



Full wwPDB X-ray Structure Validation Report ⓘ

May 28, 2020 – 09:22 pm BST

PDB ID : 1XFY
Title : Crystal structure of anthrax edema factor (EF) in complex with calmodulin
Authors : Shen, Y.; Zhukovskaya, N.L.; Guo, Q.; Florian, J.; Tang, W.J.
Deposited on : 2004-09-15
Resolution : 3.30 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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

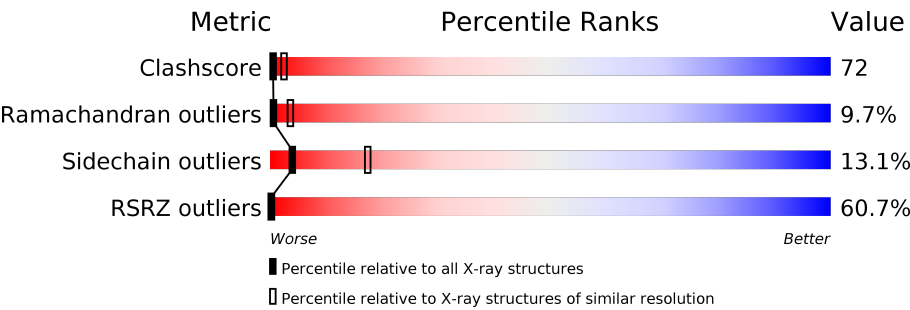
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.30 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	141614	1205 (3.34-3.26)
Ramachandran outliers	138981	1183 (3.34-3.26)
Sidechain outliers	138945	1182 (3.34-3.26)
RSRZ outliers	127900	1115 (3.34-3.26)

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 ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	777	<div><div>56%</div><div><div>23%</div><div>56%</div><div>14%</div><div>• 5%</div></div></div>
1	B	777	<div><div>57%</div><div><div>23%</div><div>56%</div><div>14%</div><div>• 5%</div></div></div>
1	C	777	<div><div>62%</div><div><div>23%</div><div>56%</div><div>14%</div><div>• 5%</div></div></div>
1	D	777	<div><div>59%</div><div><div>23%</div><div>56%</div><div>14%</div><div>• 5%</div></div></div>
1	E	777	<div><div>58%</div><div><div>23%</div><div>56%</div><div>14%</div><div>• 5%</div></div></div>
1	F	777	<div><div>58%</div><div><div>23%</div><div>56%</div><div>14%</div><div>• 5%</div></div></div>
2	O	149	<div><div>57%</div><div><div>17%</div><div>64%</div><div>16%</div><div>• •</div></div></div>

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Mol	Chain	Length	Quality of chain
2	P	149	
2	Q	149	
2	R	149	
2	S	149	
2	T	149	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MG	C	902	-	-	-	X
4	CA	P	803	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 42846 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 Calmodulin-sensitive adenylate cyclase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	B	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	C	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	D	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	E	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			
1	F	735	Total	C	N	O	S	0	0	0
			5992	3828	995	1163	6			

There are 54 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	24	MET	-	INITIATING METHIONINE	UNP P40136
A	25	HIS	-	EXPRESSION TAG	UNP P40136
A	26	HIS	-	EXPRESSION TAG	UNP P40136
A	27	HIS	-	EXPRESSION TAG	UNP P40136
A	28	HIS	-	EXPRESSION TAG	UNP P40136
A	29	HIS	-	EXPRESSION TAG	UNP P40136
A	30	HIS	-	EXPRESSION TAG	UNP P40136
A	31	ALA	-	CLONING ARTIFACT	UNP P40136
A	32	ALA	-	CLONING ARTIFACT	UNP P40136
B	24	MET	-	INITIATING METHIONINE	UNP P40136
B	25	HIS	-	EXPRESSION TAG	UNP P40136
B	26	HIS	-	EXPRESSION TAG	UNP P40136
B	27	HIS	-	EXPRESSION TAG	UNP P40136
B	28	HIS	-	EXPRESSION TAG	UNP P40136
B	29	HIS	-	EXPRESSION TAG	UNP P40136
B	30	HIS	-	EXPRESSION TAG	UNP P40136
B	31	ALA	-	CLONING ARTIFACT	UNP P40136

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Chain	Residue	Modelled	Actual	Comment	Reference
B	32	ALA	-	CLONING ARTIFACT	UNP P40136
C	24	MET	-	INITIATING METHIONINE	UNP P40136
C	25	HIS	-	EXPRESSION TAG	UNP P40136
C	26	HIS	-	EXPRESSION TAG	UNP P40136
C	27	HIS	-	EXPRESSION TAG	UNP P40136
C	28	HIS	-	EXPRESSION TAG	UNP P40136
C	29	HIS	-	EXPRESSION TAG	UNP P40136
C	30	HIS	-	EXPRESSION TAG	UNP P40136
C	31	ALA	-	CLONING ARTIFACT	UNP P40136
C	32	ALA	-	CLONING ARTIFACT	UNP P40136
D	24	MET	-	INITIATING METHIONINE	UNP P40136
D	25	HIS	-	EXPRESSION TAG	UNP P40136
D	26	HIS	-	EXPRESSION TAG	UNP P40136
D	27	HIS	-	EXPRESSION TAG	UNP P40136
D	28	HIS	-	EXPRESSION TAG	UNP P40136
D	29	HIS	-	EXPRESSION TAG	UNP P40136
D	30	HIS	-	EXPRESSION TAG	UNP P40136
D	31	ALA	-	CLONING ARTIFACT	UNP P40136
D	32	ALA	-	CLONING ARTIFACT	UNP P40136
E	24	MET	-	INITIATING METHIONINE	UNP P40136
E	25	HIS	-	EXPRESSION TAG	UNP P40136
E	26	HIS	-	EXPRESSION TAG	UNP P40136
E	27	HIS	-	EXPRESSION TAG	UNP P40136
E	28	HIS	-	EXPRESSION TAG	UNP P40136
E	29	HIS	-	EXPRESSION TAG	UNP P40136
E	30	HIS	-	EXPRESSION TAG	UNP P40136
E	31	ALA	-	CLONING ARTIFACT	UNP P40136
E	32	ALA	-	CLONING ARTIFACT	UNP P40136
F	24	MET	-	INITIATING METHIONINE	UNP P40136
F	25	HIS	-	EXPRESSION TAG	UNP P40136
F	26	HIS	-	EXPRESSION TAG	UNP P40136
F	27	HIS	-	EXPRESSION TAG	UNP P40136
F	28	HIS	-	EXPRESSION TAG	UNP P40136
F	29	HIS	-	EXPRESSION TAG	UNP P40136
F	30	HIS	-	EXPRESSION TAG	UNP P40136
F	31	ALA	-	CLONING ARTIFACT	UNP P40136
F	32	ALA	-	CLONING ARTIFACT	UNP P40136

- Molecule 2 is a protein called Calmodulin 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	O	146	Total	C	N	O	S	0	0	0
			1146	702	186	249	9			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	P	146	Total 1146	C 702	N 186	O 249	S 9	0	0	0
2	Q	146	Total 1146	C 702	N 186	O 249	S 9	0	0	0
2	R	146	Total 1146	C 702	N 186	O 249	S 9	0	0	0
2	S	146	Total 1146	C 702	N 186	O 249	S 9	0	0	0
2	T	146	Total 1146	C 702	N 186	O 249	S 9	0	0	0

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	D	1	Total 1	Mg 1	0	0
3	E	1	Total 1	Mg 1	0	0
3	B	1	Total 1	Mg 1	0	0
3	C	1	Total 1	Mg 1	0	0
3	A	1	Total 1	Mg 1	0	0
3	F	1	Total 1	Mg 1	0	0

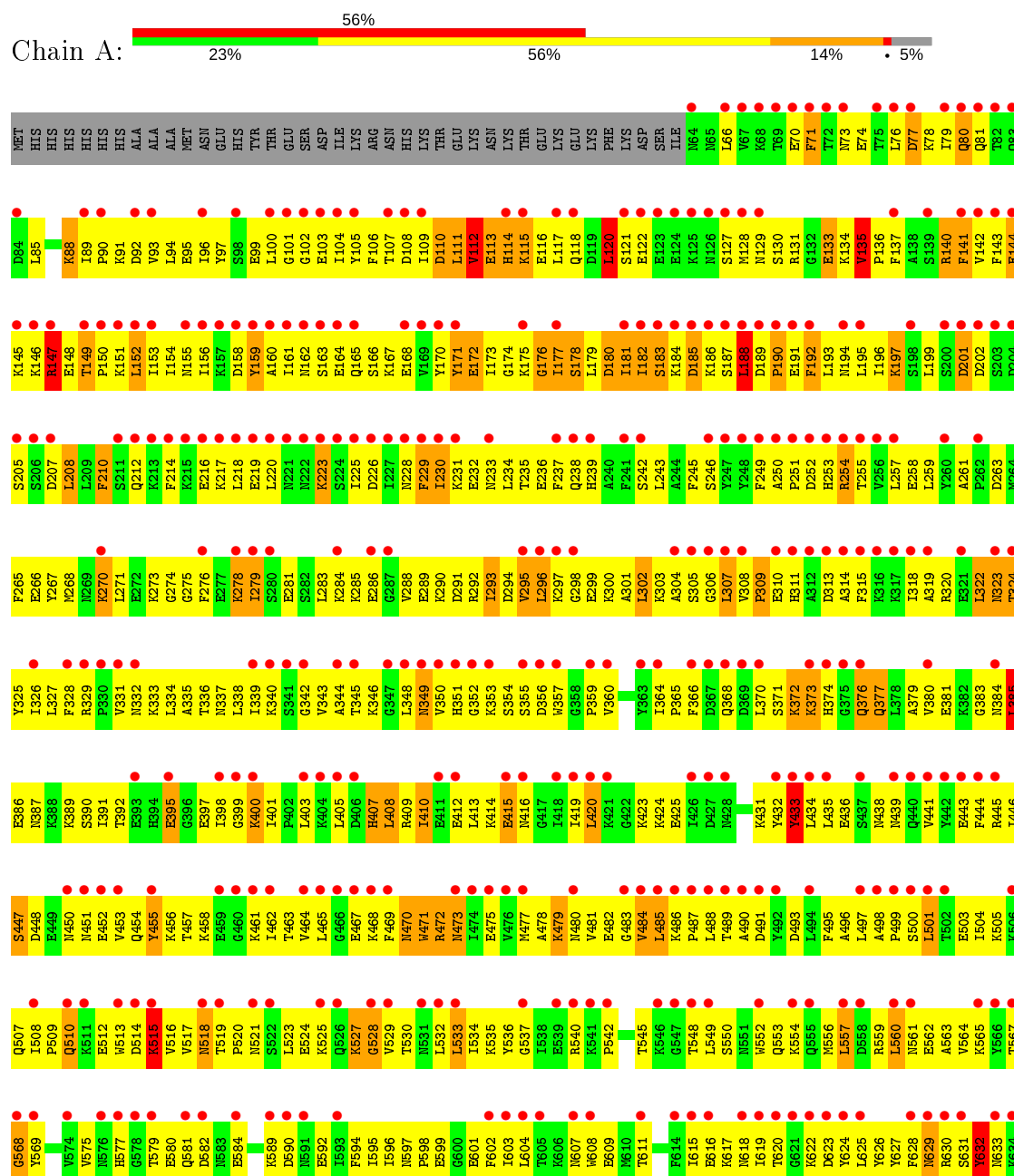
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

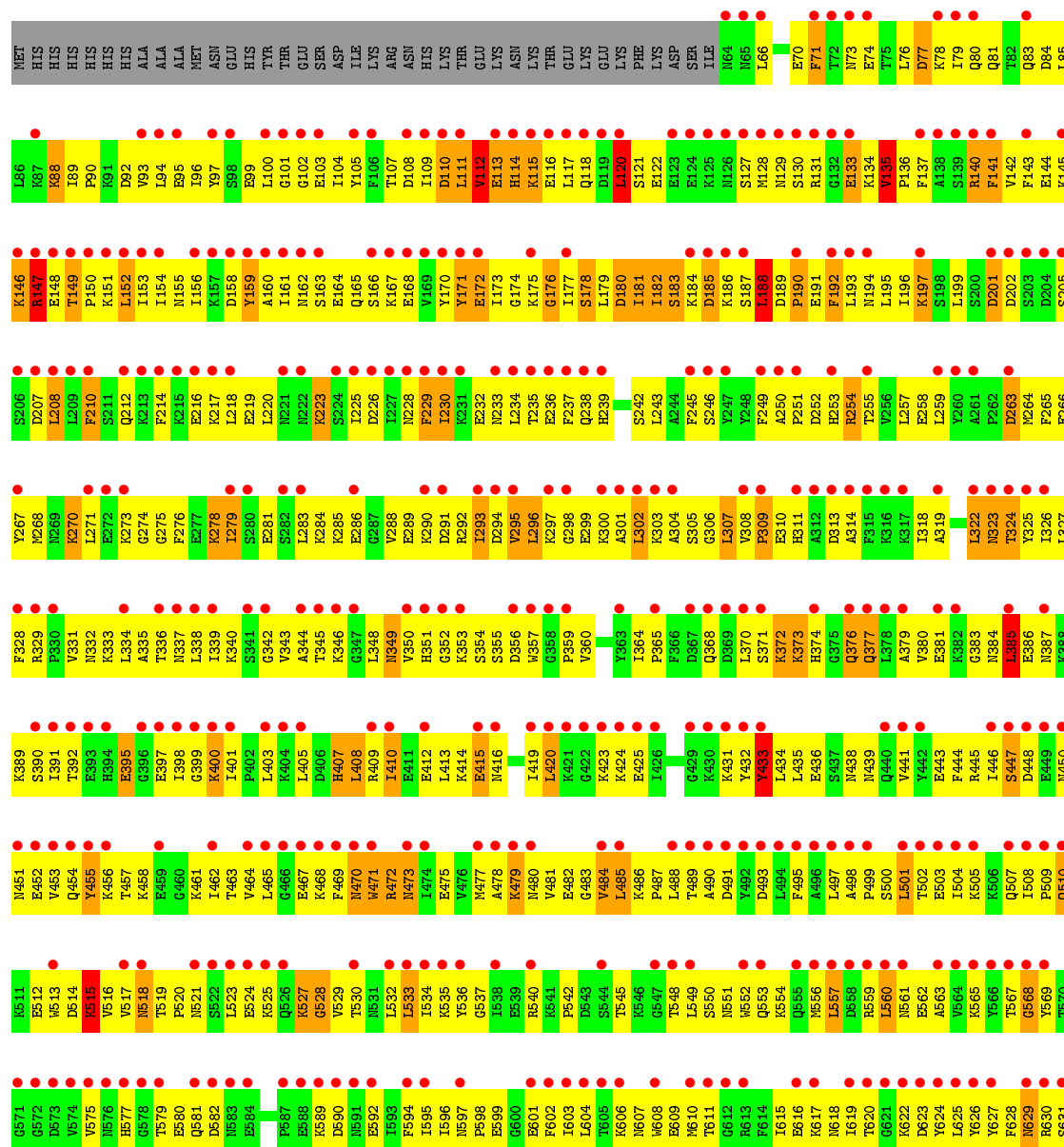
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	P	2	Total 2	Ca 2	0	0
4	Q	2	Total 2	Ca 2	0	0
4	T	2	Total 2	Ca 2	0	0
4	O	2	Total 2	Ca 2	0	0
4	R	2	Total 2	Ca 2	0	0
4	S	2	Total 2	Ca 2	0	0

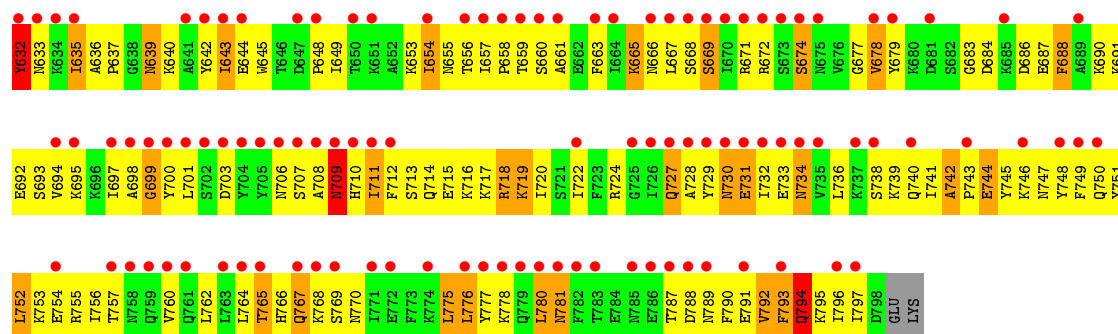
3 Residue-property plots

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.

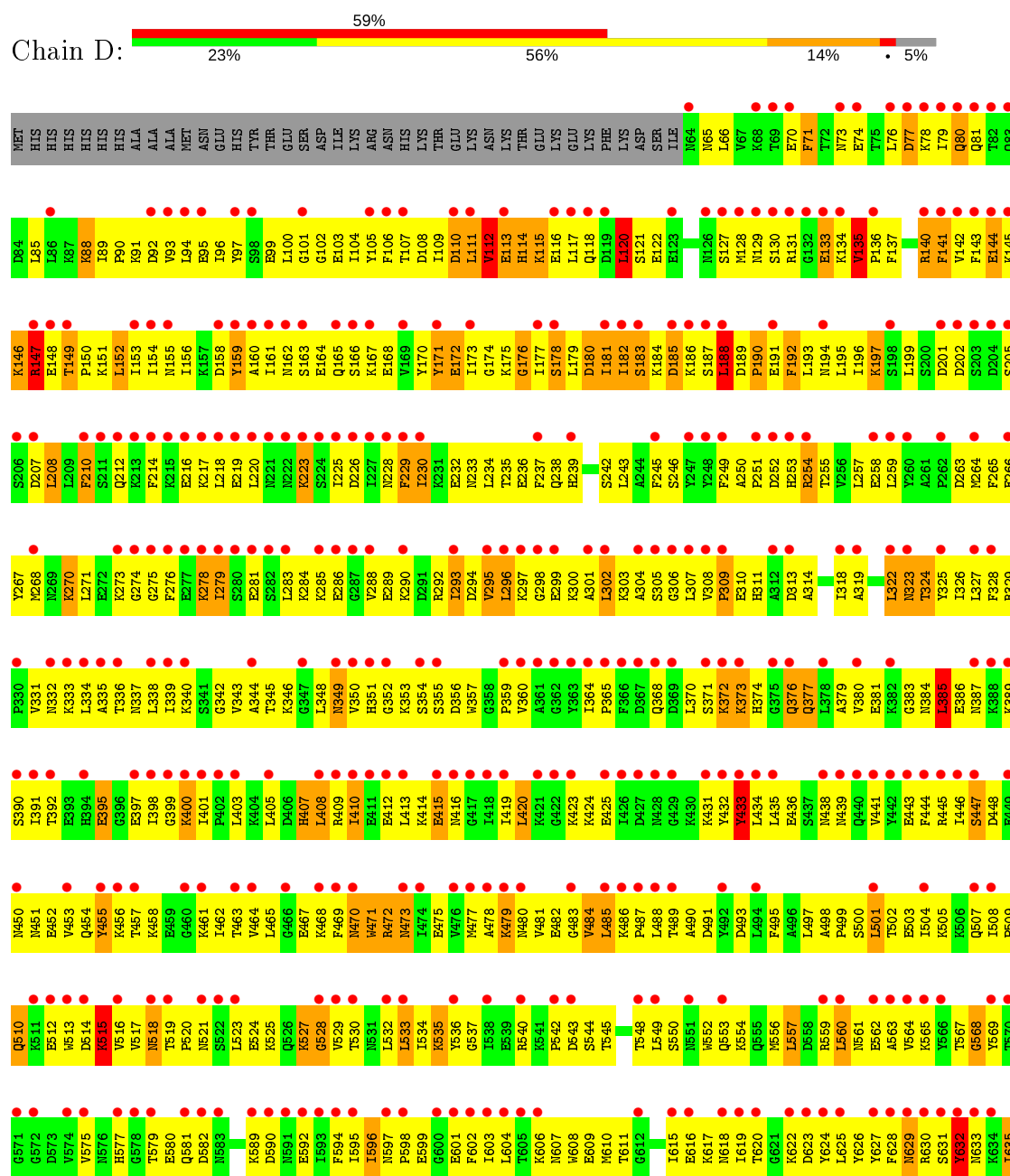
- Molecule 1: Calmodulin-sensitive adenylate cyclase

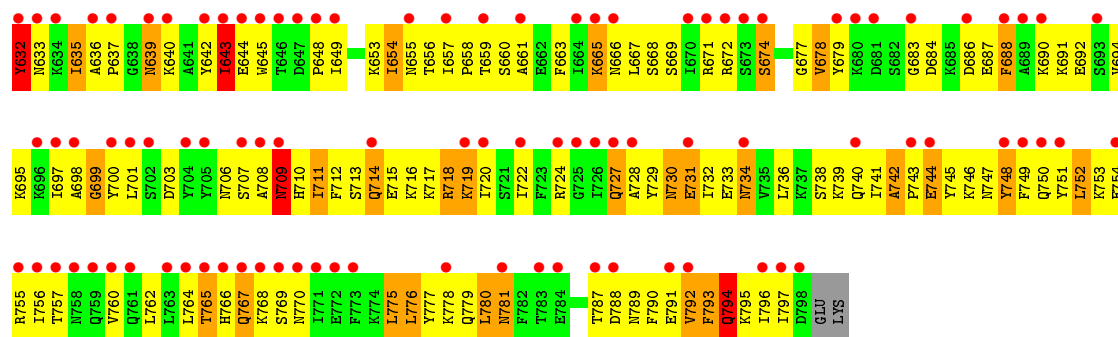




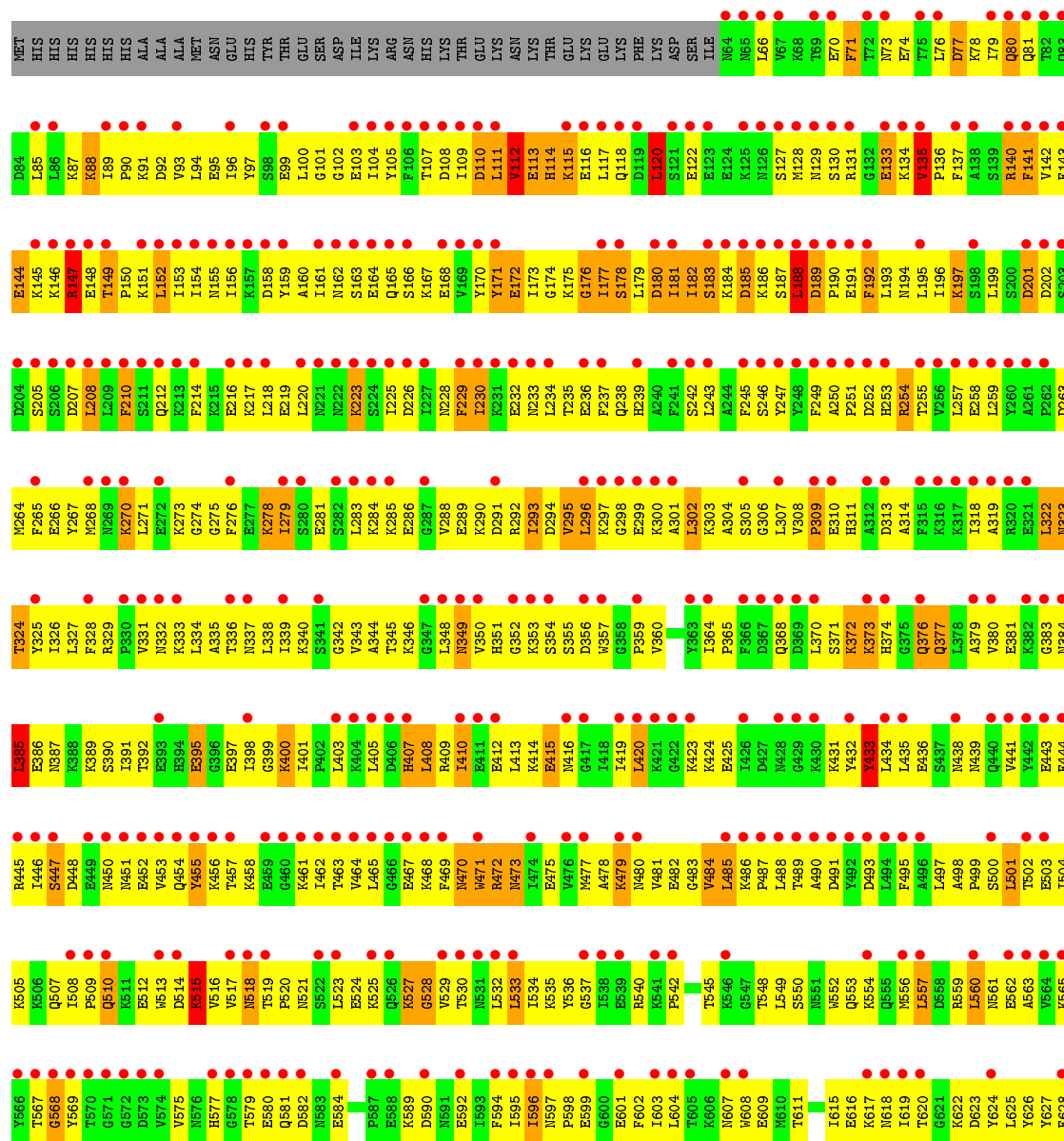


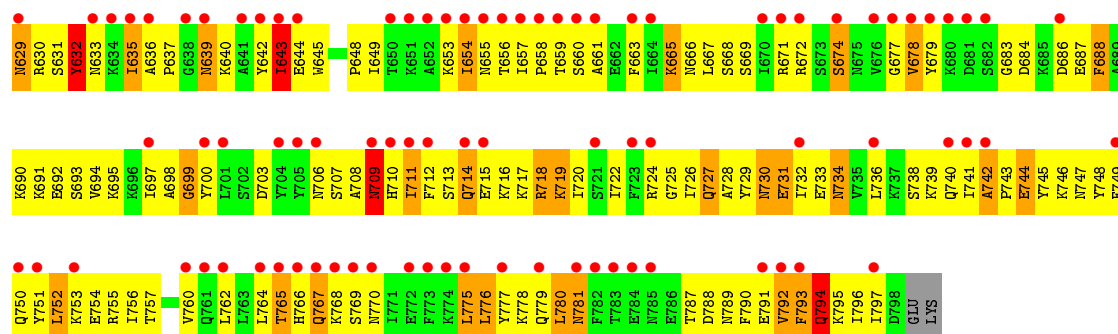
● Molecule 1: Calmodulin-sensitive adenylate cyclase





• Molecule 1: Calmodulin-sensitive adenylate cyclase





• Molecule 2: Calmodulin 2



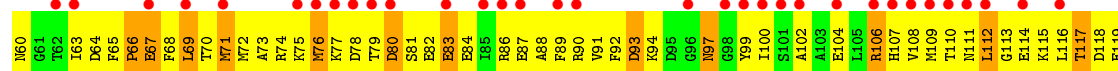
• Molecule 2: Calmodulin 2

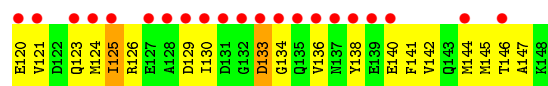


• Molecule 2: Calmodulin 2

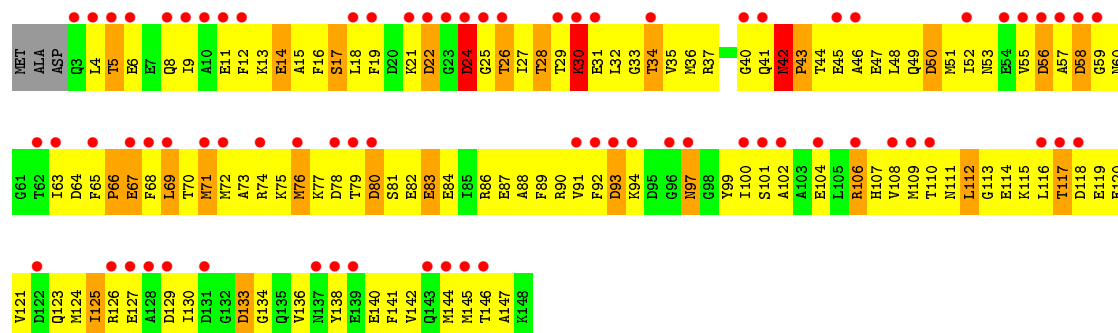


• Molecule 2: Calmodulin 2

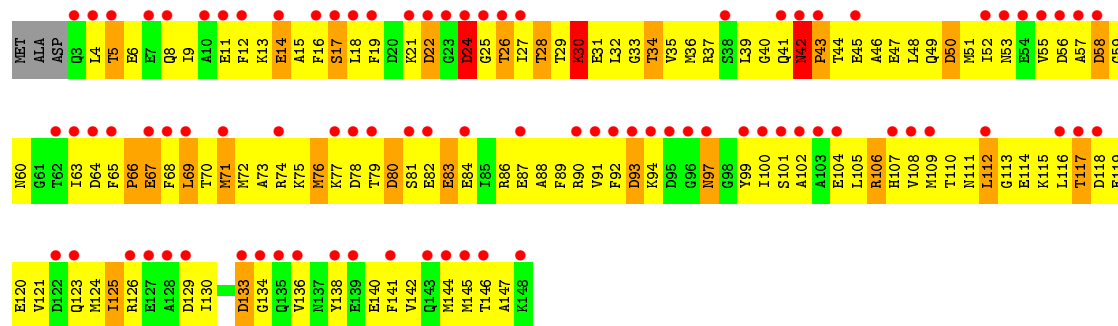




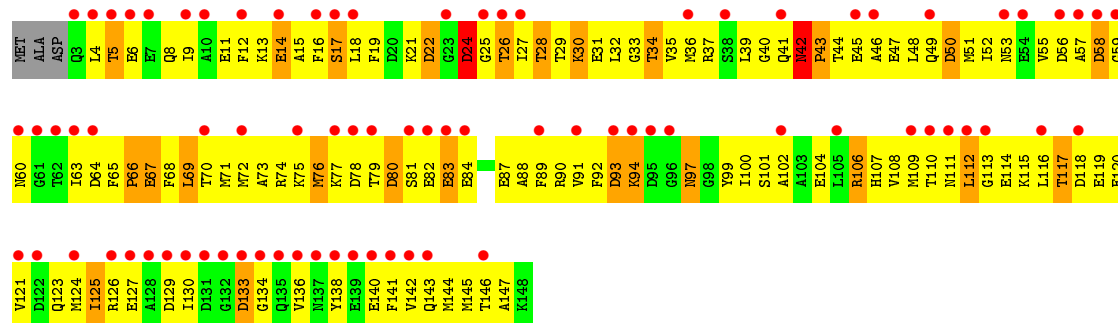
• Molecule 2: Calmodulin 2



• Molecule 2: Calmodulin 2



• Molecule 2: Calmodulin 2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	315.62Å 182.04Å 141.02Å 90.00° 89.93° 90.00°	Depositor
Resolution (Å)	10.00 – 3.30 29.82 – 3.26	Depositor EDS
% Data completeness (in resolution range)	93.9 (10.00-3.30) 91.8 (29.82-3.26)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.03	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.269 , 0.289 0.273 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	101.4	Xtriage
Anisotropy	0.113	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 56.2	EDS
L-test for twinning ¹	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.448 for -1/2*h-3/2*k,-1/2*h+1/2*k,-l 0.448 for -1/2*h+3/2*k,1/2*h+1/2*k,-l 0.448 for 1/2*h-3/2*k,-1/2*h-1/2*k,-l 0.448 for 1/2*h+3/2*k,1/2*h-1/2*k,-l 0.458 for -h,-k,l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	42846	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.18% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Theoretical 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 ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: CA, MG

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	0.54	0/6104	0.84	15/8208 (0.2%)
1	B	0.54	0/6104	0.85	15/8208 (0.2%)
1	C	0.54	0/6104	0.85	17/8208 (0.2%)
1	D	0.54	1/6104 (0.0%)	0.85	17/8208 (0.2%)
1	E	0.54	0/6104	0.85	16/8208 (0.2%)
1	F	0.54	0/6104	0.85	16/8208 (0.2%)
2	O	0.54	0/1158	0.85	4/1553 (0.3%)
2	P	0.54	0/1158	0.86	4/1553 (0.3%)
2	Q	0.54	0/1158	0.85	4/1553 (0.3%)
2	R	0.55	0/1158	0.85	4/1553 (0.3%)
2	S	0.54	0/1158	0.85	4/1553 (0.3%)
2	T	0.53	0/1158	0.85	4/1553 (0.3%)
All	All	0.54	1/43572 (0.0%)	0.85	120/58566 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	190	PRO	N-CA	-5.69	1.37	1.47

All (120) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	160	ALA	N-CA-C	9.55	136.80	111.00
1	F	160	ALA	N-CA-C	9.55	136.78	111.00
1	E	160	ALA	N-CA-C	9.54	136.76	111.00
1	A	160	ALA	N-CA-C	9.54	136.75	111.00
1	D	160	ALA	N-CA-C	9.53	136.74	111.00
1	C	160	ALA	N-CA-C	9.53	136.72	111.00
1	F	433	TYR	N-CA-C	-7.82	89.88	111.00
1	A	433	TYR	N-CA-C	-7.82	89.89	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	433	TYR	N-CA-C	-7.82	89.89	111.00
1	C	433	TYR	N-CA-C	-7.81	89.90	111.00
1	D	433	TYR	N-CA-C	-7.81	89.92	111.00
1	E	433	TYR	N-CA-C	-7.81	89.91	111.00
2	Q	22	ASP	N-CA-C	-7.43	90.94	111.00
2	O	22	ASP	N-CA-C	-7.41	90.99	111.00
2	P	22	ASP	N-CA-C	-7.36	91.14	111.00
2	R	22	ASP	N-CA-C	-7.33	91.21	111.00
2	S	22	ASP	N-CA-C	-7.33	91.21	111.00
2	T	22	ASP	N-CA-C	-7.32	91.23	111.00
1	E	433	TYR	CB-CA-C	7.25	124.89	110.40
1	C	433	TYR	CB-CA-C	7.25	124.89	110.40
1	F	433	TYR	CB-CA-C	7.24	124.88	110.40
1	A	433	TYR	CB-CA-C	7.24	124.87	110.40
1	D	433	TYR	CB-CA-C	7.24	124.87	110.40
1	B	433	TYR	CB-CA-C	7.22	124.84	110.40
1	D	322	LEU	N-CA-C	-7.14	91.71	111.00
1	A	322	LEU	N-CA-C	-7.14	91.73	111.00
1	B	322	LEU	N-CA-C	-7.14	91.73	111.00
1	F	322	LEU	N-CA-C	-7.13	91.75	111.00
1	C	322	LEU	N-CA-C	-7.13	91.75	111.00
1	E	322	LEU	N-CA-C	-7.12	91.77	111.00
1	C	188	LEU	N-CA-C	-6.77	92.72	111.00
1	F	188	LEU	N-CA-C	-6.77	92.72	111.00
1	A	188	LEU	N-CA-C	-6.76	92.74	111.00
1	E	188	LEU	N-CA-C	-6.76	92.74	111.00
1	B	188	LEU	N-CA-C	-6.76	92.76	111.00
1	D	188	LEU	N-CA-C	-6.75	92.78	111.00
1	E	183	SER	N-CA-C	-6.63	93.09	111.00
1	B	674	SER	N-CA-C	-6.62	93.12	111.00
1	F	674	SER	N-CA-C	-6.62	93.12	111.00
1	F	183	SER	N-CA-C	-6.62	93.13	111.00
1	C	183	SER	N-CA-C	-6.62	93.14	111.00
1	E	674	SER	N-CA-C	-6.62	93.14	111.00
1	A	674	SER	N-CA-C	-6.61	93.14	111.00
1	A	183	SER	N-CA-C	-6.61	93.15	111.00
1	C	674	SER	N-CA-C	-6.61	93.16	111.00
1	D	674	SER	N-CA-C	-6.61	93.16	111.00
1	D	183	SER	N-CA-C	-6.60	93.17	111.00
1	B	183	SER	N-CA-C	-6.59	93.19	111.00
1	B	159	TYR	CB-CG-CD2	-6.47	117.12	121.00
1	D	159	TYR	CB-CG-CD2	-6.44	117.14	121.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	159	TYR	CB-CG-CD2	-6.43	117.14	121.00
1	F	159	TYR	CB-CG-CD2	-6.40	117.16	121.00
1	C	147	ARG	N-CA-C	6.40	128.27	111.00
1	D	147	ARG	N-CA-C	6.39	128.27	111.00
1	B	147	ARG	N-CA-C	6.39	128.25	111.00
1	A	147	ARG	N-CA-C	6.38	128.24	111.00
1	E	147	ARG	N-CA-C	6.38	128.24	111.00
1	C	159	TYR	CB-CG-CD2	-6.38	117.17	121.00
1	F	147	ARG	N-CA-C	6.38	128.23	111.00
1	E	159	TYR	CB-CG-CD2	-6.38	117.17	121.00
2	O	25	GLY	N-CA-C	-6.29	97.36	113.10
2	T	25	GLY	N-CA-C	-6.29	97.36	113.10
2	Q	25	GLY	N-CA-C	-6.28	97.41	113.10
2	P	25	GLY	N-CA-C	-6.20	97.60	113.10
2	S	25	GLY	N-CA-C	-6.14	97.75	113.10
2	R	25	GLY	N-CA-C	-6.06	97.94	113.10
1	B	64	ASN	C-N-CA	-5.76	107.29	121.70
1	D	159	TYR	CB-CG-CD1	5.63	124.38	121.00
1	B	159	TYR	CB-CG-CD1	5.59	124.35	121.00
1	C	159	TYR	CB-CG-CD1	5.57	124.34	121.00
1	A	159	TYR	CB-CG-CD1	5.56	124.33	121.00
1	F	159	TYR	CB-CG-CD1	5.55	124.33	121.00
1	E	159	TYR	CB-CG-CD1	5.52	124.31	121.00
2	S	24	ASP	N-CA-CB	-5.36	100.95	110.60
2	O	24	ASP	N-CA-CB	-5.36	100.96	110.60
2	P	24	ASP	N-CA-CB	-5.35	100.97	110.60
1	E	120	LEU	N-CA-C	5.35	125.44	111.00
1	C	120	LEU	N-CA-C	5.35	125.44	111.00
1	D	120	LEU	N-CA-C	5.34	125.43	111.00
1	A	120	LEU	N-CA-C	5.34	125.42	111.00
1	D	190	PRO	N-CA-C	-5.34	98.21	112.10
2	Q	24	ASP	N-CA-CB	-5.34	100.99	110.60
1	F	120	LEU	N-CA-C	5.34	125.41	111.00
2	R	24	ASP	N-CA-CB	-5.33	101.00	110.60
1	B	120	LEU	N-CA-C	5.33	125.40	111.00
2	Q	24	ASP	CB-CG-OD1	-5.33	113.50	118.30
2	S	24	ASP	CB-CG-OD1	-5.33	113.50	118.30
2	T	24	ASP	CB-CG-OD1	-5.33	113.50	118.30
1	D	146	LYS	O-C-N	-5.32	114.19	122.70
2	T	24	ASP	N-CA-CB	-5.31	101.04	110.60
1	C	190	PRO	N-CA-C	-5.29	98.36	112.10
2	P	24	ASP	CB-CG-OD1	-5.28	113.55	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	632	TYR	N-CA-C	5.27	125.23	111.00
1	E	632	TYR	N-CA-C	5.26	125.20	111.00
1	B	188	LEU	CA-C-N	5.26	128.76	117.20
1	D	632	TYR	N-CA-C	5.26	125.19	111.00
1	A	632	TYR	N-CA-C	5.25	125.18	111.00
1	D	188	LEU	CA-C-N	5.25	128.75	117.20
1	C	632	TYR	N-CA-C	5.25	125.17	111.00
1	F	643	ILE	CB-CA-C	5.24	122.08	111.60
1	A	188	LEU	CA-C-N	5.24	128.73	117.20
1	C	188	LEU	CA-C-N	5.24	128.72	117.20
1	E	188	LEU	CA-C-N	5.23	128.71	117.20
1	F	632	TYR	N-CA-C	5.23	125.13	111.00
1	F	188	LEU	CA-C-N	5.21	128.66	117.20
1	E	190	PRO	N-CA-C	-5.13	98.76	112.10
1	C	146	LYS	O-C-N	-5.13	114.50	122.70
2	R	24	ASP	CB-CG-OD1	-5.13	113.69	118.30
1	E	219	GLU	N-CA-C	-5.12	97.19	111.00
1	D	160	ALA	N-CA-CB	-5.09	102.98	110.10
2	O	24	ASP	CB-CG-OD1	-5.08	113.73	118.30
1	F	160	ALA	N-CA-CB	-5.07	103.01	110.10
1	B	160	ALA	N-CA-CB	-5.06	103.01	110.10
1	E	160	ALA	N-CA-CB	-5.06	103.01	110.10
1	A	160	ALA	N-CA-CB	-5.05	103.02	110.10
1	C	160	ALA	N-CA-CB	-5.03	103.06	110.10
1	C	219	GLU	N-CA-C	-5.03	97.42	111.00
1	D	219	GLU	N-CA-C	-5.03	97.43	111.00
1	F	219	GLU	N-CA-C	-5.02	97.44	111.00
1	A	219	GLU	N-CA-C	-5.01	97.46	111.00

There are no chirality outliers.

There are no planarity outliers.

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	5992	0	6010	866	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	5992	0	6010	875	0
1	C	5992	0	6010	855	0
1	D	5992	0	6010	863	0
1	E	5992	0	6010	863	0
1	F	5992	0	6010	862	0
2	O	1146	0	1071	195	0
2	P	1146	0	1071	195	0
2	Q	1146	0	1071	189	0
2	R	1146	0	1071	196	0
2	S	1146	0	1071	196	0
2	T	1146	0	1071	192	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
4	O	2	0	0	0	0
4	P	2	0	0	0	0
4	Q	2	0	0	0	0
4	R	2	0	0	0	0
4	S	2	0	0	0	0
4	T	2	0	0	0	0
All	All	42846	0	42486	6152	0

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 72.

All (6152) 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)
1:A:183:SER:O	1:A:187:SER:CB	1.70	1.39
1:D:183:SER:O	1:D:187:SER:CB	1.70	1.38
1:F:183:SER:O	1:F:187:SER:CB	1.70	1.37
1:E:183:SER:O	1:E:187:SER:CB	1.70	1.36
1:B:183:SER:O	1:B:187:SER:CB	1.70	1.35
1:C:183:SER:O	1:C:187:SER:CB	1.70	1.35
2:P:48:LEU:HA	2:P:51:MET:HE2	1.22	1.19
1:B:120:LEU:O	1:B:120:LEU:HD13	1.43	1.18
1:A:550:SER:HB3	1:A:553:GLN:HG3	1.19	1.18
1:E:120:LEU:HD13	1:E:120:LEU:O	1.43	1.18

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:550:SER:HB3	1:C:553:GLN:HG3	1.19	1.17
1:F:550:SER:HB3	1:F:553:GLN:HG3	1.18	1.17
2:O:48:LEU:HA	2:O:51:MET:HE2	1.21	1.15
1:A:120:LEU:HD13	1:A:120:LEU:O	1.43	1.15
2:Q:48:LEU:HA	2:Q:51:MET:HE2	1.19	1.15
1:C:120:LEU:O	1:C:120:LEU:HD13	1.43	1.14
1:D:550:SER:HB3	1:D:553:GLN:HG3	1.18	1.14
1:E:550:SER:HB3	1:E:553:GLN:HG3	1.20	1.14
1:B:550:SER:HB3	1:B:553:GLN:HG3	1.18	1.14
1:F:120:LEU:O	1:F:120:LEU:HD13	1.43	1.14
1:F:183:SER:C	1:F:187:SER:HB2	1.68	1.13
1:D:765:THR:HA	1:D:769:SER:HB2	1.28	1.13
1:D:120:LEU:HD13	1:D:120:LEU:O	1.43	1.13
1:C:183:SER:C	1:C:187:SER:HB2	1.68	1.12
1:E:183:SER:C	1:E:187:SER:HB2	1.68	1.12
1:E:765:THR:HA	1:E:769:SER:HB2	1.28	1.12
1:A:765:THR:HA	1:A:769:SER:HB2	1.28	1.11
1:B:183:SER:C	1:B:187:SER:HB2	1.68	1.11
1:A:183:SER:C	1:A:187:SER:HB2	1.68	1.11
1:D:597:ASN:HD21	1:D:601:GLU:HB2	1.14	1.11
1:D:183:SER:C	1:D:187:SER:HB2	1.68	1.11
1:F:765:THR:HA	1:F:769:SER:HB2	1.29	1.10
1:C:765:THR:HA	1:C:769:SER:HB2	1.29	1.10
2:T:48:LEU:HA	2:T:51:MET:HE2	1.20	1.09
1:A:597:ASN:HD21	1:A:601:GLU:HB2	1.17	1.08
1:D:127:SER:O	1:D:133:GLU:OE2	1.71	1.08
1:E:127:SER:O	1:E:133:GLU:OE2	1.72	1.08
1:C:127:SER:O	1:C:133:GLU:OE2	1.71	1.08
1:B:765:THR:HA	1:B:769:SER:HB2	1.28	1.08
2:T:28:THR:HG23	2:T:31:GLU:HG2	1.35	1.08
1:B:597:ASN:HD21	1:B:601:GLU:HB2	1.18	1.08
1:F:127:SER:O	1:F:133:GLU:OE2	1.71	1.08
1:B:127:SER:O	1:B:133:GLU:OE2	1.72	1.07
1:A:127:SER:O	1:A:133:GLU:OE2	1.71	1.07
1:B:64:ASN:N	1:B:64:ASN:HD22	1.37	1.07
1:B:767:GLN:HG2	1:B:768:LYS:HG2	1.37	1.07
1:C:767:GLN:HG2	1:C:768:LYS:HG2	1.37	1.06
2:Q:28:THR:HG23	2:Q:31:GLU:HG2	1.37	1.06
1:A:767:GLN:HG2	1:A:768:LYS:HG2	1.37	1.06
2:R:28:THR:HG23	2:R:31:GLU:HG2	1.36	1.06
1:D:767:GLN:HG2	1:D:768:LYS:HG2	1.37	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:767:GLN:HG2	1:F:768:LYS:HG2	1.37	1.05
1:F:97:TYR:HE1	1:F:178:SER:HB2	1.19	1.05
1:E:767:GLN:HG2	1:E:768:LYS:HG2	1.37	1.04
1:E:597:ASN:HD21	1:E:601:GLU:HB2	1.18	1.04
2:O:28:THR:HG23	2:O:31:GLU:HG2	1.36	1.04
1:F:597:ASN:HD21	1:F:601:GLU:HB2	1.17	1.04
1:F:324:THR:HB	1:F:499:PRO:HA	1.39	1.04
1:C:324:THR:HB	1:C:499:PRO:HA	1.40	1.03
1:C:597:ASN:HD21	1:C:601:GLU:HB2	1.18	1.03
1:E:324:THR:HB	1:E:499:PRO:HA	1.38	1.03
1:D:324:THR:HB	1:D:499:PRO:HA	1.38	1.03
2:S:28:THR:HG23	2:S:31:GLU:HG2	1.37	1.03
2:P:28:THR:HG23	2:P:31:GLU:HG2	1.36	1.02
1:C:97:TYR:HE1	1:C:178:SER:HB2	1.21	1.02
2:S:48:LEU:HA	2:S:51:MET:HE2	1.36	1.02
2:O:51:MET:HB3	2:O:71:MET:HE2	1.42	1.02
1:E:97:TYR:HE1	1:E:178:SER:HB2	1.21	1.02
1:F:408:LEU:H	1:F:408:LEU:HD12	1.25	1.01
1:D:183:SER:O	1:D:187:SER:HB2	0.83	1.01
1:A:183:SER:O	1:A:187:SER:HB2	0.83	1.01
1:B:324:THR:HB	1:B:499:PRO:HA	1.38	1.01
1:E:183:SER:O	1:E:187:SER:HB2	0.83	1.00
1:B:97:TYR:HE1	1:B:178:SER:HB2	1.21	1.00
1:F:183:SER:O	1:F:187:SER:HB2	0.83	1.00
1:C:183:SER:O	1:C:187:SER:HB2	0.83	1.00
1:B:183:SER:O	1:B:187:SER:HB2	0.83	0.99
2:S:50:ASP:HA	2:S:53:ASN:HB3	1.44	0.99
1:E:408:LEU:H	1:E:408:LEU:HD12	1.26	0.99
1:A:324:THR:HB	1:A:499:PRO:HA	1.40	0.99
1:A:97:TYR:HE1	1:A:178:SER:HB2	1.20	0.99
1:D:97:TYR:HE1	1:D:178:SER:HB2	1.22	0.99
1:E:432:TYR:C	1:E:433:TYR:O	1.93	0.98
1:D:408:LEU:H	1:D:408:LEU:HD12	1.27	0.98
1:A:408:LEU:H	1:A:408:LEU:HD12	1.27	0.98
2:P:50:ASP:HA	2:P:53:ASN:HB3	1.44	0.98
1:D:115:LYS:HZ2	1:D:116:GLU:H	1.01	0.98
1:F:678:VAL:HG22	1:F:745:TYR:HE2	1.27	0.98
1:C:408:LEU:HD12	1:C:408:LEU:H	1.28	0.97
1:F:115:LYS:HZ2	1:F:116:GLU:H	0.98	0.97
2:Q:51:MET:HB3	2:Q:71:MET:HE2	1.42	0.97
2:T:50:ASP:HA	2:T:53:ASN:HB3	1.45	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:408:LEU:H	1:B:408:LEU:HD12	1.28	0.97
1:A:89:ILE:HG22	1:A:93:VAL:HG11	1.47	0.97
1:B:89:ILE:HG22	1:B:93:VAL:HG11	1.46	0.97
1:A:432:TYR:C	1:A:433:TYR:O	1.93	0.97
1:D:107:THR:HG21	1:D:115:LYS:HE2	1.47	0.97
2:O:50:ASP:HA	2:O:53:ASN:HB3	1.45	0.97
1:D:432:TYR:C	1:D:433:TYR:O	1.94	0.96
1:C:678:VAL:HG22	1:C:745:TYR:HE2	1.28	0.96
1:F:90:PRO:HG2	1:F:93:VAL:HB	1.47	0.96
1:A:592:GLU:HB3	1:A:604:LEU:HD11	1.47	0.96
1:D:89:ILE:HG22	1:D:93:VAL:HG11	1.46	0.96
1:F:617:LYS:HZ2	1:F:618:ASN:HD21	1.02	0.96
1:C:90:PRO:HG2	1:C:93:VAL:HB	1.46	0.96
2:Q:50:ASP:HA	2:Q:53:ASN:HB3	1.44	0.96
1:E:89:ILE:HG22	1:E:93:VAL:HG11	1.45	0.95
1:D:617:LYS:HZ2	1:D:618:ASN:HD21	1.00	0.95
1:D:678:VAL:HG22	1:D:745:TYR:HE2	1.29	0.95
1:C:115:LYS:HZ2	1:C:116:GLU:H	0.98	0.95
1:C:89:ILE:HG22	1:C:93:VAL:HG11	1.45	0.95
1:B:432:TYR:C	1:B:433:TYR:O	1.93	0.95
1:C:107:THR:HG21	1:C:115:LYS:HE2	1.48	0.95
1:E:90:PRO:HG2	1:E:93:VAL:HB	1.47	0.95
2:R:50:ASP:HA	2:R:53:ASN:HB3	1.45	0.95
1:E:115:LYS:HZ2	1:E:116:GLU:H	0.98	0.94
1:E:592:GLU:HB3	1:E:604:LEU:HD11	1.49	0.94
1:E:678:VAL:HG22	1:E:745:TYR:HE2	1.29	0.94
1:E:629:ASN:HD21	1:E:631:SER:HB2	1.32	0.94
1:B:90:PRO:HG2	1:B:93:VAL:HB	1.47	0.94
1:C:617:LYS:HZ2	1:C:618:ASN:HD21	1.03	0.94
1:E:617:LYS:HZ2	1:E:618:ASN:HD21	1.00	0.94
1:A:678:VAL:HG22	1:A:745:TYR:HE2	1.28	0.94
1:B:115:LYS:HZ2	1:B:116:GLU:H	1.00	0.94
1:B:186:LYS:HE3	1:B:234:LEU:HD12	1.49	0.94
1:C:432:TYR:C	1:C:433:TYR:O	1.94	0.94
1:D:133:GLU:HG3	1:D:133:GLU:O	1.68	0.93
1:F:89:ILE:HG22	1:F:93:VAL:HG11	1.45	0.93
2:P:51:MET:HB3	2:P:71:MET:HE2	1.50	0.93
1:B:354:SER:O	1:B:371:SER:HB2	1.68	0.93
1:F:441:VAL:HG22	1:F:461:LYS:HG2	1.51	0.93
1:F:133:GLU:O	1:F:133:GLU:HG3	1.68	0.93
1:D:592:GLU:HB3	1:D:604:LEU:HD11	1.49	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:592:GLU:HB3	1:F:604:LEU:HD11	1.49	0.93
1:A:617:LYS:HZ2	1:A:618:ASN:HD21	1.05	0.93
1:B:592:GLU:HB3	1:B:604:LEU:HD11	1.50	0.93
1:F:354:SER:O	1:F:371:SER:HB2	1.68	0.93
2:S:51:MET:HB3	2:S:71:MET:HE2	1.48	0.93
1:A:90:PRO:HG2	1:A:93:VAL:HB	1.49	0.93
1:B:678:VAL:HG22	1:B:745:TYR:HE2	1.30	0.93
1:D:90:PRO:HG2	1:D:93:VAL:HB	1.48	0.93
1:E:441:VAL:HG22	1:E:461:LYS:HG2	1.51	0.93
1:F:186:LYS:HE3	1:F:234:LEU:HD12	1.50	0.93
2:P:24:ASP:HB2	2:P:26:THR:HG23	1.50	0.93
1:A:441:VAL:HG22	1:A:461:LYS:HG2	1.50	0.93
1:E:133:GLU:HG3	1:E:133:GLU:O	1.68	0.92
1:C:133:GLU:O	1:C:133:GLU:HG3	1.68	0.92
1:D:441:VAL:HG22	1:D:461:LYS:HG2	1.51	0.92
2:Q:24:ASP:HB2	2:Q:26:THR:HG23	1.50	0.92
1:A:115:LYS:HZ2	1:A:116:GLU:H	1.01	0.92
1:A:715:GLU:HA	1:A:718:ARG:CZ	2.00	0.92
2:S:24:ASP:HB2	2:S:26:THR:HG23	1.50	0.92
1:A:629:ASN:HD21	1:A:631:SER:HB2	1.32	0.92
1:B:715:GLU:HA	1:B:718:ARG:CZ	2.00	0.92
1:F:629:ASN:HD21	1:F:631:SER:HB2	1.34	0.92
1:B:441:VAL:HG22	1:B:461:LYS:HG2	1.50	0.92
1:D:667:LEU:HD13	1:D:678:VAL:HG21	1.51	0.92
1:E:715:GLU:HA	1:E:718:ARG:CZ	2.00	0.92
2:R:51:MET:HB3	2:R:71:MET:HE2	1.51	0.92
2:R:48:LEU:HD23	2:R:51:MET:HE2	1.49	0.92
1:B:629:ASN:HD21	1:B:631:SER:HB2	1.34	0.92
1:D:715:GLU:HA	1:D:718:ARG:CZ	1.99	0.92
1:F:722:ILE:HG23	1:F:760:VAL:HG13	1.52	0.92
1:A:354:SER:O	1:A:371:SER:HB2	1.71	0.91
1:C:441:VAL:HG22	1:C:461:LYS:HG2	1.52	0.91
1:E:354:SER:O	1:E:371:SER:HB2	1.70	0.91
2:T:24:ASP:HB2	2:T:26:THR:HG23	1.50	0.91
1:A:186:LYS:HE3	1:A:234:LEU:HD12	1.50	0.91
1:B:133:GLU:HG3	1:B:133:GLU:O	1.68	0.91
1:B:617:LYS:HZ2	1:B:618:ASN:HD21	1.18	0.91
1:C:592:GLU:HB3	1:C:604:LEU:HD11	1.51	0.91
1:D:90:PRO:O	1:D:93:VAL:HG12	1.70	0.91
1:E:186:LYS:HE3	1:E:234:LEU:HD12	1.50	0.91
1:A:617:LYS:NZ	1:A:618:ASN:HD21	1.67	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:550:SER:CB	1:B:553:GLN:HG3	2.01	0.91
1:E:581:GLN:NE2	1:E:629:ASN:H	1.69	0.91
1:C:617:LYS:NZ	1:C:618:ASN:HD21	1.68	0.91
1:F:617:LYS:NZ	1:F:618:ASN:HD21	1.68	0.91
1:D:354:SER:O	1:D:371:SER:HB2	1.70	0.91
1:A:133:GLU:O	1:A:133:GLU:HG3	1.68	0.91
1:D:617:LYS:NZ	1:D:618:ASN:HD21	1.67	0.91
1:D:629:ASN:HD21	1:D:631:SER:HB2	1.33	0.91
1:C:715:GLU:HA	1:C:718:ARG:CZ	2.00	0.90
1:F:715:GLU:HA	1:F:718:ARG:CZ	2.00	0.90
1:C:354:SER:O	1:C:371:SER:HB2	1.70	0.90
1:A:581:GLN:NE2	1:A:629:ASN:H	1.69	0.90
1:A:722:ILE:HG23	1:A:760:VAL:HG13	1.52	0.90
1:A:97:TYR:CE1	1:A:178:SER:HB2	2.06	0.90
1:F:107:THR:HG21	1:F:115:LYS:HE2	1.53	0.90
1:A:667:LEU:HD13	1:A:678:VAL:HG21	1.53	0.90
1:C:186:LYS:HE3	1:C:234:LEU:HD12	1.52	0.90
1:C:629:ASN:HD21	1:C:631:SER:HB2	1.35	0.90
1:D:550:SER:CB	1:D:553:GLN:HG3	2.01	0.90
1:F:140:ARG:HA	1:F:140:ARG:HE	1.36	0.90
2:R:24:ASP:HB2	2:R:26:THR:HG23	1.52	0.90
1:F:90:PRO:O	1:F:93:VAL:HG12	1.72	0.90
2:O:24:ASP:HB2	2:O:26:THR:HG23	1.50	0.90
1:F:581:GLN:NE2	1:F:629:ASN:H	1.69	0.90
1:A:107:THR:HG21	1:A:115:LYS:HE2	1.52	0.90
1:B:722:ILE:HG23	1:B:760:VAL:HG13	1.52	0.90
1:F:97:TYR:CE1	1:F:178:SER:HB2	2.05	0.90
1:D:140:ARG:HE	1:D:140:ARG:HA	1.37	0.89
1:A:197:LYS:HB3	1:A:197:LYS:HZ2	1.38	0.89
1:A:550:SER:CB	1:A:553:GLN:HG3	2.03	0.89
1:A:724:ARG:O	1:A:727:GLN:HB2	1.72	0.89
1:F:432:TYR:C	1:F:433:TYR:O	1.93	0.89
1:C:142:VAL:HG22	1:C:154:ILE:HD12	1.55	0.89
1:E:667:LEU:HD13	1:E:678:VAL:HG21	1.53	0.89
1:D:186:LYS:HE3	1:D:234:LEU:HD12	1.52	0.89
1:E:722:ILE:HG23	1:E:760:VAL:HG13	1.53	0.89
1:E:90:PRO:O	1:E:93:VAL:HG12	1.71	0.89
1:B:617:LYS:NZ	1:B:618:ASN:HD21	1.68	0.89
1:F:142:VAL:HG22	1:F:154:ILE:HD12	1.55	0.89
1:A:140:ARG:HA	1:A:140:ARG:HE	1.36	0.89
1:C:722:ILE:HG23	1:C:760:VAL:HG13	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:722:ILE:HG23	1:D:760:VAL:HG13	1.53	0.88
1:B:667:LEU:HD13	1:B:678:VAL:HG21	1.52	0.88
1:B:715:GLU:HG3	1:B:718:ARG:HH12	1.39	0.88
1:D:581:GLN:NE2	1:D:629:ASN:H	1.71	0.88
1:B:97:TYR:CE1	1:B:178:SER:HB2	2.07	0.88
1:E:140:ARG:HA	1:E:140:ARG:HE	1.37	0.88
1:E:617:LYS:NZ	1:E:618:ASN:HD21	1.70	0.88
1:C:550:SER:CB	1:C:553:GLN:HG3	2.02	0.88
1:B:64:ASN:ND2	1:B:64:ASN:N	2.12	0.88
1:C:140:ARG:HA	1:C:140:ARG:HE	1.38	0.88
1:D:97:TYR:CE1	1:D:178:SER:HB2	2.08	0.88
1:B:90:PRO:O	1:B:93:VAL:HG12	1.71	0.88
1:C:197:LYS:HB3	1:C:197:LYS:HZ2	1.38	0.88
1:E:142:VAL:HG22	1:E:154:ILE:HD12	1.56	0.88
2:T:24:ASP:OD1	2:T:24:ASP:N	2.05	0.88
1:D:197:LYS:HZ2	1:D:197:LYS:HB3	1.39	0.88
1:E:97:TYR:CE1	1:E:178:SER:HB2	2.07	0.88
1:A:214:PHE:HB3	1:A:218:LEU:HB3	1.56	0.88
1:E:107:THR:HG21	1:E:115:LYS:HE2	1.53	0.88
1:E:214:PHE:HB3	1:E:218:LEU:HB3	1.56	0.88
1:B:724:ARG:O	1:B:727:GLN:HB2	1.73	0.88
1:C:90:PRO:O	1:C:93:VAL:HG12	1.73	0.88
1:D:142:VAL:HG22	1:D:154:ILE:HD12	1.54	0.88
1:F:154:ILE:HG13	1:F:171:TYR:CZ	2.08	0.88
1:F:667:LEU:HD13	1:F:678:VAL:HG21	1.55	0.87
1:F:724:ARG:O	1:F:727:GLN:HB2	1.73	0.87
1:C:581:GLN:NE2	1:C:629:ASN:H	1.72	0.87
1:E:76:LEU:HD22	1:E:76:LEU:H	1.40	0.87
1:B:140:ARG:HA	1:B:140:ARG:HE	1.37	0.87
1:B:142:VAL:HG22	1:B:154:ILE:HD12	1.55	0.87
1:D:214:PHE:HB3	1:D:218:LEU:HB3	1.55	0.87
1:F:254:ARG:HD2	1:F:254:ARG:H	1.39	0.87
1:C:97:TYR:CE1	1:C:178:SER:HB2	2.08	0.87
1:D:550:SER:HB3	1:D:553:GLN:CG	2.04	0.87
1:A:142:VAL:HG22	1:A:154:ILE:HD12	1.56	0.87
1:C:667:LEU:HD13	1:C:678:VAL:HG21	1.55	0.87
1:B:76:LEU:HD22	1:B:76:LEU:H	1.40	0.87
1:D:254:ARG:HD2	1:D:254:ARG:H	1.39	0.87
1:A:715:GLU:HG3	1:A:718:ARG:HH12	1.39	0.87
1:B:581:GLN:NE2	1:B:629:ASN:H	1.72	0.87
2:O:24:ASP:N	2:O:24:ASP:OD1	2.05	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:720:ILE:HD11	1:A:724:ARG:NH2	1.90	0.87
1:B:214:PHE:HB3	1:B:218:LEU:HB3	1.57	0.86
1:E:550:SER:CB	1:E:553:GLN:HG3	2.02	0.86
1:A:499:PRO:HG2	1:A:504:ILE:HD11	1.56	0.86
1:A:615:ILE:HG23	1:A:619:ILE:HD12	1.55	0.86
1:B:325:TYR:HB2	1:B:498:ALA:HB3	1.58	0.86
1:B:499:PRO:HG2	1:B:504:ILE:HD11	1.56	0.86
1:B:550:SER:HB3	1:B:553:GLN:CG	2.04	0.86
1:D:724:ARG:O	1:D:727:GLN:HB2	1.76	0.86
1:F:550:SER:CB	1:F:553:GLN:HG3	2.01	0.86
1:F:462:ILE:HG12	1:F:463:THR:H	1.40	0.86
1:F:550:SER:HB3	1:F:553:GLN:CG	2.05	0.86
1:E:715:GLU:HG3	1:E:718:ARG:HH12	1.38	0.86
1:F:197:LYS:HZ2	1:F:197:LYS:HB3	1.39	0.86
1:D:462:ILE:HG12	1:D:463:THR:H	1.39	0.86
1:D:499:PRO:HG2	1:D:504:ILE:HD11	1.56	0.86
1:A:462:ILE:HG12	1:A:463:THR:H	1.39	0.86
1:B:462:ILE:HG12	1:B:463:THR:H	1.41	0.86
1:E:254:ARG:HD2	1:E:254:ARG:H	1.39	0.86
1:E:695:LYS:HB2	2:S:18:LEU:HD22	1.55	0.86
1:A:140:ARG:NE	1:A:140:ARG:HA	1.89	0.86
1:A:254:ARG:HD2	1:A:254:ARG:H	1.38	0.86
1:B:107:THR:HG21	1:B:115:LYS:HE2	1.55	0.86
1:C:154:ILE:HG13	1:C:171:TYR:CZ	2.11	0.86
1:F:499:PRO:HG2	1:F:504:ILE:HD11	1.57	0.86
1:C:695:LYS:HB2	2:Q:18:LEU:HD22	1.57	0.86
2:S:24:ASP:OD1	2:S:24:ASP:N	2.05	0.86
1:A:90:PRO:O	1:A:93:VAL:HG12	1.76	0.86
1:C:499:PRO:HG2	1:C:504:ILE:HD11	1.58	0.86
1:C:715:GLU:HG3	1:C:718:ARG:HH12	1.38	0.86
1:C:140:ARG:HA	1:C:140:ARG:NE	1.90	0.85
1:F:76:LEU:HD22	1:F:76:LEU:H	1.40	0.85
1:F:140:ARG:HA	1:F:140:ARG:NE	1.89	0.85
1:A:550:SER:HB3	1:A:553:GLN:CG	2.05	0.85
1:B:140:ARG:NE	1:B:140:ARG:HA	1.90	0.85
1:C:214:PHE:HB3	1:C:218:LEU:HB3	1.55	0.85
1:E:326:ILE:HG22	1:E:328:PHE:CE1	2.11	0.85
1:A:154:ILE:HG13	1:A:171:TYR:CZ	2.11	0.85
1:C:254:ARG:H	1:C:254:ARG:HD2	1.40	0.85
1:D:720:ILE:HD11	1:D:724:ARG:NH2	1.92	0.85
1:E:615:ILE:HG23	1:E:619:ILE:HD12	1.58	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:325:TYR:HB2	1:A:498:ALA:HB3	1.59	0.85
1:C:720:ILE:HD11	1:C:724:ARG:NH2	1.92	0.85
1:D:140:ARG:NE	1:D:140:ARG:HA	1.90	0.85
1:E:550:SER:HB3	1:E:553:GLN:CG	2.05	0.85
1:D:615:ILE:HG23	1:D:619:ILE:HD12	1.57	0.85
1:E:288:VAL:HG23	1:E:289:GLU:H	1.40	0.85
2:T:28:THR:HG23	2:T:31:GLU:CG	2.06	0.85
1:F:715:GLU:HG3	1:F:718:ARG:HH12	1.38	0.84
1:D:325:TYR:HB2	1:D:498:ALA:HB3	1.59	0.84
1:E:479:LYS:HG2	1:E:488:LEU:HD21	1.59	0.84
2:O:28:THR:HG23	2:O:31:GLU:CG	2.06	0.84
2:R:41:GLN:C	2:R:43:PRO:HD2	1.98	0.84
1:D:154:ILE:HG13	1:D:171:TYR:CZ	2.12	0.84
2:R:28:THR:HG23	2:R:31:GLU:CG	2.06	0.84
1:C:724:ARG:O	1:C:727:GLN:HB2	1.77	0.84
1:E:197:LYS:HB3	1:E:197:LYS:HZ2	1.41	0.84
2:P:41:GLN:C	2:P:43:PRO:HD2	1.97	0.84
2:S:28:THR:HG23	2:S:31:GLU:CG	2.07	0.84
2:S:41:GLN:C	2:S:43:PRO:HD2	1.96	0.84
1:B:326:ILE:HG22	1:B:328:PHE:CE1	2.13	0.84
1:E:325:TYR:HB2	1:E:498:ALA:HB3	1.59	0.84
1:F:214:PHE:HB3	1:F:218:LEU:HB3	1.58	0.84
1:D:288:VAL:HG23	1:D:289:GLU:H	1.40	0.84
1:E:462:ILE:HG12	1:E:463:THR:H	1.40	0.84
1:A:326:ILE:HG22	1:A:328:PHE:CE1	2.13	0.84
1:B:720:ILE:HD11	1:B:724:ARG:NH2	1.92	0.84
1:C:288:VAL:HG23	1:C:289:GLU:H	1.40	0.84
1:E:720:ILE:HD11	1:E:724:ARG:NH2	1.92	0.84
1:F:720:ILE:HD11	1:F:724:ARG:NH2	1.92	0.84
2:P:28:THR:HG23	2:P:31:GLU:CG	2.07	0.84
1:B:479:LYS:HG2	1:B:488:LEU:HD21	1.59	0.84
1:E:154:ILE:HG13	1:E:171:TYR:CZ	2.12	0.84
1:E:724:ARG:O	1:E:727:GLN:HB2	1.76	0.84
2:O:47:GLU:O	2:O:51:MET:HG3	1.78	0.84
2:P:47:GLU:O	2:P:51:MET:HG3	1.78	0.84
2:Q:41:GLN:C	2:Q:43:PRO:HD2	1.98	0.84
2:T:47:GLU:O	2:T:51:MET:HG3	1.78	0.84
1:B:154:ILE:HG13	1:B:171:TYR:CZ	2.11	0.83
1:C:671:ARG:NH1	1:C:677:GLY:HA3	1.93	0.83
1:F:615:ILE:HG23	1:F:619:ILE:HD12	1.59	0.83
2:Q:28:THR:HG23	2:Q:31:GLU:CG	2.07	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:715:GLU:HG3	1:D:718:ARG:HH12	1.40	0.83
1:E:140:ARG:HA	1:E:140:ARG:NE	1.91	0.83
1:F:326:ILE:HG22	1:F:328:PHE:CE1	2.13	0.83
2:Q:24:ASP:N	2:Q:24:ASP:OD1	2.05	0.83
2:T:41:GLN:C	2:T:43:PRO:HD2	1.98	0.83
1:B:615:ILE:HG23	1:B:619:ILE:HD12	1.58	0.83
1:E:499:PRO:HG2	1:E:504:ILE:HD11	1.57	0.83
1:F:678:VAL:HG22	1:F:745:TYR:CE2	2.13	0.83
1:A:76:LEU:HD22	1:A:76:LEU:H	1.41	0.83
1:C:325:TYR:HB2	1:C:498:ALA:HB3	1.59	0.83
1:D:372:LYS:HG3	1:D:373:LYS:H	1.42	0.83
1:F:254:ARG:HB3	1:F:254:ARG:HH11	1.43	0.83
1:B:695:LYS:HB2	2:P:18:LEU:HD22	1.59	0.83
1:C:550:SER:HB3	1:C:553:GLN:CG	2.06	0.83
1:F:671:ARG:NH1	1:F:677:GLY:HA3	1.93	0.83
1:B:657:ILE:HG13	1:B:756:ILE:HD13	1.60	0.83
1:E:165:GLN:NE2	1:E:252:ASP:HB3	1.93	0.83
1:F:288:VAL:HG23	1:F:289:GLU:H	1.41	0.83
1:A:671:ARG:NH1	1:A:677:GLY:HA3	1.94	0.83
1:B:254:ARG:HD2	1:B:254:ARG:H	1.41	0.83
1:B:288:VAL:HG23	1:B:289:GLU:H	1.42	0.83
1:F:479:LYS:HG2	1:F:488:LEU:HD21	1.60	0.83
2:R:47:GLU:O	2:R:51:MET:HG3	1.79	0.83
2:S:47:GLU:O	2:S:51:MET:HG3	1.79	0.83
1:A:479:LYS:HG2	1:A:488:LEU:HD21	1.59	0.83
1:E:607:ASN:HB3	1:E:609:GLU:OE2	1.79	0.83
1:E:671:ARG:NH1	1:E:677:GLY:HA3	1.94	0.83
1:A:695:LYS:HB2	2:O:18:LEU:HD22	1.60	0.83
1:C:355:SER:CB	1:C:371:SER:HA	2.09	0.82
1:F:355:SER:HB2	1:F:371:SER:HA	1.61	0.82
1:A:678:VAL:HG22	1:A:745:TYR:CE2	2.14	0.82
1:C:607:ASN:HB3	1:C:609:GLU:OE2	1.79	0.82
1:D:165:GLN:NE2	1:D:252:ASP:HB3	1.93	0.82
1:D:479:LYS:HG2	1:D:488:LEU:HD21	1.61	0.82
1:F:345:THR:HB	1:F:491:ASP:HB3	1.61	0.82
1:B:671:ARG:NH1	1:B:677:GLY:HA3	1.94	0.82
1:E:345:THR:HB	1:E:491:ASP:HB3	1.61	0.82
1:F:722:ILE:HG23	1:F:760:VAL:CG1	2.10	0.82
1:A:254:ARG:HB3	1:A:254:ARG:HH11	1.43	0.82
1:B:154:ILE:HG13	1:B:171:TYR:CE2	2.14	0.82
1:D:607:ASN:HB3	1:D:609:GLU:OE2	1.80	0.82

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:VAL:HG23	1:A:289:GLU:H	1.42	0.82
1:E:372:LYS:HG3	1:E:373:LYS:H	1.43	0.82
2:Q:47:GLU:O	2:Q:51:MET:HG3	1.79	0.82
1:C:462:ILE:HG12	1:C:463:THR:H	1.41	0.82
1:C:678:VAL:HG22	1:C:745:TYR:CE2	2.14	0.82
1:D:678:VAL:HG22	1:D:745:TYR:CE2	2.14	0.82
1:F:154:ILE:HG13	1:F:171:TYR:CE2	2.14	0.82
1:D:326:ILE:HG22	1:D:328:PHE:CE1	2.13	0.82
1:E:355:SER:CB	1:E:371:SER:HA	2.10	0.82
1:A:345:THR:HB	1:A:491:ASP:HB3	1.61	0.82
1:A:607:ASN:HB3	1:A:609:GLU:OE2	1.79	0.82
1:A:581:GLN:HE21	1:A:629:ASN:H	1.26	0.82
1:C:76:LEU:HD22	1:C:76:LEU:H	1.44	0.82
2:P:100:ILE:HB	2:P:136:VAL:CG2	2.10	0.82
2:R:24:ASP:N	2:R:24:ASP:OD1	2.06	0.82
2:T:51:MET:HB3	2:T:71:MET:HE2	1.60	0.82
1:B:355:SER:HB2	1:B:371:SER:HA	1.62	0.82
1:E:678:VAL:HG22	1:E:745:TYR:CE2	2.15	0.82
1:A:154:ILE:HG13	1:A:171:TYR:CE2	2.15	0.81
1:A:324:THR:HB	1:A:499:PRO:CA	2.10	0.81
1:D:657:ILE:HG13	1:D:756:ILE:HD13	1.62	0.81
1:D:722:ILE:HG23	1:D:760:VAL:CG1	2.10	0.81
1:E:275:GLY:HA2	1:E:278:LYS:CD	2.10	0.81
1:E:722:ILE:HG23	1:E:760:VAL:CG1	2.09	0.81
1:A:355:SER:CB	1:A:371:SER:HA	2.11	0.81
1:C:184:LYS:O	1:C:185:ASP:C	2.19	0.81
1:D:324:THR:HB	1:D:499:PRO:CA	2.10	0.81
2:S:100:ILE:HB	2:S:136:VAL:CG2	2.10	0.81
1:A:184:LYS:O	1:A:185:ASP:C	2.19	0.81
1:B:324:THR:HB	1:B:499:PRO:CA	2.10	0.81
1:C:345:THR:HB	1:C:491:ASP:HB3	1.61	0.81
1:F:324:THR:CB	1:F:499:PRO:HA	2.10	0.81
2:O:100:ILE:HB	2:O:136:VAL:CG2	2.10	0.81
2:O:41:GLN:C	2:O:43:PRO:HD2	2.00	0.81
1:D:695:LYS:HB2	2:R:18:LEU:HD22	1.60	0.81
1:A:372:LYS:HG3	1:A:373:LYS:H	1.45	0.81
1:A:722:ILE:HG23	1:A:760:VAL:CG1	2.10	0.81
1:B:345:THR:HB	1:B:491:ASP:HB3	1.60	0.81
1:C:326:ILE:HG22	1:C:328:PHE:CE1	2.15	0.81
1:D:355:SER:CB	1:D:371:SER:HA	2.10	0.81
1:D:671:ARG:NH1	1:D:677:GLY:HA3	1.94	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:175:LYS:HB2	1:F:175:LYS:HZ2	1.44	0.81
1:C:479:LYS:HG2	1:C:488:LEU:HD21	1.62	0.81
1:C:764:LEU:C	1:C:766:HIS:H	1.83	0.81
1:F:325:TYR:HB2	1:F:498:ALA:HB3	1.61	0.81
2:R:100:ILE:HB	2:R:136:VAL:CG2	2.11	0.81
2:T:100:ILE:HB	2:T:136:VAL:CG2	2.09	0.81
1:A:355:SER:HB2	1:A:371:SER:HA	1.62	0.81
1:F:695:LYS:HB2	2:T:18:LEU:HD22	1.62	0.81
1:C:154:ILE:HG13	1:C:171:TYR:CE2	2.14	0.81
1:D:76:LEU:H	1:D:76:LEU:HD22	1.44	0.81
1:F:355:SER:CB	1:F:371:SER:HA	2.09	0.81
1:A:443:GLU:OE2	1:A:458:LYS:HG2	1.81	0.81
1:C:722:ILE:HG23	1:C:760:VAL:CG1	2.10	0.81
1:E:154:ILE:HG13	1:E:171:TYR:CE2	2.16	0.81
1:F:462:ILE:HG12	1:F:463:THR:N	1.93	0.81
2:P:24:ASP:OD1	2:P:24:ASP:N	2.05	0.81
1:B:372:LYS:HG3	1:B:373:LYS:H	1.45	0.81
1:B:607:ASN:HB3	1:B:609:GLU:OE2	1.79	0.81
1:C:275:GLY:HA2	1:C:278:LYS:CD	2.10	0.81
1:D:154:ILE:HG13	1:D:171:TYR:CE2	2.15	0.81
1:A:165:GLN:NE2	1:A:252:ASP:HB3	1.96	0.81
1:B:324:THR:CB	1:B:499:PRO:HA	2.10	0.81
1:C:355:SER:HB2	1:C:371:SER:HA	1.60	0.81
1:D:567:THR:HG23	1:D:568:GLY:N	1.96	0.81
1:E:355:SER:HB2	1:E:371:SER:HA	1.62	0.81
1:F:607:ASN:HB3	1:F:609:GLU:OE2	1.81	0.81
1:A:462:ILE:HG12	1:A:463:THR:N	1.94	0.81
1:A:324:THR:CB	1:A:499:PRO:HA	2.11	0.81
1:E:254:ARG:HH11	1:E:254:ARG:HB3	1.46	0.81
1:B:165:GLN:NE2	1:B:252:ASP:HB3	1.96	0.80
1:D:581:GLN:HE21	1:D:629:ASN:H	1.27	0.80
1:D:597:ASN:ND2	1:D:601:GLU:HB2	1.96	0.80
2:Q:100:ILE:HB	2:Q:136:VAL:CG2	2.10	0.80
1:D:275:GLY:HA2	1:D:278:LYS:CD	2.11	0.80
1:F:165:GLN:NE2	1:F:252:ASP:HB3	1.95	0.80
1:B:355:SER:CB	1:B:371:SER:HA	2.10	0.80
1:C:372:LYS:HG3	1:C:373:LYS:H	1.45	0.80
1:C:450:ASN:HD22	1:C:452:GLU:H	1.29	0.80
1:F:184:LYS:O	1:F:185:ASP:C	2.19	0.80
1:F:372:LYS:HG3	1:F:373:LYS:H	1.45	0.80
1:B:192:PHE:HA	1:B:195:LEU:HB3	1.63	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:615:ILE:HG23	1:C:619:ILE:HD12	1.61	0.80
1:D:345:THR:HB	1:D:491:ASP:HB3	1.61	0.80
1:E:184:LYS:O	1:E:185:ASP:C	2.19	0.80
1:F:184:LYS:HA	1:F:187:SER:HB3	1.63	0.80
1:A:409:ARG:NE	1:A:413:LEU:HD21	1.96	0.80
1:B:722:ILE:HG23	1:B:760:VAL:CG1	2.10	0.80
1:D:184:LYS:O	1:D:185:ASP:C	2.19	0.80
1:E:324:THR:HB	1:E:499:PRO:CA	2.10	0.80
1:E:581:GLN:HE21	1:E:629:ASN:H	1.26	0.80
1:F:324:THR:HB	1:F:499:PRO:CA	2.10	0.80
1:C:657:ILE:HG13	1:C:756:ILE:HD13	1.63	0.80
1:D:443:GLU:OE2	1:D:458:LYS:HG2	1.82	0.80
1:F:581:GLN:HE21	1:F:629:ASN:H	1.25	0.80
1:A:567:THR:HG23	1:A:568:GLY:N	1.97	0.80
1:B:450:ASN:HD22	1:B:452:GLU:H	1.30	0.80
1:B:462:ILE:HG12	1:B:463:THR:N	1.95	0.80
1:E:192:PHE:HA	1:E:195:LEU:HB3	1.64	0.80
1:F:295:VAL:C	1:F:296:LEU:HD23	2.02	0.80
1:D:462:ILE:HG12	1:D:463:THR:N	1.94	0.80
1:F:450:ASN:HD22	1:F:452:GLU:H	1.30	0.80
1:A:295:VAL:C	1:A:296:LEU:HD23	2.03	0.80
1:B:184:LYS:O	1:B:185:ASP:C	2.19	0.80
1:C:120:LEU:O	1:C:120:LEU:CD1	2.28	0.80
1:C:443:GLU:OE2	1:C:458:LYS:HG2	1.82	0.80
1:C:324:THR:CB	1:C:499:PRO:HA	2.11	0.80
1:E:657:ILE:HG13	1:E:756:ILE:HD13	1.63	0.80
1:B:175:LYS:HB2	1:B:175:LYS:HZ2	1.47	0.79
1:C:184:LYS:HA	1:C:187:SER:HB3	1.63	0.79
1:D:254:ARG:HH11	1:D:254:ARG:HB3	1.45	0.79
1:E:462:ILE:HG12	1:E:463:THR:N	1.95	0.79
1:F:764:LEU:C	1:F:766:HIS:H	1.85	0.79
1:A:472:ARG:HB3	1:A:472:ARG:HH11	1.47	0.79
1:B:189:ASP:O	1:B:191:GLU:N	2.16	0.79
1:B:275:GLY:HA2	1:B:278:LYS:CD	2.12	0.79
1:B:443:GLU:OE2	1:B:458:LYS:HG2	1.82	0.79
1:B:581:GLN:HE21	1:B:629:ASN:H	1.28	0.79
1:B:678:VAL:HG22	1:B:745:TYR:CE2	2.16	0.79
1:C:324:THR:HB	1:C:499:PRO:CA	2.11	0.79
1:A:275:GLY:HA2	1:A:278:LYS:CD	2.12	0.79
1:C:409:ARG:NE	1:C:413:LEU:HD21	1.97	0.79
1:C:462:ILE:HG12	1:C:463:THR:N	1.95	0.79

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:120:LEU:O	1:D:120:LEU:CD1	2.28	0.79
1:E:184:LYS:HA	1:E:187:SER:HB3	1.63	0.79
1:E:295:VAL:C	1:E:296:LEU:HD23	2.03	0.79
1:C:165:GLN:NE2	1:C:252:ASP:HB3	1.96	0.79
1:E:360:VAL:HG21	1:E:365:PRO:HB3	1.63	0.79
1:C:254:ARG:HH11	1:C:254:ARG:HB3	1.46	0.79
1:C:567:THR:HG23	1:C:568:GLY:N	1.97	0.79
1:C:581:GLN:HE21	1:C:629:ASN:H	1.27	0.79
1:D:324:THR:CB	1:D:499:PRO:HA	2.11	0.79
1:B:567:THR:HG23	1:B:568:GLY:N	1.98	0.79
1:D:597:ASN:HD21	1:D:601:GLU:CB	1.94	0.79
1:D:709:ASN:O	1:D:717:LYS:HE3	1.83	0.79
1:E:120:LEU:CD1	1:E:120:LEU:O	2.28	0.79
1:F:275:GLY:HA2	1:F:278:LYS:CD	2.12	0.79
1:F:597:ASN:HD21	1:F:601:GLU:CB	1.96	0.79
1:F:657:ILE:HG13	1:F:756:ILE:HD13	1.63	0.79
1:D:450:ASN:HD22	1:D:452:GLU:H	1.30	0.79
1:E:324:THR:CB	1:E:499:PRO:HA	2.10	0.79
1:F:360:VAL:HG21	1:F:365:PRO:HB3	1.64	0.79
1:A:308:VAL:HB	1:A:311:HIS:ND1	1.98	0.79
2:Q:77:LYS:O	2:Q:80:ASP:HB2	1.84	0.79
2:S:48:LEU:HA	2:S:51:MET:CE	2.13	0.79
1:A:175:LYS:HZ2	1:A:175:LYS:HB2	1.46	0.78
1:A:657:ILE:HG13	1:A:756:ILE:HD13	1.64	0.78
1:E:115:LYS:HZ2	1:E:116:GLU:N	1.79	0.78
1:F:443:GLU:OE2	1:F:458:LYS:HG2	1.82	0.78
1:B:184:LYS:HA	1:B:187:SER:HB3	1.63	0.78
1:E:658:PRO:HG3	1:E:752:LEU:HD21	1.65	0.78
2:O:77:LYS:O	2:O:80:ASP:HB2	1.84	0.78
1:B:254:ARG:HH11	1:B:254:ARG:HB3	1.48	0.78
1:E:214:PHE:CD1	1:E:218:LEU:HD23	2.19	0.78
1:E:443:GLU:OE2	1:E:458:LYS:HG2	1.83	0.78
1:D:192:PHE:HA	1:D:195:LEU:HB3	1.65	0.78
1:D:658:PRO:HG3	1:D:752:LEU:HD21	1.64	0.78
2:R:48:LEU:HA	2:R:51:MET:CE	2.14	0.78
1:A:184:LYS:HA	1:A:187:SER:HB3	1.63	0.78
1:A:360:VAL:HG21	1:A:365:PRO:HB3	1.64	0.78
1:B:293:ILE:HD13	1:B:617:LYS:HD3	1.66	0.78
1:E:450:ASN:HD22	1:E:452:GLU:H	1.31	0.78
1:B:658:PRO:HG3	1:B:752:LEU:HD21	1.66	0.78
1:C:295:VAL:C	1:C:296:LEU:HD23	2.03	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:709:ASN:O	1:C:717:LYS:HE3	1.84	0.78
1:D:355:SER:HB2	1:D:371:SER:HA	1.63	0.78
1:F:192:PHE:HA	1:F:195:LEU:HB3	1.64	0.78
1:F:409:ARG:NE	1:F:413:LEU:HD21	1.97	0.78
1:B:295:VAL:C	1:B:296:LEU:HD23	2.03	0.78
1:D:308:VAL:HB	1:D:311:HIS:ND1	1.99	0.78
1:A:112:VAL:HG12	1:A:113:GLU:H	1.47	0.78
1:A:658:PRO:HG3	1:A:752:LEU:HD21	1.66	0.78
1:B:764:LEU:C	1:B:766:HIS:H	1.86	0.78
1:D:184:LYS:HA	1:D:187:SER:HB3	1.63	0.78
1:F:658:PRO:HG3	1:F:752:LEU:HD21	1.66	0.78
1:E:409:ARG:NE	1:E:413:LEU:HD21	1.99	0.78
2:P:77:LYS:O	2:P:80:ASP:HB2	1.84	0.78
1:B:639:ASN:HD22	1:B:639:ASN:H	1.31	0.77
1:B:765:THR:HG22	1:B:769:SER:OG	1.84	0.77
1:C:776:LEU:HD23	1:C:776:LEU:O	1.84	0.77
1:D:729:TYR:HB2	1:D:756:ILE:HG21	1.67	0.77
1:A:214:PHE:CD1	1:A:218:LEU:HD23	2.19	0.77
1:C:360:VAL:HG11	1:C:370:LEU:HD22	1.67	0.77
1:A:120:LEU:O	1:A:120:LEU:CD1	2.28	0.77
1:B:409:ARG:NE	1:B:413:LEU:HD21	2.00	0.77
1:C:192:PHE:HA	1:C:195:LEU:HB3	1.64	0.77
1:E:112:VAL:HG12	1:E:113:GLU:H	1.49	0.77
1:E:567:THR:HG23	1:E:568:GLY:N	1.96	0.77
1:A:450:ASN:HD22	1:A:452:GLU:H	1.31	0.77
1:D:214:PHE:CD1	1:D:218:LEU:HD23	2.20	0.77
1:F:765:THR:HG22	1:F:769:SER:OG	1.84	0.77
2:S:77:LYS:O	2:S:80:ASP:HB2	1.84	0.77
1:C:308:VAL:HB	1:C:311:HIS:ND1	1.99	0.77
1:D:360:VAL:HG21	1:D:365:PRO:HB3	1.64	0.77
1:E:175:LYS:HB2	1:E:175:LYS:HZ2	1.49	0.77
2:R:77:LYS:O	2:R:80:ASP:HB2	1.83	0.77
1:B:639:ASN:H	1:B:639:ASN:ND2	1.83	0.77
1:C:597:ASN:HD21	1:C:601:GLU:CB	1.97	0.77
1:C:639:ASN:H	1:C:639:ASN:ND2	1.83	0.77
1:F:308:VAL:HB	1:F:311:HIS:ND1	1.99	0.77
1:C:214:PHE:CD1	1:C:218:LEU:HD23	2.19	0.77
1:D:409:ARG:NE	1:D:413:LEU:HD21	1.98	0.77
1:E:153:ILE:O	1:E:154:ILE:HD13	1.84	0.77
1:E:765:THR:HG22	1:E:769:SER:OG	1.85	0.77
1:B:214:PHE:CD1	1:B:218:LEU:HD23	2.20	0.77

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:120:LEU:CD1	1:F:120:LEU:O	2.28	0.77
1:A:115:LYS:HG3	1:A:153:ILE:HG21	1.67	0.77
1:B:360:VAL:HG21	1:B:365:PRO:HB3	1.64	0.77
1:B:472:ARG:HB3	1:B:472:ARG:HH11	1.50	0.77
1:C:360:VAL:HG21	1:C:365:PRO:HB3	1.65	0.77
1:F:472:ARG:HH11	1:F:472:ARG:HB3	1.50	0.77
1:B:788:ASP:O	1:B:792:VAL:HG23	1.85	0.77
1:D:764:LEU:C	1:D:766:HIS:H	1.85	0.77
1:A:639:ASN:HD22	1:A:639:ASN:H	1.33	0.76
1:A:639:ASN:ND2	1:A:639:ASN:H	1.83	0.76
1:B:308:VAL:HB	1:B:311:HIS:ND1	1.99	0.76
1:C:729:TYR:HB2	1:C:756:ILE:HG21	1.66	0.76
1:D:295:VAL:C	1:D:296:LEU:HD23	2.05	0.76
1:D:742:ALA:HB1	1:D:744:GLU:OE1	1.85	0.76
1:D:765:THR:HG22	1:D:769:SER:OG	1.85	0.76
1:F:165:GLN:HG2	1:F:251:PRO:HG2	1.68	0.76
1:F:639:ASN:H	1:F:639:ASN:ND2	1.84	0.76
2:T:77:LYS:O	2:T:80:ASP:HB2	1.84	0.76
1:A:293:ILE:HD13	1:A:617:LYS:HD3	1.65	0.76
1:A:764:LEU:C	1:A:766:HIS:H	1.87	0.76
1:C:293:ILE:HD13	1:C:617:LYS:HD3	1.65	0.76
1:B:112:VAL:HG12	1:B:113:GLU:H	1.50	0.76
1:D:184:LYS:HE3	1:D:191:GLU:HB2	1.67	0.76
1:E:639:ASN:ND2	1:E:639:ASN:H	1.83	0.76
1:F:112:VAL:HG12	1:F:113:GLU:H	1.49	0.76
1:A:192:PHE:HA	1:A:195:LEU:HB3	1.65	0.76
1:D:189:ASP:O	1:D:190:PRO:C	2.22	0.76
1:D:360:VAL:HG11	1:D:370:LEU:HD22	1.67	0.76
1:E:597:ASN:ND2	1:E:601:GLU:HB2	2.00	0.76
1:E:293:ILE:HD13	1:E:617:LYS:HD3	1.66	0.76
1:E:776:LEU:O	1:E:776:LEU:HD23	1.85	0.76
1:F:115:LYS:HZ2	1:F:116:GLU:N	1.81	0.76
1:F:214:PHE:CD1	1:F:218:LEU:HD23	2.20	0.76
1:F:293:ILE:HD13	1:F:617:LYS:HD3	1.67	0.76
1:C:472:ARG:HH11	1:C:472:ARG:HB3	1.50	0.76
1:C:643:ILE:HG22	1:C:644:GLU:H	1.48	0.76
1:F:499:PRO:HD3	1:F:552:TRP:CH2	2.20	0.76
1:B:120:LEU:O	1:B:120:LEU:CD1	2.28	0.76
1:D:186:LYS:HG2	1:D:186:LYS:O	1.86	0.76
1:E:308:VAL:HB	1:E:311:HIS:ND1	1.99	0.76
1:E:709:ASN:O	1:E:717:LYS:HE3	1.85	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:567:THR:HG23	1:F:568:GLY:N	1.98	0.76
1:A:765:THR:HG22	1:A:769:SER:OG	1.86	0.76
1:C:115:LYS:HZ2	1:C:116:GLU:N	1.81	0.76
1:C:333:LYS:HD2	1:C:333:LYS:H	1.51	0.76
1:C:658:PRO:HG3	1:C:752:LEU:HD21	1.67	0.76
1:D:639:ASN:H	1:D:639:ASN:HD22	1.34	0.76
1:E:333:LYS:HD2	1:E:333:LYS:H	1.51	0.76
1:C:186:LYS:HG2	1:C:186:LYS:O	1.86	0.76
1:D:589:LYS:HB2	1:D:643:ILE:HD13	1.68	0.76
1:E:499:PRO:HD3	1:E:552:TRP:CH2	2.21	0.76
1:F:357:TRP:HZ3	1:F:439:ASN:HB2	1.51	0.76
2:Q:102:ALA:HB2	2:Q:125:ILE:HG13	1.68	0.76
1:A:742:ALA:HB1	1:A:744:GLU:OE1	1.86	0.76
1:B:729:TYR:HB2	1:B:756:ILE:HG21	1.67	0.76
1:C:189:ASP:O	1:C:191:GLU:N	2.19	0.76
1:C:765:THR:HG22	1:C:769:SER:OG	1.85	0.76
2:S:100:ILE:HB	2:S:136:VAL:HG23	1.67	0.76
1:A:333:LYS:H	1:A:333:LYS:HD2	1.51	0.75
1:A:597:ASN:HD21	1:A:601:GLU:CB	1.97	0.75
1:A:709:ASN:O	1:A:717:LYS:HE3	1.86	0.75
1:C:788:ASP:O	1:C:792:VAL:HG23	1.86	0.75
1:D:175:LYS:HZ2	1:D:175:LYS:HB2	1.48	0.75
1:D:333:LYS:HD2	1:D:333:LYS:H	1.51	0.75
1:D:639:ASN:ND2	1:D:639:ASN:H	1.84	0.75
1:F:776:LEU:HD23	1:F:776:LEU:O	1.85	0.75
1:A:186:LYS:HG2	1:A:186:LYS:O	1.86	0.75
1:C:165:GLN:HG2	1:C:251:PRO:HG2	1.68	0.75
1:D:112:VAL:HG12	1:D:113:GLU:H	1.49	0.75
1:F:694:VAL:CG2	2:T:18:LEU:HD21	2.16	0.75
1:A:153:ILE:O	1:A:154:ILE:HD13	1.86	0.75
1:A:788:ASP:O	1:A:792:VAL:HG23	1.87	0.75
1:B:333:LYS:HD2	1:B:333:LYS:H	1.51	0.75
1:C:639:ASN:HD22	1:C:639:ASN:H	1.32	0.75
1:C:694:VAL:CG2	2:Q:18:LEU:HD21	2.17	0.75
2:P:100:ILE:HB	2:P:136:VAL:HG23	1.69	0.75
1:F:186:LYS:O	1:F:186:LYS:HG2	1.86	0.75
1:C:112:VAL:HG12	1:C:113:GLU:H	1.49	0.75
1:D:293:ILE:HD13	1:D:617:LYS:HD3	1.66	0.75
1:C:115:LYS:HG3	1:C:153:ILE:HG21	1.69	0.75
1:B:597:ASN:HD21	1:B:601:GLU:CB	1.97	0.75
1:C:742:ALA:HB1	1:C:744:GLU:OE1	1.87	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:472:ARG:HB3	1:D:472:ARG:HH11	1.51	0.75
1:E:115:LYS:CB	1:E:118:GLN:HG2	2.17	0.75
1:E:764:LEU:C	1:E:766:HIS:H	1.88	0.75
1:F:184:LYS:HE3	1:F:191:GLU:HB2	1.69	0.75
1:F:716:LYS:O	1:F:720:ILE:HG22	1.87	0.75
2:O:79:THR:C	2:O:81:SER:H	1.89	0.75
2:P:79:THR:C	2:P:81:SER:H	1.90	0.75
2:Q:100:ILE:HB	2:Q:136:VAL:HG23	1.67	0.75
2:R:102:ALA:HB2	2:R:125:ILE:HG13	1.68	0.75
1:B:579:THR:O	1:B:581:GLN:N	2.20	0.75
1:F:337:ASN:ND2	1:F:412:GLU:OE2	2.20	0.75
1:C:357:TRP:HZ3	1:C:439:ASN:HB2	1.52	0.74
1:D:115:LYS:HZ2	1:D:116:GLU:N	1.83	0.74
1:D:115:LYS:HG3	1:D:153:ILE:HG21	1.69	0.74
1:E:357:TRP:HZ3	1:E:439:ASN:HB2	1.51	0.74
1:E:742:ALA:HB1	1:E:744:GLU:OE1	1.87	0.74
1:F:597:ASN:ND2	1:F:601:GLU:HB2	1.99	0.74
1:F:709:ASN:O	1:F:717:LYS:HE3	1.86	0.74
1:A:115:LYS:CB	1:A:118:GLN:HG2	2.16	0.74
1:A:337:ASN:ND2	1:A:412:GLU:OE2	2.20	0.74
1:C:115:LYS:CB	1:C:118:GLN:HG2	2.17	0.74
1:C:329:ARG:HD2	1:C:590:ASP:OD2	1.87	0.74
1:D:153:ILE:O	1:D:154:ILE:HD13	1.87	0.74
1:E:353:LYS:H	1:E:368:GLN:HE22	1.33	0.74
1:F:729:TYR:HB2	1:F:756:ILE:HG21	1.67	0.74
1:A:499:PRO:HD3	1:A:552:TRP:CH2	2.21	0.74
1:A:694:VAL:CG2	2:O:18:LEU:HD21	2.17	0.74
1:D:357:TRP:HZ3	1:D:439:ASN:HB2	1.51	0.74
1:D:499:PRO:HD3	1:D:552:TRP:CH2	2.23	0.74
1:D:776:LEU:O	1:D:776:LEU:HD23	1.87	0.74
1:F:333:LYS:H	1:F:333:LYS:HD2	1.51	0.74
1:B:115:LYS:HG3	1:B:153:ILE:HG21	1.69	0.74
1:C:499:PRO:HD3	1:C:552:TRP:CH2	2.22	0.74
1:D:788:ASP:O	1:D:792:VAL:HG23	1.86	0.74
1:E:729:TYR:HB2	1:E:756:ILE:HG21	1.68	0.74
1:F:579:THR:O	1:F:581:GLN:N	2.21	0.74
1:E:694:VAL:CG2	2:S:18:LEU:HD21	2.17	0.74
1:A:357:TRP:HZ3	1:A:439:ASN:HB2	1.52	0.74
1:A:729:TYR:HB2	1:A:756:ILE:HG21	1.69	0.74
1:E:579:THR:O	1:E:581:GLN:N	2.21	0.74
2:O:110:THR:HA	2:O:114:GLU:O	1.88	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:92:PHE:O	2:P:94:LYS:N	2.21	0.74
1:B:357:TRP:HZ3	1:B:439:ASN:HB2	1.51	0.74
1:C:134:LYS:O	1:C:135:VAL:HG12	1.88	0.74
1:D:337:ASN:ND2	1:D:412:GLU:OE2	2.20	0.74
1:D:446:ILE:HD11	1:D:451:ASN:HB3	1.69	0.74
1:E:165:GLN:HG2	1:E:251:PRO:HG2	1.70	0.74
1:E:472:ARG:HH11	1:E:472:ARG:HB3	1.50	0.74
1:F:360:VAL:HG11	1:F:370:LEU:HD22	1.68	0.74
1:F:446:ILE:HD11	1:F:451:ASN:HB3	1.70	0.74
1:F:742:ALA:HB1	1:F:744:GLU:OE1	1.87	0.74
1:F:788:ASP:O	1:F:792:VAL:HG23	1.87	0.74
1:B:186:LYS:HG2	1:B:186:LYS:O	1.86	0.74
1:E:186:LYS:HG2	1:E:186:LYS:O	1.86	0.74
1:B:446:ILE:HD11	1:B:451:ASN:HB3	1.70	0.74
2:O:100:ILE:HB	2:O:136:VAL:HG23	1.69	0.74
1:B:694:VAL:CG2	2:P:18:LEU:HD21	2.17	0.74
1:B:478:ALA:HB1	1:B:486:LYS:O	1.88	0.74
1:D:401:ILE:HD13	1:D:485:LEU:O	1.88	0.74
1:E:597:ASN:HD21	1:E:601:GLU:CB	1.96	0.74
2:T:100:ILE:HB	2:T:136:VAL:HG23	1.69	0.74
1:B:360:VAL:HG11	1:B:370:LEU:HD22	1.68	0.74
1:E:639:ASN:HD22	1:E:639:ASN:H	1.33	0.74
1:F:153:ILE:O	1:F:154:ILE:HD13	1.86	0.74
1:A:401:ILE:HD13	1:A:485:LEU:O	1.88	0.73
1:B:499:PRO:HD3	1:B:552:TRP:CH2	2.23	0.73
1:C:597:ASN:ND2	1:C:601:GLU:HB2	2.00	0.73
1:D:512:GLU:O	1:D:516:VAL:HG23	1.88	0.73
1:E:360:VAL:HG11	1:E:370:LEU:HD22	1.68	0.73
1:E:401:ILE:HD13	1:E:485:LEU:O	1.87	0.73
2:R:100:ILE:HB	2:R:136:VAL:HG23	1.68	0.73
1:A:184:LYS:HE3	1:A:191:GLU:HB2	1.69	0.73
1:A:776:LEU:O	1:A:776:LEU:HD23	1.86	0.73
1:B:115:LYS:CB	1:B:118:GLN:HG2	2.18	0.73
1:D:115:LYS:CB	1:D:118:GLN:HG2	2.18	0.73
1:D:464:VAL:HG23	1:D:465:LEU:HD12	1.71	0.73
1:D:694:VAL:CG2	2:R:18:LEU:HD21	2.18	0.73
1:D:716:LYS:O	1:D:720:ILE:HG22	1.87	0.73
1:E:629:ASN:ND2	1:E:631:SER:HB2	2.03	0.73
2:R:110:THR:HA	2:R:114:GLU:O	1.88	0.73
1:A:360:VAL:HG11	1:A:370:LEU:HD22	1.68	0.73
1:A:446:ILE:HD11	1:A:451:ASN:HB3	1.70	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:709:ASN:O	1:B:717:LYS:HE3	1.87	0.73
1:C:530:THR:HG21	2:Q:145:MET:HE3	1.69	0.73
1:E:512:GLU:O	1:E:516:VAL:HG23	1.88	0.73
2:S:92:PHE:O	2:S:94:LYS:N	2.21	0.73
1:A:510:GLN:O	1:A:514:ASP:HB2	1.89	0.73
2:O:115:LYS:HZ3	2:O:115:LYS:HA	1.53	0.73
2:O:115:LYS:NZ	2:O:115:LYS:HA	2.04	0.73
1:E:142:VAL:HG22	1:E:154:ILE:HG23	1.70	0.73
1:E:446:ILE:HD11	1:E:451:ASN:HB3	1.71	0.73
1:E:530:THR:HG21	2:S:145:MET:HE3	1.70	0.73
2:S:48:LEU:O	2:S:52:ILE:HG22	1.88	0.73
1:C:337:ASN:ND2	1:C:412:GLU:OE2	2.21	0.73
1:B:353:LYS:H	1:B:368:GLN:HE22	1.34	0.73
1:B:742:ALA:HB1	1:B:744:GLU:OE1	1.88	0.73
1:C:464:VAL:HG23	1:C:465:LEU:HD12	1.71	0.73
1:F:353:LYS:H	1:F:368:GLN:HE22	1.35	0.73
2:R:79:THR:C	2:R:81:SER:H	1.89	0.73
1:A:165:GLN:HG2	1:A:251:PRO:HG2	1.70	0.73
1:B:302:LEU:HD22	1:B:602:PHE:CE1	2.24	0.73
1:B:337:ASN:ND2	1:B:412:GLU:OE2	2.21	0.73
1:B:776:LEU:HD23	1:B:776:LEU:O	1.87	0.73
1:D:302:LEU:HD22	1:D:602:PHE:CE1	2.24	0.73
1:E:329:ARG:HD2	1:E:590:ASP:OD2	1.88	0.73
1:E:788:ASP:O	1:E:792:VAL:HG23	1.87	0.73
2:T:79:THR:C	2:T:81:SER:H	1.89	0.73
1:B:165:GLN:HG2	1:B:251:PRO:HG2	1.71	0.73
1:D:142:VAL:HG22	1:D:154:ILE:HG23	1.71	0.73
1:D:329:ARG:HD2	1:D:590:ASP:OD2	1.89	0.73
1:D:615:ILE:HD12	1:D:645:TRP:HH2	1.54	0.73
2:Q:110:THR:HA	2:Q:114:GLU:O	1.88	0.73
1:A:611:THR:O	1:A:615:ILE:HG13	1.89	0.73
1:C:161:ILE:HG23	1:C:168:GLU:HB2	1.70	0.73
1:E:337:ASN:ND2	1:E:412:GLU:OE2	2.21	0.73
2:O:4:LEU:CB	2:O:8:GLN:HE21	2.02	0.73
2:T:102:ALA:HB2	2:T:125:ILE:HG13	1.71	0.73
1:E:115:LYS:HG3	1:E:153:ILE:HG21	1.69	0.72
1:C:446:ILE:HD11	1:C:451:ASN:HB3	1.71	0.72
1:D:161:ILE:HG23	1:D:168:GLU:HB2	1.69	0.72
1:F:115:LYS:CB	1:F:118:GLN:HG2	2.18	0.72
2:O:48:LEU:O	2:O:52:ILE:HG22	1.89	0.72
2:R:48:LEU:O	2:R:52:ILE:HG22	1.88	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:79:THR:C	2:S:81:SER:H	1.89	0.72
1:C:175:LYS:HZ2	1:C:175:LYS:HB2	1.53	0.72
1:C:302:LEU:HD22	1:C:602:PHE:CE1	2.23	0.72
1:E:617:LYS:HZ2	1:E:618:ASN:ND2	1.84	0.72
1:B:301:ALA:C	1:B:303:LYS:H	1.92	0.72
1:B:512:GLU:O	1:B:516:VAL:HG23	1.90	0.72
1:C:615:ILE:HD12	1:C:645:TRP:HH2	1.55	0.72
1:D:165:GLN:HG2	1:D:251:PRO:HG2	1.71	0.72
1:F:530:THR:HG21	2:T:145:MET:HE3	1.71	0.72
1:A:515:LYS:NZ	1:A:515:LYS:HB3	2.03	0.72
1:B:197:LYS:HB3	1:B:197:LYS:HZ2	1.54	0.72
1:B:297:LYS:HA	1:B:602:PHE:O	1.89	0.72
2:P:102:ALA:HB2	2:P:125:ILE:HG13	1.71	0.72
2:R:115:LYS:HA	2:R:115:LYS:NZ	2.05	0.72
2:S:102:ALA:HB2	2:S:125:ILE:HG13	1.72	0.72
1:C:512:GLU:O	1:C:516:VAL:HG23	1.90	0.72
1:E:184:LYS:HE3	1:E:191:GLU:HB2	1.72	0.72
2:T:48:LEU:O	2:T:52:ILE:HG22	1.88	0.72
1:D:611:THR:O	1:D:615:ILE:HG13	1.89	0.72
1:E:510:GLN:O	1:E:514:ASP:HB2	1.89	0.72
2:P:51:MET:HB3	2:P:71:MET:CE	2.20	0.72
1:A:115:LYS:NZ	1:A:116:GLU:H	1.85	0.72
1:A:329:ARG:HD2	1:A:590:ASP:OD2	1.89	0.72
1:A:629:ASN:ND2	1:A:631:SER:HB2	2.04	0.72
1:B:153:ILE:O	1:B:154:ILE:HD13	1.90	0.72
1:B:450:ASN:ND2	1:B:452:GLU:HG3	2.05	0.72
1:B:510:GLN:O	1:B:514:ASP:HB2	1.89	0.72
1:D:515:LYS:NZ	1:D:515:LYS:HB3	2.04	0.72
1:E:302:LEU:HD22	1:E:602:PHE:CE1	2.24	0.72
1:F:401:ILE:HD13	1:F:485:LEU:O	1.90	0.72
1:F:639:ASN:H	1:F:639:ASN:HD22	1.33	0.72
1:F:615:ILE:HD12	1:F:645:TRP:HH2	1.54	0.72
2:R:51:MET:HB3	2:R:71:MET:CE	2.20	0.72
2:T:110:THR:HA	2:T:114:GLU:O	1.89	0.72
1:D:450:ASN:ND2	1:D:452:GLU:HG3	2.04	0.72
1:E:464:VAL:HG23	1:E:465:LEU:HD12	1.72	0.72
1:F:302:LEU:HD22	1:F:602:PHE:CE1	2.24	0.72
1:F:329:ARG:HD2	1:F:590:ASP:OD2	1.90	0.72
2:Q:48:LEU:O	2:Q:52:ILE:HG22	1.88	0.72
1:F:115:LYS:HG3	1:F:153:ILE:HG21	1.71	0.72
1:F:510:GLN:O	1:F:514:ASP:HB2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:115:LYS:NZ	2:P:115:LYS:HA	2.05	0.72
1:A:615:ILE:HD12	1:A:645:TRP:HH2	1.55	0.71
1:C:579:THR:O	1:C:581:GLN:N	2.23	0.71
1:D:515:LYS:O	1:D:515:LYS:HG2	1.90	0.71
1:E:615:ILE:HD12	1:E:645:TRP:HH2	1.55	0.71
1:E:611:THR:O	1:E:615:ILE:HG13	1.90	0.71
1:F:441:VAL:HG22	1:F:461:LYS:CG	2.20	0.71
2:P:48:LEU:O	2:P:52:ILE:HG22	1.88	0.71
2:Q:79:THR:C	2:Q:81:SER:H	1.89	0.71
1:A:464:VAL:HG23	1:A:465:LEU:HD12	1.72	0.71
1:F:464:VAL:HG23	1:F:465:LEU:HD12	1.72	0.71
1:F:512:GLU:O	1:F:516:VAL:HG23	1.90	0.71
1:A:302:LEU:HD22	1:A:602:PHE:CE1	2.26	0.71
1:F:450:ASN:ND2	1:F:452:GLU:HG3	2.05	0.71
1:F:711:ILE:HG13	1:F:712:PHE:CD2	2.25	0.71
1:F:736:LEU:HD21	1:F:750:GLN:NE2	2.05	0.71
1:B:611:THR:O	1:B:615:ILE:HG13	1.91	0.71
1:D:579:THR:O	1:D:581:GLN:N	2.24	0.71
1:D:629:ASN:ND2	1:D:631:SER:HB2	2.05	0.71
1:D:711:ILE:HG13	1:D:712:PHE:CD2	2.26	0.71
1:F:408:LEU:N	1:F:408:LEU:HD12	2.04	0.71
2:P:110:THR:HA	2:P:114:GLU:O	1.90	0.71
1:C:510:GLN:O	1:C:514:ASP:HB2	1.89	0.71
1:E:630:ARG:HH11	1:E:630:ARG:HG3	1.55	0.71
2:O:102:ALA:HB2	2:O:125:ILE:HG13	1.71	0.71
2:T:92:PHE:O	2:T:94:LYS:N	2.20	0.71
1:B:464:VAL:HG23	1:B:465:LEU:HD12	1.72	0.71
1:B:716:LYS:O	1:B:720:ILE:HG22	1.89	0.71
1:C:515:LYS:NZ	1:C:515:LYS:HB3	2.06	0.71
1:C:711:ILE:HG13	1:C:712:PHE:CD2	2.26	0.71
1:C:716:LYS:O	1:C:720:ILE:HG22	1.90	0.71
1:D:301:ALA:C	1:D:303:LYS:H	1.93	0.71
1:E:589:LYS:HB2	1:E:643:ILE:HD13	1.70	0.71
2:Q:115:LYS:NZ	2:Q:115:LYS:HA	2.05	0.71
2:Q:51:MET:HB3	2:Q:71:MET:CE	2.20	0.71
1:A:353:LYS:H	1:A:368:GLN:HE22	1.36	0.71
1:C:153:ILE:O	1:C:154:ILE:HD13	1.90	0.71
1:C:409:ARG:CZ	1:C:413:LEU:HD21	2.21	0.71
1:D:142:VAL:HG13	1:D:154:ILE:CD1	2.21	0.71
1:E:338:LEU:HD21	1:E:409:ARG:CZ	2.21	0.71
1:E:441:VAL:HG22	1:E:461:LYS:CG	2.20	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:142:VAL:HG22	1:F:154:ILE:HG23	1.73	0.71
1:F:301:ALA:C	1:F:303:LYS:H	1.93	0.71
1:A:409:ARG:CZ	1:A:413:LEU:HD21	2.21	0.71
1:A:579:THR:O	1:A:581:GLN:N	2.22	0.71
1:B:441:VAL:HG22	1:B:461:LYS:CG	2.20	0.71
1:C:184:LYS:HE3	1:C:191:GLU:HB2	1.73	0.71
1:C:297:LYS:HA	1:C:602:PHE:O	1.91	0.71
1:D:441:VAL:HG22	1:D:461:LYS:CG	2.20	0.71
2:T:106:ARG:HB2	2:T:121:VAL:HG21	1.71	0.71
2:T:4:LEU:CB	2:T:8:GLN:HE21	2.03	0.71
1:A:450:ASN:ND2	1:A:452:GLU:HG3	2.05	0.71
1:B:615:ILE:HD12	1:B:645:TRP:HH2	1.55	0.71
1:C:630:ARG:CZ	2:Q:83:GLU:HG2	2.21	0.71
1:D:409:ARG:CZ	1:D:413:LEU:HD21	2.20	0.71
1:D:736:LEU:HD21	1:D:750:GLN:NE2	2.06	0.71
1:F:161:ILE:HG23	1:F:168:GLU:HB2	1.73	0.71
2:S:110:THR:HA	2:S:114:GLU:O	1.90	0.71
1:B:115:LYS:NZ	1:B:116:GLU:H	1.85	0.71
1:B:736:LEU:HD21	1:B:750:GLN:NE2	2.06	0.71
1:C:353:LYS:H	1:C:368:GLN:HE22	1.36	0.71
1:D:478:ALA:HB1	1:D:486:LYS:O	1.91	0.71
1:E:297:LYS:HA	1:E:602:PHE:O	1.91	0.71
2:R:4:LEU:CB	2:R:8:GLN:HE21	2.04	0.71
1:E:694:VAL:HG23	2:S:18:LEU:HD11	1.73	0.71
1:B:515:LYS:NZ	1:B:515:LYS:HB3	2.04	0.70
1:B:530:THR:HG21	2:P:145:MET:HE3	1.72	0.70
1:D:107:THR:CG2	1:D:115:LYS:HE2	2.21	0.70
1:D:134:LYS:O	1:D:135:VAL:HG12	1.91	0.70
1:D:353:LYS:H	1:D:368:GLN:HE22	1.35	0.70
1:D:510:GLN:O	1:D:514:ASP:HB2	1.91	0.70
1:E:716:LYS:O	1:E:720:ILE:HG22	1.91	0.70
2:O:106:ARG:HB2	2:O:121:VAL:HG21	1.72	0.70
2:P:48:LEU:HA	2:P:51:MET:CE	2.12	0.70
2:Q:92:PHE:O	2:Q:94:LYS:N	2.22	0.70
2:S:4:LEU:CB	2:S:8:GLN:HE21	2.03	0.70
1:A:301:ALA:C	1:A:303:LYS:H	1.94	0.70
1:D:355:SER:OG	1:D:371:SER:HA	1.90	0.70
1:E:355:SER:OG	1:E:371:SER:HA	1.91	0.70
1:E:409:ARG:CZ	1:E:413:LEU:HD21	2.21	0.70
1:E:450:ASN:ND2	1:E:452:GLU:HG3	2.06	0.70
1:E:736:LEU:HD21	1:E:750:GLN:NE2	2.07	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:409:ARG:CZ	1:F:413:LEU:HD21	2.21	0.70
1:F:515:LYS:HB3	1:F:515:LYS:NZ	2.06	0.70
2:O:92:PHE:O	2:O:94:LYS:N	2.23	0.70
1:B:134:LYS:O	1:B:135:VAL:HG12	1.91	0.70
1:B:338:LEU:HD21	1:B:409:ARG:CZ	2.22	0.70
1:C:142:VAL:HG22	1:C:154:ILE:HG23	1.72	0.70
1:E:134:LYS:O	1:E:135:VAL:HG12	1.91	0.70
1:E:515:LYS:HB3	1:E:515:LYS:NZ	2.05	0.70
1:A:115:LYS:HZ3	1:A:115:LYS:HA	1.56	0.70
1:B:142:VAL:HG13	1:B:154:ILE:CD1	2.21	0.70
2:O:32:LEU:HD22	2:O:63:ILE:CD1	2.21	0.70
2:P:4:LEU:CB	2:P:8:GLN:HE21	2.04	0.70
2:R:32:LEU:HD22	2:R:63:ILE:CD1	2.21	0.70
2:R:92:PHE:O	2:R:94:LYS:N	2.22	0.70
1:A:441:VAL:HG22	1:A:461:LYS:CG	2.20	0.70
1:C:671:ARG:HH12	1:C:677:GLY:HA3	1.56	0.70
1:F:540:ARG:HD3	1:F:627:TYR:OH	1.92	0.70
2:T:51:MET:HB3	2:T:71:MET:CE	2.20	0.70
1:C:764:LEU:O	1:C:766:HIS:N	2.25	0.70
1:D:279:ILE:O	1:D:283:LEU:HD13	1.92	0.70
1:A:540:ARG:HD3	1:A:627:TYR:OH	1.92	0.70
1:A:711:ILE:HG13	1:A:712:PHE:CD2	2.27	0.70
1:D:268:MET:O	1:D:271:LEU:HB2	1.92	0.70
1:F:629:ASN:ND2	1:F:631:SER:HB2	2.06	0.70
2:O:51:MET:HB3	2:O:71:MET:CE	2.20	0.70
1:A:716:LYS:O	1:A:720:ILE:HG22	1.90	0.70
1:B:329:ARG:HD2	1:B:590:ASP:OD2	1.91	0.70
1:C:408:LEU:HD12	1:C:408:LEU:N	2.06	0.70
1:C:450:ASN:ND2	1:C:452:GLU:HG3	2.06	0.70
1:F:297:LYS:HA	1:F:602:PHE:O	1.92	0.70
2:T:32:LEU:HD22	2:T:63:ILE:CD1	2.22	0.70
1:A:736:LEU:HD21	1:A:750:GLN:NE2	2.07	0.70
1:E:279:ILE:O	1:E:283:LEU:HD13	1.92	0.70
1:F:279:ILE:O	1:F:283:LEU:HD13	1.92	0.70
2:P:32:LEU:HD22	2:P:63:ILE:CD1	2.22	0.70
1:A:515:LYS:O	1:A:515:LYS:HG2	1.91	0.70
1:B:401:ILE:HD13	1:B:485:LEU:O	1.91	0.70
1:D:764:LEU:O	1:D:766:HIS:N	2.25	0.70
1:E:301:ALA:C	1:E:303:LYS:H	1.94	0.70
1:F:338:LEU:HD21	1:F:409:ARG:CZ	2.22	0.70
2:O:16:PHE:CE2	2:O:27:ILE:HD11	2.26	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:355:SER:OG	1:B:371:SER:HA	1.92	0.69
1:C:441:VAL:HG22	1:C:461:LYS:CG	2.21	0.69
1:C:401:ILE:HD13	1:C:485:LEU:O	1.91	0.69
1:C:611:THR:O	1:C:615:ILE:HG13	1.92	0.69
1:F:697:ILE:HD13	1:F:732:ILE:HD12	1.72	0.69
2:O:117:THR:HG23	2:O:120:GLU:HB2	1.74	0.69
1:B:409:ARG:CZ	1:B:413:LEU:HD21	2.22	0.69
1:E:478:ALA:HB1	1:E:486:LYS:O	1.92	0.69
2:S:32:LEU:HD22	2:S:63:ILE:CD1	2.22	0.69
1:A:142:VAL:HG22	1:A:154:ILE:HG23	1.72	0.69
1:A:279:ILE:O	1:A:283:LEU:HD13	1.92	0.69
1:A:512:GLU:O	1:A:516:VAL:HG23	1.91	0.69
1:B:142:VAL:HG22	1:B:154:ILE:HG23	1.72	0.69
1:C:142:VAL:HG13	1:C:154:ILE:CD1	2.22	0.69
1:C:279:ILE:O	1:C:283:LEU:HD13	1.91	0.69
1:C:629:ASN:ND2	1:C:631:SER:HB2	2.07	0.69
1:C:697:ILE:HD13	1:C:732:ILE:CD1	2.21	0.69
1:C:697:ILE:HD13	1:C:732:ILE:HD12	1.73	0.69
1:F:142:VAL:HG13	1:F:154:ILE:CD1	2.22	0.69
1:A:161:ILE:HG23	1:A:168:GLU:HB2	1.72	0.69
1:A:597:ASN:ND2	1:A:601:GLU:HB2	1.99	0.69
1:B:711:ILE:HG13	1:B:712:PHE:CD2	2.27	0.69
2:Q:32:LEU:HD22	2:Q:63:ILE:CD1	2.22	0.69
1:C:301:ALA:C	1:C:303:LYS:H	1.94	0.69
1:C:515:LYS:O	1:C:515:LYS:HG2	1.92	0.69
1:E:142:VAL:HG13	1:E:154:ILE:CD1	2.22	0.69
1:E:161:ILE:HG23	1:E:168:GLU:HB2	1.73	0.69
1:F:134:LYS:O	1:F:135:VAL:HG12	1.93	0.69
1:F:154:ILE:HG21	1:F:171:TYR:CE2	2.27	0.69
2:P:106:ARG:HB2	2:P:121:VAL:HG21	1.75	0.69
2:Q:48:LEU:HD23	2:Q:51:MET:HE1	1.74	0.69
1:C:736:LEU:HD21	1:C:750:GLN:NE2	2.07	0.69
1:E:515:LYS:O	1:E:515:LYS:HG2	1.91	0.69
1:A:478:ALA:HB1	1:A:486:LYS:O	1.91	0.69
1:B:201:ASP:HA	1:B:210:PHE:HE2	1.58	0.69
1:E:348:LEU:HD12	1:E:545:THR:O	1.92	0.69
1:E:697:ILE:HD13	1:E:732:ILE:CD1	2.22	0.69
1:F:405:LEU:HD13	1:F:453:VAL:HG21	1.75	0.69
1:A:630:ARG:CZ	2:O:83:GLU:HG2	2.22	0.69
1:A:355:SER:OG	1:A:371:SER:HA	1.93	0.69
1:A:671:ARG:HH12	1:A:677:GLY:HA3	1.57	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:515:LYS:O	1:B:515:LYS:HG2	1.91	0.69
1:D:297:LYS:HA	1:D:602:PHE:O	1.92	0.69
1:E:201:ASP:HA	1:E:210:PHE:HE2	1.58	0.69
1:F:189:ASP:O	1:F:191:GLU:N	2.25	0.69
1:F:201:ASP:HA	1:F:210:PHE:HE2	1.58	0.69
1:F:611:THR:O	1:F:615:ILE:HG13	1.92	0.69
1:F:711:ILE:HG13	1:F:712:PHE:CE2	2.28	0.69
1:B:694:VAL:HG23	2:P:18:LEU:HD11	1.75	0.69
1:A:189:ASP:O	1:A:191:GLU:N	2.26	0.69
1:D:711:ILE:HG13	1:D:712:PHE:CE2	2.28	0.69
1:E:457:THR:HG21	1:E:468:LYS:HA	1.75	0.69
2:T:117:THR:HG23	2:T:120:GLU:HB2	1.75	0.69
1:F:630:ARG:CZ	2:T:83:GLU:HG2	2.22	0.69
1:A:297:LYS:HA	1:A:602:PHE:O	1.92	0.69
1:A:697:ILE:HD13	1:A:732:ILE:HD12	1.75	0.69
1:B:161:ILE:HG23	1:B:168:GLU:HB2	1.73	0.69
1:B:470:ASN:O	1:B:472:ARG:HG3	1.93	0.69
1:C:338:LEU:HD21	1:C:409:ARG:CZ	2.22	0.69
1:D:540:ARG:HD3	1:D:627:TYR:OH	1.93	0.69
1:E:470:ASN:O	1:E:472:ARG:HG3	1.93	0.69
1:F:478:ALA:HB1	1:F:486:LYS:O	1.92	0.69
2:Q:49:GLN:O	2:Q:53:ASN:HB2	1.93	0.69
2:S:115:LYS:HA	2:S:115:LYS:NZ	2.07	0.69
2:S:24:ASP:CB	2:S:26:THR:HG23	2.23	0.69
2:T:115:LYS:NZ	2:T:115:LYS:HA	2.07	0.69
1:B:234:LEU:HD23	1:B:235:THR:H	1.58	0.69
1:B:457:THR:HG21	1:B:468:LYS:HA	1.75	0.69
1:B:597:ASN:ND2	1:B:601:GLU:HB2	2.00	0.69
1:C:270:LYS:O	1:C:273:LYS:HB2	1.93	0.69
2:Q:117:THR:HG23	2:Q:120:GLU:HB2	1.75	0.69
2:S:106:ARG:HB2	2:S:121:VAL:HG21	1.75	0.69
1:A:179:LEU:HD23	1:A:179:LEU:H	1.58	0.68
1:C:478:ALA:HB1	1:C:486:LYS:O	1.92	0.68
1:F:515:LYS:O	1:F:515:LYS:HG2	1.92	0.68
1:F:327:LEU:HG	1:F:595:ILE:HG12	1.75	0.68
1:F:268:MET:O	1:F:271:LEU:HB2	1.93	0.68
1:F:355:SER:OG	1:F:371:SER:HA	1.92	0.68
1:F:457:THR:HG21	1:F:468:LYS:HA	1.74	0.68
2:Q:64:ASP:HB3	2:Q:67:GLU:OE2	1.93	0.68
2:R:49:GLN:O	2:R:53:ASN:HB2	1.94	0.68
2:R:64:ASP:HB3	2:R:67:GLU:OE2	1.92	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:201:ASP:HA	1:C:210:PHE:HE2	1.58	0.68
1:C:355:SER:OG	1:C:371:SER:HA	1.91	0.68
1:C:470:ASN:O	1:C:472:ARG:HG3	1.92	0.68
1:D:179:LEU:HD23	1:D:179:LEU:H	1.58	0.68
1:D:270:LYS:O	1:D:273:LYS:HB2	1.94	0.68
1:D:530:THR:HG21	2:R:145:MET:HE3	1.74	0.68
1:D:671:ARG:HH12	1:D:677:GLY:HA3	1.58	0.68
1:F:199:LEU:C	1:F:201:ASP:H	1.96	0.68
1:B:279:ILE:O	1:B:283:LEU:HD13	1.92	0.68
1:B:711:ILE:HG13	1:B:712:PHE:CE2	2.28	0.68
1:C:630:ARG:HG3	1:C:630:ARG:HH11	1.59	0.68
1:D:630:ARG:HH11	1:D:630:ARG:HG3	1.57	0.68
1:F:201:ASP:OD1	1:F:218:LEU:HD21	1.93	0.68
1:F:470:ASN:O	1:F:472:ARG:HG3	1.93	0.68
2:Q:4:LEU:CB	2:Q:8:GLN:HE21	2.06	0.68
1:C:107:THR:CG2	1:C:115:LYS:HE2	2.24	0.68
1:E:540:ARG:HD3	1:E:627:TYR:OH	1.94	0.68
1:E:697:ILE:HD13	1:E:732:ILE:HD12	1.74	0.68
2:O:64:ASP:HB3	2:O:67:GLU:OE2	1.94	0.68
2:P:64:ASP:HB3	2:P:67:GLU:OE2	1.94	0.68
1:D:630:ARG:CZ	2:R:83:GLU:HG2	2.24	0.68
1:A:630:ARG:HH11	1:A:630:ARG:HG3	1.58	0.68
1:D:697:ILE:HD13	1:D:732:ILE:CD1	2.23	0.68
1:F:105:TYR:HE1	1:F:151:LYS:HZ2	1.41	0.68
1:F:179:LEU:HD23	1:F:179:LEU:H	1.58	0.68
1:F:186:LYS:HE3	1:F:234:LEU:CD1	2.24	0.68
1:F:671:ARG:HH12	1:F:677:GLY:HA3	1.57	0.68
2:Q:106:ARG:HB2	2:Q:121:VAL:HG21	1.74	0.68
2:S:51:MET:HB3	2:S:71:MET:CE	2.20	0.68
1:A:348:LEU:HD12	1:A:545:THR:O	1.93	0.68
1:D:470:ASN:O	1:D:472:ARG:HG3	1.93	0.68
1:D:697:ILE:HD13	1:D:732:ILE:HD12	1.74	0.68
1:E:179:LEU:HD23	1:E:179:LEU:H	1.59	0.68
1:E:711:ILE:HG13	1:E:712:PHE:CD2	2.27	0.68
2:P:24:ASP:CB	2:P:26:THR:HG23	2.23	0.68
2:S:64:ASP:HB3	2:S:67:GLU:OE2	1.94	0.68
2:T:64:ASP:HB3	2:T:67:GLU:OE2	1.94	0.68
1:A:697:ILE:HD13	1:A:732:ILE:CD1	2.24	0.68
1:C:268:MET:O	1:C:271:LEU:HB2	1.94	0.68
1:D:338:LEU:HD21	1:D:409:ARG:CZ	2.23	0.68
1:E:630:ARG:CZ	2:S:83:GLU:HG2	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:268:MET:O	1:A:271:LEU:HB2	1.93	0.68
1:E:115:LYS:HB3	1:E:118:GLN:HG2	1.76	0.68
1:E:408:LEU:N	1:E:408:LEU:HD12	2.06	0.68
2:S:115:LYS:HZ3	2:S:115:LYS:HA	1.57	0.68
1:A:326:ILE:HG22	1:A:328:PHE:HE1	1.59	0.68
1:A:478:ALA:HA	1:A:488:LEU:HG	1.75	0.68
1:A:557:LEU:HG	1:A:575:VAL:HG12	1.76	0.68
1:A:581:GLN:NE2	1:A:581:GLN:HA	2.09	0.68
1:A:711:ILE:HG13	1:A:712:PHE:CE2	2.29	0.68
1:B:115:LYS:HB3	1:B:118:GLN:HG2	1.76	0.68
1:B:115:LYS:HZ2	1:B:116:GLU:N	1.83	0.68
1:B:405:LEU:HD13	1:B:453:VAL:HG21	1.76	0.68
1:F:104:ILE:HG23	1:F:152:LEU:HD23	1.75	0.68
2:T:49:GLN:O	2:T:53:ASN:HB2	1.93	0.68
1:A:186:LYS:HE3	1:A:234:LEU:CD1	2.24	0.67
1:A:470:ASN:O	1:A:472:ARG:HG3	1.94	0.67
1:B:348:LEU:HD12	1:B:545:THR:O	1.94	0.67
1:C:711:ILE:HG13	1:C:712:PHE:CE2	2.29	0.67
1:F:115:LYS:HB3	1:F:118:GLN:HG2	1.75	0.67
1:F:697:ILE:HD13	1:F:732:ILE:CD1	2.23	0.67
1:A:457:THR:HG21	1:A:468:LYS:HA	1.75	0.67
1:A:750:GLN:O	1:A:753:LYS:HB2	1.94	0.67
1:A:764:LEU:O	1:A:766:HIS:N	2.28	0.67
1:B:478:ALA:HA	1:B:488:LEU:HG	1.76	0.67
1:B:629:ASN:ND2	1:B:631:SER:HB2	2.06	0.67
1:B:764:LEU:O	1:B:766:HIS:N	2.27	0.67
1:C:115:LYS:HB3	1:C:118:GLN:HG2	1.75	0.67
1:F:183:SER:O	1:F:187:SER:CA	2.43	0.67
1:F:557:LEU:HG	1:F:575:VAL:HG12	1.76	0.67
2:O:138:TYR:O	2:O:142:VAL:HG23	1.94	0.67
2:O:49:GLN:O	2:O:53:ASN:HB2	1.94	0.67
2:P:49:GLN:O	2:P:53:ASN:HB2	1.94	0.67
2:Q:16:PHE:CE2	2:Q:27:ILE:HD11	2.30	0.67
1:A:134:LYS:O	1:A:135:VAL:HG12	1.93	0.67
1:A:201:ASP:OD1	1:A:218:LEU:HD21	1.94	0.67
1:B:179:LEU:HG	1:B:180:ASP:N	2.08	0.67
1:C:105:TYR:HE1	1:C:151:LYS:HZ2	1.41	0.67
1:C:179:LEU:HG	1:C:180:ASP:N	2.10	0.67
1:C:201:ASP:OD1	1:C:218:LEU:HD21	1.95	0.67
1:D:348:LEU:HD12	1:D:545:THR:O	1.94	0.67
1:D:71:PHE:CD2	1:D:73:ASN:HB2	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:254:ARG:N	1:E:254:ARG:HD2	2.10	0.67
1:E:405:LEU:HD13	1:E:453:VAL:HG21	1.75	0.67
1:F:764:LEU:O	1:F:766:HIS:N	2.27	0.67
2:S:48:LEU:HD23	2:S:51:MET:HE2	1.75	0.67
1:A:270:LYS:O	1:A:273:LYS:HB2	1.94	0.67
1:A:338:LEU:HD21	1:A:409:ARG:CZ	2.24	0.67
1:C:199:LEU:C	1:C:201:ASP:H	1.97	0.67
1:C:405:LEU:HD13	1:C:453:VAL:HG21	1.76	0.67
1:D:457:THR:HG21	1:D:468:LYS:HA	1.75	0.67
1:D:478:ALA:HA	1:D:488:LEU:HG	1.76	0.67
1:F:179:LEU:HG	1:F:180:ASP:N	2.09	0.67
2:R:106:ARG:HB2	2:R:121:VAL:HG21	1.74	0.67
1:A:179:LEU:HG	1:A:180:ASP:N	2.08	0.67
1:A:199:LEU:C	1:A:201:ASP:H	1.96	0.67
1:A:540:ARG:HD3	1:A:627:TYR:CZ	2.30	0.67
1:B:199:LEU:C	1:B:201:ASP:H	1.96	0.67
1:B:540:ARG:HD3	1:B:627:TYR:OH	1.95	0.67
1:B:695:LYS:HG3	2:P:19:PHE:CE1	2.30	0.67
1:C:504:ILE:O	1:C:507:GLN:HB3	1.94	0.67
1:C:540:ARG:HD3	1:C:627:TYR:OH	1.95	0.67
1:C:78:LYS:HG3	1:C:79:ILE:N	2.09	0.67
1:D:504:ILE:O	1:D:507:GLN:HB3	1.95	0.67
2:S:49:GLN:O	2:S:53:ASN:HB2	1.93	0.67
1:A:179:LEU:HG	1:A:180:ASP:H	1.59	0.67
1:C:183:SER:O	1:C:187:SER:CA	2.43	0.67
1:C:327:LEU:HG	1:C:595:ILE:HG12	1.77	0.67
1:D:201:ASP:HA	1:D:210:PHE:HE2	1.59	0.67
1:D:201:ASP:OD1	1:D:218:LEU:HD21	1.95	0.67
1:D:405:LEU:HD13	1:D:453:VAL:HG21	1.76	0.67
1:E:630:ARG:NH1	1:E:630:ARG:HG3	2.09	0.67
1:F:694:VAL:HG23	2:T:18:LEU:HD11	1.76	0.67
1:A:254:ARG:HD2	1:A:254:ARG:N	2.09	0.67
1:B:671:ARG:HH12	1:B:677:GLY:HA3	1.57	0.67
1:D:171:TYR:HD1	1:D:171:TYR:O	1.78	0.67
1:D:617:LYS:HZ2	1:D:618:ASN:ND2	1.84	0.67
1:E:711:ILE:HG13	1:E:712:PHE:CE2	2.29	0.67
1:F:478:ALA:HA	1:F:488:LEU:HG	1.76	0.67
1:A:530:THR:HG21	2:O:145:MET:HE3	1.76	0.67
1:B:697:ILE:HD13	1:B:732:ILE:HD12	1.77	0.67
1:C:424:LYS:HB3	1:C:424:LYS:HZ2	1.60	0.67
1:E:671:ARG:HH12	1:E:677:GLY:HA3	1.57	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:ASP:HA	1:A:210:PHE:HE2	1.59	0.67
1:A:408:LEU:HD12	1:A:408:LEU:N	2.06	0.67
1:A:405:LEU:HD13	1:A:453:VAL:HG21	1.77	0.67
1:B:697:ILE:HD13	1:B:732:ILE:CD1	2.25	0.67
1:C:179:LEU:HD23	1:C:179:LEU:H	1.59	0.67
1:D:115:LYS:HB3	1:D:118:GLN:HG2	1.76	0.67
1:E:695:LYS:HG3	2:S:19:PHE:CE1	2.29	0.67
2:R:48:LEU:HA	2:R:51:MET:HE3	1.77	0.67
1:A:115:LYS:HZ2	1:A:116:GLU:N	1.85	0.67
1:B:268:MET:O	1:B:271:LEU:HB2	1.95	0.67
1:C:557:LEU:HG	1:C:575:VAL:HG12	1.76	0.67
1:D:189:ASP:O	1:D:191:GLU:N	2.28	0.67
1:F:348:LEU:HD12	1:F:545:THR:O	1.94	0.67
1:A:115:LYS:HB3	1:A:118:GLN:HG2	1.75	0.66
1:A:142:VAL:HG13	1:A:154:ILE:CD1	2.25	0.66
1:A:154:ILE:HG21	1:A:171:TYR:CE2	2.30	0.66
1:B:661:ALA:O	1:B:665:LYS:HB2	1.95	0.66
1:C:581:GLN:HA	1:C:581:GLN:NE2	2.09	0.66
1:D:557:LEU:HG	1:D:575:VAL:HG12	1.75	0.66
1:D:581:GLN:NE2	1:D:581:GLN:HA	2.09	0.66
1:E:122:GLU:O	1:E:146:LYS:HE2	1.95	0.66
1:E:199:LEU:C	1:E:201:ASP:H	1.97	0.66
1:E:557:LEU:HG	1:E:575:VAL:HG12	1.76	0.66
1:F:540:ARG:HD3	1:F:627:TYR:CZ	2.29	0.66
2:P:117:THR:HG23	2:P:120:GLU:HB2	1.77	0.66
1:C:694:VAL:HG23	2:Q:18:LEU:HD11	1.76	0.66
2:R:16:PHE:CE2	2:R:27:ILE:HD11	2.30	0.66
1:A:715:GLU:HA	1:A:718:ARG:NH1	2.10	0.66
1:B:408:LEU:N	1:B:408:LEU:HD12	2.06	0.66
1:C:189:ASP:O	1:C:190:PRO:C	2.32	0.66
1:C:397:GLU:O	1:C:479:LYS:HA	1.95	0.66
1:D:567:THR:CG2	1:D:568:GLY:N	2.58	0.66
1:E:268:MET:O	1:E:271:LEU:HB2	1.95	0.66
2:T:4:LEU:HA	2:T:8:GLN:HE21	1.60	0.66
1:C:179:LEU:HG	1:C:180:ASP:H	1.60	0.66
1:C:348:LEU:HD12	1:C:545:THR:O	1.94	0.66
1:C:478:ALA:HA	1:C:488:LEU:HG	1.78	0.66
1:D:183:SER:O	1:D:187:SER:CA	2.43	0.66
1:D:78:LYS:HG3	1:D:79:ILE:N	2.10	0.66
1:E:478:ALA:HA	1:E:488:LEU:HG	1.77	0.66
1:F:715:GLU:HA	1:F:718:ARG:NH1	2.10	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:13:LYS:HA	2:Q:65:PHE:CZ	2.30	0.66
1:D:695:LYS:HG3	2:R:19:PHE:CE1	2.30	0.66
2:S:117:THR:HG23	2:S:120:GLU:HB2	1.77	0.66
2:S:64:ASP:CG	2:S:66:PRO:HD2	2.16	0.66
1:B:115:LYS:HA	1:B:115:LYS:HZ3	1.60	0.66
1:C:457:THR:HG21	1:C:468:LYS:HA	1.75	0.66
1:A:234:LEU:HD23	1:A:235:THR:H	1.60	0.66
1:A:472:ARG:NH1	1:A:472:ARG:HB3	2.11	0.66
1:B:179:LEU:H	1:B:179:LEU:HD23	1.60	0.66
1:B:254:ARG:HD2	1:B:254:ARG:N	2.10	0.66
1:B:540:ARG:HD3	1:B:627:TYR:CZ	2.30	0.66
1:C:712:PHE:HB3	1:C:716:LYS:HG2	1.77	0.66
1:E:201:ASP:OD1	1:E:218:LEU:HD21	1.95	0.66
1:E:540:ARG:HD3	1:E:627:TYR:CZ	2.30	0.66
1:E:581:GLN:NE2	1:E:581:GLN:HA	2.10	0.66
1:F:736:LEU:HD21	1:F:750:GLN:CD	2.15	0.66
2:P:13:LYS:HA	2:P:65:PHE:CZ	2.31	0.66
1:A:171:TYR:HD1	1:A:171:TYR:O	1.79	0.66
1:B:557:LEU:HG	1:B:575:VAL:HG12	1.78	0.66
1:D:540:ARG:HD3	1:D:627:TYR:CZ	2.31	0.66
1:D:736:LEU:HD21	1:D:750:GLN:CD	2.15	0.66
1:E:764:LEU:O	1:E:766:HIS:N	2.29	0.66
1:F:504:ILE:O	1:F:507:GLN:HB3	1.96	0.66
2:P:64:ASP:CG	2:P:66:PRO:HD2	2.16	0.66
2:Q:5:THR:HG23	2:Q:8:GLN:HB2	1.78	0.66
2:R:48:LEU:HA	2:R:51:MET:HE2	1.77	0.66
2:S:16:PHE:CE2	2:S:27:ILE:HD11	2.31	0.66
1:A:424:LYS:HZ2	1:A:424:LYS:HB3	1.60	0.66
1:A:78:LYS:HG3	1:A:79:ILE:N	2.09	0.66
1:B:179:LEU:HG	1:B:180:ASP:H	1.60	0.66
1:B:217:LYS:NZ	1:B:236:GLU:HB2	2.11	0.66
1:C:115:LYS:NZ	1:C:116:GLU:H	1.85	0.66
1:C:661:ALA:O	1:C:665:LYS:HB2	1.96	0.66
1:E:154:ILE:HG21	1:E:171:TYR:CE2	2.31	0.66
1:F:480:ASN:HD21	1:F:483:GLY:H	1.44	0.66
1:F:630:ARG:HG3	1:F:630:ARG:HH11	1.59	0.66
1:D:694:VAL:HG23	2:R:18:LEU:HD11	1.76	0.66
2:T:16:PHE:CE2	2:T:27:ILE:HD11	2.31	0.66
1:B:201:ASP:OD1	1:B:218:LEU:HD21	1.95	0.66
1:B:504:ILE:O	1:B:507:GLN:HB3	1.96	0.66
1:C:171:TYR:HD1	1:C:171:TYR:O	1.79	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:LEU:C	1:D:201:ASP:H	1.96	0.66
1:D:372:LYS:HG3	1:D:373:LYS:N	2.11	0.66
2:R:13:LYS:HA	2:R:65:PHE:CZ	2.31	0.66
1:A:504:ILE:O	1:A:507:GLN:HB3	1.95	0.66
1:B:302:LEU:HD22	1:B:602:PHE:HE1	1.61	0.66
1:C:764:LEU:C	1:C:766:HIS:N	2.49	0.66
1:D:179:LEU:HG	1:D:180:ASP:N	2.10	0.66
1:D:372:LYS:O	1:D:374:HIS:N	2.29	0.66
1:D:408:LEU:N	1:D:408:LEU:HD12	2.06	0.66
1:E:171:TYR:HD1	1:E:171:TYR:O	1.79	0.66
1:E:234:LEU:HD23	1:E:235:THR:H	1.59	0.66
1:E:504:ILE:O	1:E:507:GLN:HB3	1.96	0.66
2:O:24:ASP:CB	2:O:26:THR:HG23	2.24	0.66
2:O:64:ASP:CG	2:O:66:PRO:HD2	2.16	0.66
1:B:171:TYR:O	1:B:171:TYR:HD1	1.79	0.66
1:D:105:TYR:HE1	1:D:151:LYS:HZ2	1.43	0.66
1:D:376:GLN:O	1:D:380:VAL:HG23	1.96	0.66
1:D:750:GLN:O	1:D:753:LYS:HB2	1.95	0.66
1:E:131:ARG:H	1:E:170:TYR:HE2	1.44	0.66
1:E:179:LEU:HG	1:E:180:ASP:N	2.10	0.66
1:E:397:GLU:O	1:E:479:LYS:HA	1.96	0.66
1:E:567:THR:CG2	1:E:568:GLY:N	2.58	0.66
1:F:234:LEU:HD23	1:F:235:THR:H	1.59	0.66
2:O:13:LYS:HA	2:O:65:PHE:CZ	2.31	0.66
2:Q:12:PHE:CD1	2:Q:72:MET:HG3	2.31	0.66
2:Q:42:ASN:N	2:Q:43:PRO:HD2	2.11	0.66
2:R:115:LYS:HA	2:R:115:LYS:HZ3	1.60	0.66
2:R:5:THR:HG23	2:R:8:GLN:HB2	1.78	0.66
1:A:630:ARG:HG3	1:A:630:ARG:NH1	2.10	0.65
1:B:182:ILE:O	1:B:182:ILE:HD13	1.96	0.65
1:B:700:TYR:HD1	1:B:728:ALA:N	1.95	0.65
1:B:736:LEU:HD21	1:B:750:GLN:CD	2.16	0.65
1:C:567:THR:CG2	1:C:568:GLY:N	2.59	0.65
1:D:630:ARG:HG3	1:D:630:ARG:NH1	2.10	0.65
1:E:180:ASP:CG	1:E:181:ILE:H	2.00	0.65
1:F:708:ALA:O	1:F:710:HIS:N	2.30	0.65
2:P:16:PHE:CE2	2:P:27:ILE:HD11	2.31	0.65
2:Q:64:ASP:CG	2:Q:66:PRO:HD2	2.17	0.65
2:S:13:LYS:HA	2:S:65:PHE:CZ	2.31	0.65
1:A:397:GLU:O	1:A:479:LYS:HA	1.96	0.65
1:D:518:ASN:N	1:D:518:ASN:HD22	1.95	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:736:LEU:HD21	1:E:750:GLN:CD	2.16	0.65
1:E:78:LYS:HG3	1:E:79:ILE:N	2.09	0.65
1:F:115:LYS:NZ	1:F:116:GLU:H	1.85	0.65
1:F:424:LYS:HB3	1:F:424:LYS:HZ2	1.60	0.65
2:O:12:PHE:CD1	2:O:72:MET:HG3	2.31	0.65
1:C:695:LYS:HG3	2:Q:19:PHE:CE1	2.31	0.65
2:T:138:TYR:O	2:T:142:VAL:HG23	1.96	0.65
2:T:42:ASN:N	2:T:43:PRO:HD2	2.11	0.65
1:A:183:SER:O	1:A:187:SER:CA	2.43	0.65
1:A:617:LYS:NZ	1:A:618:ASN:ND2	2.44	0.65
1:B:326:ILE:HG22	1:B:328:PHE:HE1	1.60	0.65
1:C:480:ASN:HD21	1:C:483:GLY:H	1.44	0.65
1:C:540:ARG:HD3	1:C:627:TYR:CZ	2.30	0.65
1:E:275:GLY:HA2	1:E:278:LYS:CE	2.26	0.65
1:E:372:LYS:O	1:E:374:HIS:N	2.28	0.65
1:E:643:ILE:HG22	1:E:644:GLU:H	1.61	0.65
1:F:750:GLN:O	1:F:753:LYS:HB2	1.95	0.65
2:Q:106:ARG:O	2:Q:110:THR:HG23	1.97	0.65
2:R:117:THR:HG23	2:R:120:GLU:HB2	1.78	0.65
2:T:13:LYS:HA	2:T:65:PHE:CZ	2.30	0.65
2:T:5:THR:HG23	2:T:8:GLN:HB2	1.78	0.65
1:B:154:ILE:HG21	1:B:171:TYR:CE2	2.32	0.65
1:C:517:VAL:HG23	1:C:518:ASN:HD22	1.62	0.65
1:D:175:LYS:HB2	1:D:175:LYS:NZ	2.12	0.65
1:E:302:LEU:HD22	1:E:602:PHE:HE1	1.61	0.65
1:E:715:GLU:HA	1:E:718:ARG:NH1	2.11	0.65
1:F:78:LYS:HG3	1:F:79:ILE:N	2.10	0.65
2:R:42:ASN:N	2:R:43:PRO:HD2	2.10	0.65
1:A:567:THR:CG2	1:A:568:GLY:N	2.59	0.65
1:B:567:THR:CG2	1:B:568:GLY:N	2.60	0.65
1:D:104:ILE:HG23	1:D:152:LEU:HD23	1.78	0.65
1:F:131:ARG:H	1:F:170:TYR:HE2	1.44	0.65
2:R:64:ASP:CG	2:R:66:PRO:HD2	2.16	0.65
2:R:12:PHE:CD1	2:R:72:MET:HG3	2.32	0.65
2:T:48:LEU:HD23	2:T:51:MET:CE	2.27	0.65
1:A:712:PHE:HB3	1:A:716:LYS:HG2	1.78	0.65
1:B:197:LYS:HZ3	1:B:197:LYS:C	1.99	0.65
1:B:270:LYS:O	1:B:273:LYS:HB2	1.96	0.65
1:B:750:GLN:O	1:B:753:LYS:HB2	1.96	0.65
1:C:275:GLY:HA2	1:C:278:LYS:CE	2.26	0.65
1:C:302:LEU:HD22	1:C:602:PHE:HE1	1.62	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:89:ILE:HD13	1:D:175:LYS:HE2	1.78	0.65
1:D:794:GLN:HE22	1:D:795:LYS:HG3	1.61	0.65
1:E:122:GLU:OE2	1:E:145:LYS:HE2	1.97	0.65
1:E:184:LYS:HA	1:E:187:SER:CB	2.27	0.65
2:S:42:ASN:N	2:S:43:PRO:HD2	2.10	0.65
1:A:182:ILE:O	1:A:182:ILE:HD13	1.96	0.65
1:B:131:ARG:H	1:B:170:TYR:HE2	1.44	0.65
1:B:183:SER:O	1:B:187:SER:CA	2.42	0.65
1:B:350:VAL:HG12	1:B:352:GLY:H	1.61	0.65
1:C:115:LYS:HA	1:C:115:LYS:HZ3	1.62	0.65
1:C:154:ILE:HG22	1:C:155:ASN:H	1.62	0.65
1:D:234:LEU:HD23	1:D:235:THR:H	1.59	0.65
1:F:122:GLU:OE2	1:F:145:LYS:HE2	1.97	0.65
1:F:171:TYR:HD1	1:F:171:TYR:O	1.79	0.65
2:S:48:LEU:HD23	2:S:51:MET:CE	2.26	0.65
1:A:107:THR:CG2	1:A:115:LYS:HE2	2.26	0.65
1:A:480:ASN:HD21	1:A:483:GLY:H	1.45	0.65
1:B:186:LYS:HE3	1:B:234:LEU:CD1	2.25	0.65
1:B:424:LYS:HB3	1:B:424:LYS:HZ2	1.61	0.65
1:B:718:ARG:O	1:B:722:ILE:HG13	1.97	0.65
1:C:629:ASN:ND2	1:C:631:SER:H	1.95	0.65
1:D:715:GLU:HA	1:D:718:ARG:NH1	2.10	0.65
1:E:217:LYS:NZ	1:E:236:GLU:HB2	2.12	0.65
1:E:372:LYS:HG3	1:E:373:LYS:N	2.11	0.65
1:F:217:LYS:NZ	1:F:236:GLU:HB2	2.11	0.65
1:F:712:PHE:HB3	1:F:716:LYS:HG2	1.77	0.65
1:A:695:LYS:HG3	2:O:19:PHE:CE1	2.32	0.65
2:R:72:MET:C	2:R:74:ARG:H	2.00	0.65
1:A:115:LYS:HB2	1:A:118:GLN:HG2	1.79	0.65
1:A:372:LYS:HG3	1:A:373:LYS:N	2.12	0.65
1:A:372:LYS:O	1:A:374:HIS:N	2.29	0.65
1:B:217:LYS:HZ1	1:B:233:ASN:HB3	1.61	0.65
1:B:372:LYS:HG3	1:B:373:LYS:N	2.12	0.65
1:B:794:GLN:HE22	1:B:795:LYS:HG3	1.61	0.65
1:C:104:ILE:HG23	1:C:152:LEU:HD23	1.79	0.65
1:C:630:ARG:HG3	1:C:630:ARG:NH1	2.11	0.65
1:D:182:ILE:HD13	1:D:182:ILE:O	1.97	0.65
1:E:105:TYR:HE1	1:E:151:LYS:HZ2	1.42	0.65
1:E:712:PHE:HB3	1:E:716:LYS:HG2	1.77	0.65
1:F:107:THR:CG2	1:F:115:LYS:HE2	2.27	0.65
1:F:122:GLU:O	1:F:146:LYS:HE2	1.97	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:182:ILE:O	1:F:182:ILE:HD13	1.96	0.65
2:P:42:ASN:N	2:P:43:PRO:HD2	2.10	0.65
1:A:639:ASN:HD22	1:A:639:ASN:N	1.95	0.65
1:B:184:LYS:HA	1:B:187:SER:CB	2.27	0.65
1:B:275:GLY:HA2	1:B:278:LYS:CE	2.27	0.65
1:B:630:ARG:HG3	1:B:630:ARG:HH11	1.62	0.65
1:D:311:HIS:O	1:D:314:ALA:HB3	1.96	0.65
1:E:311:HIS:O	1:E:314:ALA:HB3	1.97	0.65
1:E:521:ASN:HB3	1:E:524:GLU:HB3	1.79	0.65
1:F:326:ILE:HG22	1:F:328:PHE:HE1	1.59	0.65
1:F:376:GLN:O	1:F:380:VAL:HG23	1.96	0.65
1:B:630:ARG:CZ	2:P:83:GLU:HG2	2.27	0.65
2:Q:22:ASP:OD2	2:Q:24:ASP:OD1	2.14	0.65
2:Q:4:LEU:HA	2:Q:8:GLN:HE21	1.62	0.65
1:E:694:VAL:HG22	2:S:18:LEU:HD21	1.78	0.65
2:S:4:LEU:HA	2:S:8:GLN:HE21	1.62	0.65
2:T:115:LYS:HZ3	2:T:115:LYS:HA	1.60	0.65
1:A:327:LEU:HG	1:A:595:ILE:HG12	1.80	0.64
1:A:718:ARG:O	1:A:722:ILE:HG13	1.96	0.64
1:C:182:ILE:HD13	1:C:182:ILE:O	1.97	0.64
1:D:122:GLU:O	1:D:146:LYS:HE2	1.97	0.64
1:D:397:GLU:O	1:D:479:LYS:HA	1.96	0.64
1:D:88:LYS:NZ	1:D:172:GLU:OE2	2.29	0.64
1:E:183:SER:O	1:E:187:SER:CA	2.43	0.64
1:F:372:LYS:O	1:F:374:HIS:N	2.29	0.64
2:S:9:ILE:HD12	2:S:69:LEU:HD22	1.79	0.64
2:T:22:ASP:OD2	2:T:24:ASP:OD1	2.15	0.64
1:A:275:GLY:HA2	1:A:278:LYS:CE	2.27	0.64
1:A:700:TYR:HD1	1:A:728:ALA:N	1.96	0.64
1:A:736:LEU:HD21	1:A:750:GLN:CD	2.17	0.64
1:C:236:GLU:HA	1:C:239:HIS:CD2	2.32	0.64
1:C:794:GLN:HE22	1:C:795:LYS:HG3	1.61	0.64
1:D:179:LEU:HG	1:D:180:ASP:H	1.62	0.64
1:D:343:VAL:HG13	1:D:487:PRO:HG2	1.78	0.64
1:D:708:ALA:O	1:D:710:HIS:N	2.30	0.64
1:E:376:GLN:O	1:E:380:VAL:HG23	1.96	0.64
1:F:567:THR:CG2	1:F:568:GLY:N	2.60	0.64
1:F:700:TYR:HD1	1:F:728:ALA:N	1.95	0.64
2:Q:138:TYR:O	2:Q:142:VAL:HG23	1.97	0.64
1:A:122:GLU:O	1:A:146:LYS:HE2	1.97	0.64
1:A:661:ALA:O	1:A:665:LYS:HB2	1.96	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:794:GLN:HE22	1:A:795:LYS:HG3	1.61	0.64
1:B:472:ARG:HB3	1:B:472:ARG:NH1	2.13	0.64
1:B:397:GLU:O	1:B:479:LYS:HA	1.96	0.64
1:C:186:LYS:HE3	1:C:234:LEU:CD1	2.27	0.64
1:C:254:ARG:N	1:C:254:ARG:HD2	2.09	0.64
1:C:521:ASN:HB3	1:C:524:GLU:HB3	1.80	0.64
1:C:71:PHE:CD2	1:C:73:ASN:HB2	2.33	0.64
1:D:217:LYS:HZ1	1:D:233:ASN:HB3	1.60	0.64
1:D:275:GLY:HA2	1:D:278:LYS:CE	2.27	0.64
1:D:302:LEU:HD22	1:D:602:PHE:HE1	1.61	0.64
1:F:88:LYS:NZ	1:F:172:GLU:OE2	2.30	0.64
1:F:89:ILE:HD13	1:F:175:LYS:HE2	1.78	0.64
1:F:270:LYS:O	1:F:273:LYS:HB2	1.96	0.64
1:F:311:HIS:O	1:F:314:ALA:HB3	1.97	0.64
1:F:540:ARG:HD2	1:F:582:ASP:OD1	1.97	0.64
2:P:12:PHE:CD1	2:P:72:MET:HG3	2.31	0.64
2:Q:115:LYS:HA	2:Q:115:LYS:HZ3	1.61	0.64
2:Q:48:LEU:HD23	2:Q:51:MET:CE	2.28	0.64
2:R:48:LEU:HD23	2:R:51:MET:CE	2.27	0.64
2:T:64:ASP:CG	2:T:66:PRO:HD2	2.17	0.64
1:B:540:ARG:HD2	1:B:582:ASP:OD1	1.97	0.64
1:B:715:GLU:HA	1:B:718:ARG:NH1	2.11	0.64
1:B:78:LYS:HG3	1:B:79:ILE:N	2.11	0.64
1:C:131:ARG:H	1:C:170:TYR:HE2	1.45	0.64
1:E:182:ILE:O	1:E:182:ILE:HD13	1.97	0.64
1:E:270:LYS:O	1:E:273:LYS:HB2	1.96	0.64
2:O:72:MET:C	2:O:74:ARG:H	2.01	0.64
2:P:9:ILE:HD12	2:P:69:LEU:HD22	1.79	0.64
2:S:5:THR:HG23	2:S:8:GLN:HB2	1.79	0.64
2:T:12:PHE:CD1	2:T:72:MET:HG3	2.32	0.64
1:A:217:LYS:NZ	1:A:236:GLU:HB2	2.12	0.64
1:A:594:PHE:HE2	1:A:596:ILE:HD11	1.62	0.64
1:B:357:TRP:CZ3	1:B:439:ASN:HB2	2.33	0.64
1:C:234:LEU:HD23	1:C:235:THR:H	1.61	0.64
1:C:372:LYS:O	1:C:374:HIS:N	2.30	0.64
1:C:376:GLN:O	1:C:380:VAL:HG23	1.98	0.64
1:C:715:GLU:HA	1:C:718:ARG:NH1	2.11	0.64
1:C:750:GLN:O	1:C:753:LYS:HB2	1.96	0.64
1:D:111:LEU:HD23	1:D:155:ASN:HD21	1.63	0.64
1:D:217:LYS:NZ	1:D:236:GLU:HB2	2.11	0.64
1:D:517:VAL:HG23	1:D:518:ASN:HD22	1.61	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:764:LEU:C	1:D:766:HIS:N	2.51	0.64
1:D:79:ILE:C	1:D:81:GLN:H	2.01	0.64
1:E:700:TYR:HD1	1:E:728:ALA:N	1.96	0.64
1:E:88:LYS:NZ	1:E:172:GLU:OE2	2.30	0.64
1:F:372:LYS:HG3	1:F:373:LYS:N	2.12	0.64
1:F:397:GLU:O	1:F:479:LYS:HA	1.97	0.64
2:R:55:VAL:HG11	2:R:71:MET:HE3	1.79	0.64
2:S:12:PHE:CD1	2:S:72:MET:HG3	2.32	0.64
1:A:376:GLN:O	1:A:380:VAL:HG23	1.97	0.64
1:A:435:LEU:HG	1:A:446:ILE:HG22	1.80	0.64
1:B:712:PHE:HB3	1:B:716:LYS:HG2	1.78	0.64
1:C:372:LYS:HG3	1:C:373:LYS:N	2.12	0.64
1:C:736:LEU:HD21	1:C:750:GLN:CD	2.17	0.64
1:D:480:ASN:HD21	1:D:483:GLY:H	1.45	0.64
1:D:540:ARG:HD2	1:D:582:ASP:OD1	1.97	0.64
1:D:712:PHE:HB3	1:D:716:LYS:HG2	1.79	0.64
1:E:326:ILE:HG22	1:E:328:PHE:HE1	1.58	0.64
1:E:357:TRP:CZ3	1:E:439:ASN:HB2	2.33	0.64
1:E:518:ASN:N	1:E:518:ASN:HD22	1.94	0.64
1:A:694:VAL:HG23	2:O:18:LEU:HD11	1.78	0.64
2:O:87:GLU:O	2:O:91:VAL:HG23	1.98	0.64
2:S:76:MET:O	2:S:77:LYS:HD2	1.98	0.64
1:A:318:ILE:HG23	1:A:322:LEU:HD12	1.78	0.64
1:E:318:ILE:HG23	1:E:322:LEU:HD12	1.79	0.64
1:E:750:GLN:O	1:E:753:LYS:HB2	1.97	0.64
1:F:180:ASP:CG	1:F:181:ILE:H	2.01	0.64
1:F:184:LYS:HA	1:F:187:SER:CB	2.27	0.64
1:F:318:ILE:HG23	1:F:322:LEU:HD12	1.80	0.64
2:O:48:LEU:HD23	2:O:51:MET:HE1	1.80	0.64
1:A:122:GLU:OE2	1:A:145:LYS:HE2	1.96	0.64
1:B:115:LYS:HG3	1:B:153:ILE:HD13	1.79	0.64
1:C:154:ILE:HG21	1:C:171:TYR:CE2	2.33	0.64
1:C:180:ASP:CG	1:C:181:ILE:H	2.01	0.64
1:E:186:LYS:HE3	1:E:234:LEU:CD1	2.24	0.64
1:E:719:LYS:HG2	1:E:797:ILE:CD1	2.28	0.64
1:F:152:LEU:HD21	1:F:171:TYR:CE1	2.33	0.64
1:F:236:GLU:HA	1:F:239:HIS:CD2	2.33	0.64
1:F:617:LYS:NZ	1:F:618:ASN:ND2	2.45	0.64
1:F:794:GLN:HE22	1:F:795:LYS:HG3	1.61	0.64
2:O:16:PHE:CE2	2:O:27:ILE:CD1	2.81	0.64
2:O:4:LEU:HA	2:O:8:GLN:HE21	1.62	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:87:GLU:O	2:P:91:VAL:HG23	1.98	0.64
2:Q:24:ASP:CB	2:Q:26:THR:HG23	2.24	0.64
2:T:48:LEU:HD23	2:T:51:MET:HE1	1.79	0.64
1:A:540:ARG:HD2	1:A:582:ASP:OD1	1.97	0.64
1:B:122:GLU:OE2	1:B:145:LYS:HE2	1.98	0.64
1:B:88:LYS:NZ	1:B:172:GLU:OE2	2.31	0.64
1:C:435:LEU:HG	1:C:446:ILE:HG22	1.79	0.64
1:C:302:LEU:HB2	1:C:602:PHE:HD1	1.63	0.64
1:C:700:TYR:HD1	1:C:728:ALA:N	1.96	0.64
1:D:184:LYS:HA	1:D:187:SER:CB	2.27	0.64
1:D:220:LEU:HD11	1:D:223:LYS:HB2	1.80	0.64
2:P:48:LEU:HD23	2:P:51:MET:CE	2.27	0.64
2:P:4:LEU:HA	2:P:8:GLN:HE21	1.62	0.64
2:Q:72:MET:C	2:Q:74:ARG:H	2.00	0.64
2:R:4:LEU:HA	2:R:8:GLN:HE21	1.62	0.64
1:B:111:LEU:HD23	1:B:155:ASN:HD21	1.63	0.64
1:B:180:ASP:CG	1:B:181:ILE:H	2.01	0.64
1:B:435:LEU:HG	1:B:446:ILE:HG22	1.79	0.64
1:C:518:ASN:HD22	1:C:518:ASN:N	1.95	0.64
1:C:88:LYS:NZ	1:C:172:GLU:OE2	2.30	0.64
1:E:115:LYS:HB2	1:E:118:GLN:HG2	1.80	0.64
1:E:99:GLU:C	1:E:101:GLY:H	2.01	0.64
1:F:480:ASN:HD21	1:F:483:GLY:N	1.96	0.64
2:P:5:THR:HG23	2:P:8:GLN:HB2	1.79	0.64
1:A:104:ILE:HG23	1:A:152:LEU:HD23	1.79	0.63
1:A:105:TYR:HE1	1:A:151:LYS:HZ2	1.45	0.63
1:A:517:VAL:HG23	1:A:518:ASN:HD22	1.62	0.63
1:C:311:HIS:O	1:C:314:ALA:HB3	1.97	0.63
1:C:515:LYS:HZ2	1:C:515:LYS:HB3	1.63	0.63
1:D:186:LYS:HE3	1:D:234:LEU:CD1	2.25	0.63
1:D:236:GLU:HA	1:D:239:HIS:CD2	2.33	0.63
1:D:472:ARG:HB3	1:D:472:ARG:NH1	2.13	0.63
1:D:594:PHE:HE2	1:D:596:ILE:HD11	1.63	0.63
1:E:594:PHE:HE2	1:E:596:ILE:HD11	1.63	0.63
1:E:794:GLN:HE22	1:E:795:LYS:HG3	1.63	0.63
1:F:254:ARG:HD2	1:F:254:ARG:N	2.10	0.63
1:F:301:ALA:O	1:F:303:LYS:N	2.31	0.63
1:F:350:VAL:HG12	1:F:352:GLY:H	1.62	0.63
1:F:550:SER:H	1:F:553:GLN:HE21	1.44	0.63
1:F:581:GLN:HA	1:F:581:GLN:NE2	2.12	0.63
2:S:138:TYR:O	2:S:142:VAL:HG23	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:581:GLN:HE21	1:A:629:ASN:N	1.97	0.63
1:A:625:LEU:HD12	1:A:626:TYR:N	2.13	0.63
1:C:318:ILE:HG23	1:C:322:LEU:HD12	1.80	0.63
1:C:694:VAL:HG22	2:Q:18:LEU:HD21	1.80	0.63
1:D:173:ILE:HG23	1:D:174:GLY:H	1.63	0.63
1:D:350:VAL:HG12	1:D:352:GLY:H	1.63	0.63
1:E:104:ILE:HG23	1:E:152:LEU:HD23	1.78	0.63
1:E:115:LYS:NZ	1:E:116:GLU:H	1.85	0.63
1:E:718:ARG:O	1:E:722:ILE:HG13	1.99	0.63
1:F:175:LYS:HB2	1:F:175:LYS:NZ	2.13	0.63
1:F:302:LEU:HD22	1:F:602:PHE:HE1	1.61	0.63
1:F:731:GLU:O	1:F:734:ASN:HB3	1.97	0.63
2:O:12:PHE:CE1	2:O:72:MET:HG3	2.33	0.63
2:R:22:ASP:OD2	2:R:24:ASP:OD1	2.17	0.63
2:R:87:GLU:O	2:R:91:VAL:HG23	1.98	0.63
1:A:180:ASP:CG	1:A:181:ILE:H	2.02	0.63
1:A:184:LYS:HA	1:A:187:SER:CB	2.27	0.63
1:A:236:GLU:HA	1:A:239:HIS:CD2	2.33	0.63
1:A:357:TRP:CZ3	1:A:439:ASN:HB2	2.33	0.63
1:E:472:ARG:NH1	1:E:472:ARG:HB3	2.13	0.63
1:F:589:LYS:HE3	1:F:608:TRP:CG	2.34	0.63
2:O:22:ASP:OD2	2:O:24:ASP:OD1	2.16	0.63
2:O:5:THR:HG23	2:O:8:GLN:HB2	1.79	0.63
1:A:220:LEU:HD11	1:A:223:LYS:HB2	1.80	0.63
1:A:217:LYS:HZ1	1:A:233:ASN:HB3	1.63	0.63
1:A:302:LEU:HD22	1:A:602:PHE:HE1	1.63	0.63
1:B:581:GLN:HA	1:B:581:GLN:NE2	2.12	0.63
1:C:472:ARG:HB3	1:C:472:ARG:NH1	2.12	0.63
1:D:173:ILE:HG23	1:D:174:GLY:N	2.13	0.63
1:E:350:VAL:HG12	1:E:352:GLY:H	1.63	0.63
1:E:424:LYS:HB3	1:E:424:LYS:HZ2	1.61	0.63
1:E:517:VAL:HG23	1:E:518:ASN:HD22	1.62	0.63
1:E:625:LEU:HD12	1:E:626:TYR:N	2.13	0.63
2:O:76:MET:O	2:O:77:LYS:HD2	1.98	0.63
1:B:540:ARG:NH2	2:P:87:GLU:OE1	2.32	0.63
1:A:88:LYS:NZ	1:A:172:GLU:OE2	2.31	0.63
1:B:104:ILE:HG23	1:B:152:LEU:HD23	1.78	0.63
1:C:122:GLU:OE2	1:C:145:LYS:HE2	1.99	0.63
1:E:236:GLU:HA	1:E:239:HIS:CD2	2.33	0.63
1:F:517:VAL:HG23	1:F:518:ASN:HD22	1.62	0.63
2:O:106:ARG:O	2:O:110:THR:HG23	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:T:76:MET:O	2:T:77:LYS:HD2	1.99	0.63
1:A:518:ASN:N	1:A:518:ASN:HD22	1.95	0.63
1:A:521:ASN:HB3	1:A:524:GLU:HB3	1.79	0.63
1:B:89:ILE:HD13	1:B:175:LYS:HE2	1.80	0.63
1:B:301:ALA:O	1:B:303:LYS:N	2.32	0.63
1:B:480:ASN:HD21	1:B:483:GLY:H	1.47	0.63
1:B:521:ASN:HB3	1:B:524:GLU:HB3	1.80	0.63
1:B:625:LEU:HD12	1:B:626:TYR:N	2.13	0.63
1:B:708:ALA:O	1:B:710:HIS:N	2.32	0.63
1:C:516:VAL:HG21	1:C:532:LEU:HD11	1.81	0.63
1:C:617:LYS:NZ	1:C:618:ASN:ND2	2.45	0.63
1:D:115:LYS:HB2	1:D:118:GLN:HG2	1.81	0.63
1:D:184:LYS:CE	1:D:191:GLU:HB2	2.29	0.63
1:D:326:ILE:HG22	1:D:328:PHE:HE1	1.62	0.63
1:D:700:TYR:HD1	1:D:728:ALA:N	1.97	0.63
1:D:90:PRO:HG2	1:D:93:VAL:CB	2.26	0.63
2:O:9:ILE:HD12	2:O:69:LEU:HD22	1.81	0.63
1:A:540:ARG:NH2	2:O:87:GLU:OE1	2.32	0.63
2:Q:12:PHE:CE1	2:Q:72:MET:HG3	2.34	0.63
1:D:694:VAL:HG22	2:R:18:LEU:HD21	1.81	0.63
2:S:72:MET:C	2:S:74:ARG:H	2.00	0.63
1:A:708:ALA:O	1:A:710:HIS:N	2.32	0.63
1:B:518:ASN:N	1:B:518:ASN:HD22	1.95	0.63
1:C:122:GLU:O	1:C:146:LYS:HE2	1.99	0.63
1:C:175:LYS:NZ	1:C:175:LYS:HB2	2.13	0.63
1:D:357:TRP:CZ3	1:D:439:ASN:HB2	2.33	0.63
1:E:179:LEU:HG	1:E:180:ASP:H	1.62	0.63
1:E:589:LYS:HE3	1:E:608:TRP:CG	2.34	0.63
1:E:79:ILE:C	1:E:81:GLN:H	2.01	0.63
1:F:472:ARG:NH1	1:F:472:ARG:HB3	2.12	0.63
1:F:581:GLN:HE21	1:F:629:ASN:N	1.95	0.63
2:Q:9:ILE:HD12	2:Q:69:LEU:HD22	1.79	0.63
1:F:695:LYS:HG3	2:T:19:PHE:CE1	2.33	0.63
1:A:515:LYS:HZ2	1:A:515:LYS:HB3	1.62	0.63
1:B:311:HIS:O	1:B:314:ALA:HB3	1.99	0.63
1:C:184:LYS:HA	1:C:187:SER:CB	2.27	0.63
1:D:154:ILE:HG21	1:D:171:TYR:CE2	2.33	0.63
1:E:189:ASP:O	1:E:190:PRO:C	2.33	0.63
1:E:255:THR:O	1:E:259:LEU:N	2.28	0.63
1:E:326:ILE:CG2	1:E:328:PHE:CE1	2.82	0.63
1:E:550:SER:H	1:E:553:GLN:HE21	1.46	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:521:ASN:HB3	1:F:524:GLU:HB3	1.81	0.63
1:F:594:PHE:HE2	1:F:596:ILE:HD11	1.64	0.63
1:F:629:ASN:ND2	1:F:631:SER:H	1.97	0.63
1:F:630:ARG:NH1	1:F:630:ARG:HG3	2.12	0.63
2:S:12:PHE:CE1	2:S:72:MET:HG3	2.34	0.63
1:B:517:VAL:HG23	1:B:518:ASN:HD22	1.62	0.63
1:C:173:ILE:HG23	1:C:174:GLY:N	2.14	0.63
1:D:301:ALA:C	1:D:303:LYS:N	2.52	0.63
1:E:581:GLN:HE21	1:E:629:ASN:N	1.96	0.63
1:F:301:ALA:C	1:F:303:LYS:N	2.52	0.63
1:F:719:LYS:HG2	1:F:797:ILE:CD1	2.29	0.63
2:R:9:ILE:HD12	2:R:69:LEU:HD22	1.80	0.63
2:R:76:MET:O	2:R:77:LYS:HD2	1.98	0.63
2:T:9:ILE:HD12	2:T:69:LEU:HD22	1.80	0.63
1:A:111:LEU:HD23	1:A:155:ASN:HD21	1.64	0.62
1:B:376:GLN:O	1:B:380:VAL:HG23	1.98	0.62
1:B:629:ASN:ND2	1:B:631:SER:H	1.96	0.62
1:B:76:LEU:O	1:B:79:ILE:N	2.32	0.62
1:D:521:ASN:HB3	1:D:524:GLU:HB3	1.81	0.62
1:E:173:ILE:HG23	1:E:174:GLY:N	2.14	0.62
1:E:629:ASN:ND2	1:E:631:SER:H	1.97	0.62
1:E:76:LEU:O	1:E:79:ILE:N	2.32	0.62
1:F:302:LEU:HB2	1:F:602:PHE:HD1	1.64	0.62
2:P:55:VAL:HG11	2:P:71:MET:HE3	1.80	0.62
1:A:131:ARG:H	1:A:170:TYR:HE2	1.46	0.62
1:A:175:LYS:HB2	1:A:175:LYS:NZ	2.13	0.62
1:B:236:GLU:HA	1:B:239:HIS:CD2	2.34	0.62
1:C:111:LEU:HD23	1:C:155:ASN:HD21	1.65	0.62
1:C:220:LEU:HD11	1:C:223:LYS:HB2	1.81	0.62
1:C:708:ALA:O	1:C:710:HIS:N	2.32	0.62
1:D:617:LYS:NZ	1:D:618:ASN:ND2	2.43	0.62
1:F:435:LEU:HG	1:F:446:ILE:HG22	1.80	0.62
1:F:661:ALA:O	1:F:665:LYS:HB2	1.99	0.62
2:O:48:LEU:HD23	2:O:51:MET:CE	2.28	0.62
2:O:93:ASP:OD1	2:O:97:ASN:ND2	2.32	0.62
1:A:302:LEU:HB2	1:A:602:PHE:HD1	1.64	0.62
1:A:764:LEU:C	1:A:766:HIS:N	2.53	0.62
1:C:217:LYS:NZ	1:C:236:GLU:HB2	2.13	0.62
1:D:301:ALA:O	1:D:303:LYS:N	2.32	0.62
1:D:435:LEU:HG	1:D:446:ILE:HG22	1.81	0.62
1:D:480:ASN:HD21	1:D:483:GLY:N	1.98	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:625:LEU:HD12	1:F:626:TYR:N	2.14	0.62
2:P:72:MET:C	2:P:74:ARG:H	2.01	0.62
2:R:24:ASP:CB	2:R:26:THR:HG23	2.26	0.62
1:A:173:ILE:HG23	1:A:174:GLY:H	1.64	0.62
1:A:311:HIS:O	1:A:314:ALA:HB3	1.98	0.62
1:B:327:LEU:HG	1:B:595:ILE:HG12	1.81	0.62
1:B:617:LYS:NZ	1:B:618:ASN:ND2	2.45	0.62
1:C:255:THR:O	1:C:259:LEU:N	2.28	0.62
1:C:540:ARG:HD2	1:C:582:ASP:OD1	1.99	0.62
1:D:661:ALA:O	1:D:665:LYS:HB2	1.98	0.62
1:E:435:LEU:HG	1:E:446:ILE:HG22	1.80	0.62
1:E:516:VAL:HG21	1:E:532:LEU:HD11	1.81	0.62
1:E:708:ALA:O	1:E:710:HIS:N	2.32	0.62
1:F:179:LEU:HG	1:F:180:ASP:H	1.62	0.62
1:F:767:GLN:CG	1:F:768:LYS:HG2	2.24	0.62
2:R:138:TYR:O	2:R:142:VAL:HG23	2.00	0.62
2:S:22:ASP:OD2	2:S:24:ASP:OD1	2.18	0.62
1:F:540:ARG:NH2	2:T:87:GLU:OE1	2.32	0.62
1:C:350:VAL:HG12	1:C:352:GLY:H	1.64	0.62
1:D:254:ARG:N	1:D:254:ARG:HD2	2.10	0.62
1:F:357:TRP:CZ3	1:F:439:ASN:HB2	2.33	0.62
2:O:48:LEU:HA	2:O:51:MET:CE	2.14	0.62
2:P:138:TYR:O	2:P:142:VAL:HG23	2.00	0.62
2:T:106:ARG:O	2:T:110:THR:HG23	1.99	0.62
2:T:24:ASP:CB	2:T:26:THR:HG23	2.24	0.62
1:A:731:GLU:O	1:A:734:ASN:HB3	2.00	0.62
1:B:220:LEU:HD11	1:B:223:LYS:HB2	1.82	0.62
1:C:99:GLU:C	1:C:101:GLY:H	2.01	0.62
1:C:152:LEU:HD21	1:C:171:TYR:CE1	2.35	0.62
1:D:122:GLU:OE2	1:D:145:LYS:HE2	1.99	0.62
1:D:318:ILE:HG23	1:D:322:LEU:HD12	1.81	0.62
1:D:731:GLU:O	1:D:734:ASN:HB3	2.00	0.62
1:E:220:LEU:HD11	1:E:223:LYS:HB2	1.81	0.62
1:E:540:ARG:NH2	2:S:87:GLU:OE1	2.33	0.62
1:E:661:ALA:O	1:E:665:LYS:HB2	1.98	0.62
2:P:124:MET:O	2:P:125:ILE:C	2.38	0.62
2:Q:48:LEU:HA	2:Q:51:MET:CE	2.13	0.62
2:S:106:ARG:O	2:S:110:THR:HG23	1.98	0.62
1:C:357:TRP:CZ3	1:C:439:ASN:HB2	2.33	0.62
1:C:731:GLU:O	1:C:734:ASN:HB3	1.99	0.62
1:D:131:ARG:H	1:D:170:TYR:HE2	1.47	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:302:LEU:HB2	1:D:602:PHE:HD1	1.65	0.62
1:D:589:LYS:HE3	1:D:608:TRP:CG	2.35	0.62
1:D:636:ALA:O	1:D:640:LYS:HA	2.00	0.62
1:D:76:LEU:O	1:D:79:ILE:N	2.32	0.62
1:F:220:LEU:HD11	1:F:223:LYS:HB2	1.81	0.62
1:F:694:VAL:HG22	2:T:18:LEU:HD21	1.80	0.62
1:F:764:LEU:C	1:F:766:HIS:N	2.51	0.62
2:P:22:ASP:OD2	2:P:24:ASP:OD1	2.17	0.62
2:P:42:ASN:N	2:P:43:PRO:CD	2.63	0.62
2:P:93:ASP:OD1	2:P:97:ASN:ND2	2.32	0.62
2:Q:76:MET:O	2:Q:77:LYS:HD2	2.00	0.62
1:C:540:ARG:NH2	2:Q:87:GLU:OE1	2.33	0.62
1:D:540:ARG:NH2	2:R:87:GLU:OE1	2.33	0.62
1:B:122:GLU:O	1:B:146:LYS:HE2	1.99	0.62
1:B:589:LYS:HE3	1:B:608:TRP:CG	2.34	0.62
1:B:719:LYS:HG2	1:B:797:ILE:CD1	2.30	0.62
1:B:90:PRO:HG2	1:B:93:VAL:CB	2.24	0.62
1:C:767:GLN:CG	1:C:768:LYS:HG2	2.24	0.62
1:D:180:ASP:CG	1:D:181:ILE:H	2.03	0.62
1:E:107:THR:CG2	1:E:115:LYS:HE2	2.27	0.62
1:E:327:LEU:HG	1:E:595:ILE:HG12	1.80	0.62
1:F:184:LYS:CE	1:F:191:GLU:HB2	2.29	0.62
1:F:255:THR:O	1:F:259:LEU:N	2.27	0.62
1:F:76:LEU:O	1:F:79:ILE:N	2.32	0.62
2:O:42:ASN:N	2:O:43:PRO:HD2	2.13	0.62
1:B:694:VAL:HG22	2:P:18:LEU:HD21	1.80	0.62
2:P:76:MET:O	2:P:77:LYS:HD2	1.99	0.62
2:S:72:MET:O	2:S:74:ARG:N	2.32	0.62
1:A:480:ASN:HD21	1:A:483:GLY:N	1.98	0.62
1:A:79:ILE:C	1:A:81:GLN:H	2.02	0.62
1:B:279:ILE:HG22	1:B:283:LEU:CD1	2.30	0.62
1:B:480:ASN:HD21	1:B:483:GLY:N	1.98	0.62
1:C:581:GLN:HE21	1:C:629:ASN:N	1.98	0.62
1:D:719:LYS:HG2	1:D:797:ILE:CD1	2.30	0.62
1:E:184:LYS:CE	1:E:191:GLU:HB2	2.30	0.62
1:E:301:ALA:C	1:E:303:LYS:N	2.53	0.62
1:E:629:ASN:HD21	1:E:631:SER:CB	2.10	0.62
1:F:105:TYR:HB2	1:F:153:ILE:HG12	1.82	0.62
1:F:111:LEU:HD23	1:F:155:ASN:HD21	1.65	0.62
1:F:189:ASP:O	1:F:190:PRO:C	2.38	0.62
2:T:12:PHE:CE1	2:T:72:MET:HG3	2.35	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:173:ILE:HG23	1:B:174:GLY:N	2.14	0.62
1:B:318:ILE:HG23	1:B:322:LEU:HD12	1.80	0.62
1:B:731:GLU:O	1:B:734:ASN:HB3	2.00	0.62
1:B:728:ALA:O	1:B:732:ILE:HG12	2.00	0.62
1:D:154:ILE:HG22	1:D:155:ASN:H	1.64	0.62
1:D:424:LYS:HZ2	1:D:424:LYS:HB3	1.64	0.62
1:E:154:ILE:HG22	1:E:155:ASN:H	1.65	0.62
1:E:513:TRP:CZ2	2:S:114:GLU:HB2	2.35	0.62
1:E:731:GLU:O	1:E:734:ASN:HB3	1.99	0.62
2:Q:87:GLU:O	2:Q:91:VAL:HG23	1.99	0.62
2:R:12:PHE:CE1	2:R:72:MET:HG3	2.34	0.62
1:A:589:LYS:HE3	1:A:608:TRP:CG	2.35	0.61
1:B:173:ILE:HG23	1:B:174:GLY:H	1.64	0.61
1:B:99:GLU:C	1:B:101:GLY:H	2.02	0.61
1:C:173:ILE:HG23	1:C:174:GLY:H	1.63	0.61
1:C:89:ILE:HD13	1:C:175:LYS:HE2	1.81	0.61
1:C:719:LYS:HG2	1:C:797:ILE:CD1	2.30	0.61
1:E:480:ASN:HD21	1:E:483:GLY:H	1.47	0.61
1:F:518:ASN:N	1:F:518:ASN:HD22	1.96	0.61
1:F:516:VAL:HG21	1:F:532:LEU:HD11	1.82	0.61
1:F:718:ARG:O	1:F:722:ILE:HG13	2.00	0.61
1:A:350:VAL:HG12	1:A:352:GLY:H	1.63	0.61
1:B:217:LYS:HZ2	1:B:236:GLU:HB2	1.65	0.61
1:B:79:ILE:C	1:B:81:GLN:H	2.02	0.61
1:C:279:ILE:HG22	1:C:283:LEU:CD1	2.31	0.61
1:C:718:ARG:O	1:C:722:ILE:HG13	2.00	0.61
1:C:76:LEU:O	1:C:79:ILE:N	2.32	0.61
1:E:111:LEU:HD23	1:E:155:ASN:HD21	1.65	0.61
1:E:173:ILE:HG23	1:E:174:GLY:H	1.64	0.61
2:P:12:PHE:CE1	2:P:72:MET:HG3	2.34	0.61
2:S:93:ASP:OD1	2:S:97:ASN:ND2	2.32	0.61
1:A:301:ALA:O	1:A:303:LYS:N	2.33	0.61
1:B:630:ARG:HG3	1:B:630:ARG:NH1	2.14	0.61
1:C:79:ILE:C	1:C:81:GLN:H	2.02	0.61
1:E:175:LYS:NZ	1:E:175:LYS:HB2	2.15	0.61
1:F:275:GLY:HA2	1:F:278:LYS:CE	2.29	0.61
1:F:794:GLN:NE2	1:F:795:LYS:HG3	2.16	0.61
2:O:13:LYS:O	2:O:15:ALA:N	2.31	0.61
2:T:42:ASN:N	2:T:43:PRO:CD	2.62	0.61
2:T:72:MET:C	2:T:74:ARG:H	2.01	0.61
1:A:89:ILE:HD13	1:A:175:LYS:HE2	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:589:LYS:HE3	1:C:608:TRP:CG	2.35	0.61
2:R:124:MET:O	2:R:125:ILE:C	2.39	0.61
2:S:55:VAL:HG11	2:S:71:MET:HE3	1.82	0.61
1:B:191:GLU:O	1:B:194:ASN:N	2.34	0.61
1:B:567:THR:HG23	1:B:568:GLY:H	1.66	0.61
1:C:597:ASN:OD1	1:C:599:GLU:HB2	2.01	0.61
1:D:700:TYR:HD1	1:D:728:ALA:HA	1.65	0.61
1:F:99:GLU:C	1:F:101:GLY:H	2.02	0.61
1:A:694:VAL:HG22	2:O:18:LEU:HD21	1.82	0.61
2:R:106:ARG:O	2:R:110:THR:HG23	2.00	0.61
2:T:87:GLU:O	2:T:91:VAL:HG23	2.00	0.61
1:B:201:ASP:HA	1:B:210:PHE:CE2	2.35	0.61
1:B:326:ILE:CG2	1:B:328:PHE:CE1	2.84	0.61
1:B:372:LYS:O	1:B:374:HIS:N	2.31	0.61
1:C:636:ALA:O	1:C:640:LYS:HA	2.01	0.61
1:D:205:SER:C	1:D:207:ASP:H	2.04	0.61
1:D:327:LEU:HG	1:D:595:ILE:HG12	1.81	0.61
1:E:296:LEU:HD23	1:E:296:LEU:N	2.15	0.61
1:E:301:ALA:O	1:E:303:LYS:N	2.33	0.61
1:E:597:ASN:OD1	1:E:599:GLU:HB2	2.00	0.61
1:F:115:LYS:HB2	1:F:118:GLN:HG2	1.81	0.61
1:F:173:ILE:HG23	1:F:174:GLY:N	2.15	0.61
1:F:700:TYR:HD1	1:F:728:ALA:HA	1.65	0.61
1:C:513:TRP:CZ2	2:Q:114:GLU:HB2	2.35	0.61
1:A:719:LYS:HG2	1:A:797:ILE:CD1	2.30	0.61
1:A:767:GLN:CG	1:A:768:LYS:HG2	2.24	0.61
1:C:164:GLU:HG2	1:C:166:SER:HB3	1.83	0.61
1:C:480:ASN:HD21	1:C:483:GLY:N	1.98	0.61
1:D:567:THR:HG23	1:D:568:GLY:H	1.65	0.61
1:D:597:ASN:OD1	1:D:599:GLU:HB2	2.00	0.61
1:D:625:LEU:HD12	1:D:626:TYR:N	2.14	0.61
1:E:728:ALA:O	1:E:732:ILE:HG12	2.00	0.61
1:F:201:ASP:HA	1:F:210:PHE:CE2	2.35	0.61
1:F:513:TRP:CZ2	2:T:114:GLU:HB2	2.36	0.61
1:F:597:ASN:OD1	1:F:599:GLU:HB2	2.00	0.61
2:O:44:THR:C	2:O:46:ALA:H	2.03	0.61
2:P:115:LYS:HZ3	2:P:115:LYS:HA	1.66	0.61
1:A:105:TYR:HB2	1:A:153:ILE:HG12	1.82	0.61
1:A:521:ASN:CB	1:A:524:GLU:HB3	2.31	0.61
1:C:275:GLY:HA2	1:C:278:LYS:HE3	1.82	0.61
1:D:567:THR:CG2	1:D:568:GLY:H	2.14	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:105:TYR:HB2	1:E:153:ILE:HG12	1.82	0.61
1:E:302:LEU:HB2	1:E:602:PHE:HD1	1.64	0.61
1:F:137:PHE:O	1:F:140:ARG:HB2	2.01	0.61
1:F:326:ILE:CG2	1:F:328:PHE:CE1	2.84	0.61
2:O:4:LEU:HA	2:O:8:GLN:NE2	2.16	0.61
2:Q:16:PHE:CE2	2:Q:27:ILE:CD1	2.83	0.61
2:T:124:MET:O	2:T:125:ILE:C	2.39	0.61
2:T:4:LEU:CA	2:T:8:GLN:HE21	2.13	0.61
1:A:180:ASP:HA	1:A:183:SER:HB3	1.81	0.61
1:A:629:ASN:ND2	1:A:631:SER:H	1.98	0.61
1:B:301:ALA:C	1:B:303:LYS:N	2.52	0.61
1:C:643:ILE:HG22	1:C:644:GLU:N	2.15	0.61
1:C:700:TYR:HD1	1:C:728:ALA:HA	1.65	0.61
1:D:201:ASP:HA	1:D:210:PHE:CE2	2.36	0.61
1:F:699:GLY:O	1:F:703:ASP:N	2.34	0.61
1:F:79:ILE:C	1:F:81:GLN:H	2.02	0.61
2:Q:93:ASP:OD1	2:Q:97:ASN:ND2	2.34	0.61
2:R:42:ASN:N	2:R:43:PRO:CD	2.64	0.61
1:A:115:LYS:HG3	1:A:153:ILE:HD13	1.81	0.61
1:A:154:ILE:HG22	1:A:155:ASN:H	1.65	0.61
1:C:201:ASP:HA	1:C:210:PHE:CE2	2.35	0.61
1:C:288:VAL:HG23	1:C:289:GLU:N	2.15	0.61
1:C:625:LEU:HD12	1:C:626:TYR:N	2.15	0.61
1:D:99:GLU:C	1:D:101:GLY:H	2.04	0.61
1:D:516:VAL:HG21	1:D:532:LEU:HD11	1.81	0.61
1:D:767:GLN:CG	1:D:768:LYS:HG2	2.24	0.61
1:E:89:ILE:HD13	1:E:175:LYS:HE2	1.83	0.61
1:E:205:SER:C	1:E:207:ASP:H	2.05	0.61
1:E:201:ASP:HA	1:E:210:PHE:CE2	2.35	0.61
1:E:567:THR:CG2	1:E:568:GLY:H	2.14	0.61
1:F:115:LYS:HZ3	1:F:115:LYS:HA	1.66	0.61
1:F:639:ASN:HD22	1:F:639:ASN:N	1.95	0.61
2:P:106:ARG:O	2:P:110:THR:HG23	1.99	0.61
2:P:9:ILE:HD12	2:P:69:LEU:CD2	2.31	0.61
2:Q:9:ILE:HD12	2:Q:69:LEU:CD2	2.30	0.61
2:R:4:LEU:HA	2:R:8:GLN:NE2	2.16	0.61
2:T:4:LEU:HA	2:T:8:GLN:NE2	2.15	0.61
1:A:99:GLU:C	1:A:101:GLY:H	2.02	0.60
1:A:173:ILE:HG23	1:A:174:GLY:N	2.15	0.60
1:A:567:THR:HG23	1:A:568:GLY:H	1.66	0.60
1:A:728:ALA:O	1:A:732:ILE:HG12	2.00	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:478:ALA:CB	1:B:486:LYS:O	2.48	0.60
1:B:480:ASN:HD21	1:B:483:GLY:CA	2.14	0.60
1:B:550:SER:H	1:B:553:GLN:HE21	1.49	0.60
1:C:728:ALA:O	1:C:732:ILE:HG12	2.00	0.60
1:D:288:VAL:HG23	1:D:289:GLU:N	2.15	0.60
2:R:93:ASP:OD1	2:R:97:ASN:ND2	2.33	0.60
2:S:16:PHE:CE2	2:S:27:ILE:CD1	2.84	0.60
1:A:279:ILE:HG22	1:A:283:LEU:CD1	2.30	0.60
1:A:326:ILE:CG2	1:A:328:PHE:CE1	2.84	0.60
1:B:270:LYS:HD3	1:B:273:LYS:HD2	1.83	0.60
1:C:296:LEU:HD23	1:C:296:LEU:N	2.16	0.60
1:D:581:GLN:HE21	1:D:629:ASN:N	1.98	0.60
1:E:115:LYS:HG3	1:E:153:ILE:HD13	1.83	0.60
1:E:164:GLU:HG2	1:E:166:SER:HB3	1.83	0.60
1:E:335:ALA:O	1:E:339:ILE:HG13	2.02	0.60
1:F:173:ILE:HG23	1:F:174:GLY:H	1.65	0.60
2:O:124:MET:O	2:O:125:ILE:C	2.38	0.60
2:O:42:ASN:N	2:O:43:PRO:CD	2.64	0.60
2:T:93:ASP:OD1	2:T:97:ASN:ND2	2.34	0.60
1:A:275:GLY:HA2	1:A:278:LYS:HE3	1.82	0.60
1:B:567:THR:CG2	1:B:568:GLY:H	2.15	0.60
1:C:128:MET:HE1	1:C:235:THR:HB	1.83	0.60
1:C:616:GLU:HA	1:C:620:THR:HB	1.83	0.60
1:D:199:LEU:HD21	1:D:225:ILE:O	2.02	0.60
1:D:615:ILE:HD12	1:D:645:TRP:CH2	2.37	0.60
1:D:728:ALA:O	1:D:732:ILE:HG12	2.01	0.60
2:S:9:ILE:HD12	2:S:69:LEU:CD2	2.31	0.60
1:A:201:ASP:HA	1:A:210:PHE:CE2	2.36	0.60
1:A:90:PRO:HG2	1:A:93:VAL:CB	2.27	0.60
1:B:594:PHE:HE2	1:B:596:ILE:HD11	1.65	0.60
1:B:597:ASN:OD1	1:B:599:GLU:HB2	2.01	0.60
1:C:639:ASN:HD22	1:C:639:ASN:N	1.95	0.60
1:C:775:LEU:O	1:C:777:TYR:N	2.35	0.60
1:E:90:PRO:HG2	1:E:93:VAL:CB	2.25	0.60
1:F:335:ALA:O	1:F:339:ILE:HG13	2.02	0.60
2:Q:72:MET:O	2:Q:74:ARG:N	2.33	0.60
1:A:301:ALA:C	1:A:303:LYS:N	2.53	0.60
1:C:205:SER:C	1:C:207:ASP:H	2.05	0.60
1:D:279:ILE:HG22	1:D:283:LEU:CD1	2.31	0.60
1:D:692:GLU:OE1	2:R:21:LYS:NZ	2.32	0.60
1:E:279:ILE:HG22	1:E:283:LEU:CD1	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:504:ILE:HG12	1:E:625:LEU:HD23	1.83	0.60
1:E:767:GLN:CG	1:E:768:LYS:HG2	2.24	0.60
1:F:164:GLU:HG2	1:F:166:SER:HB3	1.83	0.60
1:F:296:LEU:N	1:F:296:LEU:HD23	2.16	0.60
2:Q:42:ASN:N	2:Q:43:PRO:CD	2.63	0.60
2:R:72:MET:O	2:R:74:ARG:N	2.32	0.60
2:S:4:LEU:HA	2:S:8:GLN:NE2	2.16	0.60
2:T:72:MET:O	2:T:74:ARG:N	2.33	0.60
1:A:700:TYR:HD1	1:A:728:ALA:HA	1.66	0.60
1:A:76:LEU:O	1:A:79:ILE:N	2.34	0.60
1:B:105:TYR:HB2	1:B:153:ILE:HG12	1.82	0.60
1:B:255:THR:O	1:B:259:LEU:N	2.27	0.60
1:B:96:ILE:HG22	1:B:100:LEU:HD11	1.83	0.60
1:C:345:THR:HA	1:C:489:THR:O	2.02	0.60
1:D:629:ASN:ND2	1:D:631:SER:H	2.00	0.60
1:D:71:PHE:CG	1:D:73:ASN:HB2	2.37	0.60
1:D:794:GLN:NE2	1:D:795:LYS:HG3	2.16	0.60
1:E:199:LEU:HD21	1:E:225:ILE:O	2.02	0.60
1:E:275:GLY:HA2	1:E:278:LYS:HE3	1.82	0.60
1:E:434:LEU:HD22	1:E:445:ARG:HB3	1.84	0.60
1:E:617:LYS:NZ	1:E:618:ASN:ND2	2.46	0.60
1:F:154:ILE:HG22	1:F:155:ASN:H	1.67	0.60
1:F:775:LEU:O	1:F:777:TYR:N	2.35	0.60
2:O:4:LEU:CA	2:O:8:GLN:HE21	2.14	0.60
2:P:16:PHE:CE2	2:P:27:ILE:CD1	2.85	0.60
2:R:102:ALA:HB1	2:R:121:VAL:HG12	1.82	0.60
2:R:16:PHE:CE2	2:R:27:ILE:CD1	2.84	0.60
2:S:4:LEU:CA	2:S:8:GLN:HE21	2.15	0.60
2:T:16:PHE:CE2	2:T:27:ILE:CD1	2.84	0.60
1:B:115:LYS:HB2	1:B:118:GLN:HG2	1.82	0.60
1:C:115:LYS:HB2	1:C:118:GLN:HG2	1.81	0.60
1:C:550:SER:H	1:C:553:GLN:HE21	1.48	0.60
1:D:326:ILE:CG2	1:D:328:PHE:CE1	2.84	0.60
1:D:775:LEU:O	1:D:777:TYR:N	2.35	0.60
1:E:184:LYS:HE3	1:E:191:GLU:CB	2.32	0.60
2:O:72:MET:O	2:O:74:ARG:N	2.32	0.60
2:P:44:THR:C	2:P:46:ALA:H	2.04	0.60
2:P:4:LEU:HA	2:P:8:GLN:NE2	2.17	0.60
2:R:44:THR:C	2:R:46:ALA:H	2.03	0.60
1:A:205:SER:C	1:A:207:ASP:H	2.05	0.60
1:A:504:ILE:HG12	1:A:625:LEU:HD23	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:629:ASN:HD21	1:A:631:SER:CB	2.11	0.60
1:A:720:ILE:HD11	1:A:724:ARG:CZ	2.32	0.60
1:A:794:GLN:NE2	1:A:795:LYS:HG3	2.16	0.60
1:B:156:ILE:HD12	1:B:156:ILE:N	2.17	0.60
1:B:184:LYS:HE3	1:B:191:GLU:HB2	1.83	0.60
1:B:275:GLY:HA2	1:B:278:LYS:HE3	1.82	0.60
1:B:513:TRP:CZ2	2:P:114:GLU:HB2	2.35	0.60
1:B:636:ALA:O	1:B:640:LYS:HA	2.00	0.60
1:C:301:ALA:O	1:C:303:LYS:N	2.35	0.60
1:C:90:PRO:HG2	1:C:93:VAL:CB	2.26	0.60
1:D:71:PHE:CB	1:D:108:ASP:HB2	2.31	0.60
1:E:275:GLY:HA2	1:E:278:LYS:HD2	1.83	0.60
1:E:480:ASN:HD21	1:E:483:GLY:N	1.99	0.60
1:E:794:GLN:NE2	1:E:795:LYS:HG3	2.17	0.60
2:T:9:ILE:HD12	2:T:69:LEU:CD2	2.32	0.60
1:A:255:THR:O	1:A:259:LEU:N	2.28	0.60
1:A:343:VAL:HG13	1:A:487:PRO:HG2	1.82	0.60
1:A:567:THR:CG2	1:A:568:GLY:H	2.15	0.60
1:B:180:ASP:HA	1:B:183:SER:HB3	1.82	0.60
1:B:434:LEU:HD22	1:B:445:ARG:HB3	1.84	0.60
1:B:478:ALA:HB1	1:B:486:LYS:C	2.22	0.60
1:C:71:PHE:CB	1:C:108:ASP:HB2	2.31	0.60
1:C:594:PHE:HE2	1:C:596:ILE:HD11	1.67	0.60
1:D:275:GLY:HA2	1:D:278:LYS:HD2	1.83	0.60
1:E:521:ASN:CB	1:E:524:GLU:HB3	2.32	0.60
1:F:184:LYS:HE3	1:F:191:GLU:CB	2.32	0.60
1:F:217:LYS:HZ1	1:F:233:ASN:HB3	1.67	0.60
1:F:520:PRO:HG2	1:F:521:ASN:H	1.66	0.60
2:Q:4:LEU:HA	2:Q:8:GLN:NE2	2.16	0.60
2:Q:97:ASN:ND2	2:Q:99:TYR:H	2.00	0.60
2:S:42:ASN:N	2:S:43:PRO:CD	2.64	0.60
1:A:96:ILE:HG22	1:A:100:LEU:HD11	1.82	0.60
1:B:154:ILE:HG22	1:B:155:ASN:H	1.66	0.60
1:B:345:THR:HA	1:B:489:THR:O	2.02	0.60
1:D:275:GLY:HA2	1:D:278:LYS:HE3	1.84	0.60
1:E:225:ILE:HG12	1:E:229:PHE:CD2	2.37	0.60
1:E:343:VAL:HG13	1:E:487:PRO:HG2	1.82	0.60
1:E:679:TYR:CD2	1:E:691:LYS:HB2	2.36	0.60
1:E:775:LEU:O	1:E:777:TYR:N	2.35	0.60
1:F:175:LYS:CB	1:F:175:LYS:HZ2	2.15	0.60
1:F:343:VAL:HG13	1:F:487:PRO:HG2	1.82	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:4:LEU:CA	2:R:8:GLN:HE21	2.15	0.60
2:R:97:ASN:ND2	2:R:99:TYR:H	2.00	0.60
2:T:114:GLU:OE2	2:T:114:GLU:HA	2.02	0.60
1:A:199:LEU:HD21	1:A:225:ILE:O	2.02	0.59
1:B:302:LEU:HB2	1:B:602:PHE:HD1	1.65	0.59
1:C:567:THR:HG23	1:C:568:GLY:H	1.66	0.59
1:D:152:LEU:HD21	1:D:171:TYR:CE1	2.37	0.59
1:D:432:TYR:CD2	1:D:447:SER:HA	2.37	0.59
1:D:550:SER:H	1:D:553:GLN:HE21	1.48	0.59
1:E:189:ASP:HB3	1:E:190:PRO:HD2	1.84	0.59
1:E:189:ASP:O	1:E:191:GLU:N	2.35	0.59
1:E:700:TYR:HD1	1:E:728:ALA:HA	1.66	0.59
1:F:205:SER:C	1:F:207:ASP:H	2.04	0.59
2:P:114:GLU:OE2	2:P:114:GLU:HA	2.02	0.59
1:A:597:ASN:OD1	1:A:599:GLU:HB2	2.02	0.59
1:A:615:ILE:HD12	1:A:645:TRP:CH2	2.37	0.59
1:B:137:PHE:O	1:B:140:ARG:HB2	2.03	0.59
1:B:480:ASN:HD21	1:B:483:GLY:HA2	1.67	0.59
1:B:521:ASN:CB	1:B:524:GLU:HB3	2.32	0.59
1:B:794:GLN:NE2	1:B:795:LYS:HG3	2.16	0.59
1:C:301:ALA:C	1:C:303:LYS:N	2.54	0.59
1:C:794:GLN:NE2	1:C:795:LYS:HG3	2.16	0.59
1:D:175:LYS:CB	1:D:175:LYS:HZ2	2.15	0.59
1:D:296:LEU:N	1:D:296:LEU:HD23	2.17	0.59
1:D:95:GLU:O	1:D:99:GLU:HB2	2.02	0.59
1:E:432:TYR:CD2	1:E:447:SER:HA	2.37	0.59
1:E:540:ARG:HD2	1:E:582:ASP:OD1	2.01	0.59
1:A:297:LYS:NZ	1:A:601:GLU:OE1	2.30	0.59
1:C:326:ILE:HG22	1:C:328:PHE:HE1	1.63	0.59
1:C:432:TYR:CD2	1:C:447:SER:HA	2.37	0.59
1:C:567:THR:CG2	1:C:568:GLY:H	2.15	0.59
1:E:275:GLY:HA2	1:E:278:LYS:HG3	1.84	0.59
1:F:297:LYS:NZ	1:F:601:GLU:OE1	2.30	0.59
2:P:4:LEU:CA	2:P:8:GLN:HE21	2.15	0.59
2:Q:13:LYS:O	2:Q:15:ALA:N	2.31	0.59
1:A:679:TYR:CD2	1:A:691:LYS:HB2	2.37	0.59
1:A:95:GLU:O	1:A:99:GLU:HB2	2.03	0.59
1:B:296:LEU:HD23	1:B:296:LEU:N	2.16	0.59
1:D:66:LEU:HD12	1:D:103:GLU:HA	1.84	0.59
1:F:180:ASP:HA	1:F:183:SER:HB3	1.83	0.59
1:F:481:VAL:O	1:F:484:VAL:HG23	2.02	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:636:ALA:O	1:F:640:LYS:HA	2.02	0.59
2:S:114:GLU:HA	2:S:114:GLU:OE2	2.03	0.59
1:A:296:LEU:HD23	1:A:296:LEU:N	2.17	0.59
1:A:480:ASN:HD21	1:A:483:GLY:CA	2.15	0.59
1:A:520:PRO:HG2	1:A:521:ASN:H	1.68	0.59
1:B:66:LEU:HD12	1:B:103:GLU:HA	1.83	0.59
1:B:775:LEU:O	1:B:777:TYR:N	2.36	0.59
1:C:243:LEU:HA	1:C:246:SER:OG	2.03	0.59
1:D:164:GLU:HG2	1:D:166:SER:HB3	1.85	0.59
1:D:478:ALA:CB	1:D:486:LYS:O	2.51	0.59
1:D:657:ILE:HG13	1:D:756:ILE:CD1	2.32	0.59
1:E:481:VAL:O	1:E:484:VAL:HG23	2.03	0.59
2:T:133:ASP:N	2:T:133:ASP:OD1	2.35	0.59
2:T:97:ASN:ND2	2:T:99:TYR:H	2.00	0.59
1:A:137:PHE:O	1:A:140:ARG:HB2	2.02	0.59
1:B:184:LYS:HE3	1:B:191:GLU:CB	2.32	0.59
1:B:199:LEU:HD21	1:B:225:ILE:O	2.03	0.59
1:B:530:THR:HG21	2:P:145:MET:CE	2.33	0.59
1:C:115:LYS:HG3	1:C:153:ILE:HD13	1.85	0.59
1:C:275:GLY:HA2	1:C:278:LYS:HD2	1.83	0.59
1:C:615:ILE:HD12	1:C:645:TRP:CH2	2.38	0.59
1:D:105:TYR:HB2	1:D:153:ILE:HG12	1.85	0.59
1:D:521:ASN:CB	1:D:524:GLU:HB3	2.32	0.59
1:E:156:ILE:N	1:E:156:ILE:HD12	2.18	0.59
1:E:180:ASP:HA	1:E:183:SER:HB3	1.84	0.59
1:E:639:ASN:HD22	1:E:639:ASN:N	1.95	0.59
1:F:480:ASN:HD21	1:F:483:GLY:CA	2.15	0.59
1:A:164:GLU:HG2	1:A:166:SER:HB3	1.84	0.59
1:B:699:GLY:O	1:B:703:ASP:N	2.36	0.59
1:C:141:PHE:HD1	1:C:141:PHE:H	1.50	0.59
1:D:616:GLU:HA	1:D:620:THR:HB	1.85	0.59
1:F:141:PHE:H	1:F:141:PHE:HD1	1.49	0.59
1:F:270:LYS:HD3	1:F:273:LYS:HD2	1.84	0.59
1:F:434:LEU:HD22	1:F:445:ARG:HB3	1.84	0.59
1:F:478:ALA:HB1	1:F:486:LYS:C	2.23	0.59
1:F:616:GLU:HA	1:F:620:THR:HB	1.85	0.59
2:S:124:MET:O	2:S:125:ILE:C	2.40	0.59
2:S:44:THR:C	2:S:46:ALA:H	2.04	0.59
1:A:335:ALA:O	1:A:339:ILE:HG13	2.02	0.59
1:A:550:SER:H	1:A:553:GLN:HE21	1.50	0.59
1:A:775:LEU:O	1:A:777:TYR:N	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:164:GLU:HG2	1:B:166:SER:HB3	1.84	0.59
1:B:175:LYS:HB2	1:B:175:LYS:NZ	2.15	0.59
1:B:700:TYR:HD1	1:B:728:ALA:HA	1.66	0.59
1:C:105:TYR:HB2	1:C:153:ILE:HG12	1.83	0.59
1:D:504:ILE:HG12	1:D:625:LEU:HD23	1.84	0.59
1:E:478:ALA:HB1	1:E:486:LYS:C	2.23	0.59
1:E:764:LEU:C	1:E:766:HIS:N	2.53	0.59
1:F:279:ILE:HG22	1:F:283:LEU:CD1	2.33	0.59
2:Q:44:THR:C	2:Q:46:ALA:H	2.03	0.59
2:R:63:ILE:HG23	2:R:67:GLU:CB	2.33	0.59
2:S:97:ASN:ND2	2:S:99:TYR:H	2.00	0.59
2:T:102:ALA:HB1	2:T:121:VAL:HG12	1.85	0.59
1:A:513:TRP:CZ2	2:O:114:GLU:HB2	2.38	0.59
1:B:335:ALA:O	1:B:339:ILE:HG13	2.02	0.59
1:C:688:PHE:C	1:C:688:PHE:CD2	2.75	0.59
1:D:137:PHE:O	1:D:140:ARG:HB2	2.03	0.59
1:D:141:PHE:H	1:D:141:PHE:HD1	1.50	0.59
1:E:480:ASN:HD21	1:E:483:GLY:CA	2.16	0.59
1:E:636:ALA:O	1:E:640:LYS:HA	2.01	0.59
1:E:692:GLU:OE1	2:S:21:LYS:NZ	2.31	0.59
1:F:96:ILE:HG22	1:F:100:LEU:HD11	1.83	0.59
2:P:102:ALA:HB1	2:P:121:VAL:HG12	1.84	0.59
1:A:472:ARG:CB	1:A:472:ARG:HH11	2.15	0.59
1:D:156:ILE:HD12	1:D:156:ILE:N	2.18	0.59
2:O:5:THR:O	2:O:9:ILE:HG12	2.03	0.59
2:P:48:LEU:HD23	2:P:51:MET:HE1	1.83	0.59
2:Q:19:PHE:CE2	2:Q:34:THR:HG22	2.38	0.59
2:R:9:ILE:HD12	2:R:69:LEU:CD2	2.33	0.59
1:A:184:LYS:O	1:A:185:ASP:O	2.21	0.58
1:A:432:TYR:CD2	1:A:447:SER:HA	2.38	0.58
1:A:434:LEU:HD22	1:A:445:ARG:HB3	1.84	0.58
1:B:184:LYS:O	1:B:185:ASP:O	2.21	0.58
1:B:657:ILE:HG13	1:B:756:ILE:CD1	2.32	0.58
1:D:180:ASP:HA	1:D:183:SER:HB3	1.85	0.58
1:D:513:TRP:CZ2	2:R:114:GLU:HB2	2.37	0.58
1:E:137:PHE:O	1:E:140:ARG:HB2	2.03	0.58
1:E:122:GLU:HG3	1:E:147:ARG:HB2	1.85	0.58
1:E:310:GLU:OE2	1:E:340:LYS:HD2	2.03	0.58
1:F:504:ILE:HG12	1:F:625:LEU:HD23	1.85	0.58
1:F:688:PHE:CD2	1:F:688:PHE:C	2.76	0.58
1:F:95:GLU:O	1:F:99:GLU:HB2	2.02	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:114:GLU:OE2	2:O:114:GLU:HA	2.03	0.58
2:Q:124:MET:O	2:Q:125:ILE:C	2.39	0.58
2:T:19:PHE:CE2	2:T:34:THR:HG22	2.38	0.58
1:A:141:PHE:H	1:A:141:PHE:HD1	1.49	0.58
1:A:184:LYS:CE	1:A:191:GLU:HB2	2.33	0.58
1:A:602:PHE:C	1:A:603:ILE:HG13	2.24	0.58
1:A:699:GLY:O	1:A:703:ASP:N	2.36	0.58
1:A:71:PHE:CD2	1:A:73:ASN:HB2	2.38	0.58
1:B:520:PRO:HG2	1:B:521:ASN:H	1.68	0.58
1:B:688:PHE:CD2	1:B:688:PHE:C	2.77	0.58
1:C:187:SER:C	1:C:188:LEU:O	2.41	0.58
1:C:335:ALA:O	1:C:339:ILE:HG13	2.03	0.58
1:C:521:ASN:CB	1:C:524:GLU:HB3	2.32	0.58
1:E:184:LYS:O	1:E:185:ASP:O	2.21	0.58
1:E:688:PHE:C	1:E:688:PHE:CD2	2.76	0.58
1:F:615:ILE:HD12	1:F:645:TRP:CH2	2.37	0.58
2:Q:4:LEU:CA	2:Q:8:GLN:HE21	2.16	0.58
1:A:616:GLU:HA	1:A:620:THR:HB	1.84	0.58
1:B:581:GLN:HE21	1:B:629:ASN:N	1.98	0.58
1:C:520:PRO:HG2	1:C:521:ASN:H	1.68	0.58
1:E:270:LYS:HD3	1:E:273:LYS:HD2	1.84	0.58
1:E:520:PRO:HG2	1:E:521:ASN:H	1.67	0.58
1:E:95:GLU:O	1:E:99:GLU:HB2	2.03	0.58
1:F:567:THR:CG2	1:F:568:GLY:H	2.16	0.58
1:F:700:TYR:HD1	1:F:728:ALA:CA	2.17	0.58
2:O:9:ILE:HD12	2:O:69:LEU:CD2	2.33	0.58
2:P:5:THR:O	2:P:9:ILE:HG12	2.04	0.58
2:Q:102:ALA:HB1	2:Q:121:VAL:HG12	1.85	0.58
1:B:97:TYR:CZ	1:B:150:PRO:HB2	2.38	0.58
1:B:205:SER:C	1:B:207:ASP:H	2.06	0.58
1:B:288:VAL:O	1:B:292:ARG:HG2	2.02	0.58
1:B:310:GLU:OE2	1:B:340:LYS:HD2	2.03	0.58
1:C:343:VAL:HG13	1:C:487:PRO:HG2	1.84	0.58
1:C:692:GLU:OE1	2:Q:21:LYS:NZ	2.33	0.58
1:F:472:ARG:HH11	1:F:472:ARG:CB	2.16	0.58
2:P:5:THR:HG23	2:P:8:GLN:CB	2.34	0.58
2:R:19:PHE:CE2	2:R:34:THR:HG22	2.38	0.58
2:S:5:THR:O	2:S:9:ILE:HG12	2.04	0.58
2:T:13:LYS:O	2:T:15:ALA:N	2.30	0.58
2:T:48:LEU:HA	2:T:51:MET:CE	2.13	0.58
1:A:102:GLY:HA3	1:A:150:PRO:HG2	1.84	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:152:LEU:HD21	1:A:171:TYR:CE1	2.38	0.58
1:A:225:ILE:HD13	1:A:237:PHE:HZ	1.67	0.58
1:A:688:PHE:C	1:A:688:PHE:CD2	2.77	0.58
1:B:481:VAL:O	1:B:484:VAL:HG23	2.03	0.58
1:B:679:TYR:CD2	1:B:691:LYS:HB2	2.38	0.58
1:C:504:ILE:HG12	1:C:625:LEU:HD23	1.84	0.58
1:E:657:ILE:HG13	1:E:756:ILE:CD1	2.33	0.58
1:F:478:ALA:CB	1:F:486:LYS:O	2.52	0.58
2:P:13:LYS:O	2:P:15:ALA:N	2.31	0.58
2:P:63:ILE:HG23	2:P:67:GLU:CB	2.34	0.58
2:P:72:MET:O	2:P:74:ARG:N	2.33	0.58
2:R:114:GLU:OE2	2:R:114:GLU:HA	2.03	0.58
2:S:87:GLU:O	2:S:91:VAL:HG23	2.03	0.58
1:A:700:TYR:HD1	1:A:728:ALA:CA	2.17	0.58
1:B:639:ASN:HD22	1:B:639:ASN:N	1.94	0.58
1:C:478:ALA:CB	1:C:486:LYS:O	2.52	0.58
1:E:225:ILE:HD13	1:E:237:PHE:HZ	1.69	0.58
1:E:480:ASN:HD21	1:E:483:GLY:HA2	1.69	0.58
1:F:617:LYS:HZ2	1:F:618:ASN:ND2	1.87	0.58
1:F:720:ILE:HD11	1:F:724:ARG:CZ	2.33	0.58
2:O:63:ILE:HG23	2:O:67:GLU:CB	2.33	0.58
2:R:133:ASP:N	2:R:133:ASP:OD1	2.37	0.58
2:R:5:THR:HG23	2:R:8:GLN:CB	2.33	0.58
2:S:5:THR:HG23	2:S:8:GLN:CB	2.34	0.58
2:T:5:THR:HG23	2:T:8:GLN:CB	2.33	0.58
1:A:97:TYR:CZ	1:A:150:PRO:HB2	2.39	0.58
1:B:102:GLY:HA3	1:B:150:PRO:HG2	1.86	0.58
1:B:141:PHE:HD1	1:B:141:PHE:H	1.49	0.58
1:B:556:MET:O	1:B:560:LEU:HD23	2.04	0.58
1:B:297:LYS:NZ	1:B:601:GLU:OE1	2.33	0.58
1:B:629:ASN:HD21	1:B:631:SER:CB	2.12	0.58
1:D:184:LYS:O	1:D:185:ASP:O	2.21	0.58
1:D:270:LYS:HD3	1:D:273:LYS:HD2	1.85	0.58
1:D:335:ALA:O	1:D:339:ILE:HG13	2.04	0.58
1:D:480:ASN:HD21	1:D:483:GLY:CA	2.16	0.58
1:E:243:LEU:HA	1:E:246:SER:OG	2.04	0.58
1:E:71:PHE:CD2	1:E:73:ASN:HB2	2.39	0.58
1:F:288:VAL:HG23	1:F:289:GLU:N	2.17	0.58
1:F:521:ASN:CB	1:F:524:GLU:HB3	2.32	0.58
2:O:102:ALA:HB1	2:O:121:VAL:HG12	1.86	0.58
2:Q:63:ILE:HG23	2:Q:67:GLU:CB	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:102:ALA:HB1	2:S:121:VAL:HG12	1.85	0.58
1:A:629:ASN:HB3	1:A:632:TYR:CD1	2.39	0.58
1:A:657:ILE:HG13	1:A:756:ILE:CD1	2.34	0.58
1:B:343:VAL:HG13	1:B:487:PRO:HG2	1.86	0.58
1:B:95:GLU:O	1:B:99:GLU:HB2	2.03	0.58
1:D:718:ARG:O	1:D:722:ILE:HG13	2.02	0.58
1:E:699:GLY:O	1:E:703:ASP:N	2.36	0.58
1:F:128:MET:HE1	1:F:235:THR:HB	1.85	0.58
1:F:275:GLY:HA2	1:F:278:LYS:HD2	1.84	0.58
1:F:432:TYR:CD2	1:F:447:SER:HA	2.38	0.58
2:Q:104:GLU:O	2:Q:108:VAL:HG23	2.04	0.58
2:R:5:THR:O	2:R:9:ILE:HG12	2.03	0.58
1:A:478:ALA:CB	1:A:486:LYS:O	2.51	0.58
1:A:636:ALA:O	1:A:640:LYS:HA	2.02	0.58
1:B:107:THR:CG2	1:B:115:LYS:HE2	2.30	0.58
1:B:515:LYS:HB3	1:B:515:LYS:HZ2	1.67	0.58
1:B:609:GLU:N	1:B:609:GLU:OE2	2.35	0.58
1:C:197:LYS:HZ2	1:C:197:LYS:CB	2.15	0.58
1:C:700:TYR:HD1	1:C:728:ALA:CA	2.17	0.58
1:D:643:ILE:HG22	1:D:644:GLU:H	1.68	0.58
1:E:478:ALA:CB	1:E:486:LYS:O	2.52	0.58
1:E:616:GLU:HA	1:E:620:THR:HB	1.84	0.58
1:F:156:ILE:HD12	1:F:156:ILE:N	2.18	0.58
1:F:728:ALA:O	1:F:732:ILE:HG12	2.03	0.58
2:O:97:ASN:ND2	2:O:99:TYR:H	2.01	0.58
2:R:13:LYS:O	2:R:15:ALA:N	2.31	0.58
1:A:128:MET:HE1	1:A:235:THR:HB	1.86	0.58
1:A:288:VAL:HG23	1:A:289:GLU:N	2.17	0.58
1:B:71:PHE:CB	1:B:108:ASP:HB2	2.34	0.58
1:B:700:TYR:HD1	1:B:728:ALA:CA	2.17	0.58
1:C:180:ASP:HA	1:C:183:SER:HB3	1.85	0.58
1:D:179:LEU:HD23	1:D:179:LEU:N	2.19	0.58
1:E:115:LYS:HA	1:E:115:LYS:HZ3	1.69	0.58
1:E:432:TYR:CD1	1:E:445:ARG:HD2	2.39	0.58
1:E:530:THR:HG21	2:S:145:MET:CE	2.34	0.58
1:F:184:LYS:O	1:F:185:ASP:O	2.22	0.58
1:F:199:LEU:HD21	1:F:225:ILE:O	2.04	0.58
1:F:225:ILE:HG12	1:F:229:PHE:CD2	2.39	0.58
2:O:5:THR:HG23	2:O:8:GLN:CB	2.34	0.58
2:S:19:PHE:CE2	2:S:34:THR:HG22	2.38	0.58
1:A:156:ILE:N	1:A:156:ILE:HD12	2.19	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:LEU:HD23	1:A:179:LEU:N	2.19	0.57
1:C:97:TYR:CZ	1:C:150:PRO:HB2	2.39	0.57
1:C:154:ILE:HG22	1:C:155:ASN:N	2.18	0.57
1:C:156:ILE:N	1:C:156:ILE:HD12	2.18	0.57
1:C:480:ASN:HD21	1:C:483:GLY:CA	2.16	0.57
1:D:478:ALA:HB1	1:D:486:LYS:C	2.24	0.57
1:D:700:TYR:HD1	1:D:728:ALA:CA	2.17	0.57
1:E:152:LEU:HD21	1:E:171:TYR:CE1	2.38	0.57
1:E:275:GLY:HA2	1:E:278:LYS:CG	2.32	0.57
1:E:629:ASN:HB3	1:E:632:TYR:CD1	2.39	0.57
2:O:19:PHE:CE2	2:O:34:THR:HG22	2.39	0.57
1:B:529:VAL:HG21	2:P:109:MET:CE	2.33	0.57
2:Q:5:THR:HG23	2:Q:8:GLN:CB	2.33	0.57
2:T:44:THR:C	2:T:46:ALA:H	2.06	0.57
1:A:345:THR:HA	1:A:489:THR:O	2.05	0.57
1:A:516:VAL:HG21	1:A:532:LEU:HD11	1.86	0.57
1:B:187:SER:C	1:B:188:LEU:O	2.41	0.57
1:B:432:TYR:CD2	1:B:447:SER:HA	2.38	0.57
1:C:602:PHE:C	1:C:603:ILE:HG13	2.24	0.57
1:D:481:VAL:O	1:D:484:VAL:HG23	2.04	0.57
1:E:115:LYS:HA	1:E:115:LYS:NZ	2.19	0.57
2:S:32:LEU:HD22	2:S:63:ILE:HD12	1.86	0.57
1:A:747:ASN:O	1:A:750:GLN:HB2	2.03	0.57
1:A:76:LEU:H	1:A:76:LEU:CD2	2.15	0.57
1:B:152:LEU:HD21	1:B:171:TYR:CE1	2.38	0.57
1:B:504:ILE:HG12	1:B:625:LEU:HD23	1.86	0.57
1:B:747:ASN:O	1:B:750:GLN:HB2	2.04	0.57
1:C:639:ASN:N	1:C:639:ASN:ND2	2.49	0.57
1:C:715:GLU:HG3	1:C:718:ARG:NH1	2.16	0.57
1:D:480:ASN:HD21	1:D:483:GLY:HA2	1.69	0.57
1:E:327:LEU:HD12	1:E:327:LEU:N	2.19	0.57
1:E:463:THR:HB	1:E:467:GLU:O	2.05	0.57
1:E:700:TYR:HD1	1:E:728:ALA:CA	2.17	0.57
1:F:225:ILE:HD13	1:F:237:PHE:HZ	1.69	0.57
1:F:76:LEU:H	1:F:76:LEU:CD2	2.14	0.57
1:F:90:PRO:HG2	1:F:93:VAL:CB	2.27	0.57
2:O:32:LEU:HD22	2:O:63:ILE:HD12	1.85	0.57
1:A:197:LYS:NZ	1:A:197:LYS:HB3	2.17	0.57
1:A:309:PRO:O	1:A:313:ASP:HB2	2.04	0.57
1:A:327:LEU:HD12	1:A:327:LEU:N	2.19	0.57
1:A:478:ALA:HB1	1:A:486:LYS:C	2.23	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:463:THR:HB	1:B:467:GLU:O	2.04	0.57
1:B:516:VAL:HG21	1:B:532:LEU:HD11	1.85	0.57
1:B:635:ILE:HD12	1:B:635:ILE:H	1.70	0.57
1:B:76:LEU:CD2	1:B:76:LEU:H	2.15	0.57
1:C:137:PHE:O	1:C:140:ARG:HB2	2.03	0.57
1:C:199:LEU:HD21	1:C:225:ILE:O	2.04	0.57
1:C:481:VAL:O	1:C:484:VAL:HG23	2.05	0.57
1:C:530:THR:HG21	2:Q:145:MET:CE	2.34	0.57
1:D:154:ILE:HG22	1:D:155:ASN:N	2.19	0.57
1:D:88:LYS:HZ3	1:D:172:GLU:CD	2.07	0.57
1:D:472:ARG:HH11	1:D:472:ARG:CB	2.17	0.57
1:D:609:GLU:OE2	1:D:609:GLU:N	2.34	0.57
1:D:699:GLY:O	1:D:703:ASP:N	2.37	0.57
1:D:747:ASN:O	1:D:750:GLN:HB2	2.03	0.57
1:E:102:GLY:HA3	1:E:150:PRO:HG2	1.87	0.57
1:E:141:PHE:H	1:E:141:PHE:HD1	1.50	0.57
1:E:217:LYS:HZ1	1:E:233:ASN:HB3	1.68	0.57
1:E:326:ILE:CG2	1:E:328:PHE:HE1	2.16	0.57
1:F:179:LEU:HD23	1:F:179:LEU:N	2.19	0.57
1:F:275:GLY:HA2	1:F:278:LYS:HE3	1.85	0.57
1:F:271:LEU:HD13	1:F:276:PHE:CE2	2.39	0.57
1:F:715:GLU:HG3	1:F:718:ARG:NH1	2.16	0.57
2:P:133:ASP:N	2:P:133:ASP:OD1	2.38	0.57
2:P:19:PHE:CE2	2:P:34:THR:HG22	2.39	0.57
2:Q:5:THR:O	2:Q:9:ILE:HG12	2.04	0.57
2:T:5:THR:O	2:T:9:ILE:HG12	2.04	0.57
1:A:71:PHE:CB	1:A:108:ASP:HB2	2.35	0.57
1:B:105:TYR:HE1	1:B:151:LYS:HZ2	1.51	0.57
1:B:692:GLU:OE1	2:P:21:LYS:NZ	2.31	0.57
1:C:478:ALA:HB1	1:C:486:LYS:C	2.25	0.57
1:C:581:GLN:O	1:C:629:ASN:HA	2.05	0.57
1:D:345:THR:HA	1:D:489:THR:O	2.03	0.57
1:E:504:ILE:HD12	1:E:504:ILE:N	2.20	0.57
1:E:76:LEU:CD2	1:E:76:LEU:H	2.14	0.57
1:F:97:TYR:CZ	1:F:150:PRO:HB2	2.38	0.57
1:F:173:ILE:HG13	1:F:242:SER:HB3	1.86	0.57
1:F:679:TYR:CD2	1:F:691:LYS:HB2	2.39	0.57
2:S:63:ILE:HG23	2:S:67:GLU:CB	2.34	0.57
1:A:275:GLY:HA2	1:A:278:LYS:HG3	1.86	0.57
1:A:504:ILE:N	1:A:504:ILE:HD12	2.19	0.57
1:C:96:ILE:HG22	1:C:100:LEU:HD11	1.86	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:270:LYS:HD3	1:C:273:LYS:HD2	1.85	0.57
1:D:225:ILE:HG12	1:D:229:PHE:CD2	2.39	0.57
1:E:556:MET:O	1:E:560:LEU:HD23	2.05	0.57
1:E:720:ILE:HD11	1:E:724:ARG:CZ	2.34	0.57
1:F:235:THR:HA	1:F:238:GLN:HG3	1.86	0.57
1:F:306:GLY:O	1:F:336:THR:HG23	2.05	0.57
1:F:345:THR:HA	1:F:489:THR:O	2.04	0.57
2:P:97:ASN:ND2	2:P:99:TYR:H	2.01	0.57
1:A:306:GLY:O	1:A:336:THR:HG23	2.04	0.57
1:B:616:GLU:HA	1:B:620:THR:HB	1.85	0.57
1:B:708:ALA:O	1:B:711:ILE:HG12	2.05	0.57
1:D:208:LEU:HD12	1:D:208:LEU:N	2.20	0.57
1:D:688:PHE:C	1:D:688:PHE:CD2	2.77	0.57
1:F:115:LYS:HG3	1:F:153:ILE:HD13	1.87	0.57
1:F:122:GLU:HG3	1:F:147:ARG:HB2	1.87	0.57
1:F:556:MET:O	1:F:560:LEU:HD23	2.05	0.57
2:Q:55:VAL:HG11	2:Q:71:MET:HE3	1.87	0.57
2:T:117:THR:OG1	2:T:119:GLU:HG2	2.05	0.57
1:A:225:ILE:HG12	1:A:229:PHE:CD2	2.40	0.57
1:A:270:LYS:HD3	1:A:273:LYS:HD2	1.87	0.57
1:A:288:VAL:O	1:A:292:ARG:HG2	2.04	0.57
1:A:310:GLU:OE2	1:A:340:LYS:HD2	2.05	0.57
1:A:635:ILE:HD12	1:A:635:ILE:H	1.70	0.57
1:B:275:GLY:HA2	1:B:278:LYS:HD2	1.85	0.57
1:C:225:ILE:HD13	1:C:237:PHE:HZ	1.69	0.57
1:C:225:ILE:HG12	1:C:229:PHE:CD2	2.39	0.57
1:C:463:THR:HB	1:C:467:GLU:O	2.05	0.57
1:C:629:ASN:HD21	1:C:631:SER:CB	2.13	0.57
1:D:639:ASN:N	1:D:639:ASN:HD22	1.96	0.57
1:D:78:LYS:O	1:D:81:GLN:HB3	2.05	0.57
1:F:71:PHE:CD2	1:F:73:ASN:HB2	2.40	0.57
2:Q:13:LYS:HA	2:Q:65:PHE:CE1	2.39	0.57
1:A:196:ILE:O	1:A:199:LEU:HB2	2.05	0.57
1:A:208:LEU:HD12	1:A:208:LEU:N	2.20	0.57
1:C:310:GLU:OE2	1:C:340:LYS:HD2	2.04	0.57
1:C:504:ILE:HD12	1:C:504:ILE:N	2.19	0.57
1:C:747:ASN:O	1:C:750:GLN:HB2	2.05	0.57
1:D:463:THR:HB	1:D:467:GLU:O	2.05	0.57
1:D:629:ASN:HD21	1:D:631:SER:CB	2.12	0.57
1:E:747:ASN:O	1:E:750:GLN:HB2	2.05	0.57
1:B:692:GLU:CD	2:P:21:LYS:HZ1	2.07	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:117:THR:OG1	2:Q:119:GLU:HG2	2.05	0.57
2:R:13:LYS:HA	2:R:65:PHE:CE1	2.40	0.57
1:A:154:ILE:HG22	1:A:155:ASN:N	2.20	0.57
1:B:234:LEU:CD2	1:B:235:THR:H	2.18	0.57
1:B:275:GLY:HA2	1:B:278:LYS:HG3	1.87	0.57
1:B:472:ARG:HH11	1:B:472:ARG:CB	2.17	0.57
1:C:185:ASP:O	1:C:190:PRO:HA	2.04	0.57
1:C:71:PHE:CG	1:C:73:ASN:HB2	2.39	0.57
1:D:96:ILE:HG22	1:D:100:LEU:HD11	1.86	0.57
1:D:102:GLY:HA3	1:D:150:PRO:HG2	1.87	0.57
1:D:309:PRO:O	1:D:313:ASP:HB2	2.05	0.57
1:E:97:TYR:CZ	1:E:150:PRO:HB2	2.40	0.57
1:E:708:ALA:O	1:E:711:ILE:HG12	2.05	0.57
1:F:71:PHE:CB	1:F:108:ASP:HB2	2.35	0.57
1:F:102:GLY:HA3	1:F:150:PRO:HG2	1.86	0.57
2:Q:133:ASP:N	2:Q:133:ASP:OD1	2.37	0.57
2:T:63:ILE:HG23	2:T:67:GLU:CB	2.35	0.57
1:B:243:LEU:HA	1:B:246:SER:OG	2.04	0.56
1:C:275:GLY:HA2	1:C:278:LYS:CG	2.34	0.56
1:C:556:MET:O	1:C:560:LEU:HD23	2.05	0.56
1:D:184:LYS:HE3	1:D:191:GLU:CB	2.34	0.56
1:E:288:VAL:HG23	1:E:289:GLU:N	2.15	0.56
1:F:243:LEU:HA	1:F:246:SER:OG	2.05	0.56
1:F:432:TYR:CD1	1:F:445:ARG:HD2	2.40	0.56
2:O:133:ASP:N	2:O:133:ASP:OD1	2.37	0.56
2:Q:114:GLU:HA	2:Q:114:GLU:OE2	2.04	0.56
2:T:104:GLU:O	2:T:108:VAL:HG23	2.05	0.56
1:A:122:GLU:HG3	1:A:147:ARG:HB2	1.86	0.56
1:B:225:ILE:HG12	1:B:229:PHE:CD2	2.41	0.56
1:B:268:MET:HA	1:B:271:LEU:HD12	1.87	0.56
1:B:720:ILE:HD11	1:B:724:ARG:CZ	2.35	0.56
1:C:184:LYS:O	1:C:185:ASP:O	2.21	0.56
1:C:326:ILE:CG2	1:C:328:PHE:CE1	2.85	0.56
1:C:432:TYR:CD1	1:C:445:ARG:HD2	2.39	0.56
1:C:472:ARG:HH11	1:C:472:ARG:CB	2.16	0.56
1:C:480:ASN:HD21	1:C:483:GLY:HA2	1.70	0.56
1:C:699:GLY:O	1:C:703:ASP:N	2.37	0.56
1:D:432:TYR:CD1	1:D:445:ARG:HD2	2.40	0.56
1:D:504:ILE:HD12	1:D:504:ILE:N	2.19	0.56
1:D:520:PRO:HG2	1:D:521:ASN:H	1.69	0.56
1:D:527:LYS:O	1:D:528:GLY:C	2.44	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:115:LYS:HB2	1:E:118:GLN:CG	2.35	0.56
1:E:275:GLY:O	1:E:278:LYS:HB2	2.05	0.56
1:E:288:VAL:O	1:E:292:ARG:HG2	2.04	0.56
1:E:615:ILE:HD12	1:E:645:TRP:CH2	2.38	0.56
1:F:310:GLU:OE2	1:F:340:LYS:HD2	2.06	0.56
1:F:480:ASN:HD21	1:F:483:GLY:HA2	1.69	0.56
1:F:747:ASN:O	1:F:750:GLN:HB2	2.05	0.56
2:S:133:ASP:N	2:S:133:ASP:OD1	2.37	0.56
2:S:13:LYS:HA	2:S:65:PHE:CE1	2.40	0.56
1:A:480:ASN:HD21	1:A:483:GLY:HA2	1.68	0.56
1:A:776:LEU:HD11	1:A:793:PHE:HE1	1.70	0.56
1:B:154:ILE:HG22	1:B:155:ASN:N	2.20	0.56
1:B:225:ILE:HD13	1:B:237:PHE:HZ	1.70	0.56
1:C:102:GLY:HA3	1:C:150:PRO:HG2	1.87	0.56
1:C:173:ILE:HG13	1:C:242:SER:HB3	1.87	0.56
1:D:217:LYS:HZ2	1:D:236:GLU:HB2	1.68	0.56
1:F:187:SER:C	1:F:188:LEU:O	2.41	0.56
1:F:463:THR:HB	1:F:467:GLU:O	2.05	0.56
1:F:692:GLU:OE1	2:T:21:LYS:NZ	2.34	0.56
1:A:66:LEU:HD12	1:A:103:GLU:HA	1.85	0.56
1:A:432:TYR:CD1	1:A:445:ARG:HD2	2.40	0.56
1:B:197:LYS:NZ	1:B:197:LYS:HB3	2.18	0.56
1:B:767:GLN:CG	1:B:768:LYS:HG2	2.24	0.56
1:C:657:ILE:HG13	1:C:756:ILE:CD1	2.34	0.56
1:D:512:GLU:HA	1:D:515:LYS:HZ2	1.70	0.56
1:E:71:PHE:CB	1:E:108:ASP:HB2	2.36	0.56
1:E:234:LEU:HG	1:E:235:THR:N	2.21	0.56
1:F:246:SER:O	1:F:250:ALA:N	2.38	0.56
1:F:629:ASN:HB3	1:F:632:TYR:CD1	2.39	0.56
2:O:117:THR:OG1	2:O:119:GLU:HG2	2.05	0.56
2:P:13:LYS:HA	2:P:65:PHE:CE1	2.40	0.56
2:Q:13:LYS:C	2:Q:15:ALA:H	2.09	0.56
2:S:117:THR:OG1	2:S:119:GLU:HG2	2.05	0.56
1:F:529:VAL:HG21	2:T:109:MET:CE	2.34	0.56
1:A:692:GLU:OE1	2:O:21:LYS:NZ	2.30	0.56
1:D:679:TYR:CD2	1:D:691:LYS:HB2	2.39	0.56
1:D:720:ILE:HD11	1:D:724:ARG:CZ	2.34	0.56
1:E:499:PRO:CG	1:E:504:ILE:HD11	2.33	0.56
1:F:326:ILE:CG2	1:F:328:PHE:HE1	2.18	0.56
1:F:512:GLU:HA	1:F:515:LYS:HZ2	1.70	0.56
1:F:530:THR:HG21	2:T:145:MET:CE	2.35	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:LYS:HB2	1:A:118:GLN:CG	2.34	0.56
1:A:609:GLU:N	1:A:609:GLU:OE2	2.34	0.56
1:B:275:GLY:HA2	1:B:278:LYS:CG	2.35	0.56
1:C:708:ALA:O	1:C:711:ILE:HG12	2.05	0.56
1:C:720:ILE:HD11	1:C:724:ARG:CZ	2.35	0.56
1:D:196:ILE:O	1:D:199:LEU:HB2	2.06	0.56
1:D:225:ILE:HD13	1:D:237:PHE:HZ	1.70	0.56
1:D:598:PRO:HG3	1:D:624:TYR:OH	2.06	0.56
1:E:196:ILE:O	1:E:199:LEU:HB2	2.06	0.56
1:E:234:LEU:CD2	1:E:235:THR:H	2.18	0.56
1:F:78:LYS:O	1:F:81:GLN:HB3	2.05	0.56
1:A:275:GLY:HA2	1:A:278:LYS:CG	2.35	0.56
1:A:271:LEU:HD13	1:A:276:PHE:CE2	2.41	0.56
1:A:431:LYS:O	1:A:448:ASP:HB2	2.06	0.56
1:A:481:VAL:O	1:A:484:VAL:HG23	2.05	0.56
1:B:432:TYR:CD1	1:B:445:ARG:HD2	2.40	0.56
1:B:666:ASN:O	1:B:669:SER:HB3	2.06	0.56
1:C:66:LEU:HD12	1:C:103:GLU:HA	1.87	0.56
1:C:115:LYS:HA	1:C:115:LYS:NZ	2.20	0.56
1:C:115:LYS:HB2	1:C:118:GLN:CG	2.36	0.56
1:C:184:LYS:CE	1:C:191:GLU:HB2	2.34	0.56
1:C:327:LEU:HD12	1:C:327:LEU:N	2.21	0.56
1:F:66:LEU:HD12	1:F:103:GLU:HA	1.86	0.56
1:F:609:GLU:N	1:F:609:GLU:OE2	2.36	0.56
2:O:104:GLU:O	2:O:108:VAL:HG23	2.04	0.56
2:T:13:LYS:C	2:T:15:ALA:H	2.09	0.56
1:A:115:LYS:NZ	1:A:115:LYS:HA	2.21	0.56
1:B:115:LYS:NZ	1:B:115:LYS:HA	2.21	0.56
1:B:196:ILE:O	1:B:199:LEU:HB2	2.06	0.56
1:C:196:ILE:O	1:C:199:LEU:HB2	2.05	0.56
1:D:128:MET:HE1	1:D:235:THR:HB	1.88	0.56
1:D:243:LEU:HA	1:D:246:SER:OG	2.06	0.56
1:D:306:GLY:O	1:D:336:THR:HG23	2.06	0.56
1:E:345:THR:HA	1:E:489:THR:O	2.05	0.56
1:F:327:LEU:HG	1:F:595:ILE:HG23	1.88	0.56
2:R:117:THR:OG1	2:R:119:GLU:HG2	2.05	0.56
1:E:529:VAL:HG21	2:S:109:MET:CE	2.35	0.56
1:A:187:SER:C	1:A:188:LEU:O	2.41	0.56
1:A:243:LEU:HA	1:A:246:SER:OG	2.05	0.56
1:B:128:MET:HE1	1:B:235:THR:HB	1.88	0.56
1:B:309:PRO:O	1:B:313:ASP:HB2	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:217:LYS:HZ1	1:C:236:GLU:HB2	1.69	0.56
1:C:217:LYS:HZ1	1:C:233:ASN:HB3	1.71	0.56
1:C:275:GLY:HA2	1:C:278:LYS:HG3	1.87	0.56
1:D:131:ARG:HG3	1:D:243:LEU:CD1	2.36	0.56
1:D:327:LEU:HD12	1:D:327:LEU:N	2.21	0.56
1:E:66:LEU:HD12	1:E:103:GLU:HA	1.87	0.56
1:E:154:ILE:HG22	1:E:155:ASN:N	2.21	0.56
1:E:172:GLU:O	1:E:175:LYS:HB3	2.05	0.56
1:E:297:LYS:NZ	1:E:601:GLU:OE1	2.30	0.56
1:E:666:ASN:O	1:E:669:SER:HB3	2.06	0.56
1:F:275:GLY:HA2	1:F:278:LYS:HG3	1.87	0.56
1:A:692:GLU:CD	2:O:21:LYS:HZ1	2.09	0.56
1:A:407:HIS:HB2	1:A:408:LEU:HD12	1.88	0.56
1:B:208:LEU:N	1:B:208:LEU:HD12	2.20	0.56
1:B:288:VAL:HG23	1:B:289:GLU:N	2.17	0.56
1:B:598:PRO:HG3	1:B:624:TYR:OH	2.06	0.56
1:B:71:PHE:CD2	1:B:73:ASN:HB2	2.40	0.56
1:C:95:GLU:O	1:C:99:GLU:HB2	2.04	0.56
1:D:118:GLN:HA	1:D:118:GLN:OE1	2.06	0.56
1:D:97:TYR:CZ	1:D:150:PRO:HB2	2.41	0.56
1:D:602:PHE:C	1:D:603:ILE:HG13	2.25	0.56
1:D:629:ASN:HB3	1:D:632:TYR:CD1	2.41	0.56
1:E:512:GLU:HA	1:E:515:LYS:HZ2	1.71	0.56
1:E:609:GLU:N	1:E:609:GLU:OE2	2.33	0.56
1:E:679:TYR:C	1:E:679:TYR:CD1	2.79	0.56
1:E:96:ILE:HG22	1:E:100:LEU:HD11	1.88	0.56
1:F:127:SER:C	1:F:133:GLU:OE2	2.44	0.56
2:O:13:LYS:HA	2:O:65:PHE:CE1	2.40	0.56
2:P:117:THR:OG1	2:P:119:GLU:HG2	2.06	0.56
1:A:368:GLN:HG3	1:A:383:GLY:C	2.27	0.56
1:B:122:GLU:HG3	1:B:147:ARG:HB2	1.88	0.56
1:B:327:LEU:HD12	1:B:327:LEU:N	2.21	0.56
1:B:504:ILE:HD12	1:B:504:ILE:N	2.20	0.56
1:C:112:VAL:HG12	1:C:113:GLU:HG3	1.87	0.56
1:C:407:HIS:HB2	1:C:408:LEU:HD12	1.88	0.56
1:C:679:TYR:CD2	1:C:691:LYS:HB2	2.40	0.56
1:D:271:LEU:HD13	1:D:276:PHE:CE2	2.41	0.56
1:E:246:SER:O	1:E:250:ALA:N	2.39	0.56
1:F:115:LYS:HB2	1:F:118:GLN:CG	2.36	0.56
1:F:208:LEU:N	1:F:208:LEU:HD12	2.20	0.56
1:A:530:THR:HG21	2:O:145:MET:CE	2.36	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:32:LEU:HD22	2:R:63:ILE:HD12	1.85	0.56
2:R:63:ILE:HG23	2:R:67:GLU:HB3	1.88	0.56
2:S:13:LYS:C	2:S:15:ALA:H	2.09	0.56
1:B:499:PRO:CG	1:B:504:ILE:HD11	2.34	0.55
1:B:629:ASN:HB3	1:B:632:TYR:CD1	2.41	0.55
1:B:794:GLN:O	1:B:797:ILE:HG12	2.06	0.55
1:C:208:LEU:HD12	1:C:208:LEU:N	2.20	0.55
1:C:306:GLY:O	1:C:336:THR:HG23	2.05	0.55
1:D:187:SER:C	1:D:188:LEU:O	2.41	0.55
1:D:76:LEU:H	1:D:76:LEU:CD2	2.17	0.55
1:E:127:SER:C	1:E:133:GLU:OE2	2.44	0.55
1:E:179:LEU:HD23	1:E:179:LEU:N	2.21	0.55
1:E:208:LEU:N	1:E:208:LEU:HD12	2.20	0.55
1:E:235:THR:HA	1:E:238:GLN:HG3	1.88	0.55
1:F:154:ILE:HG22	1:F:155:ASN:N	2.20	0.55
1:F:327:LEU:N	1:F:327:LEU:HD12	2.21	0.55
1:F:776:LEU:HD11	1:F:793:PHE:HE1	1.71	0.55
1:A:112:VAL:HG12	1:A:113:GLU:HG3	1.87	0.55
1:A:326:ILE:CG2	1:A:328:PHE:HE1	2.17	0.55
1:A:463:THR:HB	1:A:467:GLU:O	2.06	0.55
1:B:112:VAL:C	1:B:114:HIS:H	2.09	0.55
1:B:225:ILE:HG23	1:B:229:PHE:CD2	2.41	0.55
1:C:225:ILE:HG23	1:C:229:PHE:CD2	2.40	0.55
1:D:115:LYS:HB2	1:D:118:GLN:CG	2.36	0.55
1:D:115:LYS:HA	1:D:115:LYS:HZ3	1.71	0.55
1:D:434:LEU:HD22	1:D:445:ARG:HB3	1.87	0.55
1:F:309:PRO:O	1:F:313:ASP:HB2	2.05	0.55
2:R:13:LYS:C	2:R:15:ALA:H	2.10	0.55
2:T:13:LYS:HA	2:T:65:PHE:CE1	2.40	0.55
1:C:179:LEU:N	1:C:179:LEU:HD23	2.21	0.55
1:C:434:LEU:HD22	1:C:445:ARG:HB3	1.87	0.55
1:C:78:LYS:O	1:C:81:GLN:HB3	2.06	0.55
1:D:234:LEU:HG	1:D:235:THR:N	2.21	0.55
1:D:275:GLY:HA2	1:D:278:LYS:CG	2.36	0.55
1:E:115:LYS:HE3	1:E:116:GLU:HG2	1.88	0.55
1:E:173:ILE:HG13	1:E:242:SER:HB3	1.88	0.55
1:E:268:MET:HA	1:E:271:LEU:HD12	1.88	0.55
1:E:431:LYS:O	1:E:448:ASP:HB2	2.07	0.55
1:F:234:LEU:CD2	1:F:235:THR:H	2.18	0.55
1:F:288:VAL:O	1:F:292:ARG:HG2	2.05	0.55
2:P:13:LYS:C	2:P:15:ALA:H	2.08	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:104:GLU:O	2:S:108:VAL:HG23	2.06	0.55
1:A:529:VAL:HG21	2:O:109:MET:CE	2.37	0.55
1:A:643:ILE:HG22	1:A:644:GLU:H	1.71	0.55
1:B:602:PHE:C	1:B:603:ILE:HG13	2.26	0.55
1:C:297:LYS:NZ	1:C:601:GLU:OE1	2.31	0.55
1:D:326:ILE:CG2	1:D:328:PHE:HE1	2.19	0.55
1:D:368:GLN:HG3	1:D:383:GLY:C	2.27	0.55
1:E:776:LEU:HD11	1:E:793:PHE:HE1	1.70	0.55
1:F:112:VAL:HG12	1:F:113:GLU:HG3	1.88	0.55
1:F:196:ILE:O	1:F:199:LEU:HB2	2.06	0.55
1:F:234:LEU:HG	1:F:235:THR:N	2.22	0.55
1:F:275:GLY:HA2	1:F:278:LYS:CG	2.36	0.55
1:F:602:PHE:C	1:F:603:ILE:HG13	2.25	0.55
2:O:55:VAL:HG11	2:O:71:MET:HE3	1.88	0.55
2:P:63:ILE:HG23	2:P:67:GLU:HB3	1.89	0.55
1:A:275:GLY:HA2	1:A:278:LYS:HD2	1.85	0.55
1:A:450:ASN:ND2	1:A:452:GLU:CG	2.69	0.55
1:B:179:LEU:HD23	1:B:179:LEU:N	2.20	0.55
1:B:246:SER:O	1:B:250:ALA:N	2.39	0.55
1:B:431:LYS:O	1:B:448:ASP:HB2	2.07	0.55
1:C:115:LYS:HE3	1:C:116:GLU:HG2	1.89	0.55
1:C:127:SER:C	1:C:133:GLU:OE2	2.44	0.55
1:C:234:LEU:HG	1:C:235:THR:N	2.22	0.55
1:C:305:SER:HB2	1:C:594:PHE:CD1	2.42	0.55
1:C:794:GLN:O	1:C:797:ILE:HG12	2.06	0.55
1:D:310:GLU:OE2	1:D:340:LYS:HD2	2.06	0.55
1:E:567:THR:HG23	1:E:568:GLY:H	1.65	0.55
1:E:633:ASN:O	1:E:642:TYR:HE1	1.89	0.55
1:F:118:GLN:HA	1:F:118:GLN:OE1	2.07	0.55
1:F:225:ILE:HG23	1:F:229:PHE:CD2	2.42	0.55
1:F:794:GLN:O	1:F:797:ILE:HG12	2.07	0.55
2:P:32:LEU:HD22	2:P:63:ILE:HD12	1.87	0.55
1:A:234:LEU:HG	1:A:235:THR:N	2.22	0.55
1:A:777:TYR:HA	1:A:780:LEU:HD22	1.88	0.55
1:B:172:GLU:O	1:B:175:LYS:HB3	2.06	0.55
1:B:639:ASN:N	1:B:639:ASN:ND2	2.49	0.55
1:B:679:TYR:CD1	1:B:679:TYR:C	2.80	0.55
1:B:76:LEU:HD22	1:B:76:LEU:N	2.18	0.55
1:D:234:LEU:CD2	1:D:235:THR:H	2.18	0.55
1:D:305:SER:HB2	1:D:594:PHE:CD1	2.42	0.55
1:D:629:ASN:HB3	1:D:632:TYR:CE1	2.42	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:407:HIS:HB2	1:E:408:LEU:HD12	1.88	0.55
1:E:715:GLU:HG3	1:E:718:ARG:NH1	2.16	0.55
1:F:431:LYS:O	1:F:448:ASP:HB2	2.07	0.55
1:F:598:PRO:HG3	1:F:624:TYR:OH	2.07	0.55
2:R:104:GLU:O	2:R:108:VAL:HG23	2.06	0.55
1:A:118:GLN:HA	1:A:118:GLN:OE1	2.06	0.55
1:A:412:GLU:HA	1:A:415:GLU:OE2	2.07	0.55
1:A:629:ASN:HB3	1:A:632:TYR:CE1	2.42	0.55
1:A:679:TYR:C	1:A:679:TYR:CD1	2.80	0.55
1:B:173:ILE:HG13	1:B:242:SER:HB3	1.89	0.55
1:B:581:GLN:O	1:B:629:ASN:HA	2.07	0.55
1:B:777:TYR:HA	1:B:780:LEU:HD22	1.89	0.55
1:C:776:LEU:HD11	1:C:793:PHE:HE1	1.71	0.55
1:D:71:PHE:HB2	1:D:108:ASP:HB2	1.89	0.55
1:E:368:GLN:HG3	1:E:383:GLY:C	2.27	0.55
1:E:78:LYS:O	1:E:81:GLN:HB3	2.06	0.55
1:F:504:ILE:HD12	1:F:504:ILE:N	2.22	0.55
1:F:527:LYS:O	1:F:528:GLY:C	2.45	0.55
1:F:679:TYR:CD1	1:F:679:TYR:C	2.80	0.55
1:C:706:ASN:O	2:Q:130:ILE:HG23	2.06	0.55
1:E:706:ASN:O	2:S:130:ILE:HG23	2.07	0.55
1:A:234:LEU:CD2	1:A:235:THR:H	2.19	0.55
1:B:236:GLU:HA	1:B:239:HIS:HD2	1.72	0.55
1:B:326:ILE:CG2	1:B:328:PHE:HE1	2.17	0.55
1:B:724:ARG:C	1:B:727:GLN:HB2	2.27	0.55
1:B:78:LYS:O	1:B:81:GLN:HB3	2.07	0.55
1:C:172:GLU:HB3	1:C:246:SER:HA	1.89	0.55
1:C:268:MET:HA	1:C:271:LEU:HD12	1.87	0.55
1:C:412:GLU:HA	1:C:415:GLU:OE2	2.07	0.55
1:D:172:GLU:O	1:D:176:GLY:N	2.38	0.55
1:D:556:MET:O	1:D:560:LEU:HD23	2.06	0.55
1:E:697:ILE:C	1:E:699:GLY:H	2.10	0.55
1:F:445:ARG:HD3	1:F:471:TRP:CE2	2.42	0.55
1:F:596:ILE:HG22	1:F:596:ILE:O	2.07	0.55
1:F:629:ASN:HD21	1:F:631:SER:CB	2.12	0.55
1:F:639:ASN:ND2	1:F:639:ASN:N	2.50	0.55
1:F:694:VAL:HG23	2:T:18:LEU:HD21	1.89	0.55
2:T:57:ALA:C	2:T:59:GLY:H	2.10	0.55
1:A:268:MET:HA	1:A:271:LEU:HD12	1.89	0.55
1:B:115:LYS:HE3	1:B:116:GLU:HG2	1.87	0.55
1:B:473:ASN:N	1:B:473:ASN:OD1	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:708:ALA:O	1:D:711:ILE:HG12	2.06	0.55
1:E:602:PHE:C	1:E:603:ILE:HG13	2.28	0.55
1:F:88:LYS:HZ3	1:F:172:GLU:CD	2.09	0.55
1:F:407:HIS:HB2	1:F:408:LEU:HD12	1.88	0.55
2:T:32:LEU:HD22	2:T:63:ILE:HD12	1.87	0.55
1:A:445:ARG:HD3	1:A:471:TRP:CE2	2.42	0.55
1:B:445:ARG:HD3	1:B:471:TRP:CE2	2.42	0.55
1:C:131:ARG:HG3	1:C:243:LEU:CD1	2.36	0.55
1:C:499:PRO:CG	1:C:504:ILE:HD11	2.35	0.55
1:C:629:ASN:HB3	1:C:632:TYR:CD1	2.41	0.55
1:C:76:LEU:H	1:C:76:LEU:CD2	2.18	0.55
1:D:235:THR:HA	1:D:238:GLN:HG3	1.87	0.55
1:D:275:GLY:HA2	1:D:278:LYS:HG3	1.88	0.55
1:D:450:ASN:ND2	1:D:452:GLU:CG	2.69	0.55
1:D:79:ILE:O	1:D:81:GLN:N	2.40	0.55
1:E:112:VAL:C	1:E:114:HIS:H	2.10	0.55
1:E:473:ASN:OD1	1:E:473:ASN:N	2.40	0.55
1:F:115:LYS:HE3	1:F:116:GLU:HG2	1.89	0.55
1:F:293:ILE:CD1	1:F:617:LYS:HD3	2.37	0.55
2:S:13:LYS:O	2:S:15:ALA:N	2.31	0.55
2:T:107:HIS:CG	2:T:107:HIS:O	2.59	0.55
2:T:55:VAL:HG11	2:T:71:MET:HE3	1.89	0.55
1:A:556:MET:O	1:A:560:LEU:HD23	2.07	0.54
1:B:271:LEU:HD13	1:B:276:PHE:CE2	2.42	0.54
1:B:368:GLN:HG3	1:B:383:GLY:C	2.28	0.54
1:B:407:HIS:HB2	1:B:408:LEU:HD12	1.89	0.54
1:B:633:ASN:O	1:B:642:TYR:HE1	1.89	0.54
1:C:217:LYS:HB3	1:C:236:GLU:OE1	2.07	0.54
1:C:326:ILE:CG2	1:C:328:PHE:HE1	2.19	0.54
1:C:697:ILE:CD1	1:C:732:ILE:HD13	2.36	0.54
1:D:112:VAL:C	1:D:114:HIS:H	2.10	0.54
1:D:499:PRO:CG	1:D:504:ILE:HD11	2.34	0.54
1:D:85:LEU:HD12	1:D:168:GLU:OE1	2.07	0.54
1:F:197:LYS:HZ2	1:F:197:LYS:CB	2.17	0.54
1:F:450:ASN:ND2	1:F:452:GLU:CG	2.70	0.54
1:A:246:SER:O	1:A:250:ALA:N	2.38	0.54
1:C:112:VAL:C	1:C:114:HIS:H	2.10	0.54
1:C:309:PRO:O	1:C:313:ASP:HB2	2.08	0.54
1:D:351:HIS:HB2	1:D:386:GLU:CG	2.38	0.54
1:D:596:ILE:HG22	1:D:596:ILE:O	2.06	0.54
1:D:695:LYS:HE3	2:R:19:PHE:CD1	2.42	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:776:LEU:HD11	1:D:793:PHE:HE1	1.72	0.54
1:E:172:GLU:O	1:E:176:GLY:N	2.36	0.54
1:E:175:LYS:CB	1:E:175:LYS:HZ2	2.19	0.54
1:F:115:LYS:NZ	1:F:115:LYS:HA	2.22	0.54
1:F:268:MET:HA	1:F:271:LEU:HD12	1.89	0.54
1:F:444:PHE:CD2	1:F:455:TYR:HB3	2.43	0.54
1:F:629:ASN:HB3	1:F:632:TYR:CE1	2.42	0.54
1:F:633:ASN:O	1:F:642:TYR:HE1	1.89	0.54
1:B:706:ASN:O	2:P:130:ILE:HG23	2.07	0.54
1:B:234:LEU:HG	1:B:235:THR:N	2.23	0.54
1:B:351:HIS:HB2	1:B:386:GLU:CG	2.38	0.54
1:B:700:TYR:CD1	1:B:727:GLN:HB3	2.42	0.54
1:D:407:HIS:HB2	1:D:408:LEU:HD12	1.89	0.54
1:E:445:ARG:HD3	1:E:471:TRP:CE2	2.43	0.54
1:E:79:ILE:O	1:E:81:GLN:N	2.41	0.54
1:F:310:GLU:O	1:F:314:ALA:HB2	2.07	0.54
1:F:368:GLN:HG3	1:F:383:GLY:C	2.27	0.54
1:F:666:ASN:O	1:F:669:SER:HB3	2.06	0.54
2:S:57:ALA:C	2:S:59:GLY:H	2.11	0.54
1:A:172:GLU:O	1:A:176:GLY:N	2.36	0.54
1:A:308:VAL:O	1:A:311:HIS:HB2	2.08	0.54
1:A:464:VAL:HG23	1:A:465:LEU:CD1	2.38	0.54
1:A:598:PRO:HG3	1:A:624:TYR:OH	2.08	0.54
1:B:127:SER:C	1:B:133:GLU:OE2	2.44	0.54
1:B:308:VAL:O	1:B:311:HIS:HB2	2.08	0.54
1:B:293:ILE:CD1	1:B:617:LYS:HD3	2.36	0.54
1:C:777:TYR:HA	1:C:780:LEU:HD22	1.89	0.54
1:D:81:GLN:OE1	1:D:156:ILE:HG21	2.08	0.54
1:D:171:TYR:O	1:D:175:LYS:NZ	2.40	0.54
1:D:697:ILE:CD1	1:D:732:ILE:HD13	2.37	0.54
1:D:794:GLN:O	1:D:797:ILE:HG12	2.08	0.54
1:E:629:ASN:HB3	1:E:632:TYR:CE1	2.42	0.54
1:F:305:SER:HB2	1:F:594:PHE:CD1	2.42	0.54
1:A:172:GLU:O	1:A:175:LYS:HB3	2.08	0.54
1:A:408:LEU:H	1:A:408:LEU:CD1	2.02	0.54
1:A:527:LYS:O	1:A:528:GLY:C	2.46	0.54
1:A:708:ALA:O	1:A:711:ILE:HG12	2.08	0.54
1:B:118:GLN:HA	1:B:118:GLN:OE1	2.07	0.54
1:B:512:GLU:HA	1:B:515:LYS:HZ2	1.72	0.54
1:B:527:LYS:O	1:B:529:VAL:N	2.40	0.54
1:C:431:LYS:O	1:C:448:ASP:HB2	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:127:SER:C	1:D:133:GLU:OE2	2.44	0.54
1:D:179:LEU:CD2	1:D:179:LEU:H	2.21	0.54
1:D:197:LYS:NZ	1:D:197:LYS:HB3	2.19	0.54
1:D:217:LYS:HB3	1:D:236:GLU:OE1	2.06	0.54
1:D:288:VAL:O	1:D:292:ARG:HG2	2.08	0.54
1:E:217:LYS:HZ1	1:E:236:GLU:HB2	1.72	0.54
1:E:728:ALA:O	1:E:729:TYR:C	2.45	0.54
1:F:527:LYS:O	1:F:529:VAL:N	2.41	0.54
1:F:567:THR:HG23	1:F:568:GLY:H	1.67	0.54
2:O:16:PHE:CZ	2:O:27:ILE:HG12	2.43	0.54
1:C:529:VAL:HG21	2:Q:109:MET:CE	2.37	0.54
1:F:706:ASN:O	2:T:130:ILE:HG23	2.08	0.54
1:A:78:LYS:O	1:A:81:GLN:HB3	2.08	0.54
1:B:172:GLU:O	1:B:176:GLY:N	2.36	0.54
1:B:420:LEU:HD12	1:B:436:GLU:HB3	1.90	0.54
1:C:172:GLU:O	1:C:175:LYS:HB3	2.07	0.54
1:C:175:LYS:HZ2	1:C:175:LYS:CB	2.20	0.54
1:C:293:ILE:CD1	1:C:617:LYS:HD3	2.36	0.54
1:C:633:ASN:O	1:C:642:TYR:HE1	1.90	0.54
1:C:76:LEU:O	1:C:78:LYS:N	2.40	0.54
1:D:308:VAL:O	1:D:311:HIS:HB2	2.08	0.54
1:D:431:LYS:O	1:D:448:ASP:HB2	2.07	0.54
1:D:464:VAL:HG23	1:D:465:LEU:CD1	2.37	0.54
1:E:695:LYS:HE3	2:S:19:PHE:CD1	2.41	0.54
1:E:794:GLN:O	1:E:797:ILE:HG12	2.08	0.54
1:F:595:ILE:HG22	1:F:596:ILE:N	2.23	0.54
2:P:104:GLU:O	2:P:108:VAL:HG23	2.06	0.54
1:A:217:LYS:HZ2	1:A:236:GLU:HB2	1.72	0.54
1:A:235:THR:HA	1:A:238:GLN:HG3	1.89	0.54
1:A:595:ILE:HG22	1:A:596:ILE:N	2.22	0.54
1:B:112:VAL:HG12	1:B:113:GLU:HG3	1.90	0.54
1:B:175:LYS:HZ2	1:B:175:LYS:CB	2.18	0.54
1:B:217:LYS:HB3	1:B:236:GLU:OE1	2.07	0.54
1:B:275:GLY:O	1:B:278:LYS:HB2	2.08	0.54
1:B:306:GLY:O	1:B:336:THR:HG23	2.06	0.54
1:B:776:LEU:HD11	1:B:793:PHE:HE1	1.71	0.54
1:C:288:VAL:O	1:C:292:ARG:HG2	2.07	0.54
1:C:368:GLN:HG3	1:C:383:GLY:C	2.28	0.54
1:D:666:ASN:O	1:D:669:SER:HB3	2.07	0.54
1:D:679:TYR:CD1	1:D:679:TYR:C	2.80	0.54
1:E:118:GLN:HA	1:E:118:GLN:OE1	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:128:MET:HE1	1:E:235:THR:HB	1.90	0.54
1:E:515:LYS:HB3	1:E:515:LYS:HZ2	1.69	0.54
1:F:165:GLN:HG2	1:F:251:PRO:CG	2.36	0.54
1:F:464:VAL:HG23	1:F:465:LEU:CD1	2.38	0.54
1:F:724:ARG:C	1:F:727:GLN:HB2	2.28	0.54
1:A:88:LYS:HZ3	1:A:172:GLU:CD	2.09	0.54
1:A:175:LYS:CB	1:A:175:LYS:HZ2	2.16	0.54
1:A:189:ASP:O	1:A:190:PRO:C	2.46	0.54
1:A:327:LEU:HG	1:A:595:ILE:HG23	1.90	0.54
1:A:412:GLU:C	1:A:414:LYS:H	2.11	0.54
1:A:527:LYS:O	1:A:529:VAL:N	2.40	0.54
1:A:581:GLN:O	1:A:629:ASN:HA	2.08	0.54
1:C:236:GLU:HA	1:C:239:HIS:HD2	1.71	0.54
1:C:351:HIS:HB2	1:C:386:GLU:CG	2.38	0.54
1:C:617:LYS:HZ2	1:C:618:ASN:ND2	1.88	0.54
1:C:598:PRO:HG3	1:C:624:TYR:OH	2.07	0.54
1:C:679:TYR:CD1	1:C:679:TYR:C	2.81	0.54
1:D:115:LYS:HG3	1:D:153:ILE:HD13	1.88	0.54
1:D:225:ILE:HG23	1:D:229:PHE:CD2	2.42	0.54
1:D:172:GLU:HB3	1:D:246:SER:HA	1.90	0.54
1:D:529:VAL:HG21	2:R:109:MET:CE	2.38	0.54
1:D:527:LYS:O	1:D:529:VAL:N	2.40	0.54
1:D:595:ILE:HG22	1:D:596:ILE:N	2.22	0.54
1:D:700:TYR:CD1	1:D:727:GLN:HB3	2.43	0.54
1:E:112:VAL:HG12	1:E:113:GLU:HG3	1.88	0.54
1:E:697:ILE:CD1	1:E:732:ILE:HD13	2.37	0.54
1:F:112:VAL:C	1:F:114:HIS:H	2.11	0.54
1:F:172:GLU:O	1:F:176:GLY:N	2.35	0.54
1:A:127:SER:C	1:A:133:GLU:OE2	2.44	0.54
1:A:225:ILE:HG23	1:A:229:PHE:CD2	2.42	0.54
1:A:173:ILE:HG13	1:A:242:SER:HB3	1.89	0.54
1:A:666:ASN:O	1:A:669:SER:HB3	2.08	0.54
1:A:781:ASN:O	1:A:789:ASN:ND2	2.41	0.54
1:A:794:GLN:O	1:A:797:ILE:HG12	2.07	0.54
1:C:666:ASN:O	1:C:669:SER:HB3	2.08	0.54
1:D:172:GLU:O	1:D:175:LYS:HB3	2.08	0.54
1:D:173:ILE:HG13	1:D:242:SER:HB3	1.88	0.54
1:D:255:THR:O	1:D:259:LEU:N	2.27	0.54
1:D:268:MET:HA	1:D:271:LEU:HD12	1.88	0.54
1:D:530:THR:HG21	2:R:145:MET:CE	2.37	0.54
1:D:557:LEU:HG	1:D:575:VAL:CG1	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:225:ILE:HG23	1:E:229:PHE:CD2	2.43	0.54
1:E:450:ASN:ND2	1:E:452:GLU:CG	2.70	0.54
1:E:777:TYR:HA	1:E:780:LEU:HD22	1.88	0.54
1:F:217:LYS:HZ1	1:F:236:GLU:HB2	1.73	0.54
1:F:635:ILE:H	1:F:635:ILE:HD12	1.72	0.54
1:F:700:TYR:CD1	1:F:727:GLN:HB3	2.43	0.54
2:Q:79:THR:C	2:Q:81:SER:N	2.60	0.54
2:S:63:ILE:HG23	2:S:67:GLU:HB3	1.90	0.54
1:A:246:SER:O	1:A:250:ALA:HB2	2.08	0.54
1:A:351:HIS:HB2	1:A:386:GLU:CG	2.38	0.54
1:A:596:ILE:HG22	1:A:596:ILE:O	2.07	0.54
1:B:109:ILE:HG22	1:B:109:ILE:O	2.08	0.54
1:B:189:ASP:HB3	1:B:190:PRO:HD2	1.90	0.54
1:B:450:ASN:ND2	1:B:452:GLU:CG	2.69	0.54
1:B:504:ILE:H	1:B:504:ILE:HD12	1.73	0.54
1:B:695:LYS:HE3	2:P:19:PHE:CD1	2.42	0.54
1:C:443:GLU:O	1:C:455:TYR:HA	2.08	0.54
1:D:112:VAL:HG12	1:D:113:GLU:HG3	1.89	0.54
1:D:715:GLU:HG3	1:D:718:ARG:NH1	2.17	0.54
1:E:306:GLY:O	1:E:336:THR:HG23	2.07	0.54
1:E:412:GLU:HA	1:E:415:GLU:OE2	2.08	0.54
1:E:444:PHE:CD2	1:E:455:TYR:HB3	2.43	0.54
1:E:595:ILE:HG22	1:E:596:ILE:N	2.23	0.54
1:F:557:LEU:HG	1:F:575:VAL:CG1	2.37	0.54
1:F:695:LYS:HE3	2:T:19:PHE:CD1	2.43	0.54
1:F:777:TYR:HA	1:F:780:LEU:HD22	1.89	0.54
1:F:85:LEU:HD12	1:F:168:GLU:OE1	2.08	0.54
2:Q:107:HIS:CG	2:Q:107:HIS:O	2.60	0.54
2:Q:63:ILE:HG23	2:Q:67:GLU:HB3	1.90	0.54
1:D:706:ASN:O	2:R:130:ILE:HG23	2.07	0.54
1:A:172:GLU:HB3	1:A:246:SER:HA	1.90	0.53
1:A:512:GLU:HA	1:A:515:LYS:HZ2	1.73	0.53
1:A:305:SER:HB2	1:A:594:PHE:CD1	2.43	0.53
1:B:115:LYS:HB2	1:B:118:GLN:CG	2.38	0.53
1:B:464:VAL:HG23	1:B:465:LEU:CD1	2.38	0.53
1:C:81:GLN:OE1	1:C:156:ILE:HG21	2.07	0.53
1:C:444:PHE:CD2	1:C:455:TYR:HB3	2.43	0.53
1:C:450:ASN:ND2	1:C:452:GLU:CG	2.70	0.53
1:D:109:ILE:HG22	1:D:109:ILE:O	2.08	0.53
1:D:246:SER:O	1:D:250:ALA:N	2.37	0.53
1:D:420:LEU:HD12	1:D:436:GLU:HB3	1.90	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:271:LEU:HD13	1:E:276:PHE:CE2	2.43	0.53
1:E:472:ARG:CB	1:E:472:ARG:HH11	2.17	0.53
1:E:628:PHE:CD1	1:E:645:TRP:CD1	2.96	0.53
1:F:657:ILE:HG13	1:F:756:ILE:CD1	2.34	0.53
1:F:728:ALA:O	1:F:729:TYR:C	2.46	0.53
2:Q:57:ALA:C	2:Q:59:GLY:H	2.11	0.53
2:Q:12:PHE:HB3	2:Q:68:PHE:HE2	1.73	0.53
1:E:529:VAL:HG21	2:S:109:MET:HE1	1.89	0.53
1:A:112:VAL:C	1:A:114:HIS:H	2.11	0.53
1:A:236:GLU:HA	1:A:239:HIS:HD2	1.73	0.53
1:A:217:LYS:HB3	1:A:236:GLU:OE1	2.09	0.53
1:A:305:SER:OG	1:A:307:LEU:HD13	2.09	0.53
1:A:345:THR:HB	1:A:491:ASP:CB	2.36	0.53
1:A:694:VAL:HG23	2:O:18:LEU:HD21	1.87	0.53
1:C:234:LEU:CD2	1:C:235:THR:H	2.20	0.53
1:C:310:GLU:O	1:C:314:ALA:HB2	2.08	0.53
1:C:527:LYS:O	1:C:529:VAL:N	2.41	0.53
1:C:595:ILE:HG22	1:C:596:ILE:N	2.23	0.53
1:C:635:ILE:H	1:C:635:ILE:HD12	1.73	0.53
1:D:412:GLU:C	1:D:414:LYS:H	2.12	0.53
1:D:777:TYR:HA	1:D:780:LEU:HD22	1.89	0.53
1:E:305:SER:HB2	1:E:594:PHE:CD1	2.43	0.53
1:E:700:TYR:CD1	1:E:727:GLN:HB3	2.43	0.53
1:F:90:PRO:HD3	1:F:249:PHE:CE2	2.43	0.53
2:O:63:ILE:HG23	2:O:67:GLU:HB3	1.89	0.53
2:Q:32:LEU:HD22	2:Q:63:ILE:HD12	1.87	0.53
2:Q:44:THR:C	2:Q:46:ALA:N	2.62	0.53
1:A:387:ASN:HD22	1:A:387:ASN:N	2.05	0.53
1:A:456:LYS:HA	1:A:469:PHE:CE1	2.43	0.53
1:A:533:LEU:O	1:A:533:LEU:HD22	2.08	0.53
1:A:715:GLU:HG3	1:A:767:GLN:HE21	1.73	0.53
1:A:728:ALA:O	1:A:729:TYR:C	2.47	0.53
1:B:353:LYS:H	1:B:368:GLN:NE2	2.05	0.53
1:B:443:GLU:O	1:B:455:TYR:HA	2.09	0.53
1:B:628:PHE:CD1	1:B:645:TRP:CD1	2.96	0.53
1:B:629:ASN:HB3	1:B:632:TYR:CE1	2.43	0.53
1:B:615:ILE:HD12	1:B:645:TRP:CH2	2.38	0.53
1:C:109:ILE:HG22	1:C:109:ILE:O	2.08	0.53
1:C:504:ILE:H	1:C:504:ILE:HD12	1.72	0.53
1:C:527:LYS:O	1:C:528:GLY:C	2.46	0.53
1:C:700:TYR:CD1	1:C:727:GLN:HB3	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:13:LYS:C	2:O:15:ALA:H	2.09	0.53
2:O:36:MET:O	2:O:40:GLY:N	2.41	0.53
2:O:51:MET:CB	2:O:71:MET:HE2	2.29	0.53
2:T:36:MET:O	2:T:40:GLY:N	2.42	0.53
1:A:171:TYR:O	1:A:175:LYS:NZ	2.41	0.53
1:A:310:GLU:O	1:A:314:ALA:HB2	2.08	0.53
1:A:420:LEU:HD12	1:A:436:GLU:HB3	1.91	0.53
1:A:611:THR:HG22	1:A:615:ILE:HD11	1.90	0.53
1:A:628:PHE:CD1	1:A:645:TRP:CD1	2.96	0.53
1:B:310:GLU:O	1:B:314:ALA:HB2	2.08	0.53
1:C:454:GLN:HG2	1:C:473:ASN:HA	1.90	0.53
1:D:454:GLN:HG2	1:D:473:ASN:HA	1.90	0.53
1:E:187:SER:C	1:E:188:LEU:O	2.41	0.53
1:E:305:SER:OG	1:E:307:LEU:HD13	2.08	0.53
1:E:789:ASN:O	1:E:792:VAL:HB	2.08	0.53
1:F:171:TYR:O	1:F:175:LYS:NZ	2.41	0.53
1:F:597:ASN:HB2	1:F:598:PRO:HD2	1.90	0.53
1:F:76:LEU:HD22	1:F:76:LEU:N	2.17	0.53
1:F:76:LEU:O	1:F:78:LYS:N	2.42	0.53
2:R:12:PHE:HB3	2:R:68:PHE:HE2	1.72	0.53
2:T:15:ALA:HB1	2:T:35:VAL:CG1	2.39	0.53
2:T:12:PHE:HB3	2:T:68:PHE:HE2	1.73	0.53
1:A:217:LYS:CB	1:A:236:GLU:HG3	2.39	0.53
1:B:118:GLN:HE22	1:B:143:PHE:HD2	1.55	0.53
1:B:339:ILE:O	1:B:342:GLY:N	2.35	0.53
1:B:527:LYS:O	1:B:528:GLY:C	2.46	0.53
1:C:275:GLY:O	1:C:278:LYS:HB2	2.09	0.53
1:C:629:ASN:HB3	1:C:632:TYR:CE1	2.44	0.53
1:D:327:LEU:HG	1:D:595:ILE:HG23	1.90	0.53
1:E:387:ASN:N	1:E:387:ASN:HD22	2.05	0.53
1:E:443:GLU:O	1:E:455:TYR:HA	2.08	0.53
1:E:454:GLN:HG2	1:E:473:ASN:HA	1.90	0.53
1:E:533:LEU:O	1:E:533:LEU:HD22	2.08	0.53
1:F:109:ILE:O	1:F:109:ILE:HG22	2.08	0.53
1:F:781:ASN:O	1:F:789:ASN:ND2	2.41	0.53
2:P:78:ASP:C	2:P:80:ASP:H	2.12	0.53
1:A:444:PHE:CD2	1:A:455:TYR:HB3	2.43	0.53
1:B:454:GLN:HG2	1:B:473:ASN:HA	1.89	0.53
1:B:697:ILE:C	1:B:699:GLY:H	2.12	0.53
1:B:789:ASN:O	1:B:792:VAL:HB	2.09	0.53
1:C:235:THR:HA	1:C:238:GLN:HG3	1.89	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:115:LYS:HE3	1:D:116:GLU:HG2	1.91	0.53
1:D:297:LYS:NZ	1:D:601:GLU:OE1	2.33	0.53
1:E:217:LYS:CB	1:E:236:GLU:HG3	2.39	0.53
1:E:327:LEU:HG	1:E:595:ILE:HG23	1.91	0.53
1:E:724:ARG:C	1:E:727:GLN:HB2	2.29	0.53
1:F:217:LYS:HB3	1:F:236:GLU:OE1	2.08	0.53
1:F:236:GLU:HA	1:F:239:HIS:HD2	1.72	0.53
2:O:57:ALA:C	2:O:59:GLY:H	2.11	0.53
1:D:501:LEU:HD22	2:R:112:LEU:HG	1.91	0.53
1:E:694:VAL:HG23	2:S:18:LEU:HD21	1.91	0.53
1:A:115:LYS:HE3	1:A:116:GLU:HG2	1.90	0.53
1:A:275:GLY:O	1:A:278:LYS:HB2	2.09	0.53
1:A:473:ASN:OD1	1:A:473:ASN:N	2.39	0.53
1:B:597:ASN:HB2	1:B:598:PRO:HD2	1.91	0.53
1:C:180:ASP:O	1:C:183:SER:N	2.39	0.53
1:C:628:PHE:CD1	1:C:645:TRP:CD1	2.96	0.53
1:D:275:GLY:O	1:D:278:LYS:HB2	2.07	0.53
1:D:456:LYS:HA	1:D:469:PHE:CE1	2.44	0.53
1:D:515:LYS:HB3	1:D:515:LYS:HZ2	1.72	0.53
1:E:412:GLU:C	1:E:414:LYS:H	2.12	0.53
1:E:456:LYS:HA	1:E:469:PHE:CE1	2.44	0.53
1:E:71:PHE:CG	1:E:73:ASN:HB2	2.44	0.53
1:F:412:GLU:C	1:F:414:LYS:H	2.12	0.53
1:F:520:PRO:HG2	1:F:521:ASN:N	2.24	0.53
2:P:57:ALA:C	2:P:59:GLY:H	2.10	0.53
2:R:57:ALA:C	2:R:59:GLY:H	2.11	0.53
1:A:697:ILE:C	1:A:699:GLY:H	2.11	0.53
1:A:700:TYR:CD1	1:A:727:GLN:HB3	2.44	0.53
1:B:235:THR:HA	1:B:238:GLN:HG3	1.90	0.53
1:B:412:GLU:C	1:B:414:LYS:H	2.12	0.53
1:B:728:ALA:O	1:B:729:TYR:C	2.47	0.53
1:C:118:GLN:HA	1:C:118:GLN:OE1	2.08	0.53
1:C:509:PRO:HG2	1:C:512:GLU:HG3	1.91	0.53
1:C:611:THR:HG22	1:C:615:ILE:HD11	1.91	0.53
1:C:694:VAL:HG23	2:Q:18:LEU:HD21	1.90	0.53
1:D:419:ILE:HD12	1:D:435:LEU:HD13	1.91	0.53
1:D:581:GLN:O	1:D:629:ASN:HA	2.08	0.53
1:D:694:VAL:HG23	2:R:18:LEU:HD21	1.90	0.53
1:E:110:ASP:O	1:E:111:LEU:C	2.47	0.53
1:E:217:LYS:HB3	1:E:236:GLU:OE1	2.07	0.53
1:E:335:ALA:CB	1:E:489:THR:OG1	2.57	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:520:PRO:HG2	1:E:521:ASN:N	2.24	0.53
1:F:131:ARG:HG3	1:F:243:LEU:CD1	2.39	0.53
1:F:351:HIS:HB2	1:F:386:GLU:CG	2.39	0.53
1:F:387:ASN:N	1:F:387:ASN:HD22	2.06	0.53
1:F:412:GLU:HA	1:F:415:GLU:OE2	2.09	0.53
2:O:107:HIS:O	2:O:107:HIS:CG	2.62	0.53
2:T:79:THR:C	2:T:81:SER:N	2.61	0.53
1:A:443:GLU:O	1:A:455:TYR:HA	2.09	0.53
1:A:517:VAL:HB	1:A:525:LYS:HZ1	1.74	0.53
1:B:172:GLU:HB3	1:B:246:SER:HA	1.90	0.53
1:B:335:ALA:CB	1:B:489:THR:OG1	2.57	0.53
1:B:628:PHE:CE2	2:P:90:ARG:CZ	2.92	0.53
1:D:443:GLU:O	1:D:455:TYR:HA	2.08	0.53
1:D:445:ARG:HD3	1:D:471:TRP:CE2	2.43	0.53
1:D:504:ILE:HD12	1:D:504:ILE:H	1.73	0.53
1:D:635:ILE:HD12	1:D:635:ILE:H	1.74	0.53
1:D:697:ILE:CD1	1:D:732:ILE:CD1	2.87	0.53
1:F:172:GLU:O	1:F:175:LYS:HB3	2.08	0.53
1:F:628:PHE:CD1	1:F:645:TRP:CD1	2.97	0.53
1:F:739:LYS:HG2	1:F:740:GLN:H	1.74	0.53
2:P:107:HIS:CG	2:P:107:HIS:O	2.60	0.53
2:P:109:MET:O	2:P:114:GLU:HB3	2.09	0.53
1:B:694:VAL:HG23	2:P:18:LEU:HD21	1.89	0.53
2:Q:36:MET:O	2:Q:40:GLY:N	2.42	0.53
2:Q:55:VAL:O	2:Q:55:VAL:HG22	2.08	0.53
2:R:109:MET:O	2:R:114:GLU:HB3	2.09	0.53
2:R:97:ASN:HD22	2:R:97:ASN:C	2.12	0.53
2:S:36:MET:O	2:S:40:GLY:N	2.41	0.53
1:A:131:ARG:HG3	1:A:243:LEU:CD1	2.40	0.53
1:A:633:ASN:O	1:A:642:TYR:HE1	1.91	0.53
1:B:595:ILE:HG22	1:B:596:ILE:N	2.24	0.53
1:B:643:ILE:HG22	1:B:644:GLU:H	1.74	0.53
1:B:710:HIS:C	1:B:712:PHE:H	2.13	0.53
1:C:456:LYS:HA	1:C:469:PHE:CE1	2.44	0.53
1:C:533:LEU:HD22	1:C:533:LEU:O	2.08	0.53
1:C:739:LYS:HG2	1:C:740:GLN:H	1.74	0.53
1:C:776:LEU:HD23	1:C:776:LEU:C	2.29	0.53
1:D:387:ASN:N	1:D:387:ASN:HD22	2.07	0.53
1:D:444:PHE:CD2	1:D:455:TYR:HB3	2.44	0.53
1:D:517:VAL:HG23	1:D:518:ASN:ND2	2.24	0.53
1:E:310:GLU:O	1:E:314:ALA:HB2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:351:HIS:HB2	1:E:386:GLU:CG	2.38	0.53
1:E:464:VAL:HG23	1:E:465:LEU:CD1	2.38	0.53
1:E:611:THR:HG22	1:E:615:ILE:HD11	1.91	0.53
1:E:76:LEU:O	1:E:78:LYS:N	2.42	0.53
1:F:308:VAL:O	1:F:311:HIS:HB2	2.09	0.53
2:P:55:VAL:HG22	2:P:55:VAL:O	2.09	0.53
2:P:12:PHE:HB3	2:P:68:PHE:HE2	1.73	0.53
2:Q:78:ASP:C	2:Q:80:ASP:H	2.12	0.53
1:A:697:ILE:CD1	1:A:732:ILE:HD13	2.39	0.52
1:A:724:ARG:C	1:A:727:GLN:HB2	2.28	0.52
1:A:765:THR:HA	1:A:769:SER:CB	2.20	0.52
1:B:148:GLU:HG3	1:B:149:THR:N	2.24	0.52
1:C:445:ARG:HD3	1:C:471:TRP:CE2	2.43	0.52
1:C:789:ASN:O	1:C:792:VAL:HB	2.08	0.52
1:D:611:THR:HG22	1:D:615:ILE:HD11	1.92	0.52
1:D:711:ILE:C	1:D:712:PHE:HD2	2.12	0.52
1:E:309:PRO:O	1:E:313:ASP:HB2	2.07	0.52
1:E:420:LEU:HD12	1:E:436:GLU:HB3	1.90	0.52
1:E:697:ILE:CD1	1:E:732:ILE:CD1	2.87	0.52
1:E:781:ASN:O	1:E:789:ASN:ND2	2.42	0.52
1:F:305:SER:OG	1:F:307:LEU:HD13	2.09	0.52
1:F:443:GLU:O	1:F:455:TYR:HA	2.08	0.52
1:F:697:ILE:CD1	1:F:732:ILE:CD1	2.87	0.52
1:F:708:ALA:O	1:F:711:ILE:HG12	2.07	0.52
1:F:71:PHE:CG	1:F:73:ASN:HB2	2.44	0.52
2:O:51:MET:O	2:O:55:VAL:HG12	2.09	0.52
2:R:44:THR:C	2:R:46:ALA:N	2.62	0.52
2:S:15:ALA:HB1	2:S:35:VAL:CG1	2.39	0.52
2:S:55:VAL:HG22	2:S:55:VAL:O	2.09	0.52
1:A:109:ILE:O	1:A:109:ILE:HG22	2.08	0.52
1:A:148:GLU:HG3	1:A:149:THR:N	2.24	0.52
1:B:234:LEU:CD2	1:B:235:THR:HG23	2.39	0.52
1:B:412:GLU:HA	1:B:415:GLU:OE2	2.09	0.52
1:B:781:ASN:O	1:B:789:ASN:ND2	2.42	0.52
1:C:246:SER:O	1:C:250:ALA:N	2.41	0.52
1:C:271:LEU:HD13	1:C:276:PHE:CE2	2.44	0.52
1:C:697:ILE:C	1:C:699:GLY:H	2.11	0.52
1:C:724:ARG:C	1:C:727:GLN:HB2	2.29	0.52
1:C:728:ALA:O	1:C:729:TYR:C	2.47	0.52
1:D:339:ILE:O	1:D:342:GLY:N	2.35	0.52
1:D:658:PRO:HG3	1:D:752:LEU:CD2	2.37	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:109:ILE:HG22	1:E:109:ILE:O	2.09	0.52
1:E:715:GLU:HG3	1:E:767:GLN:HE21	1.74	0.52
1:F:611:THR:HG22	1:F:615:ILE:HD11	1.91	0.52
2:O:55:VAL:HG22	2:O:55:VAL:O	2.09	0.52
2:P:37:ARG:HA	2:P:41:GLN:O	2.10	0.52
2:S:109:MET:HG3	2:S:116:LEU:CD1	2.39	0.52
1:A:504:ILE:HD12	1:A:504:ILE:H	1.73	0.52
1:A:71:PHE:CG	1:A:73:ASN:HB2	2.44	0.52
1:B:501:LEU:HD22	2:P:112:LEU:HG	1.91	0.52
1:C:165:GLN:HG2	1:C:251:PRO:CG	2.38	0.52
1:C:464:VAL:HG23	1:C:465:LEU:CD1	2.37	0.52
1:C:79:ILE:O	1:C:81:GLN:N	2.43	0.52
1:D:412:GLU:HA	1:D:415:GLU:OE2	2.08	0.52
1:D:633:ASN:O	1:D:642:TYR:HE1	1.91	0.52
1:D:781:ASN:O	1:D:789:ASN:ND2	2.41	0.52
1:D:789:ASN:O	1:D:792:VAL:HB	2.09	0.52
1:E:345:THR:HB	1:E:491:ASP:CB	2.35	0.52
1:F:172:GLU:HB3	1:F:246:SER:HA	1.90	0.52
2:O:109:MET:O	2:O:114:GLU:HB3	2.09	0.52
2:R:36:MET:O	2:R:40:GLY:N	2.43	0.52
1:A:71:PHE:O	1:A:78:LYS:NZ	2.43	0.52
1:A:739:LYS:HG2	1:A:740:GLN:H	1.74	0.52
1:A:76:LEU:N	1:A:76:LEU:HD22	2.18	0.52
1:B:184:LYS:CE	1:B:191:GLU:HB2	2.40	0.52
1:B:305:SER:HB2	1:B:594:PHE:CD1	2.44	0.52
1:B:327:LEU:HG	1:B:595:ILE:HG23	1.92	0.52
1:B:715:GLU:HG3	1:B:767:GLN:HE21	1.75	0.52
1:C:71:PHE:HB2	1:C:108:ASP:HB2	1.91	0.52
1:C:473:ASN:OD1	1:C:473:ASN:N	2.40	0.52
1:C:609:GLU:N	1:C:609:GLU:OE2	2.35	0.52
1:D:118:GLN:HE22	1:D:143:PHE:HD2	1.56	0.52
1:D:171:TYR:O	1:D:171:TYR:CD1	2.62	0.52
1:D:353:LYS:H	1:D:368:GLN:NE2	2.06	0.52
1:D:371:SER:O	1:D:372:LYS:C	2.48	0.52
1:E:148:GLU:HG3	1:E:149:THR:N	2.24	0.52
1:E:171:TYR:O	1:E:175:LYS:NZ	2.42	0.52
1:E:180:ASP:CG	1:E:181:ILE:N	2.62	0.52
1:F:217:LYS:CB	1:F:236:GLU:HG3	2.40	0.52
1:F:234:LEU:CD2	1:F:235:THR:HG23	2.40	0.52
1:F:345:THR:HB	1:F:491:ASP:CB	2.35	0.52
1:F:515:LYS:HB3	1:F:515:LYS:HZ2	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:533:LEU:O	1:F:533:LEU:HD22	2.09	0.52
1:F:789:ASN:O	1:F:792:VAL:HB	2.09	0.52
1:A:706:ASN:O	2:O:130:ILE:HG23	2.08	0.52
2:O:44:THR:C	2:O:46:ALA:N	2.62	0.52
2:P:16:PHE:CZ	2:P:27:ILE:HG12	2.44	0.52
2:Q:16:PHE:CZ	2:Q:27:ILE:HG12	2.44	0.52
2:Q:49:GLN:O	2:Q:53:ASN:CB	2.58	0.52
2:R:107:HIS:CG	2:R:107:HIS:O	2.63	0.52
2:R:16:PHE:CZ	2:R:27:ILE:HG12	2.45	0.52
2:R:49:GLN:O	2:R:53:ASN:CB	2.58	0.52
2:R:78:ASP:C	2:R:80:ASP:H	2.12	0.52
2:T:100:ILE:HB	2:T:136:VAL:HG22	1.90	0.52
2:T:16:PHE:CZ	2:T:27:ILE:HG12	2.45	0.52
1:B:456:LYS:HA	1:B:469:PHE:CE1	2.44	0.52
1:B:653:LYS:O	1:B:655:ASN:N	2.42	0.52
1:B:739:LYS:HG2	1:B:740:GLN:H	1.74	0.52
1:B:79:ILE:O	1:B:81:GLN:N	2.42	0.52
1:C:308:VAL:O	1:C:311:HIS:HB2	2.09	0.52
1:C:412:GLU:C	1:C:414:LYS:H	2.12	0.52
1:C:596:ILE:O	1:C:596:ILE:HG22	2.09	0.52
1:D:217:LYS:CB	1:D:236:GLU:HG3	2.39	0.52
1:D:246:SER:O	1:D:250:ALA:HB2	2.10	0.52
1:D:305:SER:OG	1:D:307:LEU:HD13	2.10	0.52
1:D:628:PHE:CD1	1:D:645:TRP:CD1	2.98	0.52
1:D:697:ILE:C	1:D:699:GLY:H	2.12	0.52
1:D:710:HIS:C	1:D:712:PHE:H	2.13	0.52
1:E:118:GLN:HE22	1:E:143:PHE:HD2	1.57	0.52
1:E:401:ILE:HD11	1:E:487:PRO:HD3	1.92	0.52
1:E:419:ILE:HD12	1:E:435:LEU:HD13	1.90	0.52
1:E:513:TRP:CZ3	1:E:517:VAL:HG11	2.45	0.52
1:F:454:GLN:HG2	1:F:473:ASN:HA	1.91	0.52
1:F:456:LYS:HA	1:F:469:PHE:CE1	2.44	0.52
1:F:679:TYR:O	1:F:679:TYR:CD1	2.63	0.52
2:O:109:MET:HG3	2:O:116:LEU:CD1	2.40	0.52
2:P:36:MET:O	2:P:40:GLY:N	2.42	0.52
2:R:15:ALA:HB1	2:R:35:VAL:CG1	2.40	0.52
2:R:55:VAL:O	2:R:55:VAL:HG22	2.09	0.52
2:S:79:THR:C	2:S:81:SER:N	2.61	0.52
2:T:37:ARG:HA	2:T:41:GLN:O	2.10	0.52
1:A:293:ILE:CD1	1:A:617:LYS:HD3	2.37	0.52
1:B:199:LEU:C	1:B:201:ASP:N	2.63	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:217:LYS:CB	1:B:236:GLU:HG3	2.40	0.52
1:B:596:ILE:HG22	1:B:596:ILE:O	2.08	0.52
1:B:697:ILE:CD1	1:B:732:ILE:HD13	2.40	0.52
1:C:122:GLU:HG3	1:C:147:ARG:HB2	1.92	0.52
1:C:557:LEU:HG	1:C:575:VAL:CG1	2.39	0.52
1:D:739:LYS:HG2	1:D:740:GLN:H	1.74	0.52
1:D:76:LEU:O	1:D:78:LYS:N	2.43	0.52
1:E:172:GLU:HB3	1:E:246:SER:HA	1.90	0.52
1:F:419:ILE:HD12	1:F:435:LEU:HD13	1.91	0.52
1:F:480:ASN:ND2	1:F:483:GLY:HA2	2.24	0.52
2:O:15:ALA:HB1	2:O:35:VAL:CG1	2.39	0.52
2:R:79:THR:C	2:R:81:SER:N	2.61	0.52
2:S:109:MET:O	2:S:114:GLU:HB3	2.10	0.52
2:T:75:LYS:NZ	2:T:75:LYS:HB3	2.25	0.52
1:B:171:TYR:O	1:B:171:TYR:CD1	2.62	0.52
1:B:520:PRO:HG2	1:B:521:ASN:N	2.25	0.52
1:C:179:LEU:CD2	1:C:179:LEU:H	2.22	0.52
1:C:339:ILE:O	1:C:342:GLY:N	2.34	0.52
1:E:171:TYR:CD1	1:E:171:TYR:O	2.61	0.52
1:F:697:ILE:CD1	1:F:732:ILE:HD13	2.39	0.52
2:P:97:ASN:C	2:P:97:ASN:HD22	2.13	0.52
2:R:51:MET:O	2:R:55:VAL:HG12	2.10	0.52
2:S:16:PHE:CZ	2:S:27:ILE:HG12	2.44	0.52
1:A:776:LEU:C	1:A:776:LEU:HD23	2.30	0.52
1:B:180:ASP:CG	1:B:181:ILE:N	2.63	0.52
1:B:444:PHE:CD2	1:B:455:TYR:HB3	2.44	0.52
1:C:184:LYS:HE3	1:C:191:GLU:CB	2.39	0.52
1:C:517:VAL:HG23	1:C:518:ASN:ND2	2.25	0.52
1:C:85:LEU:HD12	1:C:168:GLU:OE1	2.09	0.52
1:C:88:LYS:HZ3	1:C:172:GLU:CD	2.12	0.52
1:D:115:LYS:HA	1:D:115:LYS:NZ	2.23	0.52
1:E:308:VAL:O	1:E:311:HIS:HB2	2.10	0.52
1:E:501:LEU:HD22	2:S:112:LEU:HG	1.92	0.52
1:E:557:LEU:HG	1:E:575:VAL:CG1	2.38	0.52
1:E:581:GLN:O	1:E:629:ASN:HA	2.09	0.52
1:E:635:ILE:H	1:E:635:ILE:HD12	1.75	0.52
1:E:710:HIS:C	1:E:712:PHE:H	2.13	0.52
1:F:420:LEU:HD12	1:F:436:GLU:HB3	1.91	0.52
1:F:628:PHE:CE2	2:T:90:ARG:CZ	2.93	0.52
1:F:581:GLN:O	1:F:629:ASN:HA	2.09	0.52
2:O:12:PHE:HB3	2:O:68:PHE:HE2	1.73	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:78:ASP:C	2:S:80:ASP:H	2.12	0.52
2:S:97:ASN:HD22	2:S:97:ASN:C	2.13	0.52
1:F:529:VAL:HG21	2:T:109:MET:HE1	1.90	0.52
1:A:184:LYS:HE3	1:A:191:GLU:CB	2.38	0.52
1:A:401:ILE:HD11	1:A:487:PRO:HD3	1.92	0.52
1:A:335:ALA:CB	1:A:489:THR:OG1	2.58	0.52
1:A:505:LYS:C	1:A:507:GLN:H	2.14	0.52
1:A:557:LEU:HG	1:A:575:VAL:CG1	2.39	0.52
1:A:637:PRO:O	1:A:640:LYS:HG3	2.10	0.52
1:A:695:LYS:HE3	2:O:19:PHE:CD1	2.45	0.52
1:A:715:GLU:HG3	1:A:718:ARG:NH1	2.16	0.52
1:B:711:ILE:C	1:B:712:PHE:HD2	2.13	0.52
1:B:715:GLU:HG3	1:B:718:ARG:NH1	2.16	0.52
1:C:172:GLU:O	1:C:176:GLY:N	2.37	0.52
1:C:420:LEU:HD12	1:C:436:GLU:HB3	1.92	0.52
1:D:148:GLU:HG3	1:D:149:THR:N	2.24	0.52
1:D:199:LEU:C	1:D:201:ASP:N	2.63	0.52
1:E:81:GLN:OE1	1:E:156:ILE:HG21	2.10	0.52
2:O:19:PHE:CD1	2:O:19:PHE:N	2.75	0.52
2:O:78:ASP:C	2:O:80:ASP:H	2.12	0.52
2:S:88:ALA:O	2:S:91:VAL:HB	2.10	0.52
1:A:180:ASP:O	1:A:183:SER:N	2.39	0.52
1:A:454:GLN:HG2	1:A:473:ASN:HA	1.91	0.52
1:A:480:ASN:ND2	1:A:483:GLY:HA2	2.24	0.52
1:A:520:PRO:HG2	1:A:521:ASN:N	2.25	0.52
1:A:789:ASN:O	1:A:792:VAL:HB	2.10	0.52
1:B:131:ARG:HG3	1:B:243:LEU:CD1	2.39	0.52
1:B:184:LYS:HD2	1:B:191:GLU:HB2	1.92	0.52
1:B:480:ASN:ND2	1:B:483:GLY:HA2	2.24	0.52
1:B:611:THR:HG22	1:B:615:ILE:HD11	1.91	0.52
1:B:637:PRO:O	1:B:640:LYS:HG3	2.10	0.52
1:C:628:PHE:CE2	2:Q:90:ARG:CZ	2.93	0.52
1:C:697:ILE:CD1	1:C:732:ILE:CD1	2.86	0.52
1:D:310:GLU:O	1:D:314:ALA:HB2	2.10	0.52
1:D:637:PRO:O	1:D:640:LYS:HG3	2.10	0.52
1:D:724:ARG:C	1:D:727:GLN:HB2	2.29	0.52
1:F:776:LEU:HD23	1:F:776:LEU:C	2.30	0.52
1:C:501:LEU:HD22	2:Q:112:LEU:HG	1.92	0.52
1:E:505:LYS:HD3	2:S:112:LEU:O	2.10	0.52
1:A:197:LYS:CB	1:A:197:LYS:HZ2	2.16	0.51
1:A:499:PRO:CG	1:A:504:ILE:HD11	2.34	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:513:TRP:CZ3	1:A:517:VAL:HG11	2.45	0.51
1:B:191:GLU:O	1:B:193:LEU:N	2.42	0.51
1:B:305:SER:OG	1:B:307:LEU:HD13	2.10	0.51
1:B:371:SER:O	1:B:372:LYS:C	2.48	0.51
1:B:732:ILE:HG23	1:B:749:PHE:HD1	1.75	0.51
1:C:512:GLU:HA	1:C:515:LYS:HZ2	1.75	0.51
1:C:643:ILE:CG2	1:C:644:GLU:H	2.20	0.51
1:C:666:ASN:HB2	1:C:748:TYR:OH	2.10	0.51
1:C:781:ASN:O	1:C:789:ASN:ND2	2.43	0.51
1:D:122:GLU:HG3	1:D:147:ARG:HB2	1.92	0.51
1:E:191:GLU:O	1:E:194:ASN:N	2.43	0.51
1:E:234:LEU:CD2	1:E:235:THR:HG23	2.40	0.51
1:E:364:ILE:O	1:E:477:MET:HG2	2.10	0.51
1:E:527:LYS:O	1:E:528:GLY:C	2.48	0.51
1:E:596:ILE:HG22	1:E:596:ILE:O	2.10	0.51
1:E:598:PRO:HG3	1:E:624:TYR:OH	2.10	0.51
1:F:110:ASP:O	1:F:111:LEU:C	2.48	0.51
1:F:444:PHE:HA	1:F:454:GLN:O	2.10	0.51
1:F:335:ALA:CB	1:F:489:THR:OG1	2.58	0.51
2:T:49:GLN:O	2:T:53:ASN:CB	2.58	0.51
2:T:78:ASP:C	2:T:80:ASP:H	2.13	0.51
1:A:118:GLN:HE22	1:A:143:PHE:HD2	1.57	0.51
1:A:192:PHE:O	1:A:196:ILE:HG13	2.10	0.51
1:B:171:TYR:O	1:B:175:LYS:NZ	2.43	0.51
1:B:246:SER:O	1:B:250:ALA:HB2	2.11	0.51
1:B:263:ASP:O	1:B:266:GLU:N	2.44	0.51
1:C:710:HIS:C	1:C:712:PHE:H	2.14	0.51
1:D:180:ASP:O	1:D:183:SER:N	2.41	0.51
1:D:252:ASP:CG	1:D:253:HIS:H	2.14	0.51
1:E:165:GLN:C	1:E:167:LYS:H	2.14	0.51
1:E:305:SER:C	1:E:307:LEU:H	2.14	0.51
1:F:246:SER:O	1:F:250:ALA:HB2	2.09	0.51
1:F:353:LYS:H	1:F:368:GLN:NE2	2.06	0.51
1:F:401:ILE:HD11	1:F:487:PRO:HD3	1.92	0.51
2:P:41:GLN:O	2:P:43:PRO:HD2	2.09	0.51
2:P:75:LYS:HB3	2:P:75:LYS:NZ	2.25	0.51
2:Q:19:PHE:CD2	2:Q:34:THR:HG22	2.45	0.51
2:T:63:ILE:HG23	2:T:67:GLU:HB3	1.90	0.51
1:A:102:GLY:CA	1:A:150:PRO:HG2	2.40	0.51
1:A:197:LYS:HZ3	1:A:197:LYS:C	2.13	0.51
1:A:364:ILE:O	1:A:477:MET:HG2	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:732:ILE:HG23	1:A:749:PHE:HD1	1.75	0.51
1:B:364:ILE:O	1:B:477:MET:HG2	2.10	0.51
1:B:76:LEU:O	1:B:78:LYS:N	2.43	0.51
1:C:148:GLU:HG3	1:C:149:THR:N	2.24	0.51
1:C:217:LYS:CB	1:C:236:GLU:HG3	2.39	0.51
1:D:131:ARG:HB2	1:D:243:LEU:HD21	1.92	0.51
1:D:559:ARG:O	1:D:563:ALA:HB2	2.10	0.51
1:D:76:LEU:HD22	1:D:76:LEU:N	2.19	0.51
1:E:197:LYS:HZ3	1:E:197:LYS:C	2.14	0.51
1:E:199:LEU:C	1:E:201:ASP:N	2.64	0.51
1:F:559:ARG:O	1:F:563:ALA:HB2	2.10	0.51
1:F:79:ILE:O	1:F:81:GLN:N	2.44	0.51
1:F:81:GLN:OE1	1:F:156:ILE:HG21	2.09	0.51
2:Q:15:ALA:HB1	2:Q:35:VAL:CG1	2.40	0.51
2:Q:97:ASN:HD22	2:Q:97:ASN:C	2.13	0.51
2:S:37:ARG:HA	2:S:41:GLN:O	2.10	0.51
2:S:49:GLN:O	2:S:53:ASN:CB	2.58	0.51
1:A:165:GLN:C	1:A:167:LYS:H	2.12	0.51
1:A:419:ILE:HD12	1:A:435:LEU:HD13	1.92	0.51
1:B:540:ARG:HH22	1:B:630:ARG:HE	1.59	0.51
1:B:557:LEU:HG	1:B:575:VAL:CG1	2.39	0.51
1:C:345:THR:HB	1:C:491:ASP:CB	2.36	0.51
1:C:371:SER:O	1:C:372:LYS:C	2.49	0.51
1:C:700:TYR:CD1	1:C:728:ALA:N	2.78	0.51
1:D:176:GLY:C	1:D:178:SER:N	2.62	0.51
1:D:401:ILE:HD11	1:D:487:PRO:HD3	1.92	0.51
1:D:513:TRP:CZ3	1:D:517:VAL:HG11	2.45	0.51
1:E:180:ASP:O	1:E:183:SER:N	2.37	0.51
1:E:293:ILE:CD1	1:E:617:LYS:HD3	2.38	0.51
1:E:739:LYS:HG2	1:E:740:GLN:H	1.74	0.51
1:F:118:GLN:HE22	1:F:143:PHE:HD2	1.58	0.51
1:F:165:GLN:C	1:F:167:LYS:H	2.14	0.51
2:Q:109:MET:HG3	2:Q:116:LEU:CD1	2.41	0.51
2:R:37:ARG:HA	2:R:41:GLN:O	2.10	0.51
1:A:165:GLN:HG2	1:A:251:PRO:CG	2.38	0.51
1:B:509:PRO:HG2	1:B:512:GLU:HG3	1.92	0.51
1:B:533:LEU:O	1:B:533:LEU:HD22	2.09	0.51
1:C:387:ASN:O	1:C:390:SER:HB2	2.11	0.51
1:D:189:ASP:HB3	1:D:190:PRO:HD2	1.93	0.51
1:D:345:THR:HB	1:D:491:ASP:CB	2.36	0.51
1:D:505:LYS:C	1:D:507:GLN:H	2.13	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:711:ILE:O	1:D:712:PHE:HD2	1.93	0.51
1:E:509:PRO:HG2	1:E:512:GLU:HG3	1.92	0.51
2:P:19:PHE:N	2:P:19:PHE:CD1	2.75	0.51
2:Q:66:PRO:O	2:Q:68:PHE:N	2.44	0.51
2:S:19:PHE:N	2:S:19:PHE:CD1	2.74	0.51
2:S:44:THR:C	2:S:46:ALA:N	2.63	0.51
2:S:75:LYS:HB3	2:S:75:LYS:NZ	2.25	0.51
1:A:387:ASN:O	1:A:390:SER:HB2	2.11	0.51
1:A:517:VAL:HG23	1:A:518:ASN:ND2	2.25	0.51
1:B:387:ASN:HD22	1:B:387:ASN:N	2.07	0.51
1:C:246:SER:O	1:C:250:ALA:HB2	2.10	0.51
1:C:279:ILE:HG22	1:C:283:LEU:HD13	1.93	0.51
1:C:387:ASN:HD22	1:C:387:ASN:N	2.09	0.51
1:C:520:PRO:HG2	1:C:521:ASN:N	2.25	0.51
1:D:173:ILE:C	1:D:175:LYS:N	2.64	0.51
1:D:509:PRO:HG2	1:D:512:GLU:HG3	1.91	0.51
1:D:724:ARG:HA	1:D:727:GLN:HG3	1.93	0.51
1:E:165:GLN:HG2	1:E:251:PRO:CG	2.39	0.51
1:E:371:SER:O	1:E:372:LYS:C	2.48	0.51
1:E:711:ILE:C	1:E:712:PHE:HD2	2.14	0.51
1:E:776:LEU:HD23	1:E:776:LEU:C	2.30	0.51
1:F:622:LYS:HG3	1:F:623:ASP:H	1.75	0.51
2:P:15:ALA:HB1	2:P:35:VAL:CG1	2.40	0.51
2:Q:109:MET:O	2:Q:114:GLU:HB3	2.11	0.51
2:R:19:PHE:CD2	2:R:34:THR:HG22	2.45	0.51
2:T:19:PHE:CD2	2:T:34:THR:HG22	2.46	0.51
1:A:371:SER:O	1:A:372:LYS:C	2.49	0.51
1:A:597:ASN:HB2	1:A:598:PRO:HD2	1.93	0.51
1:A:697:ILE:CD1	1:A:732:ILE:CD1	2.89	0.51
1:B:279:ILE:HG22	1:B:283:LEU:HD13	1.91	0.51
1:B:658:PRO:HB3	1:B:755:ARG:NH1	2.26	0.51
1:C:355:SER:HG	1:C:371:SER:HA	1.73	0.51
1:C:401:ILE:HD11	1:C:487:PRO:HD3	1.92	0.51
1:D:234:LEU:CG	1:D:235:THR:N	2.74	0.51
1:D:305:SER:C	1:D:307:LEU:H	2.14	0.51
1:D:520:PRO:HG2	1:D:521:ASN:N	2.25	0.51
1:D:728:ALA:O	1:D:729:TYR:C	2.46	0.51
1:E:122:GLU:HG3	1:E:147:ARG:H	1.76	0.51
1:E:444:PHE:HA	1:E:454:GLN:O	2.10	0.51
1:E:622:LYS:HG3	1:E:623:ASP:H	1.75	0.51
1:F:148:GLU:HG3	1:F:149:THR:N	2.24	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:275:GLY:O	1:F:278:LYS:HB2	2.11	0.51
1:F:711:ILE:C	1:F:712:PHE:HD2	2.14	0.51
2:P:44:THR:C	2:P:46:ALA:N	2.63	0.51
2:P:49:GLN:O	2:P:53:ASN:CB	2.58	0.51
2:Q:37:ARG:HA	2:Q:41:GLN:O	2.11	0.51
2:S:28:THR:OG1	2:S:29:THR:N	2.43	0.51
2:S:12:PHE:HB3	2:S:68:PHE:HE2	1.75	0.51
2:T:109:MET:HG3	2:T:116:LEU:CD1	2.41	0.51
1:F:501:LEU:HD22	2:T:112:LEU:HG	1.93	0.51
1:A:171:TYR:CD1	1:A:171:TYR:O	2.62	0.51
1:A:180:ASP:CG	1:A:181:ILE:N	2.64	0.51
1:A:305:SER:C	1:A:307:LEU:H	2.13	0.51
1:A:658:PRO:HG3	1:A:752:LEU:CD2	2.40	0.51
1:A:697:ILE:HG23	1:A:732:ILE:HD11	1.92	0.51
1:B:110:ASP:O	1:B:111:LEU:C	2.49	0.51
1:B:252:ASP:CG	1:B:253:HIS:H	2.15	0.51
1:B:279:ILE:HG22	1:B:283:LEU:HD11	1.93	0.51
1:B:517:VAL:HB	1:B:525:LYS:HZ1	1.76	0.51
1:B:579:THR:C	1:B:581:GLN:H	2.14	0.51
1:C:118:GLN:HE22	1:C:143:PHE:HD2	1.58	0.51
1:C:180:ASP:CG	1:C:181:ILE:N	2.64	0.51
1:C:559:ARG:O	1:C:563:ALA:HB2	2.11	0.51
1:D:364:ILE:O	1:D:477:MET:HG2	2.10	0.51
1:D:776:LEU:HD23	1:D:776:LEU:C	2.31	0.51
1:E:234:LEU:CG	1:E:235:THR:N	2.74	0.51
1:E:457:THR:HG23	1:E:469:PHE:H	1.76	0.51
1:F:371:SER:O	1:F:372:LYS:C	2.49	0.51
1:F:653:LYS:O	1:F:655:ASN:N	2.44	0.51
1:F:697:ILE:C	1:F:699:GLY:H	2.13	0.51
1:A:501:LEU:HD22	2:O:112:LEU:HG	1.93	0.51
2:O:88:ALA:O	2:O:91:VAL:HB	2.11	0.51
2:P:51:MET:O	2:P:55:VAL:HG12	2.11	0.51
2:Q:51:MET:O	2:Q:55:VAL:HG12	2.11	0.51
2:S:107:HIS:O	2:S:107:HIS:CG	2.63	0.51
2:S:52:ILE:HD13	2:S:63:ILE:HD11	1.92	0.51
2:S:51:MET:O	2:S:55:VAL:HG12	2.11	0.51
2:T:109:MET:O	2:T:114:GLU:HB3	2.10	0.51
1:A:110:ASP:O	1:A:111:LEU:C	2.49	0.51
1:A:173:ILE:C	1:A:175:LYS:N	2.63	0.51
1:A:234:LEU:CD2	1:A:235:THR:HG23	2.41	0.51
1:A:622:LYS:HG3	1:A:623:ASP:H	1.75	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:628:PHE:CE2	2:O:90:ARG:CZ	2.94	0.51
1:A:76:LEU:O	1:A:78:LYS:N	2.44	0.51
1:B:171:TYR:HD1	1:B:175:LYS:NZ	2.08	0.51
1:B:444:PHE:HA	1:B:454:GLN:O	2.11	0.51
1:B:559:ARG:O	1:B:563:ALA:HB2	2.11	0.51
1:C:173:ILE:C	1:C:175:LYS:N	2.64	0.51
1:C:176:GLY:C	1:C:178:SER:N	2.63	0.51
1:C:597:ASN:HB2	1:C:598:PRO:HD2	1.93	0.51
1:C:711:ILE:C	1:C:712:PHE:HD2	2.14	0.51
1:D:170:TYR:O	1:D:174:GLY:N	2.44	0.51
1:D:180:ASP:CG	1:D:181:ILE:N	2.65	0.51
1:D:236:GLU:HA	1:D:239:HIS:HD2	1.73	0.51
1:E:179:LEU:CD2	1:E:179:LEU:H	2.22	0.51
1:F:318:ILE:N	1:F:318:ILE:HD12	2.25	0.51
1:F:700:TYR:CD1	1:F:728:ALA:N	2.77	0.51
2:O:129:ASP:OD1	2:O:134:GLY:N	2.38	0.51
1:A:102:GLY:C	1:A:103:GLU:HG3	2.32	0.51
1:A:192:PHE:HD1	1:A:192:PHE:H	1.59	0.51
1:A:79:ILE:O	1:A:81:GLN:N	2.44	0.51
1:B:102:GLY:CA	1:B:150:PRO:HG2	2.41	0.51
1:B:345:THR:HB	1:B:491:ASP:CB	2.35	0.51
1:B:493:ASP:OD2	1:B:577:HIS:CE1	2.63	0.51
1:B:513:TRP:CZ3	1:B:517:VAL:HG11	2.46	0.51
1:C:110:ASP:O	1:C:111:LEU:C	2.48	0.51
1:C:263:ASP:O	1:C:266:GLU:N	2.44	0.51
1:C:305:SER:OG	1:C:307:LEU:HD13	2.10	0.51
1:C:505:LYS:C	1:C:507:GLN:H	2.14	0.51
1:C:76:LEU:HD22	1:C:76:LEU:N	2.19	0.51
1:D:410:ILE:HD11	1:D:435:LEU:HD11	1.93	0.51
1:D:658:PRO:HB3	1:D:755:ARG:NH1	2.25	0.51
1:E:171:TYR:HD1	1:E:175:LYS:NZ	2.09	0.51
1:E:254:ARG:NH1	1:E:254:ARG:HB3	2.23	0.51
1:E:339:ILE:O	1:E:342:GLY:N	2.36	0.51
1:E:410:ILE:HD11	1:E:435:LEU:HD11	1.92	0.51
1:F:173:ILE:C	1:F:175:LYS:N	2.63	0.51
1:F:180:ASP:O	1:F:183:SER:N	2.39	0.51
1:F:311:HIS:HE1	1:F:339:ILE:HG22	1.75	0.51
1:F:457:THR:HG23	1:F:469:PHE:H	1.76	0.51
1:F:364:ILE:O	1:F:477:MET:HG2	2.11	0.51
1:F:513:TRP:CZ3	1:F:517:VAL:HG11	2.46	0.51
2:P:19:PHE:CD2	2:P:34:THR:HG22	2.46	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:75:LYS:HB3	2:R:75:LYS:NZ	2.26	0.51
2:R:88:ALA:O	2:R:91:VAL:HB	2.11	0.51
2:S:66:PRO:O	2:S:68:PHE:N	2.44	0.51
1:A:679:TYR:O	1:A:679:TYR:CD1	2.64	0.50
1:B:173:ILE:C	1:B:175:LYS:N	2.63	0.50
1:B:679:TYR:CD1	1:B:679:TYR:O	2.65	0.50
1:C:171:TYR:O	1:C:175:LYS:NZ	2.44	0.50
1:D:165:GLN:C	1:D:167:LYS:H	2.13	0.50
1:D:529:VAL:O	1:D:532:LEU:HB2	2.11	0.50
1:D:533:LEU:HD22	1:D:533:LEU:O	2.11	0.50
1:D:622:LYS:HG3	1:D:623:ASP:H	1.75	0.50
1:E:679:TYR:CD1	1:E:679:TYR:O	2.64	0.50
1:E:724:ARG:HA	1:E:727:GLN:HG3	1.92	0.50
1:F:171:TYR:HD1	1:F:175:LYS:NZ	2.09	0.50
1:F:180:ASP:CG	1:F:181:ILE:N	2.63	0.50
2:O:37:ARG:HA	2:O:41:GLN:O	2.11	0.50
2:P:109:MET:HG3	2:P:116:LEU:CD1	2.41	0.50
2:T:97:ASN:C	2:T:97:ASN:HD22	2.13	0.50
1:A:179:LEU:CD2	1:A:179:LEU:H	2.21	0.50
1:A:318:ILE:N	1:A:318:ILE:HD12	2.25	0.50
1:A:444:PHE:HA	1:A:454:GLN:O	2.11	0.50
1:A:711:ILE:C	1:A:712:PHE:HD2	2.14	0.50
1:B:345:THR:HG22	1:B:490:ALA:O	2.10	0.50
1:B:71:PHE:CG	1:B:73:ASN:HB2	2.46	0.50
1:B:764:LEU:C	1:B:766:HIS:N	2.52	0.50
1:C:197:LYS:HD3	1:C:263:ASP:HB3	1.93	0.50
1:C:697:ILE:HG23	1:C:732:ILE:HD11	1.93	0.50
1:D:480:ASN:ND2	1:D:483:GLY:HA2	2.25	0.50
1:D:715:GLU:HG3	1:D:767:GLN:HE21	1.75	0.50
1:E:192:PHE:O	1:E:196:ILE:HG13	2.12	0.50
1:E:559:ARG:O	1:E:563:ALA:HB2	2.10	0.50
1:E:597:ASN:HB2	1:E:598:PRO:HD2	1.93	0.50
1:E:710:HIS:O	1:E:712:PHE:N	2.44	0.50
1:F:179:LEU:H	1:F:179:LEU:CD2	2.22	0.50
1:F:710:HIS:C	1:F:712:PHE:H	2.15	0.50
2:O:75:LYS:NZ	2:O:75:LYS:HB3	2.26	0.50
2:O:97:ASN:HD22	2:O:97:ASN:C	2.13	0.50
2:T:44:THR:C	2:T:46:ALA:N	2.64	0.50
2:T:66:PRO:O	2:T:68:PHE:N	2.44	0.50
1:A:559:ARG:O	1:A:563:ALA:HB2	2.11	0.50
1:A:653:LYS:O	1:A:655:ASN:N	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:LEU:CG	1:B:235:THR:N	2.75	0.50
1:C:165:GLN:C	1:C:167:LYS:H	2.14	0.50
1:C:327:LEU:HG	1:C:595:ILE:HG23	1.93	0.50
1:C:364:ILE:O	1:C:477:MET:HG2	2.11	0.50
1:C:513:TRP:CZ3	1:C:517:VAL:HG11	2.47	0.50
1:D:444:PHE:HA	1:D:454:GLN:O	2.11	0.50
1:D:322:LEU:HA	1:D:503:GLU:OE2	2.11	0.50
1:E:189:ASP:HB3	1:E:190:PRO:CD	2.38	0.50
1:E:234:LEU:N	1:E:234:LEU:HD23	2.27	0.50
1:E:76:LEU:HD22	1:E:76:LEU:N	2.17	0.50
1:F:102:GLY:CA	1:F:150:PRO:HG2	2.41	0.50
1:F:102:GLY:C	1:F:103:GLU:HG3	2.30	0.50
2:Q:75:LYS:HB3	2:Q:75:LYS:NZ	2.26	0.50
2:R:106:ARG:HH21	2:R:106:ARG:HG3	1.76	0.50
2:S:19:PHE:CD2	2:S:34:THR:HG22	2.46	0.50
2:S:56:ASP:C	2:S:58:ASP:H	2.15	0.50
1:A:234:LEU:CG	1:A:235:THR:N	2.75	0.50
1:A:85:LEU:HD12	1:A:168:GLU:OE1	2.11	0.50
1:B:179:LEU:CD2	1:B:179:LEU:H	2.22	0.50
1:B:297:LYS:HG2	1:B:603:ILE:HG12	1.94	0.50
1:B:387:ASN:O	1:B:390:SER:HB2	2.11	0.50
1:C:199:LEU:C	1:C:201:ASP:N	2.64	0.50
1:D:185:ASP:O	1:D:190:PRO:HA	2.12	0.50
1:D:473:ASN:N	1:D:473:ASN:OD1	2.41	0.50
1:D:597:ASN:HB2	1:D:598:PRO:HD2	1.94	0.50
1:E:353:LYS:N	1:E:368:GLN:HE22	2.06	0.50
1:E:518:ASN:N	1:E:518:ASN:ND2	2.60	0.50
1:E:626:TYR:CD2	1:E:627:TYR:N	2.80	0.50
1:F:279:ILE:HG22	1:F:283:LEU:HD13	1.93	0.50
1:F:504:ILE:HD12	1:F:504:ILE:H	1.75	0.50
1:F:736:LEU:HD11	1:F:750:GLN:NE2	2.27	0.50
2:Q:63:ILE:CG2	2:Q:67:GLU:HB2	2.41	0.50
1:D:628:PHE:CE2	2:R:90:ARG:CZ	2.94	0.50
2:T:104:GLU:HA	2:T:107:HIS:HB3	1.93	0.50
1:A:279:ILE:HG22	1:A:283:LEU:HD13	1.93	0.50
1:A:457:THR:HG23	1:A:469:PHE:H	1.76	0.50
1:A:629:ASN:ND2	1:A:631:SER:CB	2.73	0.50
1:B:81:GLN:OE1	1:B:156:ILE:HG21	2.11	0.50
1:B:419:ILE:HD12	1:B:435:LEU:HD13	1.93	0.50
1:C:444:PHE:HA	1:C:454:GLN:O	2.11	0.50
1:D:110:ASP:O	1:D:111:LEU:C	2.49	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:197:LYS:CB	1:D:197:LYS:HZ2	2.16	0.50
1:D:293:ILE:CD1	1:D:617:LYS:HD3	2.37	0.50
1:D:679:TYR:CD1	1:D:679:TYR:O	2.65	0.50
1:E:197:LYS:HD3	1:E:263:ASP:HB3	1.93	0.50
1:E:236:GLU:HA	1:E:239:HIS:HD2	1.73	0.50
1:E:263:ASP:O	1:E:266:GLU:N	2.45	0.50
1:E:732:ILE:HG23	1:E:749:PHE:HD1	1.76	0.50
1:F:104:ILE:HG23	1:F:152:LEU:CD2	2.41	0.50
1:F:234:LEU:CG	1:F:235:THR:N	2.74	0.50
1:F:305:SER:C	1:F:307:LEU:H	2.14	0.50
1:F:499:PRO:CG	1:F:504:ILE:HD11	2.33	0.50
2:P:66:PRO:O	2:P:68:PHE:N	2.44	0.50
1:C:505:LYS:HD3	2:Q:112:LEU:O	2.12	0.50
2:S:68:PHE:O	2:S:70:THR:N	2.45	0.50
1:A:401:ILE:HG21	1:A:485:LEU:HB3	1.94	0.50
1:B:457:THR:HG23	1:B:469:PHE:H	1.77	0.50
1:B:711:ILE:O	1:B:712:PHE:HD2	1.94	0.50
1:B:85:LEU:HD12	1:B:168:GLU:OE1	2.11	0.50
1:C:234:LEU:CD2	1:C:235:THR:HG23	2.41	0.50
1:C:234:LEU:HD23	1:C:234:LEU:N	2.27	0.50
1:C:311:HIS:HE1	1:C:339:ILE:HG22	1.76	0.50
1:E:311:HIS:HE1	1:E:339:ILE:HG22	1.77	0.50
1:E:505:LYS:C	1:E:507:GLN:H	2.15	0.50
1:E:523:LEU:HD11	2:S:144:MET:CG	2.42	0.50
1:F:197:LYS:NZ	1:F:197:LYS:HB3	2.19	0.50
1:F:252:ASP:CG	1:F:253:HIS:H	2.14	0.50
1:F:197:LYS:HD3	1:F:263:ASP:HB3	1.94	0.50
1:F:517:VAL:HG23	1:F:518:ASN:ND2	2.26	0.50
1:A:252:ASP:CG	1:A:253:HIS:H	2.15	0.50
1:A:710:HIS:C	1:A:712:PHE:H	2.14	0.50
1:A:724:ARG:HA	1:A:727:GLN:HG3	1.94	0.50
1:B:305:SER:C	1:B:307:LEU:H	2.13	0.50
1:B:622:LYS:HG3	1:B:623:ASP:H	1.75	0.50
1:B:629:ASN:ND2	1:B:631:SER:CB	2.74	0.50
1:C:715:GLU:HG3	1:C:767:GLN:HE21	1.75	0.50
1:E:173:ILE:C	1:E:175:LYS:N	2.62	0.50
1:E:527:LYS:O	1:E:529:VAL:N	2.45	0.50
1:F:234:LEU:HD23	1:F:234:LEU:N	2.27	0.50
1:F:715:GLU:HG3	1:F:767:GLN:HE21	1.76	0.50
2:P:12:PHE:O	2:P:15:ALA:HB3	2.12	0.50
2:Q:104:GLU:HA	2:Q:107:HIS:HB3	1.94	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:63:ILE:CG2	2:R:67:GLU:HB2	2.42	0.50
1:A:199:LEU:C	1:A:201:ASP:N	2.63	0.50
1:A:660:SER:O	1:A:663:PHE:HB3	2.12	0.50
1:B:122:GLU:HG3	1:B:147:ARG:H	1.77	0.50
1:B:505:LYS:C	1:B:507:GLN:H	2.15	0.50
1:C:102:GLY:C	1:C:103:GLU:HG3	2.32	0.50
1:C:234:LEU:CG	1:C:235:THR:N	2.75	0.50
1:C:353:LYS:N	1:C:368:GLN:HE22	2.08	0.50
1:D:234:LEU:CD2	1:D:235:THR:HG23	2.41	0.50
1:D:131:ARG:HG3	1:D:243:LEU:HD13	1.94	0.50
1:E:432:TYR:HE1	1:E:445:ARG:CZ	2.25	0.50
1:E:493:ASP:OD2	1:E:577:HIS:CE1	2.65	0.50
1:E:579:THR:C	1:E:581:GLN:H	2.15	0.50
1:E:637:PRO:O	1:E:640:LYS:HG3	2.11	0.50
1:F:401:ILE:HG21	1:F:485:LEU:HB3	1.94	0.50
2:P:88:ALA:O	2:P:91:VAL:HB	2.11	0.50
1:D:505:LYS:HD3	2:R:112:LEU:O	2.12	0.50
2:S:106:ARG:HH21	2:S:106:ARG:HG3	1.77	0.50
1:A:122:GLU:HG3	1:A:147:ARG:H	1.76	0.50
1:A:495:PHE:CD1	1:A:495:PHE:C	2.84	0.50
1:B:165:GLN:C	1:B:167:LYS:H	2.14	0.50
1:B:170:TYR:O	1:B:174:GLY:N	2.44	0.50
1:B:401:ILE:HD11	1:B:487:PRO:HD3	1.94	0.50
1:B:517:VAL:HG23	1:B:518:ASN:ND2	2.26	0.50
1:C:305:SER:C	1:C:307:LEU:H	2.14	0.50
1:C:622:LYS:HG3	1:C:623:ASP:H	1.75	0.50
1:D:71:PHE:O	1:D:78:LYS:NZ	2.45	0.50
1:D:700:TYR:CD1	1:D:728:ALA:N	2.78	0.50
1:E:252:ASP:CG	1:E:253:HIS:H	2.15	0.50
1:F:185:ASP:O	1:F:190:PRO:HA	2.12	0.50
1:F:509:PRO:HG2	1:F:512:GLU:HG3	1.94	0.50
2:O:56:ASP:C	2:O:58:ASP:H	2.14	0.50
2:O:63:ILE:CG2	2:O:67:GLU:HB2	2.41	0.50
2:P:104:GLU:HA	2:P:107:HIS:HB3	1.94	0.50
2:Q:41:GLN:O	2:Q:43:PRO:HD2	2.10	0.50
1:A:353:LYS:N	1:A:368:GLN:HE22	2.07	0.49
1:B:176:GLY:C	1:B:178:SER:N	2.64	0.49
1:B:493:ASP:OD2	1:B:577:HIS:HE1	1.95	0.49
1:C:131:ARG:HB2	1:C:243:LEU:HD21	1.93	0.49
1:C:171:TYR:CD1	1:C:171:TYR:O	2.62	0.49
1:C:660:SER:O	1:C:663:PHE:HB3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:142:VAL:CG2	1:E:154:ILE:HD12	2.38	0.49
1:E:246:SER:O	1:E:250:ALA:HB2	2.12	0.49
1:E:249:PHE:O	1:E:250:ALA:C	2.51	0.49
1:E:517:VAL:HG23	1:E:518:ASN:ND2	2.25	0.49
1:E:90:PRO:HD3	1:E:249:PHE:CE2	2.47	0.49
1:F:410:ILE:HD11	1:F:435:LEU:HD11	1.93	0.49
1:F:495:PHE:C	1:F:495:PHE:CD1	2.86	0.49
1:F:731:GLU:HA	1:F:734:ASN:HB2	1.94	0.49
1:F:732:ILE:HG23	1:F:749:PHE:HD1	1.76	0.49
2:O:104:GLU:HA	2:O:107:HIS:HB3	1.94	0.49
2:O:84:GLU:N	2:O:84:GLU:OE2	2.45	0.49
2:P:129:ASP:OD2	2:P:140:GLU:OE2	2.29	0.49
2:P:79:THR:C	2:P:81:SER:N	2.61	0.49
2:R:66:PRO:C	2:R:68:PHE:H	2.16	0.49
2:R:66:PRO:O	2:R:68:PHE:N	2.45	0.49
2:S:66:PRO:C	2:S:68:PHE:H	2.15	0.49
1:A:171:TYR:HD1	1:A:175:LYS:NZ	2.09	0.49
1:A:182:ILE:HA	1:A:187:SER:HA	1.94	0.49
1:A:254:ARG:NH1	1:A:254:ARG:HB3	2.20	0.49
1:A:724:ARG:HH11	1:A:724:ARG:HG3	1.77	0.49
1:A:767:GLN:HG2	1:A:768:LYS:N	2.27	0.49
1:B:180:ASP:O	1:B:183:SER:N	2.39	0.49
1:B:192:PHE:HD1	1:B:192:PHE:H	1.60	0.49
1:B:731:GLU:HA	1:B:734:ASN:HB2	1.94	0.49
1:C:755:ARG:O	1:C:756:ILE:C	2.50	0.49
1:C:719:LYS:HE3	1:C:797:ILE:HD11	1.93	0.49
1:D:165:GLN:HG2	1:D:251:PRO:CG	2.39	0.49
1:D:387:ASN:O	1:D:390:SER:HB2	2.12	0.49
1:F:658:PRO:HB3	1:F:755:ARG:NH1	2.26	0.49
1:F:671:ARG:HG3	1:F:671:ARG:HH11	1.77	0.49
2:P:63:ILE:CG2	2:P:67:GLU:HB2	2.42	0.49
1:C:529:VAL:HG21	2:Q:109:MET:HE1	1.92	0.49
2:R:72:MET:C	2:R:74:ARG:N	2.66	0.49
2:T:117:THR:C	2:T:119:GLU:N	2.66	0.49
1:A:279:ILE:HG22	1:A:283:LEU:HD11	1.93	0.49
1:A:297:LYS:HG2	1:A:603:ILE:HG12	1.94	0.49
1:B:234:LEU:N	1:B:234:LEU:HD23	2.27	0.49
1:C:170:TYR:O	1:C:174:GLY:N	2.44	0.49
1:C:279:ILE:HG22	1:C:283:LEU:HD11	1.93	0.49
1:C:318:ILE:HD12	1:C:318:ILE:N	2.27	0.49
1:C:653:LYS:O	1:C:655:ASN:N	2.44	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:724:ARG:HA	1:C:727:GLN:HG3	1.94	0.49
1:D:102:GLY:C	1:D:103:GLU:HG3	2.33	0.49
1:D:279:ILE:HG22	1:D:283:LEU:HD13	1.94	0.49
1:D:457:THR:HG23	1:D:469:PHE:H	1.76	0.49
1:E:131:ARG:HG3	1:E:243:LEU:CD1	2.43	0.49
1:E:633:ASN:O	1:E:642:TYR:CE1	2.66	0.49
1:F:100:LEU:HD22	1:F:182:ILE:HG21	1.93	0.49
2:R:104:GLU:HA	2:R:107:HIS:HB3	1.94	0.49
2:R:109:MET:HG3	2:R:116:LEU:CD1	2.41	0.49
1:D:523:LEU:HD11	2:R:144:MET:CG	2.42	0.49
2:S:117:THR:C	2:S:119:GLU:N	2.65	0.49
1:B:401:ILE:HG21	1:B:485:LEU:HB3	1.94	0.49
1:B:432:TYR:HE1	1:B:445:ARG:CZ	2.25	0.49
1:C:102:GLY:CA	1:C:150:PRO:HG2	2.42	0.49
1:C:289:GLU:HA	1:C:292:ARG:HG3	1.94	0.49
1:C:658:PRO:HB3	1:C:755:ARG:NH1	2.27	0.49
1:D:517:VAL:HB	1:D:525:LYS:HZ1	1.78	0.49
1:E:170:TYR:O	1:E:174:GLY:N	2.45	0.49
1:E:176:GLY:C	1:E:178:SER:N	2.64	0.49
1:F:263:ASP:O	1:F:266:GLU:N	2.45	0.49
1:F:339:ILE:O	1:F:342:GLY:N	2.37	0.49
1:F:432:TYR:HE1	1:F:445:ARG:CZ	2.25	0.49
1:F:505:LYS:C	1:F:507:GLN:H	2.15	0.49
2:Q:56:ASP:C	2:Q:58:ASP:H	2.14	0.49
2:T:63:ILE:CG2	2:T:67:GLU:HB2	2.43	0.49
2:T:66:PRO:C	2:T:68:PHE:H	2.16	0.49
2:T:68:PHE:O	2:T:70:THR:N	2.45	0.49
1:A:185:ASP:O	1:A:190:PRO:HA	2.13	0.49
1:A:311:HIS:HE1	1:A:339:ILE:HG22	1.77	0.49
1:A:731:GLU:HA	1:A:734:ASN:HB2	1.94	0.49
1:B:172:GLU:HG3	1:B:245:PHE:HE1	1.78	0.49
1:B:131:ARG:HB2	1:B:243:LEU:HD21	1.94	0.49
1:B:617:LYS:HZ3	1:B:618:ASN:HD21	1.58	0.49
1:B:633:ASN:O	1:B:642:TYR:CE1	2.65	0.49
1:C:192:PHE:H	1:C:192:PHE:HD1	1.61	0.49
1:C:379:ALA:O	1:C:383:GLY:N	2.45	0.49
1:C:480:ASN:HD22	1:C:481:VAL:N	2.10	0.49
1:C:695:LYS:HE3	2:Q:19:PHE:CD1	2.47	0.49
1:D:518:ASN:ND2	1:D:518:ASN:N	2.60	0.49
1:D:653:LYS:O	1:D:655:ASN:N	2.45	0.49
1:D:710:HIS:O	1:D:712:PHE:N	2.46	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:297:LYS:HB3	1:E:297:LYS:HZ3	1.77	0.49
1:E:387:ASN:O	1:E:390:SER:HB2	2.12	0.49
1:E:480:ASN:ND2	1:E:483:GLY:HA2	2.26	0.49
1:F:192:PHE:O	1:F:196:ILE:HG13	2.12	0.49
1:F:405:LEU:HD13	1:F:453:VAL:CG2	2.40	0.49
1:A:523:LEU:HD11	2:O:144:MET:CG	2.43	0.49
2:O:19:PHE:CD2	2:O:34:THR:HG22	2.48	0.49
2:O:49:GLN:O	2:O:53:ASN:CB	2.59	0.49
2:O:52:ILE:HD13	2:O:63:ILE:HD11	1.93	0.49
2:P:56:ASP:C	2:P:58:ASP:H	2.15	0.49
2:R:68:PHE:O	2:R:70:THR:N	2.45	0.49
1:A:518:ASN:ND2	1:A:518:ASN:N	2.60	0.49
1:B:104:ILE:HG23	1:B:152:LEU:CD2	2.43	0.49
1:B:724:ARG:HA	1:B:727:GLN:HG3	1.93	0.49
1:C:410:ILE:HD11	1:C:435:LEU:HD11	1.95	0.49
1:C:419:ILE:HD12	1:C:435:LEU:HD13	1.93	0.49
1:C:457:THR:HG23	1:C:469:PHE:H	1.77	0.49
1:C:480:ASN:ND2	1:C:483:GLY:HA2	2.26	0.49
1:C:637:PRO:O	1:C:640:LYS:HG3	2.12	0.49
1:D:192:PHE:O	1:D:196:ILE:HG13	2.13	0.49
1:D:234:LEU:HD23	1:D:234:LEU:N	2.27	0.49
1:E:191:GLU:O	1:E:193:LEU:N	2.45	0.49
1:E:225:ILE:HG12	1:E:229:PHE:HD2	1.77	0.49
1:E:504:ILE:HD12	1:E:504:ILE:H	1.76	0.49
1:E:690:LYS:O	1:E:691:LYS:C	2.51	0.49
1:E:711:ILE:O	1:E:712:PHE:HD2	1.95	0.49
1:F:249:PHE:O	1:F:250:ALA:C	2.51	0.49
1:F:379:ALA:O	1:F:383:GLY:N	2.44	0.49
1:F:523:LEU:HD11	2:T:144:MET:CG	2.42	0.49
1:F:579:THR:C	1:F:581:GLN:H	2.15	0.49
1:F:767:GLN:HG2	1:F:768:LYS:N	2.28	0.49
2:Q:129:ASP:OD2	2:Q:140:GLU:OE2	2.31	0.49
1:A:176:GLY:C	1:A:178:SER:N	2.64	0.49
1:A:234:LEU:N	1:A:234:LEU:HD23	2.27	0.49
1:A:172:GLU:HG3	1:A:245:PHE:HE1	1.78	0.49
1:A:579:THR:C	1:A:581:GLN:H	2.16	0.49
1:B:155:ASN:C	1:B:156:ILE:HD12	2.33	0.49
1:B:697:ILE:CD1	1:B:732:ILE:CD1	2.90	0.49
1:C:432:TYR:HE1	1:C:445:ARG:CZ	2.25	0.49
1:D:197:LYS:C	1:D:197:LYS:HZ3	2.15	0.49
1:D:755:ARG:O	1:D:756:ILE:C	2.50	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:89:ILE:HG22	1:D:90:PRO:HD2	1.94	0.49
1:E:188:LEU:HD12	1:E:191:GLU:HG3	1.94	0.49
1:E:279:ILE:HG22	1:E:283:LEU:HD11	1.93	0.49
1:F:197:LYS:C	1:F:197:LYS:HZ3	2.16	0.49
1:F:387:ASN:O	1:F:390:SER:HB2	2.12	0.49
2:O:117:THR:C	2:O:119:GLU:N	2.66	0.49
2:Q:88:ALA:O	2:Q:91:VAL:HB	2.13	0.49
2:S:100:ILE:HB	2:S:136:VAL:HG22	1.93	0.49
2:S:104:GLU:HA	2:S:107:HIS:HB3	1.94	0.49
2:T:28:THR:OG1	2:T:29:THR:N	2.44	0.49
1:B:379:ALA:O	1:B:383:GLY:N	2.45	0.49
1:C:518:ASN:ND2	1:C:518:ASN:N	2.61	0.49
1:C:671:ARG:HG3	1:C:671:ARG:HH11	1.78	0.49
1:D:192:PHE:HD1	1:D:192:PHE:H	1.61	0.49
1:D:263:ASP:O	1:D:266:GLU:N	2.45	0.49
1:D:432:TYR:HE1	1:D:445:ARG:CZ	2.26	0.49
1:D:767:GLN:HG2	1:D:768:LYS:N	2.28	0.49
1:E:254:ARG:CD	1:E:254:ARG:H	2.19	0.49
1:E:381:GLU:O	1:E:385:LEU:HD23	2.13	0.49
1:E:405:LEU:HD13	1:E:453:VAL:CG2	2.41	0.49
1:E:692:GLU:OE2	1:E:692:GLU:HA	2.13	0.49
1:E:731:GLU:HA	1:E:734:ASN:HB2	1.95	0.49
1:E:767:GLN:HG2	1:E:768:LYS:N	2.27	0.49
1:F:122:GLU:HG3	1:F:147:ARG:H	1.77	0.49
1:F:633:ASN:O	1:F:642:TYR:CE1	2.65	0.49
1:F:724:ARG:HA	1:F:727:GLN:HG3	1.93	0.49
1:F:697:ILE:HG23	1:F:732:ILE:HD11	1.94	0.49
2:O:41:GLN:O	2:O:43:PRO:HD2	2.11	0.49
2:O:79:THR:C	2:O:81:SER:N	2.60	0.49
2:P:66:PRO:C	2:P:68:PHE:H	2.15	0.49
1:D:692:GLU:CD	2:R:21:LYS:HZ1	2.15	0.49
2:S:117:THR:O	2:S:119:GLU:N	2.46	0.49
1:A:180:ASP:HA	1:A:183:SER:CB	2.43	0.49
1:A:700:TYR:CD1	1:A:728:ALA:N	2.77	0.49
1:B:182:ILE:HA	1:B:187:SER:HA	1.94	0.49
1:B:776:LEU:HD23	1:B:776:LEU:C	2.31	0.49
1:C:217:LYS:HB3	1:C:217:LYS:HZ2	1.77	0.49
1:C:353:LYS:H	1:C:368:GLN:NE2	2.06	0.49
1:C:76:LEU:O	1:C:77:ASP:C	2.51	0.49
1:D:311:HIS:HE1	1:D:339:ILE:HG22	1.78	0.49
1:D:666:ASN:HB2	1:D:748:TYR:OH	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:192:PHE:HD1	1:E:192:PHE:H	1.61	0.49
1:E:495:PHE:CD1	1:E:495:PHE:C	2.86	0.49
1:E:666:ASN:HB2	1:E:748:TYR:OH	2.12	0.49
1:E:755:ARG:O	1:E:756:ILE:C	2.51	0.49
1:E:99:GLU:C	1:E:101:GLY:N	2.66	0.49
1:F:217:LYS:HZ2	1:F:236:GLU:HB2	1.78	0.49
1:F:172:GLU:HG3	1:F:245:PHE:HE1	1.78	0.49
1:F:626:TYR:CD2	1:F:627:TYR:N	2.81	0.49
1:F:629:ASN:ND2	1:F:631:SER:CB	2.73	0.49
2:Q:66:PRO:C	2:Q:68:PHE:H	2.15	0.49
2:R:92:PHE:H	2:R:92:PHE:HD1	1.61	0.49
2:S:63:ILE:CG2	2:S:67:GLU:HB2	2.42	0.49
1:A:197:LYS:HD3	1:A:263:ASP:HB3	1.94	0.49
1:A:410:ILE:HD11	1:A:435:LEU:HD11	1.94	0.49
1:B:710:HIS:O	1:B:712:PHE:N	2.46	0.49
1:C:252:ASP:CG	1:C:253:HIS:H	2.15	0.49
1:C:493:ASP:OD2	1:C:577:HIS:CE1	2.66	0.49
1:C:731:GLU:HA	1:C:734:ASN:HB2	1.95	0.49
1:C:90:PRO:HD3	1:C:249:PHE:CE2	2.48	0.49
1:D:104:ILE:HG23	1:D:152:LEU:CD2	2.43	0.49
1:D:155:ASN:C	1:D:156:ILE:HD12	2.33	0.49
1:D:270:LYS:HA	1:D:273:LYS:HG3	1.95	0.49
1:D:456:LYS:HB2	1:D:469:PHE:O	2.13	0.49
1:E:353:LYS:H	1:E:368:GLN:NE2	2.04	0.49
1:E:379:ALA:O	1:E:383:GLY:N	2.44	0.49
1:E:446:ILE:HG13	1:E:451:ASN:O	2.13	0.49
1:E:700:TYR:CD1	1:E:728:ALA:N	2.78	0.49
1:F:131:ARG:HB2	1:F:243:LEU:HD21	1.94	0.49
1:F:381:GLU:O	1:F:385:LEU:HD23	2.13	0.49
1:F:530:THR:O	1:F:534:ILE:HG13	2.13	0.49
1:F:755:ARG:O	1:F:756:ILE:C	2.52	0.49
1:A:505:LYS:HD3	2:O:112:LEU:O	2.13	0.49
2:O:28:THR:OG1	2:O:29:THR:N	2.44	0.49
2:O:50:ASP:CA	2:O:53:ASN:HB3	2.31	0.49
2:O:68:PHE:O	2:O:70:THR:N	2.46	0.49
1:B:505:LYS:HD3	2:P:112:LEU:O	2.13	0.49
2:Q:106:ARG:HG3	2:Q:106:ARG:HH21	1.78	0.49
1:E:513:TRP:CH2	2:S:114:GLU:HB2	2.48	0.49
1:A:493:ASP:OD2	1:A:577:HIS:CE1	2.65	0.48
1:B:518:ASN:N	1:B:518:ASN:ND2	2.61	0.48
1:B:700:TYR:CD1	1:B:728:ALA:N	2.77	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:100:LEU:HD22	1:C:182:ILE:HG21	1.95	0.48
1:C:401:ILE:HG21	1:C:485:LEU:HB3	1.95	0.48
1:C:554:LYS:O	1:C:557:LEU:N	2.46	0.48
1:C:629:ASN:ND2	1:C:631:SER:CB	2.74	0.48
1:D:122:GLU:HG3	1:D:147:ARG:H	1.77	0.48
1:D:279:ILE:HG22	1:D:283:LEU:HD11	1.93	0.48
1:D:493:ASP:OD2	1:D:577:HIS:CE1	2.66	0.48
1:D:639:ASN:ND2	1:D:639:ASN:N	2.50	0.48
1:D:731:GLU:HA	1:D:734:ASN:HB2	1.95	0.48
1:E:100:LEU:HD22	1:E:182:ILE:HG21	1.94	0.48
1:E:318:ILE:N	1:E:318:ILE:HD12	2.27	0.48
1:E:432:TYR:CE1	1:E:445:ARG:CZ	2.96	0.48
1:E:671:ARG:HG3	1:E:671:ARG:HH11	1.78	0.48
1:F:182:ILE:HA	1:F:187:SER:HA	1.95	0.48
1:F:597:ASN:HD22	1:F:603:ILE:HD11	1.78	0.48
2:P:52:ILE:HD13	2:P:63:ILE:HD11	1.94	0.48
2:Q:52:ILE:HD13	2:Q:63:ILE:HD11	1.94	0.48
2:R:117:THR:C	2:R:119:GLU:N	2.65	0.48
2:R:52:ILE:HD13	2:R:63:ILE:HD11	1.94	0.48
2:T:129:ASP:OD2	2:T:140:GLU:OE2	2.31	0.48
2:T:52:ILE:HD13	2:T:63:ILE:HD11	1.93	0.48
2:T:88:ALA:O	2:T:91:VAL:HB	2.13	0.48
1:A:172:GLU:CB	1:A:246:SER:HA	2.44	0.48
1:A:322:LEU:HA	1:A:503:GLU:OE2	2.14	0.48
1:B:171:TYR:CD1	1:B:175:LYS:NZ	2.81	0.48
1:B:311:HIS:HE1	1:B:339:ILE:HG22	1.78	0.48
1:B:318:ILE:N	1:B:318:ILE:HD12	2.27	0.48
1:B:410:ILE:HD11	1:B:435:LEU:HD11	1.94	0.48
1:B:432:TYR:CE1	1:B:445:ARG:CZ	2.96	0.48
1:C:767:GLN:HG2	1:C:768:LYS:N	2.28	0.48
1:C:99:GLU:C	1:C:101:GLY:N	2.66	0.48
1:D:142:VAL:CG2	1:D:154:ILE:HD12	2.36	0.48
1:D:171:TYR:HD1	1:D:175:LYS:NZ	2.10	0.48
1:D:197:LYS:HD3	1:D:263:ASP:HB3	1.94	0.48
1:D:318:ILE:N	1:D:318:ILE:HD12	2.27	0.48
1:D:692:GLU:OE2	1:D:692:GLU:HA	2.13	0.48
1:E:279:ILE:HG22	1:E:283:LEU:HD13	1.94	0.48
2:O:129:ASP:OD2	2:O:140:GLU:OE2	2.31	0.48
2:O:66:PRO:C	2:O:68:PHE:H	2.16	0.48
2:P:106:ARG:HG3	2:P:106:ARG:HH21	1.77	0.48
1:B:523:LEU:HD11	2:P:144:MET:CG	2.43	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:P:28:THR:OG1	2:P:29:THR:N	2.44	0.48
2:Q:72:MET:C	2:Q:74:ARG:N	2.66	0.48
2:R:84:GLU:OE2	2:R:84:GLU:N	2.46	0.48
1:A:270:LYS:HA	1:A:273:LYS:HG3	1.95	0.48
1:A:405:LEU:HD13	1:A:453:VAL:CG2	2.43	0.48
1:A:432:TYR:HE1	1:A:445:ARG:CZ	2.26	0.48
1:B:142:VAL:CG2	1:B:154:ILE:HD12	2.37	0.48
1:B:100:LEU:HD22	1:B:182:ILE:HG21	1.94	0.48
1:B:767:GLN:HG2	1:B:768:LYS:N	2.28	0.48
1:C:633:ASN:O	1:C:642:TYR:CE1	2.66	0.48
1:C:732:ILE:HG23	1:C:749:PHE:HD1	1.77	0.48
1:D:102:GLY:CA	1:D:150:PRO:HG2	2.42	0.48
1:D:182:ILE:C	1:D:183:SER:O	2.52	0.48
1:D:732:ILE:HG23	1:D:749:PHE:HD1	1.77	0.48
1:D:90:PRO:HD3	1:D:249:PHE:CE2	2.47	0.48
1:E:102:GLY:CA	1:E:150:PRO:HG2	2.42	0.48
1:F:176:GLY:C	1:F:178:SER:N	2.65	0.48
1:F:182:ILE:C	1:F:183:SER:O	2.50	0.48
1:F:632:TYR:CE2	1:F:643:ILE:HG21	2.47	0.48
2:P:68:PHE:O	2:P:70:THR:N	2.45	0.48
2:Q:12:PHE:O	2:Q:15:ALA:HB3	2.13	0.48
2:S:72:MET:C	2:S:74:ARG:N	2.66	0.48
1:F:527:LYS:HG2	2:T:145:MET:SD	2.54	0.48
2:T:41:GLN:O	2:T:43:PRO:HD2	2.11	0.48
2:T:51:MET:O	2:T:55:VAL:HG12	2.12	0.48
1:A:155:ASN:C	1:A:156:ILE:HD12	2.34	0.48
1:A:131:ARG:HB2	1:A:243:LEU:HD21	1.95	0.48
1:A:81:GLN:OE1	1:A:156:ILE:HG21	2.13	0.48
1:B:351:HIS:HB2	1:B:386:GLU:HG3	1.95	0.48
1:B:660:SER:O	1:B:663:PHE:HB3	2.13	0.48
1:B:736:LEU:HD11	1:B:750:GLN:NE2	2.27	0.48
1:C:188:LEU:HD12	1:C:191:GLU:HG3	1.95	0.48
1:C:359:PRO:HG2	1:C:360:VAL:H	1.78	0.48
1:C:432:TYR:CE1	1:C:445:ARG:CZ	2.96	0.48
1:C:629:ASN:ND2	1:C:631:SER:N	2.62	0.48
1:D:77:ASP:OD1	1:D:159:TYR:HE2	1.96	0.48
1:D:235:THR:O	1:D:238:GLN:HB2	2.14	0.48
1:D:432:TYR:CE1	1:D:445:ARG:CZ	2.96	0.48
1:D:597:ASN:HD22	1:D:603:ILE:HD11	1.77	0.48
1:E:235:THR:O	1:E:238:GLN:HB2	2.14	0.48
1:E:289:GLU:HA	1:E:292:ARG:HG3	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:653:LYS:O	1:E:655:ASN:N	2.46	0.48
1:F:131:ARG:HH11	1:F:131:ARG:HG2	1.78	0.48
2:O:17:SER:OG	2:O:18:LEU:N	2.46	0.48
2:P:111:ASN:C	2:P:113:GLY:H	2.17	0.48
1:C:665:LYS:HE2	2:Q:11:GLU:OE1	2.13	0.48
2:T:117:THR:O	2:T:119:GLU:N	2.47	0.48
1:A:377:GLN:O	1:A:381:GLU:HB2	2.14	0.48
1:A:639:ASN:ND2	1:A:639:ASN:N	2.49	0.48
1:A:633:ASN:O	1:A:642:TYR:CE1	2.67	0.48
1:B:102:GLY:C	1:B:103:GLU:HG3	2.32	0.48
1:B:165:GLN:HG2	1:B:251:PRO:CG	2.40	0.48
1:B:443:GLU:HG3	1:B:458:LYS:HG2	1.96	0.48
1:B:480:ASN:ND2	1:B:481:VAL:N	2.62	0.48
1:B:617:LYS:HZ3	1:B:618:ASN:ND2	2.09	0.48
1:B:719:LYS:HE3	1:B:797:ILE:HD11	1.95	0.48
1:B:97:TYR:OH	1:B:150:PRO:HB2	2.13	0.48
1:C:171:TYR:HD1	1:C:175:LYS:NZ	2.11	0.48
1:C:249:PHE:O	1:C:250:ALA:C	2.52	0.48
1:C:351:HIS:HB2	1:C:386:GLU:HG3	1.95	0.48
1:C:480:ASN:ND2	1:C:481:VAL:N	2.60	0.48
1:E:102:GLY:C	1:E:103:GLU:HG3	2.33	0.48
1:E:660:SER:O	1:E:663:PHE:HB3	2.14	0.48
1:F:432:TYR:CE1	1:F:445:ARG:CZ	2.96	0.48
1:F:513:TRP:CH2	2:T:114:GLU:HB2	2.48	0.48
1:F:76:LEU:O	1:F:77:ASP:C	2.52	0.48
2:O:66:PRO:O	2:O:68:PHE:N	2.45	0.48
2:P:117:THR:O	2:P:119:GLU:N	2.46	0.48
2:P:117:THR:O	2:P:120:GLU:N	2.47	0.48
2:Q:28:THR:OG1	2:Q:29:THR:N	2.44	0.48
2:R:100:ILE:HB	2:R:136:VAL:HG22	1.93	0.48
2:S:32:LEU:O	2:S:32:LEU:HD12	2.13	0.48
1:A:100:LEU:HD22	1:A:182:ILE:HG21	1.95	0.48
1:A:387:ASN:N	1:A:387:ASN:ND2	2.61	0.48
1:A:456:LYS:HB2	1:A:469:PHE:O	2.14	0.48
1:A:456:LYS:HB3	1:A:471:TRP:N	2.29	0.48
1:B:480:ASN:HD22	1:B:481:VAL:N	2.11	0.48
1:C:235:THR:O	1:C:238:GLN:HB2	2.13	0.48
1:E:456:LYS:HB3	1:E:471:TRP:N	2.29	0.48
1:E:76:LEU:O	1:E:77:ASP:C	2.52	0.48
2:P:84:GLU:N	2:P:84:GLU:OE2	2.46	0.48
2:Q:19:PHE:CD1	2:Q:19:PHE:N	2.75	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:68:PHE:O	2:Q:70:THR:N	2.46	0.48
2:Q:84:GLU:OE2	2:Q:84:GLU:N	2.44	0.48
2:R:19:PHE:CD1	2:R:19:PHE:N	2.75	0.48
2:R:56:ASP:C	2:R:58:ASP:H	2.15	0.48
2:S:17:SER:OG	2:S:18:LEU:N	2.45	0.48
1:A:597:ASN:HD22	1:A:603:ILE:HD11	1.79	0.48
1:A:90:PRO:HD3	1:A:249:PHE:CE2	2.48	0.48
1:B:697:ILE:HG23	1:B:732:ILE:HD11	1.94	0.48
1:B:99:GLU:C	1:B:101:GLY:N	2.67	0.48
1:C:131:ARG:HG3	1:C:243:LEU:HD13	1.95	0.48
1:C:523:LEU:HD11	2:Q:144:MET:CG	2.44	0.48
1:C:711:ILE:O	1:C:712:PHE:HD2	1.96	0.48
1:D:456:LYS:HB3	1:D:471:TRP:N	2.28	0.48
1:E:116:GLU:HG3	1:E:117:LEU:CD2	2.44	0.48
1:E:164:GLU:O	1:E:167:LYS:HG2	2.13	0.48
1:E:401:ILE:HG21	1:E:485:LEU:HB3	1.96	0.48
1:F:155:ASN:C	1:F:156:ILE:HD12	2.34	0.48
1:F:270:LYS:HA	1:F:273:LYS:HG3	1.96	0.48
1:F:493:ASP:OD2	1:F:577:HIS:CE1	2.67	0.48
1:F:322:LEU:HA	1:F:503:GLU:OE2	2.14	0.48
1:F:517:VAL:HB	1:F:525:LYS:NZ	2.29	0.48
1:F:665:LYS:HE2	2:T:11:GLU:OE1	2.13	0.48
2:P:126:ARG:HH21	2:P:126:ARG:HG3	1.79	0.48
1:A:249:PHE:O	1:A:250:ALA:C	2.51	0.48
1:A:252:ASP:OD2	1:A:253:HIS:CD2	2.67	0.48
1:A:263:ASP:O	1:A:266:GLU:N	2.46	0.48
1:A:381:GLU:O	1:A:385:LEU:HD23	2.13	0.48
1:A:432:TYR:CE1	1:A:445:ARG:CZ	2.97	0.48
1:A:658:PRO:HB3	1:A:755:ARG:NH1	2.28	0.48
1:A:71:PHE:HB2	1:A:108:ASP:HB2	1.96	0.48
1:B:116:GLU:HG3	1:B:117:LEU:CD2	2.44	0.48
1:B:173:ILE:O	1:B:175:LYS:N	2.47	0.48
1:C:97:TYR:OH	1:C:150:PRO:HB2	2.14	0.48
1:C:298:GLY:O	1:C:300:LYS:N	2.47	0.48
1:C:381:GLU:O	1:C:385:LEU:HD23	2.14	0.48
1:C:517:VAL:HB	1:C:525:LYS:HZ1	1.79	0.48
1:C:597:ASN:HD22	1:C:603:ILE:HD11	1.78	0.48
1:D:249:PHE:O	1:D:250:ALA:C	2.51	0.48
1:D:335:ALA:CB	1:D:489:THR:OG1	2.61	0.48
1:D:697:ILE:HG23	1:D:732:ILE:HD11	1.96	0.48
1:E:131:ARG:HG2	1:E:131:ARG:HH11	1.79	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:345:THR:HG22	1:E:490:ALA:O	2.14	0.48
1:E:736:LEU:HD11	1:E:750:GLN:NE2	2.29	0.48
1:F:254:ARG:CD	1:F:254:ARG:H	2.20	0.48
1:F:456:LYS:HB3	1:F:471:TRP:N	2.28	0.48
1:F:637:PRO:O	1:F:640:LYS:HG3	2.12	0.48
2:Q:117:THR:O	2:Q:119:GLU:N	2.47	0.48
2:R:12:PHE:O	2:R:15:ALA:HB3	2.14	0.48
1:A:302:LEU:HD13	1:A:602:PHE:CE1	2.49	0.48
1:A:353:LYS:H	1:A:368:GLN:NE2	2.06	0.48
1:A:509:PRO:HG2	1:A:512:GLU:HG3	1.95	0.48
1:A:561:ASN:C	1:A:563:ALA:N	2.67	0.48
1:A:626:TYR:CD2	1:A:627:TYR:N	2.82	0.48
1:B:182:ILE:C	1:B:183:SER:O	2.50	0.48
1:B:180:ASP:HA	1:B:183:SER:CB	2.44	0.48
1:B:381:GLU:O	1:B:385:LEU:HD23	2.14	0.48
1:B:71:PHE:O	1:B:78:LYS:NZ	2.47	0.48
1:C:254:ARG:NH1	1:C:254:ARG:HB3	2.23	0.48
1:C:529:VAL:O	1:C:532:LEU:HB2	2.13	0.48
1:C:561:ASN:C	1:C:563:ALA:N	2.67	0.48
1:C:648:PRO:HD2	2:Q:90:ARG:HD3	1.95	0.48
1:C:736:LEU:HD11	1:C:750:GLN:NE2	2.29	0.48
1:C:658:PRO:HG3	1:C:752:LEU:CD2	2.40	0.48
1:D:252:ASP:OD2	1:D:253:HIS:CD2	2.67	0.48
1:D:401:ILE:HG21	1:D:485:LEU:HB3	1.96	0.48
1:D:719:LYS:HE3	1:D:797:ILE:HD11	1.95	0.48
1:E:579:THR:C	1:E:581:GLN:N	2.67	0.48
1:F:192:PHE:HD1	1:F:192:PHE:H	1.62	0.48
1:F:351:HIS:HB2	1:F:386:GLU:HG3	1.96	0.48
1:F:660:SER:O	1:F:663:PHE:HB3	2.14	0.48
1:F:690:LYS:O	1:F:691:LYS:C	2.52	0.48
1:F:711:ILE:O	1:F:712:PHE:HD2	1.96	0.48
2:P:72:MET:C	2:P:74:ARG:N	2.66	0.48
1:F:505:LYS:HD3	2:T:112:LEU:O	2.13	0.48
2:T:111:ASN:C	2:T:113:GLY:H	2.17	0.48
2:T:19:PHE:N	2:T:19:PHE:CD1	2.74	0.48
1:B:192:PHE:O	1:B:196:ILE:HG13	2.14	0.48
1:B:446:ILE:HG13	1:B:451:ASN:O	2.13	0.48
1:B:456:LYS:HB3	1:B:471:TRP:N	2.28	0.48
1:C:172:GLU:CB	1:C:246:SER:HA	2.44	0.48
1:C:357:TRP:HZ3	1:C:439:ASN:CB	2.24	0.48
1:C:692:GLU:HA	1:C:692:GLU:OE2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:446:ILE:HG13	1:D:451:ASN:O	2.14	0.48
1:D:456:LYS:HD3	1:D:471:TRP:CG	2.49	0.48
1:D:565:LYS:C	1:D:567:THR:H	2.17	0.48
1:D:629:ASN:ND2	1:D:631:SER:CB	2.73	0.48
1:D:736:LEU:HD11	1:D:750:GLN:NE2	2.28	0.48
1:E:529:VAL:O	1:E:532:LEU:HB2	2.14	0.48
1:E:629:ASN:ND2	1:E:631:SER:CB	2.71	0.48
1:F:517:VAL:HB	1:F:525:LYS:HZ1	1.78	0.48
1:F:99:GLU:C	1:F:101:GLY:N	2.67	0.48
2:O:111:ASN:C	2:O:113:GLY:H	2.17	0.48
2:O:117:THR:O	2:O:120:GLU:N	2.47	0.48
2:P:117:THR:C	2:P:119:GLU:N	2.65	0.48
1:C:513:TRP:CH2	2:Q:114:GLU:HB2	2.49	0.48
2:S:129:ASP:OD2	2:S:140:GLU:OE2	2.32	0.48
2:T:106:ARG:HG3	2:T:106:ARG:HH21	1.79	0.48
1:A:666:ASN:HB2	1:A:748:TYR:OH	2.13	0.47
1:A:736:LEU:HD11	1:A:750:GLN:NE2	2.28	0.47
1:A:755:ARG:O	1:A:756:ILE:C	2.51	0.47
1:C:192:PHE:O	1:C:196:ILE:HG13	2.14	0.47
1:C:297:LYS:HG2	1:C:603:ILE:HG12	1.95	0.47
1:C:405:LEU:HD13	1:C:453:VAL:CG2	2.43	0.47
1:D:105:TYR:HE1	1:D:151:LYS:NZ	2.12	0.47
1:D:405:LEU:HD13	1:D:453:VAL:CG2	2.43	0.47
1:E:155:ASN:C	1:E:156:ILE:HD12	2.34	0.47
1:E:718:ARG:HH12	1:E:767:GLN:HE21	1.62	0.47
1:F:164:GLU:O	1:F:167:LYS:HG2	2.14	0.47
1:F:180:ASP:HA	1:F:183:SER:CB	2.44	0.47
1:F:252:ASP:OD2	1:F:253:HIS:CD2	2.67	0.47
1:F:456:LYS:HB2	1:F:469:PHE:O	2.14	0.47
1:F:480:ASN:ND2	1:F:481:VAL:N	2.62	0.47
1:F:518:ASN:ND2	1:F:518:ASN:N	2.61	0.47
1:B:529:VAL:HG21	2:P:109:MET:HE1	1.94	0.47
2:P:17:SER:OG	2:P:18:LEU:N	2.46	0.47
1:A:345:THR:HG22	1:A:490:ALA:O	2.14	0.47
1:A:711:ILE:O	1:A:712:PHE:HD2	1.96	0.47
1:B:90:PRO:HD3	1:B:249:PHE:CE2	2.50	0.47
1:B:301:ALA:O	1:B:304:ALA:N	2.43	0.47
1:B:387:ASN:ND2	1:B:387:ASN:N	2.62	0.47
1:B:322:LEU:HA	1:B:503:GLU:OE2	2.14	0.47
1:B:561:ASN:C	1:B:563:ALA:N	2.67	0.47
1:C:579:THR:C	1:C:581:GLN:H	2.16	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:254:ARG:NH1	1:D:254:ARG:HB3	2.22	0.47
1:D:297:LYS:HG2	1:D:603:ILE:HG12	1.95	0.47
1:D:633:ASN:O	1:D:642:TYR:CE1	2.67	0.47
1:D:671:ARG:HH11	1:D:671:ARG:HG3	1.79	0.47
1:D:76:LEU:O	1:D:77:ASP:C	2.52	0.47
1:E:351:HIS:HB2	1:E:386:GLU:HG3	1.95	0.47
1:F:170:TYR:O	1:F:174:GLY:N	2.47	0.47
1:F:172:GLU:CB	1:F:246:SER:HA	2.44	0.47
1:F:297:LYS:HG2	1:F:603:ILE:HG12	1.95	0.47
1:F:298:GLY:O	1:F:300:LYS:N	2.47	0.47
1:F:443:GLU:HG3	1:F:458:LYS:HG2	1.96	0.47
1:F:719:LYS:HE3	1:F:797:ILE:HD11	1.95	0.47
2:O:117:THR:O	2:O:119:GLU:N	2.47	0.47
1:B:513:TRP:CH2	2:P:114:GLU:HB2	2.49	0.47
2:T:72:MET:C	2:T:74:ARG:N	2.67	0.47
1:A:351:HIS:HB2	1:A:386:GLU:HG3	1.95	0.47
1:A:700:TYR:CD1	1:A:728:ALA:HA	2.48	0.47
1:B:405:LEU:HD13	1:B:453:VAL:CG2	2.43	0.47
1:C:302:LEU:HD13	1:C:602:PHE:CE1	2.49	0.47
1:D:116:GLU:HG3	1:D:117:LEU:CD2	2.44	0.47
1:D:172:GLU:CB	1:D:246:SER:HA	2.45	0.47
1:D:357:TRP:HZ3	1:D:439:ASN:CB	2.23	0.47
1:D:480:ASN:HD22	1:D:481:VAL:N	2.12	0.47
1:D:579:THR:C	1:D:581:GLN:H	2.17	0.47
1:E:628:PHE:CE2	2:S:90:ARG:CZ	2.96	0.47
1:F:658:PRO:HG3	1:F:752:LEU:CD2	2.40	0.47
1:F:687:GLU:O	1:F:690:LYS:HB2	2.15	0.47
2:O:28:THR:HG23	2:O:31:GLU:CD	2.34	0.47
2:R:41:GLN:O	2:R:43:PRO:HD2	2.13	0.47
2:S:28:THR:HG23	2:S:31:GLU:CD	2.34	0.47
2:S:41:GLN:O	2:S:43:PRO:HD2	2.12	0.47
1:A:171:TYR:CD1	1:A:175:LYS:NZ	2.83	0.47
1:A:379:ALA:O	1:A:383:GLY:N	2.45	0.47
1:A:643:ILE:HG22	1:A:644:GLU:N	2.29	0.47
1:B:185:ASP:O	1:B:190:PRO:HA	2.14	0.47
1:B:197:LYS:HD3	1:B:263:ASP:HB3	1.95	0.47
1:B:357:TRP:CZ3	1:B:439:ASN:ND2	2.83	0.47
1:B:495:PHE:CD1	1:B:495:PHE:C	2.87	0.47
1:C:335:ALA:CB	1:C:489:THR:OG1	2.61	0.47
1:D:665:LYS:HE2	2:R:11:GLU:OE1	2.14	0.47
1:E:308:VAL:CG2	1:E:336:THR:O	2.62	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:432:TYR:HD1	1:E:445:ARG:HD2	1.78	0.47
1:E:456:LYS:HB2	1:E:469:PHE:O	2.14	0.47
1:E:597:ASN:HD22	1:E:603:ILE:HD11	1.80	0.47
1:E:658:PRO:HG3	1:E:752:LEU:CD2	2.39	0.47
1:E:697:ILE:HG23	1:E:732:ILE:HD11	1.94	0.47
1:E:79:ILE:C	1:E:81:GLN:N	2.68	0.47
1:F:254:ARG:NH1	1:F:254:ARG:HB3	2.20	0.47
1:F:279:ILE:HG22	1:F:283:LEU:HD11	1.96	0.47
1:F:357:TRP:HZ3	1:F:439:ASN:CB	2.23	0.47
1:F:432:TYR:HD1	1:F:445:ARG:HD2	1.79	0.47
1:F:542:PRO:HA	1:F:548:THR:HG23	1.97	0.47
2:P:12:PHE:HB3	2:P:68:PHE:CE2	2.50	0.47
2:Q:100:ILE:HB	2:Q:136:VAL:HG22	1.95	0.47
2:S:117:THR:HG23	2:S:120:GLU:CB	2.44	0.47
1:A:173:ILE:O	1:A:175:LYS:N	2.47	0.47
1:A:625:LEU:C	1:A:625:LEU:HD12	2.35	0.47
1:B:220:LEU:O	1:B:220:LEU:HG	2.15	0.47
1:B:456:LYS:HB2	1:B:469:PHE:O	2.14	0.47
1:B:666:ASN:HB2	1:B:748:TYR:OH	2.13	0.47
1:B:671:ARG:HG3	1:B:671:ARG:HH11	1.79	0.47
1:C:116:GLU:HG3	1:C:117:LEU:CD2	2.45	0.47
1:C:131:ARG:HH11	1:C:131:ARG:HG2	1.79	0.47
1:C:456:LYS:HB3	1:C:471:TRP:N	2.29	0.47
1:D:351:HIS:HB2	1:D:386:GLU:HG3	1.95	0.47
1:D:540:ARG:HD3	1:D:627:TYR:HH	1.79	0.47
1:E:180:ASP:HA	1:E:183:SER:CB	2.45	0.47
1:E:214:PHE:CB	1:E:218:LEU:HB3	2.39	0.47
1:E:387:ASN:N	1:E:387:ASN:ND2	2.62	0.47
1:E:322:LEU:HA	1:E:503:GLU:OE2	2.14	0.47
1:F:115:LYS:C	1:F:117:LEU:N	2.68	0.47
1:F:235:THR:O	1:F:238:GLN:HB2	2.14	0.47
1:F:456:LYS:HD3	1:F:471:TRP:CG	2.49	0.47
1:F:554:LYS:O	1:F:557:LEU:N	2.47	0.47
1:F:561:ASN:C	1:F:563:ALA:N	2.68	0.47
1:F:710:HIS:O	1:F:712:PHE:N	2.47	0.47
2:O:92:PHE:H	2:O:92:PHE:HD1	1.61	0.47
2:P:16:PHE:O	2:P:17:SER:C	2.52	0.47
2:Q:117:THR:C	2:Q:119:GLU:N	2.66	0.47
2:Q:63:ILE:HG23	2:Q:67:GLU:HB2	1.96	0.47
2:R:28:THR:OG1	2:R:29:THR:N	2.46	0.47
2:T:16:PHE:O	2:T:17:SER:C	2.53	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:GLU:O	1:A:167:LYS:HG2	2.14	0.47
1:A:504:ILE:O	1:A:507:GLN:CB	2.63	0.47
1:A:665:LYS:HE2	2:O:11:GLU:OE1	2.14	0.47
1:A:741:ILE:O	1:A:742:ALA:C	2.53	0.47
1:B:115:LYS:C	1:B:117:LEU:N	2.66	0.47
1:B:173:ILE:HA	1:B:242:SER:HB3	1.96	0.47
1:B:308:VAL:CG2	1:B:336:THR:O	2.62	0.47
1:B:529:VAL:O	1:B:532:LEU:HB2	2.14	0.47
1:B:579:THR:C	1:B:581:GLN:N	2.68	0.47
1:B:692:GLU:HA	1:B:692:GLU:OE2	2.15	0.47
1:C:164:GLU:O	1:C:167:LYS:HG2	2.14	0.47
1:C:254:ARG:H	1:C:254:ARG:CD	2.19	0.47
1:C:263:ASP:O	1:C:265:PHE:N	2.48	0.47
1:D:201:ASP:CA	1:D:210:PHE:HE2	2.27	0.47
1:D:305:SER:HB2	1:D:594:PHE:CE1	2.50	0.47
1:D:332:ASN:OD1	1:D:334:LEU:N	2.45	0.47
1:D:495:PHE:C	1:D:495:PHE:CD1	2.87	0.47
1:E:182:ILE:HA	1:E:187:SER:HA	1.96	0.47
1:F:359:PRO:HG2	1:F:360:VAL:H	1.79	0.47
1:F:387:ASN:N	1:F:387:ASN:ND2	2.62	0.47
1:F:629:ASN:ND2	1:F:631:SER:N	2.63	0.47
2:O:126:ARG:HG3	2:O:126:ARG:HH21	1.79	0.47
2:Q:16:PHE:O	2:Q:17:SER:C	2.52	0.47
2:Q:66:PRO:C	2:Q:68:PHE:N	2.68	0.47
1:D:513:TRP:CH2	2:R:114:GLU:HB2	2.49	0.47
1:E:665:LYS:HE2	2:S:11:GLU:OE1	2.14	0.47
1:A:115:LYS:C	1:A:117:LEU:N	2.67	0.47
1:A:540:ARG:NH1	1:A:627:TYR:CE1	2.82	0.47
1:A:671:ARG:HG3	1:A:671:ARG:HH11	1.80	0.47
1:A:692:GLU:OE2	1:A:692:GLU:HA	2.14	0.47
1:B:131:ARG:HH11	1:B:131:ARG:HG2	1.78	0.47
1:B:172:GLU:CB	1:B:246:SER:HA	2.44	0.47
1:B:201:ASP:CA	1:B:210:PHE:HE2	2.26	0.47
1:B:319:ALA:O	1:B:323:ASN:HA	2.15	0.47
1:B:343:VAL:HG12	1:B:344:ALA:O	2.14	0.47
1:B:755:ARG:O	1:B:756:ILE:C	2.52	0.47
1:C:155:ASN:C	1:C:156:ILE:HD12	2.34	0.47
1:C:710:HIS:O	1:C:712:PHE:N	2.47	0.47
1:D:700:TYR:CD1	1:D:728:ALA:HA	2.48	0.47
1:E:173:ILE:O	1:E:175:LYS:N	2.48	0.47
1:E:400:LYS:HE3	1:E:475:GLU:CD	2.35	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:658:PRO:HB3	1:E:755:ARG:NH1	2.30	0.47
1:E:724:ARG:HG3	1:E:724:ARG:HH11	1.78	0.47
1:F:115:LYS:CB	1:F:118:GLN:CG	2.92	0.47
2:O:106:ARG:HG3	2:O:106:ARG:HH21	1.79	0.47
2:O:12:PHE:O	2:O:15:ALA:HB3	2.15	0.47
2:O:100:ILE:HB	2:O:136:VAL:HG22	1.91	0.47
2:O:69:LEU:HA	2:O:69:LEU:HD23	1.75	0.47
2:P:100:ILE:HB	2:P:136:VAL:HG22	1.92	0.47
2:R:117:THR:O	2:R:119:GLU:N	2.47	0.47
2:R:32:LEU:HD12	2:R:32:LEU:O	2.14	0.47
1:A:710:HIS:O	1:A:712:PHE:N	2.47	0.47
1:B:115:LYS:CE	1:B:116:GLU:HG2	2.45	0.47
1:B:626:TYR:CD2	1:B:627:TYR:N	2.83	0.47
1:B:700:TYR:CD1	1:B:728:ALA:HA	2.48	0.47
1:B:718:ARG:HH12	1:B:767:GLN:HE21	1.62	0.47
1:C:201:ASP:CA	1:C:210:PHE:HE2	2.27	0.47
1:C:344:ALA:HA	1:C:569:TYR:OH	2.14	0.47
1:C:443:GLU:HG3	1:C:458:LYS:HG2	1.96	0.47
1:D:297:LYS:HB3	1:D:297:LYS:HZ3	1.78	0.47
1:D:741:ILE:O	1:D:742:ALA:C	2.53	0.47
1:E:218:LEU:C	1:E:220:LEU:H	2.14	0.47
1:E:302:LEU:HD13	1:E:602:PHE:CE1	2.50	0.47
1:E:700:TYR:CD1	1:E:728:ALA:HA	2.48	0.47
1:E:85:LEU:HD12	1:E:168:GLU:OE1	2.15	0.47
1:F:171:TYR:CD1	1:F:171:TYR:O	2.62	0.47
1:F:446:ILE:HG13	1:F:451:ASN:O	2.15	0.47
1:F:724:ARG:HG3	1:F:724:ARG:HH11	1.79	0.47
2:Q:117:THR:HG23	2:Q:120:GLU:CB	2.44	0.47
2:Q:146:THR:O	2:Q:147:ALA:C	2.53	0.47
2:S:109:MET:HG3	2:S:116:LEU:HD11	1.97	0.47
2:T:66:PRO:C	2:T:68:PHE:N	2.68	0.47
1:A:357:TRP:CZ3	1:A:439:ASN:ND2	2.83	0.47
1:A:513:TRP:CH2	2:O:114:GLU:HB2	2.50	0.47
1:A:90:PRO:O	1:A:93:VAL:N	2.48	0.47
1:B:263:ASP:O	1:B:265:PHE:N	2.48	0.47
1:B:391:ILE:CD1	1:B:399:GLY:HA2	2.44	0.47
1:C:322:LEU:HA	1:C:503:GLU:OE2	2.14	0.47
1:C:66:LEU:HD11	1:C:97:TYR:HD2	1.80	0.47
1:C:679:TYR:CD1	1:C:679:TYR:O	2.67	0.47
1:D:464:VAL:HG23	1:D:465:LEU:N	2.30	0.47
1:E:561:ASN:C	1:E:563:ALA:N	2.66	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:TYR:OH	1:F:150:PRO:HB2	2.15	0.47
1:F:368:GLN:CB	1:F:380:VAL:HG13	2.45	0.47
1:F:529:VAL:O	1:F:532:LEU:HB2	2.13	0.47
1:F:327:LEU:CG	1:F:595:ILE:HG12	2.43	0.47
1:F:66:LEU:HD11	1:F:97:TYR:HD2	1.80	0.47
1:F:692:GLU:HA	1:F:692:GLU:OE2	2.14	0.47
2:P:92:PHE:HD1	2:P:92:PHE:H	1.62	0.47
1:C:527:LYS:HG2	2:Q:145:MET:SD	2.55	0.47
2:Q:28:THR:HG23	2:Q:31:GLU:CD	2.35	0.47
2:Q:92:PHE:HD1	2:Q:92:PHE:H	1.62	0.47
2:R:17:SER:OG	2:R:18:LEU:N	2.47	0.47
1:D:648:PRO:HD2	2:R:90:ARG:HD3	1.97	0.47
2:S:18:LEU:HB3	2:S:19:PHE:CD1	2.50	0.47
2:S:24:ASP:HB2	2:S:26:THR:CG2	2.35	0.47
2:S:92:PHE:HD1	2:S:92:PHE:H	1.62	0.47
1:A:116:GLU:HG3	1:A:117:LEU:CD2	2.45	0.47
1:A:135:VAL:N	1:A:136:PRO:CD	2.78	0.47
1:A:235:THR:O	1:A:238:GLN:HB2	2.14	0.47
1:A:529:VAL:O	1:A:532:LEU:HB2	2.15	0.47
1:A:595:ILE:HG22	1:A:596:ILE:H	1.80	0.47
1:B:164:GLU:O	1:B:167:LYS:HG2	2.15	0.47
1:B:456:LYS:HD3	1:B:471:TRP:CG	2.50	0.47
1:B:66:LEU:HD11	1:B:97:TYR:HD2	1.80	0.47
1:B:76:LEU:O	1:B:77:ASP:C	2.53	0.47
1:C:220:LEU:O	1:C:220:LEU:HG	2.15	0.47
1:C:517:VAL:HB	1:C:525:LYS:NZ	2.30	0.47
1:D:180:ASP:HA	1:D:183:SER:CB	2.45	0.47
1:D:504:ILE:O	1:D:507:GLN:CB	2.63	0.47
1:D:656:THR:HG22	1:D:657:ILE:O	2.15	0.47
1:E:116:GLU:HG3	1:E:117:LEU:HD23	1.96	0.47
1:E:172:GLU:HG3	1:E:245:PHE:HE1	1.79	0.47
1:E:298:GLY:O	1:E:300:LYS:N	2.48	0.47
1:E:450:ASN:HD22	1:E:452:GLU:HG3	1.78	0.47
1:F:391:ILE:CD1	1:F:399:GLY:HA2	2.45	0.47
2:R:111:ASN:C	2:R:113:GLY:H	2.16	0.47
2:R:117:THR:O	2:R:120:GLU:N	2.48	0.47
2:S:111:ASN:C	2:S:113:GLY:H	2.17	0.47
2:S:16:PHE:O	2:S:17:SER:C	2.53	0.47
2:T:18:LEU:HA	2:T:18:LEU:HD23	1.75	0.47
2:T:12:PHE:HB3	2:T:68:PHE:CE2	2.50	0.47
2:T:84:GLU:OE2	2:T:84:GLU:N	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:ILE:HG23	1:A:152:LEU:CD2	2.45	0.47
1:A:170:TYR:O	1:A:174:GLY:N	2.48	0.47
1:B:115:LYS:C	1:B:117:LEU:H	2.18	0.47
1:B:249:PHE:O	1:B:250:ALA:C	2.52	0.47
1:C:197:LYS:HD3	1:C:263:ASP:OD1	2.15	0.47
1:C:456:LYS:HD3	1:C:471:TRP:CG	2.50	0.47
1:D:115:LYS:NZ	1:D:116:GLU:H	1.88	0.47
1:D:225:ILE:HG12	1:D:229:PHE:HD2	1.80	0.47
1:D:289:GLU:HA	1:D:292:ARG:HG3	1.96	0.47
1:D:302:LEU:HD13	1:D:602:PHE:CE1	2.49	0.47
1:D:308:VAL:O	1:D:311:HIS:N	2.46	0.47
1:D:595:ILE:HG22	1:D:596:ILE:H	1.79	0.47
1:D:687:GLU:O	1:D:690:LYS:HB2	2.15	0.47
1:E:377:GLN:O	1:E:381:GLU:HB2	2.15	0.47
1:E:493:ASP:OD2	1:E:577:HIS:HE1	1.98	0.47
1:F:171:TYR:HD1	1:F:175:LYS:HZ1	1.59	0.47
1:F:565:LYS:C	1:F:567:THR:H	2.18	0.47
2:Q:32:LEU:O	2:Q:32:LEU:HD12	2.14	0.47
2:R:28:THR:HG23	2:R:31:GLU:CD	2.34	0.47
2:S:12:PHE:O	2:S:15:ALA:HB3	2.15	0.47
2:S:66:PRO:C	2:S:68:PHE:N	2.68	0.47
1:A:191:GLU:O	1:A:194:ASN:N	2.47	0.46
1:A:197:LYS:HD3	1:A:263:ASP:OD1	2.15	0.46
1:A:565:LYS:C	1:A:567:THR:H	2.17	0.46
1:C:115:LYS:C	1:C:117:LEU:N	2.66	0.46
1:C:225:ILE:HG23	1:C:229:PHE:HD2	1.80	0.46
1:D:131:ARG:HH11	1:D:131:ARG:HG2	1.79	0.46
1:D:135:VAL:N	1:D:136:PRO:CD	2.78	0.46
1:D:164:GLU:O	1:D:167:LYS:HG2	2.15	0.46
1:D:636:ALA:O	1:D:640:LYS:CA	2.63	0.46
1:D:660:SER:O	1:D:663:PHE:HB3	2.15	0.46
1:E:625:LEU:C	1:E:625:LEU:HD12	2.35	0.46
1:F:453:VAL:HG12	1:F:454:GLN:N	2.30	0.46
1:F:700:TYR:CD1	1:F:728:ALA:HA	2.47	0.46
2:P:28:THR:HG23	2:P:31:GLU:CD	2.36	0.46
2:R:129:ASP:OD2	2:R:140:GLU:OE2	2.33	0.46
2:R:12:PHE:HB3	2:R:68:PHE:CE2	2.49	0.46
2:S:89:PHE:HB2	2:S:141:PHE:CD2	2.50	0.46
1:A:165:GLN:C	1:A:167:LYS:N	2.68	0.46
1:A:220:LEU:HG	1:A:220:LEU:O	2.15	0.46
1:A:446:ILE:HG13	1:A:451:ASN:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:480:ASN:ND2	1:A:481:VAL:N	2.63	0.46
1:A:493:ASP:OD2	1:A:577:HIS:HE1	1.98	0.46
1:A:656:THR:HG22	1:A:657:ILE:O	2.15	0.46
1:B:252:ASP:OD2	1:B:253:HIS:CD2	2.69	0.46
1:B:289:GLU:HA	1:B:292:ARG:HG3	1.96	0.46
1:B:656:THR:HG22	1:B:657:ILE:O	2.15	0.46
1:B:749:PHE:O	1:B:753:LYS:HG3	2.16	0.46
1:C:135:VAL:N	1:C:136:PRO:CD	2.78	0.46
1:C:122:GLU:HG3	1:C:147:ARG:H	1.78	0.46
1:C:197:LYS:HB3	1:C:197:LYS:NZ	2.19	0.46
1:C:450:ASN:HD22	1:C:452:GLU:HG3	1.80	0.46
1:D:165:GLN:C	1:D:167:LYS:N	2.69	0.46
1:D:188:LEU:HD12	1:D:191:GLU:HG3	1.96	0.46
1:D:197:LYS:HD3	1:D:263:ASP:OD1	2.15	0.46
1:D:298:GLY:O	1:D:300:LYS:N	2.48	0.46
1:E:171:TYR:HD1	1:E:175:LYS:HZ1	1.58	0.46
1:E:297:LYS:HG2	1:E:603:ILE:HG12	1.97	0.46
1:E:66:LEU:HD11	1:E:97:TYR:HD2	1.81	0.46
1:F:560:LEU:O	1:F:563:ALA:HB3	2.15	0.46
1:F:579:THR:C	1:F:581:GLN:N	2.69	0.46
1:F:697:ILE:HG12	1:F:732:ILE:HD13	1.98	0.46
2:P:48:LEU:HD23	2:P:51:MET:HE2	1.95	0.46
2:T:17:SER:OG	2:T:18:LEU:N	2.47	0.46
1:A:131:ARG:HH11	1:A:131:ARG:HG2	1.78	0.46
1:A:456:LYS:HA	1:A:469:PHE:CD1	2.50	0.46
1:A:305:SER:HB2	1:A:594:PHE:CE1	2.50	0.46
1:A:719:LYS:HE3	1:A:797:ILE:HD11	1.97	0.46
1:B:112:VAL:O	1:B:114:HIS:N	2.47	0.46
1:B:377:GLN:O	1:B:381:GLU:HB2	2.15	0.46
1:B:648:PRO:HD2	2:P:90:ARG:HD3	1.96	0.46
1:B:71:PHE:HB2	1:B:108:ASP:HB2	1.97	0.46
1:C:456:LYS:HB2	1:C:469:PHE:O	2.15	0.46
1:C:565:LYS:C	1:C:567:THR:H	2.18	0.46
1:D:182:ILE:HA	1:D:187:SER:HA	1.97	0.46
1:D:381:GLU:O	1:D:385:LEU:HD23	2.15	0.46
1:D:455:TYR:CZ	1:D:469:PHE:CZ	3.04	0.46
1:E:172:GLU:CB	1:E:246:SER:HA	2.45	0.46
1:E:191:GLU:O	1:E:192:PHE:C	2.54	0.46
1:E:308:VAL:O	1:E:311:HIS:N	2.47	0.46
1:E:565:LYS:C	1:E:567:THR:H	2.17	0.46
1:E:629:ASN:ND2	1:E:631:SER:N	2.63	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:741:ILE:O	1:E:742:ALA:C	2.53	0.46
1:E:719:LYS:HE3	1:E:797:ILE:HD11	1.97	0.46
1:F:135:VAL:N	1:F:136:PRO:CD	2.78	0.46
1:F:345:THR:HG22	1:F:490:ALA:O	2.16	0.46
1:F:344:ALA:HA	1:F:569:TYR:OH	2.15	0.46
1:F:619:ILE:O	1:F:620:THR:C	2.53	0.46
1:F:666:ASN:HB2	1:F:748:TYR:OH	2.16	0.46
2:O:63:ILE:HG23	2:O:67:GLU:HB2	1.96	0.46
2:P:63:ILE:HG23	2:P:67:GLU:HB2	1.97	0.46
2:T:92:PHE:HD1	2:T:92:PHE:H	1.62	0.46
1:A:453:VAL:HG12	1:A:454:GLN:N	2.30	0.46
1:A:445:ARG:HD3	1:A:471:TRP:CZ2	2.50	0.46
1:A:344:ALA:HA	1:A:569:TYR:OH	2.16	0.46
1:A:636:ALA:O	1:A:640:LYS:CA	2.64	0.46
1:B:391:ILE:HG12	1:B:399:GLY:HA2	1.98	0.46
1:B:597:ASN:HD22	1:B:603:ILE:HD11	1.81	0.46
1:C:104:ILE:HG23	1:C:152:LEU:CD2	2.45	0.46
1:C:700:TYR:CD1	1:C:728:ALA:HA	2.48	0.46
1:D:100:LEU:HD22	1:D:182:ILE:HG21	1.95	0.46
1:D:214:PHE:CB	1:D:218:LEU:HB3	2.38	0.46
1:D:254:ARG:CD	1:D:254:ARG:H	2.19	0.46
1:D:456:LYS:HA	1:D:469:PHE:CD1	2.50	0.46
1:D:493:ASP:OD2	1:D:577:HIS:HE1	1.99	0.46
1:E:182:ILE:C	1:E:183:SER:O	2.53	0.46
1:E:197:LYS:HB3	1:E:197:LYS:NZ	2.20	0.46
1:E:643:ILE:HG22	1:E:644:GLU:N	2.27	0.46
1:E:722:ILE:HD13	1:E:764:LEU:CD2	2.45	0.46
1:F:173:ILE:O	1:F:175:LYS:N	2.49	0.46
2:O:117:THR:HG23	2:O:120:GLU:CB	2.42	0.46
2:P:13:LYS:C	2:P:15:ALA:N	2.69	0.46
2:P:18:LEU:HB3	2:P:19:PHE:CD1	2.51	0.46
2:P:68:PHE:O	2:P:69:LEU:C	2.54	0.46
2:Q:111:ASN:C	2:Q:113:GLY:H	2.17	0.46
2:Q:126:ARG:HG3	2:Q:126:ARG:HH21	1.79	0.46
2:R:66:PRO:C	2:R:68:PHE:N	2.69	0.46
2:S:126:ARG:HH21	2:S:126:ARG:HG3	1.80	0.46
1:A:201:ASP:CA	1:A:210:PHE:HE2	2.28	0.46
1:A:173:ILE:HA	1:A:242:SER:HB3	1.97	0.46
1:A:298:GLY:O	1:A:300:LYS:N	2.49	0.46
1:A:443:GLU:HG3	1:A:458:LYS:HG2	1.97	0.46
1:A:554:LYS:O	1:A:557:LEU:N	2.49	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:687:GLU:O	1:A:690:LYS:HB2	2.15	0.46
1:A:76:LEU:O	1:A:77:ASP:C	2.54	0.46
1:B:445:ARG:HD3	1:B:471:TRP:CZ2	2.50	0.46
1:B:722:ILE:HD13	1:B:764:LEU:CD2	2.45	0.46
1:C:173:ILE:O	1:C:175:LYS:N	2.48	0.46
1:C:446:ILE:HG13	1:C:451:ASN:O	2.16	0.46
1:C:626:TYR:CD2	1:C:627:TYR:N	2.84	0.46
1:C:724:ARG:HG3	1:C:724:ARG:HH11	1.79	0.46
1:C:762:LEU:O	1:C:766:HIS:HB2	2.16	0.46
1:C:93:VAL:CG1	1:C:94:LEU:N	2.79	0.46
1:D:115:LYS:C	1:D:117:LEU:N	2.67	0.46
1:D:171:TYR:CD1	1:D:175:LYS:NZ	2.84	0.46
1:D:191:GLU:O	1:D:194:ASN:N	2.48	0.46
1:D:357:TRP:CZ3	1:D:439:ASN:ND2	2.83	0.46
1:D:480:ASN:ND2	1:D:481:VAL:N	2.62	0.46
1:D:724:ARG:HG3	1:D:724:ARG:HH11	1.80	0.46
1:E:135:VAL:N	1:E:136:PRO:CD	2.78	0.46
1:E:480:ASN:ND2	1:E:481:VAL:N	2.64	0.46
1:F:199:LEU:C	1:F:201:ASP:N	2.63	0.46
1:F:480:ASN:HD22	1:F:481:VAL:N	2.13	0.46
1:F:480:ASN:ND2	1:F:483:GLY:CA	2.79	0.46
2:Q:12:PHE:HB3	2:Q:68:PHE:CE2	2.50	0.46
2:Q:51:MET:CB	2:Q:71:MET:HE2	2.29	0.46
2:R:9:ILE:CD1	2:R:69:LEU:HD22	2.46	0.46
2:S:45:GLU:N	2:S:45:GLU:CD	2.68	0.46
1:A:400:LYS:HE3	1:A:475:GLU:CD	2.36	0.46
1:A:99:GLU:C	1:A:101:GLY:N	2.67	0.46
1:B:302:LEU:HD13	1:B:602:PHE:CE1	2.51	0.46
1:B:456:LYS:HA	1:B:469:PHE:CD1	2.51	0.46
1:B:400:LYS:HE3	1:B:475:GLU:CD	2.36	0.46
1:B:708:ALA:C	1:B:710:HIS:N	2.69	0.46
1:C:495:PHE:C	1:C:495:PHE:CD1	2.87	0.46
1:D:172:GLU:HG3	1:D:245:PHE:HE1	1.80	0.46
1:D:308:VAL:CG2	1:D:336:THR:O	2.64	0.46
1:D:353:LYS:N	1:D:368:GLN:HE22	2.08	0.46
1:D:71:PHE:CD1	1:D:108:ASP:OD1	2.68	0.46
1:E:288:VAL:CG2	1:E:289:GLU:H	2.22	0.46
1:E:443:GLU:HG3	1:E:458:LYS:HG2	1.96	0.46
1:E:464:VAL:HG23	1:E:465:LEU:N	2.31	0.46
1:E:687:GLU:O	1:E:690:LYS:HB2	2.15	0.46
1:F:201:ASP:CA	1:F:210:PHE:HE2	2.27	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:305:SER:HB2	1:F:594:PHE:CE1	2.51	0.46
1:F:71:PHE:HB2	1:F:108:ASP:HB2	1.97	0.46
2:O:115:LYS:NZ	2:O:115:LYS:CA	2.78	0.46
2:P:117:THR:C	2:P:119:GLU:H	2.19	0.46
1:B:527:LYS:HG2	2:P:145:MET:SD	2.56	0.46
2:P:50:ASP:CA	2:P:53:ASN:HB3	2.31	0.46
2:Q:18:LEU:HB3	2:Q:19:PHE:CD1	2.51	0.46
2:R:108:VAL:O	2:R:112:LEU:HD12	2.16	0.46
2:S:117:THR:O	2:S:120:GLU:N	2.49	0.46
2:T:126:ARG:HG3	2:T:126:ARG:HH21	1.79	0.46
1:B:116:GLU:HG3	1:B:117:LEU:HD23	1.97	0.46
1:B:636:ALA:O	1:B:640:LYS:CA	2.64	0.46
1:C:128:MET:HE1	1:C:235:THR:CB	2.45	0.46
1:D:359:PRO:HG2	1:D:360:VAL:H	1.80	0.46
1:D:443:GLU:HG3	1:D:458:LYS:HG2	1.96	0.46
1:D:619:ILE:O	1:D:620:THR:C	2.54	0.46
1:E:217:LYS:HZ2	1:E:236:GLU:HB2	1.81	0.46
1:E:305:SER:HB2	1:E:594:PHE:CE1	2.51	0.46
1:E:456:LYS:HA	1:E:469:PHE:CD1	2.51	0.46
1:E:530:THR:HG23	2:S:88:ALA:HB1	1.97	0.46
1:F:289:GLU:HA	1:F:292:ARG:HG3	1.97	0.46
1:F:456:LYS:HA	1:F:469:PHE:CD1	2.51	0.46
1:F:445:ARG:HD3	1:F:471:TRP:CZ2	2.50	0.46
1:F:648:PRO:HD2	2:T:90:ARG:HD3	1.96	0.46
1:F:708:ALA:C	1:F:710:HIS:H	2.18	0.46
1:F:76:LEU:O	1:F:80:GLN:N	2.47	0.46
1:A:648:PRO:HD2	2:O:90:ARG:HD3	1.97	0.46
2:T:28:THR:HG23	2:T:31:GLU:CD	2.35	0.46
1:A:131:ARG:HG3	1:A:243:LEU:HD13	1.98	0.46
1:A:142:VAL:CG2	1:A:154:ILE:HD12	2.38	0.46
1:A:214:PHE:CB	1:A:218:LEU:HB3	2.38	0.46
1:A:225:ILE:HG12	1:A:229:PHE:HD2	1.80	0.46
1:A:368:GLN:CB	1:A:380:VAL:HG13	2.46	0.46
1:A:455:TYR:CZ	1:A:469:PHE:CZ	3.04	0.46
1:A:456:LYS:HD3	1:A:471:TRP:CG	2.51	0.46
1:A:530:THR:O	1:A:534:ILE:HG13	2.14	0.46
1:A:697:ILE:HG12	1:A:732:ILE:HD13	1.98	0.46
1:A:722:ILE:HD13	1:A:764:LEU:CD2	2.45	0.46
1:B:235:THR:O	1:B:238:GLN:HB2	2.15	0.46
1:B:629:ASN:ND2	1:B:631:SER:N	2.63	0.46
1:B:792:VAL:O	1:B:796:ILE:HG12	2.16	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:79:ILE:C	1:B:81:GLN:N	2.69	0.46
1:C:270:LYS:HA	1:C:273:LYS:HG3	1.97	0.46
1:C:305:SER:HB2	1:C:594:PHE:CE1	2.51	0.46
1:C:332:ASN:OD1	1:C:334:LEU:HB2	2.16	0.46
1:C:636:ALA:O	1:C:640:LYS:CA	2.64	0.46
1:C:687:GLU:O	1:C:690:LYS:HB2	2.16	0.46
1:C:690:LYS:O	1:C:691:LYS:C	2.54	0.46
1:C:71:PHE:O	1:C:78:LYS:NZ	2.49	0.46
1:D:220:LEU:HG	1:D:220:LEU:O	2.15	0.46
1:D:360:VAL:CG1	1:D:370:LEU:HD22	2.43	0.46
1:D:377:GLN:O	1:D:381:GLU:HB2	2.15	0.46
1:D:432:TYR:HD1	1:D:445:ARG:HD2	1.79	0.46
1:D:66:LEU:HD11	1:D:97:TYR:HD2	1.80	0.46
1:E:115:LYS:C	1:E:117:LEU:N	2.67	0.46
1:E:201:ASP:CA	1:E:210:PHE:HE2	2.27	0.46
1:E:93:VAL:CG1	1:E:94:LEU:N	2.79	0.46
1:F:131:ARG:HG3	1:F:243:LEU:HD13	1.97	0.46
1:F:400:LYS:HE3	1:F:475:GLU:CD	2.36	0.46
1:F:450:ASN:HD22	1:F:452:GLU:HG3	1.80	0.46
1:F:350:VAL:HG21	1:F:488:LEU:HD12	1.98	0.46
1:F:540:ARG:NH1	1:F:627:TYR:CE1	2.83	0.46
1:F:636:ALA:O	1:F:640:LYS:CA	2.64	0.46
1:F:71:PHE:O	1:F:78:LYS:NZ	2.49	0.46
2:Q:17:SER:OG	2:Q:18:LEU:N	2.46	0.46
2:Q:18:LEU:HA	2:Q:18:LEU:HD23	1.75	0.46
2:Q:50:ASP:CA	2:Q:53:ASN:HB3	2.31	0.46
2:R:146:THR:O	2:R:147:ALA:C	2.54	0.46
2:R:63:ILE:HG23	2:R:67:GLU:HB2	1.96	0.46
2:T:117:THR:HG23	2:T:120:GLU:CB	2.43	0.46
1:F:530:THR:HG23	2:T:88:ALA:HB1	1.98	0.46
1:A:718:ARG:HH12	1:A:767:GLN:HE21	1.62	0.46
1:A:794:GLN:HE21	1:A:794:GLN:HB3	1.60	0.46
1:B:344:ALA:HA	1:B:569:TYR:OH	2.16	0.46
1:B:453:VAL:HG12	1:B:454:GLN:N	2.30	0.46
1:C:112:VAL:O	1:C:114:HIS:N	2.49	0.46
1:C:115:LYS:C	1:C:117:LEU:H	2.19	0.46
1:C:165:GLN:C	1:C:167:LYS:N	2.69	0.46
1:C:445:ARG:HD3	1:C:471:TRP:CZ2	2.51	0.46
1:C:504:ILE:H	1:C:504:ILE:CD1	2.29	0.46
1:C:327:LEU:CG	1:C:595:ILE:HG12	2.45	0.46
1:C:741:ILE:O	1:C:742:ALA:C	2.54	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:165:GLN:C	1:F:167:LYS:N	2.69	0.46
1:F:189:ASP:HB3	1:F:190:PRO:HD2	1.98	0.46
1:F:225:ILE:HG23	1:F:229:PHE:HD2	1.81	0.46
1:F:293:ILE:H	1:F:293:ILE:HG12	1.45	0.46
1:F:357:TRP:CZ3	1:F:439:ASN:ND2	2.84	0.46
1:F:79:ILE:C	1:F:81:GLN:N	2.69	0.46
2:O:16:PHE:O	2:O:17:SER:C	2.53	0.46
1:A:630:ARG:NH1	2:O:83:GLU:HG2	2.30	0.46
2:P:32:LEU:HD12	2:P:32:LEU:O	2.16	0.46
2:R:102:ALA:CB	2:R:125:ILE:HG13	2.44	0.46
2:T:146:THR:O	2:T:147:ALA:C	2.53	0.46
2:T:50:ASP:CA	2:T:53:ASN:HB3	2.31	0.46
2:T:63:ILE:HG23	2:T:67:GLU:HB2	1.97	0.46
2:T:9:ILE:CD1	2:T:69:LEU:HD22	2.46	0.46
1:A:424:LYS:O	1:A:425:GLU:OE1	2.34	0.46
1:B:359:PRO:HG2	1:B:360:VAL:H	1.80	0.46
1:B:424:LYS:O	1:B:425:GLU:OE1	2.34	0.46
1:B:432:TYR:HD1	1:B:445:ARG:HD2	1.79	0.46
1:B:741:ILE:O	1:B:742:ALA:C	2.54	0.46
1:C:214:PHE:CB	1:C:218:LEU:HB3	2.38	0.46
1:C:493:ASP:OD2	1:C:577:HIS:HE1	1.99	0.46
1:D:722:ILE:HD13	1:D:764:LEU:CD2	2.46	0.46
1:E:131:ARG:HB2	1:E:243:LEU:HD21	1.97	0.46
1:E:252:ASP:OD2	1:E:253:HIS:CD2	2.69	0.46
1:F:493:ASP:OD2	1:F:577:HIS:HE1	1.99	0.46
1:F:540:ARG:HH22	1:F:630:ARG:HE	1.64	0.46
2:P:66:PRO:C	2:P:68:PHE:N	2.68	0.46
1:C:530:THR:HG23	2:Q:88:ALA:HB1	1.98	0.46
2:R:16:PHE:O	2:R:17:SER:C	2.54	0.46
1:E:692:GLU:CD	2:S:21:LYS:HZ1	2.15	0.46
1:F:692:GLU:CD	2:T:21:LYS:HZ1	2.18	0.46
1:A:225:ILE:HG23	1:A:229:PHE:HD2	1.81	0.45
1:A:391:ILE:CD1	1:A:399:GLY:HA2	2.46	0.45
1:B:135:VAL:N	1:B:136:PRO:CD	2.78	0.45
1:B:298:GLY:O	1:B:300:LYS:N	2.49	0.45
1:B:304:ALA:HB3	1:B:604:LEU:HD22	1.98	0.45
1:C:456:LYS:HA	1:C:469:PHE:CD1	2.51	0.45
1:C:497:LEU:HD13	1:C:556:MET:HG2	1.99	0.45
1:D:332:ASN:OD1	1:D:334:LEU:HB2	2.16	0.45
1:D:445:ARG:HD3	1:D:471:TRP:CZ2	2.51	0.45
1:E:104:ILE:HG23	1:E:152:LEU:CD2	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:217:LYS:HB3	1:E:217:LYS:HZ2	1.81	0.45
1:E:319:ALA:O	1:E:323:ASN:HA	2.16	0.45
1:E:629:ASN:O	1:E:631:SER:N	2.49	0.45
1:E:71:PHE:HB2	1:E:108:ASP:HB2	1.97	0.45
1:E:765:THR:HA	1:E:769:SER:CB	2.21	0.45
1:F:116:GLU:HG3	1:F:117:LEU:CD2	2.46	0.45
1:F:302:LEU:HD13	1:F:602:PHE:CE1	2.51	0.45
1:F:377:GLN:O	1:F:381:GLU:HB2	2.15	0.45
2:O:66:PRO:C	2:O:68:PHE:N	2.69	0.45
2:O:12:PHE:HB3	2:O:68:PHE:CE2	2.50	0.45
1:A:530:THR:HG23	2:O:88:ALA:HB1	1.98	0.45
1:D:530:THR:HG23	2:R:88:ALA:HB1	1.98	0.45
2:S:12:PHE:HB3	2:S:68:PHE:CE2	2.51	0.45
1:A:359:PRO:HG2	1:A:360:VAL:H	1.81	0.45
1:B:542:PRO:HA	1:B:548:THR:HG23	1.98	0.45
1:B:629:ASN:O	1:B:631:SER:N	2.49	0.45
1:B:665:LYS:HE2	2:P:11:GLU:OE1	2.16	0.45
1:C:182:ILE:C	1:C:183:SER:O	2.53	0.45
1:C:464:VAL:HG23	1:C:465:LEU:N	2.30	0.45
1:D:170:TYR:O	1:D:174:GLY:HA3	2.17	0.45
1:D:285:LYS:O	1:D:288:VAL:HG22	2.16	0.45
1:D:504:ILE:CD1	1:D:504:ILE:H	2.29	0.45
1:D:540:ARG:NH1	1:D:627:TYR:CE1	2.84	0.45
1:D:690:LYS:O	1:D:691:LYS:C	2.52	0.45
1:D:656:THR:O	1:D:755:ARG:HD2	2.16	0.45
1:D:76:LEU:O	1:D:80:GLN:N	2.47	0.45
1:E:217:LYS:HB2	1:E:236:GLU:HG3	1.99	0.45
1:E:480:ASN:HD22	1:E:481:VAL:N	2.14	0.45
1:E:508:ILE:HG21	1:E:513:TRP:HB2	1.98	0.45
1:F:171:TYR:CD1	1:F:175:LYS:NZ	2.83	0.45
1:F:225:ILE:HG12	1:F:229:PHE:HD2	1.80	0.45
1:F:360:VAL:CG1	1:F:370:LEU:HD22	2.43	0.45
1:F:455:TYR:CZ	1:F:469:PHE:CZ	3.05	0.45
1:F:327:LEU:CD2	1:F:595:ILE:HG12	2.47	0.45
1:F:718:ARG:HH12	1:F:767:GLN:HE21	1.64	0.45
1:F:93:VAL:CG1	1:F:94:LEU:N	2.80	0.45
2:O:109:MET:HG3	2:O:116:LEU:HD11	1.98	0.45
2:P:117:THR:HG23	2:P:120:GLU:CB	2.44	0.45
2:Q:117:THR:O	2:Q:120:GLU:N	2.48	0.45
2:T:117:THR:C	2:T:119:GLU:H	2.19	0.45
1:A:295:VAL:C	1:A:296:LEU:CD2	2.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:170:TYR:O	1:B:174:GLY:HA3	2.16	0.45
1:B:197:LYS:HD3	1:B:263:ASP:OD1	2.16	0.45
1:C:97:TYR:HA	1:C:100:LEU:HD12	1.99	0.45
1:C:180:ASP:HA	1:C:183:SER:CB	2.46	0.45
1:C:179:LEU:CG	1:C:180:ASP:N	2.79	0.45
1:C:504:ILE:O	1:C:507:GLN:CB	2.63	0.45
1:C:706:ASN:OD1	1:C:707:SER:N	2.49	0.45
1:C:656:THR:O	1:C:755:ARG:HD2	2.16	0.45
1:D:387:ASN:N	1:D:387:ASN:ND2	2.63	0.45
1:D:625:LEU:C	1:D:625:LEU:HD12	2.37	0.45
1:D:730:ASN:O	1:D:733:GLU:N	2.49	0.45
1:E:115:LYS:C	1:E:117:LEU:H	2.20	0.45
1:E:220:LEU:O	1:E:220:LEU:HG	2.16	0.45
1:E:504:ILE:O	1:E:507:GLN:CB	2.64	0.45
1:E:517:VAL:HB	1:E:525:LYS:NZ	2.31	0.45
1:E:327:LEU:CD2	1:E:595:ILE:HG12	2.47	0.45
1:E:654:ILE:O	1:E:654:ILE:HG22	2.16	0.45
1:E:656:THR:HG22	1:E:657:ILE:O	2.17	0.45
1:E:708:ALA:C	1:E:710:HIS:N	2.70	0.45
1:F:197:LYS:HD3	1:F:263:ASP:OD1	2.16	0.45
1:F:656:THR:O	1:F:755:ARG:HD2	2.16	0.45
2:O:13:LYS:C	2:O:15:ALA:N	2.70	0.45
2:O:18:LEU:HB3	2:O:19:PHE:CD1	2.51	0.45
2:O:72:MET:C	2:O:74:ARG:N	2.66	0.45
2:P:115:LYS:NZ	2:P:115:LYS:CA	2.78	0.45
2:P:89:PHE:HB2	2:P:141:PHE:CD2	2.52	0.45
2:P:146:THR:O	2:P:147:ALA:C	2.54	0.45
2:R:50:ASP:CA	2:R:53:ASN:HB3	2.31	0.45
2:S:63:ILE:HG23	2:S:67:GLU:HB2	1.97	0.45
2:T:117:THR:O	2:T:120:GLU:N	2.48	0.45
1:A:480:ASN:HD22	1:A:481:VAL:N	2.14	0.45
1:B:218:LEU:C	1:B:220:LEU:H	2.15	0.45
1:B:254:ARG:CD	1:B:254:ARG:H	2.21	0.45
1:B:625:LEU:HD12	1:B:625:LEU:C	2.36	0.45
1:B:658:PRO:HG3	1:B:752:LEU:CD2	2.39	0.45
1:B:765:THR:HA	1:B:769:SER:CB	2.21	0.45
1:C:377:GLN:O	1:C:381:GLU:HB2	2.16	0.45
1:C:453:VAL:HG12	1:C:454:GLN:N	2.32	0.45
1:C:697:ILE:HG12	1:C:732:ILE:HD13	1.98	0.45
1:D:112:VAL:O	1:D:114:HIS:N	2.49	0.45
1:D:173:ILE:O	1:D:175:LYS:N	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:356:ASP:N	1:D:356:ASP:OD2	2.50	0.45
1:D:579:THR:C	1:D:581:GLN:N	2.69	0.45
1:D:626:TYR:CD2	1:D:627:TYR:N	2.84	0.45
1:D:697:ILE:HG12	1:D:732:ILE:HD13	1.98	0.45
1:D:79:ILE:C	1:D:81:GLN:N	2.68	0.45
1:D:97:TYR:HA	1:D:100:LEU:HD12	1.98	0.45
1:E:112:VAL:O	1:E:114:HIS:N	2.49	0.45
1:E:223:LYS:NZ	1:E:228:ASN:HB2	2.31	0.45
1:E:344:ALA:HA	1:E:569:TYR:OH	2.16	0.45
1:E:530:THR:O	1:E:534:ILE:HG13	2.17	0.45
1:E:554:LYS:O	1:E:557:LEU:N	2.49	0.45
1:F:97:TYR:HA	1:F:100:LEU:HD12	1.99	0.45
1:F:636:ALA:HA	1:F:637:PRO:HD3	1.82	0.45
1:F:792:VAL:O	1:F:796:ILE:HG12	2.15	0.45
2:Q:117:THR:C	2:Q:119:GLU:H	2.20	0.45
1:C:630:ARG:NH1	2:Q:83:GLU:HG2	2.32	0.45
2:T:18:LEU:HB3	2:T:19:PHE:CD1	2.51	0.45
1:A:116:GLU:HG3	1:A:117:LEU:HD23	1.98	0.45
1:A:252:ASP:O	1:A:254:ARG:HD2	2.17	0.45
1:A:619:ILE:O	1:A:620:THR:C	2.53	0.45
1:B:657:ILE:CD1	1:B:701:LEU:HD23	2.47	0.45
1:C:285:LYS:O	1:C:288:VAL:HG22	2.16	0.45
1:C:74:GLU:HB2	1:C:78:LYS:HB3	1.98	0.45
1:D:400:LYS:HE3	1:D:475:GLU:CD	2.36	0.45
1:D:560:LEU:O	1:D:563:ALA:HB3	2.16	0.45
1:E:335:ALA:HA	1:E:338:LEU:HG	1.98	0.45
1:E:455:TYR:CZ	1:E:469:PHE:CZ	3.05	0.45
1:E:595:ILE:HG22	1:E:596:ILE:H	1.81	0.45
1:F:482:GLU:HA	1:F:482:GLU:OE2	2.17	0.45
1:F:625:LEU:HD12	1:F:625:LEU:C	2.37	0.45
1:F:729:TYR:O	1:F:730:ASN:C	2.55	0.45
2:Q:89:PHE:HB2	2:Q:141:PHE:CD2	2.52	0.45
2:Q:68:PHE:O	2:Q:69:LEU:C	2.55	0.45
2:R:18:LEU:HA	2:R:18:LEU:HD23	1.74	0.45
1:A:332:ASN:OD1	1:A:334:LEU:N	2.46	0.45
1:A:339:ILE:O	1:A:342:GLY:N	2.37	0.45
1:A:351:HIS:HB2	1:A:386:GLU:HG2	1.99	0.45
1:B:191:GLU:O	1:B:192:PHE:C	2.54	0.45
1:B:464:VAL:HG23	1:B:465:LEU:N	2.32	0.45
1:B:656:THR:O	1:B:755:ARG:HD2	2.16	0.45
1:B:89:ILE:HG21	1:B:175:LYS:HE2	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:170:TYR:O	1:C:174:GLY:HA3	2.17	0.45
1:C:172:GLU:HG3	1:C:245:PHE:HE1	1.81	0.45
1:C:252:ASP:O	1:C:254:ARG:HD2	2.17	0.45
1:C:308:VAL:CG2	1:C:336:THR:O	2.65	0.45
1:C:343:VAL:HG12	1:C:344:ALA:O	2.16	0.45
1:C:391:ILE:CD1	1:C:399:GLY:HA2	2.47	0.45
1:C:708:ALA:C	1:C:710:HIS:H	2.20	0.45
1:D:391:ILE:CD1	1:D:399:GLY:HA2	2.47	0.45
1:D:344:ALA:HA	1:D:569:TYR:OH	2.17	0.45
1:D:708:ALA:C	1:D:710:HIS:H	2.19	0.45
1:D:792:VAL:O	1:D:796:ILE:HG12	2.16	0.45
1:E:184:LYS:HD2	1:E:191:GLU:HB2	1.98	0.45
1:E:252:ASP:O	1:E:254:ARG:HD2	2.17	0.45
1:E:332:ASN:OD1	1:E:334:LEU:N	2.44	0.45
1:E:445:ARG:HD3	1:E:471:TRP:CZ2	2.51	0.45
1:E:542:PRO:HA	1:E:548:THR:HG23	1.99	0.45
1:E:706:ASN:OD1	1:E:707:SER:N	2.50	0.45
1:E:729:TYR:O	1:E:730:ASN:C	2.55	0.45
1:E:88:LYS:HZ3	1:E:172:GLU:CD	2.19	0.45
1:F:308:VAL:O	1:F:311:HIS:N	2.46	0.45
2:O:32:LEU:O	2:O:32:LEU:HD12	2.17	0.45
1:A:308:VAL:O	1:A:311:HIS:N	2.46	0.45
1:A:319:ALA:O	1:A:323:ASN:HA	2.17	0.45
1:A:654:ILE:HG22	1:A:654:ILE:O	2.17	0.45
1:A:729:TYR:O	1:A:730:ASN:C	2.55	0.45
1:B:504:ILE:O	1:B:507:GLN:CB	2.65	0.45
1:C:455:TYR:CZ	1:C:469:PHE:CZ	3.05	0.45
1:C:542:PRO:HA	1:C:548:THR:HG23	1.98	0.45
1:D:189:ASP:HB3	1:D:190:PRO:CD	2.46	0.45
1:D:263:ASP:O	1:D:265:PHE:N	2.50	0.45
1:D:293:ILE:HG12	1:D:293:ILE:H	1.44	0.45
1:D:379:ALA:O	1:D:383:GLY:N	2.45	0.45
1:D:561:ASN:C	1:D:563:ALA:N	2.68	0.45
1:F:115:LYS:C	1:F:117:LEU:H	2.20	0.45
1:F:128:MET:HE1	1:F:235:THR:CB	2.46	0.45
1:F:335:ALA:HA	1:F:338:LEU:HG	1.99	0.45
1:F:447:SER:OG	1:F:448:ASP:N	2.50	0.45
1:F:595:ILE:HG22	1:F:596:ILE:H	1.81	0.45
1:F:708:ALA:C	1:F:710:HIS:N	2.68	0.45
1:F:714:GLN:O	1:F:715:GLU:C	2.55	0.45
1:F:90:PRO:HG3	1:F:249:PHE:CZ	2.51	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:97:TYR:CE1	1:F:178:SER:CB	2.91	0.45
2:O:108:VAL:O	2:O:112:LEU:HD12	2.17	0.45
2:P:108:VAL:O	2:P:112:LEU:HD12	2.17	0.45
2:R:45:GLU:N	2:R:45:GLU:CD	2.68	0.45
2:S:13:LYS:C	2:S:15:ALA:N	2.70	0.45
1:A:140:ARG:NH1	1:A:141:PHE:HE1	2.15	0.45
1:A:432:TYR:HD1	1:A:445:ARG:HD2	1.80	0.45
1:A:464:VAL:HG23	1:A:465:LEU:N	2.31	0.45
1:A:504:ILE:H	1:A:504:ILE:CD1	2.30	0.45
1:A:560:LEU:O	1:A:563:ALA:HB3	2.16	0.45
1:A:629:ASN:O	1:A:631:SER:N	2.49	0.45
1:A:96:ILE:O	1:A:100:LEU:HD12	2.17	0.45
1:A:66:LEU:HD11	1:A:97:TYR:HD2	1.81	0.45
1:B:165:GLN:C	1:B:167:LYS:N	2.69	0.45
1:B:353:LYS:N	1:B:368:GLN:HE22	2.06	0.45
1:B:351:HIS:HB2	1:B:386:GLU:HG2	1.99	0.45
1:B:530:THR:O	1:B:534:ILE:HG13	2.16	0.45
1:B:565:LYS:C	1:B:567:THR:H	2.19	0.45
1:B:627:TYR:C	1:B:627:TYR:CD1	2.90	0.45
1:B:724:ARG:HG3	1:B:724:ARG:HH11	1.81	0.45
1:C:482:GLU:HA	1:C:482:GLU:OE2	2.17	0.45
1:C:744:GLU:H	1:C:744:GLU:CD	2.20	0.45
1:C:89:ILE:HG22	1:C:90:PRO:HD2	1.99	0.45
1:D:77:ASP:OD1	1:D:159:TYR:CE2	2.70	0.45
1:D:179:LEU:CG	1:D:180:ASP:H	2.30	0.45
1:D:351:HIS:HB2	1:D:386:GLU:HG2	1.99	0.45
1:D:554:LYS:O	1:D:557:LEU:N	2.49	0.45
1:E:332:ASN:OD1	1:E:334:LEU:HB2	2.17	0.45
1:E:357:TRP:HZ3	1:E:439:ASN:CB	2.23	0.45
1:E:97:TYR:OH	1:E:150:PRO:HB2	2.16	0.45
1:F:115:LYS:CE	1:F:116:GLU:HG2	2.46	0.45
2:P:9:ILE:CD1	2:P:69:LEU:HD22	2.45	0.45
1:A:297:LYS:HZ3	1:A:297:LYS:HB3	1.82	0.45
1:A:79:ILE:C	1:A:81:GLN:N	2.69	0.45
1:B:184:LYS:CE	1:B:191:GLU:CB	2.95	0.45
1:B:225:ILE:HG23	1:B:229:PHE:HD2	1.80	0.45
1:B:254:ARG:HB3	1:B:254:ARG:NH1	2.25	0.45
1:B:401:ILE:CG2	1:B:485:LEU:HB3	2.47	0.45
1:B:70:GLU:HB2	1:B:107:THR:HG22	1.99	0.45
1:C:197:LYS:C	1:C:197:LYS:HZ3	2.20	0.45
1:C:360:VAL:CG1	1:C:370:LEU:HD22	2.43	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:368:GLN:CB	1:C:380:VAL:HG13	2.47	0.45
1:C:357:TRP:CZ3	1:C:439:ASN:ND2	2.84	0.45
1:C:627:TYR:CD1	1:C:627:TYR:C	2.91	0.45
1:D:453:VAL:HG12	1:D:454:GLN:N	2.32	0.45
1:E:115:LYS:CE	1:E:116:GLU:HG2	2.46	0.45
1:E:180:ASP:O	1:E:182:ILE:N	2.50	0.45
1:E:357:TRP:CZ3	1:E:439:ASN:ND2	2.83	0.45
1:F:220:LEU:HG	1:F:220:LEU:O	2.16	0.45
1:F:343:VAL:HG12	1:F:344:ALA:O	2.17	0.45
1:F:424:LYS:O	1:F:425:GLU:OE1	2.35	0.45
1:F:765:THR:CA	1:F:769:SER:HB2	2.22	0.45
2:Q:108:VAL:O	2:Q:112:LEU:HD12	2.17	0.45
2:Q:9:ILE:CD1	2:Q:69:LEU:HD22	2.45	0.45
1:D:527:LYS:HG2	2:R:145:MET:SD	2.57	0.45
2:S:117:THR:C	2:S:119:GLU:H	2.19	0.45
2:S:18:LEU:HA	2:S:18:LEU:HD23	1.76	0.45
2:T:68:PHE:O	2:T:69:LEU:C	2.55	0.45
1:A:289:GLU:HA	1:A:292:ARG:HG3	1.98	0.45
1:A:357:TRP:HZ3	1:A:439:ASN:CB	2.24	0.45
1:A:508:ILE:HG21	1:A:513:TRP:HB2	1.99	0.45
1:A:517:VAL:HB	1:A:525:LYS:NZ	2.30	0.45
1:B:561:ASN:C	1:B:563:ALA:H	2.21	0.45
1:B:595:ILE:HG22	1:B:596:ILE:H	1.82	0.45
1:B:697:ILE:HG12	1:B:732:ILE:HD13	1.99	0.45
1:C:173:ILE:HA	1:C:242:SER:HB3	1.98	0.45
1:C:180:ASP:O	1:C:182:ILE:N	2.51	0.45
1:C:387:ASN:ND2	1:C:387:ASN:N	2.65	0.45
1:C:540:ARG:NH1	1:C:627:TYR:CE1	2.85	0.45
1:D:193:LEU:O	1:D:197:LYS:HB2	2.17	0.45
1:D:128:MET:CE	1:D:235:THR:HB	2.47	0.45
1:D:345:THR:HG22	1:D:490:ALA:O	2.17	0.45
1:D:368:GLN:CB	1:D:380:VAL:HG13	2.47	0.45
1:D:527:LYS:HE2	1:D:527:LYS:HB3	1.84	0.45
1:D:97:TYR:OH	1:D:150:PRO:HB2	2.16	0.45
1:E:170:TYR:O	1:E:174:GLY:HA3	2.17	0.45
1:E:270:LYS:HA	1:E:273:LYS:HG3	1.99	0.45
1:E:359:PRO:HG2	1:E:360:VAL:H	1.81	0.45
1:E:424:LYS:O	1:E:425:GLU:OE1	2.35	0.45
1:E:648:PRO:HD2	2:S:90:ARG:HD3	1.98	0.45
1:F:193:LEU:O	1:F:197:LYS:HB2	2.17	0.45
1:F:288:VAL:CG2	1:F:289:GLU:H	2.23	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:630:ARG:CG	1:F:630:ARG:HH11	2.26	0.45
2:O:117:THR:C	2:O:119:GLU:H	2.20	0.45
2:O:18:LEU:HD23	2:O:18:LEU:HA	1.75	0.45
2:O:9:ILE:CD1	2:O:69:LEU:HD22	2.46	0.45
2:R:126:ARG:HH21	2:R:126:ARG:HG3	1.81	0.45
2:R:18:LEU:HB3	2:R:19:PHE:CD1	2.52	0.45
2:T:48:LEU:HD23	2:T:51:MET:HE2	2.00	0.45
1:A:360:VAL:CG1	1:A:370:LEU:HD22	2.44	0.44
1:A:450:ASN:HD22	1:A:452:GLU:HG3	1.78	0.44
1:A:706:ASN:OD1	1:A:707:SER:N	2.50	0.44
1:B:217:LYS:HB2	1:B:236:GLU:HG3	1.99	0.44
1:B:690:LYS:O	1:B:691:LYS:C	2.56	0.44
1:B:729:TYR:O	1:B:730:ASN:C	2.55	0.44
1:C:115:LYS:CB	1:C:118:GLN:CG	2.91	0.44
1:C:193:LEU:O	1:C:197:LYS:HB2	2.17	0.44
1:C:332:ASN:OD1	1:C:334:LEU:N	2.45	0.44
1:C:345:THR:HG22	1:C:490:ALA:O	2.17	0.44
1:C:480:ASN:HD22	1:C:481:VAL:H	1.65	0.44
1:C:480:ASN:ND2	1:C:483:GLY:CA	2.80	0.44
1:D:176:GLY:O	1:D:178:SER:N	2.50	0.44
1:D:329:ARG:CD	1:D:590:ASP:OD2	2.63	0.44
1:D:629:ASN:O	1:D:631:SER:N	2.50	0.44
1:E:115:LYS:CB	1:E:118:GLN:CG	2.92	0.44
1:E:173:ILE:HA	1:E:242:SER:HB3	1.98	0.44
1:E:453:VAL:HG12	1:E:454:GLN:N	2.31	0.44
1:E:513:TRP:CH2	1:E:517:VAL:HG11	2.52	0.44
1:E:730:ASN:O	1:E:733:GLU:N	2.51	0.44
1:E:697:ILE:HG12	1:E:732:ILE:HD13	1.99	0.44
1:E:792:VAL:O	1:E:796:ILE:HG12	2.16	0.44
1:F:308:VAL:CG2	1:F:336:THR:O	2.65	0.44
2:O:68:PHE:O	2:O:69:LEU:C	2.56	0.44
2:P:109:MET:HG3	2:P:116:LEU:HD11	1.99	0.44
2:S:50:ASP:CA	2:S:53:ASN:HB3	2.31	0.44
2:T:12:PHE:O	2:T:15:ALA:HB3	2.16	0.44
2:T:32:LEU:HD12	2:T:32:LEU:O	2.17	0.44
1:A:399:GLY:O	1:A:477:MET:HE3	2.18	0.44
1:A:532:LEU:HA	1:A:532:LEU:HD23	1.87	0.44
1:A:497:LEU:HD13	1:A:556:MET:HG2	1.99	0.44
1:B:230:ILE:HG13	1:B:237:PHE:CD2	2.52	0.44
1:B:335:ALA:HA	1:B:338:LEU:HG	1.98	0.44
1:B:89:ILE:HG22	1:B:90:PRO:HD2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:90:PRO:O	1:B:93:VAL:N	2.50	0.44
1:C:432:TYR:HD1	1:C:445:ARG:HD2	1.78	0.44
1:C:579:THR:C	1:C:581:GLN:N	2.69	0.44
1:D:179:LEU:CG	1:D:180:ASP:N	2.80	0.44
1:D:230:ILE:HG13	1:D:237:PHE:CD2	2.52	0.44
1:D:424:LYS:O	1:D:425:GLU:OE1	2.35	0.44
1:D:497:LEU:HD13	1:D:556:MET:HG2	1.99	0.44
1:D:706:ASN:OD1	1:D:707:SER:N	2.50	0.44
1:D:729:TYR:O	1:D:730:ASN:C	2.56	0.44
1:E:304:ALA:HB3	1:E:604:LEU:HD22	1.98	0.44
1:F:191:GLU:O	1:F:194:ASN:N	2.50	0.44
1:F:473:ASN:OD1	1:F:473:ASN:N	2.41	0.44
1:F:519:THR:HG21	1:F:525:LYS:HA	2.00	0.44
2:T:129:ASP:OD1	2:T:134:GLY:N	2.39	0.44
1:A:193:LEU:O	1:A:197:LYS:HB2	2.17	0.44
1:A:217:LYS:HB2	1:A:236:GLU:HG3	1.99	0.44
1:A:582:ASP:O	1:A:584:GLU:N	2.42	0.44
1:A:97:TYR:OH	1:A:150:PRO:HB2	2.16	0.44
1:B:175:LYS:O	1:B:176:GLY:C	2.55	0.44
1:B:218:LEU:HG	1:B:218:LEU:O	2.18	0.44
1:B:186:LYS:CE	1:B:234:LEU:HD12	2.35	0.44
1:B:288:VAL:CG2	1:B:289:GLU:H	2.23	0.44
1:B:295:VAL:C	1:B:296:LEU:CD2	2.81	0.44
1:B:368:GLN:CB	1:B:380:VAL:HG13	2.47	0.44
1:B:450:ASN:HD22	1:B:452:GLU:HG3	1.79	0.44
1:C:71:PHE:CD1	1:C:108:ASP:OD1	2.70	0.44
1:C:176:GLY:O	1:C:178:SER:N	2.51	0.44
1:C:182:ILE:HA	1:C:187:SER:HA	1.98	0.44
1:C:331:VAL:O	1:C:332:ASN:C	2.56	0.44
1:C:351:HIS:HB2	1:C:386:GLU:HG2	1.99	0.44
1:C:424:LYS:O	1:C:425:GLU:OE1	2.35	0.44
1:C:625:LEU:C	1:C:625:LEU:HD12	2.37	0.44
1:C:79:ILE:C	1:C:81:GLN:N	2.69	0.44
1:C:90:PRO:O	1:C:93:VAL:N	2.49	0.44
1:D:753:LYS:O	1:D:754:GLU:C	2.55	0.44
1:E:142:VAL:HG13	1:E:154:ILE:HD12	1.99	0.44
1:E:193:LEU:O	1:E:197:LYS:HB2	2.17	0.44
1:E:285:LYS:O	1:E:288:VAL:HG22	2.17	0.44
1:E:441:VAL:HG11	1:E:462:ILE:O	2.18	0.44
1:E:630:ARG:CG	1:E:630:ARG:HH11	2.23	0.44
1:F:329:ARG:CD	1:F:590:ASP:OD2	2.63	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:654:ILE:HG22	1:F:654:ILE:O	2.17	0.44
2:O:92:PHE:CD1	2:O:92:PHE:N	2.86	0.44
2:P:117:THR:HG23	2:P:120:GLU:CG	2.48	0.44
2:R:129:ASP:OD1	2:R:134:GLY:N	2.37	0.44
1:A:335:ALA:HA	1:A:338:LEU:HG	1.99	0.44
1:A:308:VAL:CG2	1:A:336:THR:O	2.65	0.44
1:A:730:ASN:O	1:A:733:GLU:N	2.51	0.44
1:A:732:ILE:O	1:A:733:GLU:C	2.56	0.44
1:A:792:VAL:O	1:A:796:ILE:HG12	2.18	0.44
1:C:629:ASN:O	1:C:631:SER:N	2.50	0.44
1:D:288:VAL:CG2	1:D:289:GLU:H	2.22	0.44
1:D:629:ASN:ND2	1:D:631:SER:N	2.66	0.44
1:D:74:GLU:HB2	1:D:78:LYS:HB3	1.99	0.44
1:E:560:LEU:O	1:E:563:ALA:HB3	2.18	0.44
1:F:175:LYS:O	1:F:176:GLY:C	2.55	0.44
1:F:179:LEU:CG	1:F:180:ASP:N	2.79	0.44
1:F:217:LYS:HZ2	1:F:217:LYS:HB3	1.83	0.44
1:F:319:ALA:O	1:F:323:ASN:HA	2.17	0.44
1:F:331:VAL:O	1:F:332:ASN:C	2.56	0.44
1:F:332:ASN:OD1	1:F:334:LEU:HB2	2.18	0.44
1:F:504:ILE:O	1:F:507:GLN:CB	2.64	0.44
1:F:744:GLU:CD	1:F:744:GLU:H	2.20	0.44
1:F:90:PRO:O	1:F:93:VAL:N	2.50	0.44
2:P:65:PHE:O	2:P:68:PHE:HB3	2.17	0.44
2:Q:65:PHE:HB3	2:Q:66:PRO:HD3	2.00	0.44
2:S:108:VAL:O	2:S:112:LEU:HD12	2.16	0.44
2:T:108:VAL:O	2:T:112:LEU:HD12	2.17	0.44
1:A:179:LEU:CG	1:A:180:ASP:H	2.28	0.44
1:A:179:LEU:CG	1:A:180:ASP:N	2.78	0.44
1:A:542:PRO:HA	1:A:548:THR:HG23	1.98	0.44
1:B:142:VAL:HG13	1:B:154:ILE:HD12	2.00	0.44
1:B:332:ASN:OD1	1:B:334:LEU:HB2	2.18	0.44
1:B:455:TYR:CZ	1:B:469:PHE:CZ	3.05	0.44
1:B:480:ASN:HD22	1:B:481:VAL:H	1.65	0.44
1:B:523:LEU:HD11	2:P:144:MET:HG3	2.00	0.44
1:B:687:GLU:O	1:B:690:LYS:HB2	2.16	0.44
1:B:746:LYS:HD2	1:B:747:ASN:HD22	1.82	0.44
1:B:752:LEU:HD23	1:B:752:LEU:HA	1.79	0.44
1:C:400:LYS:HE3	1:C:475:GLU:CD	2.37	0.44
1:D:668:SER:N	2:R:14:GLU:OE1	2.51	0.44
1:D:718:ARG:HH12	1:D:767:GLN:HE21	1.64	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:197:LYS:CB	1:E:197:LYS:HZ2	2.19	0.44
1:E:435:LEU:HG	1:E:446:ILE:CG2	2.47	0.44
1:E:456:LYS:HD3	1:E:471:TRP:CG	2.52	0.44
1:E:718:ARG:NH1	1:E:767:GLN:HE21	2.15	0.44
1:E:748:TYR:O	1:E:751:TYR:N	2.51	0.44
1:F:180:ASP:O	1:F:182:ILE:N	2.51	0.44
1:F:741:ILE:O	1:F:742:ALA:C	2.54	0.44
1:A:527:LYS:HG2	2:O:145:MET:SD	2.58	0.44
2:R:117:THR:C	2:R:119:GLU:H	2.20	0.44
2:R:89:PHE:HB2	2:R:141:PHE:CD2	2.51	0.44
2:R:92:PHE:N	2:R:92:PHE:CD1	2.86	0.44
2:S:129:ASP:OD1	2:S:134:GLY:N	2.37	0.44
2:T:65:PHE:HB3	2:T:66:PRO:HD3	2.00	0.44
1:A:230:ILE:HG13	1:A:237:PHE:CD2	2.53	0.44
1:A:186:LYS:CE	1:A:234:LEU:HD12	2.35	0.44
1:A:748:TYR:O	1:A:751:TYR:N	2.51	0.44
1:A:90:PRO:HG3	1:A:249:PHE:CZ	2.52	0.44
1:B:179:LEU:CG	1:B:180:ASP:H	2.28	0.44
1:B:180:ASP:O	1:B:182:ILE:N	2.51	0.44
1:B:305:SER:HB2	1:B:594:PHE:CE1	2.52	0.44
1:B:480:ASN:ND2	1:B:483:GLY:CA	2.79	0.44
1:B:619:ILE:O	1:B:620:THR:C	2.55	0.44
1:B:708:ALA:C	1:B:710:HIS:H	2.20	0.44
1:B:762:LEU:O	1:B:766:HIS:HB2	2.16	0.44
1:B:76:LEU:O	1:B:80:GLN:N	2.45	0.44
1:C:115:LYS:CE	1:C:116:GLU:HG2	2.47	0.44
1:C:319:ALA:O	1:C:323:ASN:HA	2.17	0.44
1:D:217:LYS:HB2	1:D:236:GLU:HG3	1.99	0.44
1:D:281:GLU:O	1:D:285:LYS:HG2	2.17	0.44
1:D:99:GLU:C	1:D:101:GLY:N	2.69	0.44
1:E:175:LYS:O	1:E:176:GLY:C	2.56	0.44
1:E:218:LEU:O	1:E:218:LEU:HG	2.18	0.44
1:E:368:GLN:CB	1:E:380:VAL:HG13	2.47	0.44
1:E:636:ALA:O	1:E:640:LYS:CA	2.64	0.44
1:E:684:ASP:C	1:E:686:ASP:H	2.21	0.44
1:E:92:ASP:O	1:E:93:VAL:C	2.56	0.44
1:E:97:TYR:HA	1:E:100:LEU:HD12	2.00	0.44
1:F:217:LYS:HB2	1:F:236:GLU:HG3	2.00	0.44
1:F:281:GLU:O	1:F:285:LYS:HG2	2.17	0.44
1:F:464:VAL:HG23	1:F:465:LEU:N	2.32	0.44
1:F:480:ASN:HD22	1:F:481:VAL:H	1.66	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:5:THR:OG1	2:R:6:GLU:N	2.51	0.44
2:R:68:PHE:O	2:R:69:LEU:C	2.55	0.44
2:S:101:SER:OG	2:S:104:GLU:HG2	2.17	0.44
2:S:84:GLU:N	2:S:84:GLU:OE2	2.46	0.44
1:A:182:ILE:C	1:A:183:SER:O	2.50	0.44
1:A:357:TRP:CZ2	1:A:370:LEU:HD23	2.53	0.44
1:A:549:LEU:HB2	1:A:553:GLN:HE21	1.82	0.44
1:A:708:ALA:C	1:A:710:HIS:N	2.71	0.44
1:A:752:LEU:HA	1:A:752:LEU:HD23	1.77	0.44
1:A:762:LEU:O	1:A:766:HIS:HB2	2.18	0.44
1:B:193:LEU:O	1:B:197:LYS:HB2	2.17	0.44
1:B:517:VAL:HB	1:B:525:LYS:NZ	2.31	0.44
1:B:297:LYS:HZ3	1:B:601:GLU:HB3	1.83	0.44
1:B:743:PRO:O	1:B:746:LYS:HB3	2.18	0.44
1:C:688:PHE:C	1:C:688:PHE:HD2	2.20	0.44
1:D:116:GLU:HG3	1:D:117:LEU:HD23	1.98	0.44
1:D:234:LEU:CG	1:D:235:THR:H	2.31	0.44
1:D:395:GLU:C	1:D:397:GLU:H	2.21	0.44
1:D:435:LEU:HD23	1:D:435:LEU:HA	1.80	0.44
1:D:517:VAL:HB	1:D:525:LYS:NZ	2.32	0.44
1:E:230:ILE:HG13	1:E:237:PHE:CD2	2.53	0.44
1:E:391:ILE:CD1	1:E:399:GLY:HA2	2.47	0.44
1:E:561:ASN:C	1:E:563:ALA:H	2.20	0.44
1:E:582:ASP:O	1:E:584:GLU:N	2.46	0.44
1:E:327:LEU:CG	1:E:595:ILE:HG12	2.47	0.44
1:E:540:ARG:NH1	1:E:627:TYR:CE1	2.86	0.44
1:E:762:LEU:O	1:E:766:HIS:HB2	2.17	0.44
1:E:93:VAL:HG13	1:E:94:LEU:N	2.33	0.44
1:F:353:LYS:N	1:F:368:GLN:HE22	2.07	0.44
1:F:706:ASN:OD1	1:F:707:SER:N	2.51	0.44
1:F:762:LEU:O	1:F:766:HIS:HB2	2.17	0.44
1:F:722:ILE:HD13	1:F:764:LEU:CD2	2.47	0.44
1:F:794:GLN:HB3	1:F:794:GLN:HE21	1.61	0.44
2:S:68:PHE:O	2:S:69:LEU:C	2.55	0.44
1:A:285:LYS:O	1:A:288:VAL:HG22	2.17	0.44
1:A:288:VAL:CG2	1:A:289:GLU:H	2.23	0.44
1:A:304:ALA:HB3	1:A:604:LEU:HD22	2.00	0.44
1:A:540:ARG:HH22	1:A:630:ARG:HE	1.65	0.44
1:A:687:GLU:O	1:A:690:LYS:N	2.51	0.44
1:B:350:VAL:HG21	1:B:488:LEU:HD12	1.99	0.44
1:B:435:LEU:HG	1:B:446:ILE:CG2	2.46	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:530:THR:HG23	2:P:88:ALA:HB1	2.00	0.44
1:B:74:GLU:HB2	1:B:78:LYS:HB3	2.00	0.44
1:C:622:LYS:HA	1:C:622:LYS:HD3	1.85	0.44
1:C:746:LYS:HD2	1:C:747:ASN:HD22	1.83	0.44
1:C:792:VAL:O	1:C:796:ILE:HG12	2.17	0.44
1:D:115:LYS:C	1:D:117:LEU:H	2.19	0.44
1:D:450:ASN:HD22	1:D:452:GLU:HG3	1.78	0.44
1:D:762:LEU:O	1:D:766:HIS:HB2	2.17	0.44
1:D:96:ILE:O	1:D:100:LEU:HD12	2.18	0.44
1:E:165:GLN:C	1:E:167:LYS:N	2.70	0.44
1:E:184:LYS:CE	1:E:191:GLU:CB	2.94	0.44
1:E:263:ASP:O	1:E:265:PHE:N	2.51	0.44
1:E:356:ASP:OD2	1:E:356:ASP:N	2.50	0.44
1:E:395:GLU:C	1:E:397:GLU:H	2.21	0.44
1:E:527:LYS:HG2	2:S:145:MET:SD	2.58	0.44
1:E:619:ILE:O	1:E:620:THR:C	2.56	0.44
1:F:218:LEU:HG	1:F:218:LEU:O	2.17	0.44
1:F:263:ASP:O	1:F:265:PHE:N	2.50	0.44
1:F:582:ASP:O	1:F:584:GLU:N	2.43	0.44
1:F:643:ILE:HG22	1:F:644:GLU:H	1.82	0.44
1:F:743:PRO:O	1:F:746:LYS:HB3	2.17	0.44
1:F:753:LYS:O	1:F:754:GLU:C	2.56	0.44
2:P:45:GLU:N	2:P:45:GLU:CD	2.70	0.44
2:R:117:THR:HG23	2:R:120:GLU:CB	2.46	0.44
2:S:65:PHE:O	2:S:68:PHE:HB3	2.18	0.44
2:T:117:THR:HG23	2:T:120:GLU:CG	2.47	0.44
2:T:75:LYS:HZ2	2:T:75:LYS:HB3	1.83	0.44
1:A:482:GLU:HA	1:A:482:GLU:OE2	2.17	0.44
1:A:324:THR:CG2	1:A:499:PRO:HA	2.48	0.44
1:A:636:ALA:HA	1:A:637:PRO:HD3	1.82	0.44
1:B:356:ASP:N	1:B:356:ASP:OD2	2.50	0.44
1:C:179:LEU:CG	1:C:180:ASP:H	2.29	0.44
1:C:217:LYS:HB2	1:C:236:GLU:HG3	1.99	0.44
1:C:447:SER:OG	1:C:448:ASP:N	2.51	0.44
1:C:619:ILE:O	1:C:620:THR:C	2.56	0.44
1:C:708:ALA:C	1:C:710:HIS:N	2.70	0.44
1:C:71:PHE:C	1:C:73:ASN:H	2.21	0.44
1:D:106:PHE:CZ	1:D:171:TYR:OH	2.67	0.44
1:D:301:ALA:O	1:D:304:ALA:N	2.43	0.44
1:D:331:VAL:O	1:D:332:ASN:C	2.56	0.44
1:D:508:ILE:HG21	1:D:513:TRP:HB2	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:519:THR:HG21	1:D:525:LYS:HA	2.00	0.44
1:D:684:ASP:C	1:D:686:ASP:H	2.21	0.44
1:D:713:SER:O	1:D:714:GLN:C	2.56	0.44
1:D:741:ILE:O	1:D:741:ILE:HG13	2.18	0.44
1:D:746:LYS:HD2	1:D:747:ASN:HD22	1.83	0.44
1:E:234:LEU:CG	1:E:235:THR:H	2.31	0.44
1:E:360:VAL:HA	1:E:403:LEU:HD21	2.00	0.44
1:E:679:TYR:CG	1:E:691:LYS:HB2	2.53	0.44
1:E:714:GLN:O	1:E:715:GLU:C	2.57	0.44
1:F:332:ASN:OD1	1:F:334:LEU:N	2.44	0.44
1:F:391:ILE:HG12	1:F:399:GLY:HA2	1.99	0.44
1:F:540:ARG:HD3	1:F:627:TYR:HH	1.81	0.44
1:F:684:ASP:C	1:F:686:ASP:H	2.21	0.44
2:O:117:THR:HG23	2:O:120:GLU:CG	2.48	0.44
2:P:24:ASP:HB2	2:P:26:THR:CG2	2.35	0.44
2:Q:92:PHE:N	2:Q:92:PHE:CD1	2.86	0.44
1:D:529:VAL:HG21	2:R:109:MET:HE1	1.99	0.44
2:T:89:PHE:HB2	2:T:141:PHE:CD2	2.52	0.44
1:A:255:THR:HA	1:A:258:GLU:HB3	1.99	0.43
1:A:343:VAL:HG12	1:A:344:ALA:O	2.18	0.43
1:A:356:ASP:N	1:A:356:ASP:OD2	2.51	0.43
1:A:480:ASN:ND2	1:A:483:GLY:CA	2.79	0.43
1:A:561:ASN:C	1:A:563:ALA:H	2.21	0.43
1:A:753:LYS:O	1:A:754:GLU:C	2.55	0.43
1:C:395:GLU:C	1:C:397:GLU:H	2.21	0.43
1:C:435:LEU:HG	1:C:446:ILE:CG2	2.46	0.43
1:C:513:TRP:CH2	1:C:517:VAL:HG11	2.53	0.43
1:C:540:ARG:HH22	1:C:630:ARG:HE	1.65	0.43
1:C:656:THR:HG22	1:C:657:ILE:O	2.18	0.43
1:C:722:ILE:HD13	1:C:764:LEU:CD2	2.47	0.43
1:D:173:ILE:HA	1:D:242:SER:HB3	1.99	0.43
1:D:191:GLU:O	1:D:193:LEU:N	2.51	0.43
1:D:218:LEU:O	1:D:218:LEU:HG	2.18	0.43
1:D:165:GLN:CD	1:D:252:ASP:HB3	2.39	0.43
1:D:391:ILE:HG12	1:D:399:GLY:HA2	2.01	0.43
1:D:480:ASN:ND2	1:D:483:GLY:CA	2.80	0.43
1:D:743:PRO:O	1:D:746:LYS:HB3	2.18	0.43
1:E:71:PHE:O	1:E:78:LYS:NZ	2.50	0.43
1:F:285:LYS:O	1:F:288:VAL:HG22	2.18	0.43
2:O:146:THR:O	2:O:147:ALA:C	2.54	0.43
2:P:102:ALA:CB	2:P:125:ILE:HG13	2.46	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:Q:136:VAL:HG23	2:Q:136:VAL:O	2.17	0.43
2:R:109:MET:HG3	2:R:116:LEU:HD11	2.00	0.43
2:S:9:ILE:CD1	2:S:69:LEU:HD22	2.45	0.43
1:A:115:LYS:CE	1:A:116:GLU:HG2	2.47	0.43
1:A:128:MET:HE1	1:A:235:THR:CB	2.47	0.43
1:A:690:LYS:O	1:A:691:LYS:C	2.54	0.43
1:B:331:VAL:O	1:B:332:ASN:C	2.57	0.43
1:B:335:ALA:HB1	1:B:489:THR:OG1	2.19	0.43
1:B:513:TRP:CH2	1:B:517:VAL:HG11	2.53	0.43
1:B:93:VAL:HG13	1:B:94:LEU:N	2.34	0.43
1:B:96:ILE:O	1:B:100:LEU:HD12	2.17	0.43
1:C:230:ILE:HG13	1:C:237:PHE:CD2	2.53	0.43
1:C:329:ARG:CD	1:C:590:ASP:OD2	2.61	0.43
1:C:718:ARG:HH12	1:C:767:GLN:HE21	1.64	0.43
1:C:753:LYS:O	1:C:754:GLU:C	2.57	0.43
1:C:93:VAL:HG13	1:C:94:LEU:N	2.33	0.43
1:D:653:LYS:C	1:D:655:ASN:N	2.72	0.43
1:D:708:ALA:C	1:D:710:HIS:N	2.70	0.43
1:D:765:THR:HA	1:D:769:SER:CB	2.21	0.43
1:D:792:VAL:O	1:D:793:PHE:C	2.56	0.43
1:D:90:PRO:O	1:D:93:VAL:N	2.51	0.43
1:E:281:GLU:O	1:E:285:LYS:HG2	2.17	0.43
1:E:622:LYS:HA	1:E:622:LYS:HD3	1.85	0.43
1:E:708:ALA:C	1:E:710:HIS:H	2.21	0.43
1:F:184:LYS:CE	1:F:191:GLU:CB	2.95	0.43
1:F:230:ILE:HG13	1:F:237:PHE:CD2	2.53	0.43
1:F:255:THR:HA	1:F:258:GLU:HB3	2.00	0.43
1:F:349:ASN:HB2	1:F:398:ILE:HG13	2.00	0.43
1:F:395:GLU:C	1:F:397:GLU:H	2.21	0.43
1:F:643:ILE:HG22	1:F:644:GLU:N	2.33	0.43
2:O:101:SER:OG	2:O:104:GLU:HG2	2.17	0.43
2:O:5:THR:OG1	2:O:6:GLU:N	2.50	0.43
1:C:668:SER:N	2:Q:14:GLU:OE1	2.51	0.43
2:R:97:ASN:HD22	2:R:99:TYR:H	1.64	0.43
2:T:97:ASN:HD22	2:T:99:TYR:H	1.64	0.43
1:A:115:LYS:C	1:A:117:LEU:H	2.20	0.43
1:A:513:TRP:CH2	1:A:517:VAL:HG11	2.53	0.43
1:A:629:ASN:ND2	1:A:631:SER:N	2.63	0.43
1:A:743:PRO:O	1:A:746:LYS:HB3	2.19	0.43
1:B:197:LYS:NZ	1:B:197:LYS:CB	2.81	0.43
1:B:519:THR:HG21	1:B:525:LYS:HA	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:560:LEU:O	1:B:563:ALA:HB3	2.18	0.43
1:C:225:ILE:HG12	1:C:229:PHE:HD2	1.80	0.43
1:C:304:ALA:HB3	1:C:604:LEU:HD22	1.99	0.43
1:C:384:ASN:O	1:C:386:GLU:N	2.51	0.43
1:C:671:ARG:HG3	1:C:671:ARG:NH1	2.34	0.43
1:C:687:GLU:O	1:C:690:LYS:N	2.51	0.43
1:D:218:LEU:C	1:D:220:LEU:H	2.14	0.43
1:D:304:ALA:HB3	1:D:604:LEU:HD22	2.00	0.43
1:D:420:LEU:O	1:D:420:LEU:HD13	2.18	0.43
1:E:350:VAL:HG21	1:E:488:LEU:HD12	2.00	0.43
1:E:732:ILE:O	1:E:733:GLU:C	2.57	0.43
1:F:668:SER:N	2:T:14:GLU:OE1	2.51	0.43
1:F:92:ASP:O	1:F:93:VAL:C	2.56	0.43
2:O:41:GLN:C	2:O:43:PRO:CD	2.80	0.43
2:O:65:PHE:O	2:O:68:PHE:HB3	2.18	0.43
2:S:92:PHE:CD1	2:S:92:PHE:N	2.87	0.43
1:A:218:LEU:HG	1:A:218:LEU:O	2.18	0.43
1:A:653:LYS:C	1:A:655:ASN:N	2.72	0.43
1:B:357:TRP:HZ3	1:B:439:ASN:CB	2.23	0.43
1:B:504:ILE:H	1:B:504:ILE:CD1	2.31	0.43
1:B:93:VAL:CG1	1:B:94:LEU:N	2.81	0.43
1:B:97:TYR:HA	1:B:100:LEU:HD12	2.00	0.43
1:C:128:MET:CE	1:C:235:THR:HB	2.46	0.43
1:C:349:ASN:HB2	1:C:398:ILE:HG13	2.00	0.43
1:C:360:VAL:HA	1:C:403:LEU:HD21	2.01	0.43
1:C:391:ILE:HG12	1:C:399:GLY:HA2	2.00	0.43
1:C:70:GLU:HB2	1:C:107:THR:HG22	2.00	0.43
1:D:360:VAL:HA	1:D:403:LEU:HD21	2.01	0.43
1:D:714:GLN:O	1:D:715:GLU:C	2.54	0.43
1:E:255:THR:HA	1:E:258:GLU:HB3	2.00	0.43
1:E:391:ILE:HG12	1:E:399:GLY:HA2	2.00	0.43
1:E:523:LEU:HD11	2:S:144:MET:HG3	2.00	0.43
1:E:753:LYS:O	1:E:754:GLU:C	2.56	0.43
1:E:76:LEU:O	1:E:80:GLN:N	2.48	0.43
1:F:170:TYR:O	1:F:174:GLY:HA3	2.17	0.43
1:F:279:ILE:O	1:F:283:LEU:HB2	2.18	0.43
1:F:508:ILE:HG12	1:F:536:TYR:CD2	2.53	0.43
1:F:687:GLU:O	1:F:690:LYS:N	2.52	0.43
1:F:730:ASN:O	1:F:733:GLU:N	2.51	0.43
1:F:732:ILE:O	1:F:733:GLU:C	2.56	0.43
1:F:792:VAL:O	1:F:793:PHE:C	2.56	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:706:ASN:O	2:O:130:ILE:HD13	2.18	0.43
1:B:533:LEU:HD23	2:P:112:LEU:HD21	2.01	0.43
2:P:115:LYS:HZ2	2:P:115:LYS:CA	2.32	0.43
2:Q:5:THR:OG1	2:Q:6:GLU:N	2.51	0.43
1:E:513:TRP:HZ2	2:S:114:GLU:HB2	1.82	0.43
2:S:65:PHE:HB3	2:S:66:PRO:HD3	2.00	0.43
1:A:170:TYR:O	1:A:174:GLY:HA3	2.18	0.43
1:A:205:SER:C	1:A:207:ASP:N	2.72	0.43
1:A:343:VAL:HG13	1:A:487:PRO:O	2.19	0.43
1:A:519:THR:HG21	1:A:525:LYS:HA	2.01	0.43
1:A:89:ILE:HG22	1:A:90:PRO:HD2	1.99	0.43
1:B:285:LYS:O	1:B:288:VAL:HG22	2.17	0.43
1:B:523:LEU:HD22	2:P:127:GLU:HG2	2.01	0.43
1:C:519:THR:HG21	1:C:525:LYS:HA	2.00	0.43
1:D:513:TRP:CH2	1:D:517:VAL:HG11	2.53	0.43
1:D:632:TYR:CE2	1:D:643:ILE:HG21	2.54	0.43
1:E:197:LYS:HD3	1:E:263:ASP:OD1	2.17	0.43
1:E:376:GLN:HB3	1:E:379:ALA:HB3	2.00	0.43
1:F:376:GLN:HB3	1:F:379:ALA:HB3	2.01	0.43
1:F:653:LYS:C	1:F:655:ASN:N	2.72	0.43
1:F:70:GLU:HB2	1:F:107:THR:HG22	2.00	0.43
2:P:69:LEU:HD23	2:P:69:LEU:HA	1.75	0.43
2:R:51:MET:HB2	2:R:51:MET:HE3	1.90	0.43
2:S:117:THR:HG23	2:S:120:GLU:CG	2.48	0.43
2:S:39:LEU:HD12	2:S:39:LEU:HA	1.83	0.43
2:T:143:GLN:HE21	2:T:143:GLN:HB3	1.64	0.43
1:A:218:LEU:C	1:A:220:LEU:H	2.16	0.43
1:A:384:ASN:O	1:A:386:GLU:N	2.52	0.43
1:A:350:VAL:HG21	1:A:488:LEU:HD12	2.00	0.43
1:A:714:GLN:O	1:A:715:GLU:C	2.55	0.43
1:A:775:LEU:O	1:A:778:LYS:N	2.52	0.43
1:B:184:LYS:HE3	1:B:191:GLU:HB3	1.99	0.43
1:B:131:ARG:HG3	1:B:243:LEU:HD13	1.99	0.43
1:B:384:ASN:O	1:B:386:GLU:N	2.52	0.43
1:B:420:LEU:O	1:B:420:LEU:HD13	2.18	0.43
1:B:597:ASN:C	1:B:599:GLU:H	2.22	0.43
1:C:252:ASP:OD2	1:C:253:HIS:CD2	2.70	0.43
1:C:729:TYR:O	1:C:730:ASN:C	2.56	0.43
1:C:775:LEU:O	1:C:778:LYS:N	2.52	0.43
1:C:792:VAL:O	1:C:793:PHE:C	2.57	0.43
1:D:173:ILE:CG2	1:D:174:GLY:N	2.81	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:175:LYS:O	1:D:176:GLY:C	2.57	0.43
1:D:263:ASP:O	1:D:264:MET:C	2.57	0.43
1:D:542:PRO:HA	1:D:548:THR:HG23	1.99	0.43
1:D:622:LYS:HA	1:D:622:LYS:HD3	1.85	0.43
1:D:775:LEU:O	1:D:778:LYS:N	2.52	0.43
1:E:176:GLY:O	1:E:178:SER:N	2.51	0.43
1:E:351:HIS:HB2	1:E:386:GLU:HG2	2.01	0.43
1:E:512:GLU:O	1:E:515:LYS:NZ	2.51	0.43
1:E:683:GLY:O	1:E:684:ASP:C	2.55	0.43
1:E:792:VAL:O	1:E:793:PHE:C	2.57	0.43
1:F:116:GLU:HG3	1:F:117:LEU:HD23	2.00	0.43
1:F:513:TRP:CH2	1:F:517:VAL:HG11	2.53	0.43
1:F:627:TYR:CD1	1:F:627:TYR:C	2.92	0.43
1:F:629:ASN:O	1:F:631:SER:N	2.51	0.43
1:C:533:LEU:HD23	2:Q:112:LEU:HD21	2.00	0.43
2:Q:109:MET:HG3	2:Q:116:LEU:HD11	2.00	0.43
2:Q:129:ASP:OD1	2:Q:134:GLY:N	2.39	0.43
2:R:101:SER:OG	2:R:104:GLU:HG2	2.18	0.43
2:S:29:THR:O	2:S:30:LYS:C	2.57	0.43
2:S:97:ASN:HD22	2:S:99:TYR:H	1.64	0.43
2:T:109:MET:HG3	2:T:116:LEU:HD11	2.00	0.43
2:T:68:PHE:C	2:T:70:THR:N	2.72	0.43
1:A:254:ARG:CD	1:A:254:ARG:H	2.19	0.43
1:A:435:LEU:HD23	1:A:435:LEU:HA	1.80	0.43
1:A:630:ARG:HH11	1:A:630:ARG:CG	2.24	0.43
1:A:70:GLU:HB2	1:A:107:THR:HG22	2.00	0.43
1:B:105:TYR:HE1	1:B:151:LYS:NZ	2.15	0.43
1:B:255:THR:HA	1:B:258:GLU:HB3	1.99	0.43
1:B:279:ILE:O	1:B:283:LEU:HB2	2.18	0.43
1:B:389:LYS:HA	1:B:392:THR:HB	2.01	0.43
1:B:508:ILE:HG21	1:B:513:TRP:HB2	2.00	0.43
1:B:684:ASP:C	1:B:686:ASP:H	2.21	0.43
1:B:792:VAL:O	1:B:793:PHE:C	2.56	0.43
1:B:90:PRO:HG2	1:B:93:VAL:CG1	2.48	0.43
1:C:191:GLU:O	1:C:194:ASN:N	2.50	0.43
1:C:218:LEU:HG	1:C:218:LEU:O	2.19	0.43
1:C:255:THR:HA	1:C:258:GLU:HB3	1.99	0.43
1:C:355:SER:HB2	1:C:371:SER:CA	2.41	0.43
1:C:549:LEU:HB2	1:C:553:GLN:HE21	1.82	0.43
1:C:560:LEU:O	1:C:563:ALA:HB3	2.19	0.43
1:C:657:ILE:CD1	1:C:701:LEU:HD23	2.48	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:357:TRP:CZ2	1:D:370:LEU:HD23	2.54	0.43
1:D:627:TYR:C	1:D:627:TYR:CD1	2.92	0.43
1:D:630:ARG:HH11	1:D:630:ARG:CG	2.24	0.43
1:E:131:ARG:HG3	1:E:243:LEU:HD13	2.00	0.43
1:E:746:LYS:HD2	1:E:747:ASN:HD22	1.83	0.43
1:E:765:THR:CA	1:E:769:SER:HB2	2.20	0.43
2:Q:68:PHE:C	2:Q:70:THR:N	2.72	0.43
2:T:29:THR:O	2:T:30:LYS:C	2.57	0.43
1:A:220:LEU:HG	1:A:223:LYS:HB3	2.01	0.43
1:A:234:LEU:CG	1:A:235:THR:H	2.32	0.43
1:A:331:VAL:O	1:A:332:ASN:C	2.56	0.43
1:A:395:GLU:C	1:A:397:GLU:H	2.20	0.43
1:A:648:PRO:O	1:A:649:ILE:C	2.57	0.43
1:B:144:GLU:O	1:B:144:GLU:HG3	2.18	0.43
1:B:189:ASP:HB3	1:B:190:PRO:CD	2.49	0.43
1:B:270:LYS:HA	1:B:273:LYS:HG3	1.99	0.43
1:B:305:SER:O	1:B:307:LEU:N	2.51	0.43
1:B:349:ASN:HB2	1:B:398:ILE:HG13	2.00	0.43
1:C:116:GLU:HG3	1:C:117:LEU:HD23	2.00	0.43
1:C:376:GLN:HB3	1:C:379:ALA:HB3	2.00	0.43
1:C:401:ILE:CG2	1:C:485:LEU:HB3	2.49	0.43
1:C:561:ASN:C	1:C:563:ALA:H	2.21	0.43
1:C:327:LEU:CD2	1:C:595:ILE:HG12	2.48	0.43
1:C:714:GLN:O	1:C:715:GLU:C	2.56	0.43
1:C:743:PRO:O	1:C:746:LYS:HB3	2.18	0.43
1:D:115:LYS:CE	1:D:116:GLU:HG2	2.48	0.43
1:D:188:LEU:H	1:D:188:LEU:HG	1.73	0.43
1:D:255:THR:HA	1:D:258:GLU:HB3	2.01	0.43
1:D:748:TYR:O	1:D:751:TYR:N	2.52	0.43
1:E:331:VAL:O	1:E:332:ASN:C	2.56	0.43
1:E:627:TYR:CD1	1:E:627:TYR:C	2.92	0.43
1:E:743:PRO:O	1:E:746:LYS:HB3	2.18	0.43
1:F:351:HIS:HB2	1:F:386:GLU:HG2	2.00	0.43
1:F:550:SER:H	1:F:553:GLN:NE2	2.13	0.43
1:F:656:THR:HG22	1:F:657:ILE:O	2.19	0.43
2:O:102:ALA:CB	2:O:125:ILE:HG13	2.46	0.43
2:R:29:THR:O	2:R:30:LYS:C	2.57	0.43
2:R:63:ILE:CG2	2:R:67:GLU:CB	2.97	0.43
2:S:68:PHE:C	2:S:70:THR:N	2.71	0.43
2:T:101:SER:OG	2:T:104:GLU:HG2	2.19	0.43
2:T:92:PHE:CD1	2:T:92:PHE:N	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:112:VAL:O	1:A:114:HIS:N	2.51	0.43
1:A:191:GLU:O	1:A:193:LEU:N	2.52	0.43
1:A:391:ILE:HG12	1:A:399:GLY:HA2	2.01	0.43
1:A:741:ILE:HG13	1:A:741:ILE:O	2.18	0.43
1:B:176:GLY:O	1:B:178:SER:N	2.51	0.43
1:B:345:THR:CG2	1:B:491:ASP:HA	2.49	0.43
1:B:753:LYS:O	1:B:754:GLU:C	2.56	0.43
1:C:140:ARG:NH1	1:C:141:PHE:HE1	2.16	0.43
1:C:234:LEU:CG	1:C:235:THR:H	2.32	0.43
1:D:180:ASP:O	1:D:182:ILE:N	2.52	0.43
1:D:319:ALA:O	1:D:323:ASN:HA	2.19	0.43
1:D:349:ASN:HB2	1:D:398:ILE:HG13	2.00	0.43
1:D:89:ILE:CG2	1:D:90:PRO:HD2	2.49	0.43
1:E:293:ILE:HG12	1:E:293:ILE:H	1.44	0.43
1:E:70:GLU:HB2	1:E:107:THR:HG22	2.01	0.43
1:F:435:LEU:HG	1:F:446:ILE:CG2	2.47	0.43
1:F:520:PRO:CG	1:F:521:ASN:H	2.31	0.43
2:O:105:LEU:HD21	2:O:124:MET:SD	2.59	0.43
2:P:65:PHE:HB3	2:P:66:PRO:HD3	2.00	0.43
2:Q:45:GLU:CD	2:Q:45:GLU:N	2.69	0.43
2:Q:65:PHE:O	2:Q:68:PHE:HB3	2.19	0.43
2:R:41:GLN:C	2:R:43:PRO:CD	2.80	0.43
2:T:45:GLU:N	2:T:45:GLU:CD	2.70	0.43
1:A:175:LYS:O	1:A:176:GLY:C	2.56	0.43
1:A:180:ASP:O	1:A:182:ILE:N	2.52	0.43
1:A:679:TYR:CG	1:A:691:LYS:HB2	2.54	0.43
1:A:708:ALA:C	1:A:710:HIS:H	2.22	0.43
1:B:441:VAL:HG11	1:B:462:ILE:O	2.19	0.43
1:B:482:GLU:OE2	1:B:482:GLU:HA	2.18	0.43
1:B:688:PHE:HD2	1:B:688:PHE:C	2.22	0.43
1:B:775:LEU:O	1:B:778:LYS:N	2.52	0.43
1:C:202:ASP:HB2	1:C:208:LEU:CD2	2.49	0.43
1:C:357:TRP:CZ2	1:C:370:LEU:HD23	2.54	0.43
1:C:435:LEU:HA	1:C:435:LEU:HD23	1.81	0.43
1:C:508:ILE:HG12	1:C:536:TYR:CD2	2.54	0.43
1:D:197:LYS:HD3	1:D:263:ASP:CG	2.40	0.43
1:D:271:LEU:HA	1:D:275:GLY:HA3	2.01	0.43
1:D:679:TYR:CG	1:D:691:LYS:HB2	2.54	0.43
1:E:181:ILE:O	1:E:181:ILE:HG12	2.17	0.43
1:F:205:SER:C	1:F:207:ASP:N	2.71	0.43
1:F:368:GLN:HB2	1:F:380:VAL:HG13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:29:THR:O	2:O:30:LYS:C	2.57	0.43
2:S:115:LYS:CA	2:S:115:LYS:NZ	2.81	0.43
1:E:668:SER:N	2:S:14:GLU:OE1	2.52	0.43
2:T:117:THR:HG23	2:T:120:GLU:HG3	2.00	0.43
2:T:65:PHE:O	2:T:68:PHE:HB3	2.19	0.43
1:A:656:THR:O	1:A:755:ARG:HD2	2.17	0.42
1:A:93:VAL:CG1	1:A:94:LEU:N	2.82	0.42
1:B:111:LEU:HD23	1:B:155:ASN:ND2	2.33	0.42
1:B:263:ASP:O	1:B:264:MET:C	2.57	0.42
1:B:281:GLU:O	1:B:285:LYS:HG2	2.19	0.42
1:B:308:VAL:O	1:B:311:HIS:N	2.46	0.42
1:B:376:GLN:HB3	1:B:379:ALA:HB3	2.01	0.42
1:B:368:GLN:HB2	1:B:380:VAL:HG13	2.01	0.42
1:B:554:LYS:O	1:B:557:LEU:N	2.51	0.42
1:B:748:TYR:O	1:B:751:TYR:N	2.52	0.42
1:C:77:ASP:OD1	1:C:159:TYR:HE2	2.01	0.42
1:C:335:ALA:HA	1:C:338:LEU:HG	2.01	0.42
1:C:595:ILE:HG22	1:C:596:ILE:H	1.83	0.42
1:C:730:ASN:O	1:C:733:GLU:N	2.52	0.42
1:D:111:LEU:HD23	1:D:155:ASN:ND2	2.31	0.42
1:D:732:ILE:O	1:D:733:GLU:C	2.57	0.42
1:D:752:LEU:HD23	1:D:752:LEU:HA	1.78	0.42
1:D:663:PHE:CD1	1:D:752:LEU:HD11	2.54	0.42
1:E:360:VAL:CG1	1:E:370:LEU:HD22	2.44	0.42
1:E:349:ASN:HB2	1:E:398:ILE:HG13	2.00	0.42
1:E:343:VAL:HG13	1:E:487:PRO:O	2.19	0.42
1:E:504:ILE:CD1	1:E:504:ILE:H	2.32	0.42
1:E:89:ILE:HG22	1:E:90:PRO:HD2	2.00	0.42
1:F:718:ARG:NH1	1:F:767:GLN:HE21	2.17	0.42
2:P:117:THR:HG23	2:P:120:GLU:HG3	2.00	0.42
2:P:29:THR:O	2:P:30:LYS:C	2.57	0.42
2:Q:117:THR:HG23	2:Q:120:GLU:CG	2.49	0.42
2:S:146:THR:O	2:S:147:ALA:C	2.54	0.42
2:S:70:THR:O	2:S:72:MET:N	2.52	0.42
2:T:81:SER:O	2:T:82:GLU:C	2.58	0.42
1:A:376:GLN:HB3	1:A:379:ALA:HB3	2.01	0.42
1:B:395:GLU:C	1:B:397:GLU:H	2.21	0.42
1:B:408:LEU:CD1	1:B:408:LEU:H	2.03	0.42
1:B:665:LYS:O	1:B:668:SER:HB3	2.19	0.42
1:B:679:TYR:CG	1:B:691:LYS:HB2	2.53	0.42
1:C:181:ILE:O	1:C:181:ILE:HG12	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:297:LYS:HB3	1:C:297:LYS:HZ3	1.83	0.42
1:C:732:ILE:O	1:C:733:GLU:C	2.58	0.42
1:D:252:ASP:O	1:D:254:ARG:HD2	2.20	0.42
1:D:687:GLU:O	1:D:690:LYS:N	2.52	0.42
1:D:89:ILE:HG13	1:D:89:ILE:H	1.57	0.42
1:E:295:VAL:C	1:E:296:LEU:CD2	2.81	0.42
1:E:397:GLU:O	1:E:398:ILE:HD13	2.19	0.42
1:E:401:ILE:CG2	1:E:485:LEU:HB3	2.49	0.42
1:E:517:VAL:HB	1:E:525:LYS:HZ1	1.84	0.42
1:E:665:LYS:O	1:E:668:SER:HB3	2.18	0.42
1:F:234:LEU:CG	1:F:235:THR:H	2.32	0.42
1:F:271:LEU:HB3	1:F:276:PHE:CE2	2.54	0.42
1:F:441:VAL:HG11	1:F:462:ILE:O	2.19	0.42
1:F:456:LYS:HD3	1:F:471:TRP:H	1.84	0.42
1:F:508:ILE:HG21	1:F:513:TRP:HB2	1.99	0.42
1:F:93:VAL:HG13	1:F:94:LEU:N	2.33	0.42
2:O:65:PHE:HB3	2:O:66:PRO:HD3	2.00	0.42
1:B:630:ARG:NH1	2:P:83:GLU:HG2	2.34	0.42
2:Q:29:THR:O	2:Q:30:LYS:C	2.57	0.42
2:Q:33:GLY:O	2:Q:34:THR:C	2.58	0.42
2:R:68:PHE:C	2:R:70:THR:N	2.72	0.42
2:S:86:ARG:O	2:S:86:ARG:HG2	2.18	0.42
1:A:401:ILE:CG2	1:A:485:LEU:HB3	2.49	0.42
1:A:529:VAL:HG21	2:O:109:MET:HE1	2.00	0.42
1:A:508:ILE:HG12	1:A:536:TYR:CD2	2.54	0.42
1:A:292:ARG:NE	1:A:617:LYS:HE3	2.35	0.42
1:A:657:ILE:CD1	1:A:701:LEU:HD23	2.50	0.42
1:A:97:TYR:CE1	1:A:178:SER:CB	2.92	0.42
1:B:252:ASP:O	1:B:254:ARG:HD2	2.19	0.42
1:B:398:ILE:CD1	1:B:479:LYS:HB3	2.50	0.42
1:B:540:ARG:NH1	1:B:627:TYR:CE1	2.87	0.42
1:B:764:LEU:HD23	1:B:764:LEU:HA	1.87	0.42
1:C:175:LYS:O	1:C:176:GLY:C	2.56	0.42
1:C:217:LYS:NZ	1:C:233:ASN:HB3	2.33	0.42
1:C:349:ASN:HD22	1:C:350:VAL:H	1.67	0.42
1:F:173:ILE:HA	1:F:242:SER:HB3	1.99	0.42
2:O:63:ILE:CG2	2:O:67:GLU:CB	2.97	0.42
1:B:668:SER:N	2:P:14:GLU:OE1	2.52	0.42
2:P:92:PHE:CD1	2:P:92:PHE:N	2.86	0.42
2:R:33:GLY:O	2:R:34:THR:C	2.58	0.42
2:R:65:PHE:HB3	2:R:66:PRO:HD3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:695:LYS:CB	2:S:18:LEU:HD22	2.39	0.42
2:S:81:SER:O	2:S:82:GLU:C	2.58	0.42
1:F:630:ARG:NH1	2:T:83:GLU:HG2	2.34	0.42
1:A:288:VAL:O	1:A:291:ASP:O	2.36	0.42
1:A:332:ASN:OD1	1:A:334:LEU:HB2	2.18	0.42
1:A:327:LEU:CG	1:A:595:ILE:HG12	2.48	0.42
1:A:668:SER:N	2:O:14:GLU:OE1	2.52	0.42
1:B:234:LEU:CG	1:B:235:THR:H	2.31	0.42
1:B:255:THR:C	1:B:257:LEU:N	2.73	0.42
1:B:714:GLN:O	1:B:715:GLU:C	2.57	0.42
1:B:730:ASN:O	1:B:733:GLU:N	2.52	0.42
1:B:765:THR:CA	1:B:769:SER:HB2	2.21	0.42
1:C:220:LEU:HG	1:C:223:LYS:HB3	2.02	0.42
1:C:301:ALA:O	1:C:304:ALA:N	2.46	0.42
1:D:161:ILE:CG2	1:D:168:GLU:OE2	2.68	0.42
1:D:349:ASN:HD22	1:D:350:VAL:H	1.67	0.42
1:D:389:LYS:HA	1:D:392:THR:HB	2.00	0.42
1:D:71:PHE:C	1:D:73:ASN:H	2.22	0.42
1:D:749:PHE:O	1:D:753:LYS:HG3	2.20	0.42
1:D:93:VAL:CG1	1:D:94:LEU:N	2.82	0.42
1:E:140:ARG:NH1	1:E:141:PHE:HE1	2.18	0.42
1:E:179:LEU:CG	1:E:180:ASP:H	2.31	0.42
1:E:205:SER:C	1:E:207:ASP:N	2.72	0.42
1:E:398:ILE:CD1	1:E:479:LYS:HB3	2.49	0.42
1:E:420:LEU:HD13	1:E:420:LEU:O	2.19	0.42
1:E:447:SER:OG	1:E:448:ASP:N	2.51	0.42
1:E:335:ALA:HB1	1:E:489:THR:OG1	2.19	0.42
1:E:329:ARG:CD	1:E:590:ASP:OD2	2.63	0.42
1:E:747:ASN:HD22	1:E:747:ASN:N	2.17	0.42
1:F:188:LEU:HD12	1:F:191:GLU:HG3	2.02	0.42
1:F:217:LYS:NZ	1:F:233:ASN:HB3	2.33	0.42
1:F:324:THR:CG2	1:F:499:PRO:HA	2.49	0.42
1:F:520:PRO:CG	1:F:521:ASN:N	2.83	0.42
1:F:561:ASN:C	1:F:563:ALA:H	2.22	0.42
1:F:679:TYR:CG	1:F:691:LYS:HB2	2.55	0.42
2:O:89:PHE:HB2	2:O:141:PHE:CD2	2.54	0.42
2:P:136:VAL:HG23	2:P:136:VAL:O	2.19	0.42
2:P:50:ASP:HA	2:P:53:ASN:CB	2.33	0.42
1:A:263:ASP:O	1:A:265:PHE:N	2.52	0.42
1:A:281:GLU:O	1:A:285:LYS:HG2	2.20	0.42
1:A:305:SER:O	1:A:307:LEU:N	2.51	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:420:LEU:O	1:A:420:LEU:HD13	2.20	0.42
1:A:441:VAL:HG11	1:A:462:ILE:O	2.19	0.42
1:A:329:ARG:CD	1:A:590:ASP:OD2	2.64	0.42
1:A:97:TYR:HA	1:A:100:LEU:HD12	2.00	0.42
1:B:140:ARG:NH1	1:B:141:PHE:HE1	2.18	0.42
1:B:214:PHE:CB	1:B:218:LEU:HB3	2.40	0.42
1:B:360:VAL:CG1	1:B:370:LEU:HD22	2.44	0.42
1:C:718:ARG:NH1	1:C:767:GLN:HE21	2.18	0.42
1:D:142:VAL:HG13	1:D:154:ILE:HD11	2.01	0.42
1:D:216:GLU:HG3	1:D:217:LYS:HG2	2.02	0.42
1:D:335:ALA:HA	1:D:338:LEU:HG	2.00	0.42
1:D:348:LEU:HA	1:D:348:LEU:HD23	1.93	0.42
1:D:384:ASN:O	1:D:386:GLU:N	2.52	0.42
1:D:523:LEU:HD22	2:R:127:GLU:HG2	2.02	0.42
1:D:532:LEU:HD23	1:D:532:LEU:HA	1.84	0.42
1:E:77:ASP:OD1	1:E:159:TYR:HE2	2.02	0.42
1:E:671:ARG:NH1	1:E:671:ARG:HG3	2.34	0.42
1:E:775:LEU:O	1:E:778:LYS:N	2.53	0.42
1:E:794:GLN:HE21	1:E:794:GLN:HB3	1.60	0.42
1:F:265:PHE:C	1:F:267:TYR:H	2.22	0.42
1:F:357:TRP:CZ2	1:F:370:LEU:HD23	2.54	0.42
1:F:408:LEU:H	1:F:408:LEU:CD1	2.00	0.42
1:F:504:ILE:H	1:F:504:ILE:CD1	2.33	0.42
1:F:671:ARG:HG3	1:F:671:ARG:NH1	2.33	0.42
2:O:45:GLU:CD	2:O:45:GLU:N	2.71	0.42
2:P:68:PHE:C	2:P:70:THR:N	2.72	0.42
2:R:136:VAL:O	2:R:136:VAL:HG23	2.20	0.42
2:T:5:THR:OG1	2:T:6:GLU:N	2.51	0.42
1:A:115:LYS:CB	1:A:118:GLN:CG	2.91	0.42
1:A:349:ASN:HB2	1:A:398:ILE:HG13	2.01	0.42
1:A:360:VAL:HA	1:A:403:LEU:HD21	2.01	0.42
1:A:389:LYS:HA	1:A:392:THR:HB	2.00	0.42
1:A:398:ILE:CD1	1:A:479:LYS:HB3	2.50	0.42
1:B:332:ASN:OD1	1:B:334:LEU:N	2.45	0.42
1:B:324:THR:CG2	1:B:499:PRO:HA	2.48	0.42
1:B:327:LEU:CG	1:B:595:ILE:HG12	2.49	0.42
1:C:173:ILE:HG13	1:C:242:SER:CB	2.49	0.42
1:C:653:LYS:C	1:C:655:ASN:N	2.72	0.42
1:D:480:ASN:HD22	1:D:481:VAL:H	1.66	0.42
1:D:654:ILE:O	1:D:654:ILE:HG22	2.18	0.42
1:E:197:LYS:HD3	1:E:263:ASP:CG	2.40	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:301:ALA:O	1:E:304:ALA:N	2.44	0.42
1:E:687:GLU:O	1:E:690:LYS:N	2.52	0.42
1:E:719:LYS:O	1:E:722:ILE:N	2.53	0.42
1:E:749:PHE:O	1:E:753:LYS:HG3	2.20	0.42
1:F:173:ILE:HG13	1:F:242:SER:CB	2.49	0.42
1:F:305:SER:O	1:F:307:LEU:N	2.52	0.42
2:O:117:THR:HG23	2:O:120:GLU:HG3	2.01	0.42
2:Q:9:ILE:HG23	2:Q:69:LEU:HD21	2.02	0.42
2:S:5:THR:OG1	2:S:6:GLU:N	2.51	0.42
2:T:106:ARG:CB	2:T:121:VAL:HG21	2.47	0.42
1:A:255:THR:C	1:A:257:LEU:N	2.71	0.42
1:A:279:ILE:O	1:A:283:LEU:HB2	2.19	0.42
1:A:520:PRO:CG	1:A:521:ASN:H	2.32	0.42
1:A:627:TYR:C	1:A:627:TYR:CD1	2.93	0.42
1:A:683:GLY:O	1:A:684:ASP:C	2.55	0.42
1:B:360:VAL:HA	1:B:403:LEU:HD21	2.02	0.42
1:B:671:ARG:HG3	1:B:671:ARG:NH1	2.35	0.42
1:B:683:GLY:O	1:B:684:ASP:C	2.57	0.42
1:B:706:ASN:OD1	1:B:707:SER:N	2.52	0.42
1:C:305:SER:O	1:C:307:LEU:N	2.52	0.42
1:C:520:PRO:CG	1:C:521:ASN:H	2.32	0.42
1:C:648:PRO:O	1:C:649:ILE:C	2.57	0.42
1:D:140:ARG:NH1	1:D:141:PHE:HE1	2.17	0.42
1:D:179:LEU:O	1:D:182:ILE:HG22	2.20	0.42
1:D:197:LYS:O	1:D:197:LYS:NZ	2.46	0.42
1:D:202:ASP:HB2	1:D:208:LEU:CD2	2.49	0.42
1:D:441:VAL:HG11	1:D:462:ILE:O	2.18	0.42
1:D:512:GLU:O	1:D:515:LYS:NZ	2.53	0.42
1:D:543:ASP:OD1	1:D:544:SER:N	2.53	0.42
1:D:765:THR:CA	1:D:769:SER:HB2	2.22	0.42
1:E:144:GLU:HG3	1:E:144:GLU:O	2.18	0.42
1:E:217:LYS:NZ	1:E:233:ASN:HB3	2.33	0.42
1:E:357:TRP:CZ2	1:E:370:LEU:HD23	2.54	0.42
1:E:389:LYS:HA	1:E:392:THR:HB	2.01	0.42
1:E:519:THR:HG21	1:E:525:LYS:HA	2.01	0.42
1:E:520:PRO:CG	1:E:521:ASN:H	2.32	0.42
1:E:764:LEU:HD23	1:E:764:LEU:HA	1.87	0.42
1:F:414:LYS:C	1:F:414:LYS:HD3	2.40	0.42
1:F:497:LEU:HD13	1:F:556:MET:HG2	2.02	0.42
1:F:523:LEU:HD11	2:T:144:MET:HG3	2.01	0.42
1:F:775:LEU:O	1:F:778:LYS:N	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:O:57:ALA:O	2:O:59:GLY:N	2.53	0.42
2:P:5:THR:OG1	2:P:6:GLU:N	2.52	0.42
2:R:138:TYR:CE1	2:R:142:VAL:HG22	2.55	0.42
1:D:523:LEU:HD11	2:R:144:MET:HG3	2.00	0.42
2:R:65:PHE:O	2:R:68:PHE:HB3	2.19	0.42
1:A:181:ILE:HG12	1:A:181:ILE:O	2.20	0.42
1:A:216:GLU:HG3	1:A:217:LYS:HG2	2.02	0.42
1:A:301:ALA:O	1:A:304:ALA:N	2.45	0.42
1:A:335:ALA:HB1	1:A:489:THR:OG1	2.20	0.42
1:A:622:LYS:HA	1:A:622:LYS:HD3	1.85	0.42
1:A:667:LEU:O	1:A:668:SER:C	2.58	0.42
1:A:718:ARG:NH1	1:A:767:GLN:HE21	2.16	0.42
1:B:191:GLU:C	1:B:193:LEU:N	2.73	0.42
1:B:202:ASP:HB2	1:B:208:LEU:CD2	2.49	0.42
1:B:343:VAL:HG13	1:B:487:PRO:O	2.20	0.42
1:B:551:ASN:O	1:B:554:LYS:HB3	2.20	0.42
1:B:653:LYS:C	1:B:655:ASN:N	2.71	0.42
1:B:744:GLU:H	1:B:744:GLU:CD	2.22	0.42
1:C:281:GLU:O	1:C:285:LYS:HG2	2.19	0.42
1:C:356:ASP:N	1:C:356:ASP:OD2	2.51	0.42
1:C:368:GLN:HB2	1:C:380:VAL:HG13	2.01	0.42
1:C:420:LEU:O	1:C:420:LEU:HD13	2.20	0.42
1:C:520:PRO:CG	1:C:521:ASN:N	2.83	0.42
1:C:523:LEU:HD11	2:Q:144:MET:HG3	2.01	0.42
1:D:225:ILE:HG23	1:D:229:PHE:HD2	1.82	0.42
1:D:482:GLU:OE2	1:D:482:GLU:HA	2.19	0.42
1:D:350:VAL:HG21	1:D:488:LEU:HD12	2.01	0.42
1:D:515:LYS:HZ3	1:D:515:LYS:HB3	1.83	0.42
1:D:549:LEU:HB2	1:D:553:GLN:HE21	1.84	0.42
1:D:657:ILE:CD1	1:D:701:LEU:HD23	2.50	0.42
1:D:70:GLU:HB2	1:D:107:THR:HG22	2.01	0.42
1:E:128:MET:CE	1:E:235:THR:HB	2.49	0.42
1:E:288:VAL:O	1:E:291:ASP:O	2.38	0.42
1:E:520:PRO:CG	1:E:521:ASN:N	2.83	0.42
1:E:667:LEU:O	1:E:668:SER:C	2.58	0.42
1:E:713:SER:O	1:E:714:GLN:C	2.57	0.42
1:F:181:ILE:HG12	1:F:181:ILE:O	2.19	0.42
1:F:288:VAL:O	1:F:291:ASP:O	2.38	0.42
1:F:304:ALA:HB3	1:F:604:LEU:HD22	2.01	0.42
1:F:323:ASN:HD22	1:F:598:PRO:CB	2.33	0.42
1:F:389:LYS:HA	1:F:392:THR:HB	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:401:ILE:CG2	1:F:485:LEU:HB3	2.48	0.42
1:F:622:LYS:HD3	1:F:622:LYS:HA	1.85	0.42
2:O:48:LEU:HD23	2:O:51:MET:HE2	2.01	0.42
2:P:18:LEU:HA	2:P:18:LEU:HD23	1.75	0.42
2:P:33:GLY:O	2:P:34:THR:C	2.58	0.42
2:R:117:THR:HG23	2:R:120:GLU:CG	2.49	0.42
1:A:172:GLU:HG3	1:A:245:PHE:CE1	2.55	0.42
1:B:179:LEU:CG	1:B:180:ASP:N	2.78	0.42
1:B:181:ILE:O	1:B:181:ILE:HG12	2.20	0.42
1:B:323:ASN:HD22	1:B:598:PRO:CB	2.33	0.42
1:B:357:TRP:CZ2	1:B:370:LEU:HD23	2.54	0.42
1:B:529:VAL:HG21	2:P:109:MET:HE3	2.02	0.42
1:B:654:ILE:O	1:B:654:ILE:HG22	2.20	0.42
1:C:350:VAL:HG21	1:C:488:LEU:HD12	2.01	0.42
1:C:719:LYS:O	1:C:722:ILE:N	2.52	0.42
1:C:741:ILE:O	1:C:741:ILE:HG13	2.20	0.42
1:D:88:LYS:NZ	1:D:172:GLU:CD	2.72	0.42
1:D:279:ILE:O	1:D:283:LEU:HB2	2.19	0.42
1:D:435:LEU:HG	1:D:446:ILE:CG2	2.48	0.42
1:D:447:SER:OG	1:D:448:ASP:N	2.52	0.42
1:D:561:ASN:C	1:D:563:ALA:H	2.22	0.42
1:E:173:ILE:CG2	1:E:174:GLY:N	2.82	0.42
1:E:202:ASP:HB2	1:E:208:LEU:CD2	2.50	0.42
1:E:368:GLN:C	1:E:370:LEU:H	2.23	0.42
1:E:368:GLN:HB2	1:E:380:VAL:HG13	2.02	0.42
1:E:345:THR:CG2	1:E:491:ASP:HA	2.50	0.42
1:E:508:ILE:HG12	1:E:536:TYR:CD2	2.55	0.42
1:E:653:LYS:C	1:E:655:ASN:N	2.72	0.42
1:F:140:ARG:NH1	1:F:141:PHE:HE1	2.17	0.42
1:F:144:GLU:HG3	1:F:144:GLU:O	2.19	0.42
1:F:335:ALA:HB1	1:F:489:THR:OG1	2.19	0.42
1:F:339:ILE:O	1:F:340:LYS:C	2.59	0.42
1:F:741:ILE:O	1:F:741:ILE:HG13	2.19	0.42
1:B:501:LEU:HD13	2:P:108:VAL:HG13	2.02	0.42
1:B:513:TRP:HZ2	2:P:114:GLU:HB2	1.82	0.42
2:P:57:ALA:O	2:P:59:GLY:N	2.53	0.42
1:A:77:ASP:OD1	1:A:159:TYR:HE2	2.03	0.42
1:A:176:GLY:O	1:A:178:SER:N	2.53	0.42
1:A:270:LYS:HA	1:A:273:LYS:CG	2.50	0.42
1:A:684:ASP:C	1:A:686:ASP:H	2.22	0.42
1:A:765:THR:CA	1:A:769:SER:HB2	2.21	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:96:ILE:HG22	1:A:100:LEU:CD1	2.49	0.42
1:B:220:LEU:HG	1:B:223:LYS:HB3	2.02	0.42
1:B:719:LYS:O	1:B:722:ILE:N	2.53	0.42
1:C:96:ILE:O	1:C:100:LEU:HD12	2.20	0.42
1:C:324:THR:CG2	1:C:499:PRO:HA	2.49	0.42
1:C:527:LYS:HB3	1:C:527:LYS:HE2	1.84	0.42
1:C:97:TYR:CE1	1:C:178:SER:CB	2.93	0.42
1:D:176:GLY:C	1:D:178:SER:H	2.23	0.42
1:D:181:ILE:HG12	1:D:181:ILE:O	2.20	0.42
1:D:636:ALA:HA	1:D:637:PRO:HD3	1.82	0.42
1:E:355:SER:HB2	1:E:371:SER:CA	2.43	0.42
1:E:384:ASN:O	1:E:386:GLU:N	2.53	0.42
1:E:480:ASN:HD22	1:E:481:VAL:H	1.68	0.42
1:E:480:ASN:ND2	1:E:483:GLY:CA	2.81	0.42
1:E:540:ARG:HH22	1:E:630:ARG:HE	1.68	0.42
1:E:657:ILE:CD1	1:E:701:LEU:HD23	2.50	0.42
1:F:184:LYS:HD2	1:F:191:GLU:HB2	2.02	0.42
1:F:220:LEU:HG	1:F:223:LYS:HB3	2.02	0.42
1:F:665:LYS:O	1:F:668:SER:HB3	2.20	0.42
1:F:688:PHE:HD2	1:F:688:PHE:C	2.21	0.42
1:A:533:LEU:HD23	2:O:112:LEU:HD21	2.02	0.42
2:O:65:PHE:CE2	2:O:69:LEU:HG	2.55	0.42
2:P:86:ARG:O	2:P:86:ARG:HG2	2.19	0.42
2:Q:115:LYS:NZ	2:Q:115:LYS:CA	2.79	0.42
2:Q:13:LYS:C	2:Q:15:ALA:N	2.70	0.42
2:S:89:PHE:HB2	2:S:141:PHE:CE2	2.55	0.42
2:T:138:TYR:CE1	2:T:142:VAL:HG22	2.55	0.42
1:A:127:SER:OG	1:A:135:VAL:HG21	2.20	0.41
1:A:447:SER:OG	1:A:448:ASP:N	2.52	0.41
1:A:520:PRO:CG	1:A:521:ASN:N	2.83	0.41
1:A:746:LYS:HD2	1:A:747:ASN:HD22	1.84	0.41
1:B:257:LEU:O	1:B:261:ALA:O	2.38	0.41
1:B:271:LEU:HA	1:B:275:GLY:HA3	2.02	0.41
1:B:345:THR:HG21	1:B:491:ASP:HA	2.02	0.41
1:B:549:LEU:HB2	1:B:553:GLN:HE21	1.85	0.41
1:C:441:VAL:HG11	1:C:462:ILE:O	2.19	0.41
1:C:606:LYS:HB2	1:C:610:MET:CE	2.50	0.41
1:C:679:TYR:CG	1:C:691:LYS:HB2	2.55	0.41
1:D:376:GLN:HB3	1:D:379:ALA:HB3	2.01	0.41
1:D:456:LYS:HD3	1:D:471:TRP:H	1.84	0.41
1:D:530:THR:O	1:D:534:ILE:HG13	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:744:GLU:CD	1:D:744:GLU:H	2.22	0.41
1:D:90:PRO:HG3	1:D:249:PHE:CZ	2.54	0.41
1:D:92:ASP:O	1:D:93:VAL:C	2.58	0.41
1:E:414:LYS:C	1:E:414:LYS:HD3	2.40	0.41
1:E:324:THR:CG2	1:E:499:PRO:HA	2.48	0.41
1:E:656:THR:O	1:E:755:ARG:HD2	2.20	0.41
1:F:96:ILE:O	1:F:100:LEU:HD12	2.19	0.41
1:F:111:LEU:HD23	1:F:155:ASN:ND2	2.33	0.41
1:F:179:LEU:O	1:F:182:ILE:HG22	2.20	0.41
1:F:252:ASP:O	1:F:254:ARG:HD2	2.19	0.41
1:F:356:ASP:OD2	1:F:356:ASP:N	2.52	0.41
1:F:368:GLN:C	1:F:370:LEU:H	2.24	0.41
1:F:343:VAL:HG13	1:F:487:PRO:O	2.20	0.41
2:O:81:SER:O	2:O:82:GLU:C	2.58	0.41
2:S:65:PHE:CE2	2:S:69:LEU:HG	2.55	0.41
1:A:409:ARG:O	1:A:413:LEU:HG	2.20	0.41
1:A:512:GLU:O	1:A:515:LYS:NZ	2.53	0.41
1:A:792:VAL:O	1:A:793:PHE:C	2.57	0.41
1:B:205:SER:C	1:B:207:ASP:N	2.73	0.41
1:B:229:PHE:O	1:B:231:LYS:N	2.54	0.41
1:B:718:ARG:NH1	1:B:767:GLN:HE21	2.16	0.41
1:C:105:TYR:HE1	1:C:151:LYS:NZ	2.14	0.41
1:C:171:TYR:CD1	1:C:175:LYS:NZ	2.85	0.41
1:C:218:LEU:C	1:C:220:LEU:H	2.14	0.41
1:C:265:PHE:C	1:C:267:TYR:H	2.23	0.41
1:C:389:LYS:HA	1:C:392:THR:HB	2.01	0.41
1:C:343:VAL:HG13	1:C:487:PRO:O	2.20	0.41
1:C:551:ASN:O	1:C:554:LYS:HB3	2.20	0.41
1:D:265:PHE:C	1:D:267:TYR:H	2.23	0.41
1:E:279:ILE:O	1:E:283:LEU:HB2	2.20	0.41
1:E:408:LEU:H	1:E:408:LEU:CD1	2.02	0.41
1:E:482:GLU:OE2	1:E:482:GLU:HA	2.20	0.41
1:F:154:ILE:HG21	1:F:171:TYR:CD2	2.55	0.41
1:F:725:GLY:O	1:F:726:ILE:C	2.58	0.41
2:Q:138:TYR:CE1	2:Q:142:VAL:HG22	2.55	0.41
2:Q:86:ARG:HG2	2:Q:86:ARG:O	2.20	0.41
2:R:57:ALA:O	2:R:59:GLY:N	2.54	0.41
2:S:63:ILE:CG2	2:S:67:GLU:CB	2.98	0.41
1:F:523:LEU:HD22	2:T:127:GLU:HG2	2.01	0.41
1:A:197:LYS:HD3	1:A:263:ASP:CG	2.40	0.41
1:A:349:ASN:HD22	1:A:350:VAL:H	1.68	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:504:ILE:N	1:A:504:ILE:CD1	2.84	0.41
1:B:223:LYS:NZ	1:B:228:ASN:HB2	2.35	0.41
1:B:288:VAL:O	1:B:291:ASP:O	2.38	0.41
1:B:350:VAL:HG12	1:B:351:HIS:N	2.34	0.41
1:B:512:GLU:O	1:B:515:LYS:NZ	2.53	0.41
1:C:121:SER:HB2	1:C:122:GLU:OE2	2.19	0.41
1:C:176:GLY:C	1:C:178:SER:H	2.23	0.41
1:C:368:GLN:HG3	1:C:383:GLY:HA3	2.03	0.41
1:D:270:LYS:HA	1:D:273:LYS:CG	2.50	0.41
1:D:350:VAL:HG12	1:D:351:HIS:N	2.35	0.41
1:D:401:ILE:CG2	1:D:485:LEU:HB3	2.50	0.41
1:D:508:ILE:HG12	1:D:536:TYR:CD2	2.55	0.41
1:D:540:ARG:HH22	1:D:630:ARG:HE	1.67	0.41
1:E:111:LEU:HD23	1:E:155:ASN:ND2	2.34	0.41
1:E:188:LEU:H	1:E:188:LEU:HG	1.73	0.41
1:E:165:GLN:CD	1:E:252:ASP:HB3	2.39	0.41
1:E:263:ASP:O	1:E:264:MET:C	2.58	0.41
1:E:339:ILE:O	1:E:340:LYS:C	2.58	0.41
1:E:456:LYS:HD3	1:E:471:TRP:H	1.84	0.41
1:E:648:PRO:O	1:E:649:ILE:C	2.58	0.41
1:E:744:GLU:H	1:E:744:GLU:CD	2.23	0.41
1:F:71:PHE:CD1	1:F:108:ASP:OD1	2.73	0.41
1:F:263:ASP:O	1:F:264:MET:C	2.58	0.41
1:F:635:ILE:N	1:F:635:ILE:HD12	2.36	0.41
1:F:748:TYR:O	1:F:751:TYR:N	2.53	0.41
1:F:749:PHE:O	1:F:753:LYS:HG3	2.20	0.41
1:F:790:PHE:O	1:F:791:GLU:C	2.59	0.41
2:Q:44:THR:OG1	2:Q:47:GLU:HG3	2.20	0.41
1:D:533:LEU:HD23	2:R:112:LEU:HD21	2.02	0.41
2:R:117:THR:HG23	2:R:120:GLU:HG3	2.02	0.41
2:S:117:THR:HG23	2:S:120:GLU:HG3	2.01	0.41
2:S:9:ILE:HG23	2:S:69:LEU:HD21	2.02	0.41
2:T:56:ASP:C	2:T:58:ASP:H	2.24	0.41
2:T:70:THR:O	2:T:72:MET:N	2.54	0.41
1:A:106:PHE:CZ	1:A:171:TYR:OH	2.66	0.41
1:A:188:LEU:H	1:A:188:LEU:HG	1.73	0.41
1:A:480:ASN:HD22	1:A:481:VAL:H	1.67	0.41
1:A:744:GLU:H	1:A:744:GLU:CD	2.22	0.41
1:A:76:LEU:O	1:A:80:GLN:N	2.47	0.41
1:A:790:PHE:O	1:A:791:GLU:C	2.58	0.41
1:B:115:LYS:O	1:B:117:LEU:N	2.53	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:368:GLN:HG3	1:B:383:GLY:HA3	2.03	0.41
1:B:532:LEU:HD23	1:B:532:LEU:HA	1.83	0.41
1:B:635:ILE:N	1:B:635:ILE:HD12	2.33	0.41
1:B:687:GLU:O	1:B:690:LYS:N	2.53	0.41
1:B:663:PHE:CD1	1:B:752:LEU:HD11	2.55	0.41
1:C:255:THR:C	1:C:257:LEU:N	2.72	0.41
1:C:288:VAL:CG2	1:C:289:GLU:H	2.22	0.41
1:C:292:ARG:NE	1:C:617:LYS:HE3	2.35	0.41
1:C:350:VAL:HG12	1:C:351:HIS:N	2.35	0.41
1:C:550:SER:H	1:C:553:GLN:NE2	2.16	0.41
1:C:665:LYS:O	1:C:668:SER:HB3	2.20	0.41
1:C:729:TYR:O	1:C:732:ILE:N	2.51	0.41
1:C:663:PHE:CD1	1:C:752:LEU:HD11	2.56	0.41
1:C:749:PHE:O	1:C:753:LYS:HG3	2.21	0.41
1:D:220:LEU:HG	1:D:223:LYS:HB3	2.02	0.41
1:D:451:ASN:O	1:D:452:GLU:C	2.59	0.41
1:D:520:PRO:CG	1:D:521:ASN:H	2.33	0.41
1:D:292:ARG:NE	1:D:617:LYS:HE3	2.36	0.41
1:E:741:ILE:O	1:E:741:ILE:HG13	2.21	0.41
1:F:202:ASP:HB2	1:F:208:LEU:CD2	2.51	0.41
1:F:128:MET:CE	1:F:235:THR:HB	2.49	0.41
1:F:295:VAL:C	1:F:296:LEU:CD2	2.80	0.41
1:F:301:ALA:O	1:F:304:ALA:N	2.43	0.41
1:F:350:VAL:HG12	1:F:351:HIS:N	2.35	0.41
1:F:397:GLU:O	1:F:398:ILE:HD13	2.21	0.41
1:F:397:GLU:O	1:F:480:ASN:N	2.52	0.41
1:F:420:LEU:HD13	1:F:420:LEU:O	2.20	0.41
1:F:667:LEU:O	1:F:668:SER:C	2.58	0.41
1:F:690:LYS:O	1:F:693:SER:N	2.54	0.41
1:F:87:LYS:HB3	1:F:87:LYS:HE2	1.81	0.41
2:R:65:PHE:CE2	2:R:69:LEU:HG	2.55	0.41
1:A:142:VAL:HG13	1:A:154:ILE:HD12	2.03	0.41
1:A:179:LEU:O	1:A:182:ILE:HG22	2.20	0.41
1:A:202:ASP:HB2	1:A:208:LEU:CD2	2.50	0.41
1:A:265:PHE:C	1:A:267:TYR:H	2.24	0.41
1:A:368:GLN:HB2	1:A:380:VAL:HG13	2.02	0.41
1:B:90:PRO:HG3	1:B:249:PHE:CZ	2.55	0.41
1:B:497:LEU:HD13	1:B:556:MET:HG2	2.02	0.41
1:B:520:PRO:CG	1:B:521:ASN:H	2.33	0.41
1:C:508:ILE:HG21	1:C:513:TRP:HB2	2.01	0.41
1:C:636:ALA:HA	1:C:637:PRO:HD3	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:90:PRO:HG3	1:C:249:PHE:CZ	2.55	0.41
1:D:409:ARG:O	1:D:413:LEU:HG	2.20	0.41
1:D:523:LEU:HD11	2:R:144:MET:HG2	2.03	0.41
1:D:615:ILE:CD1	1:D:645:TRP:HH2	2.29	0.41
1:D:711:ILE:C	1:D:712:PHE:CD2	2.93	0.41
1:D:90:PRO:HG2	1:D:93:VAL:CG1	2.51	0.41
1:E:217:LYS:HG3	1:E:236:GLU:HG3	2.02	0.41
1:E:403:LEU:HG	1:E:405:LEU:CD1	2.51	0.41
1:E:523:LEU:HD11	2:S:144:MET:HG2	2.02	0.41
1:E:74:GLU:HB2	1:E:78:LYS:HB3	2.03	0.41
1:E:77:ASP:OD1	1:E:159:TYR:CE2	2.73	0.41
1:E:790:PHE:O	1:E:791:GLU:C	2.59	0.41
1:F:176:GLY:O	1:F:178:SER:N	2.53	0.41
1:F:298:GLY:C	1:F:300:LYS:H	2.23	0.41
1:F:746:LYS:HD2	1:F:747:ASN:HD22	1.84	0.41
2:O:68:PHE:C	2:O:70:THR:N	2.72	0.41
2:P:138:TYR:O	2:P:141:PHE:HB3	2.20	0.41
2:Q:81:SER:O	2:Q:82:GLU:C	2.57	0.41
2:S:136:VAL:HG23	2:S:136:VAL:O	2.19	0.41
2:S:92:PHE:C	2:S:94:LYS:N	2.74	0.41
2:T:39:LEU:HD12	2:T:39:LEU:HA	1.82	0.41
1:A:197:LYS:NZ	1:A:197:LYS:CB	2.80	0.41
1:A:217:LYS:HG3	1:A:236:GLU:HG3	2.03	0.41
1:A:345:THR:CG2	1:A:491:ASP:HA	2.51	0.41
1:A:671:ARG:HG3	1:A:671:ARG:NH1	2.35	0.41
1:A:92:ASP:O	1:A:93:VAL:C	2.58	0.41
1:B:189:ASP:O	1:B:190:PRO:C	2.56	0.41
1:B:128:MET:CE	1:B:235:THR:HB	2.49	0.41
1:B:165:GLN:CD	1:B:252:ASP:HB3	2.41	0.41
1:B:414:LYS:HD3	1:B:414:LYS:C	2.41	0.41
1:B:447:SER:OG	1:B:448:ASP:N	2.52	0.41
1:B:456:LYS:HD3	1:B:471:TRP:H	1.84	0.41
1:C:131:ARG:CB	1:C:243:LEU:HD21	2.50	0.41
1:C:77:ASP:OD1	1:C:159:TYR:CE2	2.74	0.41
1:C:308:VAL:O	1:C:311:HIS:N	2.46	0.41
1:C:684:ASP:C	1:C:686:ASP:H	2.22	0.41
1:C:751:TYR:C	1:C:753:LYS:H	2.24	0.41
1:D:121:SER:HB2	1:D:122:GLU:OE2	2.20	0.41
1:D:339:ILE:O	1:D:340:LYS:C	2.58	0.41
1:D:420:LEU:CD1	1:D:436:GLU:HB3	2.51	0.41
1:D:520:PRO:CG	1:D:521:ASN:N	2.84	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:535:LYS:HD3	1:D:536:TYR:CE2	2.55	0.41
1:D:715:GLU:CG	1:D:767:GLN:HE21	2.33	0.41
1:E:197:LYS:HD3	1:E:263:ASP:CB	2.51	0.41
1:E:409:ARG:O	1:E:413:LEU:HG	2.20	0.41
1:F:360:VAL:HA	1:F:403:LEU:HD21	2.02	0.41
1:F:683:GLY:O	1:F:684:ASP:C	2.57	0.41
2:P:81:SER:O	2:P:82:GLU:C	2.58	0.41
2:R:138:TYR:O	2:R:141:PHE:HB3	2.21	0.41
2:R:13:LYS:C	2:R:15:ALA:N	2.70	0.41
2:R:81:SER:O	2:R:82:GLU:C	2.58	0.41
2:T:138:TYR:O	2:T:141:PHE:HB3	2.21	0.41
2:T:70:THR:O	2:T:71:MET:C	2.59	0.41
1:A:111:LEU:HD23	1:A:155:ASN:ND2	2.33	0.41
1:A:456:LYS:HD3	1:A:471:TRP:H	1.85	0.41
1:A:495:PHE:O	1:A:496:ALA:HB2	2.20	0.41
1:A:93:VAL:HG13	1:A:94:LEU:N	2.35	0.41
1:B:216:GLU:HG3	1:B:217:LYS:HG2	2.03	0.41
1:B:368:GLN:C	1:B:370:LEU:H	2.23	0.41
1:B:420:LEU:CD1	1:B:436:GLU:HB3	2.51	0.41
1:B:66:LEU:HD23	1:B:94:LEU:HB3	2.01	0.41
1:C:216:GLU:HG3	1:C:217:LYS:HG2	2.02	0.41
1:C:271:LEU:HA	1:C:275:GLY:HA3	2.02	0.41
1:C:279:ILE:O	1:C:283:LEU:HB2	2.20	0.41
1:C:683:GLY:O	1:C:684:ASP:C	2.56	0.41
1:C:713:SER:O	1:C:714:GLN:C	2.59	0.41
1:C:748:TYR:O	1:C:751:TYR:N	2.53	0.41
1:D:131:ARG:CB	1:D:243:LEU:HD21	2.51	0.41
1:D:144:GLU:HG3	1:D:144:GLU:O	2.19	0.41
1:D:327:LEU:CD2	1:D:595:ILE:HG12	2.51	0.41
1:E:173:ILE:C	1:E:175:LYS:H	2.23	0.41
1:F:127:SER:OG	1:F:135:VAL:HG21	2.21	0.41
1:F:384:ASN:O	1:F:386:GLU:N	2.53	0.41
1:F:297:LYS:HZ3	1:F:601:GLU:HB3	1.85	0.41
1:F:629:ASN:C	1:F:631:SER:N	2.74	0.41
2:R:86:ARG:O	2:R:86:ARG:HG2	2.21	0.41
2:T:136:VAL:HG23	2:T:136:VAL:O	2.21	0.41
1:B:110:ASP:OD1	1:B:110:ASP:N	2.53	0.41
1:B:217:LYS:HG3	1:B:236:GLU:HG3	2.03	0.41
1:B:225:ILE:HG12	1:B:229:PHE:HD2	1.81	0.41
1:B:409:ARG:O	1:B:413:LEU:HG	2.20	0.41
1:B:747:ASN:N	1:B:747:ASN:HD22	2.18	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:89:ILE:H	1:B:89:ILE:HG13	1.58	0.41
1:C:134:LYS:O	1:C:135:VAL:CG1	2.63	0.41
1:C:205:SER:C	1:C:207:ASP:N	2.72	0.41
1:C:279:ILE:HD13	1:C:279:ILE:N	2.36	0.41
1:C:368:GLN:C	1:C:370:LEU:H	2.24	0.41
1:C:408:LEU:H	1:C:408:LEU:CD1	2.03	0.41
1:C:433:TYR:N	1:C:433:TYR:CD1	2.89	0.41
1:C:752:LEU:HA	1:C:752:LEU:HD23	1.77	0.41
1:D:368:GLN:HB2	1:D:380:VAL:HG13	2.02	0.41
1:D:343:VAL:HG13	1:D:487:PRO:O	2.21	0.41
1:D:718:ARG:NH1	1:D:767:GLN:HE21	2.18	0.41
1:E:171:TYR:CD1	1:E:175:LYS:NZ	2.82	0.41
1:E:173:ILE:HG13	1:E:242:SER:CB	2.49	0.41
1:E:663:PHE:CD1	1:E:752:LEU:HD11	2.55	0.41
1:E:90:PRO:O	1:E:93:VAL:N	2.54	0.41
1:F:214:PHE:CB	1:F:218:LEU:HB3	2.40	0.41
1:F:443:GLU:HG3	1:F:458:LYS:HZ2	1.86	0.41
2:O:138:TYR:CE1	2:O:142:VAL:HG22	2.56	0.41
2:Q:138:TYR:O	2:Q:141:PHE:HB3	2.21	0.41
2:Q:97:ASN:HD22	2:Q:99:TYR:H	1.66	0.41
1:A:144:GLU:O	1:A:144:GLU:HG3	2.20	0.41
1:A:307:LEU:HD12	1:A:307:LEU:N	2.36	0.41
1:A:345:THR:HG21	1:A:491:ASP:HA	2.03	0.41
1:A:635:ILE:HD12	1:A:635:ILE:N	2.33	0.41
1:A:713:SER:O	1:A:714:GLN:C	2.58	0.41
1:A:749:PHE:O	1:A:753:LYS:HG3	2.21	0.41
1:A:89:ILE:HG13	1:A:89:ILE:H	1.55	0.41
1:B:115:LYS:CB	1:B:118:GLN:CG	2.93	0.41
1:B:173:ILE:CG2	1:B:174:GLY:N	2.83	0.41
1:B:320:ARG:NH1	1:B:599:GLU:O	2.54	0.41
1:C:223:LYS:NZ	1:C:228:ASN:HB2	2.36	0.41
1:C:298:GLY:C	1:C:300:LYS:H	2.23	0.41
1:C:339:ILE:O	1:C:340:LYS:C	2.59	0.41
1:C:715:GLU:CG	1:C:767:GLN:HE21	2.34	0.41
1:D:223:LYS:NZ	1:D:228:ASN:HB2	2.36	0.41
1:E:127:SER:OG	1:E:135:VAL:HG21	2.21	0.41
1:E:255:THR:C	1:E:257:LEU:N	2.72	0.41
1:E:257:LEU:O	1:E:261:ALA:O	2.37	0.41
1:E:305:SER:O	1:E:307:LEU:N	2.52	0.41
1:E:420:LEU:HD22	1:E:421:LYS:N	2.36	0.41
1:E:292:ARG:NE	1:E:617:LYS:HE3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:112:VAL:O	1:F:114:HIS:N	2.51	0.41
1:F:216:GLU:HG3	1:F:217:LYS:HG2	2.03	0.41
1:F:223:LYS:NZ	1:F:228:ASN:HB2	2.36	0.41
1:F:255:THR:C	1:F:257:LEU:N	2.71	0.41
1:F:279:ILE:CD1	1:F:279:ILE:H	2.33	0.41
1:F:512:GLU:O	1:F:515:LYS:NZ	2.53	0.41
1:F:658:PRO:HB3	1:F:755:ARG:HH12	1.85	0.41
1:F:74:GLU:HB2	1:F:78:LYS:HB3	2.03	0.41
2:P:33:GLY:O	2:P:35:VAL:N	2.54	0.41
1:C:692:GLU:CD	2:Q:21:LYS:HZ1	2.19	0.41
1:D:513:TRP:HZ2	2:R:114:GLU:HB2	1.84	0.41
2:S:105:LEU:HD23	2:S:121:VAL:HG13	2.03	0.41
2:T:18:LEU:HB3	2:T:19:PHE:CE1	2.56	0.41
1:A:140:ARG:NH1	1:A:141:PHE:CE1	2.89	0.41
1:A:111:LEU:CD2	1:A:155:ASN:HD21	2.33	0.41
1:A:188:LEU:HD12	1:A:191:GLU:HG3	2.02	0.41
1:A:257:LEU:O	1:A:261:ALA:O	2.39	0.41
1:A:293:ILE:H	1:A:293:ILE:HG12	1.44	0.41
1:A:368:GLN:C	1:A:370:LEU:H	2.24	0.41
1:A:435:LEU:HG	1:A:446:ILE:CG2	2.47	0.41
1:A:725:GLY:O	1:A:726:ILE:C	2.59	0.41
1:B:172:GLU:HG3	1:B:245:PHE:CE1	2.56	0.41
1:B:197:LYS:HD3	1:B:263:ASP:CG	2.41	0.41
1:B:297:LYS:HB3	1:B:297:LYS:NZ	2.36	0.41
1:B:794:GLN:HB3	1:B:794:GLN:HE21	1.61	0.41
1:C:263:ASP:O	1:C:264:MET:C	2.58	0.41
1:C:398:ILE:CD1	1:C:479:LYS:HB3	2.51	0.41
1:C:414:LYS:HD3	1:C:414:LYS:C	2.41	0.41
1:C:530:THR:O	1:C:534:ILE:HG13	2.20	0.41
1:C:654:ILE:C	1:C:655:ASN:HD22	2.24	0.41
1:C:89:ILE:CG2	1:C:90:PRO:HD2	2.51	0.41
1:E:176:GLY:C	1:E:178:SER:H	2.24	0.41
1:E:179:LEU:O	1:E:180:ASP:C	2.60	0.41
1:E:197:LYS:CB	1:E:197:LYS:NZ	2.83	0.41
1:E:90:PRO:HG3	1:E:249:PHE:CZ	2.56	0.41
1:F:142:VAL:HG13	1:F:154:ILE:HD11	2.01	0.41
1:F:297:LYS:HB3	1:F:297:LYS:HZ3	1.85	0.41
2:O:97:ASN:HD22	2:O:99:TYR:H	1.66	0.41
2:Q:18:LEU:HB3	2:Q:19:PHE:CE1	2.56	0.41
2:Q:70:THR:O	2:Q:72:MET:N	2.54	0.41
2:R:70:THR:O	2:R:72:MET:N	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:S:11:GLU:C	2:S:13:LYS:N	2.74	0.41
2:S:138:TYR:O	2:S:141:PHE:HB3	2.21	0.41
2:S:29:THR:O	2:S:32:LEU:N	2.53	0.41
2:T:13:LYS:C	2:T:15:ALA:N	2.70	0.41
1:A:223:LYS:NZ	1:A:228:ASN:HB2	2.36	0.41
1:A:420:LEU:CD1	1:A:436:GLU:HB3	2.51	0.41
1:A:663:PHE:CD1	1:A:752:LEU:HD11	2.56	0.41
1:B:142:VAL:HG13	1:B:154:ILE:HD11	2.02	0.41
1:B:173:ILE:C	1:B:175:LYS:H	2.24	0.41
1:B:298:GLY:C	1:B:300:LYS:H	2.25	0.41
1:B:508:ILE:HG12	1:B:536:TYR:CD2	2.56	0.41
1:B:582:ASP:O	1:B:584:GLU:N	2.47	0.41
1:B:711:ILE:C	1:B:712:PHE:CD2	2.94	0.41
1:B:741:ILE:O	1:B:741:ILE:HG13	2.20	0.41
1:C:530:THR:O	1:C:534:ILE:N	2.49	0.41
1:C:597:ASN:C	1:C:599:GLU:H	2.24	0.41
1:C:92:ASP:O	1:C:93:VAL:C	2.58	0.41
1:D:305:SER:O	1:D:307:LEU:N	2.52	0.41
1:D:307:LEU:HD12	1:D:307:LEU:N	2.36	0.41
1:D:561:ASN:HA	1:D:564:VAL:HG22	2.02	0.41
1:D:665:LYS:O	1:D:668:SER:HB3	2.21	0.41
1:D:671:ARG:NH1	1:D:671:ARG:HG3	2.35	0.41
1:E:343:VAL:HG12	1:E:344:ALA:O	2.20	0.41
1:E:793:PHE:HA	1:E:796:ILE:HG13	2.03	0.41
1:F:102:GLY:O	1:F:103:GLU:HG3	2.21	0.41
1:F:172:GLU:HG3	1:F:245:PHE:CE1	2.56	0.41
1:F:292:ARG:NE	1:F:617:LYS:HE3	2.35	0.41
1:F:713:SER:O	1:F:714:GLN:C	2.59	0.41
1:F:663:PHE:CD1	1:F:752:LEU:HD11	2.56	0.41
2:O:136:VAL:HG23	2:O:136:VAL:O	2.21	0.41
2:P:101:SER:OG	2:P:104:GLU:HG2	2.20	0.41
2:P:65:PHE:CE2	2:P:69:LEU:HG	2.56	0.41
2:Q:70:THR:O	2:Q:71:MET:C	2.59	0.41
2:Q:79:THR:O	2:Q:81:SER:N	2.54	0.41
2:R:106:ARG:CB	2:R:121:VAL:HG21	2.48	0.41
2:R:83:GLU:O	2:R:84:GLU:C	2.59	0.41
2:S:57:ALA:O	2:S:59:GLY:N	2.54	0.41
1:F:533:LEU:HD23	2:T:112:LEU:HD21	2.03	0.41
1:A:105:TYR:HE1	1:A:151:LYS:NZ	2.15	0.40
1:A:350:VAL:HG12	1:A:351:HIS:N	2.35	0.40
1:A:414:LYS:C	1:A:414:LYS:HD3	2.41	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:514:ASP:C	1:A:516:VAL:H	2.25	0.40
1:A:523:LEU:HD11	2:O:144:MET:HG2	2.02	0.40
1:A:561:ASN:HA	1:A:564:VAL:HG22	2.03	0.40
1:A:74:GLU:HB2	1:A:78:LYS:HB3	2.03	0.40
1:B:127:SER:OG	1:B:135:VAL:HG21	2.21	0.40
1:B:134:LYS:O	1:B:135:VAL:CG1	2.67	0.40
1:B:188:LEU:HG	1:B:188:LEU:H	1.73	0.40
1:B:173:ILE:HG13	1:B:242:SER:CB	2.50	0.40
1:B:265:PHE:C	1:B:267:TYR:H	2.25	0.40
1:B:293:ILE:H	1:B:293:ILE:HG12	1.44	0.40
1:B:88:LYS:NZ	1:B:172:GLU:CD	2.74	0.40
1:C:141:PHE:CD1	1:C:141:PHE:N	2.90	0.40
1:C:217:LYS:HG3	1:C:236:GLU:HG3	2.04	0.40
1:C:288:VAL:O	1:C:291:ASP:O	2.38	0.40
1:C:455:TYR:HA	1:C:471:TRP:CZ3	2.56	0.40
1:C:514:ASP:C	1:C:516:VAL:H	2.24	0.40
1:C:790:PHE:O	1:C:791:GLU:C	2.59	0.40
1:D:110:ASP:N	1:D:110:ASP:OD1	2.54	0.40
1:D:89:ILE:HG21	1:D:175:LYS:HE2	2.02	0.40
1:D:255:THR:C	1:D:257:LEU:N	2.73	0.40
1:D:413:LEU:HB2	1:D:419:ILE:HG12	2.03	0.40
1:D:398:ILE:CD1	1:D:479:LYS:HB3	2.51	0.40
1:D:606:LYS:HB2	1:D:610:MET:CE	2.51	0.40
1:D:729:TYR:O	1:D:732:ILE:N	2.51	0.40
1:D:736:LEU:HD21	1:D:750:GLN:OE1	2.21	0.40
1:E:71:PHE:CD1	1:E:108:ASP:OD1	2.74	0.40
1:E:179:LEU:O	1:E:182:ILE:HG22	2.21	0.40
1:E:191:GLU:C	1:E:193:LEU:N	2.75	0.40
1:E:220:LEU:HG	1:E:223:LYS:HB3	2.02	0.40
1:E:494:LEU:HD13	1:E:497:LEU:HD21	2.03	0.40
1:E:561:ASN:HA	1:E:564:VAL:HG22	2.03	0.40
1:E:89:ILE:HG21	1:E:175:LYS:HE2	2.04	0.40
1:F:197:LYS:HD3	1:F:263:ASP:CG	2.41	0.40
1:F:523:LEU:HD11	2:T:144:MET:HG2	2.03	0.40
1:F:736:LEU:HD21	1:F:750:GLN:OE1	2.21	0.40
2:O:33:GLY:O	2:O:34:THR:C	2.58	0.40
2:O:39:LEU:HA	2:O:39:LEU:HD12	1.83	0.40
2:O:70:THR:O	2:O:71:MET:C	2.59	0.40
2:P:138:TYR:CE1	2:P:142:VAL:HG22	2.57	0.40
2:P:70:THR:O	2:P:72:MET:N	2.54	0.40
2:P:92:PHE:C	2:P:94:LYS:N	2.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:R:27:ILE:HD12	2:R:32:LEU:HA	2.04	0.40
1:D:630:ARG:NH1	2:R:83:GLU:HG2	2.36	0.40
1:E:533:LEU:HD23	2:S:112:LEU:HD21	2.04	0.40
2:S:33:GLY:O	2:S:34:THR:C	2.58	0.40
1:A:339:ILE:O	1:A:340:LYS:C	2.58	0.40
1:A:529:VAL:HG21	2:O:109:MET:HE3	2.03	0.40
1:A:751:TYR:C	1:A:753:LYS:H	2.24	0.40
1:B:297:LYS:HZ3	1:B:297:LYS:HB3	1.87	0.40
1:B:397:GLU:O	1:B:398:ILE:HD13	2.21	0.40
1:B:632:TYR:HA	1:B:632:TYR:HD2	1.74	0.40
1:B:654:ILE:C	1:B:655:ASN:HD22	2.25	0.40
1:B:667:LEU:O	1:B:668:SER:C	2.59	0.40
1:B:732:ILE:O	1:B:733:GLU:C	2.59	0.40
1:C:112:VAL:C	1:C:114:HIS:N	2.75	0.40
1:C:179:LEU:O	1:C:180:ASP:C	2.59	0.40
1:C:179:LEU:O	1:C:182:ILE:HG22	2.22	0.40
1:C:323:ASN:HD22	1:C:598:PRO:HB3	1.86	0.40
1:C:409:ARG:O	1:C:413:LEU:HG	2.21	0.40
1:D:295:VAL:C	1:D:296:LEU:CD2	2.82	0.40
1:D:408:LEU:H	1:D:408:LEU:CD1	2.02	0.40
1:D:597:ASN:C	1:D:599:GLU:H	2.23	0.40
1:E:323:ASN:HD22	1:E:598:PRO:CB	2.34	0.40
1:E:365:PRO:O	1:E:366:PHE:C	2.58	0.40
1:E:504:ILE:CD1	1:E:504:ILE:N	2.84	0.40
1:F:175:LYS:O	1:F:177:ILE:N	2.54	0.40
1:F:191:GLU:O	1:F:192:PHE:C	2.59	0.40
1:F:271:LEU:HA	1:F:275:GLY:HA3	2.02	0.40
1:F:752:LEU:HD23	1:F:752:LEU:HA	1.76	0.40
2:O:36:MET:CE	2:O:48:LEU:HD21	2.52	0.40
2:O:70:THR:O	2:O:72:MET:N	2.54	0.40
2:Q:63:ILE:CG2	2:Q:67:GLU:CB	2.97	0.40
2:R:89:PHE:HB2	2:R:141:PHE:CE2	2.56	0.40
2:R:75:LYS:O	2:R:79:THR:HG22	2.22	0.40
2:R:9:ILE:HG23	2:R:69:LEU:HD21	2.03	0.40
2:S:18:LEU:HB3	2:S:19:PHE:CE1	2.56	0.40
1:A:175:LYS:O	1:A:177:ILE:N	2.55	0.40
1:A:271:LEU:HA	1:A:275:GLY:HA3	2.03	0.40
1:A:523:LEU:HD11	2:O:144:MET:HG3	2.02	0.40
1:A:632:TYR:HD2	1:A:632:TYR:HA	1.74	0.40
1:A:741:ILE:HG12	1:A:741:ILE:H	1.64	0.40
1:A:754:GLU:O	1:A:757:THR:HB	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ILE:CG2	1:A:90:PRO:HD2	2.52	0.40
1:A:89:ILE:HG21	1:A:175:LYS:HE2	2.02	0.40
1:B:131:ARG:CB	1:B:243:LEU:HD21	2.51	0.40
1:B:520:PRO:CG	1:B:521:ASN:N	2.84	0.40
1:B:629:ASN:C	1:B:631:SER:N	2.75	0.40
1:B:713:SER:O	1:B:714:GLN:C	2.59	0.40
1:C:115:LYS:O	1:C:117:LEU:N	2.54	0.40
1:C:142:VAL:HG13	1:C:154:ILE:HD11	2.02	0.40
1:C:197:LYS:O	1:C:197:LYS:NZ	2.51	0.40
1:C:357:TRP:O	1:C:357:TRP:CG	2.74	0.40
1:D:173:ILE:HG13	1:D:242:SER:CB	2.51	0.40
1:D:217:LYS:HG3	1:D:236:GLU:HG3	2.03	0.40
1:D:345:THR:CG2	1:D:491:ASP:HA	2.51	0.40
1:D:455:TYR:HA	1:D:471:TRP:CZ3	2.57	0.40
1:D:667:LEU:O	1:D:668:SER:C	2.59	0.40
1:D:687:GLU:HA	1:D:687:GLU:OE2	2.21	0.40
1:D:790:PHE:O	1:D:791:GLU:C	2.59	0.40
1:E:100:LEU:CD2	1:E:182:ILE:HG21	2.51	0.40
1:E:185:ASP:HA	1:E:194:ASN:CG	2.42	0.40
1:E:225:ILE:HG23	1:E:229:PHE:HD2	1.83	0.40
1:E:355:SER:HA	1:E:372:LYS:H	1.86	0.40
1:E:495:PHE:O	1:E:496:ALA:HB2	2.21	0.40
1:E:597:ASN:C	1:E:599:GLU:H	2.24	0.40
1:E:687:GLU:OE2	1:E:687:GLU:HA	2.20	0.40
1:F:323:ASN:HD22	1:F:598:PRO:HB3	1.85	0.40
1:F:648:PRO:O	1:F:649:ILE:C	2.59	0.40
1:F:727:GLN:O	1:F:730:ASN:HB3	2.22	0.40
2:O:18:LEU:HB3	2:O:19:PHE:CE1	2.57	0.40
2:O:64:ASP:CB	2:O:67:GLU:OE2	2.67	0.40
2:P:9:ILE:HG23	2:P:69:LEU:HD21	2.03	0.40
2:Q:27:ILE:HD12	2:Q:32:LEU:HA	2.03	0.40
2:Q:65:PHE:CE2	2:Q:69:LEU:HG	2.56	0.40
1:E:501:LEU:HD13	2:S:108:VAL:HG13	2.03	0.40
2:T:33:GLY:O	2:T:34:THR:C	2.58	0.40
2:T:64:ASP:CB	2:T:67:GLU:OE2	2.68	0.40
2:T:79:THR:O	2:T:81:SER:N	2.54	0.40
1:A:229:PHE:O	1:A:231:LYS:N	2.55	0.40
1:A:687:GLU:HA	1:A:687:GLU:OE2	2.21	0.40
1:A:747:ASN:N	1:A:747:ASN:HD22	2.18	0.40
1:B:77:ASP:OD1	1:B:159:TYR:HE2	2.03	0.40
1:B:179:LEU:O	1:B:182:ILE:HG22	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:234:LEU:N	1:B:234:LEU:CD2	2.85	0.40
1:B:263:ASP:C	1:B:265:PHE:N	2.74	0.40
1:B:283:LEU:O	1:B:287:GLY:N	2.55	0.40
1:B:339:ILE:O	1:B:340:LYS:C	2.59	0.40
1:B:355:SER:HA	1:B:372:LYS:H	1.87	0.40
1:B:292:ARG:NE	1:B:617:LYS:HE3	2.36	0.40
1:B:622:LYS:HD3	1:B:622:LYS:HA	1.85	0.40
1:B:643:ILE:HG22	1:B:644:GLU:N	2.35	0.40
1:C:159:TYR:CD1	1:C:159:TYR:N	2.90	0.40
1:C:455:TYR:HA	1:C:471:TRP:HZ3	1.86	0.40
1:C:693:SER:OG	1:C:731:GLU:OE1	2.38	0.40
1:C:83:GLN:O	1:C:84:ASP:C	2.60	0.40
1:D:208:LEU:H	1:D:208:LEU:HD12	1.86	0.40
1:D:399:GLY:O	1:D:477:MET:HE3	2.22	0.40
1:D:93:VAL:HG13	1:D:94:LEU:N	2.35	0.40
1:E:254:ARG:HH11	1:E:254:ARG:CB	2.27	0.40
1:E:514:ASP:C	1:E:516:VAL:H	2.25	0.40
1:E:549:LEU:HB2	1:E:553:GLN:HE21	1.87	0.40
1:F:197:LYS:NZ	1:F:197:LYS:O	2.48	0.40
1:F:234:LEU:CD2	1:F:234:LEU:N	2.85	0.40
1:F:131:ARG:CB	1:F:243:LEU:HD21	2.51	0.40
1:F:270:LYS:HA	1:F:273:LYS:CG	2.51	0.40
1:F:360:VAL:HG22	1:F:360:VAL:O	2.22	0.40
1:F:409:ARG:O	1:F:413:LEU:HG	2.21	0.40
1:F:399:GLY:O	1:F:477:MET:HE3	2.21	0.40
1:F:549:LEU:HB2	1:F:553:GLN:HE21	1.87	0.40
2:P:105:LEU:HD21	2:P:124:MET:SD	2.62	0.40
2:P:70:THR:O	2:P:71:MET:C	2.59	0.40
2:Q:57:ALA:O	2:Q:59:GLY:N	2.54	0.40
2:T:65:PHE:CE2	2:T:69:LEU:HG	2.56	0.40
1:A:161:ILE:HA	1:A:167:LYS:HD2	2.04	0.40
1:A:173:ILE:C	1:A:175:LYS:H	2.25	0.40
1:A:173:ILE:HG13	1:A:242:SER:CB	2.50	0.40
1:A:197:LYS:HD3	1:A:263:ASP:CB	2.51	0.40
1:A:217:LYS:HZ1	1:A:236:GLU:HB2	1.81	0.40
1:A:365:PRO:O	1:A:366:PHE:C	2.59	0.40
1:A:446:ILE:HG23	1:A:446:ILE:O	2.21	0.40
1:A:315:PHE:CD2	1:A:560:LEU:HD13	2.57	0.40
1:A:323:ASN:HD22	1:A:598:PRO:CB	2.34	0.40
1:A:320:ARG:NH1	1:A:599:GLU:O	2.55	0.40
1:A:71:PHE:CD1	1:A:108:ASP:OD1	2.75	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:365:PRO:O	1:B:366:PHE:C	2.59	0.40
1:B:514:ASP:C	1:B:516:VAL:H	2.25	0.40
1:B:716:LYS:O	1:B:717:LYS:C	2.60	0.40
1:B:790:PHE:O	1:B:791:GLU:C	2.58	0.40
1:C:254:ARG:HH11	1:C:254:ARG:CB	2.27	0.40
1:C:197:LYS:HD3	1:C:263:ASP:CG	2.41	0.40
1:C:323:ASN:HD22	1:C:598:PRO:CB	2.33	0.40
1:C:451:ASN:O	1:C:452:GLU:C	2.60	0.40
1:C:667:LEU:O	1:C:668:SER:C	2.60	0.40
1:C:794:GLN:HE21	1:C:794:GLN:HB3	1.61	0.40
1:D:205:SER:C	1:D:207:ASP:N	2.71	0.40
1:D:234:LEU:CD2	1:D:234:LEU:N	2.84	0.40
1:D:368:GLN:HG3	1:D:383:GLY:HA3	2.03	0.40
1:D:514:ASP:C	1:D:516:VAL:H	2.24	0.40
1:E:208:LEU:HD12	1:E:208:LEU:H	1.87	0.40
1:E:216:GLU:HG3	1:E:217:LYS:HG2	2.03	0.40
1:E:265:PHE:C	1:E:267:TYR:H	2.24	0.40
1:E:399:GLY:O	1:E:477:MET:HE3	2.21	0.40
1:E:688:PHE:HD2	1:E:688:PHE:C	2.22	0.40
1:F:110:ASP:OD1	1:F:110:ASP:N	2.54	0.40
1:F:142:VAL:CG2	1:F:154:ILE:HD12	2.37	0.40
1:F:179:LEU:O	1:F:180:ASP:C	2.60	0.40
1:F:243:LEU:O	1:F:247:TYR:CD1	2.74	0.40
1:F:326:ILE:C	1:F:327:LEU:HD12	2.42	0.40
1:F:398:ILE:CD1	1:F:479:LYS:HB3	2.51	0.40
1:F:455:TYR:HA	1:F:471:TRP:CZ3	2.56	0.40
2:Q:33:GLY:O	2:Q:35:VAL:N	2.54	0.40
2:R:70:THR:O	2:R:71:MET:C	2.59	0.40
2:S:27:ILE:HD12	2:S:32:LEU:HA	2.03	0.40
2:S:36:MET:CE	2:S:48:LEU:HD21	2.51	0.40
2:T:24:ASP:HB2	2:T:26:THR:CG2	2.35	0.40
2:T:9:ILE:HG23	2:T:69:LEU:HD21	2.03	0.40
2:T:92:PHE:C	2:T:94:LYS:N	2.74	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	733/777 (94%)	490 (67%)	170 (23%)	73 (10%)	0	3
1	B	733/777 (94%)	492 (67%)	171 (23%)	70 (10%)	0	4
1	C	733/777 (94%)	494 (67%)	171 (23%)	68 (9%)	0	4
1	D	733/777 (94%)	493 (67%)	170 (23%)	70 (10%)	0	4
1	E	733/777 (94%)	492 (67%)	171 (23%)	70 (10%)	0	4
1	F	733/777 (94%)	490 (67%)	172 (24%)	71 (10%)	0	3
2	O	144/149 (97%)	92 (64%)	39 (27%)	13 (9%)	1	4
2	P	144/149 (97%)	89 (62%)	39 (27%)	16 (11%)	0	2
2	Q	144/149 (97%)	90 (62%)	37 (26%)	17 (12%)	0	2
2	R	144/149 (97%)	90 (62%)	38 (26%)	16 (11%)	0	2
2	S	144/149 (97%)	90 (62%)	39 (27%)	15 (10%)	0	3
2	T	144/149 (97%)	90 (62%)	40 (28%)	14 (10%)	0	3
All	All	5262/5556 (95%)	3492 (66%)	1257 (24%)	513 (10%)	0	3

All (513) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	77	ASP
1	A	111	LEU
1	A	113	GLU
1	A	135	VAL
1	A	162	ASN
1	A	180	ASP
1	A	278	LYS
1	A	373	LYS
1	A	407	HIS
1	A	580	GLU
1	A	776	LEU
1	B	77	ASP

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Mol	Chain	Res	Type
1	B	111	LEU
1	B	113	GLU
1	B	135	VAL
1	B	162	ASN
1	B	180	ASP
1	B	278	LYS
1	B	373	LYS
1	B	407	HIS
1	B	447	SER
1	B	580	GLU
1	B	765	THR
1	B	776	LEU
1	C	77	ASP
1	C	111	LEU
1	C	113	GLU
1	C	135	VAL
1	C	162	ASN
1	C	180	ASP
1	C	278	LYS
1	C	373	LYS
1	C	407	HIS
1	C	447	SER
1	C	580	GLU
1	C	765	THR
1	C	776	LEU
1	D	77	ASP
1	D	111	LEU
1	D	113	GLU
1	D	135	VAL
1	D	162	ASN
1	D	180	ASP
1	D	278	LYS
1	D	373	LYS
1	D	407	HIS
1	D	580	GLU
1	D	765	THR
1	D	776	LEU
1	E	77	ASP
1	E	111	LEU
1	E	113	GLU
1	E	135	VAL
1	E	162	ASN

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Mol	Chain	Res	Type
1	E	180	ASP
1	E	373	LYS
1	E	407	HIS
1	E	580	GLU
1	E	776	LEU
1	F	77	ASP
1	F	111	LEU
1	F	113	GLU
1	F	135	VAL
1	F	162	ASN
1	F	180	ASP
1	F	278	LYS
1	F	373	LYS
1	F	407	HIS
1	F	580	GLU
1	F	776	LEU
1	A	80	GLN
1	A	112	VAL
1	A	176	GLY
1	A	178	SER
1	A	230	ILE
1	A	232	GLU
1	A	294	ASP
1	A	299	GLU
1	A	302	LEU
1	A	372	LYS
1	A	376	GLN
1	A	447	SER
1	A	485	LEU
1	A	510	GLN
1	A	709	ASN
1	A	711	ILE
1	A	765	THR
1	A	775	LEU
1	B	80	GLN
1	B	112	VAL
1	B	163	SER
1	B	176	GLY
1	B	178	SER
1	B	192	PHE
1	B	230	ILE
1	B	232	GLU

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Mol	Chain	Res	Type
1	B	294	ASP
1	B	299	GLU
1	B	302	LEU
1	B	372	LYS
1	B	376	GLN
1	B	485	LEU
1	B	510	GLN
1	B	709	ASN
1	B	711	ILE
1	B	727	GLN
1	B	775	LEU
1	C	80	GLN
1	C	112	VAL
1	C	176	GLY
1	C	178	SER
1	C	230	ILE
1	C	232	GLU
1	C	294	ASP
1	C	299	GLU
1	C	302	LEU
1	C	372	LYS
1	C	376	GLN
1	C	385	LEU
1	C	485	LEU
1	C	510	GLN
1	C	709	ASN
1	C	711	ILE
1	C	727	GLN
1	C	775	LEU
1	D	80	GLN
1	D	112	VAL
1	D	176	GLY
1	D	178	SER
1	D	230	ILE
1	D	232	GLU
1	D	294	ASP
1	D	299	GLU
1	D	302	LEU
1	D	372	LYS
1	D	376	GLN
1	D	447	SER
1	D	485	LEU

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Mol	Chain	Res	Type
1	D	510	GLN
1	D	709	ASN
1	D	711	ILE
1	D	775	LEU
1	E	80	GLN
1	E	112	VAL
1	E	176	GLY
1	E	178	SER
1	E	230	ILE
1	E	232	GLU
1	E	278	LYS
1	E	294	ASP
1	E	299	GLU
1	E	302	LEU
1	E	372	LYS
1	E	376	GLN
1	E	447	SER
1	E	485	LEU
1	E	510	GLN
1	E	709	ASN
1	E	711	ILE
1	E	765	THR
1	E	775	LEU
1	F	80	GLN
1	F	112	VAL
1	F	176	GLY
1	F	178	SER
1	F	230	ILE
1	F	232	GLU
1	F	294	ASP
1	F	299	GLU
1	F	302	LEU
1	F	372	LYS
1	F	376	GLN
1	F	447	SER
1	F	485	LEU
1	F	510	GLN
1	F	709	ASN
1	F	711	ILE
1	F	727	GLN
1	F	765	THR
1	F	775	LEU

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Mol	Chain	Res	Type
2	O	58	ASP
2	O	93	ASP
2	O	125	ILE
2	P	58	ASP
2	P	93	ASP
2	P	125	ILE
2	Q	58	ASP
2	Q	93	ASP
2	Q	125	ILE
2	R	58	ASP
2	R	93	ASP
2	R	125	ILE
2	S	58	ASP
2	S	93	ASP
2	S	125	ILE
2	T	58	ASP
2	T	93	ASP
2	T	125	ILE
1	A	147	ARG
1	A	163	SER
1	A	185	ASP
1	A	192	PHE
1	A	223	LYS
1	A	274	GLY
1	A	385	LEU
1	A	471	TRP
1	A	528	GLY
1	A	568	GLY
1	A	727	GLN
1	A	730	ASN
1	A	734	ASN
1	A	757	THR
1	A	787	THR
1	A	793	PHE
1	B	185	ASP
1	B	190	PRO
1	B	223	LYS
1	B	274	GLY
1	B	385	LEU
1	B	471	TRP
1	B	528	GLY
1	B	568	GLY

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Mol	Chain	Res	Type
1	B	730	ASN
1	B	734	ASN
1	B	757	THR
1	B	787	THR
1	C	147	ARG
1	C	163	SER
1	C	185	ASP
1	C	223	LYS
1	C	274	GLY
1	C	471	TRP
1	C	568	GLY
1	C	730	ASN
1	C	734	ASN
1	C	757	THR
1	C	787	THR
1	D	163	SER
1	D	185	ASP
1	D	192	PHE
1	D	223	LYS
1	D	274	GLY
1	D	385	LEU
1	D	471	TRP
1	D	528	GLY
1	D	568	GLY
1	D	727	GLN
1	D	730	ASN
1	D	731	GLU
1	D	734	ASN
1	D	757	THR
1	D	787	THR
1	E	147	ARG
1	E	163	SER
1	E	185	ASP
1	E	192	PHE
1	E	223	LYS
1	E	274	GLY
1	E	385	LEU
1	E	471	TRP
1	E	568	GLY
1	E	727	GLN
1	E	730	ASN
1	E	734	ASN

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Mol	Chain	Res	Type
1	E	757	THR
1	E	787	THR
1	F	147	ARG
1	F	163	SER
1	F	185	ASP
1	F	223	LYS
1	F	274	GLY
1	F	385	LEU
1	F	471	TRP
1	F	528	GLY
1	F	568	GLY
1	F	730	ASN
1	F	734	ASN
1	F	757	THR
1	F	787	THR
2	O	73	ALA
2	O	80	ASP
2	O	118	ASP
2	P	73	ALA
2	P	80	ASP
2	Q	67	GLU
2	Q	73	ALA
2	Q	80	ASP
2	R	67	GLU
2	R	69	LEU
2	R	73	ALA
2	R	80	ASP
2	R	118	ASP
2	S	67	GLU
2	S	69	LEU
2	S	73	ALA
2	S	80	ASP
2	T	69	LEU
2	T	73	ALA
2	T	80	ASP
1	A	91	LYS
1	A	188	LEU
1	A	290	LYS
1	A	433	TYR
1	A	535	LYS
1	A	629	ASN
1	A	654	ILE

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Mol	Chain	Res	Type
1	A	719	LYS
1	A	731	GLU
1	A	794	GLN
1	B	91	LYS
1	B	147	ARG
1	B	181	ILE
1	B	188	LEU
1	B	290	LYS
1	B	433	TYR
1	B	535	LYS
1	B	629	ASN
1	B	654	ILE
1	B	719	LYS
1	B	793	PHE
1	B	794	GLN
1	C	181	ILE
1	C	188	LEU
1	C	192	PHE
1	C	290	LYS
1	C	433	TYR
1	C	528	GLY
1	C	535	LYS
1	C	629	ASN
1	C	719	LYS
1	C	793	PHE
1	C	794	GLN
1	D	65	ASN
1	D	147	ARG
1	D	188	LEU
1	D	290	LYS
1	D	433	TYR
1	D	629	ASN
1	D	719	LYS
1	D	793	PHE
1	D	794	GLN
1	E	181	ILE
1	E	188	LEU
1	E	290	LYS
1	E	433	TYR
1	E	528	GLY
1	E	629	ASN
1	E	719	LYS

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Mol	Chain	Res	Type
1	E	731	GLU
1	E	793	PHE
1	E	794	GLN
1	F	181	ILE
1	F	188	LEU
1	F	290	LYS
1	F	433	TYR
1	F	535	LYS
1	F	629	ASN
1	F	654	ILE
1	F	719	LYS
1	F	731	GLU
1	F	793	PHE
1	F	794	GLN
2	O	14	GLU
2	O	34	THR
2	O	67	GLU
2	O	69	LEU
2	P	14	GLU
2	P	34	THR
2	P	67	GLU
2	P	69	LEU
2	P	118	ASP
2	Q	14	GLU
2	Q	34	THR
2	Q	69	LEU
2	Q	118	ASP
2	R	14	GLU
2	S	14	GLU
2	S	118	ASP
2	T	14	GLU
2	T	67	GLU
2	T	118	ASP
1	A	121	SER
1	A	181	ILE
1	A	423	LYS
1	A	515	LYS
1	A	527	LYS
1	A	748	TYR
1	A	779	GLN
1	B	423	LYS
1	B	527	LYS

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Mol	Chain	Res	Type
1	B	698	ALA
1	B	731	GLU
1	B	748	TYR
1	C	423	LYS
1	C	654	ILE
1	C	731	GLU
1	D	515	LYS
1	D	527	LYS
1	D	535	LYS
1	D	537	GLY
1	D	698	ALA
1	D	714	GLN
1	D	748	TYR
1	E	423	LYS
1	E	535	LYS
1	E	643	ILE
1	E	698	ALA
1	E	714	GLN
1	E	748	TYR
1	E	779	GLN
1	F	192	PHE
1	F	423	LYS
1	F	527	LYS
1	F	698	ALA
2	O	60	ASN
2	P	60	ASN
2	Q	60	ASN
2	R	34	THR
2	R	60	ASN
2	S	34	THR
2	S	60	ASN
2	S	71	MET
2	T	34	THR
2	T	94	LYS
1	A	201	ASP
1	A	295	VAL
1	A	307	LEU
1	A	537	GLY
1	A	669	SER
1	A	698	ALA
1	A	714	GLN
1	B	201	ASP

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Mol	Chain	Res	Type
1	B	438	ASN
1	B	537	GLY
1	B	779	GLN
1	C	201	ASP
1	C	307	LEU
1	C	515	LYS
1	C	527	LYS
1	C	537	GLY
1	C	669	SER
1	C	698	ALA
1	D	91	LYS
1	D	181	ILE
1	D	295	VAL
1	D	423	LYS
1	D	643	ILE
1	D	654	ILE
1	E	121	SER
1	E	189	ASP
1	E	201	ASP
1	E	295	VAL
1	E	527	LYS
1	E	537	GLY
1	F	91	LYS
1	F	201	ASP
1	F	295	VAL
1	F	515	LYS
1	F	537	GLY
1	F	714	GLN
1	F	779	GLN
2	P	17	SER
2	P	30	LYS
2	P	71	MET
2	Q	17	SER
2	Q	30	LYS
2	Q	56	ASP
2	Q	71	MET
2	R	30	LYS
2	R	56	ASP
2	R	71	MET
2	S	30	LYS
2	T	60	ASN
1	B	295	VAL

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Mol	Chain	Res	Type
1	C	295	VAL
1	E	654	ILE
2	O	42	ASN
2	P	42	ASN
2	P	43	PRO
2	Q	42	ASN
2	R	42	ASN
2	S	42	ASN
2	T	42	ASN
1	A	699	GLY
1	A	742	ALA
1	A	792	VAL
1	C	643	ILE
1	C	792	VAL
1	D	699	GLY
1	D	742	ALA
1	F	792	VAL
2	Q	43	PRO
2	R	43	PRO
2	S	43	PRO
2	T	43	PRO
1	A	190	PRO
1	B	699	GLY
1	B	742	ALA
1	B	792	VAL
1	C	699	GLY
1	C	742	ALA
1	D	792	VAL
1	E	699	GLY
1	E	742	ALA
1	E	792	VAL
1	F	643	ILE
1	F	699	GLY
1	F	742	ALA
2	O	43	PRO
1	B	643	ILE
1	D	596	ILE
1	F	189	ASP
1	F	596	ILE

5.3.2 Protein sidechains ⓘ

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	664/705 (94%)	580 (87%)	84 (13%)	4	19
1	B	664/705 (94%)	576 (87%)	88 (13%)	4	17
1	C	664/705 (94%)	578 (87%)	86 (13%)	4	17
1	D	664/705 (94%)	577 (87%)	87 (13%)	4	17
1	E	664/705 (94%)	578 (87%)	86 (13%)	4	17
1	F	664/705 (94%)	579 (87%)	85 (13%)	4	18
2	O	123/127 (97%)	106 (86%)	17 (14%)	3	16
2	P	123/127 (97%)	106 (86%)	17 (14%)	3	16
2	Q	123/127 (97%)	106 (86%)	17 (14%)	3	16
2	R	123/127 (97%)	106 (86%)	17 (14%)	3	16
2	S	123/127 (97%)	106 (86%)	17 (14%)	3	16
2	T	123/127 (97%)	106 (86%)	17 (14%)	3	16
All	All	4722/4992 (95%)	4104 (87%)	618 (13%)	4	17

All (618) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	71	PHE
1	A	88	LYS
1	A	110	ASP
1	A	112	VAL
1	A	114	HIS
1	A	115	LYS
1	A	120	LEU
1	A	129	ASN
1	A	130	SER
1	A	133	GLU
1	A	135	VAL
1	A	140	ARG
1	A	141	PHE
1	A	144	GLU

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Mol	Chain	Res	Type
1	A	147	ARG
1	A	149	THR
1	A	152	LEU
1	A	158	ASP
1	A	171	TYR
1	A	172	GLU
1	A	177	ILE
1	A	182	ILE
1	A	188	LEU
1	A	197	LYS
1	A	208	LEU
1	A	210	PHE
1	A	212	GLN
1	A	226	ASP
1	A	229	PHE
1	A	254	ARG
1	A	270	LYS
1	A	279	ILE
1	A	284	LYS
1	A	286	GLU
1	A	293	ILE
1	A	296	LEU
1	A	309	PRO
1	A	323	ASN
1	A	324	THR
1	A	346	LYS
1	A	349	ASN
1	A	377	GLN
1	A	385	LEU
1	A	395	GLU
1	A	400	LYS
1	A	408	LEU
1	A	410	ILE
1	A	415	GLU
1	A	416	ASN
1	A	420	LEU
1	A	438	ASN
1	A	455	TYR
1	A	470	ASN
1	A	472	ARG
1	A	473	ASN
1	A	479	LYS

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Mol	Chain	Res	Type
1	A	484	VAL
1	A	500	SER
1	A	501	LEU
1	A	515	LYS
1	A	518	ASN
1	A	533	LEU
1	A	557	LEU
1	A	560	LEU
1	A	562	GLU
1	A	632	TYR
1	A	635	ILE
1	A	639	ASN
1	A	659	THR
1	A	665	LYS
1	A	672	ARG
1	A	674	SER
1	A	678	VAL
1	A	688	PHE
1	A	709	ASN
1	A	718	ARG
1	A	738	SER
1	A	744	GLU
1	A	752	LEU
1	A	767	GLN
1	A	770	ASN
1	A	780	LEU
1	A	781	ASN
1	A	794	GLN
1	B	64	ASN
1	B	71	PHE
1	B	88	LYS
1	B	110	ASP
1	B	112	VAL
1	B	114	HIS
1	B	115	LYS
1	B	120	LEU
1	B	129	ASN
1	B	130	SER
1	B	133	GLU
1	B	135	VAL
1	B	140	ARG
1	B	141	PHE

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Mol	Chain	Res	Type
1	B	144	GLU
1	B	147	ARG
1	B	149	THR
1	B	152	LEU
1	B	158	ASP
1	B	171	TYR
1	B	172	GLU
1	B	177	ILE
1	B	182	ILE
1	B	188	LEU
1	B	197	LYS
1	B	208	LEU
1	B	210	PHE
1	B	212	GLN
1	B	226	ASP
1	B	229	PHE
1	B	254	ARG
1	B	270	LYS
1	B	279	ILE
1	B	284	LYS
1	B	286	GLU
1	B	293	ILE
1	B	296	LEU
1	B	309	PRO
1	B	323	ASN
1	B	324	THR
1	B	346	LYS
1	B	349	ASN
1	B	377	GLN
1	B	385	LEU
1	B	395	GLU
1	B	400	LYS
1	B	408	LEU
1	B	410	ILE
1	B	415	GLU
1	B	416	ASN
1	B	420	LEU
1	B	438	ASN
1	B	455	TYR
1	B	470	ASN
1	B	472	ARG
1	B	473	ASN

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Mol	Chain	Res	Type
1	B	479	LYS
1	B	484	VAL
1	B	500	SER
1	B	501	LEU
1	B	502	THR
1	B	515	LYS
1	B	518	ASN
1	B	533	LEU
1	B	557	LEU
1	B	560	LEU
1	B	562	GLU
1	B	628	PHE
1	B	632	TYR
1	B	635	ILE
1	B	639	ASN
1	B	659	THR
1	B	665	LYS
1	B	672	ARG
1	B	674	SER
1	B	678	VAL
1	B	688	PHE
1	B	709	ASN
1	B	716	LYS
1	B	718	ARG
1	B	738	SER
1	B	744	GLU
1	B	752	LEU
1	B	767	GLN
1	B	770	ASN
1	B	780	LEU
1	B	781	ASN
1	B	794	GLN
1	C	71	PHE
1	C	88	LYS
1	C	110	ASP
1	C	112	VAL
1	C	114	HIS
1	C	115	LYS
1	C	120	LEU
1	C	129	ASN
1	C	130	SER
1	C	133	GLU

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Mol	Chain	Res	Type
1	C	135	VAL
1	C	140	ARG
1	C	141	PHE
1	C	144	GLU
1	C	147	ARG
1	C	149	THR
1	C	152	LEU
1	C	158	ASP
1	C	171	TYR
1	C	172	GLU
1	C	177	ILE
1	C	182	ILE
1	C	188	LEU
1	C	197	LYS
1	C	208	LEU
1	C	210	PHE
1	C	212	GLN
1	C	226	ASP
1	C	229	PHE
1	C	254	ARG
1	C	263	ASP
1	C	270	LYS
1	C	279	ILE
1	C	284	LYS
1	C	286	GLU
1	C	293	ILE
1	C	296	LEU
1	C	309	PRO
1	C	323	ASN
1	C	324	THR
1	C	346	LYS
1	C	349	ASN
1	C	377	GLN
1	C	385	LEU
1	C	395	GLU
1	C	400	LYS
1	C	408	LEU
1	C	410	ILE
1	C	415	GLU
1	C	416	ASN
1	C	420	LEU
1	C	438	ASN

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Mol	Chain	Res	Type
1	C	455	TYR
1	C	470	ASN
1	C	472	ARG
1	C	473	ASN
1	C	479	LYS
1	C	484	VAL
1	C	500	SER
1	C	501	LEU
1	C	502	THR
1	C	515	LYS
1	C	518	ASN
1	C	533	LEU
1	C	557	LEU
1	C	560	LEU
1	C	562	GLU
1	C	632	TYR
1	C	635	ILE
1	C	639	ASN
1	C	659	THR
1	C	665	LYS
1	C	672	ARG
1	C	674	SER
1	C	678	VAL
1	C	688	PHE
1	C	709	ASN
1	C	718	ARG
1	C	738	SER
1	C	744	GLU
1	C	752	LEU
1	C	767	GLN
1	C	770	ASN
1	C	780	LEU
1	C	781	ASN
1	C	794	GLN
1	D	71	PHE
1	D	88	LYS
1	D	110	ASP
1	D	112	VAL
1	D	114	HIS
1	D	115	LYS
1	D	120	LEU
1	D	129	ASN

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Mol	Chain	Res	Type
1	D	130	SER
1	D	133	GLU
1	D	135	VAL
1	D	140	ARG
1	D	141	PHE
1	D	144	GLU
1	D	147	ARG
1	D	149	THR
1	D	152	LEU
1	D	158	ASP
1	D	171	TYR
1	D	172	GLU
1	D	177	ILE
1	D	182	ILE
1	D	188	LEU
1	D	197	LYS
1	D	208	LEU
1	D	210	PHE
1	D	212	GLN
1	D	226	ASP
1	D	229	PHE
1	D	254	ARG
1	D	270	LYS
1	D	279	ILE
1	D	284	LYS
1	D	286	GLU
1	D	293	ILE
1	D	296	LEU
1	D	309	PRO
1	D	323	ASN
1	D	324	THR
1	D	346	LYS
1	D	349	ASN
1	D	377	GLN
1	D	385	LEU
1	D	395	GLU
1	D	400	LYS
1	D	408	LEU
1	D	410	ILE
1	D	415	GLU
1	D	416	ASN
1	D	420	LEU

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Mol	Chain	Res	Type
1	D	438	ASN
1	D	455	TYR
1	D	470	ASN
1	D	472	ARG
1	D	473	ASN
1	D	479	LYS
1	D	484	VAL
1	D	500	SER
1	D	501	LEU
1	D	502	THR
1	D	515	LYS
1	D	518	ASN
1	D	533	LEU
1	D	557	LEU
1	D	560	LEU
1	D	562	GLU
1	D	632	TYR
1	D	635	ILE
1	D	639	ASN
1	D	643	ILE
1	D	659	THR
1	D	665	LYS
1	D	672	ARG
1	D	674	SER
1	D	678	VAL
1	D	688	PHE
1	D	709	ASN
1	D	716	LYS
1	D	718	ARG
1	D	738	SER
1	D	744	GLU
1	D	752	LEU
1	D	767	GLN
1	D	770	ASN
1	D	780	LEU
1	D	781	ASN
1	D	794	GLN
1	E	71	PHE
1	E	88	LYS
1	E	110	ASP
1	E	112	VAL
1	E	114	HIS

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Mol	Chain	Res	Type
1	E	115	LYS
1	E	120	LEU
1	E	129	ASN
1	E	130	SER
1	E	133	GLU
1	E	135	VAL
1	E	140	ARG
1	E	141	PHE
1	E	144	GLU
1	E	147	ARG
1	E	149	THR
1	E	152	LEU
1	E	158	ASP
1	E	171	TYR
1	E	172	GLU
1	E	177	ILE
1	E	182	ILE
1	E	188	LEU
1	E	197	LYS
1	E	208	LEU
1	E	210	PHE
1	E	212	GLN
1	E	226	ASP
1	E	229	PHE
1	E	254	ARG
1	E	270	LYS
1	E	279	ILE
1	E	284	LYS
1	E	286	GLU
1	E	293	ILE
1	E	296	LEU
1	E	309	PRO
1	E	323	ASN
1	E	324	THR
1	E	346	LYS
1	E	349	ASN
1	E	377	GLN
1	E	385	LEU
1	E	395	GLU
1	E	400	LYS
1	E	408	LEU
1	E	410	ILE

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Mol	Chain	Res	Type
1	E	415	GLU
1	E	416	ASN
1	E	420	LEU
1	E	438	ASN
1	E	455	TYR
1	E	470	ASN
1	E	472	ARG
1	E	473	ASN
1	E	479	LYS
1	E	484	VAL
1	E	500	SER
1	E	501	LEU
1	E	502	THR
1	E	515	LYS
1	E	518	ASN
1	E	533	LEU
1	E	557	LEU
1	E	560	LEU
1	E	562	GLU
1	E	632	TYR
1	E	635	ILE
1	E	639	ASN
1	E	643	ILE
1	E	659	THR
1	E	665	LYS
1	E	672	ARG
1	E	674	SER
1	E	678	VAL
1	E	688	PHE
1	E	709	ASN
1	E	718	ARG
1	E	738	SER
1	E	744	GLU
1	E	752	LEU
1	E	767	GLN
1	E	770	ASN
1	E	780	LEU
1	E	781	ASN
1	E	794	GLN
1	F	71	PHE
1	F	88	LYS
1	F	110	ASP

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Mol	Chain	Res	Type
1	F	112	VAL
1	F	114	HIS
1	F	115	LYS
1	F	120	LEU
1	F	129	ASN
1	F	130	SER
1	F	133	GLU
1	F	135	VAL
1	F	140	ARG
1	F	141	PHE
1	F	144	GLU
1	F	147	ARG
1	F	149	THR
1	F	152	LEU
1	F	158	ASP
1	F	171	TYR
1	F	172	GLU
1	F	177	ILE
1	F	182	ILE
1	F	188	LEU
1	F	197	LYS
1	F	208	LEU
1	F	210	PHE
1	F	212	GLN
1	F	226	ASP
1	F	229	PHE
1	F	254	ARG
1	F	270	LYS
1	F	279	ILE
1	F	284	LYS
1	F	286	GLU
1	F	293	ILE
1	F	296	LEU
1	F	309	PRO
1	F	323	ASN
1	F	324	THR
1	F	346	LYS
1	F	349	ASN
1	F	377	GLN
1	F	385	LEU
1	F	395	GLU
1	F	400	LYS

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Mol	Chain	Res	Type
1	F	408	LEU
1	F	410	ILE
1	F	415	GLU
1	F	416	ASN
1	F	420	LEU
1	F	438	ASN
1	F	455	TYR
1	F	470	ASN
1	F	472	ARG
1	F	473	ASN
1	F	479	LYS
1	F	484	VAL
1	F	500	SER
1	F	501	LEU
1	F	502	THR
1	F	515	LYS
1	F	518	ASN
1	F	533	LEU
1	F	557	LEU
1	F	560	LEU
1	F	562	GLU
1	F	632	TYR
1	F	635	ILE
1	F	639	ASN
1	F	659	THR
1	F	665	LYS
1	F	672	ARG
1	F	674	SER
1	F	678	VAL
1	F	688	PHE
1	F	709	ASN
1	F	718	ARG
1	F	738	SER
1	F	744	GLU
1	F	752	LEU
1	F	767	GLN
1	F	770	ASN
1	F	780	LEU
1	F	781	ASN
1	F	794	GLN
2	O	5	THR
2	O	17	SER

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Mol	Chain	Res	Type
2	O	24	ASP
2	O	26	THR
2	O	28	THR
2	O	30	LYS
2	O	42	ASN
2	O	50	ASP
2	O	66	PRO
2	O	76	MET
2	O	83	GLU
2	O	97	ASN
2	O	106	ARG
2	O	112	LEU
2	O	117	THR
2	O	123	GLN
2	O	133	ASP
2	P	5	THR
2	P	17	SER
2	P	24	ASP
2	P	26	THR
2	P	28	THR
2	P	30	LYS
2	P	42	ASN
2	P	50	ASP
2	P	66	PRO
2	P	76	MET
2	P	83	GLU
2	P	97	ASN
2	P	106	ARG
2	P	112	LEU
2	P	117	THR
2	P	123	GLN
2	P	133	ASP
2	Q	5	THR
2	Q	17	SER
2	Q	24	ASP
2	Q	26	THR
2	Q	28	THR
2	Q	30	LYS
2	Q	42	ASN
2	Q	50	ASP
2	Q	66	PRO
2	Q	76	MET

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Mol	Chain	Res	Type
2	Q	83	GLU
2	Q	97	ASN
2	Q	106	ARG
2	Q	112	LEU
2	Q	117	THR
2	Q	123	GLN
2	Q	133	ASP
2	R	5	THR
2	R	17	SER
2	R	24	ASP
2	R	26	THR
2	R	28	THR
2	R	30	LYS
2	R	42	ASN
2	R	50	ASP
2	R	66	PRO
2	R	76	MET
2	R	83	GLU
2	R	97	ASN
2	R	106	ARG
2	R	112	LEU
2	R	117	THR
2	R	123	GLN
2	R	133	ASP
2	S	5	THR
2	S	17	SER
2	S	24	ASP
2	S	26	THR
2	S	28	THR
2	S	30	LYS
2	S	42	ASN
2	S	50	ASP
2	S	66	PRO
2	S	76	MET
2	S	83	GLU
2	S	97	ASN
2	S	106	ARG
2	S	112	LEU
2	S	117	THR
2	S	123	GLN
2	S	133	ASP
2	T	5	THR

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Mol	Chain	Res	Type
2	T	17	SER
2	T	24	ASP
2	T	26	THR
2	T	28	THR
2	T	30	LYS
2	T	42	ASN
2	T	50	ASP
2	T	66	PRO
2	T	76	MET
2	T	83	GLU
2	T	97	ASN
2	T	106	ARG
2	T	112	LEU
2	T	117	THR
2	T	123	GLN
2	T	133	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (191) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	129	ASN
1	A	239	HIS
1	A	323	ASN
1	A	368	GLN
1	A	387	ASN
1	A	450	ASN
1	A	480	ASN
1	A	507	GLN
1	A	510	GLN
1	A	518	ASN
1	A	551	ASN
1	A	553	GLN
1	A	576	ASN
1	A	577	HIS
1	A	581	GLN
1	A	618	ASN
1	A	629	ASN
1	A	639	ASN
1	A	655	ASN
1	A	666	ASN
1	A	709	ASN
1	A	747	ASN

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Mol	Chain	Res	Type
1	A	750	GLN
1	A	758	ASN
1	A	767	GLN
1	A	770	ASN
1	A	781	ASN
1	A	789	ASN
1	A	794	GLN
1	B	129	ASN
1	B	239	HIS
1	B	323	ASN
1	B	368	GLN
1	B	387	ASN
1	B	450	ASN
1	B	480	ASN
1	B	507	GLN
1	B	510	GLN
1	B	518	ASN
1	B	551	ASN
1	B	553	GLN
1	B	576	ASN
1	B	577	HIS
1	B	581	GLN
1	B	618	ASN
1	B	629	ASN
1	B	639	ASN
1	B	655	ASN
1	B	666	ASN
1	B	709	ASN
1	B	747	ASN
1	B	758	ASN
1	B	767	GLN
1	B	770	ASN
1	B	781	ASN
1	B	789	ASN
1	B	794	GLN
1	C	64	ASN
1	C	129	ASN
1	C	239	HIS
1	C	323	ASN
1	C	368	GLN
1	C	387	ASN
1	C	450	ASN

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Mol	Chain	Res	Type
1	C	480	ASN
1	C	507	GLN
1	C	510	GLN
1	C	518	ASN
1	C	551	ASN
1	C	553	GLN
1	C	576	ASN
1	C	581	GLN
1	C	618	ASN
1	C	629	ASN
1	C	639	ASN
1	C	655	ASN
1	C	666	ASN
1	C	709	ASN
1	C	747	ASN
1	C	750	GLN
1	C	758	ASN
1	C	767	GLN
1	C	770	ASN
1	C	781	ASN
1	C	789	ASN
1	C	794	GLN
1	D	64	ASN
1	D	129	ASN
1	D	239	HIS
1	D	323	ASN
1	D	368	GLN
1	D	387	ASN
1	D	438	ASN
1	D	450	ASN
1	D	480	ASN
1	D	507	GLN
1	D	510	GLN
1	D	518	ASN
1	D	551	ASN
1	D	553	GLN
1	D	576	ASN
1	D	577	HIS
1	D	581	GLN
1	D	618	ASN
1	D	629	ASN
1	D	639	ASN

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Mol	Chain	Res	Type
1	D	655	ASN
1	D	666	ASN
1	D	709	ASN
1	D	747	ASN
1	D	758	ASN
1	D	767	GLN
1	D	770	ASN
1	D	781	ASN
1	D	789	ASN
1	D	794	GLN
1	E	129	ASN
1	E	239	HIS
1	E	323	ASN
1	E	368	GLN
1	E	387	ASN
1	E	450	ASN
1	E	480	ASN
1	E	507	GLN
1	E	510	GLN
1	E	518	ASN
1	E	551	ASN
1	E	553	GLN
1	E	576	ASN
1	E	577	HIS
1	E	581	GLN
1	E	618	ASN
1	E	629	ASN
1	E	639	ASN
1	E	655	ASN
1	E	666	ASN
1	E	709	ASN
1	E	747	ASN
1	E	750	GLN
1	E	758	ASN
1	E	767	GLN
1	E	770	ASN
1	E	781	ASN
1	E	789	ASN
1	E	794	GLN
1	F	64	ASN
1	F	129	ASN
1	F	239	HIS

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Mol	Chain	Res	Type
1	F	323	ASN
1	F	368	GLN
1	F	387	ASN
1	F	450	ASN
1	F	480	ASN
1	F	507	GLN
1	F	510	GLN
1	F	518	ASN
1	F	551	ASN
1	F	553	GLN
1	F	576	ASN
1	F	581	GLN
1	F	618	ASN
1	F	629	ASN
1	F	639	ASN
1	F	655	ASN
1	F	666	ASN
1	F	709	ASN
1	F	747	ASN
1	F	758	ASN
1	F	767	GLN
1	F	770	ASN
1	F	781	ASN
1	F	789	ASN
1	F	794	GLN
2	O	8	GLN
2	O	111	ASN
2	O	143	GLN
2	P	8	GLN
2	P	111	ASN
2	P	143	GLN
2	Q	8	GLN
2	Q	111	ASN
2	Q	143	GLN
2	R	8	GLN
2	R	111	ASN
2	R	143	GLN
2	S	8	GLN
2	S	111	ASN
2	S	143	GLN
2	T	8	GLN
2	T	111	ASN

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Mol	Chain	Res	Type
2	T	143	GLN

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](#)

Of 18 ligands modelled in this entry, 18 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95th 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(Å ²)	Q<0.9
1	A	735/777 (94%)	3.03	439 (59%)  	24, 83, 143, 153	0
1	B	735/777 (94%)	2.95	441 (60%)  	25, 83, 143, 153	0
1	C	735/777 (94%)	3.07	483 (65%)  	25, 83, 143, 153	0
1	D	735/777 (94%)	2.93	458 (62%)  	25, 83, 143, 153	0
1	E	735/777 (94%)	2.94	453 (61%)  	24, 83, 142, 152	0
1	F	735/777 (94%)	2.93	447 (60%)  	27, 83, 143, 154	0
2	O	146/149 (97%)	2.80	85 (58%)  	22, 74, 121, 134	0
2	P	146/149 (97%)	2.48	78 (53%)  	20, 75, 121, 135	0
2	Q	146/149 (97%)	2.49	85 (58%)  	21, 75, 121, 134	0
2	R	146/149 (97%)	2.58	75 (51%)  	20, 75, 120, 134	0
2	S	146/149 (97%)	2.67	87 (59%)  	21, 76, 121, 134	0
2	T	146/149 (97%)	2.81	80 (54%)  	21, 75, 120, 134	0
All	All	5286/5556 (95%)	2.92	3211 (60%)  	20, 80, 142, 154	0

All (3211) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	468	LYS	21.6
1	D	204	ASP	21.2
2	P	78	ASP	20.1
1	D	211	SER	19.8
1	E	593	ILE	19.8
1	A	230	ILE	18.7
1	C	205	SER	16.3
1	B	190	PRO	16.0
1	B	222	ASN	15.8
1	C	548	THR	15.0
1	B	612	GLY	14.9

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Mol	Chain	Res	Type	RSRZ
1	F	186	LYS	14.8
2	O	25	GLY	14.5
1	A	204	ASP	14.5
1	F	206	SER	14.4
1	D	224	SER	14.1
2	T	137	ASN	14.1
1	D	229	PHE	13.7
2	T	63	ILE	13.7
1	C	162	ASN	13.3
1	F	203	SER	13.2
1	A	203	SER	13.2
1	A	227	ILE	13.0
1	B	425	GLU	13.0
1	C	149	THR	13.0
1	B	156	ILE	12.5
1	B	611	THR	12.4
1	A	205	SER	12.3
1	A	187	SER	12.3
1	A	432	TYR	11.9
1	C	150	PRO	11.8
1	C	620	THR	11.7
1	F	262	PRO	11.7
1	B	419	ILE	11.7
1	D	416	ASN	11.6
1	C	422	GLY	11.5
1	D	221	ASN	11.5
1	E	225	ILE	11.5
1	F	133	GLU	11.5
1	D	225	ILE	11.4
1	D	205	SER	11.4
2	O	47	GLU	11.4
1	E	375	GLY	11.3
1	A	224	SER	11.3
1	E	216	GLU	10.8
1	E	358	GLY	10.8
1	B	204	ASP	10.8
1	E	254	ARG	10.8
1	F	187	SER	10.7
1	C	204	ASP	10.5
1	E	228	ASN	10.5
1	C	423	LYS	10.3
1	A	221	ASN	10.3

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Mol	Chain	Res	Type	RSRZ
1	D	604	LEU	10.3
1	A	184	LYS	10.3
1	C	225	ILE	10.2
2	Q	55	VAL	10.2
1	E	253	HIS	10.2
1	B	418	ILE	10.2
1	B	474	ILE	10.1
1	F	462	ILE	10.1
1	A	276	PHE	10.1
1	D	413	LEU	10.1
1	E	434	LEU	10.0
1	B	247	TYR	10.0
1	D	131	ARG	9.9
1	C	118	GLN	9.9
1	F	189	ASP	9.8
1	B	109	ILE	9.7
1	A	375	GLY	9.7
1	B	600	GLY	9.7
2	O	136	VAL	9.7
1	D	444	PHE	9.6
1	F	224	SER	9.6
1	D	230	ILE	9.6
1	F	158	ASP	9.6
1	B	230	ILE	9.5
2	R	128	ALA	9.5
2	T	79	THR	9.5
1	A	635	ILE	9.5
1	C	153	ILE	9.4
1	B	162	ASN	9.4
2	O	56	ASP	9.4
1	F	188	LEU	9.4
1	A	280	SER	9.3
1	B	205	SER	9.3
1	D	631	SER	9.3
1	A	142	VAL	9.3
1	E	218	LEU	9.2
1	C	367	ASP	9.2
1	E	80	GLN	9.2
2	R	145	MET	9.2
1	D	334	LEU	9.2
1	B	244	ALA	9.2
1	A	468	LYS	9.2

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Mol	Chain	Res	Type	RSRZ
1	D	605	THR	9.1
1	E	204	ASP	9.1
1	B	510	GLN	9.1
1	C	405	LEU	9.1
1	C	226	ASP	9.0
1	F	246	SER	9.0
1	D	410	ILE	9.0
1	C	787	THR	9.0
1	D	477	MET	9.0
1	B	374	HIS	9.0
2	T	16	PHE	9.0
1	F	560	LEU	8.9
1	D	148	GLU	8.9
1	F	72	THR	8.9
1	B	428	ASN	8.9
2	T	132	GLY	8.9
1	E	365	PRO	8.9
1	F	572	GLY	8.8
1	E	410	ILE	8.7
1	B	171	TYR	8.7
1	A	442	TYR	8.7
1	A	206	SER	8.7
1	E	413	LEU	8.6
1	C	171	TYR	8.6
1	A	494	LEU	8.6
1	C	202	ASP	8.6
1	D	418	ILE	8.6
1	E	446	ILE	8.6
1	A	215	LYS	8.6
1	B	420	LEU	8.6
1	A	185	ASP	8.6
1	B	797	ILE	8.5
1	E	380	VAL	8.5
1	D	417	GLY	8.5
1	C	312	ALA	8.5
1	E	202	ASP	8.5
1	C	605	THR	8.5
1	F	107	THR	8.5
1	F	653	LYS	8.4
1	F	296	LEU	8.4
1	A	677	GLY	8.4
1	B	302	LEU	8.4

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Mol	Chain	Res	Type	RSRZ
1	C	513	TRP	8.4
1	D	339	ILE	8.4
1	D	206	SER	8.4
1	D	286	GLU	8.3
1	F	205	SER	8.3
1	D	165	GLN	8.3
1	A	158	ASP	8.3
1	A	698	ALA	8.3
1	C	421	LYS	8.3
1	A	770	ASN	8.2
1	E	203	SER	8.2
1	A	418	ILE	8.2
1	A	186	LYS	8.2
1	A	126	ASN	8.2
1	F	147	ARG	8.2
1	E	787	THR	8.2
1	E	618	ASN	8.2
1	F	169	VAL	8.2
1	E	159	TYR	8.2
1	B	401	ILE	8.2
1	B	159	TYR	8.1
1	F	434	LEU	8.1
1	A	741	ILE	8.0
1	C	64	ASN	8.0
1	B	447	SER	8.0
1	E	205	SER	8.0
1	C	213	LYS	8.0
1	F	773	PHE	8.0
2	O	58	ASP	8.0
2	R	23	GLY	8.0
1	E	160	ALA	7.9
1	C	371	SER	7.9
1	F	168	GLU	7.9
1	D	700	TYR	7.9
1	B	377	GLN	7.9
1	B	568	GLY	7.9
1	A	419	ILE	7.9
1	B	658	PRO	7.9
1	C	557	LEU	7.9
2	S	57	ALA	7.9
1	F	89	ILE	7.9
2	S	127	GLU	7.9

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Mol	Chain	Res	Type	RSRZ
1	E	440	GLN	7.9
1	A	773	PHE	7.9
1	B	454	GLN	7.8
1	A	297	LYS	7.8
1	A	192	PHE	7.8
1	F	66	LEU	7.8
2	O	111	ASN	7.8
2	O	72	MET	7.8
1	A	156	ILE	7.8
1	F	252	ASP	7.8
1	F	127	SER	7.7
1	B	150	PRO	7.7
1	D	442	TYR	7.7
1	E	632	TYR	7.7
1	A	165	GLN	7.7
1	C	325	TYR	7.7
1	D	457	THR	7.7
1	B	126	ASN	7.7
1	F	784	GLU	7.6
2	R	26	THR	7.6
1	C	260	TYR	7.6
1	F	257	LEU	7.6
2	Q	54	GLU	7.6
2	R	52	ILE	7.6
1	F	451	ASN	7.6
1	C	156	ILE	7.6
1	C	743	PRO	7.6
2	T	7	GLU	7.6
1	F	370	LEU	7.6
1	A	439	ASN	7.6
1	F	225	ILE	7.6
1	C	157	LYS	7.6
1	B	311	HIS	7.6
1	E	572	GLY	7.6
1	C	247	TYR	7.5
2	R	4	LEU	7.5
1	D	111	LEU	7.5
1	A	189	ASP	7.5
2	O	9	ILE	7.5
1	E	469	PHE	7.4
1	A	200	SER	7.4
1	D	275	GLY	7.4

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Mol	Chain	Res	Type	RSRZ
1	C	224	SER	7.4
1	A	557	LEU	7.4
1	C	709	ASN	7.4
1	F	359	PRO	7.4
1	E	560	LEU	7.4
1	A	576	ASN	7.4
1	F	261	ALA	7.4
1	B	137	PHE	7.4
1	B	582	ASP	7.3
1	D	185	ASP	7.3
1	D	306	GLY	7.3
1	C	369	ASP	7.3
1	B	643	ILE	7.3
1	B	402	PRO	7.3
2	T	62	THR	7.3
1	E	357	TRP	7.3
2	T	111	ASN	7.3
1	D	364	ILE	7.3
1	C	339	ILE	7.3
1	D	287	GLY	7.3
2	S	144	MET	7.3
1	B	237	PHE	7.3
1	D	162	ASN	7.3
1	A	359	PRO	7.2
1	A	305	SER	7.2
1	A	226	ASP	7.2
1	B	455	TYR	7.2
1	E	457	THR	7.2
1	B	163	SER	7.1
1	C	769	SER	7.1
1	A	127	SER	7.1
2	Q	128	ALA	7.1
1	C	221	ASN	7.1
1	F	192	PHE	7.1
2	O	46	ALA	7.1
1	F	202	ASP	7.1
1	D	433	TYR	7.1
1	D	743	PRO	7.1
1	E	422	GLY	7.1
1	A	315	PHE	7.1
1	C	214	PHE	7.1
1	E	214	PHE	7.1

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Mol	Chain	Res	Type	RSRZ
2	S	78	ASP	7.1
1	F	678	VAL	7.0
1	D	434	LEU	7.0
1	D	624	TYR	7.0
1	B	489	THR	7.0
1	C	272	GLU	7.0
1	C	621	GLY	7.0
1	E	411	GLU	7.0
1	A	331	VAL	7.0
1	F	149	THR	7.0
1	C	346	LYS	7.0
1	F	259	LEU	7.0
2	T	45	GLU	7.0
1	E	227	ILE	7.0
1	B	212	GLN	6.9
1	F	380	VAL	6.9
1	A	307	LEU	6.9
2	T	93	ASP	6.9
2	R	19	PHE	6.9
1	B	225	ILE	6.9
1	C	73	ASN	6.9
2	R	68	PHE	6.9
2	R	109	MET	6.9
1	E	389	LYS	6.9
1	E	107	THR	6.9
1	B	139	SER	6.9
1	B	206	SER	6.9
1	C	524	GLU	6.8
1	D	107	THR	6.8
1	F	75	THR	6.8
1	A	216	GLU	6.8
2	T	17	SER	6.8
1	B	642	TYR	6.8
1	A	107	THR	6.8
1	D	252	ASP	6.8
1	A	90	PRO	6.8
1	A	202	ASP	6.8
1	A	207	ASP	6.8
1	A	356	ASP	6.8
1	A	788	ASP	6.8
1	E	207	ASP	6.8
2	T	6	GLU	6.8

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Mol	Chain	Res	Type	RSRZ
2	P	28	THR	6.8
1	B	452	GLU	6.7
1	B	262	PRO	6.7
1	E	621	GLY	6.7
1	C	168	GLU	6.7
2	T	112	LEU	6.7
1	F	793	PHE	6.7
1	E	75	THR	6.7
1	F	258	GLU	6.7
1	F	260	TYR	6.7
1	A	330	PRO	6.7
1	F	165	GLN	6.7
1	C	163	SER	6.7
2	O	52	ILE	6.7
1	B	226	ASP	6.6
1	D	719	LYS	6.6
2	Q	53	ASN	6.6
1	D	141	PHE	6.6
1	D	349	ASN	6.6
1	E	266	GLU	6.6
1	C	127	SER	6.6
1	B	352	GLY	6.6
1	E	433	TYR	6.6
1	F	476	VAL	6.6
1	F	556	MET	6.6
1	B	709	ASN	6.6
1	C	345	THR	6.6
1	C	279	ILE	6.6
1	A	714	GLN	6.6
1	C	564	VAL	6.6
2	O	26	THR	6.6
2	S	101	SER	6.6
1	F	356	ASP	6.5
1	F	525	LYS	6.5
1	B	490	ALA	6.5
1	C	197	LYS	6.5
1	B	437	SER	6.5
1	A	441	VAL	6.5
1	A	514	ASP	6.5
1	E	390	SER	6.5
1	E	726	ILE	6.5
1	F	467	GLU	6.5

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Mol	Chain	Res	Type	RSRZ
1	E	283	LEU	6.5
2	P	96	GLY	6.5
1	D	708	ALA	6.5
1	E	460	GLY	6.5
1	E	391	ILE	6.5
1	A	103	GLU	6.5
1	C	425	GLU	6.5
1	A	518	ASN	6.4
1	B	131	ARG	6.4
1	C	612	GLY	6.4
1	A	416	ASN	6.4
1	B	734	ASN	6.4
1	D	455	TYR	6.4
1	E	186	LYS	6.4
2	P	77	LYS	6.4
1	A	529	VAL	6.4
1	B	185	ASP	6.4
1	B	263	ASP	6.4
1	C	148	GLU	6.4
2	S	22	ASP	6.4
1	D	463	THR	6.4
1	A	542	PRO	6.4
1	D	593	ILE	6.4
2	T	61	GLY	6.4
1	E	76	LEU	6.4
1	F	152	LEU	6.4
1	C	203	SER	6.4
1	D	203	SER	6.4
1	D	280	SER	6.4
1	C	568	GLY	6.4
1	D	307	LEU	6.3
1	E	770	ASN	6.3
1	B	614	PHE	6.3
1	E	229	PHE	6.3
1	A	461	LYS	6.3
1	D	194	ASN	6.3
1	A	465	LEU	6.3
1	A	398	ILE	6.3
1	E	797	ILE	6.3
1	E	165	GLN	6.2
1	B	583	ASN	6.2
1	B	602	PHE	6.2

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Mol	Chain	Res	Type	RSRZ
1	A	433	TYR	6.2
1	A	487	PRO	6.2
1	F	530	THR	6.2
1	E	201	ASP	6.2
1	B	569	TYR	6.2
1	B	659	THR	6.2
2	Q	42	ASN	6.2
1	D	344	ALA	6.2
1	A	589	LYS	6.2
1	C	119	ASP	6.2
2	T	64	ASP	6.2
1	F	170	TYR	6.2
1	B	708	ALA	6.2
1	C	228	ASN	6.2
1	A	141	PHE	6.2
1	C	108	ASP	6.2
1	D	350	VAL	6.1
1	A	70	GLU	6.1
1	F	204	ASP	6.1
1	C	74	GLU	6.1
1	F	379	ALA	6.1
1	C	454	GLN	6.1
1	D	793	PHE	6.1
1	B	763	LEU	6.1
2	R	29	THR	6.1
1	F	607	ASN	6.1
1	A	352	GLY	6.1
1	F	782	PHE	6.1
1	C	508	ILE	6.1
2	Q	112	LEU	6.1
1	A	464	VAL	6.1
1	C	746	LYS	6.1
1	A	647	ASP	6.1
2	R	18	LEU	6.1
1	F	420	LEU	6.1
1	C	185	ASP	6.1
1	E	158	ASP	6.1
1	E	582	ASP	6.1
1	D	97	TYR	6.1
1	C	126	ASN	6.1
1	F	768	LYS	6.1
1	C	415	GLU	6.0

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Mol	Chain	Res	Type	RSRZ
1	B	64	ASN	6.0
1	A	420	LEU	6.0
1	B	197	LYS	6.0
1	D	443	GLU	6.0
1	A	590	ASP	6.0
1	D	592	GLU	6.0
1	F	121	SER	6.0
2	P	29	THR	6.0
1	F	509	PRO	6.0
1	F	569	TYR	6.0
1	D	216	GLU	6.0
1	D	461	LYS	6.0
1	E	492	TYR	6.0
1	B	367	ASP	6.0
1	D	786	GLU	6.0
1	F	297	LYS	6.0
1	A	229	PHE	6.0
1	B	473	ASN	6.0
1	C	110	ASP	6.0
2	Q	96	GLY	6.0
1	F	129	ASN	6.0
1	C	313	ASP	6.0
1	F	654	ILE	6.0
1	F	454	GLN	6.0
1	E	443	GLU	5.9
1	B	110	ASP	5.9
1	A	171	TYR	5.9
1	B	557	LEU	5.9
1	F	253	HIS	5.9
1	F	657	ILE	5.9
1	B	119	ASP	5.9
1	F	531	ASN	5.9
1	B	161	ILE	5.9
1	E	619	ILE	5.9
1	D	254	ARG	5.9
1	B	451	ASN	5.9
1	A	262	PRO	5.9
1	A	125	LYS	5.9
1	C	453	VAL	5.9
1	D	460	GLY	5.9
1	B	218	LEU	5.9
1	A	145	LYS	5.9

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Mol	Chain	Res	Type	RSRZ
1	D	80	GLN	5.9
1	C	601	GLU	5.9
1	E	181	ILE	5.9
1	F	153	ILE	5.9
1	E	222	ASN	5.9
1	A	238	GLN	5.9
1	D	335	ALA	5.9
1	A	652	ALA	5.8
1	F	268	MET	5.8
1	A	702	SER	5.8
2	S	63	ILE	5.8
1	A	399	GLY	5.8
2	P	25	GLY	5.8
1	E	798	ASP	5.8
1	A	83	GLN	5.8
1	D	130	SER	5.8
1	E	252	ASP	5.8
2	S	107	HIS	5.8
1	E	366	PHE	5.8
1	F	442	TYR	5.8
1	E	639	ASN	5.8
2	P	42	ASN	5.8
1	F	490	ALA	5.8
1	C	431	LYS	5.8
1	E	564	VAL	5.8
2	Q	39	LEU	5.8
1	E	587	PRO	5.8
1	F	90	PRO	5.8
1	F	65	ASN	5.8
1	E	624	TYR	5.8
1	C	358	GLY	5.8
1	D	601	GLU	5.7
1	A	201	ASP	5.7
1	F	298	GLY	5.7
1	E	620	THR	5.7
1	D	469	PHE	5.7
1	A	190	PRO	5.7
1	C	399	GLY	5.7
1	A	257	LEU	5.7
1	F	605	THR	5.7
1	B	132	GLY	5.7
1	D	116	GLU	5.7

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Mol	Chain	Res	Type	RSRZ
1	D	761	GLN	5.7
1	A	228	ASN	5.7
1	C	490	ALA	5.7
1	F	229	PHE	5.6
1	F	321	GLU	5.6
1	F	526	GLN	5.6
1	D	365	PRO	5.6
1	A	162	ASN	5.6
1	E	162	ASN	5.6
1	B	465	LEU	5.6
1	A	577	HIS	5.6
1	E	171	TYR	5.6
1	C	304	ALA	5.6
2	T	14	GLU	5.6
1	D	629	ASN	5.6
1	F	435	LEU	5.6
1	D	226	ASP	5.6
2	O	59	GLY	5.6
1	E	307	LEU	5.6
1	C	504	ILE	5.6
2	O	54	GLU	5.6
1	B	781	ASN	5.6
2	T	138	TYR	5.5
1	F	578	GLY	5.5
1	F	652	ALA	5.5
1	A	435	LEU	5.5
1	E	591	ASN	5.5
1	E	686	ASP	5.5
1	C	796	ILE	5.5
1	A	605	THR	5.5
1	F	494	LEU	5.5
1	C	290	LYS	5.5
1	E	442	TYR	5.5
1	C	592	GLU	5.5
1	A	490	ALA	5.5
1	B	157	LYS	5.5
1	C	442	TYR	5.5
1	D	202	ASP	5.5
1	F	376	GLN	5.5
2	Q	45	GLU	5.5
1	A	742	ALA	5.5
1	C	549	LEU	5.5

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Mol	Chain	Res	Type	RSRZ
1	B	615	ILE	5.5
1	B	136	PRO	5.5
1	D	249	PHE	5.5
1	A	653	LYS	5.5
1	D	728	ALA	5.5
1	A	168	GLU	5.5
1	E	575	VAL	5.5
1	F	178	SER	5.5
1	D	129	ASN	5.5
1	D	421	LYS	5.5
1	E	407	HIS	5.5
1	C	420	LEU	5.5
1	E	409	ARG	5.5
2	P	144	MET	5.5
1	F	571	GLY	5.5
1	C	350	VAL	5.4
1	B	324	THR	5.4
1	A	368	GLN	5.4
1	D	207	ASP	5.4
1	C	379	ALA	5.4
2	S	126	ARG	5.4
1	F	109	ILE	5.4
1	B	518	ASN	5.4
1	A	672	ARG	5.4
1	A	98	SER	5.4
1	C	308	VAL	5.4
2	S	145	MET	5.4
1	A	84	ASP	5.4
1	A	740	GLN	5.4
1	A	253	HIS	5.4
1	D	228	ASN	5.4
1	F	135	VAL	5.4
1	F	620	THR	5.4
1	B	350	VAL	5.4
1	F	618	ASN	5.4
2	S	3	GLN	5.4
1	B	698	ALA	5.4
2	T	56	ASP	5.4
1	C	494	LEU	5.4
2	R	25	GLY	5.4
1	A	251	PRO	5.4
1	C	363	TYR	5.4

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Mol	Chain	Res	Type	RSRZ
1	E	376	GLN	5.4
1	D	366	PHE	5.4
1	E	230	ILE	5.4
1	F	426	ILE	5.4
1	A	222	ASN	5.4
1	C	233	ASN	5.4
2	R	21	LYS	5.4
1	F	255	THR	5.4
1	D	705	TYR	5.4
1	C	470	ASN	5.4
1	D	574	VAL	5.3
1	E	323	ASN	5.3
1	D	428	ASN	5.3
1	C	166	SER	5.3
1	F	564	VAL	5.3
2	P	112	LEU	5.3
1	C	578	GLY	5.3
1	F	69	THR	5.3
1	A	225	ILE	5.3
1	A	248	TYR	5.3
1	A	492	TYR	5.3
1	B	381	GLU	5.3
2	Q	28	THR	5.3
1	A	194	ASN	5.3
1	F	492	TYR	5.3
2	O	128	ALA	5.3
1	D	214	PHE	5.3
1	B	160	ALA	5.3
1	C	707	SER	5.3
1	E	449	GLU	5.3
1	D	218	LEU	5.3
1	E	701	LEU	5.3
1	A	525	LYS	5.3
2	O	70	THR	5.3
1	C	250	ALA	5.2
1	A	779	GLN	5.2
1	B	760	VAL	5.2
1	E	69	THR	5.2
1	D	742	ALA	5.2
1	F	104	ILE	5.2
1	C	387	ASN	5.2
2	Q	137	ASN	5.2

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Mol	Chain	Res	Type	RSRZ
1	F	331	VAL	5.2
1	E	426	ILE	5.2
2	O	5	THR	5.2
2	O	57	ALA	5.2
2	S	135	GLN	5.2
2	P	134	GLY	5.2
1	F	143	PHE	5.2
1	B	245	PHE	5.2
1	C	113	GLU	5.2
1	C	161	ILE	5.2
1	F	421	LYS	5.2
1	E	208	LEU	5.2
1	E	367	ASP	5.2
1	E	637	PRO	5.2
1	A	159	TYR	5.2
1	D	540	ARG	5.2
1	B	694	VAL	5.2
1	D	237	PHE	5.2
1	D	264	MET	5.2
1	D	446	ILE	5.2
1	A	169	VAL	5.2
1	F	563	ALA	5.2
1	E	633	ASN	5.2
1	B	345	THR	5.2
1	E	562	GLU	5.1
1	B	248	TYR	5.1
1	D	251	PRO	5.1
1	C	230	ILE	5.1
1	D	378	LEU	5.1
1	A	344	ALA	5.1
2	R	144	MET	5.1
1	E	470	ASN	5.1
1	C	606	LYS	5.1
1	E	461	LYS	5.1
1	E	105	TYR	5.1
1	F	405	LEU	5.1
1	D	440	GLN	5.1
1	F	185	ASP	5.1
1	A	437	SER	5.1
1	D	253	HIS	5.1
1	D	126	ASN	5.1
1	E	629	ASN	5.1

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Mol	Chain	Res	Type	RSRZ
1	E	644	GLU	5.1
1	B	460	GLY	5.1
1	C	222	ASN	5.1
1	D	756	ILE	5.1
1	C	582	ASP	5.1
1	F	469	PHE	5.1
1	F	522	SER	5.1
2	O	85	ILE	5.1
1	C	496	ALA	5.1
1	D	220	LEU	5.1
2	Q	114	GLU	5.1
1	B	228	ASN	5.1
1	D	305	SER	5.1
1	C	170	TYR	5.0
2	Q	83	GLU	5.0
2	S	56	ASP	5.0
1	D	363	TYR	5.0
1	C	583	ASN	5.0
2	P	107	HIS	5.0
1	B	149	THR	5.0
1	B	217	LYS	5.0
1	C	569	TYR	5.0
2	R	146	THR	5.0
1	D	273	LYS	5.0
1	D	623	ASP	5.0
1	F	577	HIS	5.0
1	D	487	PRO	5.0
1	E	431	LYS	5.0
2	R	126	ARG	5.0
1	E	215	LYS	5.0
1	B	664	ILE	5.0
1	C	694	VAL	5.0
1	B	713	SER	5.0
1	C	489	THR	5.0
1	C	728	ALA	5.0
1	C	584	GLU	5.0
1	D	398	ILE	5.0
1	E	468	LYS	5.0
1	C	65	ASN	5.0
1	A	405	LEU	5.0
1	B	549	LEU	5.0
1	C	100	LEU	5.0

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Mol	Chain	Res	Type	RSRZ
1	F	368	GLN	5.0
1	B	207	ASP	5.0
1	B	203	SER	5.0
1	C	102	GLY	5.0
1	B	326	ILE	5.0
1	D	212	GLN	5.0
1	D	595	ILE	5.0
1	B	443	GLU	5.0
1	E	796	ILE	5.0
2	Q	76	MET	5.0
1	B	528	GLY	5.0
1	C	396	GLY	5.0
1	A	784	GLU	4.9
1	A	474	ILE	4.9
1	E	133	GLU	4.9
1	C	93	VAL	4.9
1	B	667	LEU	4.9
1	F	677	GLY	4.9
1	A	360	VAL	4.9
2	P	111	ASN	4.9
1	E	749	PHE	4.9
1	C	72	THR	4.9
2	Q	107	HIS	4.9
2	S	108	VAL	4.9
1	A	561	ASN	4.9
2	S	8	GLN	4.9
1	D	566	TYR	4.9
2	P	15	ALA	4.9
1	F	332	ASN	4.9
1	B	415	GLU	4.9
2	O	77	LYS	4.9
1	A	313	ASP	4.9
1	B	229	PHE	4.9
1	E	447	SER	4.9
1	F	403	LEU	4.9
1	F	500	SER	4.9
2	T	5	THR	4.9
1	F	398	ILE	4.9
1	E	111	LEU	4.9
1	D	709	ASN	4.9
1	F	487	PRO	4.9
1	E	604	LEU	4.8

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Mol	Chain	Res	Type	RSRZ
1	F	538	ILE	4.8
1	B	407	HIS	4.8
1	E	74	GLU	4.8
1	A	476	VAL	4.8
2	R	56	ASP	4.8
1	D	140	ARG	4.8
1	D	478	ALA	4.8
1	A	191	GLU	4.8
1	F	70	GLU	4.8
1	B	596	ILE	4.8
1	B	732	ILE	4.8
1	C	697	ILE	4.8
1	A	611	THR	4.8
1	E	417	GLY	4.8
1	A	485	LEU	4.8
1	F	221	ASN	4.8
1	E	594	PHE	4.8
1	A	467	GLU	4.8
1	B	397	GLU	4.8
2	S	26	THR	4.8
2	T	23	GLY	4.8
1	C	760	VAL	4.8
1	C	673	SER	4.8
1	D	603	ILE	4.8
1	A	72	THR	4.8
1	A	147	ARG	4.8
1	F	446	ILE	4.8
1	C	761	GLN	4.8
1	B	221	ASN	4.8
1	D	769	SER	4.8
1	F	155	ASN	4.8
1	F	190	PRO	4.8
1	A	188	LEU	4.8
1	A	256	VAL	4.8
1	A	198	SER	4.8
1	B	314	ALA	4.8
1	F	682	SER	4.8
1	E	296	LEU	4.8
1	E	643	ILE	4.8
1	A	411	GLU	4.8
1	B	363	TYR	4.8
1	B	358	GLY	4.8

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Mol	Chain	Res	Type	RSRZ
1	B	155	ASN	4.8
2	R	108	VAL	4.8
1	D	668	SER	4.8
1	C	177	ILE	4.8
1	E	771	ILE	4.8
1	F	579	THR	4.7
2	O	55	VAL	4.7
1	F	315	PHE	4.7
1	A	664	ILE	4.7
1	C	429	GLY	4.7
2	S	21	LYS	4.7
1	E	185	ASP	4.7
1	B	630	ARG	4.7
1	D	322	LEU	4.7
1	E	273	LYS	4.7
1	F	223	LYS	4.7
1	F	307	LEU	4.7
1	F	461	LYS	4.7
1	B	496	ALA	4.7
1	C	212	GLN	4.7
1	D	142	VAL	4.7
1	A	231	LYS	4.7
1	A	247	TYR	4.7
1	D	488	LEU	4.7
1	C	602	PHE	4.7
1	C	629	ASN	4.7
1	B	421	LYS	4.7
1	E	325	TYR	4.7
1	C	334	LEU	4.7
1	D	606	LYS	4.7
2	P	104	GLU	4.7
1	A	649	ILE	4.7
1	F	156	ILE	4.7
1	D	247	TYR	4.7
2	T	25	GLY	4.7
2	O	135	GLN	4.7
1	A	183	SER	4.7
1	A	370	LEU	4.7
1	E	247	TYR	4.7
1	F	222	ASN	4.7
1	F	660	SER	4.7
1	D	476	VAL	4.7

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Mol	Chain	Res	Type	RSRZ
1	E	226	ASP	4.7
1	A	82	THR	4.6
1	D	354	SER	4.6
1	D	575	VAL	4.6
1	E	256	VAL	4.6
1	A	749	PHE	4.6
1	E	109	ILE	4.6
1	B	507	GLN	4.6
1	B	621	GLY	4.6
1	A	558	ASP	4.6
1	E	474	ILE	4.6
2	O	53	ASN	4.6
1	E	386	GLU	4.6
1	E	563	ALA	4.6
1	C	190	PRO	4.6
1	B	315	PHE	4.6
1	C	526	GLN	4.6
1	B	95	GLU	4.6
1	C	502	THR	4.6
1	E	161	ILE	4.6
1	C	571	GLY	4.6
2	S	43	PRO	4.6
1	A	214	PHE	4.6
1	A	161	ILE	4.6
1	D	160	ALA	4.6
1	D	619	ILE	4.6
1	F	251	PRO	4.6
1	C	729	TYR	4.6
1	F	118	GLN	4.6
1	D	336	THR	4.6
1	D	615	ILE	4.6
1	F	117	LEU	4.6
1	A	541	LYS	4.6
1	A	554	LYS	4.6
1	C	351	HIS	4.6
1	C	484	VAL	4.6
1	B	497	LEU	4.6
1	F	749	PHE	4.6
1	B	372	LYS	4.6
1	E	647	ASP	4.6
1	C	776	LEU	4.6
1	B	414	LYS	4.6

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Mol	Chain	Res	Type	RSRZ
1	E	134	LYS	4.6
2	T	54	GLU	4.6
1	A	102	GLY	4.5
1	A	591	ASN	4.5
1	E	398	ILE	4.5
1	A	219	GLU	4.5
1	B	169	VAL	4.5
1	F	85	LEU	4.5
1	A	500	SER	4.5
1	C	245	PHE	4.5
1	E	477	MET	4.5
1	D	450	ASN	4.5
1	E	360	VAL	4.5
1	F	233	ASN	4.5
1	A	310	GLU	4.5
1	E	393	GLU	4.5
1	D	283	LEU	4.5
1	A	104	ILE	4.5
1	A	233	ASN	4.5
1	E	257	LEU	4.5
1	F	207	ASP	4.5
1	C	139	SER	4.5
1	E	302	LEU	4.5
1	D	213	LYS	4.5
2	P	39	LEU	4.5
1	A	608	TRP	4.5
1	E	83	GLN	4.5
1	A	369	ASP	4.5
1	E	553	GLN	4.5
1	C	370	LEU	4.5
1	F	465	LEU	4.5
2	S	79	THR	4.5
1	E	707	SER	4.5
1	A	160	ALA	4.5
1	D	562	GLU	4.5
1	A	252	ASP	4.5
1	A	341	SER	4.5
1	B	743	PRO	4.5
1	F	330	PRO	4.5
2	T	27	ILE	4.5
1	A	769	SER	4.5
1	D	163	SER	4.5

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Mol	Chain	Res	Type	RSRZ
1	C	781	ASN	4.5
1	E	758	ASN	4.5
1	F	523	LEU	4.5
2	T	72	MET	4.4
1	D	412	GLU	4.4
1	B	145	LYS	4.4
1	C	667	LEU	4.4
2	Q	78	ASP	4.4
1	E	421	LYS	4.4
1	B	449	GLU	4.4
1	E	116	GLU	4.4
1	E	574	VAL	4.4
1	F	350	VAL	4.4
1	A	195	LEU	4.4
1	C	631	SER	4.4
1	B	776	LEU	4.4
1	D	667	LEU	4.4
2	P	32	LEU	4.4
1	C	314	ALA	4.4
1	A	462	ILE	4.4
1	B	164	GLU	4.4
1	D	281	GLU	4.4
1	D	649	ILE	4.4
1	E	244	ALA	4.4
1	C	206	SER	4.4
1	B	215	LYS	4.4
1	B	410	ILE	4.4
1	E	571	GLY	4.4
1	D	523	LEU	4.4
1	D	560	LEU	4.4
1	F	542	PRO	4.4
1	D	127	SER	4.4
1	C	294	ASP	4.4
1	B	605	THR	4.4
1	C	238	GLN	4.4
1	C	675	ASN	4.4
1	C	347	GLY	4.4
1	B	493	ASP	4.4
1	B	525	LYS	4.4
1	F	546	LYS	4.4
1	A	250	ALA	4.4
1	E	212	GLN	4.4

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Mol	Chain	Res	Type	RSRZ
1	B	756	ILE	4.4
1	C	591	ASN	4.4
1	D	760	VAL	4.4
1	F	134	LYS	4.4
2	O	112	LEU	4.4
1	C	507	GLN	4.4
1	B	260	TYR	4.4
1	D	187	SER	4.3
2	S	23	GLY	4.4
1	A	785	ASN	4.3
1	C	786	GLU	4.3
1	A	278	LYS	4.3
1	D	297	LYS	4.3
1	E	309	PRO	4.3
1	A	376	GLN	4.3
1	D	638	GLY	4.3
1	C	111	LEU	4.3
1	C	323	ASN	4.3
1	E	439	ASN	4.3
1	D	449	GLU	4.3
1	C	239	HIS	4.3
1	E	462	ILE	4.3
1	A	121	SER	4.3
1	A	793	PHE	4.3
1	D	782	PHE	4.3
2	S	81	SER	4.3
1	A	443	GLU	4.3
1	A	636	ALA	4.3
2	S	109	MET	4.3
1	A	483	GLY	4.3
1	C	309	PRO	4.3
1	C	114	HIS	4.3
1	C	377	GLN	4.3
2	R	10	ALA	4.3
1	C	658	PRO	4.3
1	E	465	LEU	4.3
1	D	171	TYR	4.3
1	E	585	GLU	4.3
1	F	93	VAL	4.3
1	F	453	VAL	4.3
1	C	311	HIS	4.3
1	A	771	ILE	4.3

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Mol	Chain	Res	Type	RSRZ
2	S	52	ILE	4.3
2	S	68	PHE	4.3
1	A	540	ARG	4.3
1	E	251	PRO	4.3
1	A	691	LYS	4.3
1	B	548	THR	4.3
2	S	112	LEU	4.3
1	D	173	ILE	4.3
1	E	364	ILE	4.3
1	A	237	PHE	4.3
1	B	187	SER	4.3
1	D	325	TYR	4.3
1	F	445	ARG	4.3
1	C	521	ASN	4.3
1	B	287	GLY	4.3
1	A	139	SER	4.3
1	A	109	ILE	4.3
1	B	106	PHE	4.3
1	B	446	ILE	4.3
1	E	455	TYR	4.3
1	E	456	LYS	4.3
2	S	116	LEU	4.3
1	B	308	VAL	4.3
1	D	279	ILE	4.3
1	E	308	VAL	4.3
1	E	596	ILE	4.3
1	D	223	LYS	4.2
2	Q	146	THR	4.2
1	E	520	PRO	4.2
1	F	198	SER	4.2
1	C	229	PHE	4.2
1	D	735	VAL	4.2
1	A	501	LEU	4.2
2	T	116	LEU	4.2
1	A	114	HIS	4.2
1	A	678	VAL	4.2
1	B	565	LYS	4.2
1	C	209	LEU	4.2
1	A	782	PHE	4.2
1	F	216	GLU	4.2
1	A	578	GLY	4.2
1	D	132	GLY	4.2

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Mol	Chain	Res	Type	RSRZ
1	E	548	THR	4.2
2	T	128	ALA	4.2
2	S	58	ASP	4.2
1	F	76	LEU	4.2
2	O	89	PHE	4.2
2	T	96	GLY	4.2
1	B	603	ILE	4.2
1	B	98	SER	4.2
1	E	258	GLU	4.2
2	R	127	GLU	4.2
1	A	349	ASN	4.2
1	B	284	LYS	4.2
1	E	319	ALA	4.2
1	C	374	HIS	4.2
1	B	413	LEU	4.2
1	E	206	SER	4.2
1	B	594	PHE	4.2
1	F	384	ASN	4.2
2	T	59	GLY	4.2
1	A	279	ILE	4.2
1	E	424	LYS	4.2
1	E	603	ILE	4.2
1	A	705	TYR	4.2
1	C	704	TYR	4.2
1	E	282	SER	4.2
1	F	681	ASP	4.2
1	B	633	ASN	4.2
1	B	224	SER	4.2
2	O	132	GLY	4.2
1	F	230	ILE	4.2
1	A	648	PRO	4.2
1	A	223	LYS	4.2
1	E	566	TYR	4.2
1	F	363	TYR	4.2
1	E	321	GLU	4.2
1	A	618	ASN	4.2
1	C	613	ARG	4.2
2	S	42	ASN	4.2
1	A	717	LYS	4.2
1	C	657	ILE	4.2
1	D	504	ILE	4.2
1	E	99	GLU	4.2

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Mol	Chain	Res	Type	RSRZ
1	F	769	SER	4.2
1	A	353	LYS	4.1
1	E	152	LEU	4.1
1	E	269	ASN	4.1
1	E	343	VAL	4.1
1	E	760	VAL	4.1
1	B	711	ILE	4.1
1	E	772	GLU	4.1
1	E	761	GLN	4.1
1	F	750	GLN	4.1
1	A	451	ASN	4.1
1	D	627	TYR	4.1
1	F	529	VAL	4.1
2	Q	104	GLU	4.1
2	T	143	GLN	4.1
1	D	201	ASP	4.1
2	T	58	ASP	4.1
1	A	777	TYR	4.1
1	F	269	ASN	4.1
1	A	565	LYS	4.1
1	A	732	ILE	4.1
1	B	186	LYS	4.1
1	B	379	ALA	4.1
1	C	501	LEU	4.1
1	E	489	THR	4.1
1	B	279	ILE	4.1
1	C	467	GLU	4.1
1	F	279	ILE	4.1
1	A	143	PHE	4.1
1	A	694	VAL	4.1
1	F	316	LYS	4.1
2	Q	131	ASP	4.1
1	F	310	GLU	4.1
1	F	643	ILE	4.1
1	C	764	LEU	4.1
1	F	81	GLN	4.1
1	E	217	LYS	4.1
1	C	356	ASP	4.1
1	B	576	ASN	4.1
1	C	561	ASN	4.1
1	B	373	LYS	4.1
1	C	491	ASP	4.1

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Mol	Chain	Res	Type	RSRZ
1	E	622	LYS	4.1
1	F	333	LYS	4.1
1	F	479	LYS	4.1
1	D	351	HIS	4.1
1	A	426	ILE	4.1
1	C	246	SER	4.1
2	R	22	ASP	4.1
2	T	4	LEU	4.1
1	F	237	PHE	4.1
1	C	730	ASN	4.1
1	E	73	ASN	4.1
1	E	661	ALA	4.1
1	F	641	ALA	4.1
1	D	657	ILE	4.1
1	A	469	PHE	4.1
1	D	69	THR	4.1
1	F	765	THR	4.1
1	F	291	ASP	4.1
1	B	213	LYS	4.1
1	D	564	VAL	4.1
1	E	453	VAL	4.1
1	F	103	GLU	4.1
1	B	733	GLU	4.0
1	F	119	ASP	4.0
1	F	128	MET	4.0
1	F	341	SER	4.0
2	Q	135	GLN	4.0
1	E	338	LEU	4.0
1	F	741	ILE	4.0
1	C	469	PHE	4.0
1	B	317	LYS	4.0
1	B	572	GLY	4.0
1	D	258	GLU	4.0
2	P	57	ALA	4.0
1	C	130	SER	4.0
1	D	368	GLN	4.0
1	F	373	LYS	4.0
2	Q	24	ASP	4.0
2	R	79	THR	4.0
1	C	759	GLN	4.0
1	B	78	LYS	4.0
1	E	276	PHE	4.0

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Mol	Chain	Res	Type	RSRZ
1	F	450	ASN	4.0
2	O	36	MET	4.0
1	A	254	ARG	4.0
1	B	227	ILE	4.0
1	D	538	ILE	4.0
1	E	249	PHE	4.0
2	P	121	VAL	4.0
2	Q	11	GLU	4.0
1	E	132	GLY	4.0
1	B	303	LYS	4.0
1	C	783	THR	4.0
1	A	736	LEU	4.0
1	E	586	PHE	4.0
2	O	3	GLN	4.0
1	A	798	ASP	4.0
1	E	354	SER	4.0
1	A	511	LYS	4.0
1	D	763	LEU	4.0
1	D	771	ILE	4.0
2	Q	27	ILE	4.0
1	C	324	THR	4.0
2	O	94	LYS	4.0
1	B	170	TYR	4.0
1	E	221	ASN	4.0
1	A	645	TRP	4.0
1	E	479	LYS	4.0
1	A	650	THR	4.0
2	S	62	THR	4.0
1	B	328	PHE	4.0
1	B	80	GLN	4.0
1	C	768	LYS	4.0
1	C	365	PRO	4.0
1	C	517	VAL	4.0
1	A	239	HIS	4.0
1	D	695	LYS	4.0
1	B	514	ASP	4.0
2	O	78	ASP	4.0
2	S	69	LEU	4.0
1	F	635	ILE	4.0
1	A	581	GLN	3.9
1	C	416	ASN	3.9
1	E	264	MET	3.9

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Mol	Chain	Res	Type	RSRZ
2	O	64	ASP	3.9
1	A	676	VAL	3.9
1	C	485	LEU	3.9
1	B	499	PRO	3.9
2	P	73	ALA	3.9
1	F	584	GLU	3.9
1	B	357	TRP	3.9
1	C	619	ILE	3.9
1	E	444	PHE	3.9
1	B	115	LYS	3.9
1	E	577	HIS	3.9
1	A	296	LEU	3.9
1	B	399	GLY	3.9
1	E	769	SER	3.9
1	C	608	TRP	3.9
1	F	181	ILE	3.9
1	C	518	ASN	3.9
2	R	55	VAL	3.9
1	C	326	ILE	3.9
1	A	164	GLU	3.9
1	B	340	LYS	3.9
1	B	566	TYR	3.9
1	D	559	ARG	3.9
1	B	75	THR	3.9
1	B	469	PHE	3.9
1	B	783	THR	3.9
2	P	85	ILE	3.9
1	A	445	ARG	3.9
1	C	626	TYR	3.9
2	O	24	ASP	3.9
1	B	79	ILE	3.9
1	B	771	ILE	3.9
2	O	27	ILE	3.9
1	A	363	TYR	3.9
1	D	542	PRO	3.9
2	P	91	VAL	3.9
1	C	315	PHE	3.9
1	C	663	PHE	3.9
1	A	519	THR	3.9
1	E	704	TYR	3.9
1	F	770	ASN	3.9
1	A	415	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	C	616	GLU	3.9
1	E	70	GLU	3.9
1	F	151	LYS	3.9
1	A	249	PHE	3.9
1	B	759	GLN	3.9
1	D	664	ILE	3.9
1	F	108	ASP	3.9
1	F	629	ASN	3.9
1	C	777	TYR	3.9
1	B	269	ASN	3.9
1	B	577	HIS	3.9
1	B	710	HIS	3.9
1	E	368	GLN	3.9
1	D	64	ASN	3.9
1	A	66	LEU	3.8
1	D	117	LEU	3.8
1	B	267	TYR	3.8
1	F	249	PHE	3.8
1	B	238	GLN	3.8
1	D	340	LYS	3.8
1	D	726	ILE	3.8
1	F	411	GLU	3.8
2	S	84	GLU	3.8
1	B	610	MET	3.8
1	A	155	ASN	3.8
1	C	700	TYR	3.8
1	A	213	LYS	3.8
1	E	151	LYS	3.8
1	B	779	GLN	3.8
1	F	226	ASP	3.8
1	E	579	THR	3.8
1	E	655	ASN	3.8
1	A	567	THR	3.8
1	C	330	PRO	3.8
1	F	533	LEU	3.8
2	S	123	GLN	3.8
1	D	745	TYR	3.8
2	Q	134	GLY	3.8
1	C	131	ARG	3.8
1	C	703	ASP	3.8
1	D	74	GLU	3.8
1	B	360	VAL	3.8

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Mol	Chain	Res	Type	RSRZ
1	E	578	GLY	3.8
1	E	788	ASP	3.8
1	D	553	GLN	3.8
1	D	191	GLU	3.8
1	A	604	LEU	3.8
1	B	208	LEU	3.8
1	C	403	LEU	3.8
1	D	94	LEU	3.8
1	F	781	ASN	3.8
1	A	755	ARG	3.8
2	O	98	GLY	3.8
2	R	57	ALA	3.8
1	E	642	TYR	3.8
1	B	364	ILE	3.8
1	D	285	LYS	3.8
2	Q	63	ILE	3.8
1	C	488	LEU	3.8
1	F	532	LEU	3.8
1	F	64	ASN	3.8
2	O	137	ASN	3.8
1	B	184	LYS	3.8
1	D	791	GLU	3.8
1	F	517	VAL	3.8
1	A	347	GLY	3.8
1	B	124	GLU	3.8
1	C	622	LYS	3.8
2	S	143	GLN	3.8
1	A	255	THR	3.8
1	C	530	THR	3.8
1	B	189	ASP	3.8
1	B	491	ASP	3.8
1	C	175	LYS	3.8
1	C	563	ALA	3.8
1	F	580	GLU	3.8
2	R	8	GLN	3.8
1	C	726	ILE	3.8
1	E	127	SER	3.8
2	P	92	PHE	3.8
1	B	122	GLU	3.7
1	C	767	GLN	3.7
1	E	262	PRO	3.7
1	C	441	VAL	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	710	HIS	3.7
1	E	245	PHE	3.7
1	E	486	LYS	3.7
1	E	570	THR	3.7
2	Q	75	LYS	3.7
1	F	369	ASP	3.7
1	B	591	ASN	3.7
1	C	595	ILE	3.7
1	F	736	LEU	3.7
2	S	16	PHE	3.7
2	O	109	MET	3.7
2	T	146	THR	3.7
1	B	327	LEU	3.7
1	B	339	ILE	3.7
1	D	188	LEU	3.7
2	Q	125	ILE	3.7
1	C	329	ARG	3.7
1	E	131	ARG	3.7
2	P	53	ASN	3.7
1	B	744	GLU	3.7
1	E	784	GLU	3.7
1	C	301	ALA	3.7
1	E	778	LYS	3.7
1	F	125	LYS	3.7
1	B	714	GLN	3.7
1	C	426	ILE	3.7
2	Q	100	ILE	3.7
1	B	453	VAL	3.7
1	C	337	ASN	3.7
2	O	48	LEU	3.7
1	D	355	SER	3.7
1	E	118	GLN	3.7
2	O	41	GLN	3.7
1	F	634	LYS	3.7
2	R	11	GLU	3.7
1	E	129	ASN	3.7
2	P	69	LEU	3.7
1	B	376	GLN	3.7
1	A	631	SER	3.7
1	C	765	THR	3.7
1	E	350	VAL	3.7
1	C	493	ASP	3.7

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Mol	Chain	Res	Type	RSRZ
1	E	395	GLU	3.7
1	B	789	ASN	3.7
1	C	160	ALA	3.7
1	D	770	ASN	3.7
1	B	462	ILE	3.7
1	A	163	SER	3.7
1	B	769	SER	3.7
2	P	71	MET	3.7
1	A	484	VAL	3.7
1	B	432	TYR	3.7
1	B	712	PHE	3.7
1	C	293	ILE	3.7
1	C	492	TYR	3.7
1	E	363	TYR	3.7
1	A	306	GLY	3.7
1	A	522	SER	3.7
1	A	776	LEU	3.7
1	B	128	MET	3.7
1	D	296	LEU	3.7
1	F	488	LEU	3.7
1	D	167	LYS	3.7
1	E	536	TYR	3.7
1	E	538	ILE	3.7
1	A	332	ASN	3.7
1	C	140	ARG	3.7
1	E	396	GLY	3.7
1	B	202	ASP	3.7
2	R	93	ASP	3.7
2	R	92	PHE	3.7
2	Q	123	GLN	3.7
2	S	54	GLU	3.7
1	A	660	SER	3.6
1	E	149	THR	3.6
1	F	658	PRO	3.6
2	Q	109	MET	3.6
1	E	180	ASP	3.6
1	E	263	ASP	3.6
2	O	63	ILE	3.6
1	B	704	TYR	3.6
1	F	777	TYR	3.6
1	D	118	GLN	3.6
1	D	707	SER	3.6

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Mol	Chain	Res	Type	RSRZ
2	P	146	THR	3.6
1	A	687	GLU	3.6
1	C	381	GLU	3.6
1	A	101	GLY	3.6
1	A	340	LYS	3.6
1	A	510	GLN	3.6
2	R	143	GLN	3.6
1	C	560	LEU	3.6
1	E	607	ASN	3.6
1	F	655	ASN	3.6
2	O	4	LEU	3.6
1	B	749	PHE	3.6
1	A	620	THR	3.6
1	F	650	THR	3.6
1	D	333	LYS	3.6
2	R	24	ASP	3.6
2	O	18	LEU	3.6
1	A	602	PHE	3.6
1	E	387	ASN	3.6
1	D	792	VAL	3.6
1	E	670	ILE	3.6
1	F	184	LYS	3.6
2	T	136	VAL	3.6
1	F	764	LEU	3.6
1	F	272	GLU	3.6
1	C	624	TYR	3.6
1	E	751	TYR	3.6
1	E	187	SER	3.6
1	C	779	GLN	3.6
1	E	740	GLN	3.6
2	O	49	GLN	3.6
1	B	214	PHE	3.6
1	B	337	ASN	3.6
1	E	397	GLU	3.6
1	A	329	ARG	3.6
1	C	466	GLY	3.6
1	D	149	THR	3.6
1	F	82	THR	3.6
1	F	201	ASP	3.6
2	O	146	THR	3.6
2	S	118	ASP	3.6
1	B	331	VAL	3.6

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Mol	Chain	Res	Type	RSRZ
1	E	126	ASN	3.6
1	E	768	LYS	3.6
1	D	178	SER	3.6
1	D	570	THR	3.6
1	E	623	ASP	3.6
1	B	436	GLU	3.6
1	C	635	ILE	3.6
1	B	259	LEU	3.6
1	C	382	LYS	3.6
1	D	456	LYS	3.6
1	D	483	GLY	3.6
1	B	470	ASN	3.6
1	B	508	ILE	3.6
1	D	672	ARG	3.6
2	Q	29	THR	3.6
1	D	737	LYS	3.6
1	E	223	LYS	3.6
1	E	361	ALA	3.6
1	F	651	LYS	3.6
1	C	452	GLU	3.6
1	A	217	LYS	3.6
1	B	398	ILE	3.6
1	E	452	GLU	3.6
1	B	478	ALA	3.6
1	D	312	ALA	3.6
2	T	18	LEU	3.6
1	B	587	PRO	3.6
1	E	359	PRO	3.6
2	T	89	PHE	3.6
1	D	155	ASN	3.6
1	E	458	LYS	3.6
1	F	785	ASN	3.6
1	F	697	ILE	3.6
2	P	63	ILE	3.6
2	P	87	GLU	3.6
1	E	335	ALA	3.6
1	D	625	LEU	3.6
1	D	701	LEU	3.6
1	A	715	GLU	3.5
1	E	697	ILE	3.5
1	F	767	GLN	3.5
2	P	6	GLU	3.5

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Mol	Chain	Res	Type	RSRZ
1	A	351	HIS	3.5
1	D	492	TYR	3.5
1	F	248	TYR	3.5
1	B	346	LYS	3.5
1	D	411	GLU	3.5
1	D	796	ILE	3.5
1	F	212	GLN	3.5
1	D	445	ARG	3.5
1	C	368	GLN	3.5
1	D	697	ILE	3.5
1	D	301	ALA	3.5
1	E	414	LYS	3.5
1	E	791	GLU	3.5
1	D	513	TRP	3.5
1	E	645	TRP	3.5
1	E	636	ALA	3.5
1	C	141	PHE	3.5
1	E	722	ILE	3.5
1	C	151	LYS	3.5
1	F	753	LYS	3.5
2	O	32	LEU	3.5
1	C	138	ALA	3.5
1	D	319	ALA	3.5
1	F	537	GLY	3.5
2	S	122	ASP	3.5
1	E	200	SER	3.5
1	E	213	LYS	3.5
1	D	435	LEU	3.5
1	E	683	GLY	3.5
2	Q	15	ALA	3.5
1	E	459	GLU	3.5
2	T	126	ARG	3.5
2	S	53	ASN	3.5
1	C	553	GLN	3.5
1	C	660	SER	3.5
1	D	748	TYR	3.5
1	A	316	LYS	3.5
1	F	503	GLU	3.5
2	P	75	LYS	3.5
1	F	141	PHE	3.5
1	B	541	LYS	3.5
2	P	55	VAL	3.5

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Mol	Chain	Res	Type	RSRZ
1	C	533	LEU	3.5
1	D	466	GLY	3.5
1	E	573	ASP	3.5
1	F	428	ASN	3.5
1	C	737	LYS	3.5
1	C	738	SER	3.5
1	E	728	ALA	3.5
1	F	157	LYS	3.5
1	D	248	TYR	3.5
1	D	536	TYR	3.5
1	E	748	TYR	3.5
1	F	513	TRP	3.5
1	B	735	VAL	3.5
1	E	108	ASP	3.5
2	Q	57	ALA	3.5
1	B	584	GLU	3.5
1	F	471	TRP	3.5
1	B	796	ILE	3.5
2	R	63	ILE	3.5
1	B	573	ASP	3.4
1	F	116	GLU	3.4
2	O	87	GLU	3.4
1	A	569	TYR	3.4
1	E	112	VAL	3.4
2	T	142	VAL	3.4
1	D	797	ILE	3.4
1	C	478	ALA	3.4
1	A	533	LEU	3.4
1	B	622	LYS	3.4
1	C	525	LYS	3.4
1	D	79	ILE	3.4
1	D	278	LYS	3.4
1	C	237	PHE	3.4
1	F	712	PHE	3.4
2	Q	98	GLY	3.4
1	B	129	ASN	3.4
1	C	158	ASP	3.4
2	P	24	ASP	3.4
2	T	77	LYS	3.4
1	D	227	ILE	3.4
1	E	274	GLY	3.4
2	R	5	THR	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	497	LEU	3.4
1	A	549	LEU	3.4
1	C	566	TYR	3.4
1	F	775	LEU	3.4
1	E	194	ASN	3.4
2	P	56	ASP	3.4
1	B	571	GLY	3.4
1	E	102	GLY	3.4
1	A	373	LYS	3.4
1	A	783	THR	3.4
2	T	36	MET	3.4
1	E	698	ALA	3.4
1	F	234	LEU	3.4
1	C	732	ILE	3.4
1	A	71	PHE	3.4
1	D	518	ASN	3.4
1	A	146	LYS	3.4
1	D	400	LYS	3.4
2	S	7	GLU	3.4
1	F	250	ALA	3.4
1	C	763	LEU	3.4
1	B	495	PHE	3.4
1	A	491	ASP	3.4
1	D	798	ASP	3.4
1	A	452	GLU	3.4
1	B	521	ASN	3.4
1	D	332	ASN	3.4
2	T	60	ASN	3.4
2	O	102	ALA	3.4
1	E	285	LYS	3.4
1	C	352	GLY	3.4
1	D	298	GLY	3.4
1	B	299	GLU	3.4
1	D	582	ASP	3.4
2	R	71	MET	3.4
1	A	314	ALA	3.4
1	E	355	SER	3.4
1	B	534	ILE	3.4
1	D	101	GLY	3.4
1	C	286	GLU	3.4
1	B	780	LEU	3.4
1	C	661	ALA	3.4

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Mol	Chain	Res	Type	RSRZ
1	D	532	LEU	3.4
2	Q	25	GLY	3.4
1	A	404	LYS	3.4
1	D	308	VAL	3.4
2	P	136	VAL	3.4
2	T	133	ASP	3.4
1	B	492	TYR	3.4
1	F	247	TYR	3.4
1	C	579	THR	3.4
1	E	399	GLY	3.4
1	E	581	GLN	3.4
1	F	570	THR	3.4
2	P	79	THR	3.4
1	D	145	LYS	3.4
1	B	488	LEU	3.4
1	B	540	ARG	3.4
1	C	259	LEU	3.4
1	C	465	LEU	3.4
2	O	10	ALA	3.4
1	C	495	PHE	3.4
1	D	276	PHE	3.4
1	F	679	TYR	3.4
1	C	253	HIS	3.4
1	D	533	LEU	3.3
1	E	610	MET	3.4
2	O	91	VAL	3.3
1	A	92	ASP	3.3
1	D	161	ILE	3.3
1	D	313	ASP	3.3
1	D	427	ASP	3.3
1	D	645	TRP	3.3
2	Q	19	PHE	3.3
2	S	100	ILE	3.3
1	D	622	LYS	3.3
2	R	96	GLY	3.3
1	B	371	SER	3.3
1	A	380	VAL	3.3
1	C	322	LEU	3.3
1	E	516	VAL	3.3
1	F	243	LEU	3.3
1	C	698	ALA	3.3
1	D	652	ALA	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	474	ILE	3.3
1	C	670	ILE	3.3
1	A	287	GLY	3.3
1	A	466	GLY	3.3
1	A	584	GLU	3.3
1	B	158	ASP	3.3
1	B	680	LYS	3.3
1	A	473	ASN	3.3
1	D	83	GLN	3.3
1	B	625	LEU	3.3
1	D	736	LEU	3.3
1	F	604	LEU	3.3
1	A	75	THR	3.3
2	Q	35	VAL	3.3
2	Q	79	THR	3.3
2	S	38	SER	3.3
2	Q	13	LYS	3.3
1	C	448	ASP	3.3
1	F	313	ASP	3.3
2	Q	120	GLU	3.3
1	F	740	GLN	3.3
2	T	38	SER	3.3
1	A	319	ALA	3.3
1	A	797	ILE	3.3
1	A	460	GLY	3.3
1	B	627	TYR	3.3
1	D	159	TYR	3.3
1	D	474	ILE	3.3
1	E	164	GLU	3.3
1	F	573	ASP	3.3
1	F	701	LEU	3.3
1	A	400	LYS	3.3
1	C	710	HIS	3.3
1	B	570	THR	3.3
1	E	649	ILE	3.3
2	P	101	SER	3.3
1	D	432	TYR	3.3
1	F	412	GLU	3.3
1	F	357	TRP	3.3
2	R	131	ASP	3.3
1	F	328	PHE	3.3
1	A	615	ILE	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	641	ALA	3.3
1	D	98	SER	3.3
1	E	757	THR	3.3
1	F	352	GLY	3.3
1	A	513	TRP	3.3
1	D	746	LYS	3.3
2	S	148	LYS	3.3
1	D	367	ASP	3.3
2	S	71	MET	3.3
1	A	699	GLY	3.3
1	C	758	ASN	3.3
1	E	122	GLU	3.3
1	E	551	ASN	3.3
2	O	73	ALA	3.3
2	P	27	ILE	3.3
1	F	566	TYR	3.3
1	A	486	LYS	3.3
1	F	714	GLN	3.3
1	B	342	GLY	3.3
1	C	725	GLY	3.3
1	F	86	LEU	3.3
1	E	345	THR	3.3
1	A	77	ASP	3.3
1	A	539	GLU	3.3
1	B	168	GLU	3.3
1	B	590	ASP	3.3
1	C	186	LYS	3.3
1	C	401	ILE	3.3
1	E	467	GLU	3.3
2	O	13	LYS	3.3
1	A	434	LEU	3.3
1	E	98	SER	3.3
1	E	315	PHE	3.3
2	O	68	PHE	3.3
1	B	578	GLY	3.3
1	E	140	ARG	3.3
1	C	432	TYR	3.3
1	E	432	TYR	3.3
1	E	351	HIS	3.3
1	E	67	VAL	3.3
1	E	450	ASN	3.3
2	T	53	ASN	3.3

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Mol	Chain	Res	Type	RSRZ
1	C	336	THR	3.3
1	B	151	LYS	3.3
1	B	351	HIS	3.3
1	B	484	VAL	3.3
1	F	464	VAL	3.3
1	A	118	GLN	3.2
1	B	758	ASN	3.2
1	C	499	PRO	3.2
2	P	127	GLU	3.2
1	A	659	THR	3.2
1	F	287	GLY	3.2
1	B	427	ASP	3.2
1	C	80	GLN	3.2
1	F	126	ASN	3.2
2	P	109	MET	3.2
2	R	139	GLU	3.2
1	B	127	SER	3.2
1	E	625	LEU	3.2
1	A	295	VAL	3.2
1	D	106	PHE	3.2
1	B	365	PRO	3.2
1	C	534	ILE	3.2
2	P	135	GLN	3.2
1	F	73	ASN	3.2
1	B	424	LYS	3.2
1	B	329	ARG	3.2
1	B	574	VAL	3.2
1	D	369	ASP	3.2
1	E	259	LEU	3.2
1	E	648	PRO	3.2
1	F	154	ILE	3.2
1	F	474	ILE	3.2
1	F	636	ALA	3.2
1	C	642	TYR	3.2
1	C	617	LYS	3.2
2	Q	71	MET	3.2
2	R	72	MET	3.2
1	D	259	LEU	3.2
1	D	183	SER	3.2
2	T	81	SER	3.2
1	E	235	THR	3.2
1	F	463	THR	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	681	ASP	3.2
1	C	147	ARG	3.2
1	C	319	ALA	3.2
1	C	632	TYR	3.2
1	E	237	PHE	3.2
2	S	17	SER	3.2
1	A	537	GLY	3.2
1	A	560	LEU	3.2
2	Q	32	LEU	3.2
1	E	125	LYS	3.2
1	E	700	TYR	3.2
1	A	323	ASN	3.2
1	A	79	ILE	3.2
1	A	326	ILE	3.2
1	B	619	ILE	3.2
1	B	650	THR	3.2
1	A	212	GLN	3.2
1	D	590	ASP	3.2
1	E	493	ASP	3.2
1	E	590	ASP	3.2
1	B	249	PHE	3.2
1	B	325	TYR	3.2
1	C	505	LYS	3.2
2	O	108	VAL	3.2
2	Q	108	VAL	3.2
1	B	593	ILE	3.2
1	C	666	ASN	3.2
1	E	233	ASN	3.2
1	F	98	SER	3.2
1	C	685	LYS	3.2
2	Q	77	LYS	3.2
1	C	575	VAL	3.2
1	D	394	HIS	3.2
1	C	627	TYR	3.2
1	F	67	VAL	3.2
2	R	67	GLU	3.2
1	F	283	LEU	3.2
1	B	579	THR	3.2
1	C	678	VAL	3.2
2	Q	133	ASP	3.2
1	C	462	ILE	3.2
1	A	781	ASN	3.2

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Mol	Chain	Res	Type	RSRZ
1	C	477	MET	3.2
1	B	623	ASP	3.2
2	P	129	ASP	3.2
1	A	421	LYS	3.1
1	E	333	LYS	3.1
1	B	725	GLY	3.1
1	D	128	MET	3.1
1	E	540	ARG	3.1
1	B	498	ALA	3.1
1	D	698	ALA	3.1
1	F	393	GLU	3.1
1	F	115	LYS	3.1
1	B	76	LEU	3.1
1	D	419	ILE	3.1
1	D	602	PHE	3.1
1	E	503	GLU	3.1
2	S	41	GLN	3.1
2	T	57	ALA	3.1
1	C	455	TYR	3.1
1	F	130	SER	3.1
1	F	557	LEU	3.1
1	A	364	ILE	3.1
1	E	600	GLY	3.1
1	C	712	PHE	3.1
1	A	574	VAL	3.1
1	B	125	LYS	3.1
1	C	754	GLU	3.1
1	D	133	GLU	3.1
2	O	8	GLN	3.1
1	B	480	ASN	3.1
1	B	485	LEU	3.1
1	B	618	ASN	3.1
1	F	447	SER	3.1
1	D	401	ILE	3.1
1	F	347	GLY	3.1
1	F	686	ASP	3.1
1	E	106	PHE	3.1
1	F	270	LYS	3.1
2	S	139	GLU	3.1
1	F	496	ALA	3.1
1	D	750	GLN	3.1
1	B	73	ASN	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	646	THR	3.1
1	A	663	PHE	3.1
1	D	577	HIS	3.1
1	C	167	LYS	3.1
1	E	402	PRO	3.1
2	T	94	LYS	3.1
1	B	219	GLU	3.1
2	T	109	MET	3.1
2	S	138	TYR	3.1
1	C	106	PHE	3.1
1	C	771	ILE	3.1
1	D	210	PHE	3.1
1	F	663	PHE	3.1
1	C	95	GLU	3.1
1	C	263	ASP	3.1
1	F	180	ASP	3.1
1	A	403	LEU	3.1
1	A	124	GLU	3.1
1	E	148	GLU	3.1
1	E	224	SER	3.1
1	A	498	ALA	3.1
1	B	433	TYR	3.1
1	B	153	ILE	3.1
1	E	153	ILE	3.1
2	P	98	GLY	3.1
1	D	785	ASN	3.1
1	F	709	ASN	3.1
1	A	681	ASP	3.1
1	B	494	LEU	3.1
1	E	370	LEU	3.1
1	F	700	TYR	3.1
1	F	705	TYR	3.1
1	E	418	ILE	3.1
2	Q	12	PHE	3.1
1	E	232	GLU	3.1
1	D	470	ASN	3.1
1	B	646	THR	3.1
1	A	80	GLN	3.1
1	A	96	ILE	3.1
1	A	508	ILE	3.1
1	A	654	ILE	3.1
1	F	732	ILE	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	529	VAL	3.1
1	C	236	GLU	3.1
1	F	122	GLU	3.1
1	B	114	HIS	3.1
1	F	208	LEU	3.1
1	B	130	SER	3.1
1	C	540	ARG	3.1
1	A	619	ILE	3.1
1	B	670	ILE	3.1
1	F	440	GLN	3.1
2	T	134	GLY	3.1
2	T	135	GLN	3.1
1	B	412	GLU	3.1
1	F	574	VAL	3.1
2	O	6	GLU	3.1
1	A	317	LYS	3.0
1	B	706	ASN	3.0
2	Q	30	LYS	3.0
2	T	129	ASP	3.0
1	C	116	GLU	3.0
2	Q	67	GLU	3.0
1	E	167	LYS	3.0
1	E	725	GLY	3.0
1	F	231	LYS	3.0
1	A	395	GLU	3.0
1	C	750	GLN	3.0
1	D	198	SER	3.0
1	E	427	ASP	3.0
1	B	120	LEU	3.0
2	R	69	LEU	3.0
1	B	192	PHE	3.0
1	D	245	PHE	3.0
1	A	725	GLY	3.0
1	E	95	GLU	3.0
1	F	797	ILE	3.0
1	A	579	THR	3.0
2	P	30	LYS	3.0
1	A	366	PHE	3.0
1	F	628	PHE	3.0
1	B	426	ILE	3.0
1	C	298	GLY	3.0
1	C	398	ILE	3.0

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Mol	Chain	Res	Type	RSRZ
1	D	274	GLY	3.0
2	S	10	ALA	3.0
1	B	146	LYS	3.0
1	C	300	LYS	3.0
2	T	70	THR	3.0
2	P	88	ALA	3.0
1	C	772	GLU	3.0
1	C	791	GLU	3.0
1	D	93	VAL	3.0
1	E	509	PRO	3.0
1	A	117	LEU	3.0
1	A	427	ASP	3.0
1	B	243	LEU	3.0
1	C	282	SER	3.0
1	C	473	ASN	3.0
1	D	390	SER	3.0
1	F	367	ASP	3.0
2	R	58	ASP	3.0
1	C	328	PHE	3.0
1	E	567	THR	3.0
1	B	476	VAL	3.0
1	B	511	LYS	3.0
1	D	360	VAL	3.0
2	O	21	LYS	3.0
2	Q	136	VAL	3.0
1	C	66	LEU	3.0
1	A	628	PHE	3.0
1	F	305	SER	3.0
1	D	731	GLU	3.0
1	D	757	THR	3.0
1	E	101	GLY	3.0
1	C	424	LYS	3.0
1	B	405	LEU	3.0
1	F	265	PHE	3.0
1	A	655	ASN	3.0
1	D	397	GLU	3.0
1	D	486	LYS	3.0
1	E	144	GLU	3.0
1	E	666	ASN	3.0
2	T	113	GLY	3.0
2	O	79	THR	3.0
1	D	403	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	C	555	GLN	3.0
1	D	712	PHE	3.0
1	D	686	ASP	3.0
1	F	508	ILE	3.0
2	R	78	ASP	3.0
1	B	200	SER	3.0
1	C	447	SER	3.0
1	E	626	TYR	3.0
1	E	679	TYR	3.0
1	C	780	LEU	3.0
1	D	76	LEU	3.0
1	D	755	ARG	3.0
1	D	773	PHE	3.0
1	F	423	LYS	3.0
2	P	145	MET	3.0
2	T	124	MET	3.0
1	F	164	GLU	3.0
1	D	670	ILE	3.0
1	F	105	TYR	3.0
2	S	93	ASP	3.0
2	Q	101	SER	3.0
2	S	18	LEU	3.0
1	C	565	LYS	3.0
1	A	499	PRO	3.0
1	B	368	GLN	3.0
1	D	376	GLN	3.0
2	O	66	PRO	3.0
2	Q	41	GLN	3.0
1	C	201	ASP	3.0
1	C	705	TYR	3.0
1	D	569	TYR	3.0
1	E	435	LEU	3.0
1	D	633	ASN	3.0
1	D	789	ASN	3.0
1	F	416	ASN	3.0
1	F	518	ASN	3.0
1	B	107	THR	3.0
1	C	255	THR	3.0
1	F	80	GLN	3.0
2	O	45	GLU	3.0
2	R	104	GLU	3.0
1	F	441	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	108	ASP	2.9
1	B	201	ASP	2.9
1	C	788	ASP	2.9
1	D	543	ASP	2.9
2	O	30	LYS	2.9
1	A	607	ASN	2.9
1	C	522	SER	2.9
1	F	438	ASN	2.9
1	B	581	GLN	2.9
1	C	342	GLY	2.9
1	F	766	HIS	2.9
2	S	90	ARG	2.9
2	T	3	GLN	2.9
1	C	587	PRO	2.9
1	E	720	ILE	2.9
1	D	302	LEU	2.9
1	D	549	LEU	2.9
1	E	763	LEU	2.9
1	A	477	MET	2.9
1	E	731	GLU	2.9
1	F	581	GLN	2.9
1	D	134	LYS	2.9
1	D	293	ILE	2.9
2	R	94	LYS	2.9
2	T	9	ILE	2.9
1	B	406	ASP	2.9
1	D	514	ASP	2.9
1	F	491	ASP	2.9
1	C	231	LYS	2.9
2	O	143	GLN	2.9
1	D	711	ILE	2.9
1	B	604	LEU	2.9
1	F	256	VAL	2.9
2	Q	121	VAL	2.9
2	R	62	THR	2.9
1	E	141	PHE	2.9
1	C	208	LEU	2.9
2	S	97	ASN	2.9
1	B	663	PHE	2.9
1	C	317	LYS	2.9
1	F	123	GLU	2.9
1	D	169	VAL	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	508	ILE	2.9
1	D	516	VAL	2.9
1	E	533	LEU	2.9
1	F	419	ILE	2.9
2	O	116	LEU	2.9
1	D	639	ASN	2.9
1	E	689	ALA	2.9
1	A	614	PHE	2.9
2	P	148	LYS	2.9
1	B	118	GLN	2.9
1	E	484	VAL	2.9
2	O	100	ILE	2.9
2	S	136	VAL	2.9
1	A	738	SER	2.9
1	C	404	LYS	2.9
1	D	290	LYS	2.9
1	B	416	ASN	2.9
1	B	673	SER	2.9
2	P	138	TYR	2.9
1	B	562	GLU	2.9
1	B	620	THR	2.9
1	C	412	GLU	2.9
2	Q	31	GLU	2.9
2	S	117	THR	2.9
1	C	572	GLY	2.9
1	E	408	LEU	2.9
1	B	589	LYS	2.9
1	A	241	PHE	2.9
1	D	328	PHE	2.9
1	F	349	ASN	2.9
1	A	324	THR	2.9
1	C	392	THR	2.9
1	E	287	GLY	2.9
1	F	489	THR	2.9
2	P	74	ARG	2.9
1	A	780	LEU	2.9
1	C	128	MET	2.9
1	C	184	LYS	2.9
1	C	215	LYS	2.9
1	B	344	ALA	2.9
1	F	210	PHE	2.9
2	R	41	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	721	SER	2.9
1	A	153	ILE	2.9
1	B	757	THR	2.9
1	C	117	LEU	2.9
1	D	423	LYS	2.9
2	R	137	ASN	2.9
1	F	603	ILE	2.9
1	E	750	GLN	2.9
1	B	558	ASP	2.9
1	C	671	ARG	2.9
1	E	103	GLU	2.9
1	B	355	SER	2.9
1	F	383	GLY	2.9
1	C	597	ASN	2.9
1	E	322	LEU	2.9
1	E	497	LEU	2.9
1	F	162	ASN	2.9
1	C	782	PHE	2.9
1	F	659	THR	2.9
1	C	559	ARG	2.9
1	D	70	GLU	2.9
1	D	144	GLU	2.9
1	E	97	TYR	2.9
1	C	115	LYS	2.9
1	B	330	PRO	2.9
1	D	683	GLY	2.9
1	F	239	HIS	2.9
1	F	374	HIS	2.9
1	B	678	VAL	2.8
1	C	603	ILE	2.8
1	A	440	GLN	2.8
1	A	566	TYR	2.8
1	C	133	GLU	2.8
1	C	146	LYS	2.8
2	R	54	GLU	2.8
1	B	348	LEU	2.8
1	C	359	PRO	2.8
1	D	330	PRO	2.8
1	D	338	LEU	2.8
1	D	654	ILE	2.8
1	A	675	ASN	2.8
1	B	535	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	C	297	LYS	2.8
1	D	632	TYR	2.8
1	F	656	THR	2.8
1	A	308	VAL	2.8
1	C	722	ILE	2.8
1	D	628	PHE	2.8
1	E	104	ILE	2.8
2	Q	85	ILE	2.8
1	E	475	GLU	2.8
1	E	490	ALA	2.8
1	C	590	ASP	2.8
1	C	797	ILE	2.8
2	P	108	VAL	2.8
2	Q	90	ARG	2.8
1	D	402	PRO	2.8
1	B	524	GLU	2.8
1	A	211	SER	2.8
1	C	785	ASN	2.8
1	D	480	ASN	2.8
1	E	627	TYR	2.8
1	C	109	ILE	2.8
1	D	565	LYS	2.8
1	C	594	PHE	2.8
1	D	77	ASP	2.8
1	E	708	ALA	2.8
2	O	15	ALA	2.8
1	A	73	ASN	2.8
1	A	532	LEU	2.8
1	B	422	GLY	2.8
1	B	660	SER	2.8
1	B	461	LYS	2.8
1	C	630	ARG	2.8
1	D	222	ASN	2.8
1	C	210	PHE	2.8
1	C	757	THR	2.8
1	F	227	ILE	2.8
1	F	457	THR	2.8
1	C	648	PRO	2.8
1	A	455	TYR	2.8
1	A	624	TYR	2.8
1	C	193	LEU	2.8
1	C	217	LYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	D	724	ARG	2.8
1	C	338	LEU	2.8
1	C	701	LEU	2.8
1	F	163	SER	2.8
1	C	410	ILE	2.8
2	S	82	GLU	2.8
1	C	251	PRO	2.8
1	E	68	LYS	2.8
2	R	118	ASP	2.8
1	B	305	SER	2.8
1	C	480	ASN	2.8
1	B	353	LYS	2.8
1	C	650	THR	2.8
2	R	122	ASP	2.8
1	D	375	GLY	2.8
1	E	326	ILE	2.8
1	F	137	PHE	2.8
1	A	122	GLU	2.8
1	B	404	LYS	2.8
1	C	778	LYS	2.8
1	D	95	GLU	2.8
1	D	673	SER	2.8
1	F	562	GLU	2.8
1	B	72	THR	2.8
1	D	648	PRO	2.8
1	F	455	TYR	2.8
1	A	328	PHE	2.8
1	B	645	TRP	2.8
2	S	19	PHE	2.8
1	B	616	GLU	2.8
1	E	673	SER	2.8
1	B	752	LEU	2.8
1	C	789	ASN	2.8
1	C	235	THR	2.8
1	A	115	LYS	2.8
1	A	756	ILE	2.8
1	C	581	GLN	2.8
2	Q	20	ASP	2.8
1	C	588	GLU	2.8
1	E	286	GLU	2.8
1	C	341	SER	2.8
1	A	298	GLY	2.8

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Mol	Chain	Res	Type	RSRZ
2	Q	111	ASN	2.8
2	S	128	ALA	2.8
1	C	735	VAL	2.8
1	D	634	LYS	2.8
1	E	400	LYS	2.8
1	E	783	THR	2.8
1	F	502	THR	2.8
1	F	723	PHE	2.8
1	E	119	ASP	2.8
1	B	503	GLU	2.7
1	B	655	ASN	2.7
1	C	708	ALA	2.7
2	S	25	GLY	2.7
1	E	756	ILE	2.7
2	P	110	THR	2.7
1	A	406	ASP	2.7
2	P	125	ILE	2.7
2	Q	8	GLN	2.7
1	D	681	ASP	2.7
1	E	724	ARG	2.7
1	B	729	TYR	2.7
2	R	102	ALA	2.7
2	S	92	PHE	2.7
1	B	592	GLU	2.7
1	B	687	GLU	2.7
1	C	668	SER	2.7
1	D	616	GLU	2.7
1	E	163	SER	2.7
1	C	194	ASN	2.7
1	B	235	THR	2.7
1	D	479	LYS	2.7
1	E	659	THR	2.7
1	F	567	THR	2.7
1	A	488	LEU	2.7
1	B	179	LEU	2.7
1	F	477	MET	2.7
2	O	145	MET	2.7
2	T	118	ASP	2.7
2	T	131	ASP	2.7
1	D	422	GLY	2.7
1	A	67	VAL	2.7
2	R	65	PHE	2.7

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Mol	Chain	Res	Type	RSRZ
1	F	432	TYR	2.7
1	A	144	GLU	2.7
1	C	391	ILE	2.7
1	C	397	GLU	2.7
1	E	601	GLU	2.7
1	F	148	GLU	2.7
1	A	695	LYS	2.7
1	C	273	LYS	2.7
1	C	509	PRO	2.7
1	C	774	LYS	2.7
1	D	359	PRO	2.7
1	B	701	LEU	2.7
2	P	70	THR	2.7
1	C	433	TYR	2.7
1	C	731	GLU	2.7
2	Q	127	GLU	2.7
1	B	188	LEU	2.7
1	C	523	LEU	2.7
1	C	702	SER	2.7
1	E	451	ASN	2.7
1	F	241	PHE	2.7
1	B	536	TYR	2.7
1	A	643	ILE	2.7
1	F	772	GLU	2.7
1	A	629	ASN	2.7
1	C	143	PHE	2.7
1	E	773	PHE	2.7
1	F	710	HIS	2.7
1	F	608	TRP	2.7
1	A	786	GLU	2.7
1	E	589	LYS	2.7
1	E	634	LYS	2.7
1	F	495	PHE	2.7
1	A	502	THR	2.7
1	E	588	GLU	2.7
1	B	654	ILE	2.7
1	E	646	THR	2.7
2	R	129	ASP	2.7
1	A	555	GLN	2.7
1	C	249	PHE	2.7
1	A	93	VAL	2.7
1	B	354	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	C	544	SER	2.7
2	R	91	VAL	2.7
1	A	789	ASN	2.7
1	E	705	TYR	2.7
1	F	312	ALA	2.7
2	T	78	ASP	2.7
1	A	625	LEU	2.7
1	C	218	LEU	2.7
1	D	485	LEU	2.7
1	F	774	LYS	2.7
1	B	396	GLY	2.7
1	D	429	GLY	2.7
2	S	134	GLY	2.7
2	T	91	VAL	2.7
1	B	105	TYR	2.7
1	D	426	ILE	2.7
1	B	384	ASN	2.7
1	B	770	ASN	2.7
1	C	120	LEU	2.7
1	D	387	ASN	2.7
2	Q	62	THR	2.7
2	Q	129	ASP	2.7
2	T	95	ASP	2.7
1	A	81	GLN	2.7
1	B	477	MET	2.7
1	C	727	GLN	2.7
1	C	103	GLU	2.7
1	D	425	GLU	2.7
1	F	601	GLU	2.7
2	P	67	GLU	2.7
1	A	357	TRP	2.6
1	B	522	SER	2.6
1	D	636	ALA	2.7
1	E	672	ARG	2.6
2	Q	69	LEU	2.6
1	A	384	ASN	2.6
1	A	69	THR	2.6
1	D	787	THR	2.6
2	R	12	PHE	2.6
1	D	399	GLY	2.6
1	D	299	GLU	2.6
1	B	251	PRO	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	718	ARG	2.6
1	C	154	ILE	2.6
1	F	430	LYS	2.6
1	F	486	LYS	2.6
1	C	344	ALA	2.6
1	F	624	TYR	2.6
1	F	670	ILE	2.6
2	R	138	TYR	2.6
1	D	706	ASN	2.6
1	C	556	MET	2.6
1	D	372	LYS	2.6
2	T	49	GLN	2.6
1	B	253	HIS	2.6
1	D	405	LEU	2.6
1	F	642	TYR	2.6
2	O	138	TYR	2.6
1	D	522	SER	2.6
1	E	702	SER	2.6
2	S	141	PHE	2.6
1	C	129	ASN	2.6
1	C	558	ASP	2.6
1	D	521	ASN	2.6
1	E	511	LYS	2.6
1	F	145	LYS	2.6
1	F	582	ASP	2.6
1	C	611	THR	2.6
2	O	76	MET	2.6
2	Q	6	GLU	2.6
2	S	67	GLU	2.6
1	F	177	ILE	2.6
1	F	339	ILE	2.6
1	C	137	PHE	2.6
1	F	284	LYS	2.6
1	B	140	ARG	2.6
1	C	464	VAL	2.6
1	D	119	ASP	2.6
1	E	168	GLU	2.6
2	S	45	GLU	2.6
2	T	139	GLU	2.6
1	D	759	GLN	2.6
1	F	220	LEU	2.6
1	A	665	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	C	303	LYS	2.6
1	E	268	MET	2.6
1	F	674	SER	2.6
1	A	348	LEU	2.6
1	A	701	LEU	2.6
2	R	9	ILE	2.6
1	D	651	LYS	2.6
1	E	423	LYS	2.6
1	E	519	THR	2.6
2	O	107	HIS	2.6
1	E	482	GLU	2.6
1	B	702	SER	2.6
1	A	480	ASN	2.6
1	C	576	ASN	2.6
1	D	431	LYS	2.6
1	D	591	ASN	2.6
1	A	630	ARG	2.6
1	F	444	PHE	2.6
1	A	374	HIS	2.6
1	F	449	GLU	2.6
1	D	389	LYS	2.6
1	E	546	LYS	2.6
1	F	364	ILE	2.6
2	S	4	LEU	2.6
1	B	788	ASP	2.6
1	F	704	TYR	2.6
2	O	88	ALA	2.6
2	S	12	PHE	2.6
2	S	133	ASP	2.6
1	A	345	THR	2.6
1	A	735	VAL	2.6
1	C	547	GLY	2.6
1	D	408	LEU	2.6
1	E	657	ILE	2.6
1	F	510	GLN	2.6
1	B	652	ALA	2.6
1	E	448	ASP	2.6
1	E	688	PHE	2.6
1	B	290	LYS	2.6
1	B	306	GLY	2.6
1	B	567	THR	2.6
1	B	634	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	D	696	LYS	2.6
1	E	640	LYS	2.6
1	D	147	ARG	2.6
1	D	780	LEU	2.6
1	E	510	GLN	2.6
2	P	128	ALA	2.6
2	R	46	ALA	2.6
1	C	291	ASP	2.6
1	E	270	LYS	2.6
1	F	791	GLU	2.6
1	D	464	VAL	2.6
1	A	182	ILE	2.6
1	B	293	ILE	2.6
1	C	227	ILE	2.6
1	C	538	ILE	2.6
1	D	594	PHE	2.6
1	B	705	TYR	2.6
1	C	498	ALA	2.6
1	C	733	GLU	2.6
1	D	640	LYS	2.6
2	Q	132	GLY	2.6
2	S	11	GLU	2.6
2	T	83	GLU	2.6
1	C	532	LEU	2.6
1	E	374	HIS	2.6
1	A	157	LYS	2.5
1	F	715	GLU	2.5
1	F	672	ARG	2.5
1	A	100	LEU	2.5
1	B	356	ASP	2.5
1	F	166	SER	2.5
1	B	785	ASN	2.5
1	D	73	ASN	2.5
1	D	655	ASN	2.5
1	E	136	PRO	2.5
1	E	284	LYS	2.5
1	E	628	PHE	2.5
1	F	680	LYS	2.5
1	D	689	ALA	2.5
2	Q	140	GLU	2.5
2	S	87	GLU	2.5
1	C	101	GLY	2.5

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Mol	Chain	Res	Type	RSRZ
1	F	466	GLY	2.5
1	E	488	LEU	2.5
2	S	24	ASP	2.5
1	C	87	LYS	2.5
1	D	177	ILE	2.5
1	D	758	ASN	2.5
1	F	761	GLN	2.5
2	O	113	GLY	2.5
1	A	152	LEU	2.5
1	C	385	LEU	2.5
1	C	651	LYS	2.5
1	F	209	LEU	2.5
1	F	541	LYS	2.5
1	A	177	ILE	2.5
1	A	181	ILE	2.5
1	A	318	ILE	2.5
1	F	711	ILE	2.5
2	P	100	ILE	2.5
1	F	140	ARG	2.5
1	A	706	ASN	2.5
1	E	260	TYR	2.5
2	Q	139	GLU	2.5
1	B	380	VAL	2.5
1	B	608	TRP	2.5
1	F	783	THR	2.5
2	R	40	GLY	2.5
1	B	533	LEU	2.5
1	C	234	LEU	2.5
1	C	400	LYS	2.5
1	F	218	LEU	2.5
2	O	105	LEU	2.5
1	D	268	MET	2.5
1	F	131	ARG	2.5
1	D	371	SER	2.5
1	F	183	SER	2.5
1	F	514	ASP	2.5
1	E	766	HIS	2.5
1	D	382	LYS	2.5
1	E	373	LYS	2.5
1	E	545	THR	2.5
1	A	339	ILE	2.5
1	F	79	ILE	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	448	ASP	2.5
2	O	84	GLU	2.5
1	C	295	VAL	2.5
1	D	68	LYS	2.5
1	E	727	GLN	2.5
1	B	561	ASN	2.5
1	E	324	THR	2.5
2	P	5	THR	2.5
1	A	593	ILE	2.5
1	F	596	ILE	2.5
1	A	515	LYS	2.5
1	B	585	GLU	2.5
1	C	125	LYS	2.5
1	C	535	LYS	2.5
1	B	532	LEU	2.5
1	D	675	ASN	2.5
2	R	97	ASN	2.5
1	C	79	ILE	2.5
1	E	605	THR	2.5
2	P	140	GLU	2.5
1	B	464	VAL	2.5
1	E	478	ALA	2.5
1	E	743	PRO	2.5
2	Q	10	ALA	2.5
1	B	767	GLN	2.5
1	C	749	PHE	2.5
1	A	270	LYS	2.5
1	A	603	ILE	2.5
1	B	730	ASN	2.5
1	C	446	ILE	2.5
1	D	765	THR	2.5
1	E	79	ILE	2.5
1	F	353	LYS	2.5
1	B	459	GLU	2.5
1	D	219	GLU	2.5
1	A	342	GLY	2.5
1	D	166	SER	2.5
1	F	213	LYS	2.5
1	F	214	PHE	2.5
1	F	217	LYS	2.5
2	T	130	ILE	2.5
1	B	644	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	C	656	THR	2.5
1	A	304	ALA	2.5
1	E	549	LEU	2.5
2	Q	99	TYR	2.5
2	T	46	ALA	2.5
1	B	423	LYS	2.5
1	E	115	LYS	2.5
1	F	106	PHE	2.5
1	F	276	PHE	2.5
2	T	141	PHE	2.5
1	B	123	GLU	2.5
2	P	52	ILE	2.5
1	D	409	ARG	2.5
2	T	127	GLU	2.5
1	A	149	THR	2.5
1	A	521	ASN	2.5
1	A	667	LEU	2.5
1	C	169	VAL	2.5
1	D	380	VAL	2.5
1	D	551	ASN	2.5
1	D	579	THR	2.5
1	D	620	THR	2.5
1	F	676	VAL	2.5
1	B	175	LYS	2.5
1	B	717	LYS	2.5
1	E	690	LYS	2.5
2	P	21	LYS	2.5
1	B	309	PRO	2.5
2	P	68	PHE	2.5
1	E	419	ILE	2.5
1	A	64	ASN	2.4
1	B	468	LYS	2.4
1	C	271	LEU	2.4
1	F	706	ASN	2.4
2	S	146	THR	2.4
1	B	241	PHE	2.4
2	O	130	ILE	2.4
2	R	74	ARG	2.4
1	C	459	GLU	2.4
2	Q	87	GLU	2.4
1	A	284	LYS	2.4
1	B	100	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	471	TRP	2.4
1	E	128	MET	2.4
1	B	628	PHE	2.4
1	C	267	TYR	2.4
1	C	450	ASN	2.4
1	E	765	THR	2.4
1	F	245	PHE	2.4
1	A	767	GLN	2.4
1	C	510	GLN	2.4
2	Q	51	MET	2.4
1	B	513	TRP	2.4
1	A	688	PHE	2.4
1	C	71	PHE	2.4
1	D	105	TYR	2.4
2	T	102	ALA	2.4
1	D	781	ASN	2.4
1	D	714	GLN	2.4
1	F	336	THR	2.4
1	F	587	PRO	2.4
2	R	76	MET	2.4
1	F	422	GLY	2.4
2	O	40	GLY	2.4
1	A	105	TYR	2.4
1	A	137	PHE	2.4
2	P	99	TYR	2.4
1	C	634	LYS	2.4
2	R	45	GLU	2.4
1	C	497	LEU	2.4
1	F	110	ASP	2.4
2	R	59	GLY	2.4
2	T	122	ASP	2.4
1	B	138	ALA	2.4
1	C	689	ALA	2.4
1	A	393	GLU	2.4
1	C	172	GLU	2.4
1	A	220	LEU	2.4
1	B	268	MET	2.4
1	B	547	GLY	2.4
1	D	309	PRO	2.4
1	D	501	LEU	2.4
2	O	44	THR	2.4
1	C	78	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	C	187	SER	2.4
1	E	196	ILE	2.4
1	D	288	VAL	2.4
1	D	730	ASN	2.4
1	E	719	LYS	2.4
2	Q	26	THR	2.4
1	A	552	TRP	2.4
1	B	742	ALA	2.4
1	F	191	GLU	2.4
1	F	443	GLU	2.4
2	Q	138	TYR	2.4
2	S	104	GLU	2.4
1	E	178	SER	2.4
1	F	619	ILE	2.4
1	E	120	LEU	2.4
1	A	768	LYS	2.4
1	F	146	LYS	2.4
1	F	760	VAL	2.4
2	P	8	GLN	2.4
1	B	347	GLY	2.4
1	B	787	THR	2.4
1	D	618	ASN	2.4
1	E	734	ASN	2.4
1	C	105	TYR	2.4
1	F	644	GLU	2.4
1	E	552	TRP	2.4
1	C	669	SER	2.4
1	D	453	VAL	2.4
1	D	693	SER	2.4
1	E	537	GLY	2.4
2	O	16	PHE	2.4
2	P	51	MET	2.4
1	D	598	PRO	2.4
1	A	286	GLU	2.4
1	A	412	GLU	2.4
1	C	159	TYR	2.4
1	D	260	TYR	2.4
1	E	754	GLU	2.4
1	A	685	LYS	2.4
1	C	623	ASP	2.4
1	A	547	GLY	2.4
1	F	429	GLY	2.4

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Mol	Chain	Res	Type	RSRZ
1	F	779	GLN	2.4
2	T	12	PHE	2.4
1	D	630	ARG	2.4
1	D	671	ARG	2.4
2	R	6	GLU	2.4
1	D	690	LYS	2.4
1	F	96	ILE	2.4
2	T	26	THR	2.4
1	A	311	HIS	2.4
1	B	552	TRP	2.4
1	C	302	LEU	2.4
2	R	80	ASP	2.4
1	E	135	VAL	2.4
1	F	638	GLY	2.4
1	E	346	LYS	2.4
1	F	91	LYS	2.4
1	F	285	LYS	2.4
1	B	450	ASN	2.4
1	F	161	ILE	2.4
2	P	103	ALA	2.4
1	C	283	LEU	2.4
1	C	604	LEU	2.4
1	B	369	ASP	2.3
1	B	198	SER	2.3
1	B	431	LYS	2.3
1	E	425	GLU	2.3
2	P	115	LYS	2.3
1	C	625	LEU	2.3
2	R	116	LEU	2.3
1	D	530	THR	2.3
1	E	476	VAL	2.3
1	F	142	VAL	2.3
1	D	143	PHE	2.3
1	F	236	GLU	2.3
1	B	718	ARG	2.3
1	C	94	LEU	2.3
1	D	327	LEU	2.3
2	S	74	ARG	2.3
1	A	489	THR	2.3
1	E	306	GLY	2.3
1	F	300	LYS	2.3
1	F	594	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	F	633	ASN	2.3
2	P	60	ASN	2.3
1	A	623	ASP	2.3
1	A	744	GLU	2.3
1	F	299	GLU	2.3
1	B	538	ILE	2.3
1	B	613	ARG	2.3
1	C	641	ALA	2.3
1	E	305	SER	2.3
1	E	674	SER	2.3
2	S	27	ILE	2.3
1	C	192	PHE	2.3
1	D	347	GLY	2.3
1	D	571	GLY	2.3
1	C	357	TRP	2.3
2	T	82	GLU	2.3
2	T	110	THR	2.3
1	C	643	ILE	2.3
1	F	485	LEU	2.3
1	B	575	VAL	2.3
1	C	353	LYS	2.3
1	D	669	SER	2.3
1	E	693	SER	2.3
1	A	621	GLY	2.3
1	A	633	ASN	2.3
1	C	376	GLN	2.3
1	D	323	ASN	2.3
1	D	507	GLN	2.3
1	E	709	ASN	2.3
1	F	320	ARG	2.3
1	F	597	ASN	2.3
1	B	318	ILE	2.3
1	F	751	TYR	2.3
2	P	94	LYS	2.3
2	T	75	LYS	2.3
1	B	564	VAL	2.3
1	C	390	SER	2.3
1	C	699	GLY	2.3
1	F	211	SER	2.3
1	C	216	GLU	2.3
1	E	744	GLU	2.3
1	F	592	GLU	2.3

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Mol	Chain	Res	Type	RSRZ
2	Q	86	ARG	2.3
1	B	165	GLN	2.3
1	D	81	GLN	2.3
1	D	764	LEU	2.3
1	F	792	VAL	2.3
1	A	637	PRO	2.3
1	D	113	GLU	2.3
1	F	354	SER	2.3
2	O	7	GLU	2.3
1	F	617	LYS	2.3
2	O	51	MET	2.3
2	S	94	LYS	2.3
1	C	378	LEU	2.3
1	C	419	ILE	2.3
1	C	451	ASN	2.3
1	C	706	ASN	2.3
2	R	100	ILE	2.3
1	F	99	GLU	2.3
1	E	485	LEU	2.3
1	E	759	GLN	2.3
2	P	3	GLN	2.3
2	T	41	GLN	2.3
1	A	312	ALA	2.3
1	B	624	TYR	2.3
1	D	392	THR	2.3
2	S	95	ASP	2.3
1	B	74	GLU	2.3
1	F	599	GLU	2.3
1	B	501	LEU	2.3
1	E	523	LEU	2.3
1	E	532	LEU	2.3
1	F	242	SER	2.3
1	C	552	TRP	2.3
1	C	577	HIS	2.3
1	C	695	LYS	2.3
1	D	666	ASN	2.3
1	E	113	GLU	2.3
2	O	129	ASP	2.3
1	C	152	LEU	2.3
1	D	86	LEU	2.3
1	F	309	PRO	2.3
1	B	741	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	D	154	ILE	2.3
1	E	96	ILE	2.3
1	F	282	SER	2.3
1	A	753	LYS	2.3
1	B	580	GLU	2.3
1	E	483	GLY	2.3
1	A	548	THR	2.3
1	B	332	ASN	2.3
1	D	597	ASN	2.3
1	F	493	ASP	2.3
1	F	639	ASN	2.3
2	S	64	ASP	2.3
1	E	630	ARG	2.3
1	B	691	LYS	2.3
1	D	468	LYS	2.3
1	F	554	LYS	2.3
1	C	536	TYR	2.3
1	D	295	VAL	2.3
1	E	166	SER	2.3
1	E	198	SER	2.3
1	E	211	SER	2.3
1	E	441	VAL	2.3
1	E	481	VAL	2.3
1	A	568	GLY	2.2
2	S	103	ALA	2.3
1	A	616	GLU	2.2
1	A	128	MET	2.2
1	B	703	ASP	2.2
1	B	764	LEU	2.2
1	C	647	ASP	2.2
1	D	494	LEU	2.2
1	D	647	ASP	2.2
1	E	438	ASN	2.2
2	O	22	ASP	2.2
2	P	122	ASP	2.2
2	Q	18	LEU	2.2
2	Q	116	LEU	2.2
1	A	546	LYS	2.2
1	B	657	ILE	2.2
1	F	382	LYS	2.2
1	A	350	VAL	2.2
1	B	688	PHE	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	793	PHE	2.2
1	F	664	ILE	2.2
2	S	65	PHE	2.2
2	R	3	GLN	2.2
2	T	121	VAL	2.2
1	C	280	SER	2.2
1	D	674	SER	2.2
1	F	539	GLU	2.2
1	F	568	GLY	2.2
2	P	81	SER	2.2
1	C	672	ARG	2.2
1	A	622	LYS	2.2
1	C	589	LYS	2.2
1	E	611	THR	2.2
1	F	337	ASN	2.2
1	B	520	PRO	2.2
1	E	114	HIS	2.2
2	R	101	SER	2.2
1	B	231	LYS	2.2
1	B	716	LYS	2.2
1	C	567	THR	2.2
1	D	438	ASN	2.2
1	A	170	TYR	2.2
1	A	526	GLN	2.2
1	B	298	GLY	2.2
1	D	277	GLU	2.2
1	D	718	ARG	2.2
1	F	171	TYR	2.2
1	F	232	GLU	2.2
1	D	511	LYS	2.2
1	D	795	LYS	2.2
2	R	30	LYS	2.2
1	D	720	ILE	2.2
1	A	108	ASP	2.2
1	F	319	ALA	2.2
1	F	456	LYS	2.2
2	Q	102	ALA	2.2
2	T	140	GLU	2.2
1	F	721	SER	2.2
1	A	89	ILE	2.2
2	Q	124	MET	2.2
1	A	528	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	C	145	LYS	2.2
1	D	78	LYS	2.2
1	D	612	GLY	2.2
1	E	525	LYS	2.2
1	F	159	TYR	2.2
1	F	317	LYS	2.2
1	A	531	ASN	2.2
1	B	323	ASN	2.2
1	B	597	ASN	2.2
1	D	473	ASN	2.2
1	F	325	TYR	2.2
2	Q	110	THR	2.2
1	D	766	HIS	2.2
1	A	68	LYS	2.2
1	A	242	SER	2.2
1	C	456	LYS	2.2
1	C	654	ILE	2.2
1	F	366	PHE	2.2
2	O	19	PHE	2.2
1	B	731	GLU	2.2
1	D	92	ASP	2.2
1	A	787	THR	2.2
1	C	633	ASN	2.2
1	D	583	ASN	2.2
1	D	646	THR	2.2
1	D	656	THR	2.2
2	P	49	GLN	2.2
1	C	409	ARG	2.2
1	B	154	ILE	2.2
1	D	391	ILE	2.2
1	E	665	LYS	2.2
1	E	696	LYS	2.2
2	Q	144	MET	2.2
1	A	700	TYR	2.2
1	D	752	LEU	2.2
1	E	66	LEU	2.2
1	E	340	LYS	2.2
2	S	5	THR	2.2
1	A	475	GLU	2.2
2	P	54	GLU	2.2
1	B	631	SER	2.2
1	D	447	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	D	528	GLY	2.2
1	A	151	LYS	2.2
1	B	77	ASP	2.2
1	A	428	ASN	2.2
1	A	656	THR	2.2
1	E	143	PHE	2.2
1	B	595	ILE	2.2
2	R	34	THR	2.2
1	C	644	GLU	2.2
1	E	142	VAL	2.2
1	B	341	SER	2.2
1	D	373	LYS	2.2
1	D	713	SER	2.2
1	F	565	LYS	2.2
1	F	661	ALA	2.2
2	O	38	SER	2.2
1	C	123	GLU	2.2
1	E	82	THR	2.2
1	E	508	ILE	2.2
1	E	781	ASN	2.2
1	F	519	THR	2.2
2	Q	130	ILE	2.2
1	D	578	GLY	2.2
1	E	290	LYS	2.2
1	E	301	ALA	2.2
1	F	280	SER	2.2
1	D	153	ILE	2.2
1	F	452	GLU	2.2
1	F	590	ASP	2.2
1	A	129	ASN	2.2
1	A	506	LYS	2.2
1	D	217	LYS	2.2
1	D	653	LYS	2.2
1	E	78	LYS	2.2
1	E	530	THR	2.2
1	E	547	GLY	2.2
1	F	460	GLY	2.2
2	P	137	ASN	2.2
2	Q	23	GLY	2.2
1	C	748	TYR	2.1
1	E	403	LEU	2.1
1	F	195	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	246	SER	2.1
1	A	321	GLU	2.1
1	C	393	GLU	2.1
1	C	503	GLU	2.1
1	E	317	LYS	2.1
1	E	565	LYS	2.1
1	F	588	GLU	2.1
1	C	132	GLY	2.1
1	E	583	ASN	2.1
1	A	123	GLU	2.1
1	A	634	LYS	2.1
1	C	664	ILE	2.1
1	C	674	SER	2.1
1	C	711	ILE	2.1
1	D	136	PRO	2.1
1	A	582	ASP	2.1
1	D	158	ASP	2.1
1	F	406	ASP	2.1
1	A	661	ALA	2.1
1	D	82	THR	2.1
1	D	548	THR	2.1
1	E	428	ASN	2.1
1	F	480	ASN	2.1
2	Q	89	PHE	2.1
1	C	316	LYS	2.1
1	D	512	GLU	2.1
1	F	404	LYS	2.1
1	A	150	PRO	2.1
1	D	361	ALA	2.1
1	F	742	ALA	2.1
2	S	99	TYR	2.1
1	D	439	ASN	2.1
1	D	519	THR	2.1
1	B	722	ILE	2.1
1	E	154	ILE	2.1
1	F	83	GLN	2.1
1	F	410	ILE	2.1
1	F	459	GLU	2.1
2	P	45	GLU	2.1
2	S	14	GLU	2.1
2	S	55	VAL	2.1
1	E	334	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	F	417	GLY	2.1
1	C	679	TYR	2.1
1	D	589	LYS	2.1
1	D	790	PHE	2.1
1	E	681	ASP	2.1
1	F	724	ARG	2.1
2	P	58	ASP	2.1
1	D	239	HIS	2.1
2	O	11	GLU	2.1
1	B	173	ILE	2.1
1	B	726	ILE	2.1
1	E	339	ILE	2.1
1	B	385	LEU	2.1
1	E	764	LEU	2.1
1	F	111	LEU	2.1
1	F	348	LEU	2.1
1	B	382	LYS	2.1
2	Q	106	ARG	2.1
1	D	304	ALA	2.1
1	E	569	TYR	2.1
2	S	129	ASP	2.1
1	C	124	GLU	2.1
1	D	266	GLU	2.1
1	B	504	ILE	2.1
1	E	521	ASN	2.1
1	A	642	TYR	2.1
2	O	83	GLU	2.1
2	S	102	ALA	2.1
2	T	10	ALA	2.1
1	D	181	ILE	2.1
2	P	76	MET	2.1
1	D	563	ALA	2.1
1	F	138	ALA	2.1
2	O	140	GLU	2.1
1	A	453	VAL	2.1
2	S	77	LYS	2.1
2	S	91	VAL	2.1
1	C	394	HIS	2.1
1	A	76	LEU	2.1
1	B	271	LEU	2.1
1	E	671	ARG	2.1
2	R	106	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
1	C	83	GLN	2.1
2	R	110	THR	2.1
2	R	117	THR	2.1
1	C	468	LYS	2.1
1	D	282	SER	2.1
1	E	792	VAL	2.1
1	C	610	MET	2.1
1	E	602	PHE	2.1
1	B	392	THR	2.1
1	A	459	GLU	2.1
1	B	512	GLU	2.1
1	B	737	LYS	2.1
1	C	430	LYS	2.1
1	F	671	ARG	2.1
2	Q	43	PRO	2.1
1	A	355	SER	2.1
1	F	595	ILE	2.1
1	A	367	ASP	2.1
1	B	313	ASP	2.1
1	C	207	ASP	2.1
1	C	573	ASP	2.1
1	E	714	GLN	2.1
2	O	71	MET	2.1
1	B	387	ASN	2.1
1	C	479	LYS	2.1
1	B	745	TYR	2.1
1	C	734	ASN	2.1
1	D	123	GLU	2.1
1	E	463	THR	2.1
1	C	574	VAL	2.1
1	D	262	PRO	2.1
1	D	441	VAL	2.1
1	D	318	ILE	2.1
1	E	220	LEU	2.1
1	D	110	ASP	2.1
1	B	606	LYS	2.0
1	F	407	HIS	2.1
1	E	344	ALA	2.0
1	F	762	LEU	2.0
1	C	98	SER	2.0
1	E	495	PHE	2.0
1	E	680	LYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	C	440	GLN	2.0
1	A	260	TYR	2.0
1	D	704	TYR	2.0
1	A	657	ILE	2.0
1	D	182	ILE	2.0
1	D	489	THR	2.0
1	F	318	ILE	2.0
1	D	186	LYS	2.0
1	D	215	LYS	2.0
1	D	572	GLY	2.0
2	S	96	GLY	2.0
1	E	755	ARG	2.0
1	C	449	GLU	2.0
1	D	581	GLN	2.0
1	D	733	GLU	2.0
2	O	131	ASP	2.0
2	R	31	GLU	2.0
1	C	97	TYR	2.0
1	C	261	ALA	2.0
1	B	598	PRO	2.0
1	B	695	LYS	2.0
1	A	723	PHE	2.0
1	C	659	THR	2.0
1	D	362	GLY	2.0
1	D	415	GLU	2.0
2	T	84	GLU	2.0
1	D	529	VAL	2.0
2	Q	80	ASP	2.0
1	D	388	LYS	2.0
1	E	496	ALA	2.0
1	B	445	ARG	2.0
2	T	105	LEU	2.0
1	D	352	GLY	2.0
1	D	600	GLY	2.0
2	P	59	GLY	2.0
1	A	444	PHE	2.0
1	E	192	PHE	2.0
1	E	330	PRO	2.0
1	A	450	ASN	2.0
1	C	740	GLN	2.0
1	A	175	LYS	2.0
1	A	710	HIS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	218	LEU	2.0
1	E	664	ILE	2.0
1	F	301	ALA	2.0
2	P	106	ARG	2.0
1	E	172	GLU	2.0
1	E	767	GLN	2.0
1	B	370	LEU	2.0
1	D	694	VAL	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 ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	E	904	1/1	-0.20	0.34	23,23,23,23	0
4	CA	O	802	1/1	0.08	0.13	33,33,33,33	0
4	CA	S	809	1/1	0.29	0.20	29,29,29,29	0
4	CA	R	808	1/1	0.30	0.21	36,36,36,36	0
3	MG	C	902	1/1	0.33	0.57	23,23,23,23	0
4	CA	R	807	1/1	0.35	0.13	30,30,30,30	0
3	MG	D	903	1/1	0.39	0.31	21,21,21,21	0
4	CA	T	812	1/1	0.40	0.25	35,35,35,35	0
3	MG	B	901	1/1	0.40	0.29	16,16,16,16	0
4	CA	Q	806	1/1	0.41	0.16	35,35,35,35	0
4	CA	P	803	1/1	0.49	0.48	32,32,32,32	0
3	MG	A	900	1/1	0.53	0.28	23,23,23,23	0
4	CA	S	810	1/1	0.55	0.28	40,40,40,40	0
4	CA	O	801	1/1	0.60	0.13	33,33,33,33	0
4	CA	Q	805	1/1	0.65	0.21	29,29,29,29	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	CA	P	804	1/1	0.67	0.28	34,34,34,34	0
4	CA	T	811	1/1	0.79	0.23	28,28,28,28	0
3	MG	F	905	1/1	0.92	0.29	17,17,17,17	0

6.5 Other polymers [i](#)

There are no such residues in this entry.