W:249:ARG:NH1	2:g:72:ASP:CG[1_454]	2.10	0.10

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	B	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	7
1	C	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	7
1	D	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	E	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	F	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	G	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	H	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	I	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	J	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	K	565/602 (94%)	434 (77%)	88 (16%)	43 (8%)	1	8
1	L	565/602 (94%)	434 (77%)	87 (15%)	44 (8%)	1	7
1	M	565/602 (94%)	446 (79%)	81 (14%)	38 (7%)	1	11
1	N	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	10
1	O	565/602 (94%)	447 (79%)	80 (14%)	38 (7%)	1	11
1	P	565/602 (94%)	448 (79%)	79 (14%)	38 (7%)	1	11
1	Q	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	10
1	R	565/602 (94%)	448 (79%)	79 (14%)	38 (7%)	1	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	S	565/602 (94%)	443 (78%)	83 (15%)	39 (7%)	1	10
1	T	565/602 (94%)	446 (79%)	81 (14%)	38 (7%)	1	11
1	U	565/602 (94%)	447 (79%)	79 (14%)	39 (7%)	1	10
1	V	565/602 (94%)	445 (79%)	82 (14%)	38 (7%)	1	11
1	W	565/602 (94%)	448 (79%)	78 (14%)	39 (7%)	1	10
1	X	565/602 (94%)	448 (79%)	78 (14%)	39 (7%)	1	10
2	Y	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	Z	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	a	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	b	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	c	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	d	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	e	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	f	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	g	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	h	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	i	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	j	144/166 (87%)	115 (80%)	16 (11%)	13 (9%)	1	5
2	k	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	8
2	l	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	8
2	m	143/166 (86%)	115 (80%)	18 (13%)	10 (7%)	1	9
2	n	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	8
2	o	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	8
2	p	143/166 (86%)	115 (80%)	17 (12%)	11 (8%)	1	8
2	q	143/166 (86%)	113 (79%)	19 (13%)	11 (8%)	1	8
2	r	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	8
2	s	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	8
2	t	143/166 (86%)	113 (79%)	19 (13%)	11 (8%)	1	8
2	u	143/166 (86%)	114 (80%)	18 (13%)	11 (8%)	1	8
2	v	143/166 (86%)	114 (80%)	19 (13%)	10 (7%)	1	9
All	All	17004/18432 (92%)	13318 (78%)	2419 (14%)	1267 (8%)	1	8

All (1267) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	M	82	PRO
1	M	263	PHE
1	M	294	ALA
1	M	462	GLU
1	M	514	TYR
1	M	561	ASP
1	M	586	THR
1	M	588	GLU
1	N	82	PRO
1	N	263	PHE
1	N	294	ALA
1	N	462	GLU
1	N	514	TYR
1	N	561	ASP
1	N	586	THR
1	N	588	GLU
1	O	82	PRO
1	O	263	PHE
1	O	294	ALA
1	O	462	GLU
1	O	514	TYR
1	O	561	ASP
1	O	586	THR
1	O	588	GLU
1	P	82	PRO
1	P	263	PHE
1	P	294	ALA
1	P	462	GLU
1	P	514	TYR
1	P	561	ASP
1	P	586	THR
1	P	588	GLU
1	Q	82	PRO
1	Q	263	PHE
1	Q	294	ALA
1	Q	462	GLU
1	Q	514	TYR
1	Q	561	ASP
1	Q	586	THR
1	Q	588	GLU
1	R	82	PRO
1	R	263	PHE

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Mol	Chain	Res	Type
1	R	294	ALA
1	R	462	GLU
1	R	514	TYR
1	R	561	ASP
1	R	586	THR
1	R	588	GLU
1	S	82	PRO
1	S	263	PHE
1	S	294	ALA
1	S	462	GLU
1	S	514	TYR
1	S	561	ASP
1	S	586	THR
1	S	588	GLU
1	T	82	PRO
1	T	263	PHE
1	T	294	ALA
1	T	462	GLU
1	T	514	TYR
1	T	561	ASP
1	T	586	THR
1	T	588	GLU
1	U	82	PRO
1	U	263	PHE
1	U	294	ALA
1	U	462	GLU
1	U	514	TYR
1	U	561	ASP
1	U	586	THR
1	U	588	GLU
1	V	82	PRO
1	V	263	PHE
1	V	294	ALA
1	V	462	GLU
1	V	514	TYR
1	V	561	ASP
1	V	586	THR
1	V	588	GLU
1	W	82	PRO
1	W	263	PHE
1	W	294	ALA
1	W	462	GLU

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Mol	Chain	Res	Type
1	W	514	TYR
1	W	561	ASP
1	W	586	THR
1	W	588	GLU
1	X	82	PRO
1	X	263	PHE
1	X	294	ALA
1	X	462	GLU
1	X	514	TYR
1	X	561	ASP
1	X	586	THR
1	X	588	GLU
2	k	25	LEU
2	k	30	PRO
2	k	123	ALA
2	l	25	LEU
2	l	30	PRO
2	l	123	ALA
2	m	25	LEU
2	m	30	PRO
2	m	123	ALA
2	n	25	LEU
2	n	30	PRO
2	n	123	ALA
2	o	25	LEU
2	o	30	PRO
2	o	123	ALA
2	p	25	LEU
2	p	30	PRO
2	p	123	ALA
2	q	25	LEU
2	q	30	PRO
2	q	123	ALA
2	r	25	LEU
2	r	30	PRO
2	r	123	ALA
2	s	25	LEU
2	s	30	PRO
2	s	123	ALA
2	t	25	LEU
2	t	30	PRO
2	t	123	ALA

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Mol	Chain	Res	Type
2	u	25	LEU
2	u	30	PRO
2	u	123	ALA
2	v	25	LEU
2	v	30	PRO
2	v	123	ALA
1	A	41	TRP
1	A	50	THR
1	A	59	VAL
1	A	82	PRO
1	A	159	ASP
1	A	208	VAL
1	A	256	ASP
1	A	263	PHE
1	A	294	ALA
1	A	387	GLN
1	A	462	GLU
1	A	504	LYS
1	A	514	TYR
1	A	561	ASP
1	A	586	THR
1	B	41	TRP
1	B	50	THR
1	B	59	VAL
1	B	82	PRO
1	B	159	ASP
1	B	208	VAL
1	B	256	ASP
1	B	263	PHE
1	B	294	ALA
1	B	387	GLN
1	B	462	GLU
1	B	504	LYS
1	B	514	TYR
1	B	561	ASP
1	B	586	THR
1	C	41	TRP
1	C	50	THR
1	C	59	VAL
1	C	82	PRO
1	C	159	ASP
1	C	208	VAL

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Mol	Chain	Res	Type
1	C	256	ASP
1	C	263	PHE
1	C	294	ALA
1	C	387	GLN
1	C	462	GLU
1	C	504	LYS
1	C	514	TYR
1	C	561	ASP
1	C	586	THR
1	D	41	TRP
1	D	50	THR
1	D	59	VAL
1	D	82	PRO
1	D	159	ASP
1	D	208	VAL
1	D	256	ASP
1	D	263	PHE
1	D	294	ALA
1	D	387	GLN
1	D	462	GLU
1	D	504	LYS
1	D	514	TYR
1	D	561	ASP
1	D	586	THR
1	E	41	TRP
1	E	50	THR
1	E	59	VAL
1	E	82	PRO
1	E	159	ASP
1	E	208	VAL
1	E	256	ASP
1	E	263	PHE
1	E	294	ALA
1	E	387	GLN
1	E	462	GLU
1	E	504	LYS
1	E	514	TYR
1	E	561	ASP
1	E	586	THR
1	F	41	TRP
1	F	50	THR
1	F	59	VAL

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Mol	Chain	Res	Type
1	F	82	PRO
1	F	159	ASP
1	F	208	VAL
1	F	256	ASP
1	F	263	PHE
1	F	294	ALA
1	F	387	GLN
1	F	462	GLU
1	F	504	LYS
1	F	514	TYR
1	F	561	ASP
1	F	586	THR
1	G	41	TRP
1	G	50	THR
1	G	59	VAL
1	G	82	PRO
1	G	159	ASP
1	G	208	VAL
1	G	256	ASP
1	G	263	PHE
1	G	294	ALA
1	G	387	GLN
1	G	462	GLU
1	G	504	LYS
1	G	514	TYR
1	G	561	ASP
1	G	586	THR
1	H	41	TRP
1	H	50	THR
1	H	59	VAL
1	H	82	PRO
1	H	159	ASP
1	H	208	VAL
1	H	256	ASP
1	H	263	PHE
1	H	294	ALA
1	H	387	GLN
1	H	462	GLU
1	H	504	LYS
1	H	514	TYR
1	H	561	ASP
1	H	586	THR

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Mol	Chain	Res	Type
1	I	41	TRP
1	I	50	THR
1	I	59	VAL
1	I	82	PRO
1	I	159	ASP
1	I	208	VAL
1	I	256	ASP
1	I	263	PHE
1	I	294	ALA
1	I	387	GLN
1	I	462	GLU
1	I	504	LYS
1	I	514	TYR
1	I	561	ASP
1	I	586	THR
1	J	41	TRP
1	J	50	THR
1	J	59	VAL
1	J	82	PRO
1	J	159	ASP
1	J	208	VAL
1	J	256	ASP
1	J	263	PHE
1	J	294	ALA
1	J	387	GLN
1	J	462	GLU
1	J	504	LYS
1	J	514	TYR
1	J	561	ASP
1	J	586	THR
1	K	41	TRP
1	K	50	THR
1	K	59	VAL
1	K	82	PRO
1	K	208	VAL
1	K	256	ASP
1	K	263	PHE
1	K	294	ALA
1	K	387	GLN
1	K	462	GLU
1	K	504	LYS
1	K	514	TYR

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Mol	Chain	Res	Type
1	K	561	ASP
1	K	586	THR
1	L	41	TRP
1	L	50	THR
1	L	59	VAL
1	L	82	PRO
1	L	159	ASP
1	L	208	VAL
1	L	256	ASP
1	L	263	PHE
1	L	294	ALA
1	L	387	GLN
1	L	462	GLU
1	L	504	LYS
1	L	514	TYR
1	L	561	ASP
1	L	586	THR
2	Y	33	THR
2	Y	39	PRO
2	Y	75	PRO
2	Y	76	PRO
2	Y	133	LYS
2	Z	33	THR
2	Z	39	PRO
2	Z	75	PRO
2	Z	76	PRO
2	Z	133	LYS
2	a	33	THR
2	a	39	PRO
2	a	75	PRO
2	a	76	PRO
2	a	133	LYS
2	b	33	THR
2	b	39	PRO
2	b	75	PRO
2	b	76	PRO
2	b	133	LYS
2	c	33	THR
2	c	39	PRO
2	c	75	PRO
2	c	76	PRO
2	c	133	LYS

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Mol	Chain	Res	Type
2	d	33	THR
2	d	39	PRO
2	d	75	PRO
2	d	76	PRO
2	d	133	LYS
2	e	33	THR
2	e	39	PRO
2	e	75	PRO
2	e	76	PRO
2	e	133	LYS
2	f	33	THR
2	f	39	PRO
2	f	75	PRO
2	f	76	PRO
2	f	133	LYS
2	g	33	THR
2	g	39	PRO
2	g	75	PRO
2	g	76	PRO
2	g	133	LYS
2	h	33	THR
2	h	39	PRO
2	h	75	PRO
2	h	76	PRO
2	h	133	LYS
2	i	33	THR
2	i	39	PRO
2	i	75	PRO
2	i	76	PRO
2	i	133	LYS
2	j	33	THR
2	j	39	PRO
2	j	75	PRO
2	j	76	PRO
2	j	133	LYS
1	M	25	ALA
1	M	159	ASP
1	M	205	ASN
1	M	267	ALA
1	M	500	ALA
1	N	25	ALA
1	N	159	ASP

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Mol	Chain	Res	Type
1	N	205	ASN
1	N	267	ALA
1	N	295	GLY
1	N	500	ALA
1	N	513	ARG
1	O	25	ALA
1	O	76	ILE
1	O	159	ASP
1	O	205	ASN
1	O	267	ALA
1	O	295	GLY
1	O	500	ALA
1	O	513	ARG
1	P	25	ALA
1	P	49	THR
1	P	159	ASP
1	P	205	ASN
1	P	267	ALA
1	P	500	ALA
1	P	513	ARG
1	Q	25	ALA
1	Q	159	ASP
1	Q	205	ASN
1	Q	267	ALA
1	Q	500	ALA
1	R	25	ALA
1	R	159	ASP
1	R	205	ASN
1	R	267	ALA
1	R	295	GLY
1	R	500	ALA
1	S	25	ALA
1	S	49	THR
1	S	159	ASP
1	S	205	ASN
1	S	267	ALA
1	S	295	GLY
1	S	500	ALA
1	S	513	ARG
1	T	25	ALA
1	T	159	ASP
1	T	205	ASN

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Mol	Chain	Res	Type
1	T	267	ALA
1	T	500	ALA
1	T	513	ARG
1	U	25	ALA
1	U	159	ASP
1	U	205	ASN
1	U	267	ALA
1	U	295	GLY
1	U	500	ALA
1	U	513	ARG
1	V	25	ALA
1	V	159	ASP
1	V	205	ASN
1	V	267	ALA
1	V	295	GLY
1	V	500	ALA
1	W	25	ALA
1	W	159	ASP
1	W	205	ASN
1	W	267	ALA
1	W	295	GLY
1	W	500	ALA
1	X	25	ALA
1	X	76	ILE
1	X	159	ASP
1	X	205	ASN
1	X	267	ALA
1	X	295	GLY
1	X	500	ALA
2	k	66	PRO
2	k	69	GLU
2	k	124	LYS
2	k	149	PHE
2	l	66	PRO
2	l	69	GLU
2	l	124	LYS
2	l	131	ARG
2	l	149	PHE
2	m	66	PRO
2	m	124	LYS
2	m	149	PHE
2	n	66	PRO

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Mol	Chain	Res	Type
2	n	124	LYS
2	n	131	ARG
2	n	149	PHE
2	o	66	PRO
2	o	124	LYS
2	o	149	PHE
2	p	66	PRO
2	p	124	LYS
2	p	149	PHE
2	q	66	PRO
2	q	69	GLU
2	q	124	LYS
2	q	149	PHE
2	r	66	PRO
2	r	69	GLU
2	r	124	LYS
2	r	131	ARG
2	r	149	PHE
2	s	66	PRO
2	s	124	LYS
2	s	149	PHE
2	t	66	PRO
2	t	124	LYS
2	t	149	PHE
2	u	66	PRO
2	u	69	GLU
2	u	124	LYS
2	u	149	PHE
2	v	66	PRO
2	v	69	GLU
2	v	124	LYS
2	v	149	PHE
1	A	267	ALA
1	A	381	SER
1	A	388	PRO
1	A	588	GLU
1	B	267	ALA
1	B	381	SER
1	B	388	PRO
1	B	588	GLU
1	C	267	ALA
1	C	381	SER

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Mol	Chain	Res	Type
1	C	388	PRO
1	C	588	GLU
1	D	267	ALA
1	D	381	SER
1	D	388	PRO
1	D	588	GLU
1	E	267	ALA
1	E	381	SER
1	E	388	PRO
1	E	588	GLU
1	F	267	ALA
1	F	381	SER
1	F	388	PRO
1	F	588	GLU
1	G	267	ALA
1	G	381	SER
1	G	388	PRO
1	G	588	GLU
1	H	267	ALA
1	H	381	SER
1	H	388	PRO
1	H	588	GLU
1	I	267	ALA
1	I	381	SER
1	I	388	PRO
1	I	588	GLU
1	J	267	ALA
1	J	381	SER
1	J	388	PRO
1	J	588	GLU
1	K	159	ASP
1	K	267	ALA
1	K	381	SER
1	K	388	PRO
1	K	588	GLU
1	L	267	ALA
1	L	381	SER
1	L	388	PRO
1	L	588	GLU
2	Y	80	ASP
2	Y	132	ALA
2	Y	140	ARG

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Mol	Chain	Res	Type
2	Y	158	PHE
2	Z	80	ASP
2	Z	132	ALA
2	Z	140	ARG
2	Z	158	PHE
2	a	80	ASP
2	a	132	ALA
2	a	140	ARG
2	a	158	PHE
2	b	80	ASP
2	b	132	ALA
2	b	140	ARG
2	b	158	PHE
2	c	80	ASP
2	c	132	ALA
2	c	140	ARG
2	c	158	PHE
2	d	80	ASP
2	d	132	ALA
2	d	140	ARG
2	d	158	PHE
2	e	80	ASP
2	e	132	ALA
2	e	140	ARG
2	e	158	PHE
2	f	80	ASP
2	f	132	ALA
2	f	140	ARG
2	f	158	PHE
2	g	80	ASP
2	g	132	ALA
2	g	140	ARG
2	g	158	PHE
2	h	80	ASP
2	h	132	ALA
2	h	140	ARG
2	h	158	PHE
2	i	80	ASP
2	i	132	ALA
2	i	140	ARG
2	i	158	PHE
2	j	80	ASP

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Mol	Chain	Res	Type
2	j	132	ALA
2	j	140	ARG
2	j	158	PHE
1	M	8	LEU
1	M	49	THR
1	M	76	ILE
1	M	210	PRO
1	M	216	THR
1	M	295	GLY
1	M	302	PRO
1	M	381	SER
1	M	388	PRO
1	M	452	ASN
1	M	513	ARG
1	N	8	LEU
1	N	49	THR
1	N	76	ILE
1	N	210	PRO
1	N	216	THR
1	N	302	PRO
1	N	388	PRO
1	N	457	MSE
1	O	8	LEU
1	O	49	THR
1	O	210	PRO
1	O	216	THR
1	O	302	PRO
1	O	381	SER
1	O	388	PRO
1	O	452	ASN
1	O	457	MSE
1	P	8	LEU
1	P	76	ILE
1	P	210	PRO
1	P	216	THR
1	P	295	GLY
1	P	302	PRO
1	P	381	SER
1	P	388	PRO
1	P	452	ASN
1	P	457	MSE
1	Q	8	LEU

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Mol	Chain	Res	Type
1	Q	49	THR
1	Q	76	ILE
1	Q	210	PRO
1	Q	216	THR
1	Q	295	GLY
1	Q	302	PRO
1	Q	381	SER
1	Q	388	PRO
1	Q	457	MSE
1	Q	513	ARG
1	R	8	LEU
1	R	49	THR
1	R	76	ILE
1	R	210	PRO
1	R	216	THR
1	R	302	PRO
1	R	388	PRO
1	R	457	MSE
1	R	513	ARG
1	S	8	LEU
1	S	76	ILE
1	S	210	PRO
1	S	216	THR
1	S	302	PRO
1	S	381	SER
1	S	388	PRO
1	S	452	ASN
1	S	457	MSE
1	T	8	LEU
1	T	49	THR
1	T	76	ILE
1	T	210	PRO
1	T	216	THR
1	T	295	GLY
1	T	302	PRO
1	T	381	SER
1	T	388	PRO
1	T	452	ASN
1	U	8	LEU
1	U	49	THR
1	U	76	ILE
1	U	210	PRO

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Mol	Chain	Res	Type
1	U	216	THR
1	U	302	PRO
1	U	388	PRO
1	U	452	ASN
1	V	8	LEU
1	V	36	SER
1	V	49	THR
1	V	76	ILE
1	V	210	PRO
1	V	216	THR
1	V	302	PRO
1	V	388	PRO
1	V	513	ARG
1	W	8	LEU
1	W	49	THR
1	W	76	ILE
1	W	210	PRO
1	W	216	THR
1	W	302	PRO
1	W	388	PRO
1	W	452	ASN
1	W	457	MSE
1	W	513	ARG
1	X	8	LEU
1	X	49	THR
1	X	210	PRO
1	X	216	THR
1	X	302	PRO
1	X	381	SER
1	X	388	PRO
1	X	457	MSE
1	X	513	ARG
2	k	131	ARG
2	m	69	GLU
2	m	131	ARG
2	n	69	GLU
2	o	69	GLU
2	o	131	ARG
2	p	69	GLU
2	p	131	ARG
2	q	131	ARG
2	s	69	GLU

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Mol	Chain	Res	Type
2	s	131	ARG
2	t	69	GLU
2	t	131	ARG
2	u	131	ARG
2	v	131	ARG
1	A	26	ARG
1	A	36	SER
1	A	205	ASN
1	A	262	GLY
1	B	26	ARG
1	B	36	SER
1	B	205	ASN
1	B	262	GLY
1	C	26	ARG
1	C	36	SER
1	C	205	ASN
1	C	262	GLY
1	D	26	ARG
1	D	36	SER
1	D	205	ASN
1	D	262	GLY
1	E	26	ARG
1	E	36	SER
1	E	205	ASN
1	E	262	GLY
1	F	26	ARG
1	F	36	SER
1	F	205	ASN
1	F	262	GLY
1	G	26	ARG
1	G	36	SER
1	G	205	ASN
1	G	262	GLY
1	H	26	ARG
1	H	36	SER
1	H	205	ASN
1	H	262	GLY
1	I	26	ARG
1	I	36	SER
1	I	205	ASN
1	I	262	GLY
1	J	26	ARG

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Mol	Chain	Res	Type
1	J	36	SER
1	J	205	ASN
1	J	262	GLY
1	K	26	ARG
1	K	36	SER
1	K	205	ASN
1	K	262	GLY
1	L	26	ARG
1	L	36	SER
1	L	205	ASN
1	L	262	GLY
2	Y	54	ALA
2	Y	78	GLU
2	Z	54	ALA
2	Z	78	GLU
2	a	54	ALA
2	a	78	GLU
2	b	54	ALA
2	b	78	GLU
2	c	54	ALA
2	c	78	GLU
2	d	54	ALA
2	d	78	GLU
2	e	54	ALA
2	e	78	GLU
2	f	54	ALA
2	f	78	GLU
2	g	54	ALA
2	g	78	GLU
2	h	54	ALA
2	h	78	GLU
2	i	54	ALA
2	i	78	GLU
2	j	54	ALA
2	j	78	GLU
1	M	192	ASP
1	M	198	ILE
1	M	244	VAL
1	M	457	MSE
1	M	583	LYS
1	N	36	SER
1	N	192	ASP

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Mol	Chain	Res	Type
1	N	198	ILE
1	N	244	VAL
1	N	381	SER
1	N	452	ASN
1	N	583	LYS
1	O	36	SER
1	O	192	ASP
1	O	198	ILE
1	O	244	VAL
1	O	508	ASN
1	O	583	LYS
1	P	192	ASP
1	P	198	ILE
1	P	244	VAL
1	P	583	LYS
1	Q	36	SER
1	Q	192	ASP
1	Q	198	ILE
1	Q	244	VAL
1	Q	452	ASN
1	Q	583	LYS
1	R	36	SER
1	R	198	ILE
1	R	244	VAL
1	R	381	SER
1	R	452	ASN
1	R	583	LYS
1	S	36	SER
1	S	192	ASP
1	S	198	ILE
1	S	244	VAL
1	S	450	GLN
1	S	583	LYS
1	T	192	ASP
1	T	198	ILE
1	T	244	VAL
1	T	457	MSE
1	T	583	LYS
1	U	36	SER
1	U	192	ASP
1	U	198	ILE
1	U	244	VAL

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Mol	Chain	Res	Type
1	U	381	SER
1	U	457	MSE
1	U	583	LYS
1	V	192	ASP
1	V	198	ILE
1	V	244	VAL
1	V	381	SER
1	V	452	ASN
1	V	457	MSE
1	V	583	LYS
1	W	36	SER
1	W	192	ASP
1	W	198	ILE
1	W	244	VAL
1	W	381	SER
1	W	583	LYS
1	X	36	SER
1	X	192	ASP
1	X	198	ILE
1	X	244	VAL
1	X	452	ASN
1	X	583	LYS
2	k	132	MET
2	l	132	MET
2	m	132	MET
2	n	132	MET
2	o	132	MET
2	p	132	MET
2	q	132	MET
2	r	132	MET
2	s	132	MET
2	t	132	MET
2	u	132	MET
2	v	132	MET
1	A	161	ASN
1	A	198	ILE
1	A	209	PHE
1	A	216	THR
1	A	244	VAL
1	A	253	ASP
1	A	380	ASN
1	A	583	LYS

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Mol	Chain	Res	Type
1	B	161	ASN
1	B	198	ILE
1	B	209	PHE
1	B	216	THR
1	B	244	VAL
1	B	253	ASP
1	B	380	ASN
1	B	583	LYS
1	C	161	ASN
1	C	198	ILE
1	C	209	PHE
1	C	216	THR
1	C	244	VAL
1	C	253	ASP
1	C	380	ASN
1	C	583	LYS
1	D	161	ASN
1	D	198	ILE
1	D	209	PHE
1	D	216	THR
1	D	244	VAL
1	D	253	ASP
1	D	380	ASN
1	D	583	LYS
1	E	161	ASN
1	E	198	ILE
1	E	209	PHE
1	E	216	THR
1	E	244	VAL
1	E	253	ASP
1	E	380	ASN
1	E	583	LYS
1	F	161	ASN
1	F	198	ILE
1	F	209	PHE
1	F	216	THR
1	F	244	VAL
1	F	253	ASP
1	F	380	ASN
1	F	583	LYS
1	G	161	ASN
1	G	198	ILE

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Mol	Chain	Res	Type
1	G	209	PHE
1	G	216	THR
1	G	244	VAL
1	G	253	ASP
1	G	380	ASN
1	G	583	LYS
1	H	161	ASN
1	H	198	ILE
1	H	209	PHE
1	H	216	THR
1	H	244	VAL
1	H	253	ASP
1	H	380	ASN
1	H	583	LYS
1	I	161	ASN
1	I	198	ILE
1	I	209	PHE
1	I	216	THR
1	I	244	VAL
1	I	253	ASP
1	I	380	ASN
1	I	583	LYS
1	J	161	ASN
1	J	198	ILE
1	J	209	PHE
1	J	216	THR
1	J	244	VAL
1	J	253	ASP
1	J	380	ASN
1	J	583	LYS
1	K	161	ASN
1	K	198	ILE
1	K	209	PHE
1	K	216	THR
1	K	244	VAL
1	K	253	ASP
1	K	380	ASN
1	K	583	LYS
1	L	161	ASN
1	L	198	ILE
1	L	209	PHE
1	L	216	THR

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Mol	Chain	Res	Type
1	L	244	VAL
1	L	253	ASP
1	L	380	ASN
1	L	583	LYS
2	Y	141	MET
2	Y	149	PHE
2	Z	141	MET
2	Z	149	PHE
2	a	141	MET
2	a	149	PHE
2	b	141	MET
2	b	149	PHE
2	c	141	MET
2	c	149	PHE
2	d	141	MET
2	d	149	PHE
2	e	141	MET
2	e	149	PHE
2	f	141	MET
2	f	149	PHE
2	g	141	MET
2	g	149	PHE
2	h	141	MET
2	h	149	PHE
2	i	141	MET
2	i	149	PHE
2	j	141	MET
2	j	149	PHE
1	M	36	SER
1	M	344	THR
1	M	450	GLN
1	M	508	ASN
1	N	262	GLY
1	N	344	THR
1	N	508	ASN
1	O	217	ILE
1	O	344	THR
1	P	445	GLU
1	P	450	GLN
1	P	508	ASN
1	Q	262	GLY
1	Q	450	GLN

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Mol	Chain	Res	Type
1	Q	508	ASN
1	R	192	ASP
1	R	217	ILE
1	R	450	GLN
1	R	508	ASN
1	S	445	GLU
1	S	508	ASN
1	T	36	SER
1	T	217	ILE
1	T	262	GLY
1	T	450	GLN
1	T	508	ASN
1	U	262	GLY
1	U	344	THR
1	U	445	GLU
1	U	450	GLN
1	U	508	ASN
1	V	344	THR
1	V	450	GLN
1	V	508	ASN
1	W	217	ILE
1	W	344	THR
1	W	450	GLN
1	W	508	ASN
1	X	344	THR
1	X	445	GLU
1	X	508	ASN
2	k	44	MET
2	l	44	MET
2	n	44	MET
2	p	44	MET
2	q	44	MET
2	r	44	MET
1	A	76	ILE
1	A	192	ASP
1	A	206	ASP
1	A	232	ALA
1	A	295	GLY
1	A	302	PRO
1	B	76	ILE
1	B	192	ASP
1	B	206	ASP

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Mol	Chain	Res	Type
1	B	232	ALA
1	B	295	GLY
1	B	302	PRO
1	C	76	ILE
1	C	192	ASP
1	C	206	ASP
1	C	232	ALA
1	C	295	GLY
1	C	302	PRO
1	D	76	ILE
1	D	192	ASP
1	D	232	ALA
1	D	295	GLY
1	D	302	PRO
1	E	76	ILE
1	E	192	ASP
1	E	206	ASP
1	E	232	ALA
1	E	295	GLY
1	E	302	PRO
1	F	76	ILE
1	F	192	ASP
1	F	206	ASP
1	F	232	ALA
1	F	295	GLY
1	F	302	PRO
1	G	76	ILE
1	G	192	ASP
1	G	206	ASP
1	G	232	ALA
1	G	295	GLY
1	G	302	PRO
1	H	76	ILE
1	H	192	ASP
1	H	206	ASP
1	H	232	ALA
1	H	295	GLY
1	H	302	PRO
1	I	76	ILE
1	I	192	ASP
1	I	232	ALA
1	I	295	GLY

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Mol	Chain	Res	Type
1	I	302	PRO
1	J	76	ILE
1	J	192	ASP
1	J	206	ASP
1	J	232	ALA
1	J	295	GLY
1	J	302	PRO
1	K	76	ILE
1	K	192	ASP
1	K	206	ASP
1	K	232	ALA
1	K	295	GLY
1	K	302	PRO
1	L	76	ILE
1	L	192	ASP
1	L	206	ASP
1	L	232	ALA
1	L	295	GLY
1	L	302	PRO
1	M	203	ASN
1	M	217	ILE
1	M	262	GLY
1	M	397	VAL
1	N	203	ASN
1	N	217	ILE
1	N	445	GLU
1	N	450	GLN
1	O	203	ASN
1	O	262	GLY
1	O	397	VAL
1	O	450	GLN
1	P	203	ASN
1	P	262	GLY
1	P	344	THR
1	Q	203	ASN
1	Q	217	ILE
1	Q	344	THR
1	Q	397	VAL
1	Q	498	ASP
1	R	203	ASN
1	R	262	GLY
1	R	344	THR

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Mol	Chain	Res	Type
1	R	397	VAL
1	S	203	ASN
1	S	217	ILE
1	S	262	GLY
1	T	203	ASN
1	T	344	THR
1	U	203	ASN
1	U	217	ILE
1	V	203	ASN
1	V	217	ILE
1	V	262	GLY
1	W	203	ASN
1	W	262	GLY
1	W	445	GLU
1	X	203	ASN
1	X	217	ILE
1	X	262	GLY
1	X	397	VAL
1	X	450	GLN
2	o	44	MET
2	s	44	MET
2	t	44	MET
2	u	44	MET
1	A	311	GLU
1	A	384	LEU
1	B	311	GLU
1	B	384	LEU
1	B	507	LEU
1	C	311	GLU
1	C	384	LEU
1	C	507	LEU
1	D	206	ASP
1	D	311	GLU
1	D	384	LEU
1	E	311	GLU
1	E	384	LEU
1	F	311	GLU
1	F	384	LEU
1	G	311	GLU
1	G	384	LEU
1	H	311	GLU
1	H	384	LEU

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Mol	Chain	Res	Type
1	I	206	ASP
1	I	311	GLU
1	I	384	LEU
1	J	311	GLU
1	J	384	LEU
1	K	311	GLU
1	K	384	LEU
1	L	311	GLU
1	L	384	LEU
1	L	507	LEU
1	N	397	VAL
1	P	217	ILE
1	S	344	THR
1	S	397	VAL
1	T	397	VAL
1	V	397	VAL
1	W	397	VAL
2	k	140	PHE
2	l	140	PHE
2	m	140	PHE
2	n	140	PHE
2	s	140	PHE
2	t	140	PHE
2	v	140	PHE
1	A	203	ASN
1	B	203	ASN
1	C	203	ASN
1	D	203	ASN
1	E	203	ASN
1	F	203	ASN
1	G	203	ASN
1	H	203	ASN
1	I	203	ASN
1	J	203	ASN
1	K	203	ASN
1	L	203	ASN
1	P	397	VAL
2	o	140	PHE
2	p	140	PHE
2	q	140	PHE
2	r	140	PHE
2	u	140	PHE

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Mol	Chain	Res	Type
1	A	385	PRO
1	A	427	GLY
1	B	385	PRO
1	B	427	GLY
1	C	385	PRO
1	C	427	GLY
1	D	385	PRO
1	D	427	GLY
1	E	385	PRO
1	E	427	GLY
1	F	385	PRO
1	F	427	GLY
1	G	385	PRO
1	G	427	GLY
1	H	385	PRO
1	H	427	GLY
1	I	385	PRO
1	I	427	GLY
1	J	385	PRO
1	J	427	GLY
1	K	385	PRO
1	K	427	GLY
1	L	385	PRO
1	L	427	GLY
1	U	397	VAL
1	M	310	VAL
1	N	310	VAL
1	O	310	VAL
1	P	310	VAL
1	Q	310	VAL
1	R	310	VAL
1	S	310	VAL
1	T	310	VAL
1	U	310	VAL
1	V	310	VAL
1	W	310	VAL
1	X	310	VAL
1	A	210	PRO
1	B	210	PRO
1	C	210	PRO
1	D	210	PRO
1	E	210	PRO

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Mol	Chain	Res	Type
1	F	210	PRO
1	G	210	PRO
1	H	210	PRO
1	I	210	PRO
1	J	210	PRO
1	K	210	PRO
1	L	210	PRO

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	B	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	C	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	D	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	E	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	F	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	G	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	H	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	I	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	J	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	K	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	L	483/510 (95%)	412 (85%)	71 (15%)	3	17
1	M	485/510 (95%)	412 (85%)	73 (15%)	3	16
1	N	485/510 (95%)	412 (85%)	73 (15%)	3	16
1	O	485/510 (95%)	413 (85%)	72 (15%)	3	17
1	P	485/510 (95%)	413 (85%)	72 (15%)	3	17
1	Q	485/510 (95%)	412 (85%)	73 (15%)	3	16
1	R	485/510 (95%)	411 (85%)	74 (15%)	3	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	S	485/510 (95%)	411 (85%)	74 (15%)	3	15
1	T	485/510 (95%)	412 (85%)	73 (15%)	3	16
1	U	485/510 (95%)	413 (85%)	72 (15%)	3	17
1	V	485/510 (95%)	413 (85%)	72 (15%)	3	17
1	W	485/510 (95%)	413 (85%)	72 (15%)	3	17
1	X	485/510 (95%)	411 (85%)	74 (15%)	3	15
2	Y	98/132 (74%)	85 (87%)	13 (13%)	4	21
2	Z	98/132 (74%)	85 (87%)	13 (13%)	4	21
2	a	98/132 (74%)	84 (86%)	14 (14%)	4	18
2	b	98/132 (74%)	84 (86%)	14 (14%)	4	18
2	c	98/132 (74%)	85 (87%)	13 (13%)	4	21
2	d	98/132 (74%)	85 (87%)	13 (13%)	4	21
2	e	98/132 (74%)	85 (87%)	13 (13%)	4	21
2	f	98/132 (74%)	84 (86%)	14 (14%)	4	18
2	g	98/132 (74%)	84 (86%)	14 (14%)	4	18
2	h	98/132 (74%)	85 (87%)	13 (13%)	4	21
2	i	98/132 (74%)	85 (87%)	13 (13%)	4	21
2	j	98/132 (74%)	84 (86%)	14 (14%)	4	18
2	k	100/132 (76%)	88 (88%)	12 (12%)	6	26
2	l	100/132 (76%)	87 (87%)	13 (13%)	5	22
2	m	100/132 (76%)	88 (88%)	12 (12%)	6	26
2	n	100/132 (76%)	87 (87%)	13 (13%)	5	22
2	o	100/132 (76%)	85 (85%)	15 (15%)	3	16
2	p	100/132 (76%)	86 (86%)	14 (14%)	4	19
2	q	100/132 (76%)	88 (88%)	12 (12%)	6	26
2	r	100/132 (76%)	88 (88%)	12 (12%)	6	26
2	s	100/132 (76%)	87 (87%)	13 (13%)	5	22
2	t	100/132 (76%)	87 (87%)	13 (13%)	5	22
2	u	100/132 (76%)	87 (87%)	13 (13%)	5	22
2	v	100/132 (76%)	87 (87%)	13 (13%)	5	22
All	All	13992/15408 (91%)	11950 (85%)	2042 (15%)	3	17

All (2042) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	M	14	ARG
1	M	15	PHE
1	M	24	GLU
1	M	30	LYS
1	M	31	ASN
1	M	33	LEU
1	M	40	GLN
1	M	42	ASP
1	M	47	GLN
1	M	49	THR
1	M	50	THR
1	M	56	GLN
1	M	59	VAL
1	M	61	ARG
1	M	69	SER
1	M	79	LEU
1	M	94	LEU
1	M	101	ASP
1	M	123	VAL
1	M	127	ARG
1	M	133	GLU
1	M	135	GLN
1	M	144	ILE
1	M	156	VAL
1	M	157	ILE
1	M	158	TRP
1	M	161	ASN
1	M	164	LEU
1	M	174	THR
1	M	175	VAL
1	M	190	LYS
1	M	201	PHE
1	M	202	GLN
1	M	209	PHE
1	M	211	TRP
1	M	217	ILE
1	M	218	GLN
1	M	226	VAL
1	M	228	LYS
1	M	231	THR
1	M	234	ILE
1	M	246	TYR

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Mol	Chain	Res	Type
1	M	248	LYS
1	M	265	LYS
1	M	266	ILE
1	M	275	ARG
1	M	286	VAL
1	M	293	ILE
1	M	298	ILE
1	M	301	VAL
1	M	311	GLU
1	M	327	GLN
1	M	343	ARG
1	M	356	ILE
1	M	359	PHE
1	M	376	ARG
1	M	378	ASP
1	M	384	LEU
1	M	387	GLN
1	M	389	LEU
1	M	405	LEU
1	M	430	VAL
1	M	433	ASP
1	M	444	LEU
1	M	451	ASP
1	M	510	ILE
1	M	513	ARG
1	M	518	THR
1	M	541	LYS
1	M	546	THR
1	M	558	THR
1	M	592	TRP
1	M	593	LEU
1	N	14	ARG
1	N	15	PHE
1	N	24	GLU
1	N	30	LYS
1	N	31	ASN
1	N	33	LEU
1	N	40	GLN
1	N	42	ASP
1	N	47	GLN
1	N	49	THR
1	N	50	THR

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Mol	Chain	Res	Type
1	N	56	GLN
1	N	59	VAL
1	N	61	ARG
1	N	69	SER
1	N	79	LEU
1	N	94	LEU
1	N	101	ASP
1	N	123	VAL
1	N	127	ARG
1	N	133	GLU
1	N	135	GLN
1	N	144	ILE
1	N	156	VAL
1	N	157	ILE
1	N	158	TRP
1	N	161	ASN
1	N	164	LEU
1	N	174	THR
1	N	175	VAL
1	N	190	LYS
1	N	201	PHE
1	N	202	GLN
1	N	209	PHE
1	N	211	TRP
1	N	217	ILE
1	N	218	GLN
1	N	226	VAL
1	N	228	LYS
1	N	231	THR
1	N	234	ILE
1	N	246	TYR
1	N	248	LYS
1	N	265	LYS
1	N	266	ILE
1	N	273	ARG
1	N	275	ARG
1	N	286	VAL
1	N	293	ILE
1	N	298	ILE
1	N	301	VAL
1	N	327	GLN
1	N	343	ARG

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Mol	Chain	Res	Type
1	N	356	ILE
1	N	359	PHE
1	N	376	ARG
1	N	378	ASP
1	N	384	LEU
1	N	387	GLN
1	N	389	LEU
1	N	405	LEU
1	N	430	VAL
1	N	433	ASP
1	N	444	LEU
1	N	451	ASP
1	N	510	ILE
1	N	513	ARG
1	N	518	THR
1	N	541	LYS
1	N	546	THR
1	N	558	THR
1	N	592	TRP
1	N	593	LEU
1	O	14	ARG
1	O	15	PHE
1	O	24	GLU
1	O	30	LYS
1	O	31	ASN
1	O	33	LEU
1	O	40	GLN
1	O	42	ASP
1	O	47	GLN
1	O	49	THR
1	O	50	THR
1	O	56	GLN
1	O	59	VAL
1	O	61	ARG
1	O	69	SER
1	O	79	LEU
1	O	94	LEU
1	O	101	ASP
1	O	123	VAL
1	O	127	ARG
1	O	133	GLU
1	O	135	GLN

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Mol	Chain	Res	Type
1	O	144	ILE
1	O	156	VAL
1	O	157	ILE
1	O	158	TRP
1	O	161	ASN
1	O	164	LEU
1	O	174	THR
1	O	175	VAL
1	O	190	LYS
1	O	201	PHE
1	O	202	GLN
1	O	209	PHE
1	O	211	TRP
1	O	217	ILE
1	O	218	GLN
1	O	225	VAL
1	O	226	VAL
1	O	228	LYS
1	O	231	THR
1	O	234	ILE
1	O	246	TYR
1	O	248	LYS
1	O	265	LYS
1	O	266	ILE
1	O	275	ARG
1	O	286	VAL
1	O	293	ILE
1	O	298	ILE
1	O	301	VAL
1	O	327	GLN
1	O	343	ARG
1	O	356	ILE
1	O	359	PHE
1	O	376	ARG
1	O	378	ASP
1	O	384	LEU
1	O	387	GLN
1	O	389	LEU
1	O	405	LEU
1	O	433	ASP
1	O	444	LEU
1	O	451	ASP

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Mol	Chain	Res	Type
1	O	510	ILE
1	O	513	ARG
1	O	518	THR
1	O	541	LYS
1	O	546	THR
1	O	558	THR
1	O	592	TRP
1	O	593	LEU
1	P	14	ARG
1	P	15	PHE
1	P	24	GLU
1	P	30	LYS
1	P	31	ASN
1	P	33	LEU
1	P	40	GLN
1	P	42	ASP
1	P	47	GLN
1	P	49	THR
1	P	50	THR
1	P	56	GLN
1	P	59	VAL
1	P	61	ARG
1	P	69	SER
1	P	79	LEU
1	P	94	LEU
1	P	101	ASP
1	P	123	VAL
1	P	127	ARG
1	P	133	GLU
1	P	135	GLN
1	P	144	ILE
1	P	156	VAL
1	P	157	ILE
1	P	158	TRP
1	P	161	ASN
1	P	164	LEU
1	P	174	THR
1	P	175	VAL
1	P	190	LYS
1	P	201	PHE
1	P	202	GLN
1	P	209	PHE

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Mol	Chain	Res	Type
1	P	211	TRP
1	P	217	ILE
1	P	218	GLN
1	P	225	VAL
1	P	226	VAL
1	P	228	LYS
1	P	231	THR
1	P	234	ILE
1	P	246	TYR
1	P	248	LYS
1	P	265	LYS
1	P	266	ILE
1	P	275	ARG
1	P	286	VAL
1	P	293	ILE
1	P	298	ILE
1	P	301	VAL
1	P	327	GLN
1	P	343	ARG
1	P	356	ILE
1	P	359	PHE
1	P	376	ARG
1	P	378	ASP
1	P	384	LEU
1	P	387	GLN
1	P	389	LEU
1	P	430	VAL
1	P	433	ASP
1	P	444	LEU
1	P	451	ASP
1	P	510	ILE
1	P	513	ARG
1	P	518	THR
1	P	541	LYS
1	P	546	THR
1	P	558	THR
1	P	592	TRP
1	P	593	LEU
1	Q	14	ARG
1	Q	15	PHE
1	Q	24	GLU
1	Q	30	LYS

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Mol	Chain	Res	Type
1	Q	31	ASN
1	Q	33	LEU
1	Q	40	GLN
1	Q	42	ASP
1	Q	47	GLN
1	Q	49	THR
1	Q	50	THR
1	Q	56	GLN
1	Q	59	VAL
1	Q	61	ARG
1	Q	69	SER
1	Q	79	LEU
1	Q	94	LEU
1	Q	101	ASP
1	Q	123	VAL
1	Q	127	ARG
1	Q	133	GLU
1	Q	135	GLN
1	Q	144	ILE
1	Q	156	VAL
1	Q	157	ILE
1	Q	158	TRP
1	Q	161	ASN
1	Q	164	LEU
1	Q	174	THR
1	Q	175	VAL
1	Q	190	LYS
1	Q	201	PHE
1	Q	202	GLN
1	Q	209	PHE
1	Q	211	TRP
1	Q	217	ILE
1	Q	218	GLN
1	Q	225	VAL
1	Q	226	VAL
1	Q	228	LYS
1	Q	231	THR
1	Q	234	ILE
1	Q	246	TYR
1	Q	248	LYS
1	Q	265	LYS
1	Q	266	ILE

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Mol	Chain	Res	Type
1	Q	275	ARG
1	Q	286	VAL
1	Q	293	ILE
1	Q	298	ILE
1	Q	301	VAL
1	Q	327	GLN
1	Q	343	ARG
1	Q	356	ILE
1	Q	359	PHE
1	Q	376	ARG
1	Q	378	ASP
1	Q	384	LEU
1	Q	387	GLN
1	Q	389	LEU
1	Q	405	LEU
1	Q	430	VAL
1	Q	433	ASP
1	Q	444	LEU
1	Q	451	ASP
1	Q	510	ILE
1	Q	513	ARG
1	Q	518	THR
1	Q	541	LYS
1	Q	546	THR
1	Q	558	THR
1	Q	592	TRP
1	Q	593	LEU
1	R	14	ARG
1	R	15	PHE
1	R	24	GLU
1	R	30	LYS
1	R	31	ASN
1	R	33	LEU
1	R	40	GLN
1	R	42	ASP
1	R	47	GLN
1	R	49	THR
1	R	50	THR
1	R	56	GLN
1	R	59	VAL
1	R	69	SER
1	R	79	LEU

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Mol	Chain	Res	Type
1	R	94	LEU
1	R	101	ASP
1	R	123	VAL
1	R	127	ARG
1	R	133	GLU
1	R	135	GLN
1	R	144	ILE
1	R	156	VAL
1	R	157	ILE
1	R	158	TRP
1	R	161	ASN
1	R	164	LEU
1	R	174	THR
1	R	175	VAL
1	R	190	LYS
1	R	201	PHE
1	R	202	GLN
1	R	209	PHE
1	R	211	TRP
1	R	217	ILE
1	R	218	GLN
1	R	225	VAL
1	R	226	VAL
1	R	228	LYS
1	R	231	THR
1	R	234	ILE
1	R	246	TYR
1	R	248	LYS
1	R	265	LYS
1	R	266	ILE
1	R	275	ARG
1	R	286	VAL
1	R	293	ILE
1	R	298	ILE
1	R	301	VAL
1	R	311	GLU
1	R	315	VAL
1	R	327	GLN
1	R	343	ARG
1	R	356	ILE
1	R	359	PHE
1	R	376	ARG

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Mol	Chain	Res	Type
1	R	378	ASP
1	R	384	LEU
1	R	387	GLN
1	R	389	LEU
1	R	405	LEU
1	R	430	VAL
1	R	433	ASP
1	R	444	LEU
1	R	451	ASP
1	R	510	ILE
1	R	513	ARG
1	R	518	THR
1	R	541	LYS
1	R	546	THR
1	R	558	THR
1	R	592	TRP
1	R	593	LEU
1	S	14	ARG
1	S	15	PHE
1	S	24	GLU
1	S	30	LYS
1	S	31	ASN
1	S	33	LEU
1	S	40	GLN
1	S	42	ASP
1	S	47	GLN
1	S	49	THR
1	S	50	THR
1	S	56	GLN
1	S	59	VAL
1	S	61	ARG
1	S	69	SER
1	S	79	LEU
1	S	94	LEU
1	S	101	ASP
1	S	123	VAL
1	S	127	ARG
1	S	133	GLU
1	S	135	GLN
1	S	144	ILE
1	S	156	VAL
1	S	157	ILE

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Mol	Chain	Res	Type
1	S	158	TRP
1	S	161	ASN
1	S	164	LEU
1	S	174	THR
1	S	175	VAL
1	S	190	LYS
1	S	201	PHE
1	S	202	GLN
1	S	209	PHE
1	S	211	TRP
1	S	217	ILE
1	S	218	GLN
1	S	225	VAL
1	S	226	VAL
1	S	228	LYS
1	S	231	THR
1	S	234	ILE
1	S	246	TYR
1	S	248	LYS
1	S	265	LYS
1	S	266	ILE
1	S	275	ARG
1	S	286	VAL
1	S	293	ILE
1	S	298	ILE
1	S	301	VAL
1	S	311	GLU
1	S	327	GLN
1	S	343	ARG
1	S	356	ILE
1	S	359	PHE
1	S	376	ARG
1	S	378	ASP
1	S	384	LEU
1	S	387	GLN
1	S	389	LEU
1	S	405	LEU
1	S	430	VAL
1	S	433	ASP
1	S	444	LEU
1	S	451	ASP
1	S	510	ILE

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Mol	Chain	Res	Type
1	S	513	ARG
1	S	518	THR
1	S	541	LYS
1	S	546	THR
1	S	558	THR
1	S	592	TRP
1	S	593	LEU
1	T	14	ARG
1	T	15	PHE
1	T	24	GLU
1	T	30	LYS
1	T	31	ASN
1	T	33	LEU
1	T	40	GLN
1	T	42	ASP
1	T	47	GLN
1	T	49	THR
1	T	50	THR
1	T	56	GLN
1	T	59	VAL
1	T	61	ARG
1	T	69	SER
1	T	79	LEU
1	T	94	LEU
1	T	101	ASP
1	T	123	VAL
1	T	127	ARG
1	T	133	GLU
1	T	135	GLN
1	T	144	ILE
1	T	156	VAL
1	T	157	ILE
1	T	158	TRP
1	T	161	ASN
1	T	164	LEU
1	T	174	THR
1	T	175	VAL
1	T	190	LYS
1	T	201	PHE
1	T	202	GLN
1	T	209	PHE
1	T	211	TRP

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Mol	Chain	Res	Type
1	T	217	ILE
1	T	218	GLN
1	T	225	VAL
1	T	226	VAL
1	T	228	LYS
1	T	231	THR
1	T	234	ILE
1	T	246	TYR
1	T	248	LYS
1	T	265	LYS
1	T	266	ILE
1	T	275	ARG
1	T	286	VAL
1	T	293	ILE
1	T	298	ILE
1	T	301	VAL
1	T	327	GLN
1	T	343	ARG
1	T	356	ILE
1	T	359	PHE
1	T	376	ARG
1	T	378	ASP
1	T	384	LEU
1	T	387	GLN
1	T	389	LEU
1	T	405	LEU
1	T	430	VAL
1	T	433	ASP
1	T	444	LEU
1	T	451	ASP
1	T	510	ILE
1	T	513	ARG
1	T	518	THR
1	T	541	LYS
1	T	546	THR
1	T	558	THR
1	T	592	TRP
1	T	593	LEU
1	U	14	ARG
1	U	15	PHE
1	U	24	GLU
1	U	30	LYS

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Mol	Chain	Res	Type
1	U	31	ASN
1	U	33	LEU
1	U	40	GLN
1	U	42	ASP
1	U	47	GLN
1	U	49	THR
1	U	50	THR
1	U	56	GLN
1	U	59	VAL
1	U	61	ARG
1	U	69	SER
1	U	79	LEU
1	U	94	LEU
1	U	101	ASP
1	U	123	VAL
1	U	127	ARG
1	U	133	GLU
1	U	135	GLN
1	U	144	ILE
1	U	156	VAL
1	U	157	ILE
1	U	158	TRP
1	U	161	ASN
1	U	164	LEU
1	U	174	THR
1	U	175	VAL
1	U	190	LYS
1	U	201	PHE
1	U	202	GLN
1	U	209	PHE
1	U	211	TRP
1	U	217	ILE
1	U	218	GLN
1	U	226	VAL
1	U	228	LYS
1	U	231	THR
1	U	234	ILE
1	U	246	TYR
1	U	248	LYS
1	U	265	LYS
1	U	266	ILE
1	U	275	ARG

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Mol	Chain	Res	Type
1	U	286	VAL
1	U	293	ILE
1	U	298	ILE
1	U	301	VAL
1	U	327	GLN
1	U	343	ARG
1	U	356	ILE
1	U	359	PHE
1	U	376	ARG
1	U	378	ASP
1	U	384	LEU
1	U	387	GLN
1	U	389	LEU
1	U	405	LEU
1	U	430	VAL
1	U	433	ASP
1	U	444	LEU
1	U	451	ASP
1	U	510	ILE
1	U	513	ARG
1	U	518	THR
1	U	541	LYS
1	U	546	THR
1	U	558	THR
1	U	592	TRP
1	U	593	LEU
1	V	14	ARG
1	V	15	PHE
1	V	24	GLU
1	V	30	LYS
1	V	31	ASN
1	V	33	LEU
1	V	40	GLN
1	V	42	ASP
1	V	47	GLN
1	V	49	THR
1	V	50	THR
1	V	56	GLN
1	V	59	VAL
1	V	61	ARG
1	V	69	SER
1	V	79	LEU

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Mol	Chain	Res	Type
1	V	94	LEU
1	V	101	ASP
1	V	123	VAL
1	V	127	ARG
1	V	133	GLU
1	V	135	GLN
1	V	144	ILE
1	V	156	VAL
1	V	157	ILE
1	V	158	TRP
1	V	161	ASN
1	V	164	LEU
1	V	174	THR
1	V	175	VAL
1	V	190	LYS
1	V	201	PHE
1	V	202	GLN
1	V	209	PHE
1	V	211	TRP
1	V	217	ILE
1	V	218	GLN
1	V	226	VAL
1	V	228	LYS
1	V	231	THR
1	V	234	ILE
1	V	246	TYR
1	V	248	LYS
1	V	265	LYS
1	V	266	ILE
1	V	275	ARG
1	V	286	VAL
1	V	293	ILE
1	V	298	ILE
1	V	301	VAL
1	V	327	GLN
1	V	343	ARG
1	V	356	ILE
1	V	359	PHE
1	V	376	ARG
1	V	378	ASP
1	V	384	LEU
1	V	387	GLN

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Mol	Chain	Res	Type
1	V	389	LEU
1	V	405	LEU
1	V	430	VAL
1	V	433	ASP
1	V	444	LEU
1	V	451	ASP
1	V	510	ILE
1	V	513	ARG
1	V	518	THR
1	V	541	LYS
1	V	546	THR
1	V	558	THR
1	V	592	TRP
1	V	593	LEU
1	W	14	ARG
1	W	15	PHE
1	W	24	GLU
1	W	30	LYS
1	W	31	ASN
1	W	33	LEU
1	W	40	GLN
1	W	42	ASP
1	W	47	GLN
1	W	49	THR
1	W	50	THR
1	W	56	GLN
1	W	59	VAL
1	W	61	ARG
1	W	69	SER
1	W	79	LEU
1	W	94	LEU
1	W	101	ASP
1	W	123	VAL
1	W	127	ARG
1	W	133	GLU
1	W	135	GLN
1	W	144	ILE
1	W	156	VAL
1	W	157	ILE
1	W	158	TRP
1	W	161	ASN
1	W	164	LEU

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Mol	Chain	Res	Type
1	W	174	THR
1	W	175	VAL
1	W	190	LYS
1	W	201	PHE
1	W	202	GLN
1	W	209	PHE
1	W	211	TRP
1	W	217	ILE
1	W	218	GLN
1	W	225	VAL
1	W	226	VAL
1	W	228	LYS
1	W	231	THR
1	W	234	ILE
1	W	246	TYR
1	W	248	LYS
1	W	265	LYS
1	W	266	ILE
1	W	275	ARG
1	W	286	VAL
1	W	293	ILE
1	W	298	ILE
1	W	301	VAL
1	W	327	GLN
1	W	343	ARG
1	W	356	ILE
1	W	359	PHE
1	W	376	ARG
1	W	378	ASP
1	W	384	LEU
1	W	387	GLN
1	W	389	LEU
1	W	430	VAL
1	W	433	ASP
1	W	444	LEU
1	W	451	ASP
1	W	510	ILE
1	W	513	ARG
1	W	518	THR
1	W	541	LYS
1	W	546	THR
1	W	558	THR

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Mol	Chain	Res	Type
1	W	592	TRP
1	W	593	LEU
1	X	14	ARG
1	X	15	PHE
1	X	24	GLU
1	X	30	LYS
1	X	31	ASN
1	X	33	LEU
1	X	40	GLN
1	X	42	ASP
1	X	47	GLN
1	X	49	THR
1	X	50	THR
1	X	56	GLN
1	X	59	VAL
1	X	69	SER
1	X	79	LEU
1	X	94	LEU
1	X	101	ASP
1	X	123	VAL
1	X	127	ARG
1	X	133	GLU
1	X	135	GLN
1	X	144	ILE
1	X	156	VAL
1	X	157	ILE
1	X	158	TRP
1	X	161	ASN
1	X	164	LEU
1	X	174	THR
1	X	175	VAL
1	X	190	LYS
1	X	201	PHE
1	X	202	GLN
1	X	209	PHE
1	X	211	TRP
1	X	217	ILE
1	X	218	GLN
1	X	225	VAL
1	X	226	VAL
1	X	228	LYS
1	X	231	THR

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Mol	Chain	Res	Type
1	X	234	ILE
1	X	246	TYR
1	X	248	LYS
1	X	265	LYS
1	X	266	ILE
1	X	275	ARG
1	X	286	VAL
1	X	293	ILE
1	X	298	ILE
1	X	301	VAL
1	X	311	GLU
1	X	327	GLN
1	X	343	ARG
1	X	356	ILE
1	X	359	PHE
1	X	376	ARG
1	X	378	ASP
1	X	384	LEU
1	X	387	GLN
1	X	389	LEU
1	X	405	LEU
1	X	430	VAL
1	X	433	ASP
1	X	444	LEU
1	X	451	ASP
1	X	510	ILE
1	X	513	ARG
1	X	518	THR
1	X	541	LYS
1	X	546	THR
1	X	558	THR
1	X	561	ASP
1	X	592	TRP
1	X	593	LEU
2	k	16	LYS
2	k	27	ASP
2	k	29	GLU
2	k	33	MET
2	k	39	ASP
2	k	69	GLU
2	k	71	ASP
2	k	84	PHE

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Mol	Chain	Res	Type
2	k	87	LEU
2	k	130	SER
2	k	131	ARG
2	k	136	SER
2	l	16	LYS
2	l	27	ASP
2	l	29	GLU
2	l	33	MET
2	l	39	ASP
2	l	69	GLU
2	l	71	ASP
2	l	84	PHE
2	l	87	LEU
2	l	100	THR
2	l	130	SER
2	l	131	ARG
2	l	136	SER
2	m	16	LYS
2	m	27	ASP
2	m	29	GLU
2	m	33	MET
2	m	39	ASP
2	m	69	GLU
2	m	71	ASP
2	m	84	PHE
2	m	87	LEU
2	m	130	SER
2	m	131	ARG
2	m	136	SER
2	n	16	LYS
2	n	27	ASP
2	n	29	GLU
2	n	33	MET
2	n	39	ASP
2	n	56	THR
2	n	69	GLU
2	n	71	ASP
2	n	84	PHE
2	n	87	LEU
2	n	130	SER
2	n	131	ARG
2	n	136	SER

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Mol	Chain	Res	Type
2	o	16	LYS
2	o	27	ASP
2	o	29	GLU
2	o	33	MET
2	o	37	VAL
2	o	39	ASP
2	o	56	THR
2	o	69	GLU
2	o	71	ASP
2	o	84	PHE
2	o	87	LEU
2	o	100	THR
2	o	130	SER
2	o	131	ARG
2	o	136	SER
2	p	16	LYS
2	p	27	ASP
2	p	29	GLU
2	p	33	MET
2	p	37	VAL
2	p	39	ASP
2	p	56	THR
2	p	69	GLU
2	p	71	ASP
2	p	84	PHE
2	p	87	LEU
2	p	130	SER
2	p	131	ARG
2	p	136	SER
2	q	16	LYS
2	q	27	ASP
2	q	29	GLU
2	q	33	MET
2	q	39	ASP
2	q	69	GLU
2	q	71	ASP
2	q	84	PHE
2	q	87	LEU
2	q	130	SER
2	q	131	ARG
2	q	136	SER
2	r	16	LYS

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Mol	Chain	Res	Type
2	r	27	ASP
2	r	29	GLU
2	r	33	MET
2	r	39	ASP
2	r	69	GLU
2	r	71	ASP
2	r	84	PHE
2	r	87	LEU
2	r	130	SER
2	r	131	ARG
2	r	136	SER
2	s	16	LYS
2	s	27	ASP
2	s	29	GLU
2	s	33	MET
2	s	37	VAL
2	s	39	ASP
2	s	69	GLU
2	s	71	ASP
2	s	84	PHE
2	s	87	LEU
2	s	130	SER
2	s	131	ARG
2	s	136	SER
2	t	16	LYS
2	t	27	ASP
2	t	29	GLU
2	t	33	MET
2	t	39	ASP
2	t	56	THR
2	t	69	GLU
2	t	71	ASP
2	t	84	PHE
2	t	87	LEU
2	t	130	SER
2	t	131	ARG
2	t	136	SER
2	u	16	LYS
2	u	27	ASP
2	u	29	GLU
2	u	33	MET
2	u	39	ASP

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Mol	Chain	Res	Type
2	u	69	GLU
2	u	71	ASP
2	u	84	PHE
2	u	87	LEU
2	u	100	THR
2	u	130	SER
2	u	131	ARG
2	u	136	SER
2	v	16	LYS
2	v	27	ASP
2	v	29	GLU
2	v	33	MET
2	v	37	VAL
2	v	39	ASP
2	v	69	GLU
2	v	71	ASP
2	v	84	PHE
2	v	87	LEU
2	v	130	SER
2	v	131	ARG
2	v	136	SER
1	A	14	ARG
1	A	15	PHE
1	A	24	GLU
1	A	30	LYS
1	A	31	ASN
1	A	33	LEU
1	A	37	ARG
1	A	42	ASP
1	A	43	ASP
1	A	45	LEU
1	A	47	GLN
1	A	56	GLN
1	A	61	ARG
1	A	79	LEU
1	A	118	GLN
1	A	123	VAL
1	A	127	ARG
1	A	133	GLU
1	A	135	GLN
1	A	144	ILE
1	A	157	ILE

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Mol	Chain	Res	Type
1	A	158	TRP
1	A	161	ASN
1	A	164	LEU
1	A	168	SER
1	A	174	THR
1	A	190	LYS
1	A	201	PHE
1	A	202	GLN
1	A	209	PHE
1	A	211	TRP
1	A	217	ILE
1	A	218	GLN
1	A	226	VAL
1	A	234	ILE
1	A	246	TYR
1	A	248	LYS
1	A	265	LYS
1	A	266	ILE
1	A	273	ARG
1	A	275	ARG
1	A	286	VAL
1	A	293	ILE
1	A	301	VAL
1	A	315	VAL
1	A	325	ASP
1	A	327	GLN
1	A	343	ARG
1	A	359	PHE
1	A	376	ARG
1	A	384	LEU
1	A	387	GLN
1	A	389	LEU
1	A	405	LEU
1	A	421	ASP
1	A	422	THR
1	A	430	VAL
1	A	432	PHE
1	A	433	ASP
1	A	438	LEU
1	A	444	LEU
1	A	507	LEU
1	A	513	ARG

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Mol	Chain	Res	Type
1	A	518	THR
1	A	529	GLN
1	A	541	LYS
1	A	546	THR
1	A	555	GLN
1	A	592	TRP
1	A	593	LEU
1	A	597	GLN
1	B	14	ARG
1	B	15	PHE
1	B	24	GLU
1	B	30	LYS
1	B	31	ASN
1	B	33	LEU
1	B	37	ARG
1	B	42	ASP
1	B	43	ASP
1	B	45	LEU
1	B	47	GLN
1	B	56	GLN
1	B	61	ARG
1	B	79	LEU
1	B	118	GLN
1	B	123	VAL
1	B	127	ARG
1	B	133	GLU
1	B	135	GLN
1	B	144	ILE
1	B	157	ILE
1	B	158	TRP
1	B	161	ASN
1	B	164	LEU
1	B	168	SER
1	B	174	THR
1	B	190	LYS
1	B	201	PHE
1	B	202	GLN
1	B	209	PHE
1	B	211	TRP
1	B	217	ILE
1	B	218	GLN
1	B	226	VAL

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Mol	Chain	Res	Type
1	B	234	ILE
1	B	246	TYR
1	B	248	LYS
1	B	265	LYS
1	B	266	ILE
1	B	273	ARG
1	B	275	ARG
1	B	286	VAL
1	B	293	ILE
1	B	301	VAL
1	B	315	VAL
1	B	325	ASP
1	B	327	GLN
1	B	343	ARG
1	B	359	PHE
1	B	376	ARG
1	B	384	LEU
1	B	387	GLN
1	B	389	LEU
1	B	405	LEU
1	B	421	ASP
1	B	422	THR
1	B	430	VAL
1	B	432	PHE
1	B	433	ASP
1	B	438	LEU
1	B	444	LEU
1	B	507	LEU
1	B	513	ARG
1	B	518	THR
1	B	529	GLN
1	B	541	LYS
1	B	546	THR
1	B	555	GLN
1	B	592	TRP
1	B	593	LEU
1	B	597	GLN
1	C	14	ARG
1	C	15	PHE
1	C	24	GLU
1	C	30	LYS
1	C	31	ASN

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Mol	Chain	Res	Type
1	C	33	LEU
1	C	37	ARG
1	C	42	ASP
1	C	43	ASP
1	C	45	LEU
1	C	47	GLN
1	C	56	GLN
1	C	61	ARG
1	C	79	LEU
1	C	118	GLN
1	C	123	VAL
1	C	127	ARG
1	C	133	GLU
1	C	135	GLN
1	C	144	ILE
1	C	157	ILE
1	C	158	TRP
1	C	161	ASN
1	C	164	LEU
1	C	168	SER
1	C	174	THR
1	C	190	LYS
1	C	201	PHE
1	C	202	GLN
1	C	209	PHE
1	C	211	TRP
1	C	217	ILE
1	C	218	GLN
1	C	226	VAL
1	C	234	ILE
1	C	246	TYR
1	C	248	LYS
1	C	265	LYS
1	C	266	ILE
1	C	273	ARG
1	C	275	ARG
1	C	286	VAL
1	C	293	ILE
1	C	301	VAL
1	C	315	VAL
1	C	325	ASP
1	C	327	GLN

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Mol	Chain	Res	Type
1	C	343	ARG
1	C	359	PHE
1	C	376	ARG
1	C	384	LEU
1	C	387	GLN
1	C	389	LEU
1	C	405	LEU
1	C	421	ASP
1	C	422	THR
1	C	430	VAL
1	C	432	PHE
1	C	433	ASP
1	C	438	LEU
1	C	444	LEU
1	C	507	LEU
1	C	513	ARG
1	C	518	THR
1	C	529	GLN
1	C	541	LYS
1	C	546	THR
1	C	555	GLN
1	C	592	TRP
1	C	593	LEU
1	C	597	GLN
1	D	14	ARG
1	D	15	PHE
1	D	24	GLU
1	D	30	LYS
1	D	31	ASN
1	D	33	LEU
1	D	37	ARG
1	D	42	ASP
1	D	43	ASP
1	D	45	LEU
1	D	47	GLN
1	D	56	GLN
1	D	61	ARG
1	D	79	LEU
1	D	118	GLN
1	D	123	VAL
1	D	127	ARG
1	D	133	GLU

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Mol	Chain	Res	Type
1	D	135	GLN
1	D	144	ILE
1	D	157	ILE
1	D	158	TRP
1	D	161	ASN
1	D	164	LEU
1	D	168	SER
1	D	174	THR
1	D	190	LYS
1	D	201	PHE
1	D	202	GLN
1	D	209	PHE
1	D	211	TRP
1	D	217	ILE
1	D	218	GLN
1	D	226	VAL
1	D	234	ILE
1	D	246	TYR
1	D	248	LYS
1	D	265	LYS
1	D	266	ILE
1	D	273	ARG
1	D	275	ARG
1	D	286	VAL
1	D	293	ILE
1	D	301	VAL
1	D	315	VAL
1	D	325	ASP
1	D	327	GLN
1	D	343	ARG
1	D	359	PHE
1	D	376	ARG
1	D	384	LEU
1	D	387	GLN
1	D	389	LEU
1	D	405	LEU
1	D	421	ASP
1	D	422	THR
1	D	430	VAL
1	D	432	PHE
1	D	433	ASP
1	D	438	LEU

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Mol	Chain	Res	Type
1	D	444	LEU
1	D	507	LEU
1	D	513	ARG
1	D	518	THR
1	D	529	GLN
1	D	541	LYS
1	D	546	THR
1	D	555	GLN
1	D	592	TRP
1	D	593	LEU
1	D	597	GLN
1	E	14	ARG
1	E	15	PHE
1	E	24	GLU
1	E	30	LYS
1	E	31	ASN
1	E	33	LEU
1	E	37	ARG
1	E	42	ASP
1	E	43	ASP
1	E	45	LEU
1	E	47	GLN
1	E	56	GLN
1	E	61	ARG
1	E	79	LEU
1	E	118	GLN
1	E	123	VAL
1	E	127	ARG
1	E	133	GLU
1	E	135	GLN
1	E	144	ILE
1	E	157	ILE
1	E	158	TRP
1	E	161	ASN
1	E	164	LEU
1	E	168	SER
1	E	174	THR
1	E	190	LYS
1	E	201	PHE
1	E	202	GLN
1	E	209	PHE
1	E	211	TRP

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Mol	Chain	Res	Type
1	E	217	ILE
1	E	218	GLN
1	E	226	VAL
1	E	234	ILE
1	E	246	TYR
1	E	248	LYS
1	E	265	LYS
1	E	266	ILE
1	E	273	ARG
1	E	275	ARG
1	E	286	VAL
1	E	293	ILE
1	E	301	VAL
1	E	315	VAL
1	E	325	ASP
1	E	327	GLN
1	E	343	ARG
1	E	359	PHE
1	E	376	ARG
1	E	384	LEU
1	E	387	GLN
1	E	389	LEU
1	E	405	LEU
1	E	421	ASP
1	E	422	THR
1	E	430	VAL
1	E	432	PHE
1	E	433	ASP
1	E	438	LEU
1	E	444	LEU
1	E	507	LEU
1	E	513	ARG
1	E	518	THR
1	E	529	GLN
1	E	541	LYS
1	E	546	THR
1	E	555	GLN
1	E	592	TRP
1	E	593	LEU
1	E	597	GLN
1	F	14	ARG
1	F	15	PHE

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Mol	Chain	Res	Type
1	F	24	GLU
1	F	30	LYS
1	F	31	ASN
1	F	33	LEU
1	F	37	ARG
1	F	42	ASP
1	F	43	ASP
1	F	45	LEU
1	F	47	GLN
1	F	56	GLN
1	F	61	ARG
1	F	79	LEU
1	F	118	GLN
1	F	123	VAL
1	F	127	ARG
1	F	133	GLU
1	F	135	GLN
1	F	144	ILE
1	F	157	ILE
1	F	158	TRP
1	F	161	ASN
1	F	164	LEU
1	F	168	SER
1	F	174	THR
1	F	190	LYS
1	F	201	PHE
1	F	202	GLN
1	F	209	PHE
1	F	211	TRP
1	F	217	ILE
1	F	218	GLN
1	F	226	VAL
1	F	234	ILE
1	F	246	TYR
1	F	248	LYS
1	F	265	LYS
1	F	266	ILE
1	F	273	ARG
1	F	275	ARG
1	F	286	VAL
1	F	293	ILE
1	F	301	VAL

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Mol	Chain	Res	Type
1	F	315	VAL
1	F	325	ASP
1	F	327	GLN
1	F	343	ARG
1	F	359	PHE
1	F	376	ARG
1	F	384	LEU
1	F	387	GLN
1	F	389	LEU
1	F	405	LEU
1	F	421	ASP
1	F	422	THR
1	F	430	VAL
1	F	432	PHE
1	F	433	ASP
1	F	438	LEU
1	F	444	LEU
1	F	507	LEU
1	F	513	ARG
1	F	518	THR
1	F	529	GLN
1	F	541	LYS
1	F	546	THR
1	F	555	GLN
1	F	592	TRP
1	F	593	LEU
1	F	597	GLN
1	G	14	ARG
1	G	15	PHE
1	G	24	GLU
1	G	30	LYS
1	G	31	ASN
1	G	33	LEU
1	G	37	ARG
1	G	42	ASP
1	G	43	ASP
1	G	45	LEU
1	G	47	GLN
1	G	56	GLN
1	G	61	ARG
1	G	79	LEU
1	G	118	GLN

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Mol	Chain	Res	Type
1	G	123	VAL
1	G	127	ARG
1	G	133	GLU
1	G	135	GLN
1	G	144	ILE
1	G	157	ILE
1	G	158	TRP
1	G	161	ASN
1	G	164	LEU
1	G	168	SER
1	G	174	THR
1	G	190	LYS
1	G	201	PHE
1	G	202	GLN
1	G	209	PHE
1	G	211	TRP
1	G	217	ILE
1	G	218	GLN
1	G	226	VAL
1	G	234	ILE
1	G	246	TYR
1	G	248	LYS
1	G	265	LYS
1	G	266	ILE
1	G	273	ARG
1	G	275	ARG
1	G	286	VAL
1	G	293	ILE
1	G	301	VAL
1	G	315	VAL
1	G	325	ASP
1	G	327	GLN
1	G	343	ARG
1	G	359	PHE
1	G	376	ARG
1	G	384	LEU
1	G	387	GLN
1	G	389	LEU
1	G	405	LEU
1	G	421	ASP
1	G	422	THR
1	G	430	VAL

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Mol	Chain	Res	Type
1	G	432	PHE
1	G	433	ASP
1	G	438	LEU
1	G	444	LEU
1	G	507	LEU
1	G	513	ARG
1	G	518	THR
1	G	529	GLN
1	G	541	LYS
1	G	546	THR
1	G	555	GLN
1	G	592	TRP
1	G	593	LEU
1	G	597	GLN
1	H	14	ARG
1	H	15	PHE
1	H	24	GLU
1	H	30	LYS
1	H	31	ASN
1	H	33	LEU
1	H	37	ARG
1	H	42	ASP
1	H	43	ASP
1	H	45	LEU
1	H	47	GLN
1	H	56	GLN
1	H	61	ARG
1	H	79	LEU
1	H	118	GLN
1	H	123	VAL
1	H	127	ARG
1	H	133	GLU
1	H	135	GLN
1	H	144	ILE
1	H	157	ILE
1	H	158	TRP
1	H	161	ASN
1	H	164	LEU
1	H	168	SER
1	H	174	THR
1	H	190	LYS
1	H	201	PHE

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Mol	Chain	Res	Type
1	H	202	GLN
1	H	209	PHE
1	H	211	TRP
1	H	217	ILE
1	H	218	GLN
1	H	226	VAL
1	H	234	ILE
1	H	246	TYR
1	H	248	LYS
1	H	265	LYS
1	H	266	ILE
1	H	273	ARG
1	H	275	ARG
1	H	286	VAL
1	H	293	ILE
1	H	301	VAL
1	H	315	VAL
1	H	325	ASP
1	H	327	GLN
1	H	343	ARG
1	H	359	PHE
1	H	376	ARG
1	H	384	LEU
1	H	387	GLN
1	H	389	LEU
1	H	405	LEU
1	H	421	ASP
1	H	422	THR
1	H	430	VAL
1	H	432	PHE
1	H	433	ASP
1	H	438	LEU
1	H	444	LEU
1	H	507	LEU
1	H	513	ARG
1	H	518	THR
1	H	529	GLN
1	H	541	LYS
1	H	546	THR
1	H	555	GLN
1	H	592	TRP
1	H	593	LEU

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Mol	Chain	Res	Type
1	H	597	GLN
1	I	14	ARG
1	I	15	PHE
1	I	24	GLU
1	I	30	LYS
1	I	31	ASN
1	I	33	LEU
1	I	37	ARG
1	I	42	ASP
1	I	43	ASP
1	I	45	LEU
1	I	47	GLN
1	I	56	GLN
1	I	61	ARG
1	I	79	LEU
1	I	118	GLN
1	I	123	VAL
1	I	127	ARG
1	I	133	GLU
1	I	135	GLN
1	I	144	ILE
1	I	157	ILE
1	I	158	TRP
1	I	161	ASN
1	I	164	LEU
1	I	168	SER
1	I	174	THR
1	I	190	LYS
1	I	201	PHE
1	I	202	GLN
1	I	209	PHE
1	I	211	TRP
1	I	217	ILE
1	I	218	GLN
1	I	226	VAL
1	I	234	ILE
1	I	246	TYR
1	I	248	LYS
1	I	265	LYS
1	I	266	ILE
1	I	273	ARG
1	I	275	ARG

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Mol	Chain	Res	Type
1	I	286	VAL
1	I	293	ILE
1	I	301	VAL
1	I	315	VAL
1	I	325	ASP
1	I	327	GLN
1	I	343	ARG
1	I	359	PHE
1	I	376	ARG
1	I	384	LEU
1	I	387	GLN
1	I	389	LEU
1	I	405	LEU
1	I	421	ASP
1	I	422	THR
1	I	430	VAL
1	I	432	PHE
1	I	433	ASP
1	I	438	LEU
1	I	444	LEU
1	I	507	LEU
1	I	513	ARG
1	I	518	THR
1	I	529	GLN
1	I	541	LYS
1	I	546	THR
1	I	555	GLN
1	I	592	TRP
1	I	593	LEU
1	I	597	GLN
1	J	14	ARG
1	J	15	PHE
1	J	24	GLU
1	J	30	LYS
1	J	31	ASN
1	J	33	LEU
1	J	37	ARG
1	J	42	ASP
1	J	43	ASP
1	J	45	LEU
1	J	47	GLN
1	J	56	GLN

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Mol	Chain	Res	Type
1	J	61	ARG
1	J	79	LEU
1	J	118	GLN
1	J	123	VAL
1	J	127	ARG
1	J	133	GLU
1	J	135	GLN
1	J	144	ILE
1	J	157	ILE
1	J	158	TRP
1	J	161	ASN
1	J	164	LEU
1	J	168	SER
1	J	174	THR
1	J	190	LYS
1	J	201	PHE
1	J	202	GLN
1	J	209	PHE
1	J	211	TRP
1	J	217	ILE
1	J	218	GLN
1	J	226	VAL
1	J	234	ILE
1	J	246	TYR
1	J	248	LYS
1	J	265	LYS
1	J	266	ILE
1	J	273	ARG
1	J	275	ARG
1	J	286	VAL
1	J	293	ILE
1	J	301	VAL
1	J	315	VAL
1	J	325	ASP
1	J	327	GLN
1	J	343	ARG
1	J	359	PHE
1	J	376	ARG
1	J	384	LEU
1	J	387	GLN
1	J	389	LEU
1	J	405	LEU

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Mol	Chain	Res	Type
1	J	421	ASP
1	J	422	THR
1	J	430	VAL
1	J	432	PHE
1	J	433	ASP
1	J	438	LEU
1	J	444	LEU
1	J	507	LEU
1	J	513	ARG
1	J	518	THR
1	J	529	GLN
1	J	541	LYS
1	J	546	THR
1	J	555	GLN
1	J	592	TRP
1	J	593	LEU
1	J	597	GLN
1	K	14	ARG
1	K	15	PHE
1	K	24	GLU
1	K	30	LYS
1	K	31	ASN
1	K	33	LEU
1	K	37	ARG
1	K	42	ASP
1	K	43	ASP
1	K	45	LEU
1	K	47	GLN
1	K	56	GLN
1	K	61	ARG
1	K	79	LEU
1	K	118	GLN
1	K	123	VAL
1	K	127	ARG
1	K	133	GLU
1	K	135	GLN
1	K	144	ILE
1	K	157	ILE
1	K	158	TRP
1	K	161	ASN
1	K	164	LEU
1	K	168	SER

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Mol	Chain	Res	Type
1	K	174	THR
1	K	190	LYS
1	K	201	PHE
1	K	202	GLN
1	K	209	PHE
1	K	211	TRP
1	K	217	ILE
1	K	218	GLN
1	K	226	VAL
1	K	234	ILE
1	K	246	TYR
1	K	248	LYS
1	K	265	LYS
1	K	266	ILE
1	K	273	ARG
1	K	275	ARG
1	K	286	VAL
1	K	293	ILE
1	K	301	VAL
1	K	315	VAL
1	K	325	ASP
1	K	327	GLN
1	K	343	ARG
1	K	359	PHE
1	K	376	ARG
1	K	384	LEU
1	K	387	GLN
1	K	389	LEU
1	K	405	LEU
1	K	421	ASP
1	K	422	THR
1	K	430	VAL
1	K	432	PHE
1	K	433	ASP
1	K	438	LEU
1	K	444	LEU
1	K	507	LEU
1	K	513	ARG
1	K	518	THR
1	K	529	GLN
1	K	541	LYS
1	K	546	THR

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Mol	Chain	Res	Type
1	K	555	GLN
1	K	592	TRP
1	K	593	LEU
1	K	597	GLN
1	L	14	ARG
1	L	15	PHE
1	L	24	GLU
1	L	30	LYS
1	L	31	ASN
1	L	33	LEU
1	L	37	ARG
1	L	42	ASP
1	L	43	ASP
1	L	45	LEU
1	L	47	GLN
1	L	56	GLN
1	L	61	ARG
1	L	79	LEU
1	L	118	GLN
1	L	123	VAL
1	L	127	ARG
1	L	133	GLU
1	L	135	GLN
1	L	144	ILE
1	L	157	ILE
1	L	158	TRP
1	L	161	ASN
1	L	164	LEU
1	L	168	SER
1	L	174	THR
1	L	190	LYS
1	L	201	PHE
1	L	202	GLN
1	L	209	PHE
1	L	211	TRP
1	L	217	ILE
1	L	218	GLN
1	L	226	VAL
1	L	234	ILE
1	L	246	TYR
1	L	248	LYS
1	L	265	LYS

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Mol	Chain	Res	Type
1	L	266	ILE
1	L	273	ARG
1	L	275	ARG
1	L	286	VAL
1	L	293	ILE
1	L	301	VAL
1	L	315	VAL
1	L	325	ASP
1	L	327	GLN
1	L	343	ARG
1	L	359	PHE
1	L	376	ARG
1	L	384	LEU
1	L	387	GLN
1	L	389	LEU
1	L	405	LEU
1	L	421	ASP
1	L	422	THR
1	L	430	VAL
1	L	432	PHE
1	L	433	ASP
1	L	438	LEU
1	L	444	LEU
1	L	507	LEU
1	L	513	ARG
1	L	518	THR
1	L	529	GLN
1	L	541	LYS
1	L	546	THR
1	L	555	GLN
1	L	592	TRP
1	L	593	LEU
1	L	597	GLN
2	Y	26	LEU
2	Y	42	MET
2	Y	48	ASP
2	Y	49	LEU
2	Y	53	MET
2	Y	78	GLU
2	Y	80	ASP
2	Y	90	SER
2	Y	96	LEU

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Mol	Chain	Res	Type
2	Y	139	SER
2	Y	140	ARG
2	Y	145	SER
2	Y	147	ASN
2	Z	26	LEU
2	Z	42	MET
2	Z	48	ASP
2	Z	49	LEU
2	Z	53	MET
2	Z	78	GLU
2	Z	80	ASP
2	Z	90	SER
2	Z	96	LEU
2	Z	139	SER
2	Z	140	ARG
2	Z	145	SER
2	Z	147	ASN
2	a	26	LEU
2	a	42	MET
2	a	48	ASP
2	a	49	LEU
2	a	53	MET
2	a	78	GLU
2	a	80	ASP
2	a	90	SER
2	a	96	LEU
2	a	113	ILE
2	a	139	SER
2	a	140	ARG
2	a	145	SER
2	a	147	ASN
2	b	26	LEU
2	b	42	MET
2	b	48	ASP
2	b	49	LEU
2	b	53	MET
2	b	78	GLU
2	b	80	ASP
2	b	90	SER
2	b	96	LEU
2	b	113	ILE
2	b	139	SER

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Mol	Chain	Res	Type
2	b	140	ARG
2	b	145	SER
2	b	147	ASN
2	c	26	LEU
2	c	42	MET
2	c	48	ASP
2	c	49	LEU
2	c	53	MET
2	c	78	GLU
2	c	80	ASP
2	c	90	SER
2	c	96	LEU
2	c	139	SER
2	c	140	ARG
2	c	145	SER
2	c	147	ASN
2	d	26	LEU
2	d	42	MET
2	d	48	ASP
2	d	49	LEU
2	d	53	MET
2	d	78	GLU
2	d	80	ASP
2	d	90	SER
2	d	96	LEU
2	d	139	SER
2	d	140	ARG
2	d	145	SER
2	d	147	ASN
2	e	26	LEU
2	e	42	MET
2	e	48	ASP
2	e	49	LEU
2	e	53	MET
2	e	78	GLU
2	e	80	ASP
2	e	90	SER
2	e	96	LEU
2	e	139	SER
2	e	140	ARG
2	e	145	SER
2	e	147	ASN

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Mol	Chain	Res	Type
2	f	26	LEU
2	f	42	MET
2	f	48	ASP
2	f	49	LEU
2	f	53	MET
2	f	78	GLU
2	f	80	ASP
2	f	90	SER
2	f	96	LEU
2	f	113	ILE
2	f	139	SER
2	f	140	ARG
2	f	145	SER
2	f	147	ASN
2	g	26	LEU
2	g	42	MET
2	g	48	ASP
2	g	49	LEU
2	g	53	MET
2	g	78	GLU
2	g	80	ASP
2	g	90	SER
2	g	96	LEU
2	g	113	ILE
2	g	139	SER
2	g	140	ARG
2	g	145	SER
2	g	147	ASN
2	h	26	LEU
2	h	42	MET
2	h	48	ASP
2	h	49	LEU
2	h	53	MET
2	h	78	GLU
2	h	80	ASP
2	h	90	SER
2	h	96	LEU
2	h	139	SER
2	h	140	ARG
2	h	145	SER
2	h	147	ASN
2	i	26	LEU

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Mol	Chain	Res	Type
2	i	42	MET
2	i	48	ASP
2	i	49	LEU
2	i	53	MET
2	i	78	GLU
2	i	80	ASP
2	i	90	SER
2	i	96	LEU
2	i	139	SER
2	i	140	ARG
2	i	145	SER
2	i	147	ASN
2	j	26	LEU
2	j	42	MET
2	j	48	ASP
2	j	49	LEU
2	j	53	MET
2	j	78	GLU
2	j	80	ASP
2	j	90	SER
2	j	96	LEU
2	j	113	ILE
2	j	139	SER
2	j	140	ARG
2	j	145	SER
2	j	147	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (319) such sidechains are listed below:

Mol	Chain	Res	Type
1	M	31	ASN
1	M	40	GLN
1	M	508	ASN
1	M	575	GLN
1	N	31	ASN
1	N	142	GLN
1	N	508	ASN
1	N	575	GLN
1	O	31	ASN
1	O	40	GLN
1	O	135	GLN
1	O	142	GLN

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Mol	Chain	Res	Type
1	O	450	GLN
1	O	575	GLN
1	P	31	ASN
1	P	40	GLN
1	P	575	GLN
1	Q	31	ASN
1	Q	40	GLN
1	Q	508	ASN
1	Q	575	GLN
1	R	31	ASN
1	R	508	ASN
1	R	575	GLN
1	S	31	ASN
1	S	40	GLN
1	S	135	GLN
1	S	508	ASN
1	S	575	GLN
1	T	40	GLN
1	T	450	GLN
1	T	508	ASN
1	T	575	GLN
1	U	31	ASN
1	U	40	GLN
1	U	135	GLN
1	U	142	GLN
1	U	450	GLN
1	U	508	ASN
1	U	575	GLN
1	V	31	ASN
1	V	40	GLN
1	V	508	ASN
1	V	575	GLN
1	W	31	ASN
1	W	40	GLN
1	W	508	ASN
1	W	575	GLN
1	X	31	ASN
1	X	40	GLN
1	X	142	GLN
1	X	508	ASN
1	X	575	GLN
1	A	31	ASN

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Mol	Chain	Res	Type
1	A	56	GLN
1	A	73	GLN
1	A	112	ASN
1	A	118	GLN
1	A	135	GLN
1	A	161	ASN
1	A	177	HIS
1	A	182	ASN
1	A	202	GLN
1	A	214	GLN
1	A	218	GLN
1	A	236	GLN
1	A	291	GLN
1	A	297	HIS
1	A	327	GLN
1	A	337	ASN
1	A	439	ASN
1	A	529	GLN
1	A	530	GLN
1	A	555	GLN
1	A	597	GLN
1	B	31	ASN
1	B	56	GLN
1	B	73	GLN
1	B	112	ASN
1	B	118	GLN
1	B	135	GLN
1	B	161	ASN
1	B	177	HIS
1	B	182	ASN
1	B	202	GLN
1	B	214	GLN
1	B	218	GLN
1	B	236	GLN
1	B	291	GLN
1	B	297	HIS
1	B	337	ASN
1	B	439	ASN
1	B	529	GLN
1	B	530	GLN
1	B	555	GLN
1	B	597	GLN

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Mol	Chain	Res	Type
1	C	31	ASN
1	C	56	GLN
1	C	73	GLN
1	C	112	ASN
1	C	118	GLN
1	C	135	GLN
1	C	161	ASN
1	C	177	HIS
1	C	182	ASN
1	C	202	GLN
1	C	214	GLN
1	C	218	GLN
1	C	236	GLN
1	C	291	GLN
1	C	297	HIS
1	C	337	ASN
1	C	439	ASN
1	C	529	GLN
1	C	530	GLN
1	C	555	GLN
1	C	597	GLN
1	D	31	ASN
1	D	56	GLN
1	D	73	GLN
1	D	112	ASN
1	D	118	GLN
1	D	135	GLN
1	D	161	ASN
1	D	177	HIS
1	D	182	ASN
1	D	202	GLN
1	D	214	GLN
1	D	218	GLN
1	D	236	GLN
1	D	291	GLN
1	D	297	HIS
1	D	337	ASN
1	D	439	ASN
1	D	529	GLN
1	D	530	GLN
1	D	555	GLN
1	D	597	GLN

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Mol	Chain	Res	Type
1	E	31	ASN
1	E	56	GLN
1	E	73	GLN
1	E	112	ASN
1	E	118	GLN
1	E	135	GLN
1	E	161	ASN
1	E	177	HIS
1	E	182	ASN
1	E	202	GLN
1	E	214	GLN
1	E	218	GLN
1	E	236	GLN
1	E	291	GLN
1	E	297	HIS
1	E	337	ASN
1	E	439	ASN
1	E	529	GLN
1	E	530	GLN
1	E	555	GLN
1	E	597	GLN
1	F	31	ASN
1	F	56	GLN
1	F	73	GLN
1	F	112	ASN
1	F	118	GLN
1	F	135	GLN
1	F	161	ASN
1	F	177	HIS
1	F	182	ASN
1	F	202	GLN
1	F	214	GLN
1	F	218	GLN
1	F	236	GLN
1	F	291	GLN
1	F	297	HIS
1	F	327	GLN
1	F	337	ASN
1	F	439	ASN
1	F	529	GLN
1	F	530	GLN
1	F	555	GLN

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Mol	Chain	Res	Type
1	F	597	GLN
1	G	31	ASN
1	G	73	GLN
1	G	112	ASN
1	G	118	GLN
1	G	135	GLN
1	G	161	ASN
1	G	177	HIS
1	G	182	ASN
1	G	202	GLN
1	G	214	GLN
1	G	218	GLN
1	G	236	GLN
1	G	291	GLN
1	G	297	HIS
1	G	337	ASN
1	G	439	ASN
1	G	529	GLN
1	G	530	GLN
1	G	555	GLN
1	G	597	GLN
1	H	31	ASN
1	H	73	GLN
1	H	112	ASN
1	H	118	GLN
1	H	135	GLN
1	H	161	ASN
1	H	177	HIS
1	H	182	ASN
1	H	202	GLN
1	H	214	GLN
1	H	218	GLN
1	H	236	GLN
1	H	291	GLN
1	H	297	HIS
1	H	337	ASN
1	H	439	ASN
1	H	529	GLN
1	H	530	GLN
1	H	555	GLN
1	H	597	GLN
1	I	31	ASN

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Mol	Chain	Res	Type
1	I	56	GLN
1	I	73	GLN
1	I	112	ASN
1	I	118	GLN
1	I	135	GLN
1	I	161	ASN
1	I	177	HIS
1	I	182	ASN
1	I	202	GLN
1	I	214	GLN
1	I	218	GLN
1	I	236	GLN
1	I	291	GLN
1	I	297	HIS
1	I	337	ASN
1	I	439	ASN
1	I	529	GLN
1	I	530	GLN
1	I	555	GLN
1	I	597	GLN
1	J	31	ASN
1	J	73	GLN
1	J	112	ASN
1	J	118	GLN
1	J	135	GLN
1	J	161	ASN
1	J	177	HIS
1	J	182	ASN
1	J	202	GLN
1	J	214	GLN
1	J	218	GLN
1	J	236	GLN
1	J	291	GLN
1	J	297	HIS
1	J	337	ASN
1	J	439	ASN
1	J	529	GLN
1	J	530	GLN
1	J	555	GLN
1	J	597	GLN
1	K	31	ASN
1	K	56	GLN

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Mol	Chain	Res	Type
1	K	73	GLN
1	K	112	ASN
1	K	118	GLN
1	K	135	GLN
1	K	161	ASN
1	K	177	HIS
1	K	182	ASN
1	K	202	GLN
1	K	214	GLN
1	K	218	GLN
1	K	236	GLN
1	K	291	GLN
1	K	297	HIS
1	K	327	GLN
1	K	337	ASN
1	K	439	ASN
1	K	529	GLN
1	K	530	GLN
1	K	555	GLN
1	K	597	GLN
1	L	31	ASN
1	L	56	GLN
1	L	73	GLN
1	L	112	ASN
1	L	118	GLN
1	L	135	GLN
1	L	161	ASN
1	L	177	HIS
1	L	182	ASN
1	L	202	GLN
1	L	214	GLN
1	L	218	GLN
1	L	236	GLN
1	L	291	GLN
1	L	297	HIS
1	L	337	ASN
1	L	439	ASN
1	L	529	GLN
1	L	530	GLN
1	L	555	GLN
1	L	597	GLN
2	Y	94	HIS

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Mol	Chain	Res	Type
2	Z	94	HIS
2	a	94	HIS
2	b	94	HIS
2	c	40	GLN
2	c	94	HIS
2	d	40	GLN
2	d	94	HIS
2	e	94	HIS
2	f	94	HIS
2	g	94	HIS
2	h	94	HIS
2	i	94	HIS
2	j	94	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

### 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

### 5.7 Other polymers [i](#)

There are no such residues in this entry.

### 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data

### 6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å²)	Q<0.9
1	A	552/602 (91%)	2.72	282 (51%)	0	0	22, 84, 246, 379	0
1	B	552/602 (91%)	2.78	301 (54%)	0	0	23, 85, 246, 379	0
1	C	552/602 (91%)	2.76	291 (52%)	0	0	26, 84, 246, 379	0
1	D	552/602 (91%)	2.51	260 (47%)	0	0	25, 84, 246, 379	0
1	E	552/602 (91%)	2.70	273 (49%)	0	0	25, 84, 246, 379	0
1	F	552/602 (91%)	2.64	259 (46%)	0	0	25, 84, 246, 379	0
1	G	552/602 (91%)	2.66	272 (49%)	0	0	30, 84, 246, 379	0
1	H	552/602 (91%)	2.80	280 (50%)	0	0	26, 86, 246, 379	0
1	I	552/602 (91%)	2.81	289 (52%)	0	0	31, 88, 246, 379	0
1	J	552/602 (91%)	2.91	315 (57%)	0	0	33, 96, 246, 379	0
1	K	552/602 (91%)	2.95	296 (53%)	0	0	26, 88, 245, 379	0
1	L	552/602 (91%)	2.96	300 (54%)	0	0	24, 87, 246, 379	0
1	M	552/602 (91%)	2.26	228 (41%)	0	0	15, 70, 209, 327	0
1	N	552/602 (91%)	2.12	203 (36%)	0	0	18, 69, 209, 327	0
1	O	552/602 (91%)	2.09	211 (38%)	0	0	15, 69, 209, 326	0
1	P	552/602 (91%)	2.15	230 (41%)	0	0	15, 70, 209, 327	0
1	Q	552/602 (91%)	2.18	214 (38%)	0	0	15, 69, 209, 326	0
1	R	552/602 (91%)	2.22	210 (38%)	0	0	17, 69, 209, 327	0
1	S	552/602 (91%)	2.31	245 (44%)	0	0	19, 70, 209, 326	0
1	T	552/602 (91%)	2.38	226 (40%)	0	0	15, 70, 208, 326	0
1	U	552/602 (91%)	2.53	265 (48%)	0	0	17, 69, 209, 327	0
1	V	552/602 (91%)	2.42	217 (39%)	0	0	18, 70, 209, 327	0
1	W	552/602 (91%)	2.24	239 (43%)	0	0	17, 70, 209, 326	0
1	X	552/602 (91%)	2.42	231 (41%)	0	0	14, 69, 209, 326	0

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Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å <sup>2</sup> )	Q<0.9
2	Y	146/166 (87%)	3.70	84 (57%)	0	0	38, 75, 221, 304	0
2	Z	146/166 (87%)	3.56	87 (59%)	0	0	37, 73, 222, 304	0
2	a	146/166 (87%)	3.54	97 (66%)	0	0	37, 77, 221, 304	0
2	b	146/166 (87%)	3.53	94 (64%)	0	0	39, 72, 221, 304	0
2	c	146/166 (87%)	2.57	73 (50%)	0	0	39, 72, 222, 305	0
2	d	146/166 (87%)	2.97	86 (58%)	0	0	35, 72, 222, 304	0
2	e	146/166 (87%)	3.03	87 (59%)	0	0	37, 73, 220, 304	0
2	f	146/166 (87%)	3.57	98 (67%)	0	0	39, 74, 222, 304	0
2	g	146/166 (87%)	3.59	95 (65%)	0	0	44, 75, 221, 304	0
2	h	146/166 (87%)	3.57	89 (60%)	0	0	38, 75, 221, 305	0
2	i	146/166 (87%)	3.42	98 (67%)	0	0	40, 75, 221, 304	0
2	j	146/166 (87%)	4.07	118 (80%)	0	0	36, 75, 222, 305	0
2	k	145/166 (87%)	2.79	68 (46%)	0	0	25, 57, 204, 314	0
2	l	145/166 (87%)	2.73	75 (51%)	0	0	28, 56, 204, 314	0
2	m	145/166 (87%)	3.18	77 (53%)	0	0	30, 59, 203, 314	0
2	n	145/166 (87%)	2.67	63 (43%)	0	0	23, 55, 204, 314	0
2	o	145/166 (87%)	2.49	68 (46%)	0	0	26, 57, 204, 314	0
2	p	145/166 (87%)	2.87	73 (50%)	0	0	27, 57, 204, 314	0
2	q	145/166 (87%)	2.66	63 (43%)	0	0	29, 58, 204, 314	0
2	r	145/166 (87%)	2.57	63 (43%)	0	0	26, 57, 205, 314	0
2	s	145/166 (87%)	2.71	75 (51%)	0	0	30, 58, 204, 314	0
2	t	145/166 (87%)	2.81	71 (48%)	0	0	31, 58, 204, 314	0
2	u	145/166 (87%)	2.46	64 (44%)	0	0	30, 58, 204, 314	0
2	v	145/166 (87%)	1.92	49 (33%)	0	0	29, 57, 204, 314	0
All	All	16740/18432 (90%)	2.63	8052 (48%)	0	0	14, 76, 228, 379	0

All (8052) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Y	151	ASN	37.4
2	Y	152	LEU	35.1
1	D	240	THR	33.0
1	K	210	PRO	30.7
2	Y	150	PRO	29.7

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Mol	Chain	Res	Type	RSRZ
2	n	142	ASN	29.0
1	G	495	GLU	27.8
2	Z	152	LEU	27.6
2	s	150	PRO	27.0
1	V	240	THR	26.3
2	m	142	ASN	26.3
2	a	36	ASP	26.0
2	k	143	LEU	25.9
1	I	211	TRP	25.7
1	X	210	PRO	25.5
1	F	240	THR	25.4
2	t	149	PHE	25.3
2	k	141	PRO	25.1
1	V	496	VAL	24.8
2	p	144	ASN	24.7
1	A	210	PRO	23.6
2	n	150	PRO	23.5
2	j	153	ASN	23.1
1	G	211	TRP	22.3
1	V	586	THR	21.9
2	b	158	PHE	21.5
1	V	497	VAL	21.3
2	k	142	ASN	21.2
1	H	209	PHE	21.1
1	C	260	ASP	21.1
2	u	142	ASN	21.1
2	f	37	VAL	21.0
1	L	211	TRP	20.9
2	Z	151	ASN	20.7
1	F	495	GLU	20.6
1	E	240	THR	20.6
1	C	495	GLU	20.3
1	U	240	THR	20.3
2	g	152	LEU	20.2
2	m	28	VAL	20.0
1	Q	564	GLY	20.0
2	v	142	ASN	20.0
1	F	211	TRP	19.9
2	h	152	LEU	19.8
2	p	142	ASN	19.8
2	m	143	LEU	19.6
2	j	152	LEU	19.6

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Mol	Chain	Res	Type	RSRZ
2	n	149	PHE	19.4
1	R	214	GLN	19.2
1	N	602	GLY	19.0
2	q	28	VAL	19.0
1	N	240	THR	18.9
2	g	151	ASN	18.8
2	r	142	ASN	18.7
2	q	144	ASN	18.5
1	H	208	VAL	18.5
2	g	153	ASN	18.3
2	m	141	PRO	18.3
1	J	253	ASP	18.3
2	r	141	PRO	18.1
1	S	564	GLY	18.0
1	V	211	TRP	18.0
1	X	211	TRP	18.0
1	H	585	GLU	17.7
2	o	143	LEU	17.7
2	b	35	THR	17.5
2	e	14	THR	17.4
1	J	504	LYS	17.4
2	m	144	ASN	17.4
1	A	209	PHE	17.3
2	t	148	TYR	17.1
1	M	424	ALA	17.1
2	h	159	PRO	17.0
1	W	211	TRP	17.0
2	t	150	PRO	17.0
2	d	150	PRO	16.9
2	l	142	ASN	16.8
1	V	602	GLY	16.7
1	N	207	TRP	16.6
1	I	424	ALA	16.5
1	L	240	THR	16.5
2	b	159	PRO	16.5
1	N	422	THR	16.2
1	V	498	ASP	16.1
2	l	144	ASN	16.1
1	G	586	THR	16.0
1	A	186	ASP	16.0
2	n	143	LEU	16.0
2	c	159	PRO	16.0

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Mol	Chain	Res	Type	RSRZ
1	O	240	THR	15.9
1	G	498	ASP	15.9
2	g	37	VAL	15.9
1	I	495	GLU	15.9
2	Y	153	ASN	15.9
2	g	150	PRO	15.8
2	q	142	ASN	15.7
1	N	494	ALA	15.7
2	t	28	VAL	15.6
2	u	143	LEU	15.5
1	P	253	ASP	15.4
1	A	462	GLU	15.3
2	d	151	ASN	15.3
1	P	242	GLU	15.2
1	I	421	ASP	15.2
2	j	154	GLU	15.2
1	M	602	GLY	15.2
1	C	494	ALA	15.2
1	L	564	GLY	15.1
1	M	421	ASP	15.1
2	b	157	TYR	15.1
1	E	204	PRO	15.0
1	I	210	PRO	15.0
1	H	242	GLU	14.9
1	A	211	TRP	14.9
1	D	421	ASP	14.9
1	G	210	PRO	14.9
1	H	422	THR	14.8
2	f	153	ASN	14.8
2	Z	153	ASN	14.7
1	H	49	THR	14.7
1	X	461	GLY	14.6
1	K	501	THR	14.6
2	Y	35	THR	14.5
1	A	246	TYR	14.4
1	K	240	THR	14.4
1	M	601	GLN	14.4
2	r	150	PRO	14.3
2	n	141	PRO	14.3
2	l	141	PRO	14.2
2	q	141	PRO	14.1
1	J	421	ASP	14.1

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Mol	Chain	Res	Type	RSRZ
1	V	601	GLN	14.0
1	W	502	GLY	14.0
1	L	208	VAL	14.0
1	X	6	ASN	13.9
1	E	499	LEU	13.9
2	i	71	ASP	13.9
1	J	238	PRO	13.8
1	B	417	THR	13.8
1	C	425	VAL	13.7
1	V	585	GLU	13.6
1	L	183	GLY	13.6
1	M	211	TRP	13.5
1	E	261	SER	13.5
2	k	144	ASN	13.5
1	G	602	GLY	13.4
1	B	211	TRP	13.4
2	o	147	HIS	13.4
1	U	260	ASP	13.4
1	C	92	ASP	13.4
2	f	36	ASP	13.3
1	I	422	THR	13.3
2	g	36	ASP	13.3
1	M	6	ASN	13.3
1	M	210	PRO	13.3
2	m	8	ASP	13.2
1	K	216	THR	13.2
1	L	194	ASP	13.2
1	V	210	PRO	13.2
2	l	143	LEU	13.1
1	X	547	PRO	13.1
1	A	214	GLN	13.1
1	T	564	GLY	13.0
1	M	207	TRP	13.0
1	J	239	VAL	12.9
1	I	253	ASP	12.9
2	s	149	PHE	12.9
1	H	237	ASP	12.9
2	i	157	TYR	12.9
1	T	422	THR	12.8
1	L	206	ASP	12.8
1	V	424	ALA	12.7
1	C	385	PRO	12.7

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Mol	Chain	Res	Type	RSRZ
1	T	211	TRP	12.6
1	B	213	THR	12.6
1	H	424	ALA	12.5
1	K	494	ALA	12.5
2	f	38	GLU	12.5
2	q	94	ASP	12.5
1	J	197	ASP	12.5
1	W	214	GLN	12.5
2	j	159	PRO	12.4
1	W	192	ASP	12.4
2	p	28	VAL	12.4
1	H	197	ASP	12.4
2	c	151	ASN	12.4
1	K	211	TRP	12.4
1	U	386	THR	12.4
1	B	260	ASP	12.4
2	f	152	LEU	12.4
2	Y	36	ASP	12.3
2	o	150	PRO	12.3
2	c	17	ASP	12.3
1	D	598	GLN	12.3
1	J	6	ASN	12.3
2	b	74	ASN	12.3
1	C	209	PHE	12.3
1	K	386	THR	12.2
2	b	151	ASN	12.2
1	J	240	THR	12.2
1	O	424	ALA	12.2
1	R	89	ASP	12.1
1	O	208	VAL	12.1
1	N	495	GLU	12.1
2	b	48	ASP	12.1
2	Z	72	ASP	12.0
2	h	153	ASN	12.0
1	Q	495	GLU	12.0
1	J	130	THR	12.0
1	B	209	PHE	12.0
2	i	151	ASN	12.0
2	e	159	PRO	12.0
1	X	207	TRP	11.9
2	h	151	ASN	11.9
1	U	208	VAL	11.9

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Mol	Chain	Res	Type	RSRZ
1	Q	255	ILE	11.8
1	E	260	ASP	11.8
1	Q	211	TRP	11.8
1	O	211	TRP	11.8
1	Q	210	PRO	11.8
2	n	148	TYR	11.8
2	e	28	VAL	11.8
1	T	423	GLU	11.8
1	S	196	ASP	11.8
1	F	494	ALA	11.8
2	p	143	LEU	11.8
1	A	50	THR	11.8
1	J	211	TRP	11.7
2	a	74	ASN	11.6
1	A	561	ASP	11.6
1	T	586	THR	11.6
1	L	210	PRO	11.5
1	W	561	ASP	11.5
1	V	239	VAL	11.5
1	E	424	ALA	11.5
1	I	209	PHE	11.5
2	r	8	ASP	11.5
2	r	149	PHE	11.5
1	C	207	TRP	11.4
2	a	152	LEU	11.4
1	U	595	GLU	11.4
1	N	283	CYS	11.4
1	L	89	ASP	11.4
1	I	268	GLU	11.4
1	E	546	THR	11.4
1	X	213	THR	11.4
1	L	540	GLY	11.4
1	F	496	VAL	11.4
1	F	500	ALA	11.4
1	F	423	GLU	11.4
1	H	591	GLN	11.3
1	R	463	ILE	11.3
1	E	242	GLU	11.3
1	L	563	LYS	11.3
1	R	207	TRP	11.3
1	H	386	THR	11.3
1	W	424	ALA	11.3

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Mol	Chain	Res	Type	RSRZ
1	M	497	VAL	11.3
1	D	239	VAL	11.3
1	R	564	GLY	11.3
1	S	213	THR	11.2
2	o	142	ASN	11.2
1	G	186	ASP	11.2
1	F	589	GLU	11.1
1	M	586	THR	11.1
1	X	240	THR	11.1
2	d	38	GLU	11.1
2	u	149	PHE	11.1
1	J	505	GLN	11.1
1	G	267	ALA	11.1
1	B	215	ASP	11.1
1	J	210	PRO	11.0
1	D	494	ALA	11.0
1	S	565	VAL	11.0
1	S	500	ALA	11.0
1	H	496	VAL	11.0
1	W	421	ASP	11.0
2	i	153	ASN	10.9
2	e	153	ASN	10.9
1	L	550	GLN	10.9
1	T	502	GLY	10.9
2	b	34	LEU	10.9
1	K	50	THR	10.9
2	o	149	PHE	10.9
2	h	158	PHE	10.9
2	e	35	THR	10.9
1	J	252	LYS	10.9
1	S	260	ASP	10.8
2	Z	35	THR	10.8
2	d	37	VAL	10.8
1	F	501	THR	10.8
1	F	504	LYS	10.8
1	C	550	GLN	10.8
1	N	601	GLN	10.8
1	F	192	ASP	10.8
1	W	586	THR	10.8
1	S	240	THR	10.8
1	N	6	ASN	10.8
1	P	424	ALA	10.8

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Mol	Chain	Res	Type	RSRZ
2	v	141	PRO	10.8
2	s	89	CYS	10.7
1	E	262	GLY	10.7
2	l	28	VAL	10.7
2	q	145	GLU	10.7
1	D	241	GLY	10.7
2	d	77	ALA	10.7
2	a	154	GLU	10.7
2	j	34	LEU	10.7
1	A	559	LEU	10.7
1	F	424	ALA	10.7
1	G	499	LEU	10.6
2	g	16	GLY	10.6
1	Q	242	GLU	10.6
1	A	417	THR	10.6
2	h	35	THR	10.6
1	N	421	ASP	10.6
2	i	36	ASP	10.6
1	K	367	ASP	10.6
1	B	385	PRO	10.6
1	Q	240	THR	10.6
1	W	602	GLY	10.6
1	Q	245	SER	10.5
2	e	44	ASP	10.5
1	P	501	THR	10.5
1	R	205	ASN	10.5
2	a	151	ASN	10.5
1	T	238	PRO	10.5
1	H	425	VAL	10.5
1	M	5	GLU	10.5
1	D	422	THR	10.5
1	U	587	PRO	10.4
2	i	35	THR	10.4
1	E	589	GLU	10.4
1	V	207	TRP	10.4
1	R	255	ILE	10.4
1	M	253	ASP	10.4
1	E	601	GLN	10.4
1	H	260	ASP	10.4
1	L	207	TRP	10.4
1	U	211	TRP	10.3
1	V	192	ASP	10.3

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Mol	Chain	Res	Type	RSRZ
1	R	208	VAL	10.3
1	C	462	GLU	10.3
1	L	271	ILE	10.3
1	H	495	GLU	10.3
1	H	423	GLU	10.3
1	J	460	ASP	10.3
1	D	601	GLN	10.2
2	h	155	TRP	10.2
2	l	8	ASP	10.2
1	T	585	GLU	10.2
1	D	32	ASP	10.2
1	V	234	ILE	10.2
1	D	426	ASN	10.2
2	Z	73	GLU	10.1
1	B	550	GLN	10.1
1	F	422	THR	10.1
2	i	154	GLU	10.1
1	K	510	ILE	10.1
2	h	156	HIS	10.1
2	i	28	VAL	10.1
1	T	494	ALA	10.1
2	j	155	TRP	10.1
1	V	205	ASN	10.0
1	G	209	PHE	10.0
2	a	47	ASP	10.0
1	I	591	GLN	10.0
1	J	462	GLU	10.0
1	P	505	GLN	10.0
2	t	89	CYS	10.0
1	U	426	ASN	10.0
1	P	214	GLN	10.0
1	U	417	THR	9.9
1	H	601	GLN	9.9
2	j	38	GLU	9.9
1	L	205	ASN	9.9
2	Z	103	ASP	9.9
1	E	214	GLN	9.9
1	M	543	PRO	9.9
1	B	210	PRO	9.9
2	Y	16	GLY	9.9
2	a	35	THR	9.9
1	O	6	ASN	9.9

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Mol	Chain	Res	Type	RSRZ
2	k	9	LEU	9.9
1	E	561	ASP	9.9
1	V	214	GLN	9.9
2	f	35	THR	9.8
1	E	13	SER	9.8
1	T	240	THR	9.8
1	G	421	ASP	9.8
1	R	462	GLU	9.8
1	U	425	VAL	9.8
2	v	143	LEU	9.8
1	F	502	GLY	9.8
1	A	546	THR	9.7
1	G	240	THR	9.7
1	I	84	ASP	9.7
1	N	242	GLU	9.7
1	T	420	VAL	9.7
1	C	595	GLU	9.7
2	l	6	LYS	9.7
1	B	191	TYR	9.7
1	A	564	GLY	9.7
1	B	559	LEU	9.7
1	E	6	ASN	9.6
1	P	504	LYS	9.6
1	H	6	ASN	9.6
1	C	240	THR	9.6
1	W	242	GLU	9.6
2	a	37	VAL	9.6
2	h	37	VAL	9.6
1	I	232	ALA	9.6
2	u	150	PRO	9.6
1	V	215	ASP	9.6
1	E	463	ILE	9.5
1	B	248	LYS	9.5
2	g	38	GLU	9.5
2	j	100	ILE	9.5
1	C	259	ALA	9.5
1	O	253	ASP	9.5
2	j	37	VAL	9.5
1	B	597	GLN	9.5
1	R	602	GLY	9.5
1	F	203	ASN	9.5
2	q	143	LEU	9.5

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Mol	Chain	Res	Type	RSRZ
1	F	601	GLN	9.5
1	W	585	GLU	9.5
1	A	6	ASN	9.5
1	F	542	THR	9.5
2	r	28	VAL	9.5
1	U	214	GLN	9.5
1	U	92	ASP	9.5
1	T	424	ALA	9.5
1	X	546	THR	9.4
1	A	183	GLY	9.4
1	F	602	GLY	9.4
1	P	50	THR	9.4
1	V	558	THR	9.4
1	I	85	GLY	9.4
1	G	237	ASP	9.4
1	K	230	GLU	9.4
1	M	587	PRO	9.4
2	a	28	VAL	9.4
2	l	34	GLN	9.4
2	j	108	ALA	9.3
1	Q	214	GLN	9.3
1	E	565	VAL	9.3
1	S	587	PRO	9.3
1	O	212	LEU	9.3
1	X	209	PHE	9.3
1	A	245	SER	9.3
1	X	424	ALA	9.3
2	a	153	ASN	9.3
1	X	597	GLN	9.3
2	u	27	ASP	9.3
2	c	36	ASP	9.3
1	Q	228	LYS	9.3
1	L	215	ASP	9.3
1	Q	494	ALA	9.3
1	K	253	ASP	9.3
1	H	602	GLY	9.3
1	T	210	PRO	9.3
2	Z	34	LEU	9.2
2	h	150	PRO	9.2
1	S	558	THR	9.2
2	s	35	ASP	9.2
2	u	141	PRO	9.2

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Mol	Chain	Res	Type	RSRZ
1	L	188	ALA	9.2
1	H	253	ASP	9.2
1	R	245	SER	9.2
2	k	10	VAL	9.2
1	D	424	ALA	9.2
1	A	338	ALA	9.2
1	I	386	THR	9.2
2	b	28	VAL	9.2
1	M	197	ASP	9.2
1	O	422	THR	9.2
1	K	130	THR	9.2
1	W	240	THR	9.2
1	F	32	ASP	9.1
1	H	7	ARG	9.1
1	J	424	ALA	9.1
2	h	44	ASP	9.1
1	F	234	ILE	9.1
2	j	151	ASN	9.1
1	A	386	THR	9.1
1	X	495	GLU	9.1
1	T	599	ALA	9.1
1	D	420	VAL	9.1
1	A	547	PRO	9.1
1	E	501	THR	9.1
1	T	584	PRO	9.1
1	H	509	ASP	9.1
1	K	31	ASN	9.0
2	f	17	ASP	9.0
1	J	10	SER	9.0
1	R	421	ASP	9.0
1	L	285	ALA	9.0
1	M	496	VAL	9.0
1	L	239	VAL	9.0
2	s	144	ASN	9.0
1	G	494	ALA	9.0
1	X	239	VAL	9.0
1	T	284	THR	9.0
1	G	587	PRO	9.0
1	J	386	THR	9.0
1	N	250	ASP	9.0
1	E	257	ASP	8.9
2	i	48	ASP	8.9

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Mol	Chain	Res	Type	RSRZ
1	K	208	VAL	8.9
2	r	134	THR	8.9
2	q	27	ASP	8.9
1	X	499	LEU	8.9
1	D	170	ALA	8.9
2	u	55	ILE	8.9
1	W	213	THR	8.9
1	M	231	THR	8.9
1	B	208	VAL	8.9
1	O	543	PRO	8.9
1	L	420	VAL	8.9
1	V	423	GLU	8.9
1	P	246	TYR	8.9
2	f	71	ASP	8.9
1	F	212	LEU	8.8
1	C	49	THR	8.8
1	V	505	GLN	8.8
1	C	426	ASN	8.8
2	h	36	ASP	8.8
1	R	592	TRP	8.8
1	T	602	GLY	8.8
2	b	95	ASN	8.8
1	N	547	PRO	8.8
1	F	213	THR	8.8
1	R	206	ASP	8.8
1	E	588	GLU	8.7
1	G	206	ASP	8.7
1	L	268	GLU	8.7
2	r	148	TYR	8.7
2	e	37	VAL	8.7
2	i	110	ALA	8.7
1	S	424	ALA	8.7
1	T	506	VAL	8.7
1	L	417	THR	8.7
1	X	462	GLU	8.7
1	I	585	GLU	8.7
2	Z	150	PRO	8.7
1	H	8	LEU	8.7
1	B	192	ASP	8.7
1	C	211	TRP	8.7
1	C	424	ALA	8.7
2	f	74	ASN	8.7

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Mol	Chain	Res	Type	RSRZ
1	T	601	GLN	8.7
1	R	211	TRP	8.6
1	D	496	VAL	8.6
1	G	49	THR	8.6
1	I	86	ALA	8.6
1	L	203	ASN	8.6
1	F	420	VAL	8.6
1	K	592	TRP	8.6
2	j	58	GLN	8.6
1	O	503	GLU	8.6
1	R	386	THR	8.6
1	A	545	GLY	8.6
1	O	210	PRO	8.6
1	D	498	ASP	8.6
1	U	5	GLU	8.6
2	l	145	GLU	8.6
1	B	594	VAL	8.6
1	G	8	LEU	8.6
1	L	246	TYR	8.6
1	K	548	GLU	8.6
1	Q	253	ASP	8.5
1	F	92	ASP	8.5
1	V	8	LEU	8.5
1	N	211	TRP	8.5
1	I	207	TRP	8.5
1	X	48	TYR	8.5
1	F	210	PRO	8.5
1	C	538	LEU	8.5
2	Z	14	THR	8.5
1	N	267	ALA	8.5
2	h	48	ASP	8.5
1	S	259	ALA	8.5
1	L	245	SER	8.5
2	Z	19	VAL	8.5
1	E	461	GLY	8.5
1	W	496	VAL	8.5
2	u	28	VAL	8.4
1	G	177	HIS	8.4
1	F	503	GLU	8.4
2	t	64	GLU	8.4
1	H	396	GLU	8.4
1	M	232	ALA	8.4

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Mol	Chain	Res	Type	RSRZ
1	B	92	ASP	8.4
2	e	48	ASP	8.4
1	Q	8	LEU	8.4
1	D	497	VAL	8.4
1	L	386	THR	8.4
1	X	425	VAL	8.4
1	J	506	VAL	8.4
1	T	162	SER	8.4
2	v	144	ASN	8.4
2	Z	74	ASN	8.4
1	J	50	THR	8.4
1	L	463	ILE	8.4
1	J	208	VAL	8.3
1	T	561	ASP	8.3
1	K	540	GLY	8.3
2	g	31	ASP	8.3
1	T	598	GLN	8.3
2	e	15	LYS	8.3
1	W	241	GLY	8.3
2	j	47	ASP	8.3
1	Q	6	ASN	8.3
1	O	207	TRP	8.3
1	W	595	GLU	8.3
1	L	15	PHE	8.3
1	R	561	ASP	8.3
2	h	16	GLY	8.3
2	v	9	LEU	8.2
1	B	249	ARG	8.2
1	I	584	PRO	8.2
1	W	598	GLN	8.2
1	B	32	ASP	8.2
2	Z	157	TYR	8.2
1	L	242	GLU	8.2
2	n	22	ASP	8.2
2	Y	70	SER	8.2
1	J	138	THR	8.2
2	j	33	THR	8.2
1	H	211	TRP	8.2
2	f	75	PRO	8.2
1	A	597	GLN	8.2
2	b	104	TYR	8.2
1	R	256	ASP	8.2

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Mol	Chain	Res	Type	RSRZ
1	S	245	SER	8.2
2	d	17	ASP	8.2
1	T	208	VAL	8.1
1	P	585	GLU	8.1
1	M	523	SER	8.1
1	X	208	VAL	8.1
1	C	384	LEU	8.1
1	F	499	LEU	8.1
1	J	269	ARG	8.1
1	I	561	ASP	8.1
1	A	339	ASP	8.1
1	K	444	LEU	8.1
1	A	423	GLU	8.1
1	U	499	LEU	8.1
1	C	594	VAL	8.1
2	k	150	PRO	8.1
1	Q	213	THR	8.1
1	K	284	THR	8.1
2	s	143	LEU	8.1
1	W	239	VAL	8.1
1	A	208	VAL	8.1
1	K	32	ASP	8.1
1	B	261	SER	8.1
1	D	13	SER	8.1
2	Z	70	SER	8.1
1	L	515	GLU	8.1
1	T	563	LYS	8.0
1	O	558	THR	8.0
1	K	461	GLY	8.0
1	I	238	PRO	8.0
2	d	39	PRO	8.0
1	E	259	ALA	8.0
1	H	283	CYS	8.0
2	b	75	PRO	8.0
1	H	212	LEU	8.0
1	T	565	VAL	8.0
1	L	460	ASP	8.0
1	T	590	GLN	8.0
1	Q	563	LYS	8.0
1	B	259	ALA	8.0
2	a	155	TRP	8.0
2	s	27	ASP	8.0

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Mol	Chain	Res	Type	RSRZ
1	O	502	GLY	8.0
1	W	284	THR	8.0
1	X	421	ASP	8.0
1	D	563	LYS	8.0
1	K	15	PHE	7.9
2	Y	37	VAL	7.9
2	j	44	ASP	7.9
1	U	597	GLN	7.9
1	F	561	ASP	7.9
1	D	259	ALA	7.9
1	K	545	GLY	7.9
2	p	145	GLU	7.9
2	l	66	PRO	7.9
1	G	426	ASN	7.9
1	Q	283	CYS	7.9
1	A	283	CYS	7.9
1	C	559	LEU	7.9
1	G	283	CYS	7.8
1	C	262	GLY	7.8
1	E	498	ASP	7.8
2	Z	31	ASP	7.8
1	K	160	SER	7.8
1	P	564	GLY	7.8
1	P	537	GLU	7.8
1	Q	503	GLU	7.8
1	S	559	LEU	7.8
1	R	7	ARG	7.8
1	K	495	GLU	7.8
1	I	252	LYS	7.8
1	D	245	SER	7.8
2	e	38	GLU	7.8
2	f	77	ALA	7.8
1	V	233	PHE	7.8
1	Q	540	GLY	7.8
1	E	58	ASP	7.8
1	K	515	GLU	7.8
1	A	42	ASP	7.8
1	H	499	LEU	7.8
1	L	575	GLN	7.8
1	M	585	GLU	7.8
1	N	8	LEU	7.7
1	G	205	ASN	7.7

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Mol	Chain	Res	Type	RSRZ
1	R	565	VAL	7.7
1	D	162	SER	7.7
1	U	216	THR	7.7
1	I	501	THR	7.7
1	S	253	ASP	7.7
1	N	210	PRO	7.7
1	D	590	GLN	7.7
1	L	500	ALA	7.7
1	M	451	ASP	7.7
1	K	186	ASP	7.7
2	v	32	SER	7.7
1	A	8	LEU	7.7
2	b	98	CYS	7.7
1	K	198	ILE	7.7
1	L	546	THR	7.7
1	D	548	GLU	7.7
1	X	214	GLN	7.7
1	N	209	PHE	7.7
1	U	563	LYS	7.7
2	Z	62	GLY	7.7
1	I	524	PHE	7.7
2	Y	158	PHE	7.7
2	d	153	ASN	7.7
1	F	590	GLN	7.7
1	W	587	PRO	7.7
1	H	500	ALA	7.7
2	u	35	ASP	7.7
1	E	460	ASP	7.7
2	t	38	ASP	7.7
1	C	496	VAL	7.7
1	R	246	TYR	7.6
1	F	595	GLU	7.6
1	N	424	ALA	7.6
1	C	549	TYR	7.6
1	G	260	ASP	7.6
1	P	6	ASN	7.6
1	P	240	THR	7.6
1	F	260	ASP	7.6
1	L	85	GLY	7.6
2	e	24	ARG	7.6
1	S	596	ALA	7.6
1	B	421	ASP	7.6

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Mol	Chain	Res	Type	RSRZ
1	R	575	GLN	7.6
1	C	531	ASN	7.6
1	H	241	GLY	7.6
2	d	14	THR	7.6
1	C	421	ASP	7.6
1	I	260	ASP	7.6
2	a	73	GLU	7.6
2	v	31	GLN	7.6
1	A	205	ASN	7.6
1	B	383	ASP	7.6
1	J	389	LEU	7.6
1	W	259	ALA	7.6
1	J	451	ASP	7.6
2	b	84	LEU	7.6
1	V	420	VAL	7.6
1	I	202	GLN	7.6
2	t	65	ASN	7.6
1	L	77	ASP	7.6
2	b	156	HIS	7.6
1	M	242	GLU	7.6
1	J	207	TRP	7.5
1	E	558	THR	7.5
2	m	61	SER	7.5
1	W	420	VAL	7.5
2	Y	71	ASP	7.5
2	f	103	ASP	7.5
1	S	501	THR	7.5
1	D	599	ALA	7.5
2	o	35	ASP	7.5
1	I	504	LYS	7.5
1	K	13	SER	7.5
1	K	235	TYR	7.5
1	A	312	ASP	7.5
1	J	237	ASP	7.5
1	G	28	GLU	7.5
1	J	437	GLN	7.5
1	P	422	THR	7.5
1	R	215	ASP	7.5
1	T	426	ASN	7.5
1	J	584	PRO	7.5
2	Y	139	SER	7.5
2	Z	83	GLY	7.5

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Mol	Chain	Res	Type	RSRZ
1	H	256	ASP	7.5
2	i	31	ASP	7.5
1	A	267	ALA	7.5
1	H	210	PRO	7.4
1	I	7	ARG	7.4
1	O	213	THR	7.4
1	J	601	GLN	7.4
1	Q	449	PHE	7.4
1	T	421	ASP	7.4
1	P	545	GLY	7.4
1	G	547	PRO	7.4
1	H	133	GLU	7.4
1	G	32	ASP	7.4
1	U	48	TYR	7.4
1	S	211	TRP	7.4
2	r	9	LEU	7.4
2	o	148	TYR	7.4
2	h	101	ALA	7.4
1	U	259	ALA	7.4
1	E	599	ALA	7.4
1	X	422	THR	7.4
1	M	423	GLU	7.4
1	B	196	ASP	7.4
1	J	131	ASP	7.4
1	K	16	ASP	7.4
1	W	558	THR	7.4
1	B	587	PRO	7.4
1	E	339	ASP	7.4
1	K	185	GLU	7.4
1	Q	545	GLY	7.4
1	G	580	GLY	7.4
2	Y	38	GLU	7.3
2	Z	154	GLU	7.3
1	R	188	ALA	7.3
1	X	246	TYR	7.3
1	B	8	LEU	7.3
1	D	531	ASN	7.3
1	U	47	GLN	7.3
1	C	214	GLN	7.3
1	V	195	ALA	7.3
2	r	143	LEU	7.3
1	X	8	LEU	7.3

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Mol	Chain	Res	Type	RSRZ
2	t	27	ASP	7.3
1	H	264	ILE	7.3
1	T	244	VAL	7.3
1	F	204	PRO	7.3
1	Q	515	GLU	7.3
1	U	588	GLU	7.3
2	k	28	VAL	7.3
2	l	18	GLY	7.3
1	L	423	GLU	7.3
2	b	73	GLU	7.3
2	i	156	HIS	7.3
1	D	558	THR	7.3
1	A	41	TRP	7.3
1	C	15	PHE	7.3
1	S	601	GLN	7.3
1	B	48	TYR	7.3
1	N	386	THR	7.3
1	L	282	THR	7.3
1	R	239	VAL	7.3
2	s	146	TRP	7.3
2	e	155	TRP	7.3
1	U	525	GLN	7.3
2	i	158	PHE	7.3
1	Q	386	THR	7.3
1	U	585	GLU	7.3
1	G	31	ASN	7.3
1	M	209	PHE	7.3
1	T	214	GLN	7.3
2	e	104	TYR	7.3
1	D	495	GLU	7.3
1	K	422	THR	7.3
2	q	148	TYR	7.2
2	s	147	HIS	7.2
1	I	239	VAL	7.2
2	Z	155	TRP	7.2
1	X	256	ASP	7.2
1	B	570	ASP	7.2
1	J	375	ASN	7.2
2	c	14	THR	7.2
1	P	550	GLN	7.2
1	R	339	ASP	7.2
1	C	91	ALA	7.2

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Mol	Chain	Res	Type	RSRZ
1	J	25	ALA	7.2
1	N	498	ASP	7.2
1	P	425	VAL	7.2
1	I	131	ASP	7.2
1	P	252	LYS	7.2
1	G	29	ALA	7.2
1	X	498	ASP	7.2
1	K	188	ALA	7.2
1	U	264	ILE	7.2
2	Z	15	LYS	7.2
1	H	584	PRO	7.2
1	O	261	SER	7.2
1	Q	75	PRO	7.2
1	C	587	PRO	7.2
1	I	50	THR	7.2
1	N	423	GLU	7.2
1	T	495	GLU	7.2
1	I	237	ASP	7.2
1	H	523	SER	7.2
1	S	499	LEU	7.2
1	U	11	ILE	7.2
2	a	159	PRO	7.2
1	G	50	THR	7.2
2	Y	143	THR	7.2
1	Q	25	ALA	7.2
1	X	572	ALA	7.2
1	R	547	PRO	7.2
1	U	6	ASN	7.2
1	G	250	ASP	7.2
1	U	263	PHE	7.2
1	V	209	PHE	7.2
1	T	558	THR	7.1
1	X	571	TYR	7.1
1	J	410	SER	7.1
1	U	213	THR	7.1
2	t	142	ASN	7.1
1	U	590	GLN	7.1
1	T	13	SER	7.1
1	F	581	VAL	7.1
1	R	573	ASN	7.1
1	A	461	GLY	7.1
2	h	88	ALA	7.1

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Mol	Chain	Res	Type	RSRZ
1	V	89	ASP	7.1
1	B	242	GLU	7.1
1	K	539	LEU	7.1
1	B	190	LYS	7.1
1	E	566	GLU	7.1
1	B	214	GLN	7.1
1	G	378	ASP	7.1
1	J	263	PHE	7.1
1	L	25	ALA	7.1
1	E	598	GLN	7.1
1	L	597	GLN	7.1
1	O	197	ASP	7.1
1	V	182	ASN	7.1
1	I	203	ASN	7.1
1	J	422	THR	7.1
2	d	138	PRO	7.1
2	a	84	LEU	7.1
2	c	35	THR	7.1
2	o	146	TRP	7.1
1	D	575	GLN	7.1
1	R	270	GLN	7.0
1	D	595	GLU	7.0
1	J	185	GLU	7.0
2	m	70	GLY	7.0
2	i	72	ASP	7.0
1	O	421	ASP	7.0
1	X	339	ASP	7.0
2	r	94	ASP	7.0
1	D	262	GLY	7.0
1	D	602	GLY	7.0
1	X	215	ASP	7.0
1	R	189	GLU	7.0
1	J	236	GLN	7.0
1	L	255	ILE	7.0
1	Q	424	ALA	7.0
1	E	538	LEU	7.0
1	C	213	THR	7.0
1	H	451	ASP	7.0
1	R	597	GLN	7.0
1	L	189	GLU	7.0
1	G	182	ASN	7.0
2	f	18	LEU	7.0

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Mol	Chain	Res	Type	RSRZ
1	X	139	SER	7.0
1	H	421	ASP	7.0
1	L	173	CYS	7.0
2	o	22	ASP	7.0
1	A	213	THR	7.0
1	K	550	GLN	7.0
2	k	147	HIS	7.0
1	H	268	GLU	7.0
1	B	575	GLN	7.0
2	q	72	ASP	7.0
1	S	533	ALA	7.0
1	E	547	PRO	7.0
1	X	141	ASN	7.0
1	J	548	GLU	7.0
1	J	503	GLU	7.0
1	L	456	ALA	6.9
1	V	31	ASN	6.9
2	Y	34	LEU	6.9
1	I	261	SER	6.9
1	I	581	VAL	6.9
1	E	253	ASP	6.9
2	o	8	ASP	6.9
1	A	550	GLN	6.9
2	h	78	GLU	6.9
1	E	16	ASP	6.9
2	r	62	ASP	6.9
1	U	586	THR	6.9
2	n	79	ALA	6.9
1	L	367	ASP	6.9
1	F	205	ASN	6.9
1	Q	575	GLN	6.9
1	Q	173	CYS	6.9
1	A	337	ASN	6.9
2	u	56	THR	6.9
1	W	210	PRO	6.9
1	Q	548	GLU	6.9
1	F	565	VAL	6.9
1	N	31	ASN	6.9
1	J	270	GLN	6.9
2	b	69	PHE	6.9
1	U	600	LYS	6.9
1	G	194	ASP	6.9

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Mol	Chain	Res	Type	RSRZ
1	H	595	GLU	6.9
1	J	445	GLU	6.9
1	X	7	ARG	6.9
1	H	378	ASP	6.9
1	D	214	GLN	6.9
2	s	7	GLY	6.9
1	A	139	SER	6.9
1	C	32	ASP	6.9
1	J	428	GLY	6.9
1	P	20	THR	6.9
1	B	216	THR	6.9
1	I	543	PRO	6.9
2	j	150	PRO	6.9
1	Q	570	ASP	6.8
2	e	47	ASP	6.8
1	K	246	TYR	6.8
1	W	279	SER	6.8
2	a	158	PHE	6.8
1	K	202	GLN	6.8
2	m	96	ALA	6.8
2	k	145	GLU	6.8
1	F	186	ASP	6.8
2	a	46	VAL	6.8
2	t	97	LEU	6.8
2	i	23	LEU	6.8
1	A	32	ASP	6.8
1	S	497	VAL	6.8
1	D	565	VAL	6.8
2	d	35	THR	6.8
1	H	32	ASP	6.8
2	g	149	PHE	6.8
1	C	546	THR	6.8
1	C	46	SER	6.8
1	D	564	GLY	6.8
1	C	588	GLU	6.8
1	F	218	GLN	6.8
1	B	580	GLY	6.8
1	V	250	ASP	6.8
1	I	197	ASP	6.8
1	C	499	LEU	6.8
1	J	387	GLN	6.8
1	F	161	ASN	6.8

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Mol	Chain	Res	Type	RSRZ
1	V	547	PRO	6.8
1	D	561	ASP	6.8
2	p	141	PRO	6.8
1	B	26	ARG	6.7
2	a	107	GLU	6.7
1	B	563	LYS	6.7
1	S	425	VAL	6.7
1	B	573	ASN	6.7
1	N	420	VAL	6.7
2	k	30	PRO	6.7
1	K	241	GLY	6.7
2	p	147	HIS	6.7
1	M	260	ASP	6.7
1	G	584	PRO	6.7
2	a	81	ASP	6.7
2	Y	154	GLU	6.7
2	d	28	VAL	6.7
1	V	267	ALA	6.7
1	A	259	ALA	6.7
1	E	220	ALA	6.7
1	H	114	ALA	6.7
1	I	6	ASN	6.7
1	E	32	ASP	6.7
2	f	45	ALA	6.7
1	H	549	TYR	6.7
2	p	35	ASP	6.7
1	D	25	ALA	6.7
1	O	238	PRO	6.7
1	W	426	ASN	6.7
1	G	556	TYR	6.7
1	J	162	SER	6.7
1	F	580	GLY	6.7
1	O	89	ASP	6.7
1	I	198	ILE	6.7
1	O	239	VAL	6.7
2	a	150	PRO	6.7
2	h	157	TYR	6.7
1	E	205	ASN	6.6
1	F	367	ASP	6.6
1	P	254	VAL	6.6
1	E	542	THR	6.6
1	S	209	PHE	6.6

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Mol	Chain	Res	Type	RSRZ
1	H	387	GLN	6.6
1	E	50	THR	6.6
2	g	124	TYR	6.6
1	M	495	GLU	6.6
1	R	264	ILE	6.6
1	P	421	ASP	6.6
1	O	86	ALA	6.6
1	L	190	LYS	6.6
1	V	212	LEU	6.6
1	V	581	VAL	6.6
1	J	23	ASP	6.6
1	G	311	GLU	6.6
1	K	89	ASP	6.6
2	Z	47	ASP	6.6
1	U	241	GLY	6.6
1	E	279	SER	6.6
1	G	496	VAL	6.6
1	U	570	ASP	6.6
1	E	170	ALA	6.6
1	J	533	ALA	6.6
1	D	39	SER	6.6
1	K	10	SER	6.6
2	t	147	HIS	6.6
1	S	93	VAL	6.6
1	T	460	ASP	6.6
1	U	509	ASP	6.6
1	T	505	GLN	6.6
2	j	43	GLN	6.6
2	e	46	VAL	6.6
1	R	383	ASP	6.6
2	j	101	ALA	6.6
1	B	591	GLN	6.6
1	C	434	THR	6.6
2	b	152	LEU	6.5
2	s	28	VAL	6.5
1	P	180	SER	6.5
1	N	260	ASP	6.5
1	N	216	THR	6.5
1	S	238	PRO	6.5
1	E	502	GLY	6.5
1	B	424	ALA	6.5
1	X	563	LYS	6.5

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Mol	Chain	Res	Type	RSRZ
1	J	602	GLY	6.5
1	B	41	TRP	6.5
1	K	271	ILE	6.5
1	M	566	GLU	6.5
1	L	495	GLU	6.5
1	R	576	LEU	6.5
1	V	206	ASP	6.5
1	K	197	ASP	6.5
1	T	209	PHE	6.5
1	V	584	PRO	6.5
1	D	501	THR	6.5
1	A	452	ASN	6.5
1	C	242	GLU	6.5
1	Q	26	ARG	6.5
1	U	500	ALA	6.5
1	C	208	VAL	6.5
1	K	280	ILE	6.5
2	i	155	TRP	6.5
2	h	23	LEU	6.5
1	H	42	ASP	6.5
1	K	143	VAL	6.5
2	m	75	LEU	6.5
1	T	589	GLU	6.5
1	U	572	ALA	6.5
2	m	38	ASP	6.5
2	f	72	ASP	6.5
1	U	591	GLN	6.5
1	P	183	GLY	6.5
1	C	261	SER	6.5
2	h	34	LEU	6.5
1	P	503	GLU	6.5
1	U	519	ASP	6.5
1	G	242	GLU	6.5
2	v	150	PRO	6.5
1	H	202	GLN	6.5
1	T	39	SER	6.4
1	J	230	GLU	6.4
1	I	259	ALA	6.4
2	j	80	ASP	6.4
1	A	420	VAL	6.4
1	F	497	VAL	6.4
1	J	261	SER	6.4

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Mol	Chain	Res	Type	RSRZ
1	S	423	GLU	6.4
1	F	558	THR	6.4
1	O	263	PHE	6.4
1	D	58	ASP	6.4
2	l	38	ASP	6.4
2	r	7	GLY	6.4
1	W	207	TRP	6.4
1	A	422	THR	6.4
1	L	344	THR	6.4
1	R	8	LEU	6.4
2	o	144	ASN	6.4
1	S	214	GLN	6.4
1	V	194	ASP	6.4
1	E	250	ASP	6.4
2	t	145	GLU	6.4
1	D	586	THR	6.4
1	S	598	GLN	6.4
1	B	256	ASP	6.4
1	I	173	CYS	6.4
1	W	497	VAL	6.4
2	m	69	GLU	6.4
1	G	519	ASP	6.4
1	A	602	GLY	6.4
1	V	161	ASN	6.4
1	C	357	ALA	6.4
1	M	252	LYS	6.4
1	G	420	VAL	6.4
1	L	565	VAL	6.4
1	P	375	ASN	6.4
1	V	387	GLN	6.4
1	S	580	GLY	6.4
1	C	313	LYS	6.4
1	T	425	VAL	6.4
2	m	19	VAL	6.4
1	A	49	THR	6.4
1	K	20	THR	6.4
1	J	452	ASN	6.4
1	Q	421	ASP	6.4
1	S	599	ALA	6.4
1	K	433	ASP	6.4
2	r	63	ASP	6.4
2	g	19	VAL	6.4

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Mol	Chain	Res	Type	RSRZ
1	F	578	GLN	6.4
1	K	252	LYS	6.4
1	E	543	PRO	6.4
1	F	460	ASP	6.4
1	L	213	THR	6.3
1	U	559	LEU	6.3
2	f	27	GLY	6.3
1	X	186	ASP	6.3
2	f	16	GLY	6.3
1	S	254	VAL	6.3
1	J	444	LEU	6.3
2	u	148	TYR	6.3
1	R	213	THR	6.3
2	b	14	THR	6.3
1	O	271	ILE	6.3
1	V	503	GLU	6.3
1	G	456	ALA	6.3
1	K	437	GLN	6.3
1	T	587	PRO	6.3
2	c	153	ASN	6.3
1	E	586	THR	6.3
1	X	103	ARG	6.3
2	q	61	SER	6.3
1	A	256	ASP	6.3
1	V	516	CYS	6.3
1	T	461	GLY	6.3
1	B	526	SER	6.3
1	E	5	GLU	6.3
1	L	49	THR	6.3
1	R	494	ALA	6.3
1	B	531	ASN	6.3
1	G	292	LEU	6.3
1	U	461	GLY	6.3
1	C	41	TRP	6.3
1	K	546	THR	6.3
1	L	531	ASN	6.3
2	r	144	ASN	6.3
2	j	156	HIS	6.3
1	L	17	ALA	6.3
2	b	47	ASP	6.2
2	j	36	ASP	6.2
1	J	583	LYS	6.2

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Mol	Chain	Res	Type	RSRZ
1	R	540	GLY	6.2
1	E	587	PRO	6.2
1	T	239	VAL	6.2
1	K	17	ALA	6.2
1	P	283	CYS	6.2
1	H	161	ASN	6.2
1	R	25	ALA	6.2
1	L	209	PHE	6.2
1	N	586	THR	6.2
1	N	325	ASP	6.2
1	U	580	GLY	6.2
2	g	18	LEU	6.2
1	W	503	GLU	6.2
1	E	462	GLU	6.2
2	i	52	MET	6.2
1	X	200	SER	6.2
1	A	206	ASP	6.2
1	K	203	ASN	6.2
1	K	420	VAL	6.2
2	t	66	PRO	6.2
1	P	592	TRP	6.2
1	F	588	GLU	6.2
1	F	419	GLY	6.2
2	f	70	SER	6.2
1	A	388	PRO	6.2
1	L	513	ARG	6.2
1	L	516	CYS	6.2
1	C	339	ASP	6.2
1	F	282	THR	6.2
2	k	42	ALA	6.2
2	s	20	ALA	6.2
1	I	548	GLU	6.2
2	r	97	LEU	6.2
2	Y	144	GLY	6.2
1	T	339	ASP	6.2
1	L	498	ASP	6.2
1	M	589	GLU	6.2
1	B	150	HIS	6.2
1	I	204	PRO	6.2
1	I	537	GLU	6.2
1	D	550	GLN	6.2
1	P	389	LEU	6.2

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Mol	Chain	Res	Type	RSRZ
1	U	79	LEU	6.2
1	C	566	GLU	6.2
1	U	204	PRO	6.2
1	V	203	ASN	6.2
1	F	388	PRO	6.2
1	O	270	GLN	6.2
1	S	590	GLN	6.2
2	m	22	ASP	6.2
1	O	199	PRO	6.2
1	C	361	HIS	6.2
1	C	191	TYR	6.2
1	E	241	GLY	6.2
1	J	143	VAL	6.2
1	U	159	ASP	6.1
2	a	70	SER	6.1
1	W	380	ASN	6.1
1	P	444	LEU	6.1
1	S	563	LYS	6.1
1	R	550	GLN	6.1
1	S	542	THR	6.1
1	T	530	GLN	6.1
1	X	216	THR	6.1
2	m	71	ASP	6.1
1	N	543	PRO	6.1
1	F	387	GLN	6.1
1	L	561	ASP	6.1
2	t	94	ASP	6.1
1	C	596	ALA	6.1
2	Y	98	CYS	6.1
2	i	24	ARG	6.1
1	T	566	GLU	6.1
1	I	257	ASP	6.1
1	A	216	THR	6.1
1	K	283	CYS	6.1
1	V	587	PRO	6.1
1	W	590	GLN	6.1
1	B	28	GLU	6.1
1	T	257	ASP	6.1
1	F	257	ASP	6.1
1	V	542	THR	6.1
2	s	97	LEU	6.1
2	g	123	LEU	6.1

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Mol	Chain	Res	Type	RSRZ
1	S	462	GLU	6.1
2	e	157	TYR	6.1
1	J	546	THR	6.1
1	G	543	PRO	6.1
1	U	254	VAL	6.1
1	V	216	THR	6.1
1	K	542	THR	6.1
1	I	331	ASN	6.1
1	E	504	LYS	6.1
1	R	420	VAL	6.1
1	K	439	ASN	6.1
2	b	106	LEU	6.1
1	J	134	ASP	6.1
1	U	221	GLU	6.1
1	E	534	GLU	6.1
1	J	49	THR	6.1
2	j	109	THR	6.1
1	B	574	LYS	6.1
1	D	6	ASN	6.1
1	I	553	LEU	6.1
2	p	65	ASN	6.1
1	F	152	ALA	6.1
1	B	588	GLU	6.1
1	E	92	ASP	6.1
1	L	592	TRP	6.1
2	p	33	MET	6.1
1	P	386	THR	6.0
1	V	168	SER	6.0
1	D	380	ASN	6.0
1	X	494	ALA	6.0
2	h	77	ALA	6.0
1	H	541	LYS	6.0
2	r	61	SER	6.0
2	v	130	SER	6.0
2	g	28	VAL	6.0
1	A	58	ASP	6.0
1	B	159	ASP	6.0
1	I	389	LEU	6.0
1	M	49	THR	6.0
1	A	410	SER	6.0
1	J	241	GLY	6.0
2	d	73	GLU	6.0

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Mol	Chain	Res	Type	RSRZ
1	K	84	ASP	6.0
1	L	191	TYR	6.0
2	g	24	ARG	6.0
1	B	13	SER	6.0
1	W	243	PRO	6.0
1	B	204	PRO	6.0
1	B	264	ILE	6.0
1	W	495	GLU	6.0
1	I	180	SER	6.0
2	t	136	SER	6.0
1	Q	500	ALA	6.0
1	U	242	GLU	6.0
1	M	386	THR	6.0
1	U	501	THR	6.0
1	I	499	LEU	6.0
2	d	152	LEU	6.0
1	K	601	GLN	6.0
1	R	88	PRO	6.0
1	X	205	ASN	6.0
1	J	187	PHE	6.0
1	H	207	TRP	6.0
1	G	424	ALA	6.0
1	F	258	LEU	6.0
1	B	282	THR	6.0
1	B	586	THR	6.0
1	C	409	THR	6.0
1	F	243	PRO	6.0
2	j	35	THR	6.0
1	T	235	TYR	6.0
1	V	456	ALA	6.0
1	H	236	GLN	6.0
2	j	71	ASP	6.0
1	R	47	GLN	6.0
2	Y	88	ALA	6.0
2	c	132	ALA	6.0
1	E	196	ASP	6.0
2	a	59	ASP	6.0
2	b	27	GLY	6.0
1	C	386	THR	6.0
1	A	141	ASN	6.0
1	G	207	TRP	6.0
2	Z	108	ALA	6.0

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Mol	Chain	Res	Type	RSRZ
1	B	42	ASP	5.9
1	K	187	PHE	6.0
2	j	92	VAL	5.9
1	S	417	THR	5.9
1	T	261	SER	5.9
1	P	494	ALA	5.9
2	a	106	LEU	5.9
1	W	387	GLN	5.9
1	B	47	GLN	5.9
2	h	110	ALA	5.9
2	Z	61	LYS	5.9
1	P	84	ASP	5.9
1	V	367	ASP	5.9
1	F	89	ASP	5.9
1	K	462	GLU	5.9
2	r	38	ASP	5.9
1	U	385	PRO	5.9
1	E	193	LEU	5.9
2	a	52	MET	5.9
1	T	594	VAL	5.9
1	J	5	GLU	5.9
1	K	228	LYS	5.9
1	H	259	ALA	5.9
1	M	422	THR	5.9
1	G	422	THR	5.9
1	I	151	SER	5.9
1	Q	31	ASN	5.9
1	E	531	ASN	5.9
1	H	134	ASP	5.9
1	R	456	ALA	5.9
2	p	150	PRO	5.9
2	g	114	ALA	5.9
2	i	88	ALA	5.9
1	A	519	ASP	5.9
2	d	157	TYR	5.9
1	I	388	PRO	5.9
1	N	284	THR	5.9
1	S	459	ARG	5.9
1	L	284	THR	5.9
1	N	212	LEU	5.9
1	S	6	ASN	5.9
1	L	212	LEU	5.9

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Mol	Chain	Res	Type	RSRZ
1	G	233	PHE	5.9
1	I	423	GLU	5.9
1	V	506	VAL	5.9
1	E	41	TRP	5.9
1	H	576	LEU	5.9
2	p	130	SER	5.9
1	J	235	TYR	5.9
1	T	58	ASP	5.9
2	g	101	ALA	5.9
1	J	537	GLU	5.9
1	E	550	GLN	5.9
2	d	19	VAL	5.9
1	H	252	LYS	5.9
1	X	206	ASP	5.9
2	s	39	ASP	5.9
1	V	543	PRO	5.9
1	A	580	GLY	5.9
1	P	211	TRP	5.9
1	E	19	TRP	5.9
2	h	121	GLU	5.9
2	h	92	VAL	5.9
1	A	575	GLN	5.9
1	L	26	ARG	5.9
2	d	134	ARG	5.9
2	i	98	CYS	5.9
1	O	5	GLU	5.9
1	Q	169	ASP	5.9
2	u	9	LEU	5.9
1	W	498	ASP	5.8
1	E	203	ASN	5.8
1	H	397	VAL	5.8
1	H	494	ALA	5.8
2	i	87	SER	5.8
1	B	270	GLN	5.8
1	L	75	PRO	5.8
1	H	510	ILE	5.8
2	i	73	GLU	5.8
1	O	7	ARG	5.8
1	A	212	LEU	5.8
1	J	180	SER	5.8
2	g	87	SER	5.8
1	C	237	ASP	5.8

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Mol	Chain	Res	Type	RSRZ
1	B	219	ILE	5.8
1	D	540	GLY	5.8
1	K	424	ALA	5.8
2	m	7	GLY	5.8
1	H	389	LEU	5.8
1	B	501	THR	5.8
1	F	50	THR	5.8
1	F	530	GLN	5.8
2	a	69	PHE	5.8
1	V	186	ASP	5.8
1	B	252	LYS	5.8
1	L	445	GLU	5.8
2	j	102	PRO	5.8
1	H	33	LEU	5.8
1	S	422	THR	5.8
1	D	242	GLU	5.8
2	p	27	ASP	5.8
2	q	50	ASP	5.8
2	g	21	ALA	5.8
1	L	230	GLU	5.8
1	R	260	ASP	5.8
2	i	16	GLY	5.8
2	k	64	GLU	5.8
1	F	463	ILE	5.8
1	T	246	TYR	5.8
1	K	497	VAL	5.8
2	h	28	VAL	5.8
1	B	139	SER	5.8
1	H	87	ARG	5.8
1	L	87	ARG	5.8
2	f	80	ASP	5.8
2	j	98	CYS	5.8
1	L	547	PRO	5.8
1	M	509	ASP	5.8
1	X	260	ASP	5.8
1	G	563	LYS	5.8
1	J	436	ASN	5.8
1	L	182	ASN	5.8
1	M	510	ILE	5.8
1	X	263	PHE	5.8
1	J	24	GLU	5.8
1	L	16	ASP	5.8

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Mol	Chain	Res	Type	RSRZ
1	U	575	GLN	5.8
1	V	597	GLN	5.8
1	G	381	SER	5.7
1	Q	192	ASP	5.7
1	P	506	VAL	5.7
1	A	565	VAL	5.7
1	S	15	PHE	5.7
2	a	22	ALA	5.7
2	b	105	ALA	5.7
1	V	515	GLU	5.7
1	X	565	VAL	5.7
1	K	516	CYS	5.7
2	l	62	ASP	5.7
1	Q	203	ASN	5.7
1	S	600	LYS	5.7
1	I	426	ASN	5.7
1	B	227	GLU	5.7
1	K	25	ALA	5.7
1	X	385	PRO	5.7
1	N	266	ILE	5.7
1	Q	463	ILE	5.7
1	B	538	LEU	5.7
1	X	460	ASP	5.7
1	D	260	ASP	5.7
2	h	33	THR	5.7
1	E	161	ASN	5.7
1	K	596	ALA	5.7
1	T	557	PHE	5.7
1	I	601	GLN	5.7
1	R	516	CYS	5.7
2	g	73	GLU	5.7
2	e	158	PHE	5.7
1	B	91	ALA	5.7
1	G	537	GLU	5.7
2	p	26	THR	5.7
1	E	35	PHE	5.7
1	W	162	SER	5.7
1	D	10	SER	5.7
1	K	268	GLU	5.7
1	O	8	LEU	5.7
2	k	125	ARG	5.7
1	T	439	ASN	5.7

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Mol	Chain	Res	Type	RSRZ
1	E	497	VAL	5.7
1	A	421	ASP	5.7
2	a	85	ARG	5.7
1	R	209	PHE	5.7
1	B	423	GLU	5.7
1	H	137	PRO	5.7
1	H	388	PRO	5.7
1	H	91	ALA	5.7
1	L	214	GLN	5.7
1	U	15	PHE	5.7
1	G	217	ILE	5.7
1	A	81	ARG	5.7
2	c	150	PRO	5.7
1	U	155	HIS	5.7
2	o	92	ALA	5.7
1	X	41	TRP	5.7
1	C	586	THR	5.7
1	W	26	ARG	5.7
1	F	237	ASP	5.7
1	G	241	GLY	5.7
1	G	506	VAL	5.7
1	H	383	ASP	5.7
2	i	27	GLY	5.7
1	K	14	ARG	5.7
1	G	266	ILE	5.6
2	n	28	VAL	5.6
1	P	19	TRP	5.6
1	P	192	ASP	5.6
1	Q	246	TYR	5.6
1	E	386	THR	5.6
1	L	270	GLN	5.6
2	u	144	ASN	5.6
1	K	85	GLY	5.6
2	d	144	GLY	5.6
1	L	595	GLU	5.6
1	S	92	ASP	5.6
2	n	62	ASP	5.6
1	K	538	LEU	5.6
1	K	496	VAL	5.6
1	V	422	THR	5.6
1	O	516	CYS	5.6
2	Z	82	HIS	5.6

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Mol	Chain	Res	Type	RSRZ
1	T	253	ASP	5.6
1	H	561	ASP	5.6
1	K	451	ASP	5.6
2	l	63	ASP	5.6
1	P	200	SER	5.6
1	E	425	VAL	5.6
1	J	456	ALA	5.6
1	N	264	ILE	5.6
1	S	204	PRO	5.6
1	S	434	THR	5.6
1	D	600	LYS	5.6
1	K	434	THR	5.6
1	M	208	VAL	5.6
1	M	500	ALA	5.6
1	C	583	LYS	5.6
2	Y	68	VAL	5.6
2	c	28	VAL	5.6
1	K	602	GLY	5.6
2	f	52	MET	5.6
2	i	43	GLN	5.6
1	U	458	ARG	5.6
2	u	95	TYR	5.6
1	O	15	PHE	5.6
1	X	557	PHE	5.6
1	Q	85	GLY	5.6
1	S	597	GLN	5.6
1	C	585	GLU	5.6
1	C	204	PRO	5.6
1	I	269	ARG	5.6
1	S	386	THR	5.6
1	A	426	ASN	5.6
1	G	86	ALA	5.6
2	j	114	ALA	5.6
1	M	498	ASP	5.6
1	B	509	ASP	5.6
2	d	72	ASP	5.6
2	g	17	ASP	5.6
1	G	137	PRO	5.6
2	a	102	PRO	5.6
1	A	576	LEU	5.6
2	f	28	VAL	5.6
2	i	37	VAL	5.6

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Mol	Chain	Res	Type	RSRZ
1	L	29	ALA	5.6
2	s	123	ALA	5.6
2	h	53	MET	5.6
1	E	139	SER	5.6
2	Z	159	PRO	5.6
2	Z	158	PHE	5.6
1	I	420	VAL	5.6
1	T	259	ALA	5.6
2	p	29	GLU	5.6
2	c	74	ASN	5.6
2	f	146	GLY	5.6
1	V	92	ASP	5.6
1	X	92	ASP	5.6
2	j	72	ASP	5.6
1	M	565	VAL	5.6
1	A	563	LYS	5.6
1	S	560	LEU	5.5
1	F	591	GLN	5.5
1	C	206	ASP	5.5
2	a	139	SER	5.5
1	S	561	ASP	5.5
2	l	19	VAL	5.5
1	T	170	ALA	5.5
2	m	68	ALA	5.5
1	T	592	TRP	5.5
1	M	388	PRO	5.5
2	l	22	ASP	5.5
1	P	5	GLU	5.5
2	f	83	GLY	5.5
1	S	261	SER	5.5
1	L	544	GLN	5.5
1	N	5	GLU	5.5
1	Q	502	GLY	5.5
2	k	38	ASP	5.5
2	s	38	ASP	5.5
2	f	31	ASP	5.5
1	C	139	SER	5.5
2	Y	84	LEU	5.5
1	W	28	GLU	5.5
1	H	205	ASN	5.5
1	J	246	TYR	5.5
1	S	339	ASP	5.5

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Mol	Chain	Res	Type	RSRZ
1	O	25	ALA	5.5
2	c	152	LEU	5.5
1	M	240	THR	5.5
1	U	546	THR	5.5
1	V	208	VAL	5.5
1	C	565	VAL	5.5
1	F	597	GLN	5.5
2	r	10	VAL	5.5
1	P	451	ASP	5.5
1	W	195	ALA	5.5
1	C	215	ASP	5.5
2	e	34	LEU	5.5
2	i	101	ALA	5.5
1	R	26	ARG	5.5
1	A	185	GLU	5.5
1	H	48	TYR	5.5
1	J	550	GLN	5.5
1	U	576	LEU	5.5
1	D	337	ASN	5.5
1	T	169	ASP	5.5
1	F	25	ALA	5.5
1	H	519	ASP	5.5
1	K	42	ASP	5.5
2	l	79	ALA	5.5
1	L	557	PHE	5.5
1	V	242	GLU	5.5
1	B	566	GLU	5.5
2	n	64	GLU	5.5
2	q	53	GLY	5.5
1	J	494	ALA	5.5
1	K	375	ASN	5.5
2	p	12	ALA	5.5
1	C	461	GLY	5.5
1	F	151	SER	5.5
2	s	110	GLY	5.5
1	H	558	THR	5.5
1	O	547	PRO	5.5
1	U	547	PRO	5.5
1	J	7	ARG	5.5
2	m	76	ARG	5.5
2	k	94	ASP	5.5
2	f	151	ASN	5.5

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Mol	Chain	Res	Type	RSRZ
2	Y	78	GLU	5.5
1	O	556	TYR	5.5
2	j	67	TYR	5.5
1	M	261	SER	5.5
1	X	576	LEU	5.5
1	H	251	ILE	5.5
1	Q	216	THR	5.5
1	R	100	THR	5.5
1	U	599	ALA	5.5
1	X	284	THR	5.5
1	P	210	PRO	5.5
1	K	75	PRO	5.5
1	W	458	ARG	5.5
1	B	202	GLN	5.5
1	F	549	TYR	5.5
1	I	246	TYR	5.5
1	J	536	LEU	5.5
2	g	125	LYS	5.5
1	B	386	THR	5.4
1	U	594	VAL	5.4
2	m	145	GLU	5.4
2	Y	92	VAL	5.4
2	f	19	VAL	5.4
1	E	383	ASP	5.4
2	s	22	ASP	5.4
2	Z	80	ASP	5.4
1	A	525	GLN	5.4
1	M	268	GLU	5.4
1	T	497	VAL	5.4
1	H	589	GLU	5.4
2	h	142	PRO	5.4
1	S	32	ASP	5.4
1	I	206	ASP	5.4
1	L	576	LEU	5.4
1	I	578	GLN	5.4
2	e	72	ASP	5.4
1	Q	420	VAL	5.4
2	f	85	ARG	5.4
1	Q	501	THR	5.4
1	K	564	GLY	5.4
1	V	266	ILE	5.4
1	I	570	ASP	5.4

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Mol	Chain	Res	Type	RSRZ
1	V	232	ALA	5.4
1	F	259	ALA	5.4
2	u	146	TRP	5.4
1	B	151	SER	5.4
1	L	76	ILE	5.4
1	N	215	ASP	5.4
1	E	15	PHE	5.4
1	E	89	ASP	5.4
2	a	24	ARG	5.4
1	H	563	LYS	5.4
1	E	162	SER	5.4
1	B	546	THR	5.4
1	C	575	GLN	5.4
1	C	572	ALA	5.4
1	L	462	GLU	5.4
2	a	44	ASP	5.4
1	O	551	LEU	5.4
1	B	241	GLY	5.4
1	Q	271	ILE	5.4
1	F	289	ASP	5.4
1	K	192	ASP	5.4
2	c	72	ASP	5.4
2	p	91	ILE	5.4
1	C	547	PRO	5.4
1	G	601	GLN	5.4
2	h	14	THR	5.4
1	P	186	ASP	5.4
1	G	451	ASP	5.4
2	d	155	TRP	5.4
1	B	70	GLU	5.4
1	D	88	PRO	5.4
1	C	598	GLN	5.4
1	M	84	ASP	5.4
1	W	551	LEU	5.4
2	q	38	ASP	5.4
1	O	180	SER	5.4
1	C	212	LEU	5.4
1	R	443	ASP	5.4
1	C	6	ASN	5.4
1	D	585	GLU	5.4
1	S	385	PRO	5.4
1	S	550	GLN	5.4

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Mol	Chain	Res	Type	RSRZ
2	a	75	PRO	5.4
1	G	136	SER	5.4
1	K	245	SER	5.4
1	I	558	THR	5.4
2	v	48	TYR	5.4
1	R	563	LYS	5.3
1	U	34	PHE	5.3
2	j	64	ILE	5.3
1	R	595	GLU	5.3
1	H	325	ASP	5.3
1	I	425	VAL	5.3
1	W	408	ALA	5.3
1	D	29	ALA	5.3
2	f	159	PRO	5.3
1	X	36	SER	5.3
1	U	462	GLU	5.3
1	F	235	TYR	5.3
1	W	169	ASP	5.3
1	C	58	ASP	5.3
2	b	44	ASP	5.3
1	P	463	ILE	5.3
1	X	264	ILE	5.3
1	T	180	SER	5.3
2	a	157	TYR	5.3
2	f	104	TYR	5.3
1	M	576	LEU	5.3
1	W	425	VAL	5.3
1	H	89	ASP	5.3
1	K	421	ASP	5.3
1	K	448	VAL	5.3
1	S	236	GLN	5.3
1	C	508	ASN	5.3
1	D	597	GLN	5.3
1	L	259	ALA	5.3
1	U	381	SER	5.3
2	j	28	VAL	5.3
1	S	586	THR	5.3
1	U	196	ASP	5.3
1	M	597	GLN	5.3
1	O	209	PHE	5.3
1	O	428	GLY	5.3
1	P	387	GLN	5.3

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Mol	Chain	Res	Type	RSRZ
1	D	578	GLN	5.3
1	E	575	GLN	5.3
1	E	600	LYS	5.3
2	Z	84	LEU	5.3
1	N	7	ARG	5.3
2	k	15	ARG	5.3
1	T	591	GLN	5.3
1	B	525	GLN	5.3
1	S	210	PRO	5.3
1	I	510	ILE	5.3
2	q	60	PHE	5.3
1	S	591	GLN	5.3
1	P	388	PRO	5.3
1	R	210	PRO	5.3
1	O	87	ARG	5.3
1	I	205	ASN	5.3
1	W	188	ALA	5.3
2	t	18	GLY	5.3
1	U	566	GLU	5.3
2	s	41	GLU	5.3
2	v	29	GLU	5.3
1	E	238	PRO	5.3
2	f	138	PRO	5.3
1	X	241	GLY	5.3
1	N	197	ASP	5.3
1	A	544	GLN	5.3
1	I	546	THR	5.3
1	S	246	TYR	5.3
1	K	406	GLU	5.3
1	U	565	VAL	5.3
2	Z	36	ASP	5.3
1	O	557	PHE	5.3
1	D	294	ALA	5.3
2	h	105	ALA	5.3
1	T	550	GLN	5.3
1	M	215	ASP	5.2
1	N	237	ASP	5.2
1	O	237	ASP	5.2
1	G	196	ASP	5.2
1	K	239	VAL	5.3
1	H	580	GLY	5.2
1	I	240	THR	5.2

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Mol	Chain	Res	Type	RSRZ
2	r	6	LYS	5.2
1	D	31	ASN	5.2
1	H	182	ASN	5.2
1	K	234	ILE	5.2
1	N	496	VAL	5.2
1	X	550	GLN	5.2
1	W	139	SER	5.2
1	E	368	ASP	5.2
1	J	209	PHE	5.2
2	Z	144	GLY	5.2
1	X	510	ILE	5.2
2	c	77	ALA	5.2
1	Q	592	TRP	5.2
1	H	258	LEU	5.2
1	E	14	ARG	5.2
1	O	256	ASP	5.2
1	D	173	CYS	5.2
2	Y	142	PRO	5.2
2	Y	159	PRO	5.2
2	h	146	GLY	5.2
2	j	59	ASP	5.2
2	p	134	THR	5.2
2	q	75	LEU	5.2
1	T	207	TRP	5.2
1	K	129	VAL	5.2
2	t	53	GLY	5.2
1	J	196	ASP	5.2
1	X	91	ALA	5.2
1	J	285	ALA	5.2
1	O	553	LEU	5.2
1	R	258	LEU	5.2
1	H	313	LYS	5.2
1	Q	205	ASN	5.2
1	F	31	ASN	5.2
1	S	595	GLU	5.2
1	E	540	GLY	5.2
1	G	180	SER	5.2
1	E	258	LEU	5.2
1	U	317	GLU	5.2
1	K	396	GLU	5.2
2	g	78	GLU	5.2
1	S	335	SER	5.2

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Mol	Chain	Res	Type	RSRZ
1	F	136	SER	5.2
1	H	416	ALA	5.2
1	M	251	ILE	5.2
1	B	367	ASP	5.2
2	j	48	ASP	5.2
1	O	601	GLN	5.2
1	R	5	GLU	5.2
1	T	540	GLY	5.2
1	T	542	THR	5.2
1	V	386	THR	5.2
1	L	274	ARG	5.2
1	R	531	ASN	5.2
1	B	105	ASN	5.2
1	W	456	ALA	5.2
1	I	407	ALA	5.2
2	Z	51	ALA	5.2
2	j	88	ALA	5.2
1	K	297	HIS	5.2
1	B	500	ALA	5.2
1	D	209	PHE	5.2
1	R	237	ASP	5.2
1	A	495	GLU	5.2
2	Y	91	ALA	5.2
1	X	5	GLU	5.2
1	R	58	ASP	5.2
1	S	498	ASP	5.2
1	C	85	GLY	5.2
2	l	21	SER	5.2
1	S	400	ALA	5.2
2	f	136	PRO	5.1
1	O	84	ASP	5.1
1	H	200	SER	5.1
2	m	62	ASP	5.1
2	c	104	TYR	5.1
1	J	271	ILE	5.1
1	N	425	VAL	5.1
1	H	456	ALA	5.1
1	K	49	THR	5.1
2	i	109	THR	5.1
1	J	545	GLY	5.1
1	U	421	ASP	5.1
1	U	601	GLN	5.1

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Mol	Chain	Res	Type	RSRZ
1	I	505	GLN	5.1
2	a	148	SER	5.1
1	I	496	VAL	5.1
1	M	542	THR	5.1
2	Z	156	HIS	5.1
1	M	563	LYS	5.1
1	T	262	GLY	5.1
1	V	366	ASN	5.1
1	O	460	ASP	5.1
1	G	291	GLN	5.1
1	F	162	SER	5.1
1	N	456	ALA	5.1
1	G	110	ALA	5.1
1	S	548	GLU	5.1
1	W	133	GLU	5.1
1	H	230	GLU	5.1
1	J	153	CYS	5.1
2	a	66	GLY	5.1
1	M	420	VAL	5.1
1	N	202	GLN	5.1
1	C	236	GLN	5.1
2	a	100	ILE	5.1
1	A	443	ASP	5.1
1	A	265	LYS	5.1
1	G	400	ALA	5.1
1	H	390	ALA	5.1
1	L	13	SER	5.1
1	N	576	LEU	5.1
2	u	106	THR	5.1
1	B	547	PRO	5.1
1	Q	367	ASP	5.1
1	C	89	ASP	5.1
1	E	324	LYS	5.1
1	K	242	GLU	5.1
1	H	39	SER	5.1
2	n	147	HIS	5.1
2	p	146	TRP	5.1
1	B	284	THR	5.1
1	P	540	GLY	5.1
1	A	326	GLY	5.1
1	J	16	ASP	5.1
2	r	27	ASP	5.1

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Mol	Chain	Res	Type	RSRZ
1	D	539	LEU	5.1
2	j	23	LEU	5.1
2	d	57	TYR	5.1
1	J	214	GLN	5.1
1	L	387	GLN	5.1
1	X	452	ASN	5.1
1	I	114	ALA	5.1
2	p	38	ASP	5.1
1	H	41	TRP	5.1
1	H	556	TYR	5.1
2	e	156	HIS	5.1
2	n	145	GLU	5.1
2	j	142	PRO	5.1
1	A	456	ALA	5.1
1	I	357	ALA	5.1
1	A	383	ASP	5.1
1	K	589	GLU	5.1
2	i	78	GLU	5.1
1	L	419	GLY	5.1
2	u	123	ALA	5.1
1	J	283	CYS	5.1
2	s	138	ASN	5.1
1	L	139	SER	5.1
1	O	130	THR	5.1
1	B	240	THR	5.1
1	G	576	LEU	5.1
1	I	263	PHE	5.1
1	T	531	ASN	5.1
1	J	93	VAL	5.1
2	Y	80	ASP	5.1
1	U	288	LYS	5.1
1	W	136	SER	5.1
1	O	499	LEU	5.0
1	F	51	LEU	5.0
2	m	34	GLN	5.1
2	p	92	ALA	5.1
2	g	43	GLN	5.1
1	P	243	PRO	5.0
1	M	558	THR	5.0
1	B	409	THR	5.0
2	n	26	THR	5.0
1	W	423	GLU	5.0

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Mol	Chain	Res	Type	RSRZ
1	H	239	VAL	5.0
2	l	29	GLU	5.0
2	g	103	ASP	5.0
1	U	151	SER	5.0
1	B	55	GLY	5.0
2	g	159	PRO	5.0
2	Y	69	PHE	5.0
2	e	69	PHE	5.0
1	S	414	GLU	5.0
1	Q	498	ASP	5.0
1	K	368	ASP	5.0
1	E	559	LEU	5.0
1	G	374	LEU	5.0
2	l	78	SER	5.0
2	g	41	SER	5.0
1	S	547	PRO	5.0
1	L	422	THR	5.0
2	Y	99	ARG	5.0
1	D	16	ASP	5.0
2	c	51	ALA	5.0
1	T	35	PHE	5.0
1	B	324	LYS	5.0
1	D	571	TYR	5.0
2	a	55	GLU	5.0
1	Q	252	LYS	5.0
1	W	170	ALA	5.0
1	D	319	VAL	5.0
1	N	213	THR	5.0
2	p	118	THR	5.0
2	i	29	ALA	5.0
1	K	76	ILE	5.0
2	g	148	SER	5.0
1	B	313	LYS	5.0
1	B	96	GLY	5.0
1	Q	510	ILE	5.0
1	S	581	VAL	5.0
1	X	140	ASN	5.0
1	A	5	GLU	5.0
2	Y	107	GLU	5.0
2	Z	139	SER	5.0
1	V	580	GLY	5.0
1	G	382	GLY	5.0

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Mol	Chain	Res	Type	RSRZ
1	A	29	ALA	5.0
2	h	21	ALA	5.0
2	i	135	ALA	5.0
1	R	566	GLU	5.0
1	X	58	ASP	5.0
1	D	161	ASN	5.0
1	A	538	LEU	5.0
2	b	67	TYR	5.0
1	G	263	PHE	5.0
2	g	110	ALA	5.0
1	Q	505	GLN	5.0
1	E	420	VAL	5.0
1	H	217	ILE	5.0
2	f	73	GLU	5.0
1	T	570	ASP	5.0
1	G	312	ASP	5.0
1	J	84	ASP	5.0
2	f	82	HIS	5.0
1	A	26	ARG	5.0
1	E	602	GLY	5.0
2	k	65	ASN	5.0
1	Q	15	PHE	5.0
1	S	381	SER	5.0
1	S	578	GLN	5.0
1	X	505	GLN	5.0
1	E	422	THR	5.0
2	g	56	TRP	5.0
1	P	538	LEU	5.0
1	V	449	PHE	5.0
1	Q	425	VAL	5.0
1	R	232	ALA	5.0
1	X	497	VAL	5.0
1	C	420	VAL	5.0
1	K	220	ALA	5.0
1	L	202	GLN	5.0
1	W	542	THR	5.0
2	Y	109	THR	5.0
2	t	60	PHE	5.0
1	X	573	ASN	4.9
1	V	25	ALA	4.9
1	I	599	ALA	4.9
1	M	387	GLN	4.9

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Mol	Chain	Res	Type	RSRZ
1	T	41	TRP	4.9
1	T	541	LYS	4.9
1	F	562	GLY	4.9
2	u	62	ASP	4.9
1	K	595	GLU	4.9
1	I	523	SER	4.9
1	W	258	LEU	4.9
1	B	258	LEU	4.9
2	p	9	LEU	4.9
1	M	517	TYR	4.9
1	I	451	ASP	4.9
1	U	533	ALA	4.9
1	P	583	LYS	4.9
1	H	526	SER	4.9
1	K	450	GLN	4.9
1	P	235	TYR	4.9
1	I	502	GLY	4.9
1	M	506	VAL	4.9
1	S	421	ASP	4.9
1	X	443	ASP	4.9
1	A	257	ASP	4.9
1	A	299	PRO	4.9
1	K	93	VAL	4.9
2	b	81	ASP	4.9
2	g	47	ASP	4.9
1	L	337	ASN	4.9
2	t	143	LEU	4.9
1	O	550	GLN	4.9
2	d	139	SER	4.9
1	B	207	TRP	4.9
1	R	267	ALA	4.9
1	D	89	ASP	4.9
1	P	31	ASN	4.9
1	W	544	GLN	4.9
1	F	13	SER	4.9
2	q	95	TYR	4.9
2	Y	157	TYR	4.9
2	b	155	TRP	4.9
2	f	78	GLU	4.9
1	N	177	HIS	4.9
1	T	260	ASP	4.9
1	U	238	PRO	4.9

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Mol	Chain	Res	Type	RSRZ
1	W	12	LEU	4.9
1	W	494	ALA	4.9
1	C	584	PRO	4.9
1	R	6	ASN	4.9
1	K	270	GLN	4.9
1	I	600	LYS	4.9
2	n	146	TRP	4.9
2	c	46	VAL	4.9
1	T	193	LEU	4.9
1	B	576	LEU	4.9
1	D	192	ASP	4.9
1	U	327	GLN	4.9
1	B	318	GLY	4.9
2	d	62	GLY	4.9
2	g	121	GLU	4.9
2	u	37	VAL	4.9
2	l	92	ALA	4.9
1	T	243	PRO	4.9
1	G	92	ASP	4.9
1	K	18	ASP	4.9
1	L	92	ASP	4.9
2	m	67	PRO	4.9
2	u	24	THR	4.9
2	a	60	GLY	4.9
1	P	548	GLU	4.9
1	A	387	GLN	4.9
1	G	497	VAL	4.9
1	P	234	ILE	4.9
1	Q	168	SER	4.9
1	R	422	THR	4.9
1	W	460	ASP	4.9
1	W	589	GLU	4.9
1	X	47	GLN	4.9
1	K	364	ASP	4.9
1	C	141	ASN	4.9
1	C	599	ALA	4.9
1	J	357	ALA	4.9
2	l	126	ALA	4.9
2	u	44	MET	4.9
1	W	388	PRO	4.9
1	C	498	ASP	4.9
1	J	374	LEU	4.9

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Mol	Chain	Res	Type	RSRZ
1	J	553	LEU	4.9
1	K	255	ILE	4.9
1	K	577	ILE	4.9
1	I	416	ALA	4.9
2	g	52	MET	4.9
1	E	459	ARG	4.9
1	K	361	HIS	4.9
1	N	556	TYR	4.9
1	L	388	PRO	4.9
1	P	546	THR	4.8
1	J	312	ASP	4.8
1	X	564	GLY	4.8
2	Y	73	GLU	4.8
1	S	191	TYR	4.8
1	E	191	TYR	4.8
2	h	76	PRO	4.8
2	g	23	LEU	4.8
1	R	192	ASP	4.8
1	S	42	ASP	4.8
1	S	463	ILE	4.8
1	D	542	THR	4.8
2	b	33	THR	4.8
1	A	424	ALA	4.8
1	B	338	ALA	4.8
1	L	86	ALA	4.8
1	S	531	ASN	4.8
1	M	48	TYR	4.8
1	J	279	SER	4.8
2	c	148	SER	4.8
1	D	530	GLN	4.8
1	F	587	PRO	4.8
1	Q	197	ASP	4.8
1	K	509	ASP	4.8
1	I	49	THR	4.8
1	D	28	GLU	4.8
1	J	502	GLY	4.8
2	b	50	GLU	4.8
1	C	539	LEU	4.8
2	a	140	ARG	4.8
2	h	41	SER	4.8
1	K	173	CYS	4.8
1	K	229	LYS	4.8

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Mol	Chain	Res	Type	RSRZ
1	K	344	THR	4.8
2	e	27	GLY	4.8
1	K	87	ARG	4.8
1	L	458	ARG	4.8
2	Z	106	LEU	4.8
1	S	526	SER	4.8
1	I	437	GLN	4.8
1	J	75	PRO	4.8
1	K	600	LYS	4.8
1	M	169	ASP	4.8
1	O	548	GLU	4.8
1	C	5	GLU	4.8
1	E	206	ASP	4.8
1	F	461	GLY	4.8
1	L	237	ASP	4.8
2	d	34	LEU	4.8
2	j	124	TYR	4.8
1	Q	557	PHE	4.8
1	T	203	ASN	4.8
1	B	299	PRO	4.8
1	I	387	GLN	4.8
1	K	209	PHE	4.8
2	o	141	PRO	4.8
2	f	76	PRO	4.8
1	N	400	ALA	4.8
1	C	602	GLY	4.8
1	F	456	ALA	4.8
1	G	379	GLU	4.8
1	H	232	ALA	4.8
2	d	31	ASP	4.8
1	W	283	CYS	4.8
1	A	48	TYR	4.8
1	F	425	VAL	4.8
1	I	115	VAL	4.8
1	D	41	TRP	4.8
1	Q	230	GLU	4.8
1	C	335	SER	4.8
1	G	151	SER	4.8
1	J	388	PRO	4.8
2	n	92	ALA	4.8
2	q	45	ALA	4.8
2	b	91	ALA	4.8

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Mol	Chain	Res	Type	RSRZ
2	h	45	ALA	4.8
1	P	244	VAL	4.8
1	V	32	ASP	4.8
1	A	367	ASP	4.8
2	a	34	LEU	4.8
1	U	35	PHE	4.8
1	A	409	THR	4.8
1	T	537	GLU	4.8
1	E	508	ASN	4.8
1	N	378	ASP	4.8
2	f	59	ASP	4.8
1	G	524	PHE	4.8
2	o	91	ILE	4.8
1	B	595	GLU	4.8
1	E	597	GLN	4.8
1	E	290	LYS	4.8
2	m	20	ALA	4.8
1	I	559	LEU	4.8
1	W	16	ASP	4.8
2	m	29	GLU	4.8
1	F	52	GLN	4.8
1	B	452	ASN	4.8
1	G	508	ASN	4.8
2	q	59	VAL	4.8
1	E	280	ILE	4.8
1	S	242	GLU	4.8
1	O	183	GLY	4.8
1	T	386	THR	4.8
2	d	156	HIS	4.8
2	d	63	ILE	4.7
2	h	147	ASN	4.7
1	B	564	GLY	4.7
1	K	131	ASP	4.7
2	j	31	ASP	4.7
2	t	20	ALA	4.7
1	M	88	PRO	4.7
1	T	458	ARG	4.7
1	C	249	ARG	4.7
1	X	187	PHE	4.7
1	H	452	ASN	4.7
2	g	154	GLU	4.7
1	D	134	ASP	4.7

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Mol	Chain	Res	Type	RSRZ
1	Q	212	LEU	4.7
2	t	96	ALA	4.7
1	E	252	LYS	4.7
1	E	377	THR	4.7
1	I	503	GLU	4.7
1	I	517	TYR	4.7
1	N	261	SER	4.7
1	T	205	ASN	4.7
1	V	540	GLY	4.7
2	m	21	SER	4.7
1	E	248	LYS	4.7
1	X	417	THR	4.7
2	r	147	HIS	4.7
1	N	234	ILE	4.7
2	g	76	PRO	4.7
2	k	61	SER	4.7
2	Y	23	LEU	4.7
1	A	327	GLN	4.7
1	G	114	ALA	4.7
1	J	592	TRP	4.7
2	m	59	VAL	4.7
2	a	45	ALA	4.7
1	O	535	ILE	4.7
1	F	546	THR	4.7
1	C	576	LEU	4.7
1	D	8	LEU	4.7
2	f	84	LEU	4.7
1	E	237	ASP	4.7
1	I	41	TRP	4.7
1	O	230	GLU	4.7
1	V	26	ARG	4.7
1	T	305	GLY	4.7
1	V	283	CYS	4.7
2	b	49	LEU	4.7
1	S	141	ASN	4.7
1	C	591	GLN	4.7
1	H	46	SER	4.7
1	H	578	GLN	4.7
1	L	267	ALA	4.7
1	K	39	SER	4.7
2	h	38	GLU	4.7
1	Q	422	THR	4.7

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Mol	Chain	Res	Type	RSRZ
1	T	213	THR	4.7
1	U	552	LEU	4.7
2	b	62	GLY	4.7
1	X	259	ALA	4.7
1	M	452	ASN	4.7
1	P	230	GLU	4.7
1	W	31	ASN	4.7
1	X	105	ASN	4.7
1	F	531	ASN	4.7
2	l	16	LYS	4.7
2	u	139	SER	4.7
1	P	237	ASP	4.7
1	T	43	ASP	4.7
1	Q	444	LEU	4.7
1	F	539	LEU	4.7
1	O	420	VAL	4.7
1	C	100	THR	4.7
1	B	288	LYS	4.7
2	j	55	GLU	4.7
1	J	535	ILE	4.7
1	I	212	LEU	4.7
2	t	114	LEU	4.7
2	v	27	ASP	4.7
2	j	17	ASP	4.7
1	G	238	PRO	4.7
1	K	249	ARG	4.7
1	O	501	THR	4.7
1	D	188	ALA	4.7
2	Z	33	THR	4.7
1	H	550	GLN	4.7
1	X	384	LEU	4.7
1	G	168	SER	4.7
2	Z	95	ASN	4.7
2	d	18	LEU	4.7
2	j	144	GLY	4.7
1	J	265	LYS	4.7
1	M	595	GLU	4.7
1	X	396	GLU	4.7
1	B	317	GLU	4.7
1	D	314	GLU	4.7
1	I	500	ALA	4.7
1	S	87	ARG	4.7

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Mol	Chain	Res	Type	RSRZ
1	F	183	GLY	4.7
2	e	152	LEU	4.7
1	P	205	ASN	4.7
1	C	35	PHE	4.7
1	T	595	GLU	4.7
1	K	445	GLU	4.7
1	X	270	GLN	4.6
1	L	586	THR	4.6
1	U	326	GLY	4.6
1	V	565	VAL	4.6
1	B	335	SER	4.6
1	I	309	PHE	4.6
1	G	131	ASP	4.6
1	I	92	ASP	4.6
1	J	42	ASP	4.6
2	s	65	ASN	4.6
2	h	145	SER	4.6
1	F	242	GLU	4.6
2	h	50	GLU	4.6
1	C	601	GLN	4.6
1	Q	254	VAL	4.6
1	X	34	PHE	4.6
1	K	449	PHE	4.6
1	Q	160	SER	4.6
1	Q	443	ASP	4.6
1	B	353	PRO	4.6
2	p	72	ASP	4.6
2	d	103	ASP	4.6
2	i	50	GLU	4.6
2	k	29	GLU	4.6
2	i	56	TRP	4.6
1	V	289	ASP	4.6
2	n	65	ASN	4.6
2	j	94	HIS	4.6
1	S	536	LEU	4.6
1	X	580	GLY	4.6
1	G	236	GLN	4.6
1	G	208	VAL	4.6
1	H	254	VAL	4.6
1	K	233	PHE	4.6
1	F	582	LYS	4.6
1	P	238	PRO	4.6

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Mol	Chain	Res	Type	RSRZ
1	S	368	ASP	4.6
1	G	234	ILE	4.6
2	Z	102	PRO	4.6
2	e	36	ASP	4.6
2	h	58	GLN	4.6
1	N	208	VAL	4.6
1	G	63	VAL	4.6
1	S	534	GLU	4.6
2	b	24	ARG	4.6
1	M	499	LEU	4.6
1	S	237	ASP	4.6
1	V	502	GLY	4.6
1	B	519	ASP	4.6
1	H	23	ASP	4.6
2	e	70	SER	4.6
2	e	71	ASP	4.6
1	B	35	PHE	4.6
2	g	30	SER	4.6
1	C	597	GLN	4.6
1	D	459	ARG	4.6
1	G	47	GLN	4.6
2	l	64	GLU	4.6
1	I	576	LEU	4.6
1	S	96	GLY	4.6
1	V	421	ASP	4.6
1	W	582	LYS	4.6
2	d	80	ASP	4.6
1	J	566	GLU	4.6
1	V	213	THR	4.6
1	C	558	THR	4.6
1	I	231	THR	4.6
1	A	96	GLY	4.6
1	P	423	GLU	4.6
1	U	279	SER	4.6
1	C	571	TYR	4.6
1	K	436	ASN	4.6
1	L	396	GLU	4.6
1	Q	208	VAL	4.6
1	V	47	GLN	4.6
1	E	199	PRO	4.6
1	N	169	ASP	4.6
1	I	283	CYS	4.6

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Mol	Chain	Res	Type	RSRZ
1	B	384	LEU	4.6
1	M	357	ALA	4.6
1	N	416	ALA	4.6
1	J	596	ALA	4.6
1	E	211	TRP	4.6
2	t	146	TRP	4.6
2	j	93	PHE	4.6
1	O	214	GLN	4.6
1	S	566	GLU	4.6
1	E	515	GLU	4.6
2	q	150	PRO	4.6
1	N	182	ASN	4.6
1	U	154	SER	4.6
1	G	7	ARG	4.6
1	U	248	LYS	4.6
1	D	529	GLN	4.6
1	G	62	PRO	4.6
1	G	501	THR	4.6
2	g	20	ARG	4.6
1	P	134	ASP	4.6
1	T	499	LEU	4.6
1	F	325	ASP	4.6
1	R	424	ALA	4.5
1	A	494	ALA	4.5
1	M	227	GLU	4.5
1	R	37	ARG	4.5
1	S	19	TRP	4.5
1	V	589	GLU	4.5
1	F	28	GLU	4.5
1	L	448	VAL	4.5
1	H	47	GLN	4.5
1	H	501	THR	4.5
1	K	387	GLN	4.5
1	Q	186	ASP	4.5
1	C	519	ASP	4.5
2	b	72	ASP	4.5
2	d	71	ASP	4.5
1	D	502	GLY	4.5
2	n	110	GLY	4.5
2	p	79	ALA	4.5
1	O	389	LEU	4.5
1	R	417	THR	4.5

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Mol	Chain	Res	Type	RSRZ
1	D	52	GLN	4.5
2	m	26	THR	4.5
1	W	234	ILE	4.5
1	G	169	ASP	4.5
1	I	390	ALA	4.5
1	J	443	ASP	4.5
2	p	8	ASP	4.5
2	v	42	ALA	4.5
2	a	27	GLY	4.5
1	N	46	SER	4.5
1	T	242	GLU	4.5
1	B	7	ARG	4.5
1	V	380	ASN	4.5
2	b	154	GLU	4.5
1	C	388	PRO	4.5
1	M	494	ALA	4.5
1	T	367	ASP	4.5
2	d	124	TYR	4.5
1	T	56	GLN	4.5
1	B	228	LYS	4.5
1	D	547	PRO	4.5
1	M	230	GLU	4.5
1	W	49	THR	4.5
1	L	50	THR	4.5
1	U	93	VAL	4.5
2	b	51	ALA	4.5
1	B	58	ASP	4.5
1	L	32	ASP	4.5
2	s	16	LYS	4.5
2	f	123	LEU	4.5
1	S	575	GLN	4.5
1	G	578	GLN	4.5
1	S	543	PRO	4.5
1	O	423	GLU	4.5
1	S	28	GLU	4.5
1	A	497	VAL	4.5
1	G	342	ALA	4.5
1	L	195	ALA	4.5
2	s	26	THR	4.5
1	P	539	LEU	4.5
2	p	78	SER	4.5
1	X	218	GLN	4.5

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Mol	Chain	Res	Type	RSRZ
1	F	182	ASN	4.5
2	o	110	GLY	4.5
2	d	82	HIS	4.5
1	B	50	THR	4.5
1	P	269	ARG	4.5
1	X	570	ASP	4.5
1	B	554	LEU	4.5
1	H	586	THR	4.5
1	L	231	THR	4.5
1	P	76	ILE	4.5
1	X	529	GLN	4.5
2	p	77	SER	4.5
1	F	228	LYS	4.5
1	G	462	GLU	4.5
2	m	73	HIS	4.5
1	L	216	THR	4.5
2	t	118	THR	4.5
2	h	109	THR	4.5
2	i	34	LEU	4.5
1	S	134	ASP	4.5
1	V	460	ASP	4.5
1	X	336	PHE	4.5
1	T	366	ASN	4.5
1	C	430	VAL	4.5
1	K	267	ALA	4.5
2	j	42	MET	4.5
2	Y	67	TYR	4.5
1	P	251	ILE	4.5
1	X	42	ASP	4.5
2	k	63	ASP	4.5
1	T	283	CYS	4.5
1	T	575	GLN	4.5
1	I	555	GLN	4.5
1	K	296	GLU	4.5
1	U	239	VAL	4.5
1	B	459	ARG	4.5
1	F	46	SER	4.5
1	X	508	ASN	4.5
1	K	407	ALA	4.5
1	D	243	PRO	4.5
1	P	534	GLU	4.5
1	D	92	ASP	4.5

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Mol	Chain	Res	Type	RSRZ
1	G	558	THR	4.5
1	H	537	GLU	4.5
1	J	356	ILE	4.5
2	j	66	GLY	4.5
1	K	225	VAL	4.5
1	A	592	TRP	4.5
1	F	195	ALA	4.5
1	F	200	SER	4.5
1	R	337	ASN	4.5
1	I	31	ASN	4.5
2	q	14	LEU	4.5
1	V	238	PRO	4.5
1	N	233	PHE	4.5
2	m	115	TYR	4.5
2	c	158	PHE	4.5
1	U	70	GLU	4.4
1	W	215	ASP	4.4
1	W	581	VAL	4.4
1	A	323	THR	4.4
1	H	84	ASP	4.4
2	m	63	ASP	4.4
2	g	105	ALA	4.4
1	L	229	LYS	4.4
1	W	263	PHE	4.4
1	M	87	ARG	4.4
1	O	27	ARG	4.4
1	Q	537	GLU	4.4
1	D	515	GLU	4.4
1	T	538	LEU	4.4
1	W	52	GLN	4.4
1	G	284	THR	4.4
2	f	58	GLN	4.4
1	T	204	PRO	4.4
1	T	380	ASN	4.4
1	A	62	PRO	4.4
2	o	65	ASN	4.4
2	u	66	PRO	4.4
2	g	86	SER	4.4
1	X	506	VAL	4.4
1	J	129	VAL	4.4
1	V	563	LYS	4.4
1	P	206	ASP	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	77	ASP	4.4
1	C	79	LEU	4.4
2	q	39	ASP	4.4
1	N	136	SER	4.4
1	R	183	GLY	4.4
1	O	504	LYS	4.4
1	P	555	GLN	4.4
1	Q	86	ALA	4.4
1	S	529	GLN	4.4
1	E	51	LEU	4.4
1	L	554	LEU	4.4
1	U	449	PHE	4.4
1	H	50	THR	4.4
2	o	26	THR	4.4
2	i	104	TYR	4.4
2	h	117	LYS	4.4
1	W	47	GLN	4.4
1	G	516	CYS	4.4
1	K	557	PHE	4.4
2	f	101	ALA	4.4
1	O	134	ASP	4.4
1	P	255	ILE	4.4
1	X	217	ILE	4.4
1	G	589	GLU	4.4
1	J	461	GLY	4.4
1	L	602	GLY	4.4
2	j	46	VAL	4.4
1	W	599	ALA	4.4
1	B	518	THR	4.4
1	I	344	THR	4.4
2	u	39	ASP	4.4
1	K	389	LEU	4.4
1	V	523	SER	4.4
1	C	410	SER	4.4
1	L	155	HIS	4.4
1	A	142	GLN	4.4
1	G	25	ALA	4.4
2	i	22	ALA	4.4
1	W	186	ASP	4.4
1	C	219	ILE	4.4
1	H	198	ILE	4.4
1	H	420	VAL	4.4

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Mol	Chain	Res	Type	RSRZ
1	L	156	VAL	4.4
2	m	97	LEU	4.4
2	t	26	THR	4.4
1	A	398	PRO	4.4
2	a	98	CYS	4.4
1	M	313	LYS	4.4
1	P	263	PHE	4.4
2	i	30	SER	4.4
1	K	24	GLU	4.4
1	E	246	TYR	4.4
1	F	255	ILE	4.4
1	I	535	ILE	4.4
2	Y	100	ILE	4.4
1	W	253	ASP	4.4
1	I	506	VAL	4.4
1	I	519	ASP	4.4
2	t	19	VAL	4.4
2	u	87	LEU	4.4
2	a	103	ASP	4.4
1	X	15	PHE	4.4
1	H	34	PHE	4.4
1	C	220	ALA	4.4
1	T	5	GLU	4.4
1	D	589	GLU	4.4
1	L	28	GLU	4.4
1	L	590	GLN	4.4
2	u	64	GLU	4.4
1	O	31	ASN	4.4
1	O	439	ASN	4.4
1	O	545	GLY	4.4
1	A	556	TYR	4.4
1	G	549	TYR	4.4
2	k	148	TYR	4.4
1	B	560	LEU	4.4
2	i	152	LEU	4.4
1	S	41	TRP	4.4
1	D	339	ASP	4.4
1	J	199	PRO	4.4
1	R	338	ALA	4.4
2	f	105	ALA	4.4
1	I	545	GLY	4.4
1	L	160	SER	4.4

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Mol	Chain	Res	Type	RSRZ
1	L	580	GLY	4.4
1	U	313	LYS	4.4
1	U	498	ASP	4.4
1	L	41	TRP	4.4
2	j	81	ASP	4.4
1	I	213	THR	4.4
1	M	8	LEU	4.3
1	O	246	TYR	4.3
1	C	553	LEU	4.3
1	H	263	PHE	4.3
2	n	94	ASP	4.3
2	a	31	ASP	4.3
1	Q	50	THR	4.3
1	Q	229	LYS	4.3
1	T	529	GLN	4.3
1	U	538	LEU	4.3
1	I	234	ILE	4.3
2	r	75	LEU	4.3
2	s	148	TYR	4.3
1	S	572	ALA	4.3
1	X	456	ALA	4.3
2	b	132	ALA	4.3
1	N	502	GLY	4.3
1	P	26	ARG	4.3
1	Q	434	THR	4.3
1	C	177	HIS	4.3
1	A	560	LEU	4.3
2	r	55	ILE	4.3
1	V	46	SER	4.3
1	K	36	SER	4.3
1	K	582	LYS	4.3
1	T	533	ALA	4.3
1	U	220	ALA	4.3
1	B	131	ASP	4.3
1	E	21	ALA	4.3
1	U	243	PRO	4.3
1	X	255	ILE	4.3
1	B	81	ARG	4.3
1	E	395	PRO	4.3
1	I	498	ASP	4.3
2	Y	19	VAL	4.3
2	f	62	GLY	4.3

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Mol	Chain	Res	Type	RSRZ
2	a	108	ALA	4.3
2	e	74	ASN	4.3
1	Q	89	ASP	4.3
1	V	12	LEU	4.3
1	A	192	ASP	4.3
1	Q	550	GLN	4.3
1	U	83	LYS	4.3
2	n	6	LYS	4.3
2	p	148	TYR	4.3
1	N	133	GLU	4.3
1	E	532	ARG	4.3
1	R	506	VAL	4.3
1	U	506	VAL	4.3
1	X	19	TRP	4.3
2	m	53	GLY	4.3
1	C	270	GLN	4.3
1	H	327	GLN	4.3
2	t	16	LYS	4.3
2	Z	98	CYS	4.3
1	R	546	THR	4.3
1	U	558	THR	4.3
1	I	27	ARG	4.3
1	I	542	THR	4.3
1	B	160	SER	4.3
1	J	107	ALA	4.3
2	h	22	ALA	4.3
1	P	129	VAL	4.3
1	F	290	LYS	4.3
2	f	133	LYS	4.3
1	C	573	ASN	4.3
1	M	291	GLN	4.3
1	M	584	PRO	4.3
1	C	263	PHE	4.3
1	H	498	ASP	4.3
1	I	199	PRO	4.3
2	h	31	ASP	4.3
1	D	249	ARG	4.3
1	T	501	THR	4.3
1	P	245	SER	4.3
1	C	294	ALA	4.3
2	l	14	LEU	4.3
2	v	28	VAL	4.3

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Mol	Chain	Res	Type	RSRZ
2	Y	96	LEU	4.3
1	K	410	SER	4.3
1	H	199	PRO	4.3
1	R	296	GLU	4.3
1	W	534	GLU	4.3
2	Y	72	ASP	4.3
1	R	574	LYS	4.3
1	Q	507	LEU	4.3
1	O	198	ILE	4.3
1	A	156	VAL	4.3
1	B	11	ILE	4.3
1	K	285	ALA	4.3
1	P	233	PHE	4.3
1	R	187	PHE	4.3
1	H	36	SER	4.3
2	g	85	ARG	4.3
1	P	197	ASP	4.3
1	G	366	ASN	4.3
1	H	361	HIS	4.3
1	L	383	ASP	4.3
2	b	94	HIS	4.3
1	S	244	VAL	4.3
1	U	100	THR	4.3
1	V	400	ALA	4.3
1	X	558	THR	4.3
2	h	119	GLY	4.3
1	M	238	PRO	4.3
1	P	270	GLN	4.3
1	D	248	LYS	4.3
1	F	573	ASN	4.3
1	K	88	PRO	4.3
2	o	6	LYS	4.3
1	I	256	ASP	4.3
1	K	561	ASP	4.3
1	L	394	ASN	4.3
2	n	144	ASN	4.3
2	g	48	ASP	4.3
1	A	258	LEU	4.3
1	P	93	VAL	4.3
1	Q	17	ALA	4.3
1	A	271	ILE	4.3
1	C	533	ALA	4.3

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>	<b>RSRZ</b>
1	H	532	ARG	4.3
1	S	546	THR	4.3
2	m	140	PHE	4.3
1	X	227	GLU	4.3
1	C	248	LYS	4.3
1	N	36	SER	4.3
1	G	73	GLN	4.3
1	C	543	PRO	4.3
2	m	66	PRO	4.3
1	N	194	ASP	4.3
1	R	194	ASP	4.3
1	R	269	ARG	4.3
1	S	58	ASP	4.3
1	U	134	ASP	4.3
1	V	27	ARG	4.3
1	B	337	ASN	4.3
1	D	253	ASP	4.3
1	G	561	ASP	4.3
1	J	390	ALA	4.3
1	E	190	LYS	4.2
2	m	6	LYS	4.2
1	T	597	GLN	4.2
1	R	388	PRO	4.2
1	F	459	ARG	4.2
1	M	198	ILE	4.2
1	X	318	GLY	4.2
1	J	108	LYS	4.2
1	L	197	ASP	4.2
1	L	449	PHE	4.2
1	A	590	GLN	4.2
1	H	560	LEU	4.2
1	J	438	LEU	4.2
1	X	96	GLY	4.2
2	Y	90	SER	4.2
1	C	280	ILE	4.2
2	a	101	ALA	4.2
1	D	274	ARG	4.2
1	Q	586	THR	4.2
1	D	386	THR	4.2
2	j	126	GLN	4.2
1	P	15	PHE	4.2
1	R	96	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
1	S	279	SER	4.2
1	I	11	ILE	4.2
2	f	134	ARG	4.2
1	X	591	GLN	4.2
1	S	594	VAL	4.2
1	B	420	VAL	4.2
1	H	417	THR	4.2
2	j	27	GLY	4.2
1	C	537	GLU	4.2
1	F	160	SER	4.2
1	L	273	ARG	4.2
1	W	101	ASP	4.2
2	m	72	ASP	4.2
1	F	246	TYR	4.2
1	N	47	GLN	4.2
1	A	591	GLN	4.2
1	P	542	THR	4.2
1	K	41	TRP	4.2
2	k	68	ALA	4.2
2	b	102	PRO	4.2
1	E	541	LYS	4.2
1	L	410	SER	4.2
1	Q	536	LEU	4.2
1	L	499	LEU	4.2
2	k	62	ASP	4.2
1	B	182	ASN	4.2
2	i	118	TYR	4.2
1	R	387	GLN	4.2
1	A	236	GLN	4.2
1	K	236	GLN	4.2
1	A	395	PRO	4.2
1	D	534	GLU	4.2
2	g	35	THR	4.2
2	g	39	PRO	4.2
2	i	14	THR	4.2
1	U	33	LEU	4.2
1	K	279	SER	4.2
1	X	509	ASP	4.2
1	K	169	ASP	4.2
2	Y	18	LEU	4.2
1	G	590	GLN	4.2
1	L	7	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
1	O	406	GLU	4.2
1	S	284	THR	4.2
1	T	220	ALA	4.2
1	A	173	CYS	4.2
1	C	338	ALA	4.2
1	L	185	GLU	4.2
2	n	133	PRO	4.2
2	g	75	PRO	4.2
1	U	191	TYR	4.2
1	O	449	PHE	4.2
1	B	34	PHE	4.2
1	E	295	GLY	4.2
1	K	237	ASP	4.2
2	n	27	ASP	4.2
2	u	38	ASP	4.2
2	f	47	ASP	4.2
1	O	387	GLN	4.2
1	E	439	ASN	4.2
1	J	266	ILE	4.2
1	A	28	GLU	4.2
1	A	25	ALA	4.2
1	K	79	LEU	4.2
2	m	127	PRO	4.2
2	h	98	CYS	4.2
1	V	286	VAL	4.2
1	I	383	ASP	4.2
1	K	320	VAL	4.2
2	f	30	SER	4.2
1	E	134	ASP	4.2
1	E	414	GLU	4.2
1	K	281	ILE	4.2
1	L	452	ASN	4.2
1	P	213	THR	4.2
1	O	581	VAL	4.2
1	E	496	VAL	4.2
1	W	260	ASP	4.2
1	G	585	GLU	4.2
2	t	39	ASP	4.2
2	c	71	ASP	4.2
1	R	29	ALA	4.2
1	U	195	ALA	4.2
1	A	51	LEU	4.2

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Mol	Chain	Res	Type	RSRZ
1	F	207	TRP	4.2
2	k	146	TRP	4.2
2	i	49	LEU	4.2
1	C	210	PRO	4.2
1	M	540	GLY	4.2
1	X	32	ASP	4.1
1	D	261	SER	4.2
1	E	178	SER	4.2
2	f	121	GLU	4.2
2	q	71	ASP	4.1
2	h	90	SER	4.2
1	P	533	ALA	4.1
2	l	20	ALA	4.1
1	G	161	ASN	4.1
1	U	207	TRP	4.1
1	K	391	TYR	4.1
2	Z	56	TRP	4.1
2	p	133	PRO	4.1
1	V	455	THR	4.1
2	p	69	GLU	4.1
2	f	113	ILE	4.1
1	U	32	ASP	4.1
1	W	237	ASP	4.1
1	K	23	ASP	4.1
1	L	8	LEU	4.1
1	L	538	LEU	4.1
2	s	8	ASP	4.1
2	t	17	LEU	4.1
1	T	263	PHE	4.1
1	B	15	PHE	4.1
2	m	149	PHE	4.1
1	P	143	VAL	4.1
1	S	147	GLU	4.1
1	I	230	GLU	4.1
2	p	15	ARG	4.1
1	E	313	LYS	4.1
1	X	338	ALA	4.1
1	G	507	LEU	4.1
1	S	35	PHE	4.1
1	M	439	ASN	4.1
1	U	564	GLY	4.1
2	n	91	ILE	4.1

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Mol	Chain	Res	Type	RSRZ
1	D	546	THR	4.1
1	I	8	LEU	4.1
1	L	20	THR	4.1
1	Q	459	ARG	4.1
1	J	15	PHE	4.1
1	L	42	ASP	4.1
2	t	78	SER	4.1
2	j	103	ASP	4.1
1	H	308	GLY	4.1
1	I	244	VAL	4.1
2	t	95	TYR	4.1
1	M	31	ASN	4.1
1	M	205	ASN	4.1
1	R	268	GLU	4.1
1	F	515	GLU	4.1
1	B	398	PRO	4.1
1	L	161	ASN	4.1
1	M	114	ALA	4.1
1	U	91	ALA	4.1
1	H	214	GLN	4.1
1	C	570	ASP	4.1
1	J	425	VAL	4.1
1	L	260	ASP	4.1
2	h	15	LYS	4.1
1	N	28	GLU	4.1
1	Q	74	ASN	4.1
1	B	140	ASN	4.1
1	J	543	PRO	4.1
1	P	551	LEU	4.1
1	H	507	LEU	4.1
1	N	304	PHE	4.1
2	Z	109	THR	4.1
1	Q	76	ILE	4.1
1	T	32	ASP	4.1
1	V	312	ASP	4.1
1	A	92	ASP	4.1
1	D	367	ASP	4.1
1	D	537	GLU	4.1
1	E	421	ASP	4.1
1	H	136	SER	4.1
1	H	160	SER	4.1
1	J	498	ASP	4.1

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Mol	Chain	Res	Type	RSRZ
1	L	192	ASP	4.1
2	n	21	SER	4.1
2	a	104	TYR	4.1
2	i	44	ASP	4.1
1	S	426	ASN	4.1
1	G	51	LEU	4.1
1	L	573	ASN	4.1
1	B	504	LYS	4.1
1	Q	506	VAL	4.1
1	R	586	THR	4.1
1	E	564	GLY	4.1
1	G	64	VAL	4.1
2	o	89	CYS	4.1
2	j	16	GLY	4.1
1	O	16	ASP	4.1
1	R	253	ASP	4.1
2	p	71	ASP	4.1
2	Y	31	ASP	4.1
1	Q	533	ALA	4.1
1	U	508	ASN	4.1
2	b	153	ASN	4.1
2	Z	66	GLY	4.1
1	G	386	THR	4.1
1	T	368	ASP	4.1
1	E	215	ASP	4.1
1	H	229	LYS	4.1
1	A	407	ALA	4.1
1	G	285	ALA	4.1
1	J	267	ALA	4.1
2	o	7	GLY	4.1
2	s	37	VAL	4.1
2	u	65	ASN	4.1
2	a	29	ALA	4.1
2	b	43	GLN	4.1
1	E	235	TYR	4.1
1	E	535	ILE	4.1
1	L	252	LYS	4.1
1	L	323	THR	4.1
2	a	96	LEU	4.1
1	F	173	CYS	4.1
2	b	31	ASP	4.1
1	E	25	ALA	4.1

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Mol	Chain	Res	Type	RSRZ
1	E	82	PRO	4.1
2	Y	110	ALA	4.1
1	O	331	ASN	4.1
1	G	6	ASN	4.1
1	I	227	GLU	4.1
1	U	549	TYR	4.1
1	D	549	TYR	4.1
1	F	556	TYR	4.1
1	W	446	THR	4.1
1	H	304	PHE	4.1
1	C	19	TRP	4.1
1	M	396	GLU	4.1
1	Q	437	GLN	4.1
1	Q	565	VAL	4.1
1	D	584	PRO	4.1
2	o	33	MET	4.1
2	p	119	ALA	4.1
1	F	600	LYS	4.1
1	G	505	GLN	4.1
2	s	145	GLU	4.1
1	C	337	ASN	4.1
1	J	359	PHE	4.0
1	T	250	ASP	4.0
1	K	257	ASP	4.0
1	L	248	LYS	4.0
2	p	76	ARG	4.0
1	P	160	SER	4.0
1	A	261	SER	4.0
1	B	326	GLY	4.0
1	D	594	VAL	4.0
2	m	130	SER	4.0
2	e	142	PRO	4.0
1	U	176	ILE	4.0
1	V	551	LEU	4.0
1	X	51	LEU	4.0
1	A	31	ASN	4.0
1	H	331	ASN	4.0
1	L	536	LEU	4.0
1	V	600	LYS	4.0
1	M	325	ASP	4.0
1	W	41	TRP	4.0
1	W	501	THR	4.0

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Mol	Chain	Res	Type	RSRZ
1	A	107	ALA	4.0
1	A	377	THR	4.0
1	C	358	GLY	4.0
1	G	423	GLU	4.0
1	K	21	ALA	4.0
1	K	184	TRP	4.0
1	L	58	ASP	4.0
2	j	127	THR	4.0
2	i	130	SER	4.0
1	C	11	ILE	4.0
1	U	30	LYS	4.0
1	X	35	PHE	4.0
1	J	331	ASN	4.0
1	W	515	GLU	4.0
1	C	540	GLY	4.0
1	K	174	THR	4.0
2	q	96	ALA	4.0
1	B	181	GLN	4.0
1	E	367	ASP	4.0
2	Y	81	ASP	4.0
1	M	11	ILE	4.0
1	K	8	LEU	4.0
2	n	14	LEU	4.0
2	a	87	SER	4.0
2	c	102	PRO	4.0
2	d	64	ILE	4.0
1	O	26	ARG	4.0
2	j	95	ASN	4.0
1	D	244	VAL	4.0
1	J	63	VAL	4.0
1	O	500	ALA	4.0
1	U	294	ALA	4.0
2	p	88	ALA	4.0
2	Y	108	ALA	4.0
1	S	56	GLN	4.0
1	W	597	GLN	4.0
1	X	159	ASP	4.0
1	B	510	ILE	4.0
1	F	12	LEU	4.0
2	c	142	PRO	4.0
2	h	43	GLN	4.0
1	O	173	CYS	4.0

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Mol	Chain	Res	Type	RSRZ
1	O	599	ALA	4.0
1	E	173	CYS	4.0
1	G	232	ALA	4.0
2	n	88	ALA	4.0
2	e	91	ALA	4.0
1	O	163	LYS	4.0
1	T	61	ARG	4.0
1	E	554	LEU	4.0
1	F	569	ARG	4.0
1	M	206	ASP	4.0
1	U	598	GLN	4.0
1	X	543	PRO	4.0
1	D	101	ASP	4.0
1	G	82	PRO	4.0
2	i	119	GLY	4.0
1	C	463	ILE	4.0
1	O	524	PHE	4.0
1	Q	387	GLN	4.0
1	B	517	TYR	4.0
1	U	543	PRO	4.0
1	A	570	ASP	4.0
1	B	557	PHE	4.0
1	G	387	GLN	4.0
1	F	194	ASP	4.0
1	H	240	THR	4.0
2	e	154	GLU	4.0
1	F	528	LYS	4.0
1	H	582	LYS	4.0
2	c	111	LYS	4.0
2	g	49	LEU	4.0
2	j	29	ALA	4.0
1	K	300	ILE	4.0
2	c	64	ILE	4.0
1	E	591	GLN	4.0
2	f	56	TRP	4.0
2	f	124	TYR	4.0
1	R	283	CYS	4.0
1	W	257	ASP	4.0
1	A	406	GLU	4.0
2	o	39	ASP	4.0
2	r	133	PRO	4.0
1	I	288	LYS	4.0

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Mol	Chain	Res	Type	RSRZ
2	e	50	GLU	4.0
1	M	239	VAL	4.0
1	I	155	HIS	4.0
1	N	114	ALA	4.0
1	A	573	ASN	4.0
1	L	31	ASN	4.0
1	N	206	ASP	4.0
1	U	60	VAL	4.0
1	G	323	THR	4.0
1	J	38	VAL	4.0
2	a	68	VAL	4.0
1	P	261	SER	4.0
1	G	258	LEU	4.0
1	J	538	LEU	4.0
2	q	132	MET	4.0
2	s	36	ALA	4.0
2	h	42	MET	4.0
1	V	255	ILE	4.0
1	C	350	PHE	4.0
2	d	104	TYR	4.0
1	N	503	GLU	4.0
1	W	218	GLN	4.0
1	X	426	ASN	4.0
1	I	550	GLN	4.0
1	H	506	VAL	4.0
1	R	79	LEU	4.0
1	B	193	LEU	4.0
1	L	339	ASP	4.0
1	J	255	ILE	4.0
1	K	390	ALA	4.0
2	v	33	MET	4.0
1	S	535	ILE	4.0
1	B	36	SER	4.0
2	m	104	ILE	4.0
2	n	89	CYS	4.0
2	b	148	SER	4.0
1	T	314	GLU	4.0
1	I	117	GLU	4.0
1	X	31	ASN	4.0
1	O	241	GLY	4.0
1	E	545	GLY	4.0
1	J	184	TRP	4.0

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Mol	Chain	Res	Type	RSRZ
2	s	93	PRO	4.0
1	A	89	ASP	4.0
1	N	87	ARG	4.0
1	G	264	ILE	4.0
2	a	105	ALA	4.0
1	I	189	GLU	3.9
1	N	508	ASN	3.9
1	S	461	GLY	3.9
1	I	452	ASN	3.9
2	i	95	ASN	3.9
1	M	91	ALA	3.9
1	R	519	ASP	3.9
1	W	32	ASP	3.9
1	W	134	ASP	3.9
1	E	342	ALA	3.9
1	J	364	ASP	3.9
2	p	99	ALA	3.9
2	Y	17	ASP	3.9
1	O	517	TYR	3.9
1	C	13	SER	3.9
1	G	162	SER	3.9
1	H	315	VAL	3.9
1	K	590	GLN	3.9
2	g	92	VAL	3.9
1	A	193	LEU	3.9
1	V	388	PRO	3.9
1	B	426	ASN	3.9
1	M	524	PHE	3.9
1	R	247	PHE	3.9
1	H	557	PHE	3.9
2	c	53	MET	3.9
1	N	519	ASP	3.9
1	P	196	ASP	3.9
1	A	11	ILE	3.9
1	G	257	ASP	3.9
2	e	121	GLU	3.9
1	M	151	SER	3.9
1	M	581	VAL	3.9
1	F	8	LEU	3.9
1	F	575	GLN	3.9
1	I	399	GLN	3.9
1	J	244	VAL	3.9

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Mol	Chain	Res	Type	RSRZ
1	K	38	VAL	3.9
2	d	30	SER	3.9
2	e	41	SER	3.9
1	G	103	ARG	3.9
2	k	18	GLY	3.9
1	X	109	ILE	3.9
2	c	52	MET	3.9
2	d	74	ASN	3.9
2	f	114	ALA	3.9
1	M	588	GLU	3.9
1	Q	215	ASP	3.9
1	V	595	GLU	3.9
1	B	5	GLU	3.9
1	E	423	GLU	3.9
1	G	445	GLU	3.9
2	l	39	ASP	3.9
1	P	586	THR	3.9
1	L	409	THR	3.9
1	A	46	SER	3.9
1	C	170	ALA	3.9
1	F	41	TRP	3.9
1	P	268	GLU	3.9
1	C	401	ASN	3.9
1	H	173	CYS	3.9
1	N	196	ASP	3.9
2	v	8	ASP	3.9
2	Z	71	ASP	3.9
2	d	85	ARG	3.9
2	f	20	ARG	3.9
1	G	130	THR	3.9
1	D	264	ILE	3.9
1	H	356	ILE	3.9
1	F	584	PRO	3.9
1	G	398	PRO	3.9
2	b	110	ALA	3.9
1	M	98	TYR	3.9
1	P	436	ASN	3.9
2	e	147	ASN	3.9
1	J	499	LEU	3.9
2	k	22	ASP	3.9
2	h	47	ASP	3.9
1	M	50	THR	3.9

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Mol	Chain	Res	Type	RSRZ
1	K	218	GLN	3.9
1	X	449	PHE	3.9
1	E	245	SER	3.9
1	O	585	GLU	3.9
1	R	423	GLU	3.9
1	I	87	ARG	3.9
1	J	41	TRP	3.9
2	l	96	ALA	3.9
2	i	77	ALA	3.9
2	i	121	GLU	3.9
1	P	203	ASN	3.9
2	l	65	ASN	3.9
2	Z	37	VAL	3.9
1	Q	364	ASP	3.9
1	V	237	ASP	3.9
1	D	427	GLY	3.9
1	G	253	ASP	3.9
1	K	215	ASP	3.9
2	e	66	GLY	3.9
1	O	323	THR	3.9
1	O	410	SER	3.9
1	W	46	SER	3.9
1	I	13	SER	3.9
2	t	61	SER	3.9
1	W	193	LEU	3.9
1	D	310	VAL	3.9
1	F	571	TYR	3.9
1	F	206	ASP	3.9
2	d	15	LYS	3.9
1	B	537	GLU	3.9
1	G	213	THR	3.9
2	p	89	CYS	3.9
2	j	110	ALA	3.9
2	j	143	THR	3.9
1	P	410	SER	3.9
2	e	130	SER	3.9
1	M	553	LEU	3.9
1	V	183	GLY	3.9
1	B	155	HIS	3.9
1	F	529	GLN	3.9
1	I	172	HIS	3.9
1	S	5	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	577	ILE	3.9
2	f	43	GLN	3.9
2	Y	42	MET	3.9
2	f	108	ALA	3.9
1	R	410	SER	3.9
1	T	59	VAL	3.9
1	W	261	SER	3.9
1	H	235	TYR	3.9
1	D	14	ARG	3.9
2	o	67	PRO	3.9
2	Y	62	GLY	3.9
1	N	256	ASP	3.9
1	O	189	GLU	3.9
1	R	32	ASP	3.9
1	E	337	ASN	3.9
1	G	383	ASP	3.9
1	J	89	ASP	3.9
1	K	155	HIS	3.9
1	M	541	LYS	3.9
1	D	30	LYS	3.9
1	J	115	VAL	3.9
2	k	124	LYS	3.9
2	o	19	VAL	3.9
2	u	124	LYS	3.9
1	O	41	TRP	3.9
1	V	246	TYR	3.9
2	e	65	THR	3.9
2	g	115	THR	3.9
1	F	592	TRP	3.9
1	R	217	ILE	3.9
1	J	311	GLU	3.9
1	K	535	ILE	3.9
2	s	98	GLU	3.9
1	O	42	ASP	3.9
1	L	253	ASP	3.9
1	M	33	LEU	3.8
1	I	63	VAL	3.8
1	I	287	LEU	3.8
2	l	114	LEU	3.8
2	q	99	ALA	3.9
2	f	106	LEU	3.8
1	G	282	THR	3.8

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Mol	Chain	Res	Type	RSRZ
1	V	590	GLN	3.8
1	Q	259	ALA	3.8
1	T	192	ASP	3.8
1	W	58	ASP	3.8
1	B	257	ASP	3.8
1	D	64	VAL	3.8
1	H	196	ASP	3.8
2	g	84	LEU	3.8
1	U	80	TYR	3.8
2	h	118	TYR	3.8
1	Q	49	THR	3.8
1	C	314	GLU	3.8
1	C	563	LYS	3.8
1	I	376	ARG	3.8
2	g	126	GLN	3.8
1	R	254	VAL	3.8
1	S	239	VAL	3.8
1	D	506	VAL	3.8
1	C	561	ASP	3.8
1	G	433	ASP	3.8
1	V	34	PHE	3.8
1	V	571	TYR	3.8
1	H	394	ASN	3.8
1	K	141	ASN	3.8
1	C	288	LYS	3.8
1	X	386	THR	3.8
1	B	344	THR	3.8
2	Z	30	SER	3.8
1	D	591	GLN	3.8
1	A	425	VAL	3.8
2	l	17	LEU	3.8
1	E	131	ASP	3.8
1	U	459	ARG	3.8
1	V	7	ARG	3.8
2	g	33	THR	3.8
1	W	538	LEU	3.8
1	F	598	GLN	3.8
1	A	574	LYS	3.8
1	B	549	TYR	3.8
1	I	262	GLY	3.8
2	f	69	PHE	3.8
1	P	589	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
1	S	337	ASN	3.8
1	B	569	ARG	3.8
1	E	401	ASN	3.8
1	K	92	ASP	3.8
1	T	234	ILE	3.8
1	Q	207	TRP	3.8
1	S	582	LYS	3.8
1	W	13	SER	3.8
1	F	599	ALA	3.8
1	J	13	SER	3.8
2	a	145	SER	3.8
1	J	191	TYR	3.8
1	A	147	GLU	3.8
1	E	570	ASP	3.8
2	e	31	ASP	3.8
1	T	337	ASN	3.8
1	D	234	ILE	3.8
1	J	337	ASN	3.8
1	V	425	VAL	3.8
1	W	184	TRP	3.8
1	A	225	VAL	3.8
1	H	497	VAL	3.8
1	J	420	VAL	3.8
2	s	66	PRO	3.8
1	O	386	THR	3.8
1	O	416	ALA	3.8
1	R	160	SER	3.8
1	I	160	SER	3.8
1	V	196	ASP	3.8
1	T	51	LEU	3.8
1	M	202	GLN	3.8
1	A	458	ARG	3.8
1	C	564	GLY	3.8
1	H	309	PHE	3.8
1	I	236	GLN	3.8
2	r	53	GLY	3.8
2	h	108	ALA	3.8
1	G	39	SER	3.8
1	S	361	HIS	3.8
1	J	589	GLU	3.8
1	S	197	ASP	3.8
1	U	554	LEU	3.8

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Mol	Chain	Res	Type	RSRZ
1	P	141	ASN	3.8
1	A	105	ASN	3.8
1	M	107	ALA	3.8
1	N	388	PRO	3.8
1	P	408	ALA	3.8
1	K	505	GLN	3.8
2	Y	66	GLY	3.8
1	S	556	TYR	3.8
1	U	534	GLU	3.8
1	G	9	GLU	3.8
1	J	516	CYS	3.8
1	S	507	LEU	3.8
1	B	109	ILE	3.8
1	P	215	ASP	3.8
2	i	47	ASP	3.8
1	M	401	ASN	3.8
1	P	75	PRO	3.8
1	S	205	ASN	3.8
1	V	295	GLY	3.8
1	W	530	GLN	3.8
1	E	590	GLN	3.8
1	J	259	ALA	3.8
1	K	19	TRP	3.8
2	n	101	ALA	3.8
1	K	583	LYS	3.8
1	U	277	TYR	3.8
1	N	249	ARG	3.8
1	E	284	THR	3.8
1	S	384	LEU	3.8
1	V	180	SER	3.8
1	F	283	CYS	3.8
2	b	129	ILE	3.8
1	P	187	PHE	3.8
1	C	187	PHE	3.8
1	D	237	ASP	3.8
2	f	44	ASP	3.8
1	M	462	GLU	3.8
1	N	203	ASN	3.8
1	P	199	PRO	3.8
1	U	135	GLN	3.8
1	B	396	GLU	3.8
2	r	64	GLU	3.8

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Mol	Chain	Res	Type	RSRZ
2	d	78	GLU	3.8
1	G	61	ARG	3.8
1	B	552	LEU	3.8
1	U	139	SER	3.8
1	V	136	SER	3.8
1	I	254	VAL	3.8
1	P	169	ASP	3.7
1	P	195	ALA	3.7
1	R	90	ALA	3.7
1	V	495	GLU	3.7
1	A	498	ASP	3.7
1	J	495	GLU	3.7
1	L	186	ASP	3.7
1	L	424	ALA	3.7
2	d	54	ALA	3.7
1	P	41	TRP	3.7
1	S	555	GLN	3.7
1	V	525	GLN	3.7
1	W	575	GLN	3.7
1	C	327	GLN	3.7
1	C	578	GLN	3.7
2	j	107	GLU	3.7
1	G	375	ASN	3.7
1	H	141	ASN	3.7
1	L	141	ASN	3.7
1	O	12	LEU	3.7
1	K	536	LEU	3.7
1	M	129	VAL	3.7
1	O	506	VAL	3.7
1	Q	546	THR	3.7
1	J	344	THR	3.7
1	V	160	SER	3.7
2	t	7	GLY	3.7
1	N	387	GLN	3.7
1	Q	134	ASP	3.7
1	X	411	ALA	3.7
1	X	416	ALA	3.7
1	U	387	GLN	3.7
1	U	571	TYR	3.7
1	J	202	GLN	3.7
1	M	426	ASN	3.7
1	R	271	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	264	ILE	3.7
1	C	551	LEU	3.7
2	a	67	TYR	3.7
1	F	217	ILE	3.7
2	Z	63	ILE	3.7
1	O	252	LYS	3.7
1	O	254	VAL	3.7
1	R	458	ARG	3.7
1	U	284	THR	3.7
1	I	410	SER	3.7
2	j	78	GLU	3.7
1	N	32	ASP	3.7
1	R	385	PRO	3.7
1	S	207	TRP	3.7
1	V	325	ASP	3.7
1	V	539	LEU	3.7
1	F	62	PRO	3.7
1	L	421	ASP	3.7
1	L	444	LEU	3.7
2	s	95	TYR	3.7
2	t	75	LEU	3.7
2	b	96	LEU	3.7
2	g	113	ILE	3.7
1	O	269	ARG	3.7
1	O	407	ALA	3.7
1	U	409	THR	3.7
1	W	564	GLY	3.7
1	B	558	THR	3.7
1	C	28	GLU	3.7
1	G	216	THR	3.7
1	I	130	THR	3.7
2	k	73	HIS	3.7
2	l	7	GLY	3.7
2	c	50	GLU	3.7
1	J	195	ALA	3.7
2	s	96	ALA	3.7
1	X	191	TYR	3.7
1	D	236	GLN	3.7
1	O	519	ASP	3.7
1	S	592	TRP	3.7
1	U	367	ASP	3.7
1	U	592	TRP	3.7

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Mol	Chain	Res	Type	RSRZ
2	Z	17	ASP	3.7
1	H	35	PHE	3.7
2	v	10	VAL	3.7
2	h	89	VAL	3.7
2	g	74	ASN	3.7
1	X	147	GLU	3.7
1	B	230	GLU	3.7
1	Q	600	LYS	3.7
1	F	596	ALA	3.7
1	G	455	THR	3.7
2	m	92	ALA	3.7
2	n	126	ALA	3.7
1	U	550	GLN	3.7
1	E	560	LEU	3.7
1	G	327	GLN	3.7
1	I	98	TYR	3.7
1	L	335	SER	3.7
1	I	356	ILE	3.7
1	L	281	ILE	3.7
1	R	186	ASP	3.7
1	L	247	PHE	3.7
2	Z	75	PRO	3.7
1	J	183	GLY	3.7
1	K	195	ALA	3.7
2	c	32	ALA	3.7
1	K	33	LEU	3.7
1	Q	139	SER	3.7
1	V	235	TYR	3.7
1	V	236	GLN	3.7
1	F	168	SER	3.7
2	j	24	ARG	3.7
1	N	451	ASP	3.7
1	X	595	GLU	3.7
2	s	53	GLY	3.7
1	M	283	CYS	3.7
1	U	424	ALA	3.7
2	o	138	ASN	3.7
1	B	287	LEU	3.7
1	L	14	ARG	3.7
2	i	97	ALA	3.7
1	Q	601	GLN	3.7
1	J	510	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
2	k	115	TYR	3.7
1	J	233	PHE	3.7
1	U	19	TRP	3.7
1	W	541	LYS	3.7
1	C	196	ASP	3.7
1	J	250	ASP	3.7
2	a	16	GLY	3.7
1	P	552	LEU	3.7
1	Q	572	ALA	3.7
1	X	559	LEU	3.7
1	O	264	ILE	3.7
1	C	281	ILE	3.7
1	M	591	GLN	3.7
1	Q	516	CYS	3.7
1	U	270	GLN	3.7
1	A	47	GLN	3.7
1	G	52	GLN	3.7
1	G	214	GLN	3.7
2	i	92	VAL	3.7
1	C	160	SER	3.7
1	M	398	PRO	3.7
1	O	584	PRO	3.7
1	D	588	GLU	3.7
1	I	5	GLU	3.7
2	i	55	GLU	3.7
1	M	27	ARG	3.7
1	K	498	ASP	3.7
1	R	389	LEU	3.7
1	L	453	LEU	3.7
1	N	48	TYR	3.7
1	X	337	ASN	3.7
1	J	399	GLN	3.7
1	T	534	GLU	3.7
1	V	200	SER	3.7
1	D	200	SER	3.7
1	E	20	THR	3.7
1	F	88	PRO	3.7
2	k	67	PRO	3.7
2	q	78	SER	3.7
2	b	123	LEU	3.7
1	I	574	LYS	3.7
2	k	102	LYS	3.7

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Mol	Chain	Res	Type	RSRZ
1	M	34	PHE	3.7
1	H	63	VAL	3.7
1	G	296	GLU	3.7
1	H	40	GLN	3.7
2	b	121	GLU	3.7
1	O	559	LEU	3.7
1	I	33	LEU	3.7
2	f	90	SER	3.7
1	M	267	ALA	3.7
1	E	533	ALA	3.7
1	H	90	ALA	3.7
2	r	71	ASP	3.7
2	e	45	ALA	3.7
2	Z	100	ILE	3.7
2	f	68	VAL	3.7
1	A	529	GLN	3.7
1	E	249	ARG	3.7
1	L	227	GLU	3.7
2	p	53	GLY	3.6
2	e	83	GLY	3.6
1	M	216	THR	3.6
1	P	547	PRO	3.6
1	S	50	THR	3.6
1	S	523	SER	3.6
1	U	41	TRP	3.6
1	I	547	PRO	3.6
1	K	552	LEU	3.6
2	e	75	PRO	3.6
2	j	26	LEU	3.6
1	J	381	SER	3.6
1	X	383	ASP	3.6
1	U	249	ARG	3.6
1	I	301	VAL	3.6
2	k	19	VAL	3.6
1	M	578	GLN	3.6
1	W	445	GLU	3.6
1	B	327	GLN	3.6
1	C	379	GLU	3.6
1	N	580	GLY	3.6
1	G	183	GLY	3.6
1	H	419	GLY	3.6
2	r	135	GLY	3.6

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Mol	Chain	Res	Type	RSRZ
2	u	117	GLN	3.6
2	d	83	GLY	3.6
2	g	58	GLN	3.6
1	H	384	LEU	3.6
1	P	513	ARG	3.6
1	Q	22	SER	3.6
1	B	572	ALA	3.6
1	F	417	THR	3.6
1	H	299	PRO	3.6
1	J	188	ALA	3.6
2	n	140	PHE	3.6
1	N	239	VAL	3.6
1	T	64	VAL	3.6
1	J	192	ASP	3.6
1	T	6	ASN	3.6
1	B	508	ASN	3.6
1	G	203	ASN	3.6
1	J	141	ASN	3.6
2	n	138	ASN	3.6
1	S	220	ALA	3.6
2	s	119	ALA	3.6
1	C	518	THR	3.6
2	t	54	ILE	3.6
1	M	570	ASP	3.6
1	P	42	ASP	3.6
1	P	383	ASP	3.6
1	R	197	ASP	3.6
1	S	194	ASP	3.6
1	T	237	ASP	3.6
1	T	582	LYS	3.6
1	V	582	LYS	3.6
1	C	48	TYR	3.6
1	D	381	SER	3.6
1	F	139	SER	3.6
1	J	200	SER	3.6
2	Z	92	VAL	3.6
1	J	368	ASP	3.6
1	L	134	ASP	3.6
2	i	90	SER	3.6
1	B	118	GLN	3.6
1	E	382	GLY	3.6
1	Q	233	PHE	3.6

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Mol	Chain	Res	Type	RSRZ
1	W	209	PHE	3.6
1	E	263	PHE	3.6
1	P	11	ILE	3.6
1	S	293	ILE	3.6
1	Q	462	GLU	3.6
1	T	60	VAL	3.6
1	T	600	LYS	3.6
1	V	290	LYS	3.6
1	D	587	PRO	3.6
1	G	152	ALA	3.6
1	K	500	ALA	3.6
1	R	216	THR	3.6
1	K	323	THR	3.6
1	L	364	ASP	3.6
2	k	53	GLY	3.6
2	b	103	ASP	3.6
1	L	283	CYS	3.6
1	N	445	GLU	3.6
1	W	341	VAL	3.6
1	D	566	GLU	3.6
1	I	534	GLU	3.6
1	L	5	GLU	3.6
1	M	122	GLY	3.6
1	M	580	GLY	3.6
1	N	383	ASP	3.6
1	B	422	THR	3.6
1	B	553	LEU	3.6
1	C	26	ARG	3.6
1	E	49	THR	3.6
1	F	545	GLY	3.6
1	G	249	ARG	3.6
1	K	168	SER	3.6
2	k	136	SER	3.6
1	I	291	GLN	3.6
2	q	8	ASP	3.6
2	s	94	ASP	3.6
1	R	265	LYS	3.6
1	W	222	PHE	3.6
1	J	163	LYS	3.6
2	b	46	VAL	3.6
1	Q	439	ASN	3.6
1	T	19	TRP	3.6

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Mol	Chain	Res	Type	RSRZ
1	U	105	ASN	3.6
1	X	331	ASN	3.6
1	F	352	TRP	3.6
2	t	144	ASN	3.6
1	N	100	THR	3.6
1	T	554	LEU	3.6
1	N	180	SER	3.6
1	O	505	GLN	3.6
1	D	196	ASP	3.6
1	J	409	THR	3.6
2	k	26	THR	3.6
2	Y	126	GLN	3.6
2	d	70	SER	3.6
2	Y	82	HIS	3.6
1	Q	24	GLU	3.6
1	U	596	ALA	3.6
1	X	125	ALA	3.6
1	X	232	ALA	3.6
2	Y	135	ALA	3.6
1	A	366	ASN	3.6
1	M	163	LYS	3.6
1	C	252	LYS	3.6
1	D	560	LEU	3.6
1	H	55	GLY	3.6
2	a	83	GLY	3.6
2	j	83	GLY	3.6
1	Q	450	GLN	3.6
1	Q	509	ASP	3.6
1	V	73	GLN	3.6
2	c	41	SER	3.6
2	e	53	MET	3.6
1	B	220	ALA	3.6
1	J	423	GLU	3.6
1	N	541	LYS	3.6
1	T	583	LYS	3.6
1	D	562	GLY	3.6
2	j	117	LYS	3.6
1	R	141	ASN	3.6
1	S	401	ASN	3.6
1	L	366	ASN	3.6
1	N	367	ASP	3.6
1	P	446	THR	3.6

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Mol	Chain	Res	Type	RSRZ
1	Q	497	VAL	3.6
1	R	11	ILE	3.6
1	S	460	ASP	3.6
1	T	279	SER	3.6
1	U	58	ASP	3.6
1	W	60	VAL	3.6
1	X	561	ASP	3.6
1	H	261	SER	3.6
1	I	143	VAL	3.6
1	J	198	ILE	3.6
2	l	77	SER	3.6
2	o	29	GLU	3.6
2	p	122	ARG	3.6
2	j	30	SER	3.6
1	B	177	HIS	3.6
1	E	17	ALA	3.6
1	U	55	GLY	3.6
1	X	262	GLY	3.6
1	D	365	GLY	3.6
1	E	552	LEU	3.6
2	b	60	GLY	3.6
1	P	426	ASN	3.6
1	Q	34	PHE	3.6
1	V	204	PRO	3.6
1	W	543	PRO	3.6
1	D	207	TRP	3.6
1	L	74	ASN	3.6
1	O	206	ASP	3.6
1	Q	460	ASP	3.6
1	R	425	VAL	3.6
1	T	245	SER	3.6
1	U	237	ASP	3.6
1	C	42	ASP	3.6
1	G	261	SER	3.6
1	H	186	ASP	3.6
1	I	129	VAL	3.6
1	K	221	GLU	3.6
2	q	37	VAL	3.6
2	q	54	ILE	3.6
1	L	232	ALA	3.6
2	f	115	THR	3.6
1	S	571	TYR	3.6

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Mol	Chain	Res	Type	RSRZ
1	B	372	TYR	3.6
1	D	580	GLY	3.6
1	F	193	LEU	3.6
1	U	209	PHE	3.6
2	k	149	PHE	3.6
2	b	142	PRO	3.6
1	S	31	ASN	3.6
1	B	203	ASN	3.6
1	E	202	GLN	3.6
1	E	293	ILE	3.6
1	E	548	GLU	3.6
1	F	313	LYS	3.6
1	I	327	GLN	3.6
1	I	397	VAL	3.6
1	L	296	GLU	3.6
2	a	50	GLU	3.6
1	W	151	SER	3.6
1	X	586	THR	3.6
1	B	279	SER	3.6
1	E	194	ASP	3.6
1	S	94	LEU	3.6
1	J	172	HIS	3.6
1	G	247	PHE	3.5
1	I	108	LYS	3.5
2	e	117	LYS	3.5
2	f	39	PRO	3.5
1	B	565	VAL	3.5
1	C	589	GLU	3.5
2	j	25	LYS	3.5
1	O	205	ASN	3.5
1	R	203	ASN	3.5
1	K	355	GLN	3.5
2	s	86	ASN	3.5
2	e	58	GLN	3.5
2	g	68	VAL	3.5
2	h	100	ILE	3.5
1	Q	408	ALA	3.5
1	B	29	ALA	3.5
1	C	381	SER	3.5
2	l	15	ARG	3.5
2	j	90	SER	3.5
2	j	145	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	F	359	PHE	3.5
1	L	228	LYS	3.5
2	c	93	PHE	3.5
1	X	142	GLN	3.5
1	A	397	VAL	3.5
1	H	379	GLU	3.5
1	H	581	VAL	3.5
2	o	93	PRO	3.5
2	o	133	PRO	3.5
2	i	58	GLN	3.5
1	O	375	ASN	3.5
1	J	416	ALA	3.5
2	q	40	LEU	3.5
2	d	84	LEU	3.5
2	g	88	ALA	3.5
2	j	45	ALA	3.5
2	j	91	ALA	3.5
1	M	213	THR	3.5
1	I	192	ASP	3.5
1	J	369	TYR	3.5
1	N	200	SER	3.5
1	W	200	SER	3.5
2	p	39	ASP	3.5
2	b	30	SER	3.5
1	M	319	VAL	3.5
1	E	595	GLU	3.5
1	F	341	VAL	3.5
2	p	10	VAL	3.5
1	B	418	LEU	3.5
1	G	532	ARG	3.5
1	I	533	ALA	3.5
1	L	461	GLY	3.5
2	j	97	ALA	3.5
1	O	451	ASP	3.5
1	A	166	ASP	3.5
1	J	43	ASP	3.5
1	P	462	GLU	3.5
1	Q	10	SER	3.5
1	X	279	SER	3.5
1	C	50	THR	3.5
2	u	147	HIS	3.5
1	Q	93	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	V	293	ILE	3.5
1	J	320	VAL	3.5
1	P	207	TRP	3.5
1	T	578	GLN	3.5
1	D	19	TRP	3.5
1	D	353	PRO	3.5
1	K	144	ILE	3.5
1	K	204	PRO	3.5
1	F	374	LEU	3.5
1	K	499	LEU	3.5
2	j	128	ALA	3.5
1	U	396	GLU	3.5
1	A	70	GLU	3.5
1	C	548	GLU	3.5
1	I	250	ASP	3.5
1	P	420	VAL	3.5
1	U	569	ARG	3.5
1	J	145	ARG	3.5
2	p	54	ILE	3.5
2	c	115	THR	3.5
1	M	108	LYS	3.5
1	U	560	LEU	3.5
1	H	88	PRO	3.5
1	T	55	GLY	3.5
1	U	227	GLU	3.5
1	K	74	ASN	3.5
1	T	92	ASP	3.5
1	A	239	VAL	3.5
2	h	80	ASP	3.5
1	C	582	LYS	3.5
1	D	255	ILE	3.5
1	H	163	LYS	3.5
2	q	52	LYS	3.5
1	U	399	GLN	3.5
1	B	543	PRO	3.5
1	O	187	PHE	3.5
1	D	211	TRP	3.5
1	X	423	GLU	3.5
1	B	585	GLU	3.5
1	C	532	ARG	3.5
1	G	565	VAL	3.5
1	H	112	ASN	3.5

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Mol	Chain	Res	Type	RSRZ
2	Z	68	VAL	3.5
1	P	339	ASP	3.5
1	A	217	ILE	3.5
1	G	58	ASP	3.5
1	U	160	SER	3.5
1	U	518	THR	3.5
1	J	262	GLY	3.5
1	L	10	SER	3.5
2	j	70	SER	3.5
1	N	584	PRO	3.5
1	R	587	PRO	3.5
1	T	395	PRO	3.5
1	F	35	PHE	3.5
1	F	294	ALA	3.5
1	T	254	VAL	3.5
1	B	439	ASN	3.5
1	H	559	LEU	3.5
2	k	71	ASP	3.5
2	n	39	ASP	3.5
2	t	62	ASP	3.5
2	e	96	LEU	3.5
1	S	512	GLY	3.5
1	U	173	CYS	3.5
1	O	50	THR	3.5
1	E	233	PHE	3.5
1	I	174	THR	3.5
2	c	58	GLN	3.5
1	M	445	GLU	3.5
1	B	221	GLU	3.5
2	r	145	GLU	3.5
1	N	581	VAL	3.5
1	D	208	VAL	3.5
1	P	507	LEU	3.5
1	A	444	LEU	3.5
2	s	40	LEU	3.5
1	M	561	ASP	3.5
1	P	364	ASP	3.5
1	P	512	GLY	3.5
1	S	540	GLY	3.5
1	U	7	ARG	3.5
1	H	215	ASP	3.5
1	N	291	GLN	3.5

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Mol	Chain	Res	Type	RSRZ
1	W	25	ALA	3.5
1	W	386	THR	3.5
1	I	447	TYR	3.5
1	I	549	TYR	3.5
1	K	138	THR	3.5
2	r	139	SER	3.5
1	M	320	VAL	3.5
1	M	594	VAL	3.5
1	I	565	VAL	3.5
2	c	19	VAL	3.5
2	t	25	LEU	3.5
1	B	269	ARG	3.5
2	u	85	HIS	3.5
1	R	452	ASN	3.5
1	M	327	GLN	3.5
1	M	530	GLN	3.5
1	M	555	GLN	3.5
1	S	43	ASP	3.5
1	V	378	ASP	3.5
1	B	339	ASP	3.5
1	R	48	TYR	3.5
1	D	5	GLU	3.5
1	I	530	GLN	3.5
1	G	200	SER	3.5
2	m	95	TYR	3.5
2	e	145	SER	3.5
1	Q	576	LEU	3.5
1	H	577	ILE	3.5
2	h	24	ARG	3.5
2	i	123	LEU	3.5
1	R	31	ASN	3.4
1	U	224	GLU	3.4
1	U	230	GLU	3.4
1	U	573	ASN	3.4
1	J	161	ASN	3.4
2	m	27	ASP	3.4
2	m	50	ASP	3.4
1	Q	13	SER	3.4
1	T	49	THR	3.4
1	M	356	ILE	3.4
1	T	343	ARG	3.4
1	B	100	THR	3.4

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Mol	Chain	Res	Type	RSRZ
2	k	66	PRO	3.4
1	C	458	ARG	3.4
1	D	271	ILE	3.4
1	J	333	ILE	3.4
2	k	90	ARG	3.4
2	m	114	LEU	3.4
1	C	304	PHE	3.4
1	H	350	PHE	3.4
1	O	537	GLU	3.4
1	G	361	HIS	3.4
2	v	147	HIS	3.4
1	O	425	VAL	3.4
1	R	182	ASN	3.4
1	H	27	ARG	3.4
2	t	22	ASP	3.4
1	Q	41	TRP	3.4
1	W	560	LEU	3.4
1	A	384	LEU	3.4
1	J	243	PRO	3.4
1	K	541	LYS	3.4
1	L	346	LYS	3.4
2	Z	18	LEU	3.4
2	f	150	PRO	3.4
1	E	39	SER	3.4
1	X	173	CYS	3.4
1	W	110	ALA	3.4
1	C	408	ALA	3.4
2	o	79	ALA	3.4
2	u	41	GLU	3.4
2	e	107	GLU	3.4
2	j	73	GLU	3.4
1	P	181	GLN	3.4
1	L	27	ARG	3.4
2	o	49	GLN	3.4
1	C	134	ASP	3.4
1	L	204	PRO	3.4
2	b	136	PRO	3.4
2	h	63	ILE	3.4
1	P	502	GLY	3.4
1	W	262	GLY	3.4
1	B	187	PHE	3.4
1	C	359	PHE	3.4

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Mol	Chain	Res	Type	RSRZ
2	r	130	SER	3.4
1	C	190	LYS	3.4
1	C	400	ALA	3.4
1	D	503	GLU	3.4
1	E	456	ALA	3.4
1	M	191	TYR	3.4
1	T	581	VAL	3.4
1	X	525	GLN	3.4
1	U	536	LEU	3.4
1	J	319	VAL	3.4
1	N	299	PRO	3.4
1	O	587	PRO	3.4
1	C	250	ASP	3.4
1	I	243	PRO	3.4
1	J	547	PRO	3.4
1	L	251	ILE	3.4
2	d	36	ASP	3.4
1	P	318	GLY	3.4
1	W	562	GLY	3.4
1	C	377	THR	3.4
1	H	342	ALA	3.4
2	o	96	ALA	3.4
1	A	79	LEU	3.4
1	H	98	TYR	3.4
1	H	597	GLN	3.4
2	h	67	TYR	3.4
1	N	205	ASN	3.4
1	O	215	ASP	3.4
1	R	557	PHE	3.4
1	V	247	PHE	3.4
1	W	584	PRO	3.4
1	B	263	PHE	3.4
1	C	378	ASP	3.4
1	H	31	ASN	3.4
2	s	74	GLY	3.4
2	u	86	ASN	3.4
2	h	56	TRP	3.4
2	t	41	GLU	3.4
1	X	402	ALA	3.4
1	D	50	THR	3.4
1	H	431	ALA	3.4
1	U	505	GLN	3.4

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Mol	Chain	Res	Type	RSRZ
1	R	15	PHE	3.4
1	N	62	PRO	3.4
1	V	253	ASP	3.4
1	J	186	ASP	3.4
1	O	452	ASN	3.4
1	C	140	ASN	3.4
1	E	331	ASN	3.4
2	Z	38	GLU	3.4
1	R	496	VAL	3.4
1	T	285	ALA	3.4
1	D	425	VAL	3.4
1	J	22	SER	3.4
1	K	29	ALA	3.4
1	L	174	THR	3.4
2	j	84	LEU	3.4
1	Q	209	PHE	3.4
1	B	361	HIS	3.4
1	I	264	ILE	3.4
1	L	437	GLN	3.4
1	B	449	PHE	3.4
2	e	64	ILE	3.4
2	i	100	ILE	3.4
1	N	16	ASP	3.4
1	P	224	GLU	3.4
1	S	185	GLU	3.4
1	K	423	GLU	3.4
2	t	141	PRO	3.4
2	Z	138	PRO	3.4
2	h	55	GLU	3.4
1	P	439	ASN	3.4
1	R	416	ALA	3.4
1	T	553	LEU	3.4
1	W	533	ALA	3.4
1	D	152	ALA	3.4
1	F	245	SER	3.4
1	L	193	LEU	3.4
2	j	96	LEU	3.4
1	X	249	ARG	3.4
1	I	201	PHE	3.4
2	s	124	LYS	3.4
1	B	388	PRO	3.4
2	b	76	PRO	3.4

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Mol	Chain	Res	Type	RSRZ
2	c	155	TRP	3.4
2	f	81	ASP	3.4
1	G	520	VAL	3.4
2	d	51	ALA	3.4
1	M	218	GLN	3.4
1	S	530	GLN	3.4
1	T	236	GLN	3.4
1	U	335	SER	3.4
1	F	247	PHE	3.4
2	b	112	ILE	3.4
2	g	104	TYR	3.4
2	i	124	TYR	3.4
1	B	529	GLN	3.4
1	D	323	THR	3.4
1	J	598	GLN	3.4
1	P	445	GLU	3.4
1	R	495	GLU	3.4
1	S	537	GLU	3.4
1	C	311	GLU	3.4
2	o	145	GLU	3.4
1	N	137	PRO	3.4
1	O	312	ASP	3.4
1	S	86	ALA	3.4
1	W	51	LEU	3.4
1	D	26	ARG	3.4
1	L	494	ALA	3.4
2	q	9	LEU	3.4
2	f	49	LEU	3.4
2	g	22	ALA	3.4
1	B	247	PHE	3.4
1	E	48	TYR	3.4
1	G	112	ASN	3.4
1	L	140	ASN	3.4
1	P	437	GLN	3.4
1	W	516	CYS	3.4
2	e	86	SER	3.4
1	C	534	GLU	3.4
1	H	462	GLU	3.4
1	P	7	ARG	3.4
1	W	459	ARG	3.4
1	D	458	ARG	3.4
1	E	551	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
2	d	141	MET	3.4
1	B	169	ASP	3.4
1	B	443	ASP	3.4
1	D	570	ASP	3.4
2	Y	47	ASP	3.4
1	P	535	ILE	3.4
1	T	161	ASN	3.4
1	X	98	TYR	3.4
2	m	60	PHE	3.4
1	W	56	GLN	3.4
1	B	461	GLY	3.4
1	E	537	GLU	3.4
2	b	58	GLN	3.4
1	P	541	LYS	3.4
1	J	335	SER	3.4
1	T	459	ARG	3.4
1	S	208	VAL	3.3
1	U	353	PRO	3.3
1	A	336	PHE	3.3
1	E	207	TRP	3.3
1	I	587	PRO	3.3
1	R	340	ILE	3.3
1	G	289	ASP	3.3
1	G	300	ILE	3.3
1	J	11	ILE	3.3
1	J	166	ASP	3.3
1	L	577	ILE	3.3
2	t	63	ASP	3.3
1	N	591	GLN	3.3
1	W	112	ASN	3.3
1	C	52	GLN	3.3
2	Z	107	GLU	3.3
1	Q	552	LEU	3.3
1	U	150	HIS	3.3
1	A	455	THR	3.3
1	N	407	ALA	3.3
1	P	29	ALA	3.3
1	S	195	ALA	3.3
1	L	336	PHE	3.3
2	m	13	ALA	3.3
2	q	42	ALA	3.3
2	h	97	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	M	556	TYR	3.3
1	N	257	ASP	3.3
1	X	312	ASP	3.3
2	Z	81	ASP	3.3
1	L	436	ASN	3.3
1	K	178	SER	3.3
1	L	389	LEU	3.3
2	i	143	THR	3.3
1	N	357	ALA	3.3
1	U	232	ALA	3.3
1	X	388	PRO	3.3
1	D	408	ALA	3.3
1	H	238	PRO	3.3
2	n	96	ALA	3.3
1	M	250	ASP	3.3
1	R	312	ASP	3.3
1	U	24	GLU	3.3
1	W	537	GLU	3.3
1	X	28	GLU	3.3
1	G	502	GLY	3.3
1	U	164	LEU	3.3
1	E	553	LEU	3.3
1	F	576	LEU	3.3
2	i	74	ASN	3.3
1	O	546	THR	3.3
1	F	10	SER	3.3
1	F	222	PHE	3.3
2	s	56	THR	3.3
2	a	109	THR	3.3
2	i	41	SER	3.3
1	M	264	ILE	3.3
1	X	189	GLU	3.3
1	A	311	GLU	3.3
1	F	191	TYR	3.3
2	g	27	GLY	3.3
1	Q	202	GLN	3.3
1	V	193	LEU	3.3
1	N	563	LYS	3.3
1	V	276	VAL	3.3
1	F	239	VAL	3.3
1	F	426	ASN	3.3
1	H	115	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
1	H	565	VAL	3.3
1	A	449	PHE	3.3
1	G	449	PHE	3.3
1	K	6	ASN	3.3
2	d	95	ASN	3.3
2	e	93	PHE	3.3
1	M	549	TYR	3.3
1	S	514	TYR	3.3
1	J	20	THR	3.3
1	I	602	GLY	3.3
1	M	256	ASP	3.3
1	X	598	GLN	3.3
1	X	601	GLN	3.3
1	A	578	GLN	3.3
1	D	169	ASP	3.3
2	q	17	LEU	3.3
2	f	125	LYS	3.3
2	h	96	LEU	3.3
2	p	59	VAL	3.3
2	Z	69	PHE	3.3
1	T	573	ASN	3.3
1	I	508	ASN	3.3
1	N	595	GLU	3.3
1	V	526	SER	3.3
1	B	154	SER	3.3
1	F	180	SER	3.3
2	b	55	GLU	3.3
1	M	199	PRO	3.3
1	Q	270	GLN	3.3
2	f	15	LYS	3.3
1	C	289	ASP	3.3
2	n	80	VAL	3.3
2	e	81	ASP	3.3
1	M	90	ALA	3.3
1	N	356	ILE	3.3
1	Q	390	ALA	3.3
1	U	109	ILE	3.3
1	A	379	GLU	3.3
2	l	104	ILE	3.3
2	o	41	GLU	3.3
1	X	124	GLY	3.3
1	B	39	SER	3.3

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Mol	Chain	Res	Type	RSRZ
1	F	386	THR	3.3
1	H	522	PRO	3.3
1	V	184	TRP	3.3
1	B	590	GLN	3.3
1	G	315	VAL	3.3
1	P	18	ASP	3.3
1	H	572	ALA	3.3
1	I	107	ALA	3.3
1	L	11	ILE	3.3
2	p	98	GLU	3.3
1	T	571	TYR	3.3
1	L	514	TYR	3.3
1	P	204	PRO	3.3
1	H	151	SER	3.3
1	J	51	LEU	3.3
1	U	434	THR	3.3
1	T	142	GLN	3.3
1	A	187	PHE	3.3
1	J	524	PHE	3.3
1	K	134	ASP	3.3
2	n	35	ASP	3.3
1	D	596	ALA	3.3
2	t	122	ARG	3.3
2	e	97	ALA	3.3
1	V	499	LEU	3.3
1	W	573	ASN	3.3
1	K	508	ASN	3.3
1	R	526	SER	3.3
1	A	247	PHE	3.3
1	D	35	PHE	3.3
1	E	57	PHE	3.3
1	H	587	PRO	3.3
1	E	216	THR	3.3
1	L	180	SER	3.3
1	F	327	GLN	3.3
2	j	56	TRP	3.3
1	A	589	GLU	3.3
1	F	24	GLU	3.3
2	f	107	GLU	3.3
1	N	86	ALA	3.3
1	S	338	ALA	3.3
1	W	378	ASP	3.3

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Mol	Chain	Res	Type	RSRZ
1	J	570	ASP	3.3
1	K	339	ASP	3.3
2	c	54	ALA	3.3
1	U	405	LEU	3.3
1	J	517	TYR	3.3
1	E	573	ASN	3.3
1	G	304	PHE	3.3
1	J	201	PHE	3.3
1	K	594	VAL	3.3
1	V	575	GLN	3.3
1	D	313	LYS	3.3
1	J	346	LYS	3.3
2	v	30	PRO	3.3
2	e	150	PRO	3.3
1	N	23	ASP	3.3
1	E	96	GLY	3.3
1	H	257	ASP	3.3
2	l	105	ALA	3.3
1	P	549	TYR	3.3
1	H	447	TYR	3.3
1	Q	187	PHE	3.3
1	R	38	VAL	3.3
1	U	303	VAL	3.3
1	F	44	TRP	3.2
1	F	537	GLU	3.2
1	O	390	ALA	3.2
1	A	282	THR	3.2
1	F	308	GLY	3.2
1	G	259	ALA	3.2
2	u	88	ALA	3.2
1	Q	206	ASP	3.2
1	X	131	ASP	3.2
1	G	89	ASP	3.2
1	G	367	ASP	3.2
1	I	536	LEU	3.2
1	T	26	ARG	3.2
2	k	140	PHE	3.2
1	M	161	ASN	3.2
1	P	360	GLU	3.2
1	A	370	PRO	3.2
1	R	13	SER	3.2
1	U	510	ILE	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	112	ASN	3.2
1	F	238	PRO	3.2
2	k	93	PRO	3.2
2	c	38	GLU	3.2
1	N	285	ALA	3.2
1	B	180	SER	3.2
1	J	160	SER	3.2
2	l	103	ILE	3.2
1	Q	20	THR	3.2
1	U	329	LEU	3.2
1	W	212	LEU	3.2
1	F	514	TYR	3.2
1	J	229	LYS	3.2
2	l	148	TYR	3.2
2	c	18	LEU	3.2
1	N	509	ASP	3.2
1	P	23	ASP	3.2
1	H	153	CYS	3.2
1	J	254	VAL	3.2
1	I	217	ILE	3.2
2	p	34	GLN	3.2
1	Q	508	ASN	3.2
1	W	439	ASN	3.2
1	A	182	ASN	3.2
2	q	57	GLY	3.2
2	s	142	ASN	3.2
2	t	86	ASN	3.2
2	a	147	ASN	3.2
1	E	10	SER	3.2
1	G	178	SER	3.2
2	c	88	ALA	3.2
2	e	26	LEU	3.2
1	V	282	THR	3.2
1	E	343	ARG	3.2
1	K	511	ARG	3.2
2	v	148	TYR	3.2
2	h	124	TYR	3.2
2	j	131	ARG	3.2
1	N	42	ASP	3.2
1	Q	239	VAL	3.2
2	l	94	ASP	3.2
1	D	9	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	F	153	CYS	3.2
1	F	360	GLU	3.2
1	N	308	GLY	3.2
1	V	217	ILE	3.2
1	E	291	GLN	3.2
1	F	248	LYS	3.2
2	e	42	MET	3.2
1	G	308	GLY	3.2
1	P	500	ALA	3.2
1	O	235	TYR	3.2
1	G	447	TYR	3.2
1	J	321	ARG	3.2
2	h	20	ARG	3.2
1	O	455	THR	3.2
1	X	412	VAL	3.2
1	P	89	ASP	3.2
1	P	443	ASP	3.2
1	T	306	GLU	3.2
1	T	588	GLU	3.2
1	F	312	ASP	3.2
2	q	62	ASP	3.2
2	u	72	ASP	3.2
1	U	177	HIS	3.2
1	R	444	LEU	3.2
1	T	292	LEU	3.2
1	A	218	GLN	3.2
1	F	384	LEU	3.2
1	H	453	LEU	3.2
1	J	173	CYS	3.2
1	B	75	PRO	3.2
2	o	66	PRO	3.2
2	p	75	LEU	3.2
2	f	23	LEU	3.2
1	H	400	ALA	3.2
1	I	557	PHE	3.2
1	C	279	SER	3.2
1	K	319	VAL	3.2
1	L	434	THR	3.2
2	q	98	GLU	3.2
2	h	154	GLU	3.2
1	A	196	ASP	3.2
1	C	367	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
2	k	35	ASP	3.2
2	m	35	ASP	3.2
1	O	255	ILE	3.2
1	B	293	ILE	3.2
1	R	449	PHE	3.2
1	U	299	PRO	3.2
1	X	75	PRO	3.2
1	C	137	PRO	3.2
1	E	232	ALA	3.2
1	I	15	PHE	3.2
2	g	77	ALA	3.2
1	J	19	TRP	3.2
1	H	375	ASN	3.2
1	H	445	GLU	3.2
2	b	145	SER	3.2
1	Q	145	ARG	3.2
1	D	343	ARG	3.2
1	U	262	GLY	3.2
1	F	16	ASP	3.2
1	L	18	ASP	3.2
1	U	118	GLN	3.2
1	H	267	ALA	3.2
1	S	541	LYS	3.2
1	B	315	VAL	3.2
1	E	277	TYR	3.2
2	j	69	PHE	3.2
1	L	574	LYS	3.2
1	B	314	GLU	3.2
1	N	151	SER	3.2
1	X	26	ARG	3.2
1	J	439	ASN	3.2
1	B	200	SER	3.2
1	O	49	THR	3.2
1	J	542	THR	3.2
2	l	106	THR	3.2
1	M	400	ALA	3.2
1	M	115	VAL	3.2
1	M	132	TYR	3.2
1	R	252	LYS	3.2
1	C	86	ALA	3.2
2	p	31	GLN	3.2
1	I	313	LYS	3.2

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Mol	Chain	Res	Type	RSRZ
1	K	62	PRO	3.2
1	S	133	GLU	3.2
1	U	158	TRP	3.2
2	o	15	ARG	3.2
1	W	531	ASN	3.2
1	C	405	LEU	3.2
1	E	251	ILE	3.2
1	I	384	LEU	3.2
2	c	130	SER	3.2
1	W	30	LYS	3.2
1	C	422	THR	3.2
2	l	26	THR	3.2
1	Q	368	ASP	3.2
1	U	454	ALA	3.2
1	A	15	PHE	3.2
1	D	256	ASP	3.2
1	B	226	VAL	3.2
2	f	94	HIS	3.2
2	t	76	ARG	3.2
2	c	107	GLU	3.2
1	H	158	TRP	3.2
1	Q	573	ASN	3.2
1	B	33	LEU	3.2
1	J	74	ASN	3.2
2	p	32	SER	3.2
1	N	131	ASP	3.2
1	B	434	THR	3.2
1	I	40	GLN	3.2
1	I	93	VAL	3.2
1	J	106	THR	3.2
1	W	48	TYR	3.2
1	J	448	VAL	3.2
1	H	147	GLU	3.2
1	L	363	TYR	3.2
1	R	62	PRO	3.2
1	W	238	PRO	3.2
1	R	536	LEU	3.2
1	S	51	LEU	3.2
1	W	290	LYS	3.2
1	A	389	LEU	3.2
2	l	9	LEU	3.2
2	o	137	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	M	425	VAL	3.2
1	R	259	ALA	3.2
1	S	136	SER	3.2
1	X	27	ARG	3.2
1	K	394	ASN	3.2
2	j	99	ARG	3.2
1	U	357	ALA	3.2
1	X	226	VAL	3.2
1	F	285	ALA	3.2
2	l	23	ALA	3.2
1	S	289	ASP	3.2
1	T	101	ASP	3.2
1	C	556	TYR	3.2
1	G	48	TYR	3.2
2	h	103	ASP	3.2
2	j	14	THR	3.2
1	Q	388	PRO	3.1
1	B	395	PRO	3.1
1	V	419	GLY	3.1
1	A	124	GLY	3.1
1	I	183	GLY	3.1
2	r	70	GLY	3.1
1	R	529	GLN	3.1
1	U	494	ALA	3.1
1	F	105	ASN	3.1
1	I	406	GLU	3.1
2	o	69	GLU	3.1
2	Z	101	ALA	3.1
2	n	63	ASP	3.1
2	q	100	THR	3.1
2	v	102	LYS	3.1
1	C	593	LEU	3.1
1	E	584	PRO	3.1
1	G	81	ARG	3.1
1	H	234	ILE	3.1
2	g	136	PRO	3.1
1	T	532	ARG	3.1
1	A	103	ARG	3.1
2	i	60	GLY	3.1
1	N	218	GLN	3.1
1	I	462	GLU	3.1
2	a	121	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	N	426	ASN	3.1
1	A	279	SER	3.1
1	D	439	ASN	3.1
1	Q	539	LEU	3.1
1	R	364	ASP	3.1
1	S	26	ARG	3.1
1	T	65	ARG	3.1
1	V	256	ASP	3.1
1	B	377	THR	3.1
1	C	155	HIS	3.1
1	F	197	ASP	3.1
1	F	421	ASP	3.1
2	n	100	THR	3.1
1	M	109	ILE	3.1
1	Q	183	GLY	3.1
1	D	158	TRP	3.1
2	j	141	MET	3.1
1	V	294	ALA	3.1
1	X	133	GLU	3.1
1	P	202	GLN	3.1
2	v	68	ALA	3.1
1	X	556	TYR	3.1
1	H	517	TYR	3.1
1	F	458	ARG	3.1
1	I	10	SER	3.1
1	I	375	ASN	3.1
2	e	95	ASN	3.1
2	j	57	TYR	3.1
1	T	178	SER	3.1
1	U	51	LEU	3.1
1	U	526	SER	3.1
1	X	150	HIS	3.1
1	C	287	LEU	3.1
1	D	507	LEU	3.1
1	K	127	ARG	3.1
1	K	438	LEU	3.1
1	L	418	LEU	3.1
2	p	113	LEU	3.1
1	N	241	GLY	3.1
1	B	323	THR	3.1
1	B	325	ASP	3.1
1	C	256	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	M	15	PHE	3.1
1	I	106	THR	3.1
1	G	341	VAL	3.1
1	L	184	TRP	3.1
1	I	342	ALA	3.1
1	I	516	CYS	3.1
1	S	387	GLN	3.1
1	W	529	GLN	3.1
1	C	202	GLN	3.1
1	F	214	GLN	3.1
1	G	437	GLN	3.1
1	G	539	LEU	3.1
1	U	172	HIS	3.1
1	W	6	ASN	3.1
1	W	203	ASN	3.1
1	F	39	SER	3.1
1	J	449	PHE	3.1
2	t	91	ILE	3.1
1	O	92	ASP	3.1
1	Q	272	LYS	3.1
1	N	585	GLU	3.1
1	C	497	VAL	3.1
2	l	10	VAL	3.1
1	W	596	ALA	3.1
2	k	36	ALA	3.1
2	n	15	ARG	3.1
1	N	214	GLN	3.1
1	R	530	GLN	3.1
1	T	507	LEU	3.1
1	L	142	GLN	3.1
2	v	115	TYR	3.1
2	a	58	GLN	3.1
1	M	305	GLY	3.1
1	Q	461	GLY	3.1
1	T	535	ILE	3.1
1	U	602	GLY	3.1
2	e	151	ASN	3.1
2	h	120	LYS	3.1
1	M	237	ASP	3.1
1	R	230	GLU	3.1
1	W	88	PRO	3.1
1	B	120	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	D	423	GLU	3.1
1	F	315	VAL	3.1
1	J	310	VAL	3.1
2	f	48	ASP	3.1
1	U	402	ALA	3.1
1	G	357	ALA	3.1
2	u	82	ALA	3.1
2	a	54	ALA	3.1
1	M	583	LYS	3.1
1	O	530	GLN	3.1
1	Q	590	GLN	3.1
1	F	453	LEU	3.1
1	F	544	GLN	3.1
1	K	504	LYS	3.1
1	A	266	ILE	3.1
1	O	515	GLU	3.1
1	R	257	ASP	3.1
1	T	319	VAL	3.1
1	U	531	ASN	3.1
1	E	380	ASN	3.1
1	I	9	GLU	3.1
1	I	59	VAL	3.1
1	K	140	ASN	3.1
1	P	250	ASP	3.1
1	M	592	TRP	3.1
1	U	455	THR	3.1
1	B	49	THR	3.1
1	B	455	THR	3.1
1	C	443	ASP	3.1
1	K	586	THR	3.1
2	h	59	ASP	3.1
1	P	556	TYR	3.1
1	T	12	LEU	3.1
1	I	338	ALA	3.1
1	T	191	TYR	3.1
1	I	556	TYR	3.1
1	A	577	ILE	3.1
1	F	34	PHE	3.1
1	F	209	PHE	3.1
2	b	66	GLY	3.1
1	Q	155	HIS	3.1
1	A	24	GLU	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	172	HIS	3.1
1	A	396	GLU	3.1
2	t	73	HIS	3.1
2	e	82	HIS	3.1
1	P	367	ASP	3.1
1	T	23	ASP	3.1
1	U	215	ASP	3.1
1	V	162	SER	3.1
1	V	451	ASP	3.1
1	A	194	ASP	3.1
1	A	215	ASP	3.1
1	B	46	SER	3.1
2	Y	103	ASP	3.1
1	M	390	ALA	3.1
1	P	267	ALA	3.1
1	L	107	ALA	3.1
2	d	97	ALA	3.1
1	E	571	TYR	3.1
2	l	115	TYR	3.1
1	C	264	ILE	3.1
1	J	300	ILE	3.1
1	B	534	GLU	3.1
1	E	503	GLU	3.1
1	I	594	VAL	3.1
1	O	383	ASP	3.1
1	P	74	ASN	3.1
1	Q	32	ASP	3.1
1	U	338	ALA	3.1
1	V	18	ASP	3.1
1	W	166	ASP	3.1
1	W	381	SER	3.1
1	B	456	ALA	3.1
2	t	8	ASP	3.1
2	v	123	ALA	3.1
2	a	123	LEU	3.1
2	b	71	ASP	3.1
2	d	130	SER	3.1
2	f	135	ALA	3.1
1	Q	556	TYR	3.1
1	Q	234	ILE	3.1
1	R	34	PHE	3.1
1	B	542	THR	3.1

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Mol	Chain	Res	Type	RSRZ
1	J	434	THR	3.1
1	K	282	THR	3.1
2	l	95	TYR	3.1
1	T	291	GLN	3.1
1	C	271	ILE	3.1
1	B	462	GLU	3.1
1	H	504	LYS	3.1
1	M	94	LEU	3.1
1	M	32	ASP	3.1
1	Q	188	ALA	3.1
1	T	21	ALA	3.1
1	X	587	PRO	3.1
1	B	292	LEU	3.1
1	I	538	LEU	3.1
1	L	104	HIS	3.1
1	L	297	HIS	3.1
1	T	498	ASP	3.1
1	U	439	ASN	3.1
1	B	103	ARG	3.1
1	E	90	ALA	3.1
2	n	66	PRO	3.1
2	d	159	PRO	3.1
1	F	166	ASP	3.1
2	e	110	ALA	3.1
1	X	434	THR	3.1
1	A	202	GLN	3.1
1	A	434	THR	3.1
1	C	557	PHE	3.1
1	G	363	TYR	3.1
1	S	47	GLN	3.1
1	D	535	ILE	3.1
1	E	236	GLN	3.1
1	K	598	GLN	3.1
1	O	63	VAL	3.1
1	V	227	GLU	3.1
1	W	248	LYS	3.1
1	X	120	GLU	3.1
1	E	563	LYS	3.1
2	o	16	LYS	3.1
1	P	212	LEU	3.1
1	W	554	LEU	3.1
1	I	12	LEU	3.1

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Mol	Chain	Res	Type	RSRZ
1	J	559	LEU	3.1
1	N	385	PRO	3.0
1	I	385	PRO	3.0
2	g	157	TYR	3.0
2	h	102	PRO	3.0
1	U	89	ASP	3.0
1	U	253	ASP	3.0
1	W	545	GLY	3.0
2	t	137	GLY	3.0
2	Y	79	GLY	3.0
1	X	387	GLN	3.0
1	G	218	GLN	3.0
1	E	93	VAL	3.0
2	Y	55	GLU	3.0
2	c	73	GLU	3.0
1	A	249	ARG	3.0
1	M	86	ALA	3.0
2	o	68	ALA	3.0
1	M	318	GLY	3.0
1	Q	333	ILE	3.0
1	S	324	LYS	3.0
1	S	340	ILE	3.0
1	U	337	ASN	3.0
1	L	196	ASP	3.0
2	t	47	TRP	3.0
2	f	147	ASN	3.0
1	S	63	VAL	3.0
1	U	276	VAL	3.0
1	H	174	THR	3.0
1	I	14	ARG	3.0
1	W	29	ALA	3.0
1	B	107	ALA	3.0
2	j	111	LYS	3.0
1	M	414	GLU	3.0
1	U	217	ILE	3.0
1	W	295	GLY	3.0
1	H	5	GLU	3.0
1	H	243	PRO	3.0
2	m	48	TYR	3.0
2	s	70	GLY	3.0
1	B	589	GLU	3.0
1	J	585	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	O	196	ASP	3.0
1	O	327	GLN	3.0
1	P	561	ASP	3.0
1	A	496	VAL	3.0
1	D	60	VAL	3.0
1	E	140	ASN	3.0
1	H	77	ASP	3.0
1	L	368	ASP	3.0
2	k	86	ASN	3.0
2	Z	145	SER	3.0
1	U	551	LEU	3.0
1	J	8	LEU	3.0
2	d	115	THR	3.0
1	N	449	PHE	3.0
1	N	572	ALA	3.0
1	O	283	CYS	3.0
1	O	533	ALA	3.0
1	E	350	PHE	3.0
1	V	241	GLY	3.0
1	D	461	GLY	3.0
2	p	135	GLY	3.0
1	P	249	ARG	3.0
1	B	445	GLU	3.0
2	m	30	PRO	3.0
1	H	38	VAL	3.0
1	I	310	VAL	3.0
1	M	10	SER	3.0
1	M	89	ASP	3.0
1	B	250	ASP	3.0
1	I	525	GLN	3.0
1	F	380	ASN	3.0
1	I	178	SER	3.0
1	R	409	THR	3.0
1	M	416	ALA	3.0
1	S	263	PHE	3.0
1	S	494	ALA	3.0
1	W	247	PHE	3.0
2	s	60	PHE	3.0
2	v	24	THR	3.0
1	U	445	GLU	3.0
1	X	37	ARG	3.0
1	C	72	ARG	3.0

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Mol	Chain	Res	Type	RSRZ
1	L	277	TYR	3.0
1	L	326	GLY	3.0
1	L	534	GLU	3.0
2	m	64	GLU	3.0
1	Q	299	PRO	3.0
1	C	93	VAL	3.0
1	M	560	LEU	3.0
1	A	207	TRP	3.0
1	L	236	GLN	3.0
2	e	25	LYS	3.0
2	e	84	LEU	3.0
2	g	155	TRP	3.0
1	D	57	PHE	3.0
1	S	91	ALA	3.0
1	U	316	TYR	3.0
1	W	219	ILE	3.0
1	W	280	ILE	3.0
1	X	602	GLY	3.0
1	A	219	ILE	3.0
1	A	534	GLU	3.0
2	o	115	TYR	3.0
2	f	64	ILE	3.0
2	g	63	ILE	3.0
1	N	520	VAL	3.0
1	P	587	PRO	3.0
2	f	46	VAL	3.0
2	f	61	LYS	3.0
1	L	47	GLN	3.0
2	f	102	PRO	3.0
2	j	122	LEU	3.0
1	N	61	ARG	3.0
1	R	367	ASP	3.0
2	k	33	MET	3.0
1	K	269	ARG	3.0
2	i	59	ASP	3.0
1	O	426	ASN	3.0
1	L	6	ASN	3.0
1	Q	406	GLU	3.0
1	F	358	GLY	3.0
2	b	100	ILE	3.0
2	f	137	TYR	3.0
2	i	21	ALA	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	244	VAL	3.0
1	L	552	LEU	3.0
2	a	23	LEU	3.0
2	l	89	CYS	3.0
1	P	495	GLU	3.0
1	R	408	ALA	3.0
1	V	311	GLU	3.0
1	X	439	ASN	3.0
1	S	549	TYR	3.0
1	H	403	TYR	3.0
1	K	189	GLU	3.0
2	Y	97	ALA	3.0
2	s	100	THR	3.0
1	X	418	LEU	3.0
1	I	560	LEU	3.0
1	M	449	PHE	3.0
1	N	236	GLN	3.0
1	N	327	GLN	3.0
1	E	530	GLN	3.0
1	A	184	TRP	3.0
1	K	108	LYS	3.0
2	m	47	TRP	3.0
1	N	433	ASP	3.0
1	O	305	GLY	3.0
1	A	9	GLU	3.0
1	C	227	GLU	3.0
1	D	227	GLU	3.0
1	G	189	GLU	3.0
2	v	45	ALA	3.0
2	b	146	GLY	3.0
1	F	391	TYR	3.0
1	H	381	SER	3.0
1	L	36	SER	3.0
2	Z	90	SER	3.0
2	j	135	ALA	3.0
1	C	303	VAL	3.0
1	C	439	ASN	3.0
1	K	274	ARG	3.0
1	N	34	PHE	3.0
1	A	229	LYS	3.0
1	C	600	LYS	3.0
2	m	124	LYS	3.0

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Mol	Chain	Res	Type	RSRZ
1	U	124	GLY	3.0
1	U	589	GLU	3.0
1	H	318	GLY	3.0
1	J	317	GLU	3.0
2	s	57	GLY	3.0
1	O	510	ILE	3.0
1	V	494	ALA	3.0
1	C	253	ASP	3.0
1	F	101	ASP	3.0
2	d	88	ALA	3.0
2	i	32	ALA	3.0
1	Q	389	LEU	3.0
1	T	593	LEU	3.0
1	Q	201	PHE	3.0
1	R	50	THR	3.0
1	J	417	THR	3.0
1	I	52	GLN	3.0
2	l	147	HIS	3.0
2	r	60	PHE	3.0
1	U	584	PRO	3.0
2	d	42	MET	3.0
1	Q	18	ASP	3.0
1	S	513	ARG	3.0
1	X	271	ILE	3.0
2	b	63	ILE	3.0
1	R	12	LEU	3.0
1	B	89	ASP	3.0
1	D	257	ASP	3.0
1	E	256	ASP	3.0
1	K	164	LEU	3.0
1	I	105	ASN	3.0
2	u	138	ASN	3.0
2	d	86	SER	3.0
2	d	145	SER	3.0
1	O	589	GLU	3.0
1	R	461	GLY	2.9
1	D	445	GLU	3.0
1	E	427	GLY	2.9
1	M	572	ALA	2.9
1	T	14	ARG	2.9
1	X	65	ARG	2.9
1	Q	38	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	506	VAL	2.9
1	L	19	TRP	2.9
1	K	191	TYR	2.9
2	l	13	ALA	2.9
2	o	88	ALA	2.9
2	q	23	ALA	2.9
2	e	128	ALA	2.9
2	g	15	LYS	2.9
2	g	137	TYR	2.9
2	i	116	ALA	2.9
1	D	538	LEU	2.9
1	S	570	ASP	2.9
1	N	117	GLU	2.9
1	O	598	GLN	2.9
1	P	282	THR	2.9
1	W	224	GLU	2.9
1	A	75	PRO	2.9
1	A	376	ARG	2.9
1	B	273	ARG	2.9
1	D	387	GLN	2.9
1	F	104	HIS	2.9
1	G	106	THR	2.9
1	H	117	GLU	2.9
1	J	525	GLN	2.9
2	p	117	GLN	2.9
2	u	15	ARG	2.9
2	Z	140	ARG	2.9
2	c	156	HIS	2.9
2	d	143	THR	2.9
1	S	11	ILE	2.9
1	G	371	TYR	2.9
1	I	163	LYS	2.9
2	m	148	TYR	2.9
2	b	29	ALA	2.9
2	e	49	LEU	2.9
1	N	263	PHE	2.9
1	B	312	ASP	2.9
1	I	32	ASP	2.9
1	M	399	GLN	2.9
1	S	181	GLN	2.9
1	S	202	GLN	2.9
1	T	445	GLU	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	160	SER	2.9
1	K	575	GLN	2.9
2	a	30	SER	2.9
2	b	70	SER	2.9
2	h	30	SER	2.9
1	R	231	THR	2.9
1	K	340	ILE	2.9
2	v	133	PRO	2.9
2	g	82	HIS	2.9
1	R	277	TYR	2.9
1	W	8	LEU	2.9
1	W	506	VAL	2.9
1	W	539	LEU	2.9
1	B	175	VAL	2.9
1	F	184	TRP	2.9
1	H	45	LEU	2.9
1	H	94	LEU	2.9
2	r	96	ALA	2.9
2	a	116	ALA	2.9
2	h	54	ALA	2.9
1	U	257	ASP	2.9
1	X	367	ASP	2.9
1	I	513	ARG	2.9
1	K	459	ARG	2.9
2	o	94	ASP	2.9
1	W	5	GLU	2.9
1	G	5	GLU	2.9
1	H	104	HIS	2.9
1	H	105	ASN	2.9
2	Z	60	GLY	2.9
2	e	43	GLN	2.9
2	f	95	ASN	2.9
1	P	216	THR	2.9
1	A	385	PRO	2.9
1	D	213	THR	2.9
1	D	238	PRO	2.9
1	E	276	VAL	2.9
1	J	174	THR	2.9
1	L	220	ALA	2.9
2	t	14	LEU	2.9
2	a	138	PRO	2.9
1	W	549	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
1	C	246	TYR	2.9
1	B	147	GLU	2.9
1	C	541	LYS	2.9
1	D	541	LYS	2.9
1	E	28	GLU	2.9
1	I	89	ASP	2.9
1	L	570	ASP	2.9
2	v	46	GLU	2.9
2	a	61	LYS	2.9
1	S	55	GLY	2.9
1	N	217	ILE	2.9
1	P	13	SER	2.9
1	U	280	ILE	2.9
1	W	291	GLN	2.9
1	E	355	GLN	2.9
1	I	448	VAL	2.9
1	K	337	ASN	2.9
1	L	264	ILE	2.9
2	Y	40	GLN	2.9
1	B	63	VAL	2.9
2	k	45	ALA	2.9
2	b	147	ASN	2.9
2	e	18	LEU	2.9
1	L	395	PRO	2.9
1	N	130	THR	2.9
2	i	57	TYR	2.9
1	M	19	TRP	2.9
1	U	423	GLU	2.9
1	A	296	GLU	2.9
1	P	194	ASP	2.9
1	E	580	GLY	2.9
1	F	196	ASP	2.9
1	H	250	ASP	2.9
1	H	305	GLY	2.9
2	k	135	GLY	2.9
2	p	74	GLY	2.9
2	b	53	MET	2.9
1	E	581	VAL	2.9
1	F	219	ILE	2.9
1	K	12	LEU	2.9
2	o	87	LEU	2.9
2	h	122	LEU	2.9

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Mol	Chain	Res	Type	RSRZ
1	M	259	ALA	2.9
1	O	155	HIS	2.9
1	P	170	ALA	2.9
1	P	390	ALA	2.9
1	V	110	ALA	2.9
1	X	407	ALA	2.9
1	A	543	PRO	2.9
1	C	7	ARG	2.9
1	F	353	PRO	2.9
1	I	53	TYR	2.9
1	K	112	ASN	2.9
1	K	139	SER	2.9
2	p	126	ALA	2.9
2	r	73	HIS	2.9
2	s	42	ALA	2.9
2	j	116	ALA	2.9
1	R	35	PHE	2.9
1	U	557	PHE	2.9
1	R	49	THR	2.9
2	v	118	THR	2.9
1	J	306	GLU	2.9
1	M	217	ILE	2.9
1	M	397	VAL	2.9
1	O	202	GLN	2.9
1	T	412	VAL	2.9
1	C	63	VAL	2.9
1	E	169	ASP	2.9
1	E	555	GLN	2.9
1	G	325	ASP	2.9
1	L	601	GLN	2.9
2	r	22	ASP	2.9
2	c	43	GLN	2.9
2	d	26	LEU	2.9
1	Q	504	LYS	2.9
1	U	46	SER	2.9
1	U	361	HIS	2.9
1	B	363	TYR	2.9
1	G	336	PHE	2.9
1	H	247	PHE	2.9
2	m	116	LYS	2.9
2	s	23	ALA	2.9
2	v	119	ALA	2.9

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Mol	Chain	Res	Type	RSRZ
2	b	108	ALA	2.9
1	F	375	ASN	2.9
1	I	200	SER	2.9
2	r	93	PRO	2.9
2	i	147	ASN	2.9
1	S	588	GLU	2.9
1	U	49	THR	2.9
1	A	174	THR	2.9
1	D	49	THR	2.9
1	J	446	THR	2.9
2	u	98	GLU	2.9
2	d	55	GLU	2.9
1	L	382	GLY	2.9
2	m	18	GLY	2.9
1	W	319	VAL	2.9
1	D	569	ARG	2.9
1	G	111	VAL	2.9
1	H	113	ILE	2.9
1	J	293	ILE	2.9
1	K	430	VAL	2.9
2	s	103	ILE	2.9
2	Z	64	ILE	2.9
2	j	85	ARG	2.9
1	R	218	GLN	2.9
1	U	289	ASP	2.9
1	X	247	PHE	2.9
1	A	232	ALA	2.9
1	L	338	ALA	2.9
2	k	20	ALA	2.9
2	v	22	ASP	2.9
1	Q	200	SER	2.9
1	E	155	HIS	2.9
1	U	205	ASN	2.9
1	B	74	ASN	2.9
1	G	534	GLU	2.9
1	H	185	GLU	2.9
1	J	31	ASN	2.9
2	k	130	SER	2.9
2	a	95	ASN	2.9
1	W	330	ARG	2.9
1	C	545	GLY	2.9
1	H	284	THR	2.9

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Mol	Chain	Res	Type	RSRZ
2	m	137	GLY	2.9
2	s	18	GLY	2.9
2	u	74	GLY	2.9
2	Z	24	ARG	2.9
2	Z	143	THR	2.9
2	Z	146	GLY	2.9
1	O	93	VAL	2.9
1	A	315	VAL	2.9
1	A	507	LEU	2.9
1	F	167	LYS	2.9
1	G	559	LEU	2.9
1	N	201	PHE	2.9
1	H	291	GLN	2.9
1	J	400	ALA	2.9
1	K	170	ALA	2.9
1	K	201	PHE	2.9
1	A	277	TYR	2.9
1	K	443	ASP	2.9
2	r	35	ASP	2.9
2	r	92	ALA	2.9
1	F	406	GLU	2.9
2	p	21	SER	2.9
2	s	133	PRO	2.9
1	Q	182	ASN	2.9
1	S	190	LYS	2.9
1	F	140	ASN	2.9
1	P	208	VAL	2.9
1	T	446	THR	2.9
1	U	520	VAL	2.9
1	A	520	VAL	2.9
1	E	130	THR	2.9
1	F	251	ILE	2.9
1	G	409	THR	2.9
1	G	581	VAL	2.9
1	I	377	THR	2.9
1	J	496	VAL	2.9
2	o	37	VAL	2.9
2	s	25	LEU	2.9
1	R	236	GLN	2.9
1	N	561	ASP	2.9
1	P	132	TYR	2.9
1	W	571	TYR	2.9

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Mol	Chain	Res	Type	RSRZ
2	i	114	ALA	2.9
1	P	296	GLU	2.9
1	E	585	GLU	2.9
2	s	63	ASP	2.9
1	R	75	PRO	2.9
1	S	348	LYS	2.9
2	t	52	LYS	2.9
2	h	79	GLY	2.9
1	W	173	CYS	2.9
1	L	244	VAL	2.9
2	s	19	VAL	2.9
1	M	138	THR	2.9
1	S	350	PHE	2.9
1	U	422	THR	2.9
2	o	106	THR	2.9
1	S	437	GLN	2.9
1	B	56	GLN	2.9
1	M	246	TYR	2.9
1	S	532	ARG	2.9
1	W	246	TYR	2.9
1	I	588	GLU	2.9
1	L	571	TYR	2.9
2	q	41	GLU	2.9
1	M	600	LYS	2.9
1	W	228	LYS	2.9
1	J	324	LYS	2.9
1	S	155	HIS	2.9
1	B	62	PRO	2.9
1	K	299	PRO	2.9
2	a	62	GLY	2.9
2	j	39	PRO	2.9
1	U	401	ASN	2.8
1	A	526	SER	2.8
1	L	526	SER	2.8
2	q	65	ASN	2.8
2	j	139	SER	2.8
1	N	417	THR	2.8
1	N	542	THR	2.8
1	V	152	ALA	2.8
1	V	459	ARG	2.8
1	V	544	GLN	2.8
1	A	195	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	416	ALA	2.8
1	E	26	ARG	2.8
1	G	100	THR	2.8
1	H	516	CYS	2.8
1	J	21	ALA	2.8
1	J	52	GLN	2.8
1	P	368	ASP	2.8
1	X	192	ASP	2.8
1	R	384	LEU	2.8
1	N	115	VAL	2.8
1	S	388	PRO	2.8
1	S	395	PRO	2.8
1	G	594	VAL	2.8
1	L	370	PRO	2.8
1	M	41	TRP	2.8
1	Q	269	ARG	2.8
1	U	261	SER	2.8
2	m	43	MET	2.8
2	v	149	PHE	2.8
1	G	30	LYS	2.8
2	m	138	ASN	2.8
2	j	74	ASN	2.8
1	R	534	GLU	2.8
1	T	596	ALA	2.8
1	C	90	ALA	2.8
2	h	91	ALA	2.8
1	R	173	CYS	2.8
1	M	196	ASP	2.8
1	O	192	ASP	2.8
1	G	33	LEU	2.8
1	G	551	LEU	2.8
2	g	72	ASP	2.8
1	E	557	PHE	2.8
2	u	104	ILE	2.8
2	Y	113	ILE	2.8
2	h	141	MET	2.8
1	Q	220	ALA	2.8
1	X	245	SER	2.8
1	A	160	SER	2.8
1	E	596	ALA	2.8
1	G	595	GLU	2.8
1	L	279	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	571	TYR	2.8
1	L	218	GLN	2.8
2	t	46	GLU	2.8
1	P	417	THR	2.8
1	U	138	THR	2.8
1	A	453	LEU	2.8
1	C	67	LEU	2.8
1	L	33	LEU	2.8
1	L	258	LEU	2.8
2	s	75	LEU	2.8
1	M	516	CYS	2.8
1	P	248	LYS	2.8
1	D	532	ARG	2.8
1	F	368	ASP	2.8
1	I	175	VAL	2.8
1	W	361	HIS	2.8
1	A	351	PHE	2.8
1	F	199	PRO	2.8
1	G	385	PRO	2.8
1	J	228	LYS	2.8
1	L	433	ASP	2.8
2	i	76	PRO	2.8
1	S	589	GLU	2.8
1	T	372	TYR	2.8
1	U	400	ALA	2.8
1	U	495	GLU	2.8
1	N	523	SER	2.8
2	o	32	SER	2.8
2	Y	155	TRP	2.8
1	C	437	GLN	2.8
1	F	369	TYR	2.8
1	I	142	GLN	2.8
2	h	57	TYR	2.8
1	S	8	LEU	2.8
1	S	269	ARG	2.8
1	W	422	THR	2.8
1	X	507	LEU	2.8
1	T	496	VAL	2.8
1	U	324	LYS	2.8
1	C	344	THR	2.8
1	K	417	THR	2.8
1	C	535	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
1	F	208	VAL	2.8
2	p	83	VAL	2.8
2	e	100	ILE	2.8
1	M	433	ASP	2.8
1	N	368	ASP	2.8
1	S	173	CYS	2.8
1	E	42	ASP	2.8
1	F	370	PRO	2.8
1	L	361	HIS	2.8
2	l	43	MET	2.8
2	r	69	GLU	2.8
1	M	389	LEU	2.8
1	O	381	SER	2.8
1	U	202	GLN	2.8
2	k	31	GLN	2.8
2	p	115	TYR	2.8
2	Y	124	TYR	2.8
2	c	157	TYR	2.8
1	P	508	ASN	2.8
1	A	87	ARG	2.8
1	D	12	LEU	2.8
1	F	295	GLY	2.8
2	v	122	ARG	2.8
2	i	70	SER	2.8
2	i	86	SER	2.8
1	X	377	THR	2.8
2	j	149	PHE	2.8
1	P	460	ASP	2.8
1	S	77	ASP	2.8
1	T	503	GLU	2.8
2	l	67	PRO	2.8
2	d	102	PRO	2.8
1	B	25	ALA	2.8
1	U	593	LEU	2.8
1	V	262	GLY	2.8
1	X	288	LYS	2.8
1	A	429	GLN	2.8
1	C	459	ARG	2.8
1	D	246	TYR	2.8
1	F	236	GLN	2.8
1	G	122	GLY	2.8
1	H	575	GLN	2.8

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Mol	Chain	Res	Type	RSRZ
2	n	124	LYS	2.8
2	r	58	TYR	2.8
2	f	99	ARG	2.8
1	P	419	GLY	2.8
1	J	539	LEU	2.8
1	X	335	SER	2.8
2	Y	83	GLY	2.8
1	N	105	ASN	2.8
1	D	203	ASN	2.8
1	T	546	THR	2.8
1	R	445	GLU	2.8
1	Q	23	ASP	2.8
1	J	33	LEU	2.8
1	J	86	ALA	2.8
1	J	171	ARG	2.8
1	N	384	LEU	2.8
1	L	556	TYR	2.8
1	S	602	GLY	2.8
1	N	60	VAL	2.8
1	U	175	VAL	2.8
1	A	516	CYS	2.8
2	e	40	GLN	2.8
1	D	151	SER	2.8
1	E	136	SER	2.8
1	H	222	PHE	2.8
1	L	168	SER	2.8
2	r	54	ILE	2.8
2	g	130	SER	2.8
1	Q	323	THR	2.8
1	V	28	GLU	2.8
1	W	216	THR	2.8
1	X	138	THR	2.8
1	A	566	GLU	2.8
1	I	100	THR	2.8
2	j	53	MET	2.8
1	E	30	LYS	2.8
2	d	111	LYS	2.8
1	N	549	TYR	2.8
1	Q	172	HIS	2.8
1	V	188	ALA	2.8
1	X	299	PRO	2.8
1	V	191	TYR	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	159	ASP	2.8
1	J	349	PRO	2.8
2	m	147	HIS	2.8
2	Z	91	ALA	2.8
1	N	525	GLN	2.8
1	R	327	GLN	2.8
1	E	505	GLN	2.8
1	I	293	ILE	2.8
2	i	63	ILE	2.8
1	S	46	SER	2.8
1	U	31	ASN	2.8
1	C	423	GLU	2.8
1	E	269	ARG	2.8
1	K	22	SER	2.8
1	E	426	ASN	2.8
2	t	6	LYS	2.8
2	j	15	LYS	2.8
1	N	20	THR	2.8
1	N	409	THR	2.8
1	S	377	THR	2.8
1	E	213	THR	2.8
2	s	106	THR	2.8
1	M	85	GLY	2.8
1	R	42	ASP	2.8
1	V	16	ASP	2.8
1	A	191	TYR	2.8
1	C	195	ALA	2.8
1	E	289	ASP	2.8
1	H	58	ASP	2.8
1	H	152	ALA	2.8
1	K	86	ALA	2.8
2	u	73	HIS	2.8
2	g	29	ALA	2.8
1	B	336	PHE	2.8
2	c	63	ILE	2.8
2	d	69	PHE	2.8
1	N	589	GLU	2.8
1	N	600	LYS	2.8
1	Q	87	ARG	2.8
1	F	163	LYS	2.8
2	d	52	MET	2.8
2	i	38	GLU	2.8

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Mol	Chain	Res	Type	RSRZ
2	Y	74	ASN	2.8
2	d	98	CYS	2.8
1	V	564	GLY	2.8
1	A	138	THR	2.8
2	a	127	THR	2.8
2	d	49	LEU	2.8
1	D	48	TYR	2.8
1	V	35	PHE	2.8
1	W	57	PHE	2.8
1	X	237	ASP	2.8
1	D	199	PRO	2.8
1	G	388	PRO	2.8
1	K	349	PRO	2.8
1	G	598	GLN	2.8
2	m	83	VAL	2.8
2	q	22	ASP	2.8
2	s	84	PHE	2.8
1	U	293	ILE	2.8
1	U	120	GLU	2.8
1	M	453	LEU	2.8
1	C	136	SER	2.8
1	H	180	SER	2.8
1	T	25	ALA	2.8
1	C	138	THR	2.8
1	C	372	TYR	2.8
1	D	382	GLY	2.8
1	D	533	ALA	2.8
1	L	105	ASN	2.8
2	q	89	CYS	2.8
1	N	108	LYS	2.8
1	O	388	PRO	2.8
1	T	388	PRO	2.8
1	V	50	THR	2.8
1	P	16	ASP	2.8
1	W	415	VAL	2.8
1	H	543	PRO	2.8
2	Z	76	PRO	2.8
1	R	142	GLN	2.7
1	S	52	GLN	2.7
1	C	399	GLN	2.7
2	q	31	GLN	2.7
1	F	33	LEU	2.7

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Mol	Chain	Res	Type	RSRZ
1	X	500	ALA	2.7
1	B	54	ARG	2.7
1	F	107	ALA	2.7
1	F	413	LYS	2.7
1	H	376	ARG	2.7
1	I	125	ALA	2.7
1	F	415	VAL	2.7
1	I	403	TYR	2.7
2	l	110	GLY	2.7
2	Y	15	LYS	2.7
2	b	45	ALA	2.7
1	T	341	VAL	2.7
1	D	341	VAL	2.7
1	A	104	HIS	2.7
1	D	446	THR	2.7
1	G	20	THR	2.7
1	H	398	PRO	2.7
1	K	238	PRO	2.7
2	t	56	THR	2.7
2	u	26	THR	2.7
2	d	142	PRO	2.7
1	Q	268	GLU	2.7
1	J	509	ASP	2.7
1	L	181	GLN	2.7
2	f	141	MET	2.7
1	U	8	LEU	2.7
1	V	164	LEU	2.7
1	C	569	ARG	2.7
2	q	87	LEU	2.7
1	O	259	ALA	2.7
1	V	382	GLY	2.7
1	C	402	ALA	2.7
1	H	107	ALA	2.7
1	L	154	SER	2.7
1	L	201	PHE	2.7
2	g	62	GLY	2.7
2	j	22	ALA	2.7
1	M	537	GLU	2.7
1	N	558	THR	2.7
1	A	595	GLU	2.7
1	G	133	GLU	2.7
1	H	588	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	J	157	ILE	2.7
1	J	242	GLU	2.7
1	J	282	THR	2.7
2	l	47	TRP	2.7
1	N	539	LEU	2.7
1	P	459	ARG	2.7
1	R	212	LEU	2.7
1	B	87	ARG	2.7
1	E	539	LEU	2.7
1	Q	21	ALA	2.7
1	T	545	GLY	2.7
1	X	111	VAL	2.7
1	B	239	VAL	2.7
1	B	277	TYR	2.7
1	B	571	TYR	2.7
1	H	29	ALA	2.7
1	H	357	ALA	2.7
1	I	408	ALA	2.7
1	J	222	PHE	2.7
1	L	497	VAL	2.7
2	l	80	VAL	2.7
2	h	32	ALA	2.7
1	R	335	SER	2.7
1	D	217	ILE	2.7
2	n	41	GLU	2.7
2	n	104	ILE	2.7
2	i	148	SER	2.7
1	R	578	GLN	2.7
1	D	210	PRO	2.7
1	F	361	HIS	2.7
1	I	112	ASN	2.7
1	N	116	ARG	2.7
1	S	519	ASP	2.7
1	S	551	LEU	2.7
1	T	134	ASP	2.7
1	T	539	LEU	2.7
1	X	458	ARG	2.7
1	C	159	ASP	2.7
2	m	9	LEU	2.7
2	t	35	ASP	2.7
2	g	122	LEU	2.7
1	W	540	GLY	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	25	ALA	2.7
1	C	580	GLY	2.7
1	H	407	ALA	2.7
1	L	562	GLY	2.7
2	u	83	VAL	2.7
1	P	279	SER	2.7
1	R	178	SER	2.7
1	S	13	SER	2.7
1	V	69	SER	2.7
1	A	136	SER	2.7
1	C	515	GLU	2.7
1	U	181	GLN	2.7
1	G	278	LYS	2.7
1	A	177	HIS	2.7
1	I	539	LEU	2.7
1	B	19	TRP	2.7
1	L	451	ASP	2.7
2	l	27	ASP	2.7
1	C	500	ALA	2.7
1	Q	221	GLU	2.7
1	Q	423	GLU	2.7
1	J	251	ILE	2.7
1	J	280	ILE	2.7
1	L	9	GLU	2.7
1	W	327	GLN	2.7
1	W	370	PRO	2.7
1	M	375	ASN	2.7
1	I	215	ASP	2.7
1	W	163	LYS	2.7
1	H	116	ARG	2.7
1	H	255	ILE	2.7
1	H	274	ARG	2.7
1	J	294	ALA	2.7
2	g	108	ALA	2.7
1	C	173	CYS	2.7
1	E	181	GLN	2.7
1	G	155	HIS	2.7
1	I	335	SER	2.7
2	l	139	SER	2.7
2	q	66	PRO	2.7
1	W	366	ASN	2.7
1	D	290	LYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	305	GLY	2.7
1	F	394	ASN	2.7
1	G	564	GLY	2.7
1	H	426	ASN	2.7
1	I	401	ASN	2.7
1	K	263	PHE	2.7
1	V	383	ASP	2.7
1	E	197	ASP	2.7
1	F	383	ASP	2.7
1	G	515	GLU	2.7
1	H	314	GLU	2.7
1	H	542	THR	2.7
1	I	319	VAL	2.7
1	I	456	ALA	2.7
2	k	37	VAL	2.7
2	c	47	ASP	2.7
1	P	281	ILE	2.7
1	U	548	GLU	2.7
1	W	588	GLU	2.7
1	B	379	GLU	2.7
1	K	70	GLU	2.7
2	g	127	THR	2.7
2	e	113	ILE	2.7
1	S	270	GLN	2.7
1	P	228	LYS	2.7
1	A	39	SER	2.7
1	B	173	CYS	2.7
1	B	122	GLY	2.7
1	J	512	GLY	2.7
2	l	61	SER	2.7
2	s	21	SER	2.7
1	M	77	ASP	2.7
1	N	25	ALA	2.7
1	X	296	GLU	2.7
1	B	6	ASN	2.7
1	D	366	ASN	2.7
1	I	19	TRP	2.7
1	J	408	ALA	2.7
1	J	508	ASN	2.7
1	O	549	TYR	2.7
1	P	174	THR	2.7
1	K	224	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	E	266	ILE	2.7
2	e	132	ALA	2.7
2	f	33	THR	2.7
2	i	80	ASP	2.7
1	J	453	LEU	2.7
2	k	17	LEU	2.7
2	k	97	LEU	2.7
2	d	23	LEU	2.7
1	O	555	GLN	2.7
1	T	504	LYS	2.7
1	V	557	PHE	2.7
1	A	413	LYS	2.7
1	D	291	GLN	2.7
1	G	582	LYS	2.7
1	J	73	GLN	2.7
1	Q	602	GLY	2.7
1	E	177	HIS	2.7
1	M	407	ALA	2.7
1	R	242	GLU	2.7
1	G	46	SER	2.7
1	J	39	SER	2.7
1	A	408	ALA	2.7
1	V	169	ASP	2.7
1	B	592	TRP	2.7
1	K	360	GLU	2.7
2	c	91	ALA	2.7
1	I	134	ASP	2.7
2	j	113	ILE	2.7
1	O	324	LYS	2.7
1	P	374	LEU	2.7
1	V	167	LYS	2.7
1	B	389	LEU	2.7
1	C	536	LEU	2.7
1	R	590	GLN	2.7
1	X	327	GLN	2.7
1	I	449	PHE	2.7
1	J	382	GLY	2.7
1	J	427	GLY	2.7
1	F	296	GLU	2.7
2	g	138	PRO	2.7
1	N	39	SER	2.7
1	R	442	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	X	86	ALA	2.7
1	A	69	SER	2.7
1	A	335	SER	2.7
2	o	21	SER	2.7
2	t	85	HIS	2.7
1	M	229	LYS	2.7
1	O	337	ASN	2.7
1	P	112	ASN	2.7
1	X	190	LYS	2.7
1	X	283	CYS	2.7
1	E	549	TYR	2.7
1	J	577	ILE	2.7
1	O	586	THR	2.7
1	Q	58	ASP	2.7
1	Q	237	ASP	2.7
1	A	582	LYS	2.7
1	D	216	THR	2.7
1	D	389	LEU	2.7
1	K	446	THR	2.7
2	c	23	LEU	2.7
2	e	115	THR	2.7
1	H	218	GLN	2.7
1	L	35	PHE	2.7
1	S	495	GLU	2.7
1	J	497	VAL	2.7
2	k	69	GLU	2.7
2	b	107	GLU	2.7
1	P	599	ALA	2.7
1	N	258	LEU	2.6
1	N	551	LEU	2.6
1	P	12	LEU	2.6
1	Q	178	SER	2.6
1	S	264	ILE	2.7
1	C	348	LYS	2.6
1	F	21	ALA	2.7
1	K	83	LYS	2.6
2	o	12	ALA	2.7
2	a	118	TYR	2.6
2	g	112	ILE	2.7
2	h	94	HIS	2.7
1	L	79	LEU	2.6
2	v	146	TRP	2.6

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Mol	Chain	Res	Type	RSRZ
1	X	519	ASP	2.6
1	H	166	ASP	2.6
1	J	215	ASP	2.6
1	U	231	THR	2.6
1	P	38	VAL	2.6
1	T	9	GLU	2.6
1	B	303	VAL	2.6
1	E	270	GLN	2.6
1	G	202	GLN	2.6
1	I	589	GLU	2.6
1	Q	324	LYS	2.6
1	J	62	PRO	2.6
2	p	93	PRO	2.6
2	g	25	LYS	2.6
2	i	125	LYS	2.6
1	S	458	ARG	2.6
1	V	103	ARG	2.6
1	X	107	ALA	2.6
2	v	95	TYR	2.6
2	j	32	ALA	2.6
1	T	258	LEU	2.6
1	A	523	SER	2.6
1	I	554	LEU	2.6
1	L	69	SER	2.6
2	e	148	SER	2.6
1	M	141	ASN	2.6
1	C	383	ASP	2.6
1	G	443	ASP	2.6
1	I	439	ASN	2.6
2	Y	149	PHE	2.6
1	O	602	GLY	2.6
1	W	580	GLY	2.6
2	v	53	GLY	2.6
2	a	38	GLU	2.6
2	c	109	THR	2.6
1	I	229	LYS	2.6
1	X	81	ARG	2.6
1	A	125	ALA	2.6
1	A	285	ALA	2.6
1	A	418	LEU	2.6
1	C	243	PRO	2.6
2	u	133	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
2	c	140	ARG	2.6
2	b	26	LEU	2.6
2	h	116	ALA	2.6
1	X	592	TRP	2.6
1	A	557	PHE	2.6
1	C	178	SER	2.6
1	J	178	SER	2.6
1	S	291	GLN	2.6
1	U	244	VAL	2.6
1	V	433	ASP	2.6
1	E	529	GLN	2.6
1	I	216	THR	2.6
1	I	445	GLU	2.6
1	L	425	VAL	2.6
2	s	80	VAL	2.6
2	b	36	ASP	2.6
1	P	434	THR	2.6
1	W	106	THR	2.6
1	J	47	GLN	2.6
1	J	532	ARG	2.6
2	d	126	GLN	2.6
1	S	235	TYR	2.6
1	E	198	ILE	2.6
1	F	416	ALA	2.6
1	H	395	PRO	2.6
1	J	556	TYR	2.6
2	r	66	PRO	2.6
2	r	107	ALA	2.6
1	N	336	PHE	2.6
1	N	69	SER	2.6
1	W	592	TRP	2.6
1	W	249	ARG	2.6
1	B	602	GLY	2.6
2	t	121	SER	2.6
1	Q	383	ASP	2.6
1	U	250	ASP	2.6
1	W	325	ASP	2.6
1	D	77	ASP	2.6
1	K	26	ARG	2.6
1	I	218	GLN	2.6
1	J	433	ASP	2.6
2	r	29	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
2	t	43	MET	2.6
2	b	80	ASP	2.6
1	N	251	ILE	2.6
1	I	195	ALA	2.6
1	J	76	ILE	2.6
2	m	106	THR	2.6
2	a	14	THR	2.6
1	X	599	ALA	2.6
1	R	370	PRO	2.6
1	E	229	LYS	2.6
1	H	528	LYS	2.6
2	s	6	LYS	2.6
2	i	94	HIS	2.6
1	N	305	GLY	2.6
1	Q	227	GLU	2.6
1	W	565	VAL	2.6
1	D	406	GLU	2.6
2	l	70	GLY	2.6
2	v	131	ARG	2.6
2	Y	46	VAL	2.6
2	j	41	SER	2.6
1	N	499	LEU	2.6
1	P	140	ASN	2.6
1	T	206	ASP	2.6
1	P	264	ILE	2.6
1	W	337	ASN	2.6
1	G	530	GLN	2.6
1	L	443	ASP	2.6
2	m	65	ASN	2.6
2	h	95	ASN	2.6
1	U	372	TYR	2.6
1	W	449	PHE	2.6
1	A	108	LYS	2.6
1	G	246	TYR	2.6
1	G	572	ALA	2.6
2	i	51	ALA	2.6
2	i	115	THR	2.6
1	C	82	PRO	2.6
1	D	388	PRO	2.6
2	l	30	PRO	2.6
2	u	84	PHE	2.6
2	i	133	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	540	GLY	2.6
1	F	516	CYS	2.6
1	G	360	GLU	2.6
1	K	585	GLU	2.6
1	A	22	SER	2.6
2	i	53	MET	2.6
1	M	193	LEU	2.6
1	R	83	LYS	2.6
1	A	260	ASP	2.6
1	B	113	ILE	2.6
1	D	463	ILE	2.6
1	J	383	ASP	2.6
2	p	40	LEU	2.6
2	t	87	LEU	2.6
2	p	123	ALA	2.6
2	q	86	ASN	2.6
2	u	119	ALA	2.6
1	U	26	ARG	2.6
1	G	518	THR	2.6
2	c	149	PHE	2.6
1	B	370	PRO	2.6
1	F	299	PRO	2.6
1	X	63	VAL	2.6
2	o	46	GLU	2.6
2	j	89	VAL	2.6
2	q	146	TRP	2.6
1	S	504	LYS	2.6
1	S	528	LYS	2.6
2	b	130	SER	2.6
1	R	92	ASP	2.6
1	E	23	ASP	2.6
1	J	17	ALA	2.6
1	O	129	VAL	2.6
1	D	295	GLY	2.6
1	D	545	GLY	2.6
1	H	435	VAL	2.6
1	L	59	VAL	2.6
2	c	94	HIS	2.6
1	N	389	LEU	2.6
1	O	236	GLN	2.6
1	V	202	GLN	2.6
1	D	298	ILE	2.6

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Mol	Chain	Res	Type	RSRZ
1	E	81	ARG	2.6
1	G	591	GLN	2.6
1	J	218	GLN	2.6
2	Z	85	ARG	2.6
2	j	40	GLN	2.6
1	O	335	SER	2.6
1	S	257	ASP	2.6
1	X	364	ASP	2.6
1	E	335	SER	2.6
1	K	556	TYR	2.6
2	n	71	ASP	2.6
2	u	8	ASP	2.6
2	f	132	ALA	2.6
1	S	585	GLU	2.6
1	P	138	THR	2.6
1	U	497	VAL	2.6
1	W	406	GLU	2.6
1	A	445	GLU	2.6
1	E	138	THR	2.6
1	E	239	VAL	2.6
1	F	30	LYS	2.6
1	F	108	LYS	2.6
1	F	397	VAL	2.6
1	I	124	GLY	2.6
2	c	65	THR	2.6
1	P	418	LEU	2.6
1	U	87	ARG	2.6
1	C	269	ARG	2.6
1	D	171	ARG	2.6
1	H	128	LEU	2.6
2	a	63	ILE	2.6
1	T	387	GLN	2.6
1	L	578	GLN	2.6
2	b	40	GLN	2.6
1	S	313	LYS	2.6
1	U	166	ASP	2.6
1	W	43	ASP	2.6
1	N	112	ASN	2.6
1	N	565	VAL	2.6
1	R	366	ASN	2.6
1	U	96	GLY	2.6
1	A	227	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	562	GLY	2.6
1	C	360	GLU	2.6
1	D	583	LYS	2.6
1	F	462	GLU	2.6
1	I	166	ASP	2.6
2	u	22	ASP	2.6
2	Z	27	GLY	2.6
1	S	243	PRO	2.6
1	W	532	ARG	2.6
1	X	238	PRO	2.6
1	P	33	LEU	2.6
2	c	127	THR	2.6
2	f	143	THR	2.6
1	I	109	ILE	2.6
1	R	233	PHE	2.6
1	V	454	ALA	2.6
2	Z	104	TYR	2.6
1	N	134	ASP	2.6
1	O	13	SER	2.6
1	T	580	GLY	2.6
1	A	59	VAL	2.6
1	A	122	GLY	2.6
1	B	289	ASP	2.6
1	C	194	ASP	2.6
1	D	410	SER	2.6
1	C	441	ARG	2.6
1	E	192	ASP	2.6
1	F	594	VAL	2.6
2	k	32	SER	2.6
1	O	141	ASN	2.6
1	T	401	ASN	2.6
1	T	543	PRO	2.6
1	C	353	PRO	2.6
1	D	204	PRO	2.6
2	f	34	LEU	2.6
1	R	344	THR	2.6
1	V	356	ILE	2.6
1	D	293	ILE	2.6
1	H	20	THR	2.6
2	v	54	ILE	2.6
2	g	143	THR	2.6
1	S	57	PHE	2.5

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Mol	Chain	Res	Type	RSRZ
1	X	233	PHE	2.5
1	S	525	GLN	2.5
1	V	270	GLN	2.5
1	W	601	GLN	2.5
1	A	53	TYR	2.5
1	K	429	GLN	2.5
2	u	36	ALA	2.5
2	j	105	ALA	2.5
1	F	534	GLU	2.5
1	N	458	ARG	2.5
1	W	559	LEU	2.5
1	X	134	ASP	2.5
1	C	39	SER	2.5
2	u	136	SER	2.5
1	T	547	PRO	2.5
1	C	395	PRO	2.5
1	J	463	ILE	2.5
2	q	91	ILE	2.5
2	f	42	MET	2.5
1	O	108	LYS	2.5
1	R	20	THR	2.5
1	D	516	CYS	2.5
1	I	138	THR	2.5
1	I	586	THR	2.5
1	K	350	PHE	2.5
1	S	120	GLU	2.5
1	W	19	TRP	2.5
1	E	592	TRP	2.5
2	o	112	GLU	2.5
2	c	99	ARG	2.5
1	O	156	VAL	2.5
1	U	59	VAL	2.5
1	N	12	LEU	2.5
1	O	131	ASP	2.5
1	T	312	ASP	2.5
1	G	166	ASP	2.5
1	L	438	LEU	2.5
1	R	199	PRO	2.5
2	k	132	MET	2.5
1	E	458	ARG	2.5
1	L	172	HIS	2.5
1	M	447	TYR	2.5

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Mol	Chain	Res	Type	RSRZ
1	W	235	TYR	2.5
1	K	578	GLN	2.5
2	e	51	ALA	2.5
2	e	124	TYR	2.5
2	j	77	ALA	2.5
1	P	320	VAL	2.5
1	Q	496	VAL	2.5
1	V	341	VAL	2.5
1	I	540	GLY	2.5
1	J	540	GLY	2.5
1	O	265	LYS	2.5
1	R	453	LEU	2.5
1	J	164	LEU	2.5
1	K	190	LYS	2.5
2	n	16	LYS	2.5
2	q	6	LYS	2.5
1	P	359	PHE	2.5
1	R	266	ILE	2.5
1	V	222	PHE	2.5
1	A	76	ILE	2.5
1	E	333	ILE	2.5
2	u	60	PHE	2.5
2	d	81	ASP	2.5
1	C	349	PRO	2.5
1	E	385	PRO	2.5
1	P	259	ALA	2.5
1	T	28	GLU	2.5
1	T	406	GLU	2.5
1	A	515	GLU	2.5
1	B	133	GLU	2.5
1	Q	19	TRP	2.5
1	Q	344	THR	2.5
1	Q	542	THR	2.5
1	C	80	TYR	2.5
1	E	450	GLN	2.5
1	J	361	HIS	2.5
1	K	223	TYR	2.5
2	u	29	GLU	2.5
1	B	502	GLY	2.5
2	e	143	THR	2.5
1	X	538	LEU	2.5
1	I	373	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	I	593	LEU	2.5
1	S	7	ARG	2.5
1	P	10	SER	2.5
1	V	561	ASP	2.5
1	D	168	SER	2.5
1	E	43	ASP	2.5
1	I	458	ARG	2.5
1	K	82	PRO	2.5
1	K	388	PRO	2.5
2	t	21	SER	2.5
1	B	403	TYR	2.5
2	f	57	TYR	2.5
2	g	57	TYR	2.5
1	O	539	LEU	2.5
1	W	50	THR	2.5
2	m	100	THR	2.5
2	o	113	LEU	2.5
1	O	340	ILE	2.5
1	O	356	ILE	2.5
1	U	247	PHE	2.5
1	B	298	ILE	2.5
1	B	513	ARG	2.5
2	p	84	PHE	2.5
2	Y	131	ARG	2.5
2	g	100	ILE	2.5
1	O	160	SER	2.5
1	P	39	SER	2.5
1	V	317	GLU	2.5
1	H	178	SER	2.5
1	I	312	ASP	2.5
2	l	71	ASP	2.5
2	r	67	PRO	2.5
1	S	276	VAL	2.5
1	S	517	TYR	2.5
1	E	63	VAL	2.5
1	K	415	VAL	2.5
2	o	83	VAL	2.5
1	W	507	LEU	2.5
1	C	389	LEU	2.5
1	C	507	LEU	2.5
1	G	329	LEU	2.5
2	p	73	HIS	2.5

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Mol	Chain	Res	Type	RSRZ
1	E	366	ASN	2.5
1	K	366	ASN	2.5
1	Q	284	THR	2.5
2	o	100	THR	2.5
1	D	263	PHE	2.5
1	D	309	PHE	2.5
1	R	227	GLU	2.5
1	R	515	GLU	2.5
1	X	515	GLU	2.5
1	G	147	GLU	2.5
1	M	137	PRO	2.5
1	M	243	PRO	2.5
1	S	420	VAL	2.5
1	V	428	GLY	2.5
1	W	92	ASP	2.5
1	W	367	ASP	2.5
1	A	36	SER	2.5
1	D	514	TYR	2.5
1	G	427	GLY	2.5
1	K	43	ASP	2.5
1	K	456	ALA	2.5
2	o	81	SER	2.5
2	v	35	ASP	2.5
2	Y	54	ALA	2.5
2	d	90	SER	2.5
1	N	79	LEU	2.5
1	Q	384	LEU	2.5
1	S	418	LEU	2.5
1	S	569	ARG	2.5
1	B	429	GLN	2.5
1	B	536	LEU	2.5
1	G	193	LEU	2.5
1	L	355	GLN	2.5
1	A	331	ASN	2.5
1	Q	174	THR	2.5
1	B	20	THR	2.5
1	C	336	PHE	2.5
1	G	105	ASN	2.5
1	O	133	GLU	2.5
1	O	600	LYS	2.5
1	R	396	GLU	2.5
1	T	528	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	L	24	GLU	2.5
2	k	43	MET	2.5
2	l	116	LYS	2.5
1	O	456	ALA	2.5
1	O	178	SER	2.5
1	P	516	CYS	2.5
1	Q	312	ASP	2.5
1	W	220	ALA	2.5
1	W	451	ASP	2.5
1	B	458	ARG	2.5
1	C	326	GLY	2.5
1	C	427	GLY	2.5
1	D	444	LEU	2.5
1	E	84	ASP	2.5
1	E	94	LEU	2.5
1	F	378	ASP	2.5
1	F	547	PRO	2.5
1	K	171	ARG	2.5
1	J	291	GLN	2.5
1	K	374	LEU	2.5
1	K	392	TYR	2.5
1	K	513	ARG	2.5
2	Y	116	ALA	2.5
2	j	87	SER	2.5
1	K	172	HIS	2.5
1	W	359	PHE	2.5
1	I	35	PHE	2.5
1	V	112	ASN	2.5
1	A	203	ASN	2.5
1	J	144	ILE	2.5
1	J	205	ASN	2.5
1	S	81	ARG	2.5
1	K	330	ARG	2.5
1	M	554	LEU	2.5
1	P	517	TYR	2.5
1	Q	442	ALA	2.5
1	V	374	LEU	2.5
1	F	86	ALA	2.5
1	I	453	LEU	2.5
2	o	9	LEU	2.5
2	a	132	ALA	2.5
1	M	519	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	P	312	ASP	2.5
1	T	186	ASP	2.5
1	W	42	ASP	2.5
1	D	325	ASP	2.5
1	F	433	ASP	2.5
2	n	38	ASP	2.5
2	g	80	ASP	2.5
1	X	69	SER	2.5
1	D	15	PHE	2.5
1	K	324	LYS	2.5
2	b	133	LYS	2.5
1	G	293	ILE	2.5
1	M	311	GLU	2.5
1	B	495	GLU	2.5
2	s	112	GLU	2.5
2	a	42	MET	2.5
1	T	282	THR	2.5
1	U	274	ARG	2.5
1	V	14	ARG	2.5
1	W	569	ARG	2.5
2	q	76	ARG	2.5
1	N	80	TYR	2.5
1	V	593	LEU	2.5
1	B	556	TYR	2.5
1	H	553	LEU	2.5
1	I	267	ALA	2.5
2	r	99	ALA	2.5
2	j	104	TYR	2.5
1	X	56	GLN	2.5
1	E	137	PRO	2.5
1	F	498	ASP	2.5
1	L	62	PRO	2.5
1	F	177	HIS	2.5
1	H	157	ILE	2.5
2	j	86	SER	2.5
1	A	268	GLU	2.5
1	D	153	CYS	2.5
1	I	532	ARG	2.5
1	R	315	VAL	2.5
1	S	562	GLY	2.5
1	N	29	ALA	2.5
1	T	30	LYS	2.5

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Mol	Chain	Res	Type	RSRZ
1	X	258	LEU	2.5
1	G	190	LYS	2.5
1	I	551	LEU	2.5
2	j	146	GLY	2.5
2	b	128	ALA	2.5
1	S	82	PRO	2.5
1	C	47	GLN	2.5
1	E	210	PRO	2.5
1	R	103	ARG	2.5
1	K	194	ASP	2.5
2	s	122	ARG	2.5
2	t	77	SER	2.5
1	O	427	GLY	2.4
1	U	418	LEU	2.4
1	V	64	VAL	2.4
1	F	366	ASN	2.4
2	q	137	GLY	2.4
2	Z	23	LEU	2.4
2	f	122	LEU	2.4
2	i	25	LYS	2.4
1	O	357	ALA	2.4
1	J	363	TYR	2.4
1	K	408	ALA	2.4
2	r	82	ALA	2.4
1	D	222	PHE	2.4
1	L	359	PHE	2.4
1	O	321	ARG	2.4
1	P	144	ILE	2.4
1	X	291	GLN	2.4
1	G	510	ILE	2.4
1	H	204	PRO	2.4
1	I	450	GLN	2.4
1	I	511	ARG	2.4
1	J	148	PRO	2.4
1	S	131	ASP	2.4
1	J	147	GLU	2.4
1	L	101	ASP	2.4
1	R	200	SER	2.4
1	U	420	VAL	2.4
1	E	254	VAL	2.4
1	F	435	VAL	2.4
2	r	74	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
2	a	146	GLY	2.4
1	M	411	ALA	2.4
1	F	449	PHE	2.4
1	G	80	TYR	2.4
1	G	500	ALA	2.4
2	e	67	TYR	2.4
2	f	54	ALA	2.4
1	O	284	THR	2.4
1	X	231	THR	2.4
1	A	27	ARG	2.4
1	A	330	ARG	2.4
1	E	455	THR	2.4
1	I	455	THR	2.4
1	P	147	GLU	2.4
1	R	238	PRO	2.4
1	T	52	GLN	2.4
1	X	221	GLU	2.4
1	A	414	GLU	2.4
1	D	333	ILE	2.4
1	F	566	GLU	2.4
1	G	550	GLN	2.4
1	J	181	GLN	2.4
2	u	127	PRO	2.4
1	N	253	ASP	2.4
1	P	155	HIS	2.4
1	D	43	ASP	2.4
1	K	58	ASP	2.4
1	T	295	GLY	2.4
1	G	295	GLY	2.4
1	J	412	VAL	2.4
2	Y	106	LEU	2.4
2	c	144	GLY	2.4
1	M	263	PHE	2.4
1	S	369	TYR	2.4
1	C	403	TYR	2.4
1	F	316	TYR	2.4
1	K	48	TYR	2.4
2	p	68	ALA	2.4
2	Z	116	ALA	2.4
1	B	331	ASN	2.4
1	P	271	ILE	2.4
1	F	396	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	J	450	GLN	2.4
1	K	409	THR	2.4
1	L	377	THR	2.4
1	O	522	PRO	2.4
1	X	398	PRO	2.4
2	a	133	LYS	2.4
1	O	143	VAL	2.4
1	Q	538	LEU	2.4
1	T	115	VAL	2.4
1	U	256	ASP	2.4
1	W	256	ASP	2.4
1	C	412	VAL	2.4
1	C	460	ASP	2.4
1	I	18	ASP	2.4
1	Q	410	SER	2.4
1	F	381	SER	2.4
1	J	26	ARG	2.4
1	P	21	ALA	2.4
1	U	235	TYR	2.4
1	Q	296	GLU	2.4
1	Q	360	GLU	2.4
1	X	74	ASN	2.4
1	B	268	GLU	2.4
1	D	163	LYS	2.4
2	u	6	LYS	2.4
2	Z	78	GLU	2.4
1	Q	56	GLN	2.4
1	U	377	THR	2.4
1	C	417	THR	2.4
1	J	355	GLN	2.4
2	p	106	THR	2.4
1	N	82	PRO	2.4
2	l	127	PRO	2.4
1	S	45	LEU	2.4
1	L	123	VAL	2.4
2	n	19	VAL	2.4
2	t	80	VAL	2.4
2	a	53	MET	2.4
1	S	16	ASP	2.4
1	X	84	ASP	2.4
1	B	364	ASP	2.4
1	P	442	ALA	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	272	LYS	2.4
1	E	294	ALA	2.4
1	H	454	ALA	2.4
1	J	442	ALA	2.4
1	K	335	SER	2.4
1	L	390	ALA	2.4
2	l	12	ALA	2.4
2	a	120	LYS	2.4
2	i	108	ALA	2.4
1	S	379	GLU	2.4
2	q	64	GLU	2.4
1	N	286	VAL	2.4
1	O	405	LEU	2.4
1	Q	513	ARG	2.4
1	A	394	ASN	2.4
1	B	161	ASN	2.4
1	D	135	GLN	2.4
1	G	554	LEU	2.4
1	J	441	ARG	2.4
2	u	34	GLN	2.4
1	U	62	PRO	2.4
1	A	88	PRO	2.4
1	A	94	LEU	2.4
1	C	238	PRO	2.4
1	C	315	VAL	2.4
1	D	100	THR	2.4
2	s	87	LEU	2.4
2	d	65	THR	2.4
1	K	183	GLY	2.4
2	c	16	GLY	2.4
2	i	142	PRO	2.4
1	N	364	ASP	2.4
1	O	570	ASP	2.4
1	P	209	PHE	2.4
1	R	77	ASP	2.4
1	G	413	LYS	2.4
1	F	188	ALA	2.4
2	h	128	ALA	2.4
1	M	139	SER	2.4
1	P	217	ILE	2.4
1	V	306	GLU	2.4
1	V	360	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	W	10	SER	2.4
1	D	462	GLU	2.4
1	E	523	SER	2.4
1	I	76	ILE	2.4
1	I	147	GLU	2.4
2	b	85	ARG	2.4
1	P	438	LEU	2.4
1	N	238	PRO	2.4
1	N	243	PRO	2.4
1	V	60	VAL	2.4
1	B	521	GLY	2.4
1	D	225	VAL	2.4
1	G	254	VAL	2.4
1	G	384	LEU	2.4
1	I	444	LEU	2.4
2	q	97	LEU	2.4
1	D	370	PRO	2.4
1	L	233	PHE	2.4
1	B	311	GLU	2.4
1	B	416	ALA	2.4
1	H	393	GLU	2.4
1	L	403	TYR	2.4
2	n	23	ALA	2.4
1	I	441	ARG	2.4
1	T	552	LEU	2.4
1	M	582	LYS	2.4
1	A	73	GLN	2.4
1	P	382	GLY	2.4
1	B	496	VAL	2.4
1	G	212	LEU	2.4
1	G	525	GLN	2.4
1	M	522	PRO	2.4
1	P	231	THR	2.4
1	F	284	THR	2.4
1	I	395	PRO	2.4
1	J	353	PRO	2.4
2	k	118	THR	2.4
2	l	129	PRO	2.4
2	t	93	PRO	2.4
2	i	138	PRO	2.4
1	N	431	ALA	2.4
1	V	445	GLU	2.4

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Mol	Chain	Res	Type	RSRZ
1	X	408	ALA	2.4
1	E	195	ALA	2.4
1	I	48	TYR	2.4
1	I	110	ALA	2.4
1	I	220	ALA	2.4
2	m	107	ALA	2.4
2	r	131	ARG	2.4
1	W	293	ILE	2.4
1	C	176	ILE	2.4
1	C	510	ILE	2.4
1	P	173	CYS	2.4
1	S	129	VAL	2.4
1	U	73	GLN	2.4
1	W	73	GLN	2.4
1	W	427	GLY	2.4
1	B	59	VAL	2.4
1	B	412	VAL	2.4
1	C	530	GLN	2.4
1	H	320	VAL	2.4
2	e	68	VAL	2.4
2	j	130	SER	2.4
1	E	359	PHE	2.4
1	J	309	PHE	2.4
1	V	299	PRO	2.4
1	K	345	PRO	2.4
1	L	82	PRO	2.4
2	e	76	PRO	2.4
1	R	17	ALA	2.4
1	U	379	GLU	2.4
1	B	246	TYR	2.4
1	K	273	ARG	2.4
1	L	455	THR	2.4
2	r	41	GLU	2.4
2	j	51	ALA	2.4
1	O	109	ILE	2.4
1	R	229	LYS	2.4
1	W	374	LEU	2.4
1	X	193	LEU	2.4
1	G	560	LEU	2.4
1	L	292	LEU	2.4
1	L	413	LYS	2.4
2	c	61	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	M	180	SER	2.4
1	G	160	SER	2.4
1	K	162	SER	2.4
1	S	153	CYS	2.4
1	B	345	PRO	2.4
1	Q	48	TYR	2.4
1	C	117	GLU	2.4
1	C	185	GLU	2.4
1	R	240	THR	2.4
1	J	392	TYR	2.4
2	u	20	ALA	2.4
2	c	124	TYR	2.4
1	M	361	HIS	2.4
1	T	198	ILE	2.4
1	L	217	ILE	2.4
1	K	44	TRP	2.4
1	X	420	VAL	2.4
1	B	254	VAL	2.4
1	U	529	GLN	2.4
1	X	87	ARG	2.4
1	E	569	ARG	2.4
1	G	399	GLN	2.4
1	I	187	PHE	2.4
2	t	49	GLN	2.4
1	Q	189	GLU	2.4
1	M	29	ALA	2.4
1	S	48	TYR	2.4
1	S	252	LYS	2.4
1	T	456	ALA	2.4
1	W	583	LYS	2.4
1	F	114	ALA	2.4
1	J	48	TYR	2.4
1	J	114	ALA	2.4
1	K	353	PRO	2.4
2	v	145	GLU	2.4
2	u	48	TYR	2.4
2	g	118	TYR	2.4
1	Q	409	THR	2.4
1	B	141	ASN	2.4
1	C	144	ILE	2.4
2	i	122	LEU	2.4
1	P	87	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
1	Q	458	ARG	2.3
1	B	60	VAL	2.3
1	B	460	ASP	2.3
1	D	156	VAL	2.3
1	I	44	TRP	2.3
1	I	116	ARG	2.3
1	L	415	VAL	2.3
1	M	236	GLN	2.3
1	D	252	LYS	2.3
1	D	379	GLU	2.3
1	F	379	GLU	2.3
1	G	227	GLU	2.3
1	H	288	LYS	2.3
1	L	30	LYS	2.3
2	v	121	SER	2.3
2	i	117	LYS	2.3
1	R	204	PRO	2.3
1	J	302	PRO	2.3
1	J	407	ALA	2.3
1	K	403	TYR	2.3
1	T	444	LEU	2.3
1	O	594	VAL	2.3
1	U	182	ASN	2.3
1	V	106	THR	2.3
1	W	161	ASN	2.3
1	B	329	LEU	2.3
1	U	273	ARG	2.3
1	A	328	ARG	2.3
1	B	65	ARG	2.3
1	C	319	VAL	2.3
1	D	401	ASN	2.3
2	r	56	THR	2.3
2	Y	140	ARG	2.3
1	P	256	ASP	2.3
1	S	89	ASP	2.3
1	W	35	PHE	2.3
1	H	15	PHE	2.3
1	I	352	TRP	2.3
1	J	77	ASP	2.3
1	K	34	PHE	2.3
1	B	30	LYS	2.3
2	b	117	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	120	GLU	2.3
2	b	78	GLU	2.3
1	M	329	LEU	2.3
1	S	121	ALA	2.3
1	V	411	ALA	2.3
1	D	139	SER	2.3
1	H	392	TYR	2.3
2	q	21	SER	2.3
2	b	90	SER	2.3
1	A	109	ILE	2.3
1	A	37	ARG	2.3
1	A	438	LEU	2.3
1	D	395	PRO	2.3
2	k	129	PRO	2.3
1	M	331	ASN	2.3
1	P	409	THR	2.3
1	Q	512	GLY	2.3
1	V	336	PHE	2.3
1	X	265	LYS	2.3
1	A	155	HIS	2.3
2	o	80	VAL	2.3
1	A	284	THR	2.3
1	D	282	THR	2.3
1	G	377	THR	2.3
1	H	138	THR	2.3
2	p	102	LYS	2.3
2	b	83	GLY	2.3
1	O	169	ASP	2.3
1	O	591	GLN	2.3
1	Q	339	ASP	2.3
1	S	378	ASP	2.3
1	G	429	GLN	2.3
1	H	52	GLN	2.3
1	T	526	SER	2.3
1	U	407	ALA	2.3
1	V	285	ALA	2.3
1	X	116	ARG	2.3
1	B	116	ARG	2.3
1	C	416	ALA	2.3
1	I	255	ILE	2.3
1	J	139	SER	2.3
1	K	395	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	322	LEU	2.3
2	l	109	TYR	2.3
2	q	36	ALA	2.3
2	a	99	ARG	2.3
2	h	29	ALA	2.3
1	N	254	VAL	2.3
1	O	85	GLY	2.3
1	E	562	GLY	2.3
1	K	222	PHE	2.3
1	N	221	GLU	2.3
1	O	534	GLU	2.3
1	W	197	ASP	2.3
1	W	339	ASP	2.3
1	W	578	GLN	2.3
1	X	409	THR	2.3
1	B	380	ASN	2.3
1	L	221	GLU	2.3
1	L	426	ASN	2.3
1	P	601	GLN	2.3
1	J	18	ASP	2.3
2	d	58	GLN	2.3
1	J	511	ARG	2.3
2	j	20	ARG	2.3
1	M	405	LEU	2.3
1	N	342	ALA	2.3
1	C	198	ILE	2.3
1	L	48	TYR	2.3
1	L	356	ILE	2.3
2	e	32	ALA	2.3
1	M	63	VAL	2.3
1	S	88	PRO	2.3
1	X	353	PRO	2.3
1	I	162	SER	2.3
1	I	353	PRO	2.3
1	L	302	PRO	2.3
2	q	19	VAL	2.3
2	j	125	LYS	2.3
1	C	351	PHE	2.3
1	L	365	GLY	2.3
1	O	203	ASN	2.3
1	X	155	HIS	2.3
1	E	445	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	406	GLU	2.3
2	l	41	GLU	2.3
1	W	54	ARG	2.3
1	A	118	GLN	2.3
1	D	56	GLN	2.3
1	D	437	GLN	2.3
1	M	18	ASP	2.3
1	O	186	ASP	2.3
1	Q	433	ASP	2.3
1	U	443	ASP	2.3
1	C	84	ASP	2.3
1	C	312	ASP	2.3
1	E	444	LEU	2.3
1	J	206	ASP	2.3
1	P	17	ALA	2.3
1	R	572	ALA	2.3
1	C	293	ILE	2.3
1	K	372	TYR	2.3
1	L	408	ALA	2.3
2	Z	67	TYR	2.3
2	c	117	LYS	2.3
2	f	120	LYS	2.3
2	i	113	ILE	2.3
1	T	88	PRO	2.3
1	B	78	VAL	2.3
1	D	233	PHE	2.3
1	L	78	VAL	2.3
1	L	430	VAL	2.3
2	l	83	VAL	2.3
2	j	79	GLY	2.3
1	X	585	GLU	2.3
1	B	185	GLU	2.3
1	F	445	GLU	2.3
1	U	297	HIS	2.3
1	J	81	ARG	2.3
2	m	125	ARG	2.3
2	c	131	ARG	2.3
1	M	74	ASN	2.3
1	N	578	GLN	2.3
1	O	399	GLN	2.3
1	N	33	LEU	2.3
1	N	159	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	P	130	THR	2.3
1	U	578	GLN	2.3
1	C	525	GLN	2.3
1	H	108	LYS	2.3
1	H	323	THR	2.3
1	H	450	GLN	2.3
1	Q	438	LEU	2.3
1	D	378	ASP	2.3
1	L	250	ASP	2.3
1	A	412	VAL	2.3
1	A	506	VAL	2.3
1	H	351	PHE	2.3
1	L	93	VAL	2.3
1	Q	127	ARG	2.3
1	R	28	GLU	2.3
1	R	398	PRO	2.3
2	n	81	SER	2.3
2	s	64	GLU	2.3
2	Y	75	PRO	2.3
2	c	66	GLY	2.3
1	C	147	GLU	2.3
1	E	133	GLU	2.3
1	I	154	SER	2.3
1	L	376	ARG	2.3
2	e	30	SER	2.3
1	M	287	LEU	2.3
1	O	450	GLN	2.3
1	R	41	TRP	2.3
1	R	437	GLN	2.3
1	P	182	ASN	2.3
1	U	452	ASN	2.3
1	U	553	LEU	2.3
1	W	418	LEU	2.3
2	m	25	LEU	2.3
2	Z	96	LEU	2.3
2	c	40	GLN	2.3
1	E	394	ASN	2.3
1	N	594	VAL	2.3
1	B	111	VAL	2.3
1	E	187	PHE	2.3
1	H	594	VAL	2.3
1	J	303	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
2	v	63	ASP	2.3
2	d	46	VAL	2.3
1	U	54	ARG	2.3
1	U	61	ARG	2.3
1	D	96	GLY	2.3
1	E	37	ARG	2.3
1	H	269	ARG	2.3
1	V	265	LYS	2.3
1	L	345	PRO	2.3
1	W	526	SER	2.3
2	f	139	SER	2.3
1	Q	12	LEU	2.3
1	R	155	HIS	2.3
1	S	405	LEU	2.3
1	T	212	LEU	2.3
1	B	79	LEU	2.3
1	D	51	LEU	2.3
1	F	538	LEU	2.3
1	H	418	LEU	2.3
1	O	48	TYR	2.3
1	S	25	ALA	2.3
1	S	277	TYR	2.3
1	D	251	ILE	2.3
1	T	241	GLY	2.3
1	T	513	ARG	2.3
1	V	417	THR	2.3
1	C	254	VAL	2.3
1	H	411	ALA	2.3
1	K	182	ASN	2.3
2	j	54	ALA	2.3
1	C	257	ASP	2.3
1	F	427	GLY	2.3
1	K	378	ASP	2.3
2	m	39	ASP	2.3
2	s	72	ASP	2.3
2	Z	59	ASP	2.3
1	O	495	GLU	2.3
1	A	324	LYS	2.3
2	b	25	LYS	2.3
1	S	552	LEU	2.3
1	X	151	SER	2.3
1	N	530	GLN	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	181	GLN	2.3
1	V	48	TYR	2.3
1	V	81	ARG	2.3
1	A	403	TYR	2.3
1	E	223	TYR	2.3
1	F	103	ARG	2.3
1	H	44	TRP	2.3
1	K	57	PHE	2.3
1	K	145	ARG	2.3
1	L	21	ALA	2.3
1	L	99	ARG	2.3
1	L	397	VAL	2.3
2	I	101	ALA	2.3
1	M	265	LYS	2.3
1	O	174	THR	2.3
1	A	531	ASN	2.3
1	B	138	THR	2.3
1	C	83	LYS	2.3
1	D	228	LYS	2.3
1	C	230	GLU	2.3
1	E	314	GLU	2.3
1	H	203	ASN	2.3
1	L	23	ASP	2.3
1	L	257	ASP	2.3
2	a	80	ASP	2.3
1	S	292	LEU	2.3
1	T	536	LEU	2.3
1	J	299	PRO	2.3
2	I	25	LEU	2.3
1	A	200	SER	2.3
1	B	27	ARG	2.3
1	B	255	ILE	2.3
1	B	410	SER	2.3
1	C	61	ARG	2.3
2	Z	43	GLN	2.3
2	a	112	ILE	2.3
1	N	152	ALA	2.3
1	T	454	ALA	2.3
1	V	153	CYS	2.3
1	W	316	TYR	2.3
1	G	173	CYS	2.3
1	H	129	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	L	108	LYS	2.3
2	Z	105	ALA	2.3
2	j	68	VAL	2.3
1	M	262	GLY	2.3
1	W	462	GLU	2.3
1	F	117	GLU	2.3
1	J	124	GLY	2.3
1	K	147	GLU	2.3
2	q	7	GLY	2.3
2	t	57	GLY	2.3
2	b	79	GLY	2.3
1	Q	256	ASP	2.3
1	Q	366	ASN	2.3
1	R	378	ASP	2.3
1	X	203	ASN	2.3
1	G	18	ASP	2.3
1	G	256	ASP	2.3
1	I	169	ASP	2.3
2	a	33	THR	2.3
1	N	164	LEU	2.3
1	N	569	ARG	2.3
1	S	212	LEU	2.3
1	D	258	LEU	2.3
1	E	507	LEU	2.3
2	i	39	PRO	2.3
1	V	228	LYS	2.3
1	E	113	ILE	2.3
1	S	80	TYR	2.3
1	W	555	GLN	2.3
1	W	591	GLN	2.3
1	X	410	SER	2.3
1	C	151	SER	2.3
1	G	403	TYR	2.3
1	H	399	GLN	2.3
1	K	351	PHE	2.3
1	J	500	ALA	2.3
1	L	399	GLN	2.3
2	v	84	PHE	2.3
1	S	70	GLU	2.2
1	B	358	GLY	2.2
2	q	18	GLY	2.2
2	d	50	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	N	45	LEU	2.2
1	N	312	ASP	2.2
1	Q	436	ASN	2.2
1	E	7	ARG	2.2
1	I	194	ASP	2.2
1	J	14	ARG	2.2
2	l	138	ASN	2.2
2	m	17	LEU	2.2
2	o	86	ASN	2.2
2	Z	49	LEU	2.2
2	b	17	ASP	2.2
2	c	84	LEU	2.2
2	d	106	LEU	2.2
1	N	278	LYS	2.2
1	P	370	PRO	2.2
1	P	385	PRO	2.2
1	D	543	PRO	2.2
1	G	356	ILE	2.2
2	u	91	ILE	2.2
2	e	61	LYS	2.2
1	M	38	VAL	2.2
1	O	201	PHE	2.2
1	N	514	TYR	2.2
1	R	397	VAL	2.2
1	H	64	VAL	2.2
1	L	496	VAL	2.2
2	l	37	VAL	2.2
1	O	540	GLY	2.2
1	L	521	GLY	2.2
2	m	12	ALA	2.2
2	o	95	TYR	2.2
1	T	177	HIS	2.2
1	T	352	TRP	2.2
1	U	36	SER	2.2
1	V	19	TRP	2.2
1	B	414	GLU	2.2
1	J	117	GLU	2.2
2	p	107	ALA	2.2
1	M	269	ARG	2.2
1	P	536	LEU	2.2
1	U	163	LYS	2.2
1	Q	518	THR	2.2

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Mol	Chain	Res	Type	RSRZ
1	R	289	ASP	2.2
1	A	18	ASP	2.2
1	B	541	LYS	2.2
1	H	551	LEU	2.2
2	f	26	LEU	2.2
2	f	117	LYS	2.2
2	j	49	LEU	2.2
1	I	417	THR	2.2
2	Y	59	ASP	2.2
1	K	333	ILE	2.2
2	Y	129	ILE	2.2
1	U	448	VAL	2.2
1	K	310	VAL	2.2
1	M	342	ALA	2.2
1	Q	52	GLN	2.2
1	W	294	ALA	2.2
1	A	588	GLU	2.2
1	I	133	GLU	2.2
1	K	571	TYR	2.2
2	o	51	GLY	2.2
2	u	49	GLN	2.2
1	G	27	ARG	2.2
1	J	273	ARG	2.2
1	L	151	SER	2.2
1	L	178	SER	2.2
2	a	86	SER	2.2
1	R	30	LYS	2.2
1	H	574	LYS	2.2
2	i	96	LEU	2.2
2	c	42	MET	2.2
1	N	573	ASN	2.2
1	T	280	ILE	2.2
1	U	50	THR	2.2
1	J	169	ASP	2.2
1	L	84	ASP	2.2
1	T	181	GLN	2.2
1	U	514	TYR	2.2
1	X	555	GLN	2.2
1	A	517	TYR	2.2
1	B	90	ALA	2.2
1	C	118	GLN	2.2
1	F	227	GLU	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	360	GLU	2.2
2	n	107	ALA	2.2
2	b	101	ALA	2.2
2	i	45	ALA	2.2
1	A	278	LYS	2.2
1	A	600	LYS	2.2
1	C	504	LYS	2.2
1	J	348	LYS	2.2
1	M	559	LEU	2.2
1	O	523	SER	2.2
1	X	526	SER	2.2
1	D	559	LEU	2.2
1	O	217	ILE	2.2
1	P	577	ILE	2.2
1	P	452	ASN	2.2
1	V	257	ASP	2.2
1	A	581	VAL	2.2
2	Y	63	ILE	2.2
1	S	349	PRO	2.2
1	V	395	PRO	2.2
1	V	416	ALA	2.2
1	W	9	GLU	2.2
1	A	231	THR	2.2
1	B	366	ASN	2.2
1	E	61	ARG	2.2
1	F	27	ARG	2.2
1	F	132	TYR	2.2
1	G	369	TYR	2.2
1	I	396	GLU	2.2
1	K	549	TYR	2.2
1	L	249	ARG	2.2
1	L	353	PRO	2.2
2	k	76	ARG	2.2
2	m	11	ARG	2.2
2	e	140	ARG	2.2
1	A	399	GLN	2.2
1	E	408	ALA	2.2
1	O	384	LEU	2.2
1	S	12	LEU	2.2
1	W	389	LEU	2.2
1	J	12	LEU	2.2
2	k	21	SER	2.2

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Mol	Chain	Res	Type	RSRZ
2	s	121	SER	2.2
1	J	175	VAL	2.2
1	L	103	ARG	2.2
1	P	185	GLU	2.2
1	V	562	GLY	2.2
1	W	89	ASP	2.2
1	X	185	GLU	2.2
1	A	133	GLU	2.2
1	F	256	ASP	2.2
1	H	53	TYR	2.2
1	H	206	ASP	2.2
1	I	515	GLU	2.2
1	K	419	GLY	2.2
2	l	112	GLU	2.2
2	r	57	GLY	2.2
2	t	112	GLU	2.2
1	O	370	PRO	2.2
1	S	439	ASN	2.2
2	Z	118	TYR	2.2
2	i	103	ASP	2.2
1	V	550	GLN	2.2
1	F	216	THR	2.2
1	H	446	THR	2.2
1	I	355	GLN	2.2
2	k	134	THR	2.2
1	V	173	CYS	2.2
1	A	536	LEU	2.2
1	E	45	LEU	2.2
2	p	25	LEU	2.2
2	c	34	LEU	2.2
1	P	280	ILE	2.2
1	R	523	SER	2.2
1	U	350	PHE	2.2
1	X	22	SER	2.2
1	X	532	ARG	2.2
1	B	350	PHE	2.2
1	D	119	ILE	2.2
1	D	359	PHE	2.2
1	G	35	PHE	2.2
1	J	350	PHE	2.2
2	s	140	PHE	2.2
2	d	56	TRP	2.2

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Mol	Chain	Res	Type	RSRZ
1	T	276	VAL	2.2
2	Y	87	SER	2.2
2	f	92	VAL	2.2
1	D	326	GLY	2.2
1	E	311	GLU	2.2
1	G	540	GLY	2.2
1	J	9	GLU	2.2
1	O	191	TYR	2.2
1	I	372	TYR	2.2
2	u	18	GLY	2.2
1	V	368	ASP	2.2
1	O	380	ASN	2.2
1	Q	558	THR	2.2
1	S	380	ASN	2.2
1	W	137	PRO	2.2
2	n	93	PRO	2.2
2	p	128	TYR	2.2
2	Y	102	PRO	2.2
2	a	48	ASP	2.2
1	C	554	LEU	2.2
1	E	417	THR	2.2
1	H	106	THR	2.2
1	I	436	ASN	2.2
1	J	501	THR	2.2
1	O	532	ARG	2.2
1	P	449	PHE	2.2
1	W	44	TRP	2.2
1	A	30	LYS	2.2
1	E	352	TRP	2.2
1	M	315	VAL	2.2
1	P	221	GLU	2.2
1	Q	64	VAL	2.2
1	R	136	SER	2.2
1	S	358	GLY	2.2
1	B	124	GLY	2.2
1	F	133	GLU	2.2
2	g	119	GLY	2.2
1	M	42	ASP	2.2
1	Q	170	ALA	2.2
1	Q	235	TYR	2.2
1	P	433	ASP	2.2
1	R	16	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	U	460	ASP	2.2
1	V	88	PRO	2.2
1	V	166	ASP	2.2
1	W	364	ASP	2.2
1	A	237	ASP	2.2
1	B	206	ASP	2.2
1	D	357	ALA	2.2
1	G	509	ASP	2.2
1	I	494	ALA	2.2
2	n	25	LEU	2.2
2	r	39	ASP	2.2
2	r	42	ALA	2.2
2	e	114	ALA	2.2
2	j	118	TYR	2.2
1	T	569	ARG	2.2
1	A	35	PHE	2.2
1	D	557	PHE	2.2
1	D	582	LYS	2.2
1	G	87	ARG	2.2
1	E	351	PHE	2.2
1	G	583	LYS	2.2
1	K	563	LYS	2.2
2	f	65	THR	2.2
1	R	361	HIS	2.2
1	B	356	ILE	2.2
1	K	5	GLU	2.2
1	Q	279	SER	2.2
1	I	241	GLY	2.2
2	s	77	SER	2.2
1	M	214	GLN	2.2
1	O	576	LEU	2.2
1	P	79	LEU	2.2
1	B	152	ALA	2.2
1	I	91	ALA	2.2
1	I	294	ALA	2.2
1	V	530	GLN	2.2
1	B	253	ASP	2.2
1	C	16	ASP	2.2
1	D	7	ARG	2.2
1	E	388	PRO	2.2
1	F	135	GLN	2.2
1	H	194	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	159	ASP	2.2
1	J	561	ASP	2.2
1	K	272	LYS	2.2
1	L	378	ASP	2.2
2	m	102	LYS	2.2
2	t	133	PRO	2.2
2	Y	85	ARG	2.2
2	Z	40	GLN	2.2
2	a	72	ASP	2.2
2	h	40	GLN	2.2
1	C	331	ASN	2.2
1	T	271	ILE	2.2
1	F	106	THR	2.2
2	a	129	ILE	2.2
1	T	427	GLY	2.2
1	J	419	GLY	2.2
1	N	560	LEU	2.2
1	U	228	LYS	2.2
1	D	391	TYR	2.2
1	G	45	LEU	2.2
1	I	292	LEU	2.2
1	K	91	ALA	2.2
1	L	39	SER	2.2
1	L	51	LEU	2.2
2	t	58	TYR	2.2
2	g	34	LEU	2.2
2	g	111	LYS	2.2
1	J	142	GLN	2.2
1	Q	351	PHE	2.2
1	V	426	ASN	2.2
1	W	417	THR	2.2
1	A	189	GLU	2.2
1	C	24	GLU	2.2
1	E	117	GLU	2.2
1	H	216	THR	2.2
1	J	216	THR	2.2
1	K	537	GLU	2.2
2	q	26	THR	2.2
2	r	19	VAL	2.2
2	j	147	ASN	2.2
1	A	297	HIS	2.2
1	U	513	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	592	TRP	2.2
1	G	158	TRP	2.2
2	a	82	HIS	2.2
1	M	258	LEU	2.2
1	M	384	LEU	2.2
1	C	407	ALA	2.2
1	D	235	TYR	2.2
2	m	109	TYR	2.2
2	d	140	ARG	2.2
1	G	416	ALA	2.2
2	Y	77	ALA	2.2
1	R	336	PHE	2.2
1	O	257	ASP	2.2
1	T	215	ASP	2.2
1	V	385	PRO	2.2
1	G	199	PRO	2.2
1	G	222	PHE	2.2
1	A	364	ASP	2.2
1	B	84	ASP	2.2
1	D	215	ASP	2.2
1	L	509	ASP	2.2
2	n	132	MET	2.2
2	r	98	GLU	2.2
2	u	63	ASP	2.2
2	Y	44	ASP	2.2
2	i	150	PRO	2.2
1	J	221	GLU	2.2
1	O	171	ARG	2.2
1	Q	141	ASN	2.2
1	T	326	GLY	2.2
1	U	540	GLY	2.2
1	W	321	ARG	2.2
1	H	150	HIS	2.2
1	H	546	THR	2.2
1	J	231	THR	2.2
2	b	61	LYS	2.2
2	g	109	THR	2.2
1	C	517	TYR	2.1
1	D	456	ALA	2.1
1	I	572	ALA	2.1
1	M	505	GLN	2.1
1	S	154	SER	2.1

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Mol	Chain	Res	Type	RSRZ
1	U	530	GLN	2.1
1	W	557	PHE	2.1
1	A	233	PHE	2.1
1	C	387	GLN	2.1
2	a	149	PHE	2.1
1	M	534	GLU	2.1
1	O	166	ASP	2.1
1	P	300	ILE	2.1
1	P	333	ILE	2.1
1	W	199	PRO	2.1
1	A	320	VAL	2.1
1	D	412	VAL	2.1
1	W	288	LYS	2.1
1	E	296	GLU	2.1
1	K	370	PRO	2.1
2	q	93	PRO	2.1
2	s	55	ILE	2.1
1	I	583	LYS	2.1
2	Z	52	MET	2.1
2	e	133	LYS	2.1
1	M	155	HIS	2.1
1	M	373	LEU	2.1
1	U	258	LEU	2.1
1	K	331	ASN	2.1
1	I	235	TYR	2.1
1	I	514	TYR	2.1
2	n	56	THR	2.1
2	b	143	THR	2.1
2	c	118	TYR	2.1
2	d	127	THR	2.1
2	g	156	HIS	2.1
1	P	596	ALA	2.1
1	D	17	ALA	2.1
1	F	336	PHE	2.1
1	M	146	ARG	2.1
1	N	162	SER	2.1
2	d	40	GLN	2.1
1	S	303	VAL	2.1
1	U	281	ILE	2.1
1	A	353	PRO	2.1
1	F	293	ILE	2.1
1	K	149	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
2	k	46	GLU	2.1
2	p	90	ARG	2.1
2	g	64	ILE	2.1
1	T	383	ASP	2.1
1	E	183	GLY	2.1
1	E	326	GLY	2.1
1	F	215	ASP	2.1
2	o	18	GLY	2.1
2	t	72	ASP	2.1
2	a	17	ASP	2.1
2	d	53	MET	2.1
2	e	103	ASP	2.1
1	G	553	LEU	2.1
1	N	361	HIS	2.1
1	O	29	ALA	2.1
1	P	344	THR	2.1
1	S	366	ASN	2.1
1	V	556	TYR	2.1
1	A	411	ALA	2.1
1	A	447	TYR	2.1
2	h	135	ALA	2.1
2	j	137	TYR	2.1
1	I	57	PHE	2.1
1	J	57	PHE	2.1
1	O	227	GLU	2.1
1	V	578	GLN	2.1
2	r	76	ARG	2.1
2	u	122	ARG	2.1
2	v	15	ARG	2.1
1	E	448	VAL	2.1
1	P	154	SER	2.1
1	S	10	SER	2.1
1	S	326	GLY	2.1
1	X	137	PRO	2.1
1	B	540	GLY	2.1
1	C	69	SER	2.1
1	K	11	ILE	2.1
1	I	302	PRO	2.1
1	L	46	SER	2.1
2	k	54	ILE	2.1
1	L	502	GLY	2.1
2	s	61	SER	2.1

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Mol	Chain	Res	Type	RSRZ
2	f	41	SER	2.1
2	f	79	GLY	2.1
1	X	77	ASP	2.1
1	G	134	ASP	2.1
1	L	539	LEU	2.1
1	M	112	ASN	2.1
1	N	366	ASN	2.1
1	O	232	ALA	2.1
1	Q	290	LYS	2.1
1	S	402	ALA	2.1
1	B	80	TYR	2.1
1	D	172	HIS	2.1
1	G	145	ARG	2.1
1	H	126	TRP	2.1
2	n	95	TYR	2.1
2	o	124	LYS	2.1
2	e	94	HIS	2.1
2	a	65	THR	2.1
1	O	24	GLU	2.1
1	S	117	GLU	2.1
1	X	11	ILE	2.1
1	X	320	VAL	2.1
1	B	73	GLN	2.1
1	D	360	GLU	2.1
1	E	510	ILE	2.1
1	H	109	ILE	2.1
1	L	254	VAL	2.1
2	b	38	GLU	2.1
2	d	92	VAL	2.1
1	T	183	GLY	2.1
1	T	382	GLY	2.1
1	X	358	GLY	2.1
1	H	554	LEU	2.1
1	J	154	SER	2.1
2	o	44	MET	2.1
2	o	40	LEU	2.1
2	b	41	SER	2.1
1	S	61	ARG	2.1
1	V	569	ARG	2.1
1	W	23	ASP	2.1
1	C	228	LYS	2.1
1	E	54	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	229	LYS	2.1
1	F	376	ARG	2.1
1	G	197	ASP	2.1
1	J	223	TYR	2.1
1	K	163	LYS	2.1
2	l	128	TYR	2.1
2	m	45	ALA	2.1
2	c	137	TYR	2.1
2	i	105	ALA	2.1
1	M	105	ASN	2.1
1	M	106	THR	2.1
1	P	448	VAL	2.1
1	V	6	ASN	2.1
1	T	144	ILE	2.1
1	X	175	VAL	2.1
1	E	231	THR	2.1
1	G	573	ASN	2.1
2	r	106	THR	2.1
2	Z	28	VAL	2.1
2	j	115	THR	2.1
2	i	126	GLN	2.1
1	N	96	GLY	2.1
1	F	521	GLY	2.1
1	U	388	PRO	2.1
1	A	137	PRO	2.1
2	n	114	LEU	2.1
1	N	37	ARG	2.1
1	R	249	ARG	2.1
1	U	99	ARG	2.1
1	W	171	ARG	2.1
1	B	532	ARG	2.1
1	D	54	ARG	2.1
1	F	523	SER	2.1
1	H	245	SER	2.1
1	K	154	SER	2.1
2	d	87	SER	2.1
2	h	148	SER	2.1
1	S	342	ALA	2.1
1	J	256	ASP	2.1
1	T	117	GLU	2.1
1	T	311	GLU	2.1
1	U	28	GLU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	286	VAL	2.1
1	D	38	VAL	2.1
1	D	133	GLU	2.1
1	D	592	TRP	2.1
1	E	379	GLU	2.1
1	J	158	TRP	2.1
1	M	417	THR	2.1
1	M	295	GLY	2.1
1	T	118	GLN	2.1
1	M	551	LEU	2.1
1	N	582	LYS	2.1
1	Q	164	LEU	2.1
1	V	292	LEU	2.1
1	W	563	LYS	2.1
1	E	376	ARG	2.1
1	G	458	ARG	2.1
1	T	154	SER	2.1
1	W	39	SER	2.1
2	a	41	SER	2.1
1	M	194	ASP	2.1
1	O	32	ASP	2.1
1	R	195	ALA	2.1
1	V	534	GLU	2.1
1	W	566	GLU	2.1
1	C	131	ASP	2.1
1	J	411	ALA	2.1
2	l	69	GLU	2.1
2	n	112	GLU	2.1
2	o	99	ALA	2.1
1	O	172	HIS	2.1
1	T	143	VAL	2.1
1	D	59	VAL	2.1
2	v	73	HIS	2.1
1	N	461	GLY	2.1
1	U	450	GLN	2.1
1	X	228	LYS	2.1
1	X	569	ARG	2.1
1	C	164	LEU	2.1
1	C	229	LYS	2.1
1	E	344	THR	2.1
1	G	67	LEU	2.1
1	I	575	GLN	2.1

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Mol	Chain	Res	Type	RSRZ
2	r	118	THR	2.1
1	N	302	PRO	2.1
1	C	88	PRO	2.1
1	F	351	PHE	2.1
2	i	102	PRO	2.1
1	M	503	GLU	2.1
1	N	516	CYS	2.1
1	Q	9	GLU	2.1
1	Q	125	ALA	2.1
1	H	223	TYR	2.1
1	J	549	TYR	2.1
1	K	363	TYR	2.1
2	p	81	SER	2.1
2	p	109	TYR	2.1
2	s	92	ALA	2.1
2	s	99	ALA	2.1
2	s	130	SER	2.1
2	v	69	GLU	2.1
2	Z	22	ALA	2.1
2	a	90	SER	2.1
1	M	312	ASP	2.1
1	P	319	VAL	2.1
1	W	313	LYS	2.1
1	A	378	ASP	2.1
1	B	497	VAL	2.1
1	C	197	ASP	2.1
2	r	91	ILE	2.1
2	c	59	ASP	2.1
1	O	307	TRP	2.1
1	A	521	GLY	2.1
1	D	44	TRP	2.1
2	Y	20	ARG	2.1
2	c	113	ILE	2.1
1	O	429	GLN	2.1
1	J	56	GLN	2.1
1	J	552	LEU	2.1
1	J	593	LEU	2.1
2	d	27	GLY	2.1
1	R	426	ASN	2.1
1	T	323	THR	2.1
1	W	375	ASN	2.1
2	f	109	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	U	210	PRO	2.1
1	L	199	PRO	2.1
2	h	39	PRO	2.1
1	O	306	GLU	2.1
1	R	400	ALA	2.1
1	W	152	ALA	2.1
1	B	189	GLU	2.1
1	H	548	GLU	2.1
1	L	566	GLU	2.1
1	R	139	SER	2.1
1	U	574	LYS	2.1
1	V	260	ASP	2.1
1	V	300	ILE	2.1
1	A	38	VAL	2.1
1	B	283	CYS	2.1
1	D	226	VAL	2.1
1	I	208	VAL	2.1
1	K	276	VAL	2.1
1	K	376	ARG	2.1
1	L	320	VAL	2.1
2	k	11	ARG	2.1
2	o	54	ILE	2.1
2	v	136	SER	2.1
1	M	538	LEU	2.1
1	P	43	ASP	2.1
1	S	538	LEU	2.1
1	A	43	ASP	2.1
1	D	84	ASP	2.1
1	G	16	ASP	2.1
2	g	99	ARG	2.1
2	g	129	ILE	2.1
2	n	113	LEU	2.1
2	e	123	LEU	2.1
2	g	40	GLN	2.1
1	B	304	PHE	2.1
1	M	20	THR	2.1
1	P	284	THR	2.1
1	D	205	ASN	2.1
1	G	359	PHE	2.1
2	d	149	PHE	2.1
2	m	118	THR	2.1
2	s	24	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	O	229	LYS	2.1
1	Q	514	TYR	2.1
1	T	556	TYR	2.1
1	U	328	ARG	2.1
1	B	195	ALA	2.1
1	G	14	ARG	2.1
1	G	541	LYS	2.1
1	K	411	ALA	2.1
1	K	447	TYR	2.1
1	H	273	ARG	2.1
2	v	20	ALA	2.1
2	g	32	ALA	2.1
1	K	251	ILE	2.1
1	L	510	ILE	2.1
1	X	172	HIS	2.1
1	X	183	GLY	2.1
1	H	43	ASP	2.1
1	J	358	GLY	2.1
2	n	70	GLY	2.1
2	n	78	SER	2.1
2	Y	30	SER	2.1
1	X	44	TRP	2.1
1	E	186	ASP	2.1
1	P	544	GLN	2.1
1	G	135	GLN	2.1
1	U	414	GLU	2.1
1	B	515	GLU	2.1
1	C	574	LYS	2.1
1	N	411	ALA	2.1
1	O	385	PRO	2.1
1	Q	243	PRO	2.1
1	T	121	ALA	2.1
1	T	514	TYR	2.1
1	V	549	TYR	2.1
1	C	216	THR	2.1
1	C	542	THR	2.1
1	D	117	GLU	2.1
1	K	227	GLU	2.1
1	A	188	ALA	2.1
2	n	48	TYR	2.1
2	n	106	THR	2.1
2	Y	115	THR	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	244	VAL	2.1
2	p	30	PRO	2.1
2	v	66	PRO	2.1
1	R	554	LEU	2.1
1	X	340	ILE	2.1
1	X	389	LEU	2.1
1	A	280	ILE	2.1
1	F	418	LEU	2.1
1	G	251	ILE	2.1
2	Z	129	ILE	2.1
1	V	261	SER	2.1
1	C	154	SER	2.1
1	D	419	GLY	2.1
1	I	428	GLY	2.1
2	o	77	SER	2.1
2	q	130	SER	2.1
1	M	187	PHE	2.0
1	P	509	ASP	2.1
1	Q	451	ASP	2.1
1	Q	519	ASP	2.1
1	C	172	HIS	2.1
1	J	194	ASP	2.1
2	b	59	ASP	2.1
1	A	7	ARG	2.0
1	A	441	ARG	2.0
1	E	224	GLU	2.0
1	H	127	ARG	2.0
2	n	29	GLU	2.0
1	G	349	PRO	2.0
1	H	213	THR	2.0
1	H	226	VAL	2.0
1	J	426	ASN	2.0
1	J	522	PRO	2.0
1	K	599	ALA	2.0
1	L	90	ALA	2.0
2	o	123	ALA	2.0
2	Z	137	TYR	2.0
1	X	401	ASN	2.0
1	A	344	THR	2.0
2	j	132	ALA	2.0
1	W	271	ILE	2.0
1	Q	326	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	R	365	GLY	2.0
1	C	94	LEU	2.0
1	V	159	ASP	2.0
1	W	160	SER	2.0
1	W	201	PHE	2.0
1	B	348	LYS	2.0
1	F	22	SER	2.0
1	H	449	PHE	2.0
2	s	32	SER	2.0
2	b	125	LYS	2.0
1	R	27	ARG	2.0
1	B	44	TRP	2.0
1	B	172	HIS	2.0
1	E	172	HIS	2.0
1	I	307	TRP	2.0
1	J	339	ASP	2.0
1	X	379	GLU	2.0
1	F	5	GLU	2.0
1	L	133	GLU	2.0
1	N	107	ALA	2.0
1	P	411	ALA	2.0
1	S	341	VAL	2.0
1	W	191	TYR	2.0
1	B	64	VAL	2.0
1	G	411	ALA	2.0
1	J	277	TYR	2.0
1	L	369	TYR	2.0
1	L	520	VAL	2.0
1	S	241	GLY	2.0
1	T	62	PRO	2.0
1	P	229	LYS	2.0
1	V	248	LYS	2.0
1	V	413	LYS	2.0
1	X	562	GLY	2.0
1	F	323	THR	2.0
1	F	543	PRO	2.0
1	J	284	THR	2.0
1	X	459	ARG	2.0
1	P	335	SER	2.0
1	R	185	GLU	2.0
1	V	519	ASP	2.0
1	C	218	GLN	2.0

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Mol	Chain	Res	Type	RSRZ
1	D	40	GLN	2.0
1	H	525	GLN	2.0
1	K	101	ASP	2.0
2	l	146	TRP	2.0
2	p	63	ASP	2.0
2	g	44	ASP	2.0
1	W	442	ALA	2.0
1	A	276	VAL	2.0
1	C	53	TYR	2.0
1	I	405	LEU	2.0
1	J	170	ALA	2.0
2	m	23	ALA	2.0
2	r	128	TYR	2.0
2	Y	89	VAL	2.0
2	c	68	VAL	2.0
2	h	46	VAL	2.0
1	T	389	LEU	2.0
1	M	153	CYS	2.0
1	S	419	GLY	2.0
1	V	171	ARG	2.0
1	X	545	GLY	2.0
1	L	545	GLY	2.0
2	o	111	LYS	2.0
1	G	446	THR	2.0
2	e	138	PRO	2.0
2	k	60	PHE	2.0
1	Q	544	GLN	2.0
1	R	544	GLN	2.0
1	F	355	GLN	2.0
2	f	40	GLN	2.0
1	E	184	TRP	2.0
1	F	261	SER	2.0
2	a	156	HIS	2.0
2	h	70	SER	2.0
1	M	83	LYS	2.0
1	O	175	VAL	2.0
1	V	514	TYR	2.0
1	G	175	VAL	2.0
1	F	281	ILE	2.0
1	G	338	ALA	2.0
1	H	294	ALA	2.0
1	K	248	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	L	517	TYR	2.0
2	i	68	VAL	2.0
1	Q	275	ARG	2.0
1	R	67	LEU	2.0
1	L	572	ALA	2.0
2	c	112	ILE	2.0
2	d	116	ALA	2.0
2	i	26	LEU	2.0
1	W	183	GLY	2.0
1	E	365	GLY	2.0
1	F	540	GLY	2.0
2	g	79	GLY	2.0
2	i	79	GLY	2.0
1	C	398	PRO	2.0
1	O	417	THR	2.0
1	O	542	THR	2.0
1	W	153	CYS	2.0
1	E	112	ASN	2.0
1	S	24	GLU	2.0
1	E	185	GLU	2.0
1	F	429	GLN	2.0
1	G	221	GLU	2.0
1	H	529	GLN	2.0
2	c	121	GLU	2.0
1	M	574	LYS	2.0
1	O	496	VAL	2.0
1	Q	248	LYS	2.0
1	W	108	LYS	2.0
1	F	389	LEU	2.0
1	F	559	LEU	2.0
1	G	215	ASP	2.0
1	J	297	HIS	2.0
1	K	397	VAL	2.0
1	M	234	ILE	2.0
1	O	188	ALA	2.0
1	R	274	ARG	2.0
1	S	554	LEU	2.0
1	A	14	ARG	2.0
1	C	81	ARG	2.0
1	C	258	LEU	2.0
1	C	342	ALA	2.0
1	C	442	ALA	2.0

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Mol	Chain	Res	Type	RSRZ
1	E	373	LEU	2.0
1	G	113	ILE	2.0
1	H	25	ALA	2.0
1	I	113	ILE	2.0
1	I	258	LEU	2.0
2	k	27	ASP	2.0
2	Z	87	SER	2.0
2	a	51	ALA	2.0
2	b	116	ALA	2.0
2	d	44	ASP	2.0
1	N	382	GLY	2.0
1	S	74	ASN	2.0
1	W	205	ASN	2.0
1	Q	429	GLN	2.0
1	B	290	LYS	2.0
1	D	375	ASN	2.0
1	X	118	GLN	2.0
1	A	450	GLN	2.0
1	E	83	LYS	2.0
1	K	399	GLN	2.0
1	A	552	LEU	2.0
1	B	415	VAL	2.0
1	D	103	ARG	2.0
1	J	61	ARG	2.0
1	J	292	LEU	2.0

## 6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

There are no ligands in this entry.

## 6.5 Other polymers [i](#)

There are no such residues in this entry.