



Full wwPDB X-ray Structure Validation Report ⓘ

May 21, 2020 – 11:33 am BST

PDB ID : 3GKF
Title : Crystal Structure of E. coli LsrF
Authors : Miller, S.T.; Diaz, Z.C.
Deposited on : 2009-03-10
Resolution : 2.90 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

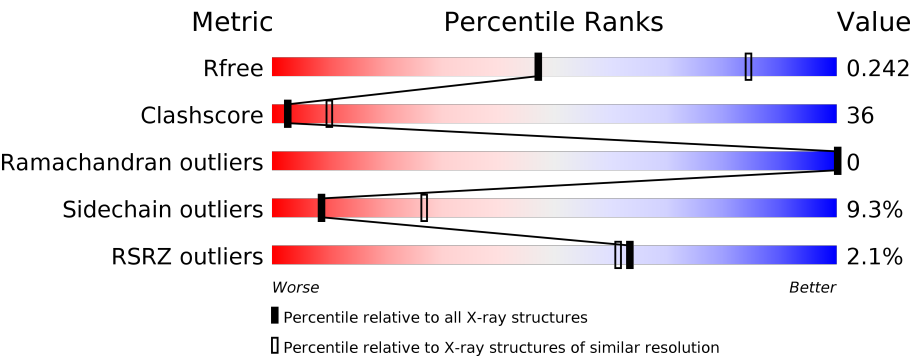
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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))
R_{free}	130704	1957 (2.90-2.90)
Clashscore	141614	2172 (2.90-2.90)
Ramachandran outliers	138981	2115 (2.90-2.90)
Sidechain outliers	138945	2117 (2.90-2.90)
RSRZ outliers	127900	1906 (2.90-2.90)

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	293	<div><div>4%</div><div></div><div>50%</div><div>38%</div><div>6%</div><div>6%</div></div>
1	B	293	<div><div>%</div><div></div><div>46%</div><div>43%</div><div>5%</div><div>6%</div></div>
1	C	293	<div><div>%</div><div></div><div>48%</div><div>40%</div><div>6%</div><div>6%</div></div>
1	D	293	<div><div>%</div><div></div><div>48%</div><div>41%</div><div>5%</div><div>6%</div></div>
1	E	293	<div><div>4%</div><div></div><div>48%</div><div>41%</div><div>5%</div><div>6%</div></div>
1	F	293	<div><div>%</div><div></div><div>51%</div><div>39%</div><div>5%</div><div>6%</div></div>

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Mol	Chain	Length	Quality of chain
1	G	293	
1	H	293	
1	I	293	
1	J	293	
1	K	293	
1	L	293	
1	M	293	
1	N	293	
1	O	293	
1	P	293	
1	Q	293	
1	R	293	
1	S	293	
1	T	293	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 42541 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 Aldolase lsrF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	O	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	L	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	M	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	N	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	K	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	F	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	I	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	H	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	G	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	J	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	S	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	P	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	Q	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	R	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	T	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	E	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	B	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	C	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	D	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			
1	A	276	Total	C	N	O	S	0	0	0
			2115	1332	374	392	17			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-1	GLY	-	EXPRESSION TAG	UNP P76143
O	0	SER	-	EXPRESSION TAG	UNP P76143
L	-1	GLY	-	EXPRESSION TAG	UNP P76143
L	0	SER	-	EXPRESSION TAG	UNP P76143
M	-1	GLY	-	EXPRESSION TAG	UNP P76143
M	0	SER	-	EXPRESSION TAG	UNP P76143
N	-1	GLY	-	EXPRESSION TAG	UNP P76143
N	0	SER	-	EXPRESSION TAG	UNP P76143
K	-1	GLY	-	EXPRESSION TAG	UNP P76143
K	0	SER	-	EXPRESSION TAG	UNP P76143
F	-1	GLY	-	EXPRESSION TAG	UNP P76143
F	0	SER	-	EXPRESSION TAG	UNP P76143
I	-1	GLY	-	EXPRESSION TAG	UNP P76143
I	0	SER	-	EXPRESSION TAG	UNP P76143
H	-1	GLY	-	EXPRESSION TAG	UNP P76143
H	0	SER	-	EXPRESSION TAG	UNP P76143
G	-1	GLY	-	EXPRESSION TAG	UNP P76143
G	0	SER	-	EXPRESSION TAG	UNP P76143
J	-1	GLY	-	EXPRESSION TAG	UNP P76143
J	0	SER	-	EXPRESSION TAG	UNP P76143
S	-1	GLY	-	EXPRESSION TAG	UNP P76143
S	0	SER	-	EXPRESSION TAG	UNP P76143
P	-1	GLY	-	EXPRESSION TAG	UNP P76143
P	0	SER	-	EXPRESSION TAG	UNP P76143
Q	-1	GLY	-	EXPRESSION TAG	UNP P76143
Q	0	SER	-	EXPRESSION TAG	UNP P76143
R	-1	GLY	-	EXPRESSION TAG	UNP P76143
R	0	SER	-	EXPRESSION TAG	UNP P76143
T	-1	GLY	-	EXPRESSION TAG	UNP P76143
T	0	SER	-	EXPRESSION TAG	UNP P76143
E	-1	GLY	-	EXPRESSION TAG	UNP P76143

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Chain	Residue	Modelled	Actual	Comment	Reference
E	0	SER	-	EXPRESSION TAG	UNP P76143
B	-1	GLY	-	EXPRESSION TAG	UNP P76143
B	0	SER	-	EXPRESSION TAG	UNP P76143
C	-1	GLY	-	EXPRESSION TAG	UNP P76143
C	0	SER	-	EXPRESSION TAG	UNP P76143
D	-1	GLY	-	EXPRESSION TAG	UNP P76143
D	0	SER	-	EXPRESSION TAG	UNP P76143
A	-1	GLY	-	EXPRESSION TAG	UNP P76143
A	0	SER	-	EXPRESSION TAG	UNP P76143

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	O	13	Total O 13 13	0	0
2	L	11	Total O 11 11	0	0
2	M	13	Total O 13 13	0	0
2	N	16	Total O 16 16	0	0
2	K	6	Total O 6 6	0	0
2	F	9	Total O 9 9	0	0
2	I	9	Total O 9 9	0	0
2	H	20	Total O 20 20	0	0
2	G	16	Total O 16 16	0	0
2	J	10	Total O 10 10	0	0
2	S	10	Total O 10 10	0	0
2	P	5	Total O 5 5	0	0
2	Q	10	Total O 10 10	0	0
2	R	6	Total O 6 6	0	0
2	T	7	Total O 7 7	0	0

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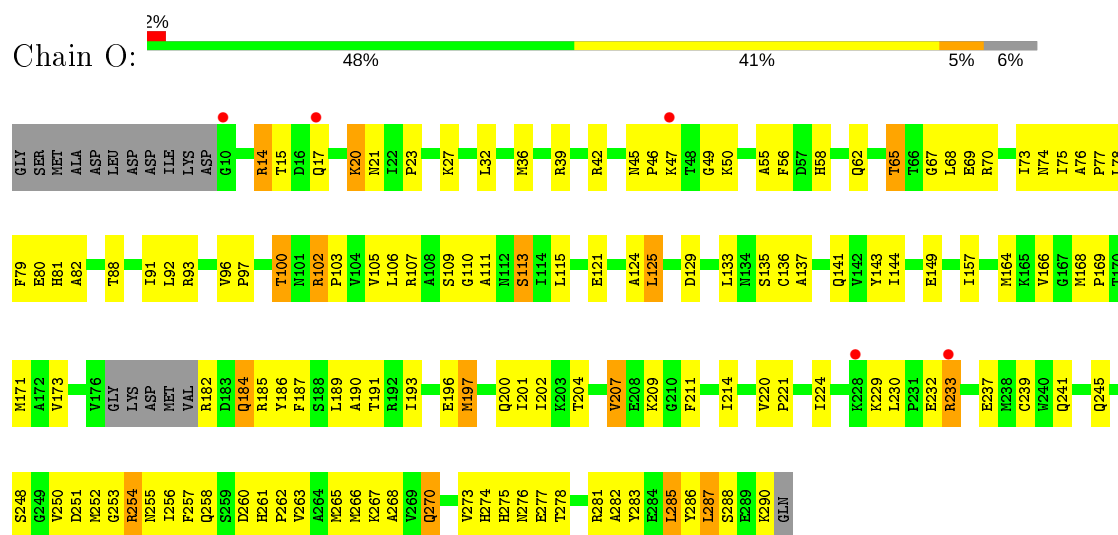
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	E	6	Total 6	O 6	0	0
2	B	10	Total 10	O 10	0	0
2	C	35	Total 35	O 35	0	0
2	D	18	Total 18	O 18	0	0
2	A	11	Total 11	O 11	0	0

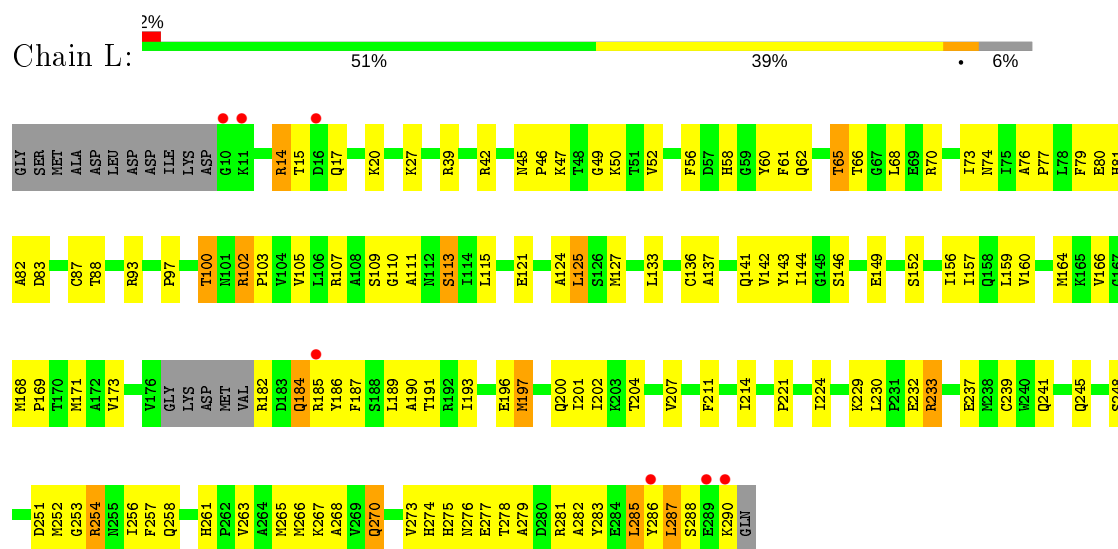
3 Residue-property plots [i](#)

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: Aldolase lsrF

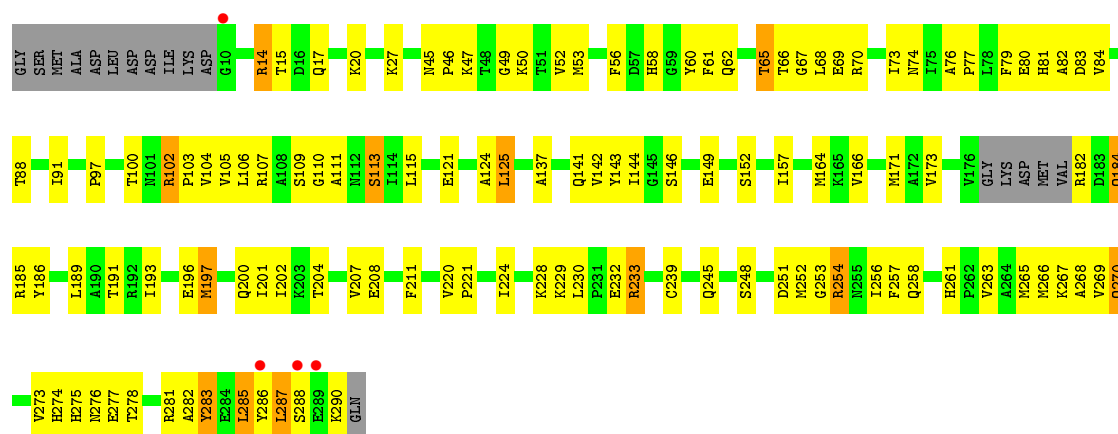


• Molecule 1: Aldolase lsrF

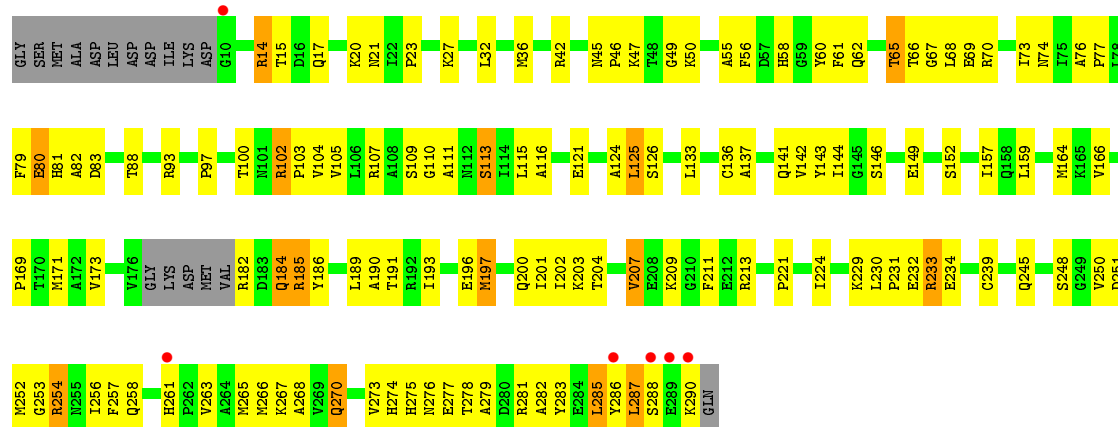


• Molecule 1: Aldolase lsrF

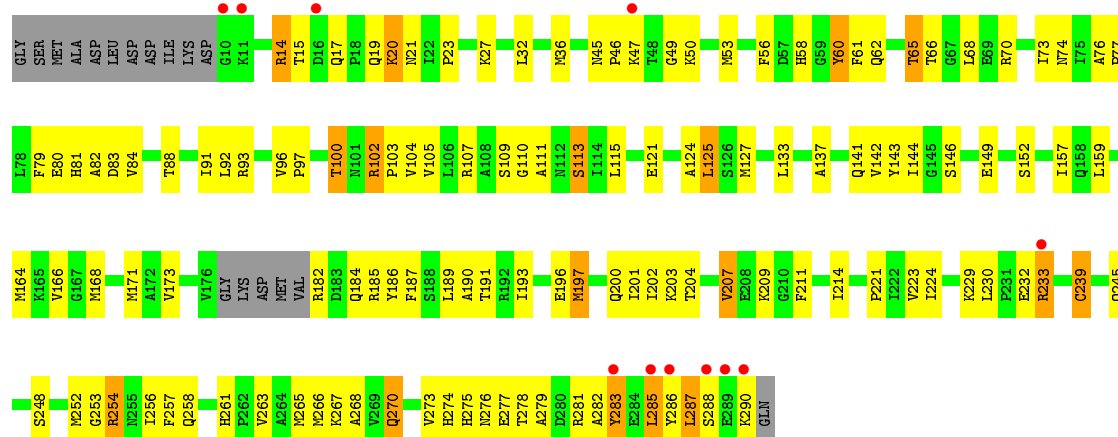




• Molecule 1: Aldolase lsrF



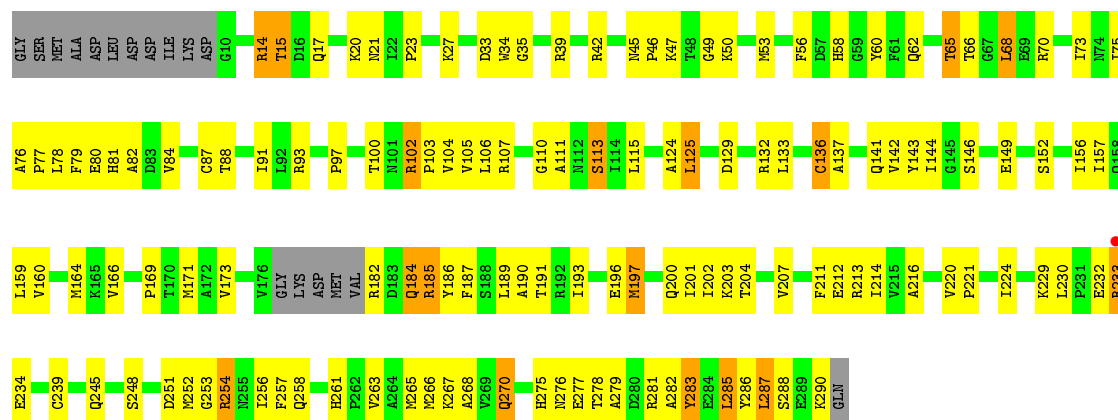
• Molecule 1: Aldolase lsrF



• Molecule 1: Aldolase lsrF

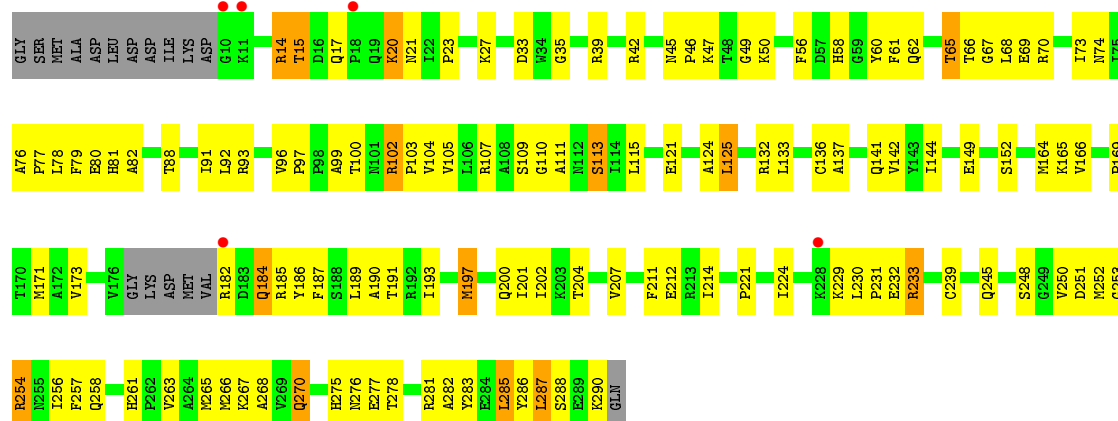
- Molecule 1: Aldolase lsrF

Chain G:  48% 40% 6% 6%



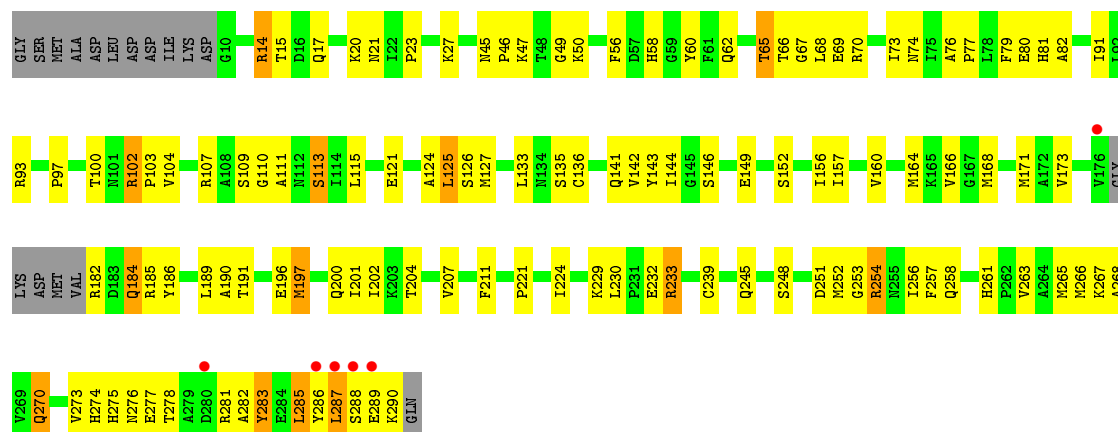
- Molecule 1: Aldolase lsrF

Chain J: 

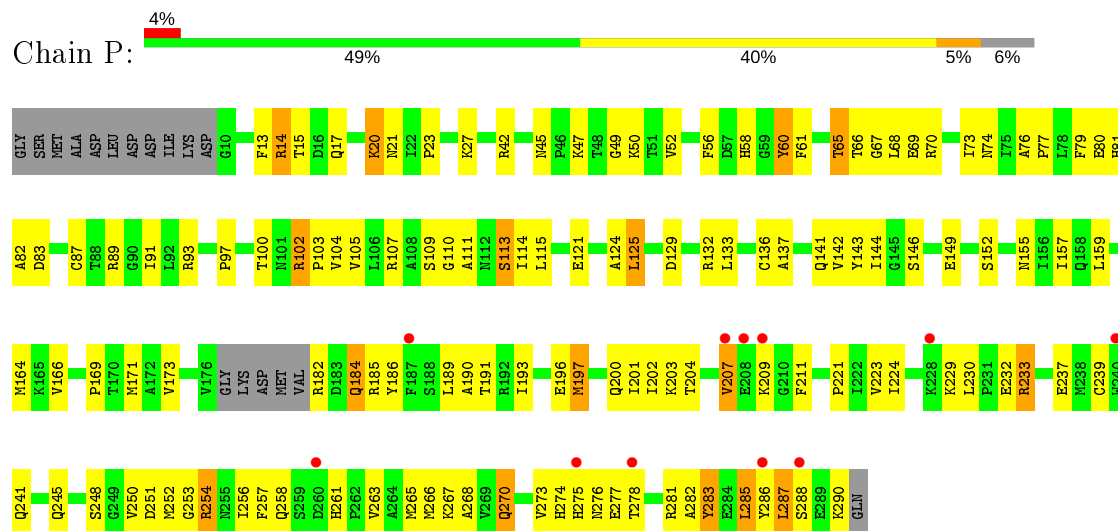


- Molecule 1: Aldolase lsrF

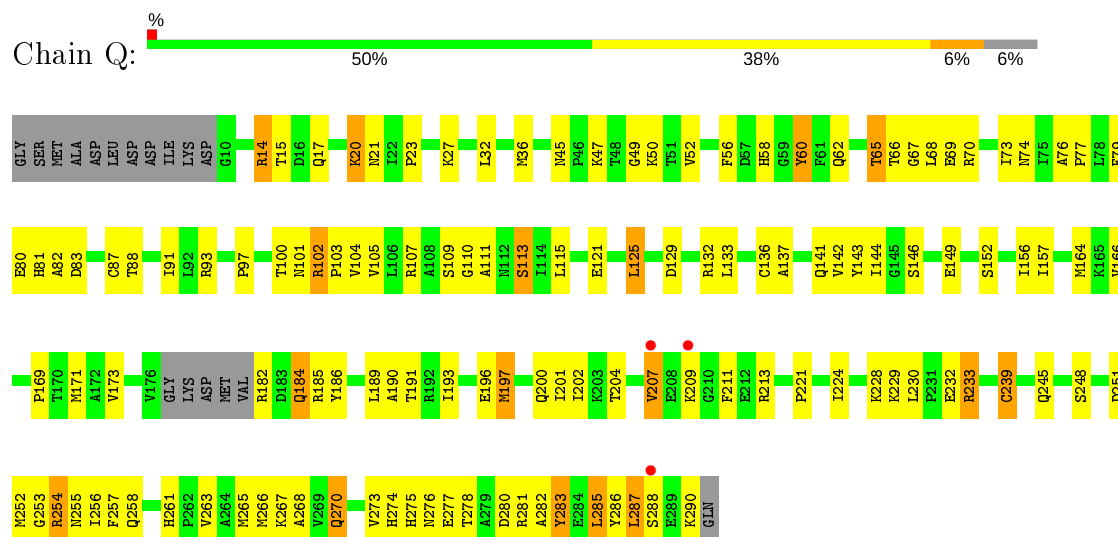
Chain S: 



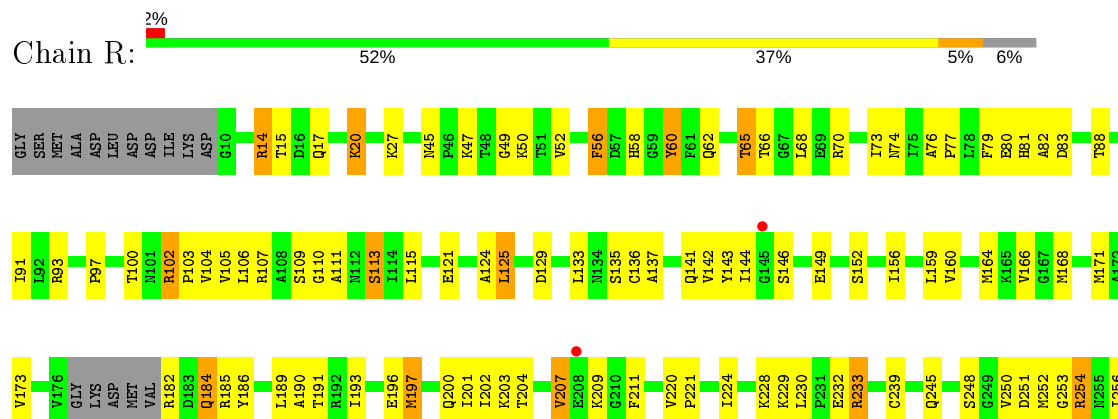
- Molecule 1: Aldolase lsrF



- Molecule 1: Aldolase lsrF

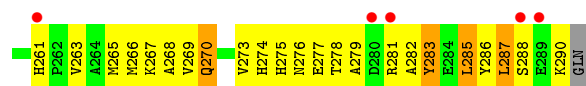
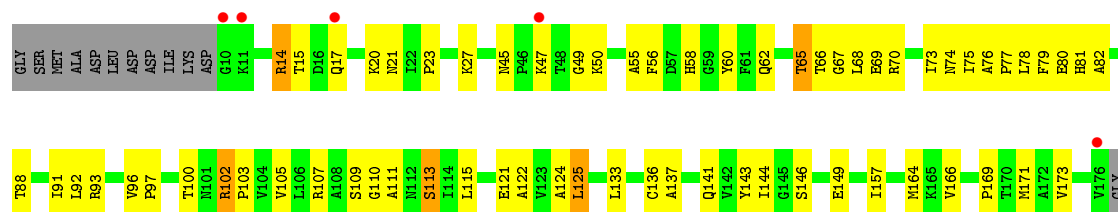


- Molecule 1: Aldolase lsrF





• Molecule 1: Aldolase lsrF

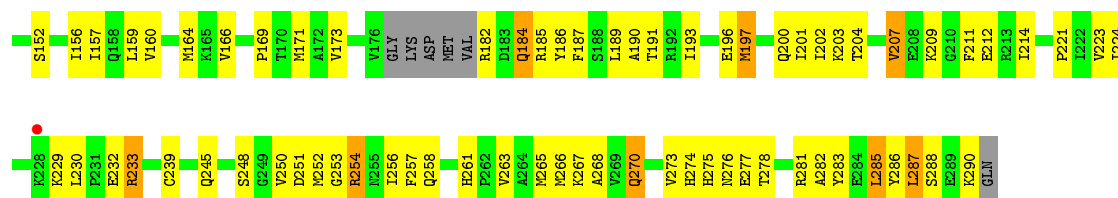


• Molecule 1: Aldolase lsrF

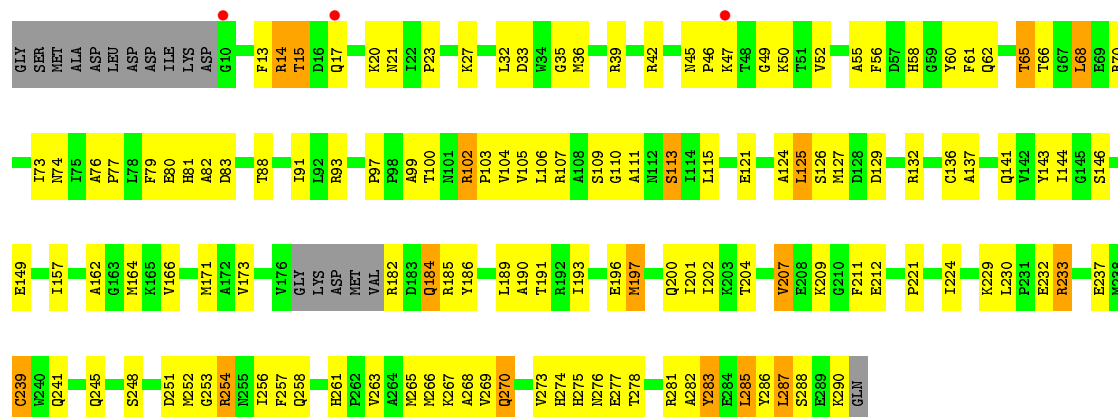


• Molecule 1: Aldolase lsrF

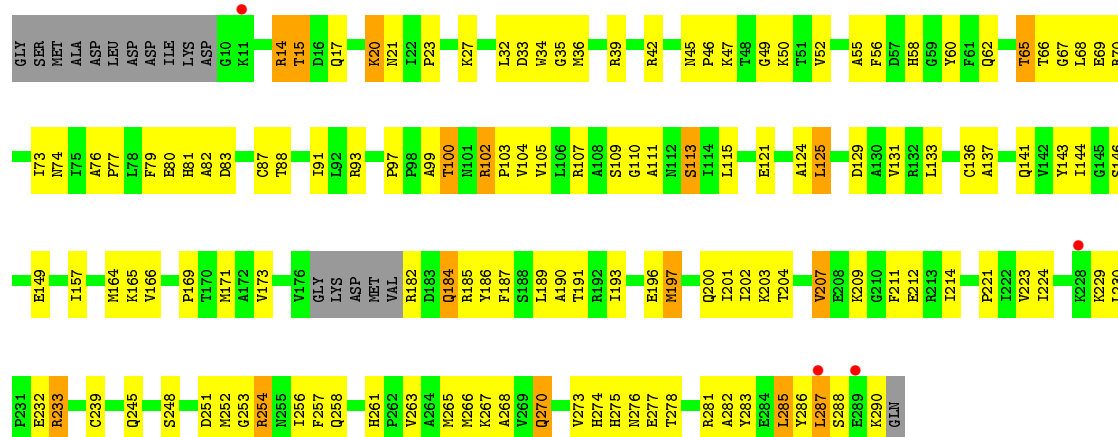




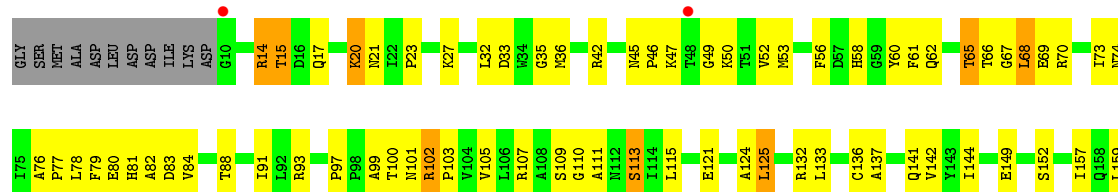
• Molecule 1: Aldolase lsrF

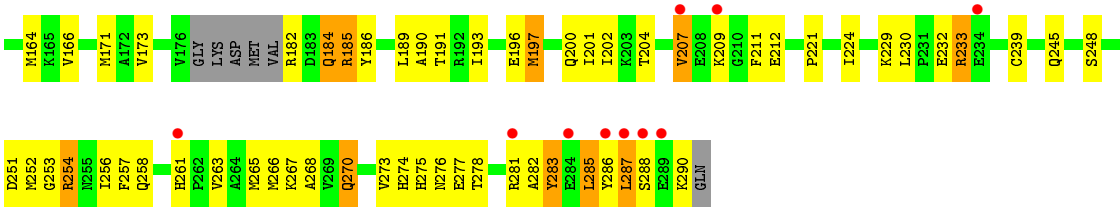


• Molecule 1: Aldolase lsrF



• Molecule 1: Aldolase lsrF





4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	78.50Å 104.61Å 171.67Å 89.88° 79.31° 89.61°	Depositor
Resolution (Å)	29.64 – 2.90 29.65 – 2.90	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.64-2.90) 95.4 (29.65-2.90)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.90Å)	Xtriage
Refinement program	REFMAC 5.5.0066	Depositor
R, R_{free}	0.209 , 0.229 0.227 , 0.242	Depositor DCC
R_{free} test set	5685 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	47.1	Xtriage
Anisotropy	0.424	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 38.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.025 for h,-k,h-l 0.036 for -h,k,-l 0.013 for -h,-k,-h+l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	42541	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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 [i](#)

5.1 Standard geometry [i](#)

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	0.63	0/2153	0.70	0/2911
1	B	0.65	0/2153	0.69	0/2911
1	C	0.75	1/2153 (0.0%)	0.73	0/2911
1	D	0.65	0/2153	0.70	0/2911
1	E	0.62	1/2153 (0.0%)	0.68	0/2911
1	F	0.63	0/2153	0.68	0/2911
1	G	0.69	1/2153 (0.0%)	0.71	0/2911
1	H	0.72	1/2153 (0.0%)	0.72	0/2911
1	I	0.65	0/2153	0.71	0/2911
1	J	0.62	0/2153	0.70	0/2911
1	K	0.64	1/2153 (0.0%)	0.70	0/2911
1	L	0.69	0/2153	0.72	0/2911
1	M	0.71	0/2153	0.71	0/2911
1	N	0.71	0/2153	0.70	0/2911
1	O	0.62	0/2153	0.68	0/2911
1	P	0.60	0/2153	0.68	0/2911
1	Q	0.66	1/2153 (0.0%)	0.69	0/2911
1	R	0.70	0/2153	0.70	0/2911
1	S	0.64	0/2153	0.69	0/2911
1	T	0.61	0/2153	0.69	0/2911
All	All	0.66	6/43060 (0.0%)	0.70	0/58220

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	Q	239	CYS	CB-SG	-6.83	1.70	1.82
1	E	136	CYS	CB-SG	-6.11	1.71	1.82
1	C	239	CYS	CB-SG	-5.75	1.72	1.81
1	H	239	CYS	CB-SG	-5.74	1.72	1.81
1	K	239	CYS	CB-SG	-5.70	1.72	1.81
1	G	136	CYS	CB-SG	-5.00	1.73	1.81

There are no bond angle outliers.

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	2115	0	2126	170	0
1	B	2115	0	2126	177	1
1	C	2115	0	2126	179	0
1	D	2115	0	2126	178	2
1	E	2115	0	2126	173	1
1	F	2115	0	2125	158	0
1	G	2115	0	2126	190	0
1	H	2115	0	2126	171	0
1	I	2115	0	2126	173	0
1	J	2115	0	2126	157	2
1	K	2115	0	2126	154	0
1	L	2115	0	2126	151	3
1	M	2115	0	2126	145	3
1	N	2115	0	2126	177	1
1	O	2115	0	2126	170	3
1	P	2115	0	2126	160	0
1	Q	2115	0	2126	160	0
1	R	2115	0	2126	156	0
1	S	2115	0	2126	150	0
1	T	2115	0	2126	159	0
2	A	11	0	0	0	0
2	B	10	0	0	2	0
2	C	35	0	0	4	0
2	D	18	0	0	2	0
2	E	6	0	0	0	0
2	F	9	0	0	1	0
2	G	16	0	0	0	0
2	H	20	0	0	4	0
2	I	9	0	0	0	0
2	J	10	0	0	1	0
2	K	6	0	0	1	0
2	L	11	0	0	0	0
2	M	13	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	N	16	0	0	4	0
2	O	13	0	0	0	0
2	P	5	0	0	1	0
2	Q	10	0	0	5	0
2	R	6	0	0	0	0
2	S	10	0	0	1	0
2	T	7	0	0	4	0
All	All	42541	0	42519	3016	8

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 36.

All (3016) 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:N:287:LEU:HD21	1:G:275:HIS:CE1	1.20	1.70
1:B:283:TYR:HE2	1:B:287:LEU:CD1	1.19	1.55
1:O:283:TYR:HE2	1:O:287:LEU:CD1	1.19	1.54
1:J:283:TYR:HE2	1:J:287:LEU:CD1	1.15	1.53
1:N:283:TYR:HE2	1:N:287:LEU:CD1	1.22	1.52
1:S:283:TYR:HE2	1:S:287:LEU:CD1	1.20	1.52
1:R:283:TYR:HE2	1:R:287:LEU:CD1	1.23	1.52
1:P:283:TYR:HE2	1:P:287:LEU:CD1	1.21	1.51
1:K:283:TYR:HE2	1:K:287:LEU:CD1	1.22	1.51
1:M:283:TYR:HE2	1:M:287:LEU:CD1	1.20	1.50
1:E:283:TYR:HE2	1:E:287:LEU:CD1	1.21	1.50
1:F:283:TYR:HE2	1:F:287:LEU:CD1	1.23	1.49
1:G:283:TYR:HE2	1:G:287:LEU:CD1	1.26	1.49
1:A:283:TYR:HE2	1:A:287:LEU:CD1	1.25	1.49
1:F:239:CYS:SG	1:F:252:MET:CE	2.02	1.48
1:I:283:TYR:HE2	1:I:287:LEU:CD1	1.25	1.48
1:F:239:CYS:SG	1:F:252:MET:HE2	1.52	1.47
1:H:283:TYR:HE2	1:H:287:LEU:CD1	1.21	1.47
1:Q:283:TYR:HE2	1:Q:287:LEU:CD1	1.25	1.47
1:T:283:TYR:HE2	1:T:287:LEU:CD1	1.21	1.46
1:D:283:TYR:HE2	1:D:287:LEU:CD1	1.27	1.46
1:L:283:TYR:HE2	1:L:287:LEU:CD1	1.26	1.45
1:J:283:TYR:CE2	1:J:287:LEU:HD12	1.52	1.45
1:E:283:TYR:CE2	1:E:287:LEU:HD12	1.53	1.44
1:I:239:CYS:SG	1:I:252:MET:HE2	1.57	1.44
1:B:283:TYR:CE2	1:B:287:LEU:HD12	1.53	1.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:239:CYS:SG	1:L:252:MET:CE	2.07	1.42
1:S:283:TYR:CE2	1:S:287:LEU:HD12	1.54	1.41
1:M:283:TYR:CE2	1:M:287:LEU:HD12	1.54	1.41
1:S:239:CYS:SG	1:S:252:MET:HE2	1.60	1.41
1:C:283:TYR:HE2	1:C:287:LEU:CD1	1.32	1.40
1:K:283:TYR:CE2	1:K:287:LEU:HD12	1.56	1.40
1:E:239:CYS:SG	1:E:252:MET:CE	2.10	1.40
1:H:283:TYR:CE2	1:H:287:LEU:HD12	1.55	1.40
1:C:239:CYS:SG	1:C:252:MET:HE2	1.62	1.40
1:N:239:CYS:SG	1:N:252:MET:CE	2.10	1.39
1:P:239:CYS:SG	1:P:252:MET:HE2	1.61	1.39
1:M:239:CYS:SG	1:M:252:MET:CE	2.11	1.39
1:O:283:TYR:CE2	1:O:287:LEU:HD12	1.56	1.39
1:E:239:CYS:SG	1:E:252:MET:HE2	1.59	1.39
1:T:239:CYS:SG	1:T:252:MET:HE2	1.62	1.39
1:T:283:TYR:CE2	1:T:287:LEU:HD12	1.56	1.38
1:S:239:CYS:SG	1:S:252:MET:CE	2.10	1.38
1:M:239:CYS:SG	1:M:252:MET:HE2	1.60	1.38
1:P:283:TYR:CE2	1:P:287:LEU:HD12	1.57	1.38
1:D:239:CYS:SG	1:D:252:MET:HE2	1.61	1.38
1:R:283:TYR:CE2	1:R:287:LEU:HD12	1.58	1.38
1:D:239:CYS:SG	1:D:252:MET:CE	2.11	1.37
1:N:239:CYS:SG	1:N:252:MET:HE2	1.62	1.37
1:I:283:TYR:CE2	1:I:287:LEU:HD12	1.59	1.36
1:L:239:CYS:SG	1:L:252:MET:HE2	1.63	1.36
1:I:239:CYS:SG	1:I:252:MET:CE	2.11	1.36
1:O:239:CYS:SG	1:O:252:MET:HE2	1.65	1.35
1:H:239:CYS:SG	1:H:252:MET:HE3	1.64	1.35
1:F:283:TYR:CE2	1:F:287:LEU:HD12	1.59	1.35
1:N:283:TYR:CE2	1:N:287:LEU:HD12	1.60	1.35
1:Q:283:TYR:CE2	1:Q:287:LEU:HD12	1.60	1.35
1:D:283:TYR:CE2	1:D:287:LEU:HD12	1.60	1.35
1:R:239:CYS:SG	1:R:252:MET:HE2	1.66	1.34
1:T:239:CYS:SG	1:T:252:MET:CE	2.16	1.34
1:B:239:CYS:SG	1:B:252:MET:HE2	1.66	1.34
1:C:239:CYS:SG	1:C:252:MET:CE	2.15	1.34
1:N:287:LEU:CD2	1:G:275:HIS:CE1	2.09	1.34
1:G:239:CYS:SG	1:G:252:MET:HE2	1.67	1.33
1:A:239:CYS:SG	1:A:252:MET:HE2	1.67	1.33
1:A:283:TYR:CE2	1:A:287:LEU:HD12	1.60	1.33
1:P:239:CYS:SG	1:P:252:MET:CE	2.16	1.32

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:283:TYR:CE2	1:G:287:LEU:HD12	1.62	1.32
1:L:283:TYR:CE2	1:L:287:LEU:HD12	1.64	1.31
1:O:239:CYS:SG	1:O:252:MET:CE	2.19	1.31
1:J:283:TYR:CE2	1:J:287:LEU:CD1	2.08	1.31
1:R:239:CYS:SG	1:R:252:MET:CE	2.19	1.31
1:K:239:CYS:SG	1:K:252:MET:HE2	1.70	1.30
1:K:239:CYS:SG	1:K:252:MET:CE	2.19	1.30
1:B:283:TYR:CE2	1:B:287:LEU:CD1	2.11	1.30
1:J:239:CYS:SG	1:J:252:MET:HE2	1.71	1.30
1:H:239:CYS:SG	1:H:252:MET:CE	2.19	1.30
1:T:283:TYR:CE2	1:T:287:LEU:CD1	2.14	1.29
1:Q:239:CYS:SG	1:Q:252:MET:HE2	1.72	1.29
1:O:283:TYR:CE2	1:O:287:LEU:CD1	2.12	1.28
1:B:239:CYS:SG	1:B:252:MET:CE	2.22	1.28
1:C:283:TYR:CE2	1:C:287:LEU:HD12	1.69	1.28
1:F:283:TYR:CE2	1:F:287:LEU:CD1	2.15	1.28
1:J:239:CYS:SG	1:J:252:MET:CE	2.23	1.27
1:A:239:CYS:SG	1:A:252:MET:CE	2.21	1.27
1:N:283:TYR:CE2	1:N:287:LEU:CD1	2.14	1.27
1:R:283:TYR:CE2	1:R:287:LEU:CD1	2.15	1.26
1:S:283:TYR:CE2	1:S:287:LEU:CD1	2.12	1.26
1:Q:283:TYR:CE2	1:Q:287:LEU:CD1	2.18	1.25
1:G:283:TYR:CE2	1:G:287:LEU:CD1	2.18	1.25
1:G:239:CYS:SG	1:G:252:MET:CE	2.23	1.25
1:M:283:TYR:CE2	1:M:287:LEU:CD1	2.13	1.25
1:E:283:TYR:CE2	1:E:287:LEU:CD1	2.14	1.25
1:N:234:GLU:OE2	1:G:281:ARG:NH1	1.71	1.24
1:P:283:TYR:CE2	1:P:287:LEU:CD1	2.14	1.24
1:A:283:TYR:CE2	1:A:287:LEU:CD1	2.18	1.22
1:D:283:TYR:CE2	1:D:287:LEU:CD1	2.20	1.21
1:Q:239:CYS:SG	1:Q:252:MET:CE	2.28	1.21
1:A:125:LEU:HD12	1:A:125:LEU:O	1.38	1.20
1:I:283:TYR:CE2	1:I:287:LEU:CD1	2.18	1.20
1:H:283:TYR:CE2	1:H:287:LEU:CD1	2.13	1.20
1:L:125:LEU:HD12	1:L:125:LEU:O	1.39	1.19
1:K:283:TYR:CE2	1:K:287:LEU:CD1	2.15	1.18
1:R:125:LEU:HD12	1:R:125:LEU:O	1.39	1.18
1:C:283:TYR:CE2	1:C:287:LEU:CD1	2.24	1.16
1:L:283:TYR:CE2	1:L:287:LEU:CD1	2.19	1.16
1:G:233:ARG:HG2	1:G:233:ARG:HH11	1.12	1.14
1:Q:233:ARG:HG2	1:Q:233:ARG:HH11	1.13	1.14

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:283:TYR:HE2	1:C:287:LEU:HD12	0.97	1.12
1:T:233:ARG:HH11	1:T:233:ARG:HG2	1.12	1.12
1:T:125:LEU:O	1:T:125:LEU:HD12	1.47	1.12
1:C:285:LEU:HD22	1:C:285:LEU:C	1.67	1.12
1:J:125:LEU:O	1:J:125:LEU:HD12	1.50	1.12
1:I:233:ARG:HH11	1:I:233:ARG:HG2	1.12	1.12
1:O:125:LEU:HD12	1:O:125:LEU:O	1.48	1.11
1:D:282:ALA:O	1:D:285:LEU:HD13	1.50	1.11
1:E:233:ARG:HH11	1:E:233:ARG:HG2	1.13	1.10
1:T:285:LEU:C	1:T:285:LEU:HD22	1.72	1.10
1:N:233:ARG:HG2	1:N:233:ARG:HH11	1.15	1.09
1:S:233:ARG:HH11	1:S:233:ARG:HG2	1.15	1.09
1:Q:107:ARG:HH12	1:Q:141:GLN:HG2	1.16	1.09
1:P:233:ARG:HH11	1:P:233:ARG:HG2	1.12	1.09
1:D:233:ARG:HG2	1:D:233:ARG:HH11	1.16	1.08
1:D:285:LEU:HD22	1:D:285:LEU:C	1.71	1.08
1:P:282:ALA:O	1:P:285:LEU:HD13	1.52	1.08
1:O:285:LEU:HD22	1:O:285:LEU:C	1.74	1.08
1:O:282:ALA:O	1:O:285:LEU:HD13	1.52	1.08
1:J:233:ARG:HH11	1:J:233:ARG:HG2	1.09	1.08
1:L:283:TYR:HE2	1:L:287:LEU:HD12	0.92	1.08
1:F:233:ARG:HG2	1:F:233:ARG:HH11	1.11	1.08
1:F:285:LEU:C	1:F:285:LEU:HD22	1.74	1.08
1:P:125:LEU:O	1:P:125:LEU:HD12	1.54	1.08
1:M:233:ARG:HH11	1:M:233:ARG:HG2	1.13	1.07
1:O:283:TYR:HE2	1:O:287:LEU:HD11	1.17	1.07
1:N:283:TYR:HE2	1:N:287:LEU:HD11	1.15	1.07
1:I:285:LEU:HD22	1:I:285:LEU:C	1.74	1.07
1:H:233:ARG:HG2	1:H:233:ARG:HH11	1.13	1.07
1:B:233:ARG:HH11	1:B:233:ARG:HG2	1.14	1.07
1:F:282:ALA:O	1:F:285:LEU:HD13	1.53	1.06
1:O:283:TYR:O	1:O:286:TYR:HB3	1.52	1.06
1:F:283:TYR:HE2	1:F:287:LEU:HD11	1.19	1.06
1:L:283:TYR:HE2	1:L:287:LEU:HD11	1.20	1.06
1:J:283:TYR:HE2	1:J:287:LEU:HD11	1.15	1.06
1:B:283:TYR:HE2	1:B:287:LEU:HD11	1.19	1.06
1:H:125:LEU:HD12	1:H:125:LEU:O	1.54	1.06
1:J:285:LEU:HD22	1:J:285:LEU:C	1.76	1.06
1:N:234:GLU:HG2	1:G:281:ARG:NH2	1.69	1.05
1:C:125:LEU:HD12	1:C:125:LEU:O	1.55	1.05
1:N:283:TYR:O	1:N:286:TYR:HB3	1.56	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:233:ARG:HH11	1:O:233:ARG:HG2	1.16	1.05
1:D:283:TYR:O	1:D:286:TYR:HB3	1.55	1.05
1:L:233:ARG:HH11	1:L:233:ARG:HG2	1.14	1.05
1:Q:282:ALA:O	1:Q:285:LEU:HD13	1.57	1.05
1:R:233:ARG:HG2	1:R:233:ARG:HH11	1.17	1.05
1:N:282:ALA:O	1:N:285:LEU:HD13	1.57	1.05
1:B:283:TYR:O	1:B:286:TYR:HB3	1.56	1.05
1:G:283:TYR:HE2	1:G:287:LEU:HD12	0.91	1.05
1:S:283:TYR:O	1:S:286:TYR:HB3	1.57	1.05
1:I:282:ALA:O	1:I:285:LEU:HD13	1.57	1.04
1:S:97:PRO:O	1:S:100:THR:OG1	1.75	1.04
1:J:282:ALA:O	1:J:285:LEU:HD13	1.56	1.04
1:G:212:GLU:HB3	1:C:15:THR:HG21	1.40	1.04
1:K:233:ARG:HG2	1:K:233:ARG:HH11	1.14	1.04
1:A:233:ARG:HG2	1:A:233:ARG:HH11	1.13	1.04
1:S:282:ALA:O	1:S:285:LEU:HD13	1.58	1.04
1:I:283:TYR:HE2	1:I:287:LEU:HD12	0.87	1.04
1:C:233:ARG:HH11	1:C:233:ARG:HG2	1.17	1.03
1:A:283:TYR:HE2	1:A:287:LEU:HD11	1.22	1.03
1:P:283:TYR:HE2	1:P:287:LEU:HD11	1.19	1.03
1:Q:283:TYR:HE2	1:Q:287:LEU:HD11	1.22	1.03
1:T:282:ALA:O	1:T:285:LEU:HD13	1.56	1.03
1:A:282:ALA:O	1:A:285:LEU:HD13	1.56	1.03
1:F:107:ARG:HH12	1:F:141:GLN:HG2	1.23	1.03
1:B:125:LEU:HD12	1:B:125:LEU:O	1.58	1.03
1:M:285:LEU:HD22	1:M:285:LEU:C	1.78	1.03
1:R:282:ALA:O	1:R:285:LEU:HD13	1.59	1.03
1:R:283:TYR:HE2	1:R:287:LEU:HD11	1.19	1.03
1:G:283:TYR:O	1:G:286:TYR:HB3	1.59	1.03
1:L:282:ALA:O	1:L:285:LEU:HD13	1.58	1.03
1:G:283:TYR:HE2	1:G:287:LEU:HD11	1.20	1.02
1:I:283:TYR:O	1:I:286:TYR:HB3	1.58	1.02
1:A:283:TYR:O	1:A:286:TYR:HB3	1.59	1.02
1:I:283:TYR:HE2	1:I:287:LEU:HD11	1.22	1.02
1:B:285:LEU:C	1:B:285:LEU:HD22	1.80	1.02
1:M:107:ARG:HH12	1:M:141:GLN:HG2	1.20	1.02
1:A:285:LEU:HD22	1:A:285:LEU:C	1.80	1.02
1:N:107:ARG:HH12	1:N:141:GLN:HG2	1.23	1.02
1:M:283:TYR:HE2	1:M:287:LEU:HD11	1.23	1.02
1:B:107:ARG:HH12	1:B:141:GLN:HG2	1.23	1.02
1:I:125:LEU:HD12	1:I:125:LEU:O	1.59	1.01

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:283:TYR:HE2	1:N:287:LEU:HD12	0.90	1.01
1:T:283:TYR:HE2	1:T:287:LEU:HD11	1.20	1.01
1:E:282:ALA:O	1:E:285:LEU:HD13	1.57	1.01
1:G:125:LEU:O	1:G:125:LEU:HD12	1.59	1.01
1:P:107:ARG:HH12	1:P:141:GLN:HG2	1.24	1.01
1:L:107:ARG:HH12	1:L:141:GLN:HG2	1.22	1.01
1:N:125:LEU:O	1:N:125:LEU:HD12	1.61	1.01
1:Q:283:TYR:HE2	1:Q:287:LEU:HD12	0.87	1.01
1:S:283:TYR:HE2	1:S:287:LEU:HD11	1.21	1.01
1:T:283:TYR:HE2	1:T:287:LEU:HD12	0.84	1.01
1:D:125:LEU:HD12	1:D:125:LEU:O	1.61	1.01
1:M:283:TYR:O	1:M:286:TYR:HB3	1.59	1.01
1:H:283:TYR:HE2	1:H:287:LEU:HD11	1.21	1.01
1:H:282:ALA:O	1:H:285:LEU:HD13	1.60	1.01
1:F:277:GLU:OE1	1:F:281:ARG:CB	2.08	1.01
1:E:253:GLY:C	1:E:257:PHE:CE2	2.34	1.00
1:H:285:LEU:HD22	1:H:285:LEU:C	1.79	1.00
1:K:283:TYR:O	1:K:286:TYR:HB3	1.58	1.00
1:K:282:ALA:O	1:K:285:LEU:HD13	1.59	1.00
1:N:285:LEU:HD22	1:N:285:LEU:C	1.82	1.00
1:O:283:TYR:HE2	1:O:287:LEU:HD12	0.86	1.00
1:O:277:GLU:OE1	1:O:281:ARG:CB	2.09	1.00
1:G:282:ALA:O	1:G:285:LEU:HD13	1.62	1.00
1:C:283:TYR:O	1:C:286:TYR:HB3	1.62	1.00
1:O:107:ARG:HH12	1:O:141:GLN:HG2	1.25	1.00
1:C:282:ALA:O	1:C:285:LEU:HD13	1.60	0.99
1:F:283:TYR:O	1:F:286:TYR:HB3	1.61	0.99
1:T:283:TYR:O	1:T:286:TYR:HB3	1.61	0.99
1:F:277:GLU:OE1	1:F:281:ARG:HB3	1.62	0.99
1:C:277:GLU:OE1	1:C:281:ARG:CB	2.10	0.99
1:D:97:PRO:O	1:D:100:THR:OG1	1.78	0.99
1:D:107:ARG:HH12	1:D:141:GLN:HG2	1.24	0.99
1:B:282:ALA:O	1:B:285:LEU:HD13	1.60	0.99
1:R:283:TYR:O	1:R:286:TYR:HB3	1.63	0.99
1:K:283:TYR:HE2	1:K:287:LEU:HD11	1.23	0.99
1:B:97:PRO:O	1:B:100:THR:OG1	1.81	0.99
1:P:285:LEU:C	1:P:285:LEU:HD22	1.80	0.99
1:D:283:TYR:HE2	1:D:287:LEU:HD11	1.26	0.99
1:G:285:LEU:HD22	1:G:285:LEU:C	1.83	0.99
1:L:239:CYS:SG	1:L:252:MET:HE3	2.00	0.99
1:I:277:GLU:OE1	1:I:281:ARG:HB3	1.63	0.98

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:253:GLY:C	1:O:257:PHE:CE2	2.35	0.98
1:K:283:TYR:HE2	1:K:287:LEU:HD12	0.82	0.98
1:J:283:TYR:O	1:J:286:TYR:HB3	1.60	0.98
1:P:253:GLY:C	1:P:257:PHE:CE2	2.36	0.98
1:B:283:TYR:HE2	1:B:287:LEU:HD12	0.83	0.98
1:K:125:LEU:HD12	1:K:125:LEU:O	1.61	0.98
1:E:107:ARG:HH12	1:E:141:GLN:HG2	1.29	0.98
1:E:283:TYR:HE2	1:E:287:LEU:HD11	1.27	0.98
1:F:253:GLY:C	1:F:257:PHE:CE2	2.37	0.98
1:T:253:GLY:C	1:T:257:PHE:CE2	2.36	0.98
1:I:277:GLU:OE1	1:I:281:ARG:CB	2.11	0.98
1:N:97:PRO:O	1:N:100:THR:OG1	1.81	0.98
1:Q:97:PRO:O	1:Q:100:THR:OG1	1.82	0.98
1:D:283:TYR:HE2	1:D:287:LEU:HD12	0.86	0.98
1:E:283:TYR:O	1:E:286:TYR:HB3	1.63	0.98
1:F:15:THR:HG21	1:B:212:GLU:HB3	1.43	0.98
1:F:125:LEU:O	1:F:125:LEU:HD12	1.62	0.97
1:G:107:ARG:HH12	1:G:141:GLN:HG2	1.29	0.97
1:O:277:GLU:OE1	1:O:281:ARG:HB3	1.63	0.97
1:R:285:LEU:HD22	1:R:285:LEU:C	1.85	0.97
1:A:277:GLU:OE1	1:A:281:ARG:CB	2.12	0.97
1:B:277:GLU:OE1	1:B:281:ARG:CB	2.12	0.97
1:H:233:ARG:HB2	2:H:310:HOH:O	1.62	0.97
1:J:277:GLU:OE1	1:J:281:ARG:CB	2.12	0.97
1:D:277:GLU:OE1	1:D:281:ARG:CB	2.12	0.97
1:Q:283:TYR:O	1:Q:286:TYR:HB3	1.62	0.97
1:R:65:THR:HB	1:R:68:LEU:HD12	1.44	0.97
1:S:285:LEU:C	1:S:285:LEU:HD22	1.84	0.97
1:Q:285:LEU:C	1:Q:285:LEU:HD22	1.83	0.97
1:A:253:GLY:C	1:A:257:PHE:CE2	2.36	0.97
1:K:107:ARG:HH12	1:K:141:GLN:HG2	1.30	0.97
1:C:233:ARG:HH11	1:C:233:ARG:CG	1.77	0.97
1:T:277:GLU:OE1	1:T:281:ARG:CB	2.13	0.97
1:C:277:GLU:OE1	1:C:281:ARG:HB3	1.65	0.97
1:C:283:TYR:HE2	1:C:287:LEU:HD11	1.22	0.97
1:F:97:PRO:O	1:F:100:THR:OG1	1.80	0.96
1:K:285:LEU:C	1:K:285:LEU:HD22	1.84	0.96
1:L:253:GLY:C	1:L:257:PHE:CE2	2.38	0.96
1:R:107:ARG:HH12	1:R:141:GLN:HG2	1.27	0.96
1:S:253:GLY:C	1:S:257:PHE:CE2	2.38	0.96
1:H:283:TYR:O	1:H:286:TYR:HB3	1.64	0.96

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:233:ARG:HH11	1:K:233:ARG:CG	1.79	0.96
1:Q:233:ARG:HH11	1:Q:233:ARG:CG	1.78	0.96
1:G:65:THR:HB	1:G:68:LEU:HD12	1.47	0.96
1:M:277:GLU:OE1	1:M:281:ARG:HB3	1.64	0.96
1:S:65:THR:HB	1:S:68:LEU:HD12	1.48	0.96
1:C:107:ARG:HH12	1:C:141:GLN:HG2	1.27	0.96
1:L:283:TYR:O	1:L:286:TYR:HB3	1.64	0.96
1:N:233:ARG:HH11	1:N:233:ARG:CG	1.79	0.96
1:A:107:ARG:HH12	1:A:141:GLN:HG2	1.27	0.96
1:B:277:GLU:OE1	1:B:281:ARG:HB3	1.66	0.96
1:M:253:GLY:C	1:M:257:PHE:CE2	2.39	0.96
1:H:277:GLU:OE1	1:H:281:ARG:CB	2.14	0.96
1:J:283:TYR:HE2	1:J:287:LEU:HD12	0.82	0.96
1:J:283:TYR:CE2	1:J:287:LEU:HD11	1.92	0.95
1:P:65:THR:HB	1:P:68:LEU:HD12	1.49	0.95
1:Q:125:LEU:HD12	1:Q:125:LEU:O	1.66	0.95
1:E:233:ARG:HH11	1:E:233:ARG:CG	1.76	0.95
1:M:277:GLU:OE1	1:M:281:ARG:CB	2.13	0.95
1:O:65:THR:HB	1:O:68:LEU:HD12	1.48	0.95
1:S:107:ARG:HH12	1:S:141:GLN:HG2	1.25	0.95
1:F:283:TYR:HE2	1:F:287:LEU:HD12	0.88	0.95
1:H:107:ARG:HH12	1:H:141:GLN:HG2	1.28	0.95
1:J:233:ARG:HH11	1:J:233:ARG:CG	1.77	0.95
1:O:97:PRO:O	1:O:100:THR:OG1	1.81	0.95
1:F:233:ARG:CG	1:F:233:ARG:HH11	1.79	0.95
1:N:285:LEU:HA	1:N:288:SER:HB3	1.49	0.95
1:P:277:GLU:OE1	1:P:281:ARG:CB	2.14	0.95
1:P:283:TYR:HE2	1:P:287:LEU:HD12	0.86	0.95
1:S:277:GLU:OE1	1:S:281:ARG:CB	2.14	0.95
1:G:212:GLU:CB	1:C:15:THR:HG21	1.95	0.95
1:P:233:ARG:HH11	1:P:233:ARG:CG	1.78	0.95
1:E:285:LEU:HD22	1:E:285:LEU:C	1.87	0.95
1:M:97:PRO:O	1:M:100:THR:OG1	1.84	0.95
1:A:233:ARG:HH11	1:A:233:ARG:CG	1.80	0.94
1:E:125:LEU:O	1:E:125:LEU:HD12	1.66	0.94
1:E:97:PRO:O	1:E:100:THR:OG1	1.84	0.94
1:L:277:GLU:OE1	1:L:281:ARG:CB	2.15	0.94
1:L:285:LEU:C	1:L:285:LEU:HD22	1.87	0.94
1:T:233:ARG:HH11	1:T:233:ARG:CG	1.79	0.94
1:I:97:PRO:O	1:I:100:THR:OG1	1.84	0.94
1:M:283:TYR:HE2	1:M:287:LEU:HD12	0.80	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:125:LEU:O	1:M:125:LEU:HD12	1.67	0.94
1:T:107:ARG:HH12	1:T:141:GLN:HG2	1.32	0.94
1:J:253:GLY:C	1:J:257:PHE:CE2	2.40	0.94
1:E:277:GLU:OE1	1:E:281:ARG:CB	2.15	0.94
1:E:277:GLU:OE1	1:E:281:ARG:HB3	1.68	0.94
1:K:253:GLY:C	1:K:257:PHE:CE2	2.41	0.94
1:G:212:GLU:HB3	1:C:15:THR:CG2	1.97	0.94
1:G:97:PRO:O	1:G:100:THR:OG1	1.84	0.94
1:H:233:ARG:CG	1:H:233:ARG:HH11	1.80	0.94
1:Q:233:ARG:NH1	1:Q:233:ARG:HG2	1.78	0.94
1:G:253:GLY:C	1:G:257:PHE:CE2	2.40	0.94
1:A:283:TYR:HE2	1:A:287:LEU:HD12	0.88	0.94
1:I:107:ARG:HH12	1:I:141:GLN:HG2	1.30	0.94
1:I:233:ARG:CG	1:I:233:ARG:HH11	1.79	0.94
1:I:65:THR:HB	1:I:68:LEU:HD12	1.49	0.94
1:A:277:GLU:OE1	1:A:281:ARG:HB3	1.69	0.93
1:H:283:TYR:HE2	1:H:287:LEU:HD12	0.82	0.93
1:M:282:ALA:O	1:M:285:LEU:HD13	1.67	0.93
1:P:283:TYR:O	1:P:286:TYR:HB3	1.66	0.93
1:D:253:GLY:C	1:D:257:PHE:CE2	2.40	0.93
1:G:277:GLU:OE1	1:G:281:ARG:HB3	1.69	0.93
1:J:277:GLU:OE1	1:J:281:ARG:HB3	1.67	0.93
1:Q:277:GLU:OE1	1:Q:281:ARG:CB	2.16	0.93
1:H:285:LEU:HA	1:H:288:SER:HB3	1.51	0.93
1:R:285:LEU:HA	1:R:288:SER:HB3	1.51	0.93
1:N:234:GLU:HG2	1:G:281:ARG:CZ	1.98	0.93
1:S:283:TYR:HE2	1:S:287:LEU:HD12	0.81	0.93
1:M:233:ARG:HH11	1:M:233:ARG:CG	1.82	0.92
1:R:233:ARG:CG	1:R:233:ARG:HH11	1.82	0.92
1:L:233:ARG:CG	1:L:233:ARG:HH11	1.81	0.92
1:T:277:GLU:OE1	1:T:281:ARG:HB3	1.68	0.92
1:N:287:LEU:HD21	1:G:275:HIS:HE1	1.20	0.92
1:D:277:GLU:OE1	1:D:281:ARG:HB3	1.68	0.92
1:B:65:THR:HB	1:B:68:LEU:HD12	1.50	0.92
1:H:97:PRO:O	1:H:100:THR:OG1	1.85	0.92
1:K:65:THR:HB	1:K:68:LEU:HD12	1.48	0.92
1:R:283:TYR:HE2	1:R:287:LEU:HD12	0.88	0.92
1:D:233:ARG:CG	1:D:233:ARG:HH11	1.83	0.92
1:P:233:ARG:HG2	1:P:233:ARG:NH1	1.79	0.92
1:S:233:ARG:NH1	1:S:233:ARG:HG2	1.83	0.92
1:G:233:ARG:HH11	1:G:233:ARG:CG	1.82	0.92

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:125:LEU:HD12	1:R:125:LEU:C	1.88	0.91
1:R:277:GLU:OE1	1:R:281:ARG:CB	2.18	0.91
1:G:233:ARG:NH1	1:G:233:ARG:HG2	1.81	0.91
1:E:65:THR:HB	1:E:68:LEU:HD12	1.52	0.91
1:J:97:PRO:O	1:J:100:THR:OG1	1.88	0.91
1:Q:65:THR:HB	1:Q:68:LEU:HD12	1.50	0.91
1:A:125:LEU:HD12	1:A:125:LEU:C	1.89	0.91
1:N:239:CYS:SG	1:N:252:MET:HE3	2.10	0.91
1:S:233:ARG:HH11	1:S:233:ARG:CG	1.82	0.91
1:F:233:ARG:NH1	1:F:233:ARG:HG2	1.78	0.91
1:J:65:THR:HB	1:J:68:LEU:HD12	1.51	0.91
1:K:97:PRO:O	1:K:100:THR:OG1	1.86	0.91
1:K:277:GLU:OE1	1:K:281:ARG:CB	2.18	0.91
1:S:277:GLU:OE1	1:S:281:ARG:HB3	1.69	0.91
1:D:239:CYS:SG	1:D:252:MET:HE3	2.08	0.91
1:F:65:THR:HB	1:F:68:LEU:HD12	1.51	0.91
1:M:233:ARG:NH1	1:M:233:ARG:HG2	1.82	0.91
1:M:283:TYR:CE2	1:M:287:LEU:HD11	1.99	0.91
1:G:277:GLU:OE1	1:G:281:ARG:CB	2.17	0.91
1:L:285:LEU:HA	1:L:288:SER:HB3	1.51	0.91
1:Q:277:GLU:OE1	1:Q:281:ARG:HB3	1.70	0.91
1:F:212:GLU:HB3	1:B:15:THR:HG21	1.53	0.91
1:N:253:GLY:C	1:N:257:PHE:CE2	2.44	0.91
1:N:283:TYR:CE2	1:N:287:LEU:HD11	1.94	0.91
1:M:65:THR:HB	1:M:68:LEU:HD12	1.53	0.91
1:I:15:THR:HG21	1:E:212:GLU:HB3	1.54	0.90
1:H:277:GLU:OE1	1:H:281:ARG:HB3	1.70	0.90
1:B:233:ARG:NH1	1:B:233:ARG:HG2	1.82	0.90
1:A:125:LEU:CD1	1:A:125:LEU:O	2.18	0.90
1:K:285:LEU:HA	1:K:288:SER:HB3	1.54	0.90
1:L:233:ARG:NH1	1:L:233:ARG:HG2	1.81	0.90
1:O:233:ARG:CG	1:O:233:ARG:HH11	1.85	0.90
1:E:283:TYR:HE2	1:E:287:LEU:HD12	0.77	0.90
1:Q:285:LEU:HA	1:Q:288:SER:HB3	1.54	0.90
1:B:253:GLY:C	1:B:257:PHE:CE2	2.44	0.90
1:D:65:THR:HB	1:D:68:LEU:HD12	1.52	0.90
1:F:285:LEU:HA	1:F:288:SER:HB3	1.54	0.90
1:Q:253:GLY:C	1:Q:257:PHE:CE2	2.44	0.90
1:S:285:LEU:HA	1:S:288:SER:HB3	1.52	0.90
1:L:277:GLU:OE1	1:L:281:ARG:HB3	1.68	0.90
1:P:277:GLU:OE1	1:P:281:ARG:HB3	1.71	0.90

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:285:LEU:HA	1:A:288:SER:HB3	1.52	0.90
1:R:97:PRO:O	1:R:100:THR:OG1	1.89	0.90
1:B:233:ARG:CG	1:B:233:ARG:HH11	1.83	0.89
1:H:253:GLY:C	1:H:257:PHE:CE2	2.45	0.89
1:G:285:LEU:HA	1:G:288:SER:HB3	1.52	0.89
1:R:275:HIS:O	1:R:276:ASN:HB2	1.72	0.89
1:S:125:LEU:HD12	1:S:125:LEU:O	1.72	0.89
1:T:65:THR:HB	1:T:68:LEU:HD12	1.52	0.89
1:N:65:THR:HB	1:N:68:LEU:HD12	1.53	0.89
1:A:65:THR:HB	1:A:68:LEU:HD12	1.51	0.89
1:C:65:THR:HB	1:C:68:LEU:HD12	1.53	0.89
1:A:97:PRO:O	1:A:100:THR:OG1	1.88	0.89
1:A:233:ARG:HG2	1:A:233:ARG:NH1	1.80	0.89
1:K:233:ARG:NH1	1:K:233:ARG:HG2	1.79	0.89
1:N:277:GLU:OE1	1:N:281:ARG:CB	2.21	0.89
1:A:277:GLU:OE1	1:A:281:ARG:CD	2.21	0.89
1:H:65:THR:HB	1:H:68:LEU:HD12	1.53	0.89
1:T:233:ARG:NH1	1:T:233:ARG:HG2	1.79	0.89
1:F:239:CYS:SG	1:F:252:MET:HE3	2.11	0.88
1:O:283:TYR:CE2	1:O:287:LEU:HD11	1.95	0.88
1:P:97:PRO:O	1:P:100:THR:OG1	1.89	0.88
1:E:283:TYR:CE2	1:E:287:LEU:HD11	2.03	0.88
1:I:253:GLY:C	1:I:257:PHE:CE2	2.47	0.88
1:M:285:LEU:HA	1:M:288:SER:HB3	1.55	0.88
1:I:233:ARG:NH1	1:I:233:ARG:HG2	1.80	0.88
1:P:275:HIS:O	1:P:276:ASN:HB2	1.74	0.88
1:J:125:LEU:C	1:J:125:LEU:HD12	1.88	0.88
1:K:277:GLU:OE1	1:K:281:ARG:HB3	1.72	0.88
1:R:253:GLY:C	1:R:257:PHE:CE2	2.46	0.88
1:P:285:LEU:HA	1:P:288:SER:HB3	1.55	0.88
1:L:97:PRO:O	1:L:100:THR:OG1	1.92	0.88
1:N:287:LEU:HD21	1:G:275:HIS:NE2	1.89	0.88
1:H:283:TYR:HE1	2:H:310:HOH:O	1.58	0.87
1:L:65:THR:HB	1:L:68:LEU:HD12	1.55	0.87
1:T:125:LEU:C	1:T:125:LEU:HD12	1.90	0.87
1:E:171:MET:HG3	1:E:201:ILE:HB	1.57	0.87
1:L:125:LEU:C	1:L:125:LEU:HD12	1.90	0.87
1:C:141:GLN:OE1	1:C:173:VAL:HB	1.75	0.87
1:O:277:GLU:OE2	1:C:281:ARG:NE	2.08	0.87
1:H:283:TYR:CE2	1:H:287:LEU:HD11	1.98	0.87
1:B:285:LEU:HA	1:B:288:SER:HB3	1.55	0.87

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:285:LEU:HA	1:T:288:SER:HB3	1.57	0.87
1:R:125:LEU:CD1	1:R:125:LEU:C	2.43	0.87
1:A:125:LEU:CD1	1:A:125:LEU:C	2.42	0.86
1:O:233:ARG:NH1	1:O:233:ARG:HG2	1.85	0.86
1:O:285:LEU:HA	1:O:288:SER:HB3	1.56	0.86
1:T:97:PRO:O	1:T:100:THR:OG1	1.92	0.86
1:B:283:TYR:CE2	1:B:287:LEU:HD11	1.97	0.86
1:I:212:GLU:HB3	1:E:15:THR:HG21	1.57	0.86
1:I:285:LEU:HA	1:I:288:SER:HB3	1.57	0.86
1:O:125:LEU:HD12	1:O:125:LEU:C	1.93	0.86
1:O:141:GLN:OE1	1:O:173:VAL:HB	1.75	0.86
1:E:285:LEU:HA	1:E:288:SER:HB3	1.55	0.86
1:P:283:TYR:CE2	1:P:287:LEU:HD11	1.97	0.86
1:T:283:TYR:CE2	1:T:287:LEU:HD11	1.98	0.86
1:D:285:LEU:HA	1:D:288:SER:HB3	1.56	0.86
1:L:125:LEU:O	1:L:125:LEU:CD1	2.23	0.86
1:C:285:LEU:HA	1:C:288:SER:HB3	1.56	0.85
1:L:125:LEU:C	1:L:125:LEU:CD1	2.45	0.85
1:I:164:MET:CE	1:I:200:GLN:HE22	1.90	0.85
1:R:277:GLU:OE1	1:R:281:ARG:HB3	1.75	0.85
1:S:283:TYR:CE2	1:S:287:LEU:HD11	1.98	0.85
1:J:285:LEU:HA	1:J:288:SER:HB3	1.59	0.85
1:C:233:ARG:NH1	1:C:233:ARG:HG2	1.80	0.85
1:E:239:CYS:SG	1:E:252:MET:HE1	2.14	0.85
1:R:125:LEU:O	1:R:125:LEU:CD1	2.23	0.85
1:C:285:LEU:CD2	1:C:285:LEU:C	2.45	0.84
1:Q:171:MET:HG3	1:Q:201:ILE:HB	1.59	0.84
1:R:283:TYR:CE2	1:R:287:LEU:HD11	1.99	0.84
1:J:233:ARG:HG2	1:J:233:ARG:NH1	1.77	0.84
1:J:107:ARG:HH12	1:J:141:GLN:HG2	1.39	0.84
1:N:277:GLU:OE1	1:N:281:ARG:HB3	1.78	0.84
1:S:171:MET:HG3	1:S:201:ILE:HB	1.59	0.84
1:F:15:THR:HG21	1:B:212:GLU:CB	2.07	0.84
1:T:125:LEU:C	1:T:125:LEU:CD1	2.46	0.84
1:H:171:MET:HG3	1:H:201:ILE:HB	1.59	0.84
1:I:141:GLN:OE1	1:I:173:VAL:HB	1.77	0.84
1:Q:283:TYR:CE2	1:Q:287:LEU:HD11	2.01	0.84
1:J:283:TYR:CD2	1:J:287:LEU:HD12	2.12	0.84
1:B:141:GLN:OE1	1:B:173:VAL:HB	1.77	0.84
1:N:234:GLU:CG	1:G:281:ARG:CZ	2.55	0.84
1:P:125:LEU:C	1:P:125:LEU:HD12	1.95	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:275:HIS:O	1:E:276:ASN:HB2	1.78	0.84
1:J:125:LEU:C	1:J:125:LEU:CD1	2.45	0.84
1:S:275:HIS:O	1:S:276:ASN:HB2	1.77	0.84
1:N:287:LEU:CD2	1:G:275:HIS:HE1	1.74	0.83
1:G:283:TYR:CE2	1:G:287:LEU:HD11	2.00	0.83
1:J:171:MET:HG3	1:J:201:ILE:HB	1.60	0.83
1:D:171:MET:HG3	1:D:201:ILE:HB	1.59	0.83
1:K:283:TYR:CE2	1:K:287:LEU:HD11	2.01	0.83
1:D:275:HIS:O	1:D:276:ASN:HB2	1.77	0.83
1:I:283:TYR:CE2	1:I:287:LEU:HD11	2.01	0.83
1:O:232:GLU:N	1:O:232:GLU:OE1	2.10	0.83
1:T:171:MET:HG3	1:T:201:ILE:HB	1.59	0.83
1:C:275:HIS:O	1:C:276:ASN:HB2	1.78	0.83
1:A:283:TYR:CE2	1:A:287:LEU:HD11	2.01	0.83
1:L:141:GLN:OE1	1:L:173:VAL:HB	1.78	0.83
1:S:239:CYS:SG	1:S:252:MET:HE3	2.18	0.83
1:K:275:HIS:O	1:K:276:ASN:HB2	1.79	0.82
1:R:65:THR:CB	1:R:68:LEU:HD12	2.09	0.82
1:G:15:THR:HG21	1:C:212:GLU:HB3	1.60	0.82
1:F:15:THR:CG2	1:B:212:GLU:HB3	2.09	0.82
1:H:15:THR:HG21	1:D:212:GLU:HB3	1.62	0.82
1:H:275:HIS:O	1:H:276:ASN:HB2	1.79	0.82
1:O:125:LEU:CD1	1:O:125:LEU:C	2.48	0.82
1:C:253:GLY:C	1:C:257:PHE:CE2	2.53	0.82
1:L:277:GLU:OE1	1:L:281:ARG:CD	2.27	0.82
1:Q:141:GLN:OE1	1:Q:173:VAL:HB	1.80	0.82
1:M:275:HIS:O	1:M:276:ASN:HB2	1.78	0.82
1:D:285:LEU:CD2	1:D:285:LEU:C	2.47	0.82
1:L:283:TYR:CE2	1:L:287:LEU:HD11	2.00	0.82
1:N:80:GLU:HG2	2:N:303:HOH:O	1.80	0.82
1:D:277:GLU:OE1	1:D:281:ARG:CD	2.28	0.81
1:H:125:LEU:HD12	1:H:125:LEU:C	1.97	0.81
1:P:171:MET:HG3	1:P:201:ILE:HB	1.62	0.81
1:E:233:ARG:NH1	1:E:233:ARG:HG2	1.78	0.81
1:N:141:GLN:OE1	1:N:173:VAL:HB	1.81	0.81
1:N:233:ARG:HG2	1:N:233:ARG:NH1	1.80	0.81
1:O:171:MET:HG3	1:O:201:ILE:HB	1.60	0.81
1:P:141:GLN:OE1	1:P:173:VAL:HB	1.80	0.81
1:T:285:LEU:C	1:T:285:LEU:CD2	2.49	0.81
1:B:277:GLU:OE1	1:B:281:ARG:CD	2.29	0.81
1:F:171:MET:HG3	1:F:201:ILE:HB	1.62	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:125:LEU:C	1:G:125:LEU:HD12	1.99	0.81
1:F:283:TYR:CE2	1:F:287:LEU:HD11	1.97	0.81
1:S:277:GLU:OE1	1:S:281:ARG:CD	2.29	0.81
1:T:277:GLU:OE1	1:T:281:ARG:CD	2.28	0.81
1:H:212:GLU:HB3	1:D:15:THR:HG21	1.62	0.81
1:C:97:PRO:O	1:C:100:THR:OG1	1.97	0.80
1:A:232:GLU:N	1:A:232:GLU:OE1	2.14	0.80
1:D:141:GLN:OE1	1:D:173:VAL:HB	1.81	0.80
1:H:233:ARG:HG2	1:H:233:ARG:NH1	1.80	0.80
1:K:277:GLU:OE1	1:K:281:ARG:CD	2.29	0.80
1:H:212:GLU:CB	1:D:15:THR:HG21	2.11	0.80
1:R:283:TYR:CD2	1:R:287:LEU:HD12	2.16	0.80
1:M:239:CYS:SG	1:M:252:MET:HE3	2.21	0.80
1:B:283:TYR:CD2	1:B:287:LEU:HD12	2.15	0.80
1:F:239:CYS:SG	1:F:252:MET:HE1	2.17	0.80
1:F:275:HIS:O	1:F:276:ASN:HB2	1.80	0.80
1:G:277:GLU:OE1	1:G:281:ARG:CD	2.30	0.80
1:K:125:LEU:HD12	1:K:125:LEU:C	1.99	0.80
1:N:234:GLU:CG	1:G:281:ARG:NH2	2.44	0.80
1:P:149:GLU:OE2	1:T:113:SER:OG	2.00	0.80
1:P:232:GLU:N	1:P:232:GLU:OE1	2.14	0.80
1:H:191:THR:HG22	1:H:202:ILE:HG21	1.63	0.79
1:S:141:GLN:OE1	1:S:173:VAL:HB	1.82	0.79
1:H:141:GLN:OE1	1:H:173:VAL:HB	1.82	0.79
1:T:239:CYS:SG	1:T:252:MET:HE3	2.22	0.79
1:O:277:GLU:OE1	1:O:281:ARG:CD	2.30	0.79
1:P:125:LEU:C	1:P:125:LEU:CD1	2.50	0.79
1:R:277:GLU:OE1	1:R:281:ARG:CD	2.30	0.79
1:I:65:THR:CB	1:I:68:LEU:HD12	2.13	0.79
1:L:275:HIS:O	1:L:276:ASN:HB2	1.79	0.79
1:D:233:ARG:HG2	1:D:233:ARG:NH1	1.84	0.79
1:I:285:LEU:CD2	1:I:285:LEU:C	2.51	0.79
1:B:171:MET:HG3	1:B:201:ILE:HB	1.65	0.79
1:I:239:CYS:SG	1:I:252:MET:HE3	2.20	0.79
1:M:141:GLN:OE1	1:M:173:VAL:HB	1.81	0.79
1:Q:232:GLU:OE1	1:Q:232:GLU:N	2.14	0.79
1:S:283:TYR:CD2	1:S:287:LEU:HD12	2.17	0.79
1:P:65:THR:CB	1:P:68:LEU:HD12	2.12	0.79
1:O:275:HIS:O	1:O:276:ASN:HB2	1.80	0.78
1:S:65:THR:CB	1:S:68:LEU:HD12	2.13	0.78
1:C:125:LEU:HD12	1:C:125:LEU:C	2.01	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:125:LEU:HD12	1:D:125:LEU:C	2.00	0.78
1:A:275:HIS:O	1:A:276:ASN:HB2	1.82	0.78
1:K:171:MET:HG3	1:K:201:ILE:HB	1.66	0.78
1:I:125:LEU:HD12	1:I:125:LEU:C	2.03	0.78
1:I:232:GLU:N	1:I:232:GLU:OE1	2.16	0.78
1:A:171:MET:HG3	1:A:201:ILE:HB	1.65	0.78
1:O:283:TYR:CD2	1:O:287:LEU:HD12	2.15	0.78
1:H:125:LEU:CD1	1:H:125:LEU:C	2.51	0.78
1:N:283:TYR:CD2	1:N:287:LEU:HD12	2.17	0.78
1:P:277:GLU:OE1	1:P:281:ARG:CD	2.31	0.78
1:P:283:TYR:CD2	1:P:287:LEU:HD12	2.18	0.78
1:P:113:SER:OG	1:Q:149:GLU:OE2	2.01	0.78
1:R:233:ARG:HG2	1:R:233:ARG:NH1	1.84	0.78
1:J:65:THR:CB	1:J:68:LEU:HD12	2.14	0.78
1:N:275:HIS:O	1:N:276:ASN:HB2	1.82	0.78
1:C:277:GLU:OE1	1:C:281:ARG:CD	2.32	0.77
1:I:171:MET:HG3	1:I:201:ILE:HB	1.67	0.77
1:J:141:GLN:OE1	1:J:173:VAL:HB	1.84	0.77
1:O:285:LEU:C	1:O:285:LEU:CD2	2.51	0.77
1:F:283:TYR:CD2	1:F:287:LEU:HD12	2.17	0.77
1:K:125:LEU:C	1:K:125:LEU:CD1	2.53	0.77
1:T:285:LEU:O	1:T:285:LEU:HD22	1.85	0.77
1:F:277:GLU:OE1	1:F:281:ARG:CD	2.32	0.77
1:M:171:MET:HG3	1:M:201:ILE:HB	1.64	0.77
1:B:125:LEU:C	1:B:125:LEU:HD12	2.00	0.77
1:G:15:THR:HG21	1:C:212:GLU:CB	2.14	0.77
1:S:102:ARG:HG3	1:S:103:PRO:HD2	1.65	0.77
1:B:65:THR:CB	1:B:68:LEU:HD12	2.14	0.77
1:E:277:GLU:OE1	1:E:281:ARG:CD	2.33	0.77
1:Q:275:HIS:O	1:Q:276:ASN:HB2	1.83	0.77
1:R:171:MET:HG3	1:R:201:ILE:HB	1.66	0.77
1:T:125:LEU:O	1:T:125:LEU:CD1	2.32	0.77
1:C:239:CYS:SG	1:C:252:MET:HE1	2.25	0.77
1:H:283:TYR:CD2	1:H:287:LEU:HD12	2.18	0.77
1:J:275:HIS:O	1:J:276:ASN:HB2	1.83	0.77
1:E:164:MET:CE	1:E:200:GLN:HE22	1.98	0.76
1:I:275:HIS:O	1:I:276:ASN:HB2	1.82	0.76
1:O:70:ARG:NH2	1:O:73:ILE:HD12	1.99	0.76
1:E:232:GLU:N	1:E:232:GLU:OE1	2.18	0.76
1:J:277:GLU:OE1	1:J:281:ARG:CD	2.32	0.76
1:T:283:TYR:CD2	1:T:287:LEU:HD12	2.19	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:277:GLU:OE1	1:I:281:ARG:CD	2.33	0.76
1:N:125:LEU:C	1:N:125:LEU:CD1	2.54	0.76
1:B:232:GLU:OE1	1:B:232:GLU:N	2.18	0.76
1:F:125:LEU:C	1:F:125:LEU:HD12	2.04	0.76
1:G:283:TYR:CD2	1:G:287:LEU:HD12	2.19	0.76
1:I:15:THR:HG21	1:E:212:GLU:CB	2.15	0.76
1:B:125:LEU:C	1:B:125:LEU:CD1	2.54	0.76
1:F:212:GLU:HB3	1:B:15:THR:CG2	2.16	0.76
1:C:125:LEU:CD1	1:C:125:LEU:C	2.54	0.76
1:G:65:THR:CB	1:G:68:LEU:HD12	2.16	0.76
1:I:283:TYR:CD2	1:I:287:LEU:HD12	2.19	0.76
1:T:65:THR:CB	1:T:68:LEU:HD12	2.16	0.76
1:F:212:GLU:CB	1:B:15:THR:HG21	2.15	0.76
1:G:275:HIS:O	1:G:276:ASN:HB2	1.85	0.76
1:M:277:GLU:OE1	1:M:281:ARG:CD	2.34	0.76
1:N:125:LEU:C	1:N:125:LEU:HD12	2.01	0.76
1:P:164:MET:CE	1:P:200:GLN:HE22	1.98	0.76
1:K:232:GLU:N	1:K:232:GLU:OE1	2.19	0.76
1:K:283:TYR:CD2	1:K:287:LEU:HD12	2.19	0.76
1:M:232:GLU:N	1:M:232:GLU:OE1	2.18	0.76
1:S:239:CYS:SG	1:S:252:MET:HE1	2.24	0.76
1:E:253:GLY:CA	1:E:257:PHE:HE2	1.99	0.75
1:M:191:THR:HG22	1:M:202:ILE:HG21	1.68	0.75
1:N:232:GLU:OE1	1:N:232:GLU:N	2.17	0.75
1:O:65:THR:CB	1:O:68:LEU:HD12	2.14	0.75
1:G:171:MET:HG3	1:G:201:ILE:HB	1.66	0.75
1:O:125:LEU:CD1	1:O:125:LEU:O	2.32	0.75
1:B:164:MET:CE	1:B:200:GLN:HE22	1.99	0.75
1:F:285:LEU:C	1:F:285:LEU:CD2	2.51	0.75
1:L:232:GLU:N	1:L:232:GLU:OE1	2.19	0.75
1:J:15:THR:HG21	1:A:212:GLU:HB3	1.69	0.75
1:D:282:ALA:O	1:D:285:LEU:CD1	2.32	0.75
1:H:15:THR:HG21	1:D:212:GLU:CB	2.16	0.75
1:L:171:MET:HG3	1:L:201:ILE:HB	1.68	0.75
1:D:285:LEU:HD22	1:D:285:LEU:O	1.85	0.75
1:I:212:GLU:CB	1:E:15:THR:HG21	2.15	0.75
1:K:65:THR:CB	1:K:68:LEU:HD12	2.16	0.75
1:A:253:GLY:CA	1:A:257:PHE:HE2	2.00	0.75
1:F:125:LEU:C	1:F:125:LEU:CD1	2.54	0.75
1:K:141:GLN:OE1	1:K:173:VAL:HB	1.87	0.75
1:D:232:GLU:N	1:D:232:GLU:OE1	2.20	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:277:GLU:OE1	1:N:281:ARG:CD	2.34	0.75
1:O:113:SER:OG	1:K:149:GLU:OE2	2.04	0.75
1:F:232:GLU:OE1	1:F:232:GLU:N	2.20	0.75
1:Q:283:TYR:CD2	1:Q:287:LEU:HD12	2.20	0.75
1:R:252:MET:HB2	1:R:256:ILE:HG13	1.67	0.75
1:T:275:HIS:O	1:T:276:ASN:HB2	1.86	0.75
1:A:252:MET:HB2	1:A:256:ILE:HG13	1.69	0.74
1:H:232:GLU:OE1	1:H:232:GLU:N	2.19	0.74
1:C:171:MET:HG3	1:C:201:ILE:HB	1.69	0.74
1:G:191:THR:HG22	1:G:202:ILE:HG21	1.70	0.74
1:A:285:LEU:CD2	1:A:285:LEU:C	2.56	0.74
1:G:15:THR:CG2	1:C:212:GLU:HB3	2.17	0.74
1:D:283:TYR:CD2	1:D:287:LEU:HD12	2.21	0.74
1:M:283:TYR:CD2	1:M:287:LEU:HD12	2.18	0.74
1:Q:65:THR:CB	1:Q:68:LEU:HD12	2.17	0.74
1:A:164:MET:CE	1:A:200:GLN:HE22	1.99	0.74
1:B:285:LEU:CD2	1:B:285:LEU:C	2.56	0.74
1:C:283:TYR:CE2	1:C:287:LEU:HD11	2.04	0.74
1:J:285:LEU:CD2	1:J:285:LEU:C	2.52	0.74
1:M:113:SER:OG	1:N:149:GLU:OE2	2.04	0.74
1:B:275:HIS:O	1:B:276:ASN:HB2	1.87	0.74
1:H:15:THR:CG2	1:D:212:GLU:HB3	2.18	0.74
1:E:125:LEU:HD12	1:E:125:LEU:C	2.05	0.74
1:F:141:GLN:OE1	1:F:173:VAL:HB	1.87	0.74
1:H:65:THR:CB	1:H:68:LEU:HD12	2.16	0.74
1:B:239:CYS:SG	1:B:252:MET:HE3	2.27	0.74
1:H:277:GLU:OE1	1:H:281:ARG:CD	2.35	0.74
1:K:70:ARG:NH2	1:K:73:ILE:HD12	2.03	0.74
1:E:65:THR:CB	1:E:68:LEU:HD12	2.18	0.74
1:D:125:LEU:C	1:D:125:LEU:CD1	2.56	0.74
1:D:70:ARG:NH2	1:D:73:ILE:HD12	2.02	0.74
1:S:232:GLU:OE1	1:S:232:GLU:N	2.21	0.74
1:H:283:TYR:C	1:H:283:TYR:CD2	2.60	0.73
1:C:65:THR:CB	1:C:68:LEU:HD12	2.19	0.73
1:L:283:TYR:CD2	1:L:287:LEU:HD12	2.21	0.73
1:A:277:GLU:OE1	1:A:281:ARG:HD3	1.86	0.73
1:K:253:GLY:CA	1:K:257:PHE:HE2	2.01	0.73
1:C:285:LEU:HD22	1:C:285:LEU:O	1.87	0.73
1:K:239:CYS:SG	1:K:252:MET:HE3	2.25	0.73
1:M:239:CYS:SG	1:M:252:MET:HE1	2.23	0.73
1:Q:283:TYR:CD2	1:Q:283:TYR:C	2.60	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:191:THR:HG22	1:R:202:ILE:HG21	1.70	0.73
1:D:283:TYR:CE2	1:D:287:LEU:HD11	2.06	0.73
1:E:283:TYR:CD2	1:E:287:LEU:HD12	2.20	0.73
1:E:70:ARG:NH2	1:E:73:ILE:HD12	2.03	0.73
1:M:285:LEU:CD2	1:M:285:LEU:C	2.54	0.73
1:S:125:LEU:HD12	1:S:125:LEU:C	2.07	0.73
1:G:232:GLU:N	1:G:232:GLU:OE1	2.22	0.73
1:N:182:ARG:HG2	1:N:182:ARG:HH11	1.53	0.73
1:O:282:ALA:O	1:O:285:LEU:CD1	2.34	0.73
1:R:232:GLU:OE1	1:R:232:GLU:N	2.21	0.73
1:R:267:LYS:HA	1:R:270:GLN:HG3	1.71	0.73
1:G:125:LEU:CD1	1:G:125:LEU:C	2.57	0.73
1:M:164:MET:CE	1:M:200:GLN:HE22	2.02	0.73
1:P:282:ALA:O	1:P:285:LEU:CD1	2.35	0.73
1:A:102:ARG:HG3	1:A:103:PRO:HD2	1.71	0.73
1:H:212:GLU:HB3	1:D:15:THR:CG2	2.18	0.73
1:I:149:GLU:OE2	1:J:113:SER:OG	2.07	0.73
1:J:164:MET:CE	1:J:200:GLN:HE22	2.01	0.73
1:J:285:LEU:O	1:J:285:LEU:HD22	1.89	0.73
1:M:102:ARG:HG3	1:M:103:PRO:HD2	1.71	0.73
1:C:283:TYR:CD2	1:C:287:LEU:HD12	2.24	0.72
1:I:125:LEU:CD1	1:I:125:LEU:C	2.58	0.72
1:L:277:GLU:OE1	1:L:281:ARG:HD3	1.88	0.72
1:P:125:LEU:CD1	1:P:125:LEU:O	2.36	0.72
1:Q:125:LEU:HD12	1:Q:125:LEU:C	2.08	0.72
1:A:141:GLN:OE1	1:A:173:VAL:HB	1.88	0.72
1:E:149:GLU:OE2	1:D:113:SER:OG	2.07	0.72
1:P:253:GLY:CA	1:P:257:PHE:HE2	2.02	0.72
1:M:65:THR:CB	1:M:68:LEU:HD12	2.18	0.72
1:F:65:THR:CB	1:F:68:LEU:HD12	2.19	0.72
1:N:285:LEU:CD2	1:N:285:LEU:C	2.58	0.72
1:D:65:THR:CB	1:D:68:LEU:HD12	2.18	0.72
1:E:141:GLN:OE1	1:E:173:VAL:HB	1.89	0.72
1:F:27:LYS:O	1:F:221:PRO:HD3	1.89	0.72
1:F:252:MET:HB2	1:F:256:ILE:HG13	1.70	0.72
1:P:239:CYS:SG	1:P:252:MET:HE1	2.26	0.72
1:T:253:GLY:CA	1:T:257:PHE:HE2	2.01	0.72
1:A:283:TYR:CD2	1:A:287:LEU:HD12	2.21	0.72
1:B:277:GLU:OE1	1:B:281:ARG:HD3	1.90	0.72
1:I:15:THR:CG2	1:E:212:GLU:HB3	2.19	0.72
1:T:232:GLU:OE1	1:T:232:GLU:N	2.22	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:TYR:C	1:A:283:TYR:CD2	2.64	0.72
1:A:285:LEU:HD22	1:A:285:LEU:O	1.89	0.72
1:A:65:THR:CB	1:A:68:LEU:HD12	2.19	0.72
1:L:253:GLY:CA	1:L:257:PHE:HE2	2.03	0.72
1:N:171:MET:HG3	1:N:201:ILE:HB	1.70	0.72
1:E:239:CYS:SG	1:E:252:MET:HE3	2.27	0.71
1:I:252:MET:HB2	1:I:256:ILE:HG13	1.72	0.71
1:Q:277:GLU:OE1	1:Q:281:ARG:CD	2.38	0.71
1:S:125:LEU:CD1	1:S:125:LEU:C	2.59	0.71
1:S:285:LEU:CD2	1:S:285:LEU:C	2.59	0.71
1:E:125:LEU:CD1	1:E:125:LEU:C	2.59	0.71
1:I:212:GLU:HB3	1:E:15:THR:CG2	2.20	0.71
1:K:164:MET:CE	1:K:200:GLN:HE22	2.03	0.71
1:O:239:CYS:SG	1:O:252:MET:HE3	2.29	0.71
1:O:253:GLY:CA	1:O:257:PHE:HE2	2.03	0.71
1:E:113:SER:OG	1:A:149:GLU:OE2	2.06	0.71
1:D:267:LYS:HA	1:D:270:GLN:HG3	1.73	0.71
1:J:125:LEU:CD1	1:J:125:LEU:O	2.35	0.71
1:Q:164:MET:CE	1:Q:200:GLN:HE22	2.02	0.71
1:C:239:CYS:SG	1:C:252:MET:HE3	2.28	0.71
1:K:285:LEU:O	1:K:285:LEU:HD22	1.90	0.71
1:L:191:THR:HG22	1:L:202:ILE:HG21	1.73	0.71
1:O:285:LEU:HD22	1:O:285:LEU:O	1.90	0.71
1:F:253:GLY:CA	1:F:257:PHE:HE2	2.03	0.71
1:F:70:ARG:NH2	1:F:73:ILE:HD12	2.05	0.71
1:G:164:MET:CE	1:G:200:GLN:HE22	2.04	0.71
1:G:256:ILE:HD13	1:G:266:MET:HG2	1.72	0.71
1:R:102:ARG:HG3	1:R:103:PRO:HD2	1.71	0.71
1:S:253:GLY:CA	1:S:257:PHE:HE2	2.03	0.71
1:S:70:ARG:NH2	1:S:73:ILE:HD12	2.06	0.71
1:F:149:GLU:OE2	1:G:113:SER:OG	2.08	0.71
1:G:277:GLU:OE1	1:G:281:ARG:HD3	1.90	0.71
1:P:283:TYR:C	1:P:283:TYR:CD2	2.64	0.71
1:B:107:ARG:NH1	1:B:141:GLN:HG2	2.04	0.71
1:I:239:CYS:SG	1:I:252:MET:HE1	2.28	0.71
1:I:285:LEU:HD22	1:I:285:LEU:O	1.91	0.71
1:M:253:GLY:CA	1:M:257:PHE:HE2	2.04	0.71
1:M:285:LEU:O	1:M:285:LEU:HD22	1.88	0.71
1:Q:125:LEU:C	1:Q:125:LEU:CD1	2.59	0.71
1:D:164:MET:CE	1:D:200:GLN:HE22	2.03	0.71
1:F:282:ALA:O	1:F:285:LEU:CD1	2.34	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:252:MET:HB2	1:H:256:ILE:HG13	1.73	0.71
1:P:267:LYS:HA	1:P:270:GLN:HG3	1.73	0.71
1:T:191:THR:HG22	1:T:202:ILE:HG21	1.72	0.71
1:N:252:MET:HB2	1:N:256:ILE:HG13	1.73	0.70
1:R:239:CYS:SG	1:R:252:MET:HE1	2.30	0.70
1:D:191:THR:HG22	1:D:202:ILE:HG21	1.71	0.70
1:E:252:MET:HB2	1:E:256:ILE:HG13	1.72	0.70
1:M:113:SER:OG	1:N:149:GLU:CD	2.30	0.70
1:N:65:THR:CB	1:N:68:LEU:HD12	2.21	0.70
1:Q:253:GLY:CA	1:Q:257:PHE:HE2	2.05	0.70
1:E:283:TYR:C	1:E:283:TYR:CD2	2.62	0.70
1:K:252:MET:HB2	1:K:256:ILE:HG13	1.72	0.70
1:P:252:MET:HB2	1:P:256:ILE:HG13	1.71	0.70
1:Q:107:ARG:NH1	1:Q:141:GLN:HG2	2.00	0.70
1:R:239:CYS:SG	1:R:252:MET:HE3	2.30	0.70
1:C:232:GLU:OE1	1:C:232:GLU:N	2.24	0.70
1:L:252:MET:HB2	1:L:256:ILE:HG13	1.73	0.70
1:Q:191:THR:HG22	1:Q:202:ILE:HG21	1.73	0.70
1:C:164:MET:CE	1:C:200:GLN:HE22	2.04	0.70
1:J:232:GLU:OE1	1:J:232:GLU:N	2.25	0.70
1:M:283:TYR:CD2	1:M:283:TYR:C	2.64	0.70
1:P:149:GLU:CD	1:T:113:SER:OG	2.30	0.70
1:P:70:ARG:NH2	1:P:73:ILE:HD12	2.06	0.70
1:E:282:ALA:O	1:E:285:LEU:CD1	2.39	0.70
1:N:191:THR:HG22	1:N:202:ILE:HG21	1.72	0.70
1:Q:285:LEU:C	1:Q:285:LEU:CD2	2.59	0.70
1:B:102:ARG:HG3	1:B:103:PRO:HD2	1.71	0.70
1:T:252:MET:HB2	1:T:256:ILE:HG13	1.72	0.70
1:F:285:LEU:O	1:F:285:LEU:HD22	1.91	0.70
1:K:285:LEU:CD2	1:K:285:LEU:C	2.59	0.70
1:M:27:LYS:O	1:M:221:PRO:HD3	1.91	0.70
1:O:253:GLY:C	1:O:257:PHE:HE2	1.94	0.70
1:T:283:TYR:C	1:T:283:TYR:CD2	2.65	0.70
1:D:107:ARG:NH1	1:D:141:GLN:HG2	2.05	0.70
1:M:107:ARG:NH1	1:M:141:GLN:HG2	2.01	0.70
1:S:164:MET:CE	1:S:200:GLN:HE22	2.04	0.69
1:G:141:GLN:OE1	1:G:173:VAL:HB	1.92	0.69
1:P:102:ARG:HG3	1:P:103:PRO:HD2	1.74	0.69
1:A:239:CYS:SG	1:A:252:MET:HE3	2.28	0.69
1:H:125:LEU:CD1	1:H:125:LEU:O	2.36	0.69
1:J:252:MET:HB2	1:J:256:ILE:HG13	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:283:TYR:C	1:C:283:TYR:CD2	2.65	0.69
1:H:285:LEU:CD2	1:H:285:LEU:C	2.55	0.69
1:N:256:ILE:HD13	1:N:266:MET:HG2	1.74	0.69
1:T:141:GLN:OE1	1:T:173:VAL:HB	1.92	0.69
1:D:165:LYS:HE2	2:D:308:HOH:O	1.92	0.69
1:I:164:MET:HE2	1:I:200:GLN:HE22	1.58	0.69
1:N:283:TYR:CD2	1:N:283:TYR:C	2.66	0.69
1:O:102:ARG:HG3	1:O:103:PRO:HD2	1.75	0.69
1:O:277:GLU:OE1	1:O:281:ARG:HB2	1.93	0.69
1:S:283:TYR:CD2	1:S:283:TYR:C	2.65	0.69
1:I:282:ALA:O	1:I:285:LEU:CD1	2.39	0.69
1:J:283:TYR:C	1:J:283:TYR:CD2	2.66	0.69
1:O:164:MET:CE	1:O:200:GLN:HE22	2.05	0.69
1:R:141:GLN:OE1	1:R:173:VAL:HB	1.92	0.69
1:S:252:MET:HB2	1:S:256:ILE:HG13	1.73	0.69
1:A:191:THR:HG22	1:A:202:ILE:HG21	1.75	0.69
1:G:70:ARG:NH2	1:G:73:ILE:HD12	2.08	0.69
1:J:191:THR:HG22	1:J:202:ILE:HG21	1.75	0.69
1:L:107:ARG:NH1	1:L:141:GLN:HG2	2.03	0.69
1:L:283:TYR:CD2	1:L:283:TYR:C	2.66	0.69
1:P:256:ILE:HD13	1:P:266:MET:HG2	1.75	0.69
1:S:253:GLY:O	1:S:257:PHE:CE2	2.46	0.69
1:A:14:ARG:HD2	1:A:17:GLN:OE1	1.92	0.69
1:B:125:LEU:CD1	1:B:125:LEU:O	2.39	0.69
1:B:149:GLU:OE2	1:A:113:SER:OG	2.10	0.69
1:Q:282:ALA:O	1:Q:285:LEU:CD1	2.38	0.69
1:S:253:GLY:C	1:S:257:PHE:HE2	1.96	0.69
1:B:239:CYS:HG	1:B:252:MET:HE2	1.54	0.69
1:N:116:ALA:HB1	2:N:305:HOH:O	1.93	0.69
1:O:107:ARG:NH1	1:O:141:GLN:HG2	2.05	0.69
1:E:191:THR:HG22	1:E:202:ILE:HG21	1.75	0.69
1:F:33:ASP:OD1	1:A:93:ARG:NH1	2.26	0.69
1:I:191:THR:HG22	1:I:202:ILE:HG21	1.75	0.69
1:Q:252:MET:HB2	1:Q:256:ILE:HG13	1.74	0.69
1:A:107:ARG:NH1	1:A:141:GLN:HG2	2.06	0.69
1:F:102:ARG:HG3	1:F:103:PRO:HD2	1.73	0.69
1:F:125:LEU:O	1:F:125:LEU:CD1	2.40	0.69
1:G:239:CYS:SG	1:G:252:MET:HE3	2.31	0.69
1:R:285:LEU:C	1:R:285:LEU:CD2	2.60	0.69
1:S:277:GLU:OE1	1:S:281:ARG:HD3	1.91	0.69
1:E:285:LEU:CD2	1:E:285:LEU:C	2.61	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:70:ARG:NH2	1:R:73:ILE:HD12	2.08	0.68
1:C:267:LYS:HA	1:C:270:GLN:HG3	1.74	0.68
1:C:70:ARG:NH2	1:C:73:ILE:HD12	2.08	0.68
1:K:283:TYR:C	1:K:283:TYR:CD2	2.64	0.68
1:N:285:LEU:HD22	1:N:285:LEU:O	1.93	0.68
1:O:252:MET:HB2	1:O:256:ILE:HG13	1.74	0.68
1:Q:182:ARG:HG2	1:Q:182:ARG:HH11	1.58	0.68
1:S:285:LEU:HD22	1:S:285:LEU:O	1.92	0.68
1:C:282:ALA:O	1:C:285:LEU:CD1	2.40	0.68
1:D:283:TYR:CD2	1:D:283:TYR:C	2.66	0.68
1:G:253:GLY:CA	1:G:257:PHE:HE2	2.07	0.68
1:J:256:ILE:HD13	1:J:266:MET:HG2	1.75	0.68
1:K:256:ILE:HD13	1:K:266:MET:HG2	1.76	0.68
1:J:253:GLY:CA	1:J:257:PHE:HE2	2.07	0.68
1:K:191:THR:HG22	1:K:202:ILE:HG21	1.74	0.68
1:O:267:LYS:HA	1:O:270:GLN:HG3	1.76	0.68
1:C:125:LEU:CD1	1:C:125:LEU:O	2.37	0.68
1:M:125:LEU:C	1:M:125:LEU:HD12	2.12	0.68
1:D:277:GLU:OE1	1:D:281:ARG:HD3	1.91	0.68
1:E:285:LEU:HD22	1:E:285:LEU:O	1.93	0.68
1:I:65:THR:CG2	1:I:68:LEU:HD12	2.24	0.68
1:P:65:THR:CG2	1:P:68:LEU:HD12	2.23	0.68
1:H:70:ARG:NH2	1:H:73:ILE:HD12	2.08	0.68
1:I:164:MET:CE	1:I:200:GLN:NE2	2.57	0.68
1:O:113:SER:OG	1:K:149:GLU:CD	2.32	0.68
1:N:107:ARG:NH1	1:N:141:GLN:HG2	2.05	0.68
1:O:277:GLU:OE1	1:O:281:ARG:HD3	1.94	0.68
1:C:285:LEU:HD22	1:C:286:TYR:N	2.09	0.68
1:F:253:GLY:O	1:F:257:PHE:CE2	2.45	0.68
1:K:282:ALA:O	1:K:285:LEU:CD1	2.40	0.68
1:E:27:LYS:O	1:E:221:PRO:HD3	1.94	0.68
1:I:14:ARG:HD2	1:I:17:GLN:OE1	1.93	0.68
1:L:27:LYS:O	1:L:221:PRO:HD3	1.94	0.68
1:D:253:GLY:CA	1:D:257:PHE:HE2	2.07	0.67
1:G:283:TYR:C	1:G:283:TYR:CD2	2.67	0.67
1:N:282:ALA:O	1:N:285:LEU:CD1	2.39	0.67
1:N:70:ARG:NH2	1:N:73:ILE:HD12	2.09	0.67
1:I:93:ARG:NH1	1:D:33:ASP:OD1	2.27	0.67
1:F:277:GLU:OE1	1:F:281:ARG:HB2	1.93	0.67
1:J:102:ARG:HG3	1:J:103:PRO:HD2	1.75	0.67
1:L:149:GLU:OE2	1:K:113:SER:OG	2.12	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:27:LYS:O	1:Q:221:PRO:HD3	1.95	0.67
1:R:275:HIS:O	1:R:276:ASN:CB	2.43	0.67
1:D:277:GLU:OE1	1:D:281:ARG:HB2	1.94	0.67
1:G:285:LEU:CD2	1:G:285:LEU:C	2.59	0.67
1:D:182:ARG:HG2	1:D:182:ARG:HH11	1.59	0.67
1:L:65:THR:CB	1:L:68:LEU:HD12	2.24	0.67
1:S:267:LYS:HA	1:S:270:GLN:HG3	1.77	0.67
1:H:277:GLU:OE1	1:H:281:ARG:HB2	1.94	0.67
1:L:285:LEU:O	1:L:285:LEU:HD22	1.93	0.67
1:O:239:CYS:SG	1:O:252:MET:HE1	2.32	0.67
1:P:285:LEU:C	1:P:285:LEU:CD2	2.56	0.67
1:R:164:MET:CE	1:R:200:GLN:HE22	2.08	0.67
1:B:100:THR:HG23	2:B:292:HOH:O	1.95	0.67
1:D:252:MET:HB2	1:D:256:ILE:HG13	1.77	0.67
1:E:253:GLY:O	1:E:257:PHE:CE2	2.48	0.67
1:H:164:MET:CE	1:H:200:GLN:HE22	2.06	0.67
1:P:275:HIS:O	1:P:276:ASN:CB	2.42	0.67
1:A:282:ALA:O	1:A:285:LEU:CD1	2.38	0.67
1:C:113:SER:OG	1:D:149:GLU:OE2	2.11	0.67
1:H:285:LEU:O	1:H:285:LEU:HD22	1.95	0.67
1:I:283:TYR:C	1:I:283:TYR:CD2	2.67	0.67
1:J:212:GLU:HB3	1:A:15:THR:HG21	1.76	0.67
1:A:27:LYS:O	1:A:221:PRO:HD3	1.95	0.67
1:B:283:TYR:CD2	1:B:283:TYR:C	2.68	0.67
1:I:256:ILE:HD13	1:I:266:MET:HG2	1.76	0.67
1:R:277:GLU:OE1	1:R:281:ARG:HD3	1.95	0.67
1:D:14:ARG:HD2	1:D:17:GLN:OE1	1.94	0.67
1:E:204:THR:O	1:E:224:ILE:HA	1.95	0.67
1:B:252:MET:HB2	1:B:256:ILE:HG13	1.77	0.66
1:M:267:LYS:HA	1:M:270:GLN:HG3	1.77	0.66
1:O:283:TYR:C	1:O:283:TYR:CD2	2.68	0.66
1:B:253:GLY:CA	1:B:257:PHE:HE2	2.08	0.66
1:G:102:ARG:HG3	1:G:103:PRO:HD2	1.77	0.66
1:H:267:LYS:HA	1:H:270:GLN:HG3	1.77	0.66
1:M:125:LEU:CD1	1:M:125:LEU:C	2.64	0.66
1:T:277:GLU:OE1	1:T:281:ARG:HD3	1.94	0.66
1:C:256:ILE:HD13	1:C:266:MET:HG2	1.75	0.66
1:D:253:GLY:C	1:D:257:PHE:HE2	1.98	0.66
1:B:14:ARG:HD2	1:B:17:GLN:OE1	1.96	0.66
1:B:285:LEU:O	1:B:285:LEU:HD22	1.95	0.66
1:H:283:TYR:CD2	1:H:283:TYR:O	2.48	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:125:LEU:O	1:N:125:LEU:CD1	2.41	0.66
1:P:253:GLY:O	1:P:257:PHE:CE2	2.48	0.66
1:G:107:ARG:NH1	1:G:141:GLN:HG2	2.07	0.66
1:I:277:GLU:OE1	1:I:281:ARG:HD3	1.95	0.66
1:T:277:GLU:OE1	1:T:281:ARG:HB2	1.96	0.66
1:N:277:GLU:OE1	1:N:281:ARG:HD3	1.96	0.66
1:P:113:SER:OG	1:Q:149:GLU:CD	2.34	0.66
1:P:277:GLU:OE1	1:P:281:ARG:HD3	1.95	0.66
1:R:65:THR:CG2	1:R:68:LEU:HD12	2.26	0.66
1:E:267:LYS:HA	1:E:270:GLN:HG3	1.76	0.66
1:H:282:ALA:O	1:H:285:LEU:CD1	2.41	0.66
1:N:164:MET:CE	1:N:200:GLN:HE22	2.08	0.66
1:N:234:GLU:OE2	1:G:281:ARG:CZ	2.43	0.66
1:O:189:LEU:O	1:O:193:ILE:HG13	1.96	0.66
1:Q:14:ARG:HD2	1:Q:17:GLN:OE1	1.95	0.66
1:C:102:ARG:HG3	1:C:103:PRO:HD2	1.78	0.66
1:E:164:MET:CE	1:E:200:GLN:NE2	2.59	0.66
1:L:164:MET:CE	1:L:200:GLN:HE22	2.08	0.66
1:O:14:ARG:HD2	1:O:17:GLN:OE1	1.96	0.66
1:O:197:MET:CE	1:N:110:GLY:HA3	2.26	0.66
1:Q:267:LYS:HA	1:Q:270:GLN:HG3	1.78	0.66
1:G:212:GLU:HB2	1:C:15:THR:HG21	1.77	0.66
1:K:102:ARG:HG3	1:K:103:PRO:HD2	1.76	0.66
1:K:14:ARG:HD2	1:K:17:GLN:OE1	1.96	0.66
1:N:267:LYS:HA	1:N:270:GLN:HG3	1.78	0.66
1:P:14:ARG:HD2	1:P:17:GLN:OE1	1.96	0.66
1:T:102:ARG:HG3	1:T:103:PRO:HD2	1.76	0.66
1:F:191:THR:HG22	1:F:202:ILE:HG21	1.78	0.66
1:K:277:GLU:OE1	1:K:281:ARG:HD3	1.94	0.66
1:O:182:ARG:HH11	1:O:182:ARG:HG2	1.61	0.66
1:I:267:LYS:HA	1:I:270:GLN:HG3	1.77	0.65
1:J:15:THR:HG21	1:A:212:GLU:CB	2.25	0.65
1:P:239:CYS:SG	1:P:252:MET:HE3	2.32	0.65
1:S:149:GLU:OE2	1:R:113:SER:OG	2.13	0.65
1:I:107:ARG:NH1	1:I:141:GLN:HG2	2.09	0.65
1:K:267:LYS:HA	1:K:270:GLN:HG3	1.78	0.65
1:H:65:THR:CG2	1:H:68:LEU:HD12	2.26	0.65
1:P:191:THR:HG22	1:P:202:ILE:HG21	1.78	0.65
1:H:239:CYS:SG	1:H:252:MET:HE1	2.29	0.65
1:N:102:ARG:HG3	1:N:103:PRO:HD2	1.77	0.65
1:O:277:GLU:OE2	1:C:281:ARG:CZ	2.44	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:107:ARG:NH1	1:P:141:GLN:HG2	2.06	0.65
1:C:277:GLU:OE1	1:C:281:ARG:HD3	1.96	0.65
1:G:252:MET:HB2	1:G:256:ILE:HG13	1.77	0.65
1:H:182:ARG:HG2	1:H:182:ARG:HH11	1.62	0.65
1:N:253:GLY:CA	1:N:257:PHE:HE2	2.10	0.65
1:F:283:TYR:C	1:F:283:TYR:CD2	2.69	0.65
1:G:27:LYS:O	1:G:221:PRO:HD3	1.97	0.65
1:M:252:MET:HB2	1:M:256:ILE:HG13	1.77	0.65
1:T:256:ILE:HD13	1:T:266:MET:HG2	1.77	0.65
1:T:70:ARG:NH2	1:T:73:ILE:HD12	2.12	0.65
1:A:70:ARG:NH2	1:A:73:ILE:HD12	2.11	0.65
1:D:265:MET:O	1:D:268:ALA:HB3	1.97	0.65
1:M:253:GLY:C	1:M:257:PHE:HE2	2.00	0.65
1:O:253:GLY:O	1:O:257:PHE:CE2	2.49	0.65
1:C:27:LYS:O	1:C:221:PRO:HD3	1.97	0.65
1:J:267:LYS:HA	1:J:270:GLN:HG3	1.79	0.65
1:O:191:THR:HG22	1:O:202:ILE:HG21	1.78	0.65
1:E:149:GLU:CD	1:D:113:SER:OG	2.35	0.65
1:P:285:LEU:O	1:P:285:LEU:HD22	1.96	0.65
1:A:267:LYS:HA	1:A:270:GLN:HG3	1.79	0.64
1:B:70:ARG:NH2	1:B:73:ILE:HD12	2.12	0.64
1:E:277:GLU:OE1	1:E:281:ARG:HD3	1.97	0.64
1:L:14:ARG:HD2	1:L:17:GLN:OE1	1.97	0.64
1:S:282:ALA:O	1:S:285:LEU:CD1	2.41	0.64
1:S:65:THR:CG2	1:S:68:LEU:HD12	2.28	0.64
1:B:277:GLU:OE1	1:B:281:ARG:HB2	1.96	0.64
1:F:110:GLY:O	1:F:111:ALA:HB3	1.97	0.64
1:L:282:ALA:O	1:L:285:LEU:CD1	2.40	0.64
1:O:65:THR:HB	1:O:68:LEU:CD1	2.26	0.64
1:P:277:GLU:OE1	1:P:281:ARG:HB2	1.94	0.64
1:E:253:GLY:C	1:E:257:PHE:HE2	1.93	0.64
1:J:277:GLU:OE1	1:J:281:ARG:HD3	1.96	0.64
1:B:191:THR:HG22	1:B:202:ILE:HG21	1.80	0.64
1:C:14:ARG:HD2	1:C:17:GLN:OE1	1.97	0.64
1:C:277:GLU:OE1	1:C:281:ARG:HB2	1.92	0.64
1:E:283:TYR:CD2	1:E:283:TYR:O	2.51	0.64
1:T:107:ARG:NH1	1:T:141:GLN:HG2	2.10	0.64
1:B:224:ILE:O	1:B:224:ILE:HG13	1.98	0.64
1:B:267:LYS:HA	1:B:270:GLN:HG3	1.78	0.64
1:E:107:ARG:NH1	1:E:141:GLN:HG2	2.09	0.64
1:E:275:HIS:O	1:E:276:ASN:CB	2.46	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:14:ARG:HD2	1:G:17:GLN:OE1	1.97	0.64
1:Q:70:ARG:NH2	1:Q:73:ILE:HD12	2.13	0.64
1:D:285:LEU:HD22	1:D:286:TYR:N	2.12	0.64
1:H:14:ARG:HD2	1:H:17:GLN:OE1	1.98	0.64
1:L:102:ARG:HG3	1:L:103:PRO:HD2	1.79	0.64
1:A:265:MET:O	1:A:268:ALA:HB3	1.98	0.64
1:E:14:ARG:HD2	1:E:17:GLN:OE1	1.97	0.64
1:G:267:LYS:HA	1:G:270:GLN:HG3	1.78	0.64
1:Q:189:LEU:O	1:Q:193:ILE:HG13	1.98	0.64
1:T:253:GLY:O	1:T:257:PHE:CE2	2.51	0.64
1:K:239:CYS:SG	1:K:252:MET:HE1	2.32	0.64
1:O:197:MET:HE3	1:N:110:GLY:HA3	1.80	0.64
1:S:107:ARG:NH1	1:S:141:GLN:HG2	2.08	0.64
1:I:102:ARG:HG3	1:I:103:PRO:HD2	1.79	0.64
1:J:253:GLY:C	1:J:257:PHE:HE2	2.01	0.64
1:M:277:GLU:OE1	1:M:281:ARG:HD3	1.97	0.64
1:P:164:MET:CE	1:P:200:GLN:NE2	2.60	0.64
1:S:256:ILE:HD13	1:S:266:MET:HG2	1.80	0.64
1:H:253:GLY:CA	1:H:257:PHE:HE2	2.11	0.63
1:Q:125:LEU:O	1:Q:125:LEU:CD1	2.42	0.63
1:T:164:MET:CE	1:T:200:GLN:HE22	2.10	0.63
1:E:102:ARG:HG3	1:E:103:PRO:HD2	1.81	0.63
1:L:110:GLY:O	1:L:111:ALA:HB3	1.98	0.63
1:L:267:LYS:HA	1:L:270:GLN:HG3	1.80	0.63
1:Q:277:GLU:OE1	1:Q:281:ARG:HB2	1.98	0.63
1:Q:283:TYR:CD2	1:Q:283:TYR:O	2.51	0.63
1:Q:113:SER:OG	1:R:149:GLU:OE2	2.16	0.63
1:F:164:MET:CE	1:F:200:GLN:HE22	2.11	0.63
1:F:256:ILE:HD13	1:F:266:MET:HG2	1.80	0.63
1:K:27:LYS:O	1:K:221:PRO:HD3	1.98	0.63
1:R:283:TYR:CD2	1:R:283:TYR:C	2.71	0.63
1:T:282:ALA:O	1:T:285:LEU:CD1	2.39	0.63
1:H:111:ALA:H	1:G:197:MET:HE2	1.61	0.63
1:G:285:LEU:O	1:G:285:LEU:HD22	1.97	0.63
1:J:164:MET:HE2	1:J:200:GLN:HE22	1.62	0.63
1:J:277:GLU:OE1	1:J:281:ARG:HB2	1.95	0.63
1:P:204:THR:O	1:P:224:ILE:HA	1.99	0.63
1:F:204:THR:O	1:F:224:ILE:HA	1.97	0.63
1:H:113:SER:OG	1:G:149:GLU:OE2	2.17	0.63
1:Q:101:ASN:HA	2:Q:296:HOH:O	1.97	0.63
1:S:275:HIS:O	1:S:276:ASN:CB	2.44	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:239:CYS:SG	1:T:252:MET:HE1	2.33	0.63
1:K:125:LEU:O	1:K:125:LEU:CD1	2.43	0.63
1:S:265:MET:O	1:S:268:ALA:HB3	1.98	0.63
1:B:65:THR:CG2	1:B:68:LEU:HD12	2.28	0.63
1:G:229:LYS:NZ	1:G:230:LEU:O	2.31	0.63
1:J:239:CYS:SG	1:J:252:MET:HE3	2.33	0.63
1:J:282:ALA:O	1:J:285:LEU:CD1	2.40	0.63
1:K:229:LYS:NZ	1:K:230:LEU:O	2.31	0.63
1:Q:285:LEU:O	1:Q:285:LEU:HD22	1.99	0.63
1:F:113:SER:OG	1:J:149:GLU:OE2	2.17	0.63
1:O:265:MET:O	1:O:268:ALA:HB3	1.99	0.63
1:R:65:THR:HB	1:R:68:LEU:CD1	2.22	0.63
1:T:14:ARG:HD2	1:T:17:GLN:OE1	1.99	0.63
1:E:197:MET:HE1	1:D:110:GLY:HA3	1.80	0.63
1:H:107:ARG:NH1	1:H:141:GLN:HG2	2.09	0.63
1:K:113:SER:HB2	1:K:115:LEU:H	1.64	0.63
1:B:164:MET:CE	1:B:200:GLN:NE2	2.62	0.62
1:D:102:ARG:HG3	1:D:103:PRO:HD2	1.81	0.62
1:K:110:GLY:O	1:K:111:ALA:HB3	1.98	0.62
1:S:277:GLU:OE1	1:S:281:ARG:HB2	1.98	0.62
1:E:229:LYS:NZ	1:E:230:LEU:O	2.32	0.62
1:S:191:THR:HG22	1:S:202:ILE:HG21	1.80	0.62
1:S:27:LYS:O	1:S:221:PRO:HD3	1.99	0.62
1:S:65:THR:HB	1:S:68:LEU:CD1	2.28	0.62
1:T:65:THR:CG2	1:T:68:LEU:HD12	2.29	0.62
1:C:252:MET:HB2	1:C:256:ILE:HG13	1.81	0.62
1:I:277:GLU:OE1	1:I:281:ARG:HB2	1.97	0.62
1:J:239:CYS:SG	1:J:252:MET:HE1	2.32	0.62
1:J:211:PHE:HB3	1:J:245:GLN:OE1	1.99	0.62
1:K:164:MET:CE	1:K:200:GLN:NE2	2.62	0.62
1:L:285:LEU:CD2	1:L:285:LEU:C	2.62	0.62
1:P:65:THR:HB	1:P:68:LEU:CD1	2.27	0.62
1:B:256:ILE:HD13	1:B:266:MET:HG2	1.81	0.62
1:J:265:MET:O	1:J:268:ALA:HB3	1.99	0.62
1:I:233:ARG:NH1	1:I:233:ARG:CG	2.50	0.62
1:L:229:LYS:NZ	1:L:230:LEU:O	2.31	0.62
1:N:234:GLU:CD	1:G:281:ARG:CZ	2.67	0.62
1:Q:102:ARG:HG3	1:Q:103:PRO:HD2	1.80	0.62
1:Q:111:ALA:H	1:R:197:MET:HE1	1.63	0.62
1:E:113:SER:OG	1:A:149:GLU:CD	2.38	0.62
1:J:65:THR:CG2	1:J:68:LEU:HD12	2.30	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:277:GLU:OE1	1:R:281:ARG:HB2	1.99	0.62
1:B:149:GLU:CD	1:A:113:SER:OG	2.38	0.62
1:F:267:LYS:HA	1:F:270:GLN:HG3	1.80	0.62
1:G:253:GLY:O	1:G:257:PHE:CE2	2.51	0.62
1:H:102:ARG:HG3	1:H:103:PRO:HD2	1.82	0.62
1:J:14:ARG:HD2	1:J:17:GLN:OE1	2.00	0.62
1:B:124:ALA:HA	1:C:157:ILE:HD13	1.81	0.62
1:I:149:GLU:CD	1:J:113:SER:OG	2.38	0.62
1:J:113:SER:HB2	1:J:115:LEU:H	1.65	0.62
1:L:256:ILE:HD13	1:L:266:MET:HG2	1.80	0.62
1:N:277:GLU:OE1	1:N:281:ARG:HB2	2.00	0.62
1:Q:164:MET:CE	1:Q:200:GLN:NE2	2.62	0.62
1:R:253:GLY:CA	1:R:257:PHE:HE2	2.12	0.62
1:A:164:MET:CE	1:A:200:GLN:NE2	2.62	0.62
1:A:229:LYS:NZ	1:A:230:LEU:O	2.32	0.62
1:F:265:MET:O	1:F:268:ALA:HB3	2.00	0.62
1:F:277:GLU:OE1	1:F:281:ARG:HD3	1.98	0.62
1:L:253:GLY:O	1:L:257:PHE:CE2	2.52	0.62
1:M:70:ARG:NH2	1:M:73:ILE:HD12	2.14	0.62
1:O:283:TYR:O	1:O:286:TYR:CB	2.40	0.62
1:A:224:ILE:HG13	1:A:224:ILE:O	2.00	0.62
1:I:253:GLY:CA	1:I:257:PHE:HE2	2.13	0.62
1:K:107:ARG:NH1	1:K:141:GLN:HG2	2.11	0.62
1:H:212:GLU:HB2	1:D:15:THR:HG21	1.82	0.61
1:F:14:ARG:HD2	1:F:17:GLN:OE1	2.00	0.61
1:F:253:GLY:O	1:F:257:PHE:CD2	2.52	0.61
1:H:33:ASP:OD1	1:C:93:ARG:NH1	2.32	0.61
1:K:265:MET:O	1:K:268:ALA:HB3	1.99	0.61
1:B:285:LEU:HB3	2:B:295:HOH:O	1.98	0.61
1:D:65:THR:CG2	1:D:68:LEU:HD12	2.30	0.61
1:M:224:ILE:O	1:M:224:ILE:HG13	2.01	0.61
1:B:27:LYS:O	1:B:221:PRO:HD3	1.99	0.61
1:G:204:THR:O	1:G:224:ILE:HA	2.00	0.61
1:J:253:GLY:O	1:J:257:PHE:CE2	2.53	0.61
1:R:282:ALA:O	1:R:285:LEU:CD1	2.43	0.61
1:S:197:MET:CE	1:R:110:GLY:HA3	2.30	0.61
1:F:113:SER:HB2	1:F:115:LEU:H	1.65	0.61
1:L:149:GLU:CD	1:K:113:SER:OG	2.39	0.61
1:N:113:SER:HB2	1:N:115:LEU:H	1.66	0.61
1:O:275:HIS:O	1:O:276:ASN:CB	2.47	0.61
1:O:79:PHE:CD2	1:O:100:THR:HG21	2.36	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:229:LYS:NZ	1:T:230:LEU:O	2.33	0.61
1:I:110:GLY:HA3	1:H:197:MET:CE	2.31	0.61
1:R:256:ILE:HD13	1:R:266:MET:HG2	1.83	0.61
1:T:265:MET:O	1:T:268:ALA:HB3	1.99	0.61
1:J:164:MET:CE	1:J:200:GLN:NE2	2.63	0.61
1:J:229:LYS:NZ	1:J:230:LEU:O	2.31	0.61
1:P:229:LYS:NZ	1:P:230:LEU:O	2.32	0.61
1:S:285:LEU:CA	1:S:288:SER:HB3	2.29	0.61
1:T:267:LYS:HA	1:T:270:GLN:HG3	1.81	0.61
1:B:102:ARG:HG3	1:B:103:PRO:CD	2.31	0.61
1:E:253:GLY:O	1:E:257:PHE:CD2	2.54	0.61
1:E:256:ILE:HD13	1:E:266:MET:HG2	1.82	0.61
1:B:182:ARG:HG2	1:B:182:ARG:HH11	1.66	0.61
1:C:182:ARG:HH11	1:C:182:ARG:HG2	1.66	0.61
1:C:275:HIS:O	1:C:276:ASN:CB	2.46	0.61
1:K:204:THR:O	1:K:224:ILE:HA	2.00	0.61
1:L:204:THR:O	1:L:224:ILE:HA	2.01	0.61
1:P:27:LYS:O	1:P:221:PRO:HD3	2.01	0.61
1:Q:65:THR:CG2	1:Q:68:LEU:HD12	2.31	0.61
1:F:149:GLU:CD	1:G:113:SER:OG	2.38	0.61
1:I:58:HIS:O	1:I:62:GLN:HB2	2.01	0.61
1:F:111:ALA:H	1:J:197:MET:HE1	1.66	0.61
1:M:283:TYR:O	1:M:283:TYR:CD2	2.54	0.61
1:N:14:ARG:HD2	1:N:17:GLN:OE1	2.00	0.61
1:N:275:HIS:O	1:N:276:ASN:CB	2.48	0.61
1:B:65:THR:HB	1:B:68:LEU:CD1	2.30	0.60
1:H:277:GLU:OE1	1:H:281:ARG:HD3	2.01	0.60
1:I:113:SER:HB2	1:I:115:LEU:H	1.66	0.60
1:I:224:ILE:O	1:I:224:ILE:HG13	2.00	0.60
1:R:285:LEU:HD22	1:R:285:LEU:O	1.99	0.60
1:S:110:GLY:O	1:S:111:ALA:HB3	2.01	0.60
1:A:256:ILE:HD13	1:A:266:MET:HG2	1.83	0.60
1:C:113:SER:OG	1:D:149:GLU:CD	2.40	0.60
1:C:191:THR:HG22	1:C:202:ILE:HG21	1.82	0.60
1:I:285:LEU:HD22	1:I:286:TYR:N	2.16	0.60
1:N:189:LEU:O	1:N:193:ILE:HG13	2.01	0.60
1:Q:283:TYR:HD2	1:Q:283:TYR:C	2.04	0.60
1:J:15:THR:CG2	1:A:212:GLU:HB3	2.31	0.60
1:L:239:CYS:SG	1:L:252:MET:HE1	2.31	0.60
1:L:70:ARG:NH2	1:L:73:ILE:HD12	2.15	0.60
1:O:65:THR:CG2	1:O:68:LEU:HD12	2.32	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:GLU:OE1	1:A:281:ARG:HB2	1.97	0.60
1:F:285:LEU:HD22	1:F:286:TYR:N	2.16	0.60
1:H:113:SER:HB2	1:H:115:LEU:H	1.66	0.60
1:H:204:THR:O	1:H:224:ILE:HA	2.01	0.60
1:K:283:TYR:O	1:K:283:TYR:CD2	2.54	0.60
1:Q:265:MET:O	1:Q:268:ALA:HB3	2.01	0.60
1:N:283:TYR:O	1:N:286:TYR:CB	2.43	0.60
1:P:182:ARG:HH11	1:P:182:ARG:HG2	1.67	0.60
1:Q:254:ARG:O	1:Q:258:GLN:HB2	2.02	0.60
1:R:27:LYS:O	1:R:221:PRO:HD3	2.01	0.60
1:S:204:THR:O	1:S:224:ILE:HA	2.01	0.60
1:B:282:ALA:O	1:B:285:LEU:CD1	2.43	0.60
1:I:239:CYS:HG	1:I:252:MET:HE2	1.61	0.60
1:K:224:ILE:HG13	1:K:224:ILE:O	2.00	0.60
1:B:113:SER:HB2	1:B:115:LEU:H	1.64	0.60
1:I:265:MET:O	1:I:268:ALA:HB3	2.01	0.60
1:Q:256:ILE:HD13	1:Q:266:MET:HG2	1.81	0.60
1:S:254:ARG:O	1:S:258:GLN:HB2	2.02	0.60
1:C:65:THR:CG2	1:C:68:LEU:HD12	2.32	0.60
1:H:100:THR:HG23	2:H:308:HOH:O	2.01	0.60
1:H:229:LYS:NZ	1:H:230:LEU:O	2.34	0.60
1:J:275:HIS:O	1:J:276:ASN:CB	2.49	0.60
1:M:277:GLU:OE1	1:M:281:ARG:HB2	1.99	0.60
1:D:204:THR:O	1:D:224:ILE:HA	2.01	0.60
1:G:164:MET:CE	1:G:200:GLN:NE2	2.65	0.60
1:P:113:SER:HB2	1:P:115:LEU:H	1.66	0.60
1:S:253:GLY:O	1:S:257:PHE:CD2	2.55	0.60
1:T:122:ALA:HA	2:T:298:HOH:O	2.00	0.60
1:D:165:LYS:CE	2:D:308:HOH:O	2.49	0.60
1:N:285:LEU:CA	1:N:288:SER:HB3	2.30	0.60
1:E:110:GLY:HA3	1:A:197:MET:CE	2.32	0.59
1:A:253:GLY:O	1:A:257:PHE:CE2	2.55	0.59
1:H:256:ILE:HD13	1:H:266:MET:HG2	1.83	0.59
1:O:256:ILE:HD13	1:O:266:MET:HG2	1.84	0.59
1:O:285:LEU:HD22	1:O:286:TYR:N	2.17	0.59
1:A:275:HIS:O	1:A:276:ASN:CB	2.47	0.59
1:C:45:ASN:O	1:C:49:GLY:N	2.30	0.59
1:D:113:SER:HB2	1:D:115:LEU:H	1.66	0.59
1:E:283:TYR:C	1:E:283:TYR:HD2	2.05	0.59
1:H:191:THR:HG22	1:H:202:ILE:CG2	2.31	0.59
1:H:65:THR:HB	1:H:68:LEU:CD1	2.31	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:277:GLU:OE1	1:K:281:ARG:HB2	2.01	0.59
1:Q:224:ILE:O	1:Q:224:ILE:HG13	2.01	0.59
1:Q:239:CYS:SG	1:Q:252:MET:HE3	2.39	0.59
1:Q:277:GLU:OE1	1:Q:281:ARG:HD3	2.01	0.59
1:D:79:PHE:CD2	1:D:100:THR:HG21	2.36	0.59
1:E:277:GLU:OE1	1:E:281:ARG:HB2	2.01	0.59
1:H:27:LYS:O	1:H:221:PRO:HD3	2.02	0.59
1:H:275:HIS:O	1:H:276:ASN:CB	2.46	0.59
1:K:275:HIS:O	1:K:276:ASN:CB	2.45	0.59
1:L:182:ARG:HH11	1:L:182:ARG:HG2	1.66	0.59
1:O:27:LYS:O	1:O:221:PRO:HD3	2.02	0.59
1:E:65:THR:CG2	1:E:68:LEU:HD12	2.32	0.59
1:G:265:MET:O	1:G:268:ALA:HB3	2.03	0.59
1:J:27:LYS:O	1:J:221:PRO:HD3	2.02	0.59
1:K:50:LYS:HA	1:K:248:SER:O	2.03	0.59
1:R:81:HIS:O	1:R:266:MET:HE2	2.02	0.59
1:M:113:SER:HB2	1:M:115:LEU:H	1.66	0.59
1:M:275:HIS:O	1:M:276:ASN:CB	2.46	0.59
1:N:253:GLY:O	1:N:257:PHE:CE2	2.55	0.59
1:O:70:ARG:NH2	1:O:73:ILE:CD1	2.64	0.59
1:P:253:GLY:O	1:P:257:PHE:CD2	2.56	0.59
1:M:14:ARG:HD2	1:M:17:GLN:OE1	2.01	0.59
1:T:285:LEU:HD22	1:T:286:TYR:N	2.17	0.59
1:B:113:SER:OG	1:C:149:GLU:OE2	2.20	0.59
1:D:253:GLY:O	1:D:257:PHE:CE2	2.53	0.59
1:D:93:ARG:CZ	1:D:133:LEU:HD21	2.32	0.59
1:O:58:HIS:O	1:O:62:GLN:HB2	2.03	0.59
1:P:105:VAL:HG22	1:P:137:ALA:HB3	1.84	0.59
1:P:283:TYR:O	1:P:283:TYR:CD2	2.56	0.59
1:R:14:ARG:HD2	1:R:17:GLN:OE1	2.02	0.59
1:B:76:ALA:N	1:B:77:PRO:HD2	2.17	0.59
1:H:265:MET:O	1:H:268:ALA:HB3	2.03	0.59
1:J:93:ARG:NH1	1:E:33:ASP:OD1	2.35	0.59
1:M:65:THR:CG2	1:M:68:LEU:HD12	2.33	0.59
1:N:253:GLY:C	1:N:257:PHE:HE2	2.04	0.59
1:E:110:GLY:HA3	1:A:197:MET:HE3	1.85	0.59
1:B:113:SER:OG	1:C:149:GLU:CD	2.41	0.59
1:B:265:MET:O	1:B:268:ALA:HB3	2.01	0.59
1:C:253:GLY:CA	1:C:257:PHE:HE2	2.16	0.59
1:G:282:ALA:O	1:G:285:LEU:CD1	2.45	0.59
1:H:164:MET:CE	1:H:200:GLN:NE2	2.66	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:204:THR:O	1:N:224:ILE:HA	2.02	0.59
1:O:211:PHE:HB3	1:O:245:GLN:OE1	2.01	0.59
1:S:14:ARG:HD2	1:S:17:GLN:OE1	2.01	0.59
1:E:182:ARG:HG2	1:E:182:ARG:HH11	1.68	0.59
1:E:265:MET:O	1:E:268:ALA:HB3	2.02	0.59
1:G:76:ALA:N	1:G:77:PRO:HD2	2.17	0.59
1:O:113:SER:HB2	1:O:115:LEU:H	1.67	0.59
1:O:253:GLY:O	1:O:257:PHE:CD2	2.56	0.59
1:S:102:ARG:HG3	1:S:103:PRO:CD	2.32	0.59
1:F:58:HIS:H	1:F:58:HIS:CD2	2.20	0.58
1:G:182:ARG:HH11	1:G:182:ARG:HG2	1.67	0.58
1:K:60:TYR:OH	1:K:121:GLU:OE2	2.17	0.58
1:M:45:ASN:O	1:M:49:GLY:N	2.34	0.58
1:D:164:MET:CE	1:D:200:GLN:NE2	2.67	0.58
1:F:93:ARG:NH1	1:A:33:ASP:OD1	2.37	0.58
1:H:105:VAL:HG22	1:H:137:ALA:HB3	1.84	0.58
1:J:182:ARG:HG2	1:J:182:ARG:HH11	1.68	0.58
1:S:239:CYS:HG	1:S:252:MET:CE	2.13	0.58
1:G:212:GLU:HB3	1:C:15:THR:HG22	1.85	0.58
1:E:164:MET:HE1	1:E:200:GLN:HE22	1.68	0.58
1:E:197:MET:HE2	1:D:111:ALA:H	1.67	0.58
1:L:275:HIS:O	1:L:276:ASN:CB	2.48	0.58
1:R:107:ARG:NH1	1:R:141:GLN:HG2	2.08	0.58
1:C:283:TYR:O	1:C:283:TYR:CD2	2.57	0.58
1:C:285:LEU:CD2	1:C:285:LEU:O	2.51	0.58
1:F:229:LYS:NZ	1:F:230:LEU:O	2.36	0.58
1:H:283:TYR:C	1:H:283:TYR:HD2	2.04	0.58
1:I:125:LEU:CD1	1:I:125:LEU:O	2.43	0.58
1:I:275:HIS:O	1:I:276:ASN:CB	2.49	0.58
1:C:164:MET:CE	1:C:200:GLN:NE2	2.66	0.58
1:G:110:GLY:O	1:G:111:ALA:HB3	2.04	0.58
1:N:234:GLU:CD	1:G:281:ARG:NH2	2.57	0.58
1:H:239:CYS:SG	1:H:252:MET:HE2	2.35	0.58
1:O:50:LYS:HA	1:O:248:SER:O	2.03	0.58
1:P:265:MET:O	1:P:268:ALA:HB3	2.04	0.58
1:R:56:PHE:N	1:R:56:PHE:CD2	2.72	0.58
1:T:182:ARG:HH11	1:T:182:ARG:HG2	1.68	0.58
1:D:27:LYS:O	1:D:221:PRO:HD3	2.03	0.58
1:R:164:MET:CE	1:R:200:GLN:NE2	2.67	0.58
1:S:164:MET:CE	1:S:200:GLN:NE2	2.66	0.58
1:F:76:ALA:N	1:F:77:PRO:HD2	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:M:111:ALA:H	1:N:197:MET:HE1	1.68	0.58
1:T:164:MET:CE	1:T:200:GLN:NE2	2.67	0.58
1:I:182:ARG:HG2	1:I:182:ARG:HH11	1.68	0.58
1:L:157:ILE:HD13	1:K:124:ALA:HA	1.86	0.58
1:S:113:SER:OG	1:T:149:GLU:OE2	2.20	0.58
1:T:253:GLY:C	1:T:257:PHE:HE2	1.95	0.58
1:A:50:LYS:HA	1:A:248:SER:O	2.03	0.58
1:A:283:TYR:CD2	1:A:283:TYR:O	2.57	0.58
1:I:110:GLY:HA3	1:H:197:MET:HE3	1.86	0.58
1:I:27:LYS:O	1:I:221:PRO:HD3	2.04	0.58
1:L:224:ILE:HG13	1:L:224:ILE:O	2.02	0.58
1:M:283:TYR:C	1:M:283:TYR:HD2	2.07	0.58
1:R:253:GLY:C	1:R:257:PHE:HE2	2.06	0.58
1:A:283:TYR:HD2	1:A:283:TYR:C	2.07	0.58
1:D:70:ARG:NH2	1:D:73:ILE:CD1	2.67	0.58
1:M:189:LEU:O	1:M:193:ILE:HG13	2.04	0.58
1:P:144:ILE:HG22	1:T:115:LEU:HD12	1.86	0.58
1:S:124:ALA:HA	1:T:157:ILE:HD13	1.85	0.58
1:G:275:HIS:O	1:G:276:ASN:CB	2.51	0.57
1:G:79:PHE:CD2	1:G:100:THR:HG21	2.39	0.57
1:O:157:ILE:HD13	1:N:124:ALA:HA	1.85	0.57
1:N:254:ARG:O	1:N:258:GLN:HB2	2.04	0.57
1:P:189:LEU:O	1:P:193:ILE:HG13	2.04	0.57
1:R:285:LEU:CA	1:R:288:SER:HB3	2.31	0.57
1:S:110:GLY:HA3	1:T:197:MET:HE1	1.85	0.57
1:G:277:GLU:OE1	1:G:281:ARG:HB2	2.03	0.57
1:O:110:GLY:HA3	1:K:197:MET:CE	2.34	0.57
1:Q:233:ARG:NH1	1:Q:233:ARG:CG	2.48	0.57
1:R:182:ARG:HH11	1:R:182:ARG:HG2	1.70	0.57
1:T:283:TYR:HD2	1:T:283:TYR:C	2.07	0.57
1:C:189:LEU:O	1:C:193:ILE:HG13	2.04	0.57
1:H:93:ARG:NH1	1:C:33:ASP:OD1	2.36	0.57
1:C:110:GLY:HA3	1:D:197:MET:CE	2.34	0.57
1:E:105:VAL:HG22	1:E:137:ALA:HB3	1.85	0.57
1:K:283:TYR:HD2	1:K:283:TYR:C	2.07	0.57
1:L:110:GLY:HA3	1:M:197:MET:CE	2.34	0.57
1:N:213:ARG:NH1	2:N:293:HOH:O	2.37	0.57
1:S:197:MET:HE1	1:R:111:ALA:H	1.70	0.57
1:B:197:MET:HE1	1:A:111:ALA:H	1.70	0.57
1:G:65:THR:CG2	1:G:68:LEU:HD12	2.35	0.57
1:L:283:TYR:CD2	1:L:283:TYR:O	2.58	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:113:SER:OG	1:M:149:GLU:OE2	2.22	0.57
1:T:110:GLY:O	1:T:111:ALA:HB3	2.05	0.57
1:T:253:GLY:O	1:T:257:PHE:CD2	2.57	0.57
1:A:182:ARG:HH11	1:A:182:ARG:HG2	1.70	0.57
1:L:58:HIS:H	1:L:58:HIS:CD2	2.20	0.57
1:M:253:GLY:O	1:M:257:PHE:CE2	2.56	0.57
1:N:27:LYS:O	1:N:221:PRO:HD3	2.04	0.57
1:O:229:LYS:NZ	1:O:230:LEU:O	2.33	0.57
1:A:204:THR:O	1:A:224:ILE:HA	2.04	0.57
1:B:275:HIS:O	1:B:276:ASN:CB	2.52	0.57
1:G:65:THR:HB	1:G:68:LEU:CD1	2.29	0.57
1:P:110:GLY:HA3	1:Q:197:MET:CE	2.35	0.57
1:A:45:ASN:O	1:A:49:GLY:N	2.38	0.57
1:B:239:CYS:HG	1:B:252:MET:CE	2.09	0.57
1:C:58:HIS:O	1:C:62:GLN:HB2	2.05	0.57
1:M:102:ARG:HG3	1:M:103:PRO:CD	2.34	0.57
1:O:105:VAL:HG22	1:O:137:ALA:HB3	1.87	0.57
1:T:27:LYS:O	1:T:221:PRO:HD3	2.05	0.57
1:B:211:PHE:HB3	1:B:245:GLN:OE1	2.03	0.57
1:R:253:GLY:O	1:R:257:PHE:CE2	2.58	0.57
1:S:197:MET:HE1	1:R:110:GLY:HA3	1.86	0.57
1:H:76:ALA:N	1:H:77:PRO:HD2	2.20	0.57
1:I:189:LEU:O	1:I:193:ILE:HG13	2.05	0.57
1:M:256:ILE:HD13	1:M:266:MET:HG2	1.86	0.57
1:R:211:PHE:HB3	1:R:245:GLN:OE1	2.05	0.57
1:T:76:ALA:N	1:T:77:PRO:HD2	2.20	0.57
1:G:239:CYS:SG	1:G:252:MET:HE1	2.41	0.57
1:H:285:LEU:HD22	1:H:286:TYR:N	2.19	0.57
1:J:253:GLY:O	1:J:257:PHE:CD2	2.58	0.57
1:O:110:GLY:HA3	1:K:197:MET:HE3	1.87	0.57
1:L:164:MET:CE	1:L:200:GLN:NE2	2.68	0.57
1:O:76:ALA:N	1:O:77:PRO:HD2	2.19	0.57
1:Q:253:GLY:CA	1:Q:257:PHE:CE2	2.84	0.57
1:T:275:HIS:O	1:T:276:ASN:CB	2.51	0.57
1:G:224:ILE:HG13	1:G:224:ILE:O	2.04	0.56
1:I:211:PHE:HB3	1:I:245:GLN:OE1	2.04	0.56
1:I:70:ARG:NH2	1:I:73:ILE:HD12	2.19	0.56
1:I:197:MET:HE3	1:J:110:GLY:HA3	1.87	0.56
1:J:254:ARG:O	1:J:258:GLN:HB2	2.04	0.56
1:K:253:GLY:CA	1:K:257:PHE:CE2	2.83	0.56
1:P:196:GLU:OE2	1:T:91:ILE:HG13	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:S:283:TYR:O	1:S:283:TYR:CD2	2.57	0.56
1:E:261:HIS:CG	1:E:290:LYS:HG2	2.40	0.56
1:E:65:THR:HB	1:E:68:LEU:CD1	2.33	0.56
1:F:164:MET:CE	1:F:200:GLN:NE2	2.68	0.56
1:G:189:LEU:O	1:G:193:ILE:HG13	2.05	0.56
1:L:76:ALA:N	1:L:77:PRO:HD2	2.20	0.56
1:M:265:MET:O	1:M:268:ALA:HB3	2.06	0.56
1:N:224:ILE:O	1:N:224:ILE:HG13	2.05	0.56
1:N:50:LYS:HA	1:N:248:SER:O	2.05	0.56
1:C:283:TYR:C	1:C:283:TYR:HD2	2.08	0.56
1:G:253:GLY:O	1:G:257:PHE:CD2	2.58	0.56
1:K:76:ALA:N	1:K:77:PRO:HD2	2.19	0.56
1:O:204:THR:O	1:O:224:ILE:HA	2.05	0.56
1:P:211:PHE:HB3	1:P:245:GLN:OE1	2.04	0.56
1:D:211:PHE:HB3	1:D:245:GLN:OE1	2.06	0.56
1:E:197:MET:CE	1:D:110:GLY:HA3	2.34	0.56
1:J:65:THR:HB	1:J:68:LEU:CD1	2.29	0.56
1:P:285:LEU:HD22	1:P:286:TYR:N	2.20	0.56
1:H:211:PHE:HB3	1:H:245:GLN:OE1	2.05	0.56
1:J:212:GLU:CB	1:A:15:THR:HG21	2.34	0.56
1:K:254:ARG:O	1:K:258:GLN:HB2	2.06	0.56
1:M:229:LYS:NZ	1:M:230:LEU:O	2.36	0.56
1:Q:110:GLY:HA3	1:R:197:MET:CE	2.35	0.56
1:T:224:ILE:HG13	1:T:224:ILE:O	2.04	0.56
1:K:182:ARG:HG2	1:K:182:ARG:HH11	1.69	0.56
1:N:164:MET:CE	1:N:200:GLN:NE2	2.68	0.56
1:N:45:ASN:O	1:N:49:GLY:N	2.36	0.56
1:O:261:HIS:CG	1:O:290:LYS:HG2	2.40	0.56
1:P:124:ALA:HA	1:Q:157:ILE:HD13	1.87	0.56
1:P:283:TYR:HD2	1:P:283:TYR:C	2.08	0.56
1:P:93:ARG:CZ	1:P:133:LEU:HD21	2.36	0.56
1:S:109:SER:HB2	1:S:121:GLU:OE1	2.06	0.56
1:T:285:LEU:O	1:T:285:LEU:CD2	2.51	0.56
1:T:65:THR:HB	1:T:68:LEU:CD1	2.31	0.56
1:A:211:PHE:HB3	1:A:245:GLN:OE1	2.06	0.56
1:M:58:HIS:O	1:M:62:GLN:HB2	2.05	0.56
1:R:102:ARG:HG3	1:R:103:PRO:CD	2.36	0.56
1:R:224:ILE:HG13	1:R:224:ILE:O	2.06	0.56
1:S:149:GLU:CD	1:R:113:SER:OG	2.43	0.56
1:T:204:THR:O	1:T:224:ILE:HA	2.06	0.56
1:B:50:LYS:HA	1:B:248:SER:O	2.05	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:107:ARG:NH1	1:C:141:GLN:HG2	2.10	0.56
1:G:211:PHE:HB3	1:G:245:GLN:OE1	2.04	0.56
1:J:102:ARG:HG3	1:J:103:PRO:CD	2.36	0.56
1:L:277:GLU:OE1	1:L:281:ARG:HB2	2.01	0.56
1:M:164:MET:CE	1:M:200:GLN:NE2	2.67	0.56
1:M:285:LEU:CD2	1:M:285:LEU:O	2.54	0.56
1:O:184:GLN:NE2	1:O:185:ARG:HA	2.21	0.56
1:S:224:ILE:O	1:S:224:ILE:HG13	2.04	0.56
1:G:33:ASP:OD1	1:B:93:ARG:NH1	2.39	0.56
1:E:113:SER:HB2	1:E:115:LEU:H	1.70	0.56
1:E:76:ALA:N	1:E:77:PRO:HD2	2.21	0.56
1:F:263:VAL:O	1:F:267:LYS:HG3	2.05	0.56
1:F:45:ASN:O	1:F:49:GLY:N	2.37	0.56
1:I:65:THR:HB	1:I:68:LEU:CD1	2.29	0.56
1:T:238:MET:CE	2:T:296:HOH:O	2.53	0.56
1:B:204:THR:O	1:B:224:ILE:HA	2.06	0.56
1:D:109:SER:HB2	1:D:121:GLU:OE1	2.06	0.56
1:K:102:ARG:HG3	1:K:103:PRO:CD	2.36	0.56
1:L:253:GLY:O	1:L:257:PHE:CD2	2.59	0.56
1:N:110:GLY:O	1:N:111:ALA:HB3	2.06	0.56
1:N:184:GLN:NE2	1:N:185:ARG:HA	2.21	0.56
1:Q:204:THR:O	1:Q:224:ILE:HA	2.06	0.56
1:S:229:LYS:NZ	1:S:230:LEU:O	2.38	0.56
1:D:58:HIS:H	1:D:58:HIS:CD2	2.23	0.56
1:K:287:LEU:HA	1:K:290:LYS:HD3	1.88	0.56
1:M:125:LEU:CD1	1:M:125:LEU:O	2.47	0.56
1:F:197:MET:CE	1:G:110:GLY:HA3	2.36	0.55
1:I:45:ASN:O	1:I:49:GLY:N	2.38	0.55
1:J:107:ARG:NH1	1:J:141:GLN:HG2	2.17	0.55
1:K:65:THR:HB	1:K:68:LEU:CD1	2.29	0.55
1:T:283:TYR:O	1:T:283:TYR:CD2	2.59	0.55
1:B:110:GLY:HA3	1:C:197:MET:CE	2.36	0.55
1:F:182:ARG:HH11	1:F:182:ARG:HG2	1.71	0.55
1:G:113:SER:HB2	1:G:115:LEU:H	1.71	0.55
1:G:283:TYR:C	1:G:283:TYR:HD2	2.09	0.55
1:H:50:LYS:HA	1:H:248:SER:O	2.06	0.55
1:K:65:THR:CG2	1:K:68:LEU:HD12	2.35	0.55
1:N:253:GLY:O	1:N:257:PHE:CD2	2.58	0.55
1:B:197:MET:CE	1:A:110:GLY:HA3	2.35	0.55
1:B:285:LEU:HD22	1:B:286:TYR:N	2.21	0.55
1:C:211:PHE:HB3	1:C:245:GLN:OE1	2.06	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:283:TYR:C	1:N:283:TYR:HD2	2.09	0.55
1:S:45:ASN:O	1:S:49:GLY:N	2.39	0.55
1:C:105:VAL:HG22	1:C:137:ALA:HB3	1.89	0.55
1:D:256:ILE:HD13	1:D:266:MET:HG2	1.88	0.55
1:J:33:ASP:OD1	1:E:93:ARG:NH1	2.39	0.55
1:F:254:ARG:O	1:F:258:GLN:HB2	2.06	0.55
1:F:70:ARG:NH2	1:F:73:ILE:CD1	2.70	0.55
1:N:234:GLU:CD	1:G:281:ARG:NH1	2.55	0.55
1:H:58:HIS:CD2	1:H:58:HIS:H	2.23	0.55
1:L:211:PHE:HB3	1:L:245:GLN:OE1	2.06	0.55
1:L:263:VAL:O	1:L:267:LYS:HG3	2.06	0.55
1:M:182:ARG:HH11	1:M:182:ARG:HG2	1.71	0.55
1:O:196:GLU:HG3	1:N:88:THR:HG21	1.87	0.55
1:R:229:LYS:NZ	1:R:230:LEU:O	2.39	0.55
1:B:93:ARG:CZ	1:B:133:LEU:HD21	2.36	0.55
1:C:113:SER:HB2	1:C:115:LEU:H	1.71	0.55
1:D:105:VAL:HG22	1:D:137:ALA:HB3	1.87	0.55
1:D:275:HIS:O	1:D:276:ASN:CB	2.46	0.55
1:D:58:HIS:O	1:D:62:GLN:HB2	2.06	0.55
1:G:45:ASN:O	1:G:49:GLY:N	2.39	0.55
1:I:113:SER:OG	1:H:149:GLU:OE2	2.24	0.55
1:J:165:LYS:HB3	2:J:296:HOH:O	2.06	0.55
1:N:93:ARG:CZ	1:N:133:LEU:HD21	2.37	0.55
1:O:58:HIS:CD2	1:O:58:HIS:H	2.23	0.55
1:P:157:ILE:HD13	1:T:124:ALA:HA	1.89	0.55
1:P:58:HIS:CD2	1:P:58:HIS:H	2.22	0.55
1:R:204:THR:O	1:R:224:ILE:HA	2.07	0.55
1:S:211:PHE:HB3	1:S:245:GLN:OE1	2.07	0.55
1:H:113:SER:OG	1:G:149:GLU:CD	2.45	0.55
1:G:285:LEU:CA	1:G:288:SER:HB3	2.31	0.55
1:H:251:ASP:OD1	1:H:251:ASP:C	2.45	0.55
1:J:283:TYR:O	1:J:283:TYR:CD2	2.59	0.55
1:K:79:PHE:CD2	1:K:100:THR:HG21	2.42	0.55
1:M:65:THR:HB	1:M:68:LEU:CD1	2.33	0.55
1:O:197:MET:HE1	1:N:111:ALA:H	1.70	0.55
1:N:81:HIS:HB2	1:N:266:MET:HE2	1.89	0.55
1:O:164:MET:HE2	1:O:200:GLN:HE22	1.71	0.55
1:P:197:MET:CE	1:T:110:GLY:HA3	2.36	0.55
1:T:58:HIS:O	1:T:62:GLN:HB2	2.06	0.55
1:B:45:ASN:O	1:B:49:GLY:N	2.37	0.55
1:C:50:LYS:HA	1:C:248:SER:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:107:ARG:NH1	1:F:141:GLN:HG2	2.06	0.55
1:F:144:ILE:HA	1:F:149:GLU:HG3	1.89	0.55
1:F:50:LYS:HA	1:F:248:SER:O	2.07	0.55
1:F:58:HIS:O	1:F:62:GLN:HB2	2.07	0.55
1:G:213:ARG:HG2	1:C:13:PHE:CD2	2.42	0.55
1:K:105:VAL:HG22	1:K:137:ALA:HB3	1.88	0.55
1:N:185:ARG:HG2	1:N:186:TYR:N	2.21	0.55
1:Q:229:LYS:NZ	1:Q:230:LEU:O	2.40	0.55
1:D:285:LEU:CD2	1:D:285:LEU:O	2.51	0.55
1:J:204:THR:O	1:J:224:ILE:HA	2.07	0.55
1:M:124:ALA:HA	1:N:157:ILE:HD13	1.89	0.55
1:Q:65:THR:HB	1:Q:68:LEU:CD1	2.32	0.55
1:S:285:LEU:HA	1:S:288:SER:CB	2.31	0.55
1:S:50:LYS:HA	1:S:248:SER:O	2.07	0.55
1:A:76:ALA:N	1:A:77:PRO:HD2	2.22	0.55
1:F:211:PHE:HB3	1:F:245:GLN:OE1	2.07	0.55
1:H:124:ALA:HA	1:G:157:ILE:HD13	1.89	0.55
1:H:285:LEU:CA	1:H:288:SER:HB3	2.33	0.55
1:R:93:ARG:CZ	1:R:133:LEU:HD21	2.37	0.55
1:T:113:SER:HB2	1:T:115:LEU:H	1.72	0.55
1:A:110:GLY:O	1:A:111:ALA:HB3	2.07	0.55
1:D:253:GLY:O	1:D:257:PHE:CD2	2.60	0.55
1:E:110:GLY:O	1:E:111:ALA:HB3	2.06	0.55
1:E:287:LEU:HA	1:E:290:LYS:HD3	1.89	0.55
1:K:211:PHE:HB3	1:K:245:GLN:OE1	2.06	0.55
1:K:253:GLY:O	1:K:257:PHE:CE2	2.60	0.55
1:N:211:PHE:HB3	1:N:245:GLN:OE1	2.07	0.55
1:P:76:ALA:N	1:P:77:PRO:HD2	2.21	0.55
1:T:254:ARG:O	1:T:258:GLN:HB2	2.07	0.55
1:G:233:ARG:NH1	1:G:233:ARG:CG	2.53	0.54
1:G:50:LYS:HA	1:G:248:SER:O	2.06	0.54
1:I:136:CYS:O	1:I:169:PRO:HD2	2.07	0.54
1:I:229:LYS:NZ	1:I:230:LEU:O	2.37	0.54
1:I:76:ALA:N	1:I:77:PRO:HD2	2.21	0.54
1:J:189:LEU:O	1:J:193:ILE:HG13	2.07	0.54
1:N:102:ARG:HG3	1:N:103:PRO:CD	2.36	0.54
1:R:50:LYS:HA	1:R:248:SER:O	2.06	0.54
1:R:254:ARG:O	1:R:258:GLN:HB2	2.07	0.54
1:J:212:GLU:HB3	1:A:15:THR:CG2	2.37	0.54
1:A:277:GLU:OE1	1:A:281:ARG:HD2	2.03	0.54
1:H:253:GLY:O	1:H:257:PHE:CE2	2.61	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:50:LYS:HA	1:L:248:SER:O	2.07	0.54
1:R:58:HIS:CD2	1:R:58:HIS:H	2.24	0.54
1:D:50:LYS:HA	1:D:248:SER:O	2.06	0.54
1:D:283:TYR:CD2	1:D:283:TYR:O	2.60	0.54
1:I:197:MET:CE	1:J:110:GLY:HA3	2.37	0.54
1:J:14:ARG:O	1:J:14:ARG:HG3	2.07	0.54
1:N:45:ASN:OD1	1:N:47:LYS:N	2.39	0.54
1:Q:109:SER:HB2	1:Q:121:GLU:OE1	2.07	0.54
1:A:58:HIS:O	1:A:62:GLN:HB2	2.08	0.54
1:C:76:ALA:N	1:C:77:PRO:HD2	2.23	0.54
1:E:70:ARG:NH2	1:E:73:ILE:CD1	2.71	0.54
1:F:261:HIS:CG	1:F:290:LYS:HG2	2.42	0.54
1:J:70:ARG:NH2	1:J:73:ILE:HD12	2.22	0.54
1:M:211:PHE:HB3	1:M:245:GLN:OE1	2.06	0.54
1:N:239:CYS:SG	1:N:252:MET:HE1	2.32	0.54
1:Q:76:ALA:N	1:Q:77:PRO:HD2	2.22	0.54
1:R:277:GLU:OE1	1:R:281:ARG:HD2	2.07	0.54
1:S:157:ILE:HD13	1:R:124:ALA:HA	1.89	0.54
1:T:261:HIS:CG	1:T:290:LYS:HG2	2.42	0.54
1:C:65:THR:HB	1:C:68:LEU:CD1	2.31	0.54
1:D:76:ALA:N	1:D:77:PRO:HD2	2.22	0.54
1:I:254:ARG:O	1:I:258:GLN:HB2	2.08	0.54
1:K:144:ILE:HA	1:K:149:GLU:HG3	1.87	0.54
1:L:196:GLU:OE2	1:K:91:ILE:HG13	2.07	0.54
1:N:283:TYR:CD2	1:N:283:TYR:O	2.61	0.54
1:S:81:HIS:HB2	1:S:266:MET:HE2	1.89	0.54
1:B:164:MET:HE2	1:B:200:GLN:HE22	1.69	0.54
1:I:99:ALA:HB1	1:D:46:PRO:HB3	1.89	0.54
1:J:110:GLY:O	1:J:111:ALA:HB3	2.07	0.54
1:J:285:LEU:O	1:J:285:LEU:CD2	2.55	0.54
1:Q:184:GLN:NE2	1:Q:185:ARG:HA	2.23	0.54
1:Q:113:SER:OG	1:R:149:GLU:CD	2.46	0.54
1:S:287:LEU:HA	1:S:290:LYS:HD3	1.89	0.54
1:E:164:MET:HE1	1:E:200:GLN:NE2	2.21	0.54
1:F:102:ARG:HG3	1:F:103:PRO:CD	2.38	0.54
1:G:287:LEU:HA	1:G:290:LYS:HD3	1.90	0.54
1:H:287:LEU:HA	1:H:290:LYS:HD3	1.89	0.54
1:L:189:LEU:O	1:L:193:ILE:HG13	2.08	0.54
1:O:224:ILE:HG13	1:O:224:ILE:O	2.07	0.54
1:O:254:ARG:O	1:O:258:GLN:HB2	2.07	0.54
1:R:261:HIS:CG	1:R:290:LYS:HG2	2.43	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ARG:HG3	1:A:103:PRO:CD	2.38	0.54
1:A:144:ILE:HA	1:A:149:GLU:HG3	1.90	0.54
1:F:109:SER:HB2	1:F:121:GLU:OE1	2.08	0.54
1:L:45:ASN:O	1:L:49:GLY:N	2.35	0.54
1:S:184:GLN:NE2	1:S:185:ARG:HA	2.23	0.54
1:A:58:HIS:H	1:A:58:HIS:CD2	2.25	0.54
1:E:224:ILE:HG13	1:E:224:ILE:O	2.06	0.54
1:L:14:ARG:O	1:L:14:ARG:HG3	2.08	0.54
1:M:254:ARG:O	1:M:258:GLN:HB2	2.07	0.54
1:O:149:GLU:OE2	1:N:113:SER:OG	2.25	0.54
1:O:233:ARG:CG	1:O:233:ARG:NH1	2.55	0.54
1:Q:275:HIS:O	1:Q:276:ASN:CB	2.50	0.54
1:T:211:PHE:HB3	1:T:245:GLN:OE1	2.07	0.54
1:D:261:HIS:CG	1:D:290:LYS:HG2	2.43	0.54
1:F:275:HIS:O	1:F:276:ASN:CB	2.49	0.54
1:H:144:ILE:HA	1:H:149:GLU:HG3	1.88	0.54
1:I:144:ILE:HG22	1:J:115:LEU:HD12	1.89	0.54
1:I:204:THR:O	1:I:224:ILE:HA	2.08	0.54
1:L:261:HIS:CG	1:L:290:LYS:HG2	2.43	0.54
1:P:50:LYS:HA	1:P:248:SER:O	2.08	0.54
1:A:65:THR:CG2	1:A:68:LEU:HD12	2.38	0.53
1:C:184:GLN:NE2	1:C:185:ARG:HA	2.22	0.53
1:J:76:ALA:N	1:J:77:PRO:HD2	2.23	0.53
1:O:164:MET:CE	1:O:200:GLN:NE2	2.71	0.53
1:Q:253:GLY:O	1:Q:257:PHE:CE2	2.61	0.53
1:S:113:SER:HB2	1:S:115:LEU:H	1.73	0.53
1:T:277:GLU:OE1	1:T:281:ARG:HD2	2.08	0.53
1:C:110:GLY:HA3	1:D:197:MET:HE1	1.90	0.53
1:F:142:VAL:HA	1:F:152:SER:HB2	1.90	0.53
1:F:157:ILE:HD13	1:G:124:ALA:HA	1.89	0.53
1:J:105:VAL:HG22	1:J:137:ALA:HB3	1.88	0.53
1:M:105:VAL:HG22	1:M:137:ALA:HB3	1.90	0.53
1:O:45:ASN:O	1:O:49:GLY:N	2.39	0.53
1:B:253:GLY:CA	1:B:257:PHE:CE2	2.90	0.53
1:E:50:LYS:HA	1:E:248:SER:O	2.08	0.53
1:E:58:HIS:CD2	1:E:58:HIS:H	2.26	0.53
1:G:58:HIS:H	1:G:58:HIS:CD2	2.25	0.53
1:J:224:ILE:O	1:J:224:ILE:HG13	2.09	0.53
1:J:285:LEU:HD22	1:J:286:TYR:N	2.20	0.53
1:L:142:VAL:HA	1:L:152:SER:HB2	1.89	0.53
1:N:58:HIS:CD2	1:N:58:HIS:H	2.24	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:184:GLN:NE2	1:P:185:ARG:HA	2.23	0.53
1:Q:110:GLY:HA3	1:R:197:MET:HE3	1.91	0.53
1:S:283:TYR:O	1:S:286:TYR:CB	2.45	0.53
1:S:70:ARG:NH2	1:S:73:ILE:CD1	2.72	0.53
1:I:197:MET:HE1	1:J:111:ALA:H	1.74	0.53
1:M:204:THR:O	1:M:224:ILE:HA	2.08	0.53
1:E:113:SER:HG	1:A:149:GLU:CD	2.12	0.53
1:A:263:VAL:O	1:A:267:LYS:HG3	2.08	0.53
1:C:164:MET:HE2	1:C:200:GLN:HE22	1.72	0.53
1:D:125:LEU:O	1:D:125:LEU:CD1	2.45	0.53
1:D:144:ILE:HA	1:D:149:GLU:HG3	1.91	0.53
1:I:109:SER:HB2	1:I:121:GLU:OE1	2.08	0.53
1:A:65:THR:HB	1:A:68:LEU:CD1	2.31	0.53
1:D:184:GLN:NE2	1:D:185:ARG:HA	2.24	0.53
1:C:111:ALA:H	1:D:197:MET:HE2	1.74	0.53
1:D:283:TYR:HD2	1:D:283:TYR:C	2.12	0.53
1:G:263:VAL:O	1:G:267:LYS:HG3	2.08	0.53
1:H:224:ILE:HG13	1:H:224:ILE:O	2.09	0.53
1:I:50:LYS:HA	1:I:248:SER:O	2.09	0.53
1:J:58:HIS:H	1:J:58:HIS:CD2	2.24	0.53
1:L:287:LEU:HA	1:L:290:LYS:HD3	1.91	0.53
1:C:185:ARG:HG2	1:C:186:TYR:N	2.24	0.53
1:C:254:ARG:O	1:C:258:GLN:HB2	2.09	0.53
1:D:239:CYS:SG	1:D:252:MET:HE1	2.37	0.53
1:D:45:ASN:OD1	1:D:47:LYS:N	2.41	0.53
1:E:125:LEU:O	1:E:125:LEU:CD1	2.49	0.53
1:F:56:PHE:CD2	1:F:56:PHE:N	2.77	0.53
1:F:65:THR:CG2	1:F:68:LEU:HD12	2.39	0.53
1:H:110:GLY:HA3	1:G:197:MET:CE	2.39	0.53
1:M:76:ALA:N	1:M:77:PRO:HD2	2.22	0.53
1:M:91:ILE:HG13	1:N:196:GLU:OE2	2.09	0.53
1:O:149:GLU:CD	1:N:113:SER:OG	2.46	0.53
1:A:254:ARG:O	1:A:258:GLN:HB2	2.08	0.53
1:B:263:VAL:O	1:B:267:LYS:HG3	2.09	0.53
1:D:189:LEU:O	1:D:193:ILE:HG13	2.09	0.53
1:F:185:ARG:HG2	1:F:186:TYR:N	2.24	0.53
1:G:105:VAL:HG22	1:G:137:ALA:HB3	1.91	0.53
1:H:126:SER:HB2	2:H:305:HOH:O	2.08	0.53
1:H:81:HIS:HB2	1:H:266:MET:HE2	1.91	0.53
1:J:58:HIS:O	1:J:62:GLN:HB2	2.08	0.53
1:J:93:ARG:CZ	1:J:133:LEU:HD21	2.39	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:65:THR:CG2	1:N:68:LEU:HD12	2.39	0.53
1:A:261:HIS:CG	1:A:290:LYS:HG2	2.44	0.53
1:K:58:HIS:CD2	1:K:58:HIS:H	2.25	0.53
1:R:265:MET:O	1:R:268:ALA:HB3	2.09	0.53
1:T:14:ARG:HG3	1:T:14:ARG:O	2.09	0.53
1:A:285:LEU:HD22	1:A:286:TYR:N	2.24	0.53
1:B:105:VAL:HG22	1:B:137:ALA:HB3	1.91	0.53
1:E:45:ASN:O	1:E:49:GLY:N	2.41	0.53
1:G:283:TYR:O	1:G:283:TYR:CD2	2.62	0.53
1:K:184:GLN:NE2	1:K:185:ARG:HA	2.24	0.53
1:L:265:MET:O	1:L:268:ALA:HB3	2.08	0.53
1:N:287:LEU:HA	1:N:290:LYS:HD3	1.91	0.53
1:Q:164:MET:HE1	1:Q:200:GLN:NE2	2.24	0.53
1:S:283:TYR:C	1:S:283:TYR:HD2	2.10	0.53
1:T:189:LEU:O	1:T:193:ILE:HG13	2.09	0.53
1:T:45:ASN:O	1:T:49:GLY:N	2.40	0.53
1:F:35:GLY:HA3	1:A:132:ARG:O	2.08	0.52
1:B:229:LYS:NZ	1:B:230:LEU:O	2.38	0.52
1:B:110:GLY:HA3	1:C:197:MET:HE2	1.92	0.52
1:E:142:VAL:HA	1:E:152:SER:HB2	1.91	0.52
1:F:283:TYR:O	1:F:283:TYR:CD2	2.62	0.52
1:H:263:VAL:O	1:H:267:LYS:HG3	2.09	0.52
1:I:283:TYR:O	1:I:283:TYR:CD2	2.63	0.52
1:I:56:PHE:N	1:I:56:PHE:CD2	2.77	0.52
1:R:189:LEU:O	1:R:193:ILE:HG13	2.09	0.52
1:T:238:MET:HE3	2:T:296:HOH:O	2.09	0.52
1:A:253:GLY:O	1:A:257:PHE:CD2	2.61	0.52
1:D:191:THR:HG22	1:D:202:ILE:CG2	2.39	0.52
1:F:14:ARG:HG3	1:F:14:ARG:O	2.08	0.52
1:F:65:THR:HB	1:F:68:LEU:CD1	2.31	0.52
1:F:79:PHE:CD2	1:F:100:THR:HG21	2.44	0.52
1:L:197:MET:CE	1:K:110:GLY:HA3	2.40	0.52
1:Q:211:PHE:HB3	1:Q:245:GLN:OE1	2.10	0.52
1:Q:88:THR:HA	2:Q:300:HOH:O	2.10	0.52
1:S:261:HIS:CG	1:S:290:LYS:HG2	2.43	0.52
1:T:50:LYS:HA	1:T:248:SER:O	2.09	0.52
1:B:109:SER:HB2	1:B:121:GLU:OE1	2.10	0.52
1:C:224:ILE:O	1:C:224:ILE:HG13	2.09	0.52
1:H:110:GLY:O	1:H:111:ALA:HB3	2.10	0.52
1:L:110:GLY:HA3	1:M:197:MET:HE1	1.90	0.52
1:M:56:PHE:CD2	1:M:56:PHE:N	2.76	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:45:ASN:OD1	1:P:47:LYS:N	2.42	0.52
1:Q:50:LYS:HA	1:Q:248:SER:O	2.08	0.52
1:C:229:LYS:NZ	1:C:230:LEU:O	2.40	0.52
1:C:33:ASP:HB3	2:C:307:HOH:O	2.09	0.52
1:F:105:VAL:HG22	1:F:137:ALA:HB3	1.91	0.52
1:I:253:GLY:O	1:I:257:PHE:CE2	2.62	0.52
1:N:65:THR:HB	1:N:68:LEU:CD1	2.34	0.52
1:Q:113:SER:HB2	1:Q:115:LEU:H	1.75	0.52
1:R:113:SER:HB2	1:R:115:LEU:H	1.74	0.52
1:S:142:VAL:HA	1:S:152:SER:HB2	1.90	0.52
1:S:93:ARG:CZ	1:S:133:LEU:HD21	2.39	0.52
1:D:229:LYS:NZ	1:D:230:LEU:O	2.39	0.52
1:E:157:ILE:HD13	1:D:124:ALA:HA	1.92	0.52
1:I:196:GLU:OE2	1:J:91:ILE:HG13	2.10	0.52
1:J:45:ASN:OD1	1:J:47:LYS:N	2.42	0.52
1:P:224:ILE:O	1:P:224:ILE:HG13	2.09	0.52
1:R:283:TYR:CD2	1:R:283:TYR:O	2.63	0.52
1:S:76:ALA:N	1:S:77:PRO:HD2	2.24	0.52
1:T:253:GLY:CA	1:T:257:PHE:CE2	2.85	0.52
1:F:224:ILE:HG13	1:F:224:ILE:O	2.09	0.52
1:G:93:ARG:NH1	1:B:33:ASP:OD1	2.43	0.52
1:I:283:TYR:HD2	1:I:283:TYR:C	2.11	0.52
1:I:82:ALA:O	1:I:102:ARG:HD3	2.10	0.52
1:K:82:ALA:O	1:K:102:ARG:HD3	2.10	0.52
1:N:182:ARG:HG2	1:N:182:ARG:NH1	2.22	0.52
1:P:102:ARG:HG3	1:P:103:PRO:CD	2.38	0.52
1:S:125:LEU:O	1:S:125:LEU:CD1	2.51	0.52
1:S:185:ARG:CG	1:S:186:TYR:N	2.72	0.52
1:O:45:ASN:OD1	1:O:47:LYS:N	2.43	0.52
1:Q:285:LEU:HD22	1:Q:286:TYR:N	2.24	0.52
1:R:105:VAL:HG22	1:R:137:ALA:HB3	1.92	0.52
1:D:32:LEU:HD13	1:D:36:MET:SD	2.50	0.52
1:I:105:VAL:HG22	1:I:137:ALA:HB3	1.91	0.52
1:J:109:SER:HB2	1:J:121:GLU:OE1	2.09	0.52
1:O:111:ALA:H	1:K:197:MET:HE1	1.75	0.52
1:K:45:ASN:O	1:K:49:GLY:N	2.41	0.52
1:S:58:HIS:CD2	1:S:58:HIS:H	2.27	0.52
1:A:109:SER:HB2	1:A:121:GLU:OE1	2.09	0.52
1:B:185:ARG:HG2	1:B:186:TYR:N	2.25	0.52
1:M:253:GLY:O	1:M:257:PHE:CD2	2.63	0.52
1:P:287:LEU:HA	1:P:290:LYS:HD3	1.90	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:91:ILE:HG13	1:R:196:GLU:OE2	2.09	0.52
1:A:239:CYS:SG	1:A:252:MET:HE1	2.37	0.52
1:E:144:ILE:HA	1:E:149:GLU:HG3	1.90	0.52
1:G:15:THR:HG21	1:C:212:GLU:HB2	1.90	0.52
1:K:142:VAL:HA	1:K:152:SER:HB2	1.90	0.52
1:O:102:ARG:HG3	1:O:103:PRO:CD	2.40	0.52
1:P:261:HIS:CG	1:P:290:LYS:HG2	2.44	0.52
1:P:45:ASN:O	1:P:49:GLY:N	2.42	0.52
1:R:273:VAL:HG12	1:R:274:HIS:HD2	1.75	0.52
1:G:285:LEU:HA	1:G:288:SER:CB	2.34	0.51
1:H:15:THR:HG21	1:D:212:GLU:HB2	1.92	0.51
1:H:81:HIS:O	1:H:266:MET:HE2	2.10	0.51
1:L:56:PHE:N	1:L:56:PHE:CD2	2.77	0.51
1:O:263:VAL:O	1:O:267:LYS:HG3	2.09	0.51
1:P:109:SER:HB2	1:P:121:GLU:OE1	2.10	0.51
1:B:197:MET:HE3	1:A:110:GLY:HA3	1.92	0.51
1:A:82:ALA:O	1:A:102:ARG:HD3	2.10	0.51
1:C:58:HIS:CD2	1:C:58:HIS:H	2.26	0.51
1:E:81:HIS:O	1:E:266:MET:HE2	2.09	0.51
1:I:110:GLY:O	1:I:111:ALA:HB3	2.10	0.51
1:I:81:HIS:O	1:I:266:MET:HE2	2.10	0.51
1:J:79:PHE:CD2	1:J:100:THR:HG21	2.44	0.51
1:L:143:TYR:O	1:L:149:GLU:HB2	2.09	0.51
1:L:283:TYR:HD2	1:L:283:TYR:C	2.10	0.51
1:B:65:THR:CG2	1:B:66:THR:N	2.72	0.51
1:C:126:SER:HB2	2:C:310:HOH:O	2.09	0.51
1:J:283:TYR:HD2	1:J:283:TYR:C	2.10	0.51
1:P:79:PHE:CD2	1:P:100:THR:HG21	2.45	0.51
1:P:273:VAL:HG12	1:P:274:HIS:HD2	1.75	0.51
1:B:287:LEU:HA	1:B:290:LYS:HD3	1.93	0.51
1:F:184:GLN:NE2	1:F:185:ARG:HA	2.25	0.51
1:K:70:ARG:NH2	1:K:73:ILE:CD1	2.73	0.51
1:M:144:ILE:HA	1:M:149:GLU:HG3	1.92	0.51
1:L:124:ALA:HA	1:M:157:ILE:HD13	1.93	0.51
1:M:58:HIS:H	1:M:58:HIS:CD2	2.27	0.51
1:P:81:HIS:HB2	1:P:266:MET:HE2	1.91	0.51
1:S:113:SER:OG	1:T:149:GLU:CD	2.49	0.51
1:G:144:ILE:HA	1:G:149:GLU:HG3	1.92	0.51
1:I:111:ALA:H	1:H:197:MET:HE1	1.76	0.51
1:M:191:THR:HG22	1:M:202:ILE:CG2	2.39	0.51
1:P:164:MET:HE2	1:P:200:GLN:HE22	1.76	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:136:CYS:O	1:Q:169:PRO:HD2	2.11	0.51
1:G:234:GLU:OE2	1:Q:280:ASP:OD2	2.29	0.51
1:R:76:ALA:N	1:R:77:PRO:HD2	2.25	0.51
1:A:164:MET:HE2	1:A:200:GLN:HE22	1.72	0.51
1:G:191:THR:HG22	1:G:202:ILE:CG2	2.39	0.51
1:G:283:TYR:O	1:G:286:TYR:CB	2.47	0.51
1:K:81:HIS:HB2	1:K:266:MET:HE2	1.92	0.51
1:M:285:LEU:HD22	1:M:286:TYR:N	2.23	0.51
1:S:91:ILE:HG13	1:T:196:GLU:OE2	2.11	0.51
1:E:211:PHE:HB3	1:E:245:GLN:OE1	2.11	0.51
1:F:287:LEU:HA	1:F:290:LYS:HD3	1.91	0.51
1:I:157:ILE:HD13	1:J:124:ALA:HA	1.93	0.51
1:L:105:VAL:HG22	1:L:137:ALA:HB3	1.93	0.51
1:O:103:PRO:HB3	1:O:136:CYS:SG	2.50	0.51
1:S:182:ARG:HG2	1:S:182:ARG:HH11	1.75	0.51
1:B:157:ILE:HD13	1:A:124:ALA:HA	1.92	0.51
1:B:283:TYR:CD2	1:B:283:TYR:O	2.64	0.51
1:D:21:ASN:O	1:D:23:PRO:HD3	2.11	0.51
1:E:184:GLN:NE2	1:E:185:ARG:HA	2.25	0.51
1:G:70:ARG:NH2	1:G:73:ILE:CD1	2.72	0.51
1:K:277:GLU:OE1	1:K:281:ARG:HD2	2.09	0.51
1:O:39:ARG:O	1:O:42:ARG:HB2	2.11	0.51
1:S:45:ASN:OD1	1:S:47:LYS:N	2.44	0.51
1:C:110:GLY:O	1:C:111:ALA:HB3	2.10	0.51
1:D:185:ARG:HG2	1:D:186:TYR:N	2.26	0.51
1:M:142:VAL:HA	1:M:152:SER:HB2	1.92	0.51
1:M:50:LYS:HA	1:M:248:SER:O	2.11	0.51
1:S:143:TYR:HB3	1:S:146:SER:HB2	1.92	0.51
1:C:102:ARG:HG3	1:C:103:PRO:CD	2.41	0.51
1:C:45:ASN:OD1	1:C:47:LYS:N	2.44	0.51
1:F:253:GLY:C	1:F:257:PHE:HE2	1.98	0.51
1:F:285:LEU:CA	1:F:288:SER:HB3	2.36	0.51
1:L:113:SER:OG	1:M:149:GLU:CD	2.49	0.51
1:M:283:TYR:O	1:M:286:TYR:CB	2.48	0.51
1:M:110:GLY:HA3	1:N:197:MET:CE	2.41	0.51
1:N:229:LYS:NZ	1:N:230:LEU:O	2.41	0.51
1:N:261:HIS:CG	1:N:290:LYS:HG2	2.45	0.51
1:N:265:MET:O	1:N:268:ALA:HB3	2.11	0.51
1:N:65:THR:CG2	1:N:66:THR:N	2.74	0.51
1:P:110:GLY:O	1:P:111:ALA:HB3	2.09	0.51
1:B:142:VAL:HA	1:B:152:SER:HB2	1.93	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:253:GLY:O	1:B:257:PHE:CE2	2.63	0.50
1:B:91:ILE:HG13	1:C:196:GLU:OE2	2.12	0.50
1:D:65:THR:HB	1:D:68:LEU:CD1	2.33	0.50
1:F:93:ARG:CZ	1:F:133:LEU:HD21	2.41	0.50
1:P:197:MET:HE1	1:T:110:GLY:HA3	1.93	0.50
1:B:58:HIS:CD2	1:B:58:HIS:H	2.28	0.50
1:D:42:ARG:HD3	1:D:136:CYS:SG	2.51	0.50
1:D:164:MET:HE2	1:D:200:GLN:HE22	1.76	0.50
1:E:254:ARG:O	1:E:258:GLN:HB2	2.12	0.50
1:H:110:GLY:HA3	1:G:197:MET:HE1	1.93	0.50
1:J:144:ILE:HA	1:J:149:GLU:HG3	1.93	0.50
1:O:81:HIS:O	1:O:266:MET:HE2	2.11	0.50
1:P:65:THR:CG2	1:P:68:LEU:CD1	2.89	0.50
1:T:76:ALA:HA	1:T:79:PHE:CE2	2.47	0.50
1:B:164:MET:HE2	1:B:200:GLN:NE2	2.25	0.50
1:F:81:HIS:O	1:F:266:MET:HE2	2.11	0.50
1:G:285:LEU:HD22	1:G:286:TYR:N	2.26	0.50
1:L:285:LEU:CA	1:L:288:SER:HB3	2.32	0.50
1:P:254:ARG:O	1:P:258:GLN:HB2	2.11	0.50
1:P:56:PHE:CD2	1:P:56:PHE:N	2.80	0.50
1:S:185:ARG:HG2	1:S:186:TYR:N	2.26	0.50
1:H:253:GLY:O	1:H:257:PHE:CD2	2.64	0.50
1:K:285:LEU:O	1:K:285:LEU:CD2	2.59	0.50
1:N:285:LEU:HD22	1:N:286:TYR:N	2.26	0.50
1:Q:251:ASP:OD1	1:Q:251:ASP:C	2.45	0.50
1:R:253:GLY:O	1:R:257:PHE:CD2	2.65	0.50
1:B:79:PHE:CD2	1:B:100:THR:HG21	2.47	0.50
1:B:81:HIS:O	1:B:266:MET:HE2	2.10	0.50
1:B:58:HIS:O	1:B:62:GLN:HB2	2.11	0.50
1:D:261:HIS:ND1	1:D:290:LYS:HG2	2.27	0.50
1:E:14:ARG:HG3	1:E:14:ARG:O	2.11	0.50
1:E:185:ARG:HG2	1:E:186:TYR:N	2.27	0.50
1:E:253:GLY:CA	1:E:257:PHE:CE2	2.83	0.50
1:O:93:ARG:CZ	1:O:133:LEU:HD21	2.41	0.50
1:Q:144:ILE:HA	1:Q:149:GLU:HG3	1.94	0.50
1:Q:45:ASN:O	1:Q:49:GLY:N	2.42	0.50
1:R:285:LEU:HD22	1:R:286:TYR:N	2.24	0.50
1:T:283:TYR:O	1:T:286:TYR:CB	2.49	0.50
1:B:239:CYS:SG	1:B:252:MET:HE1	2.41	0.50
1:C:263:VAL:O	1:C:267:LYS:HG3	2.12	0.50
1:D:273:VAL:HG12	1:D:274:HIS:HD2	1.76	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:197:MET:HE1	1:G:111:ALA:H	1.77	0.50
1:H:185:ARG:HG2	1:H:186:TYR:N	2.27	0.50
1:K:285:LEU:CA	1:K:288:SER:HB3	2.34	0.50
1:O:91:ILE:HG13	1:K:196:GLU:OE2	2.11	0.50
1:P:21:ASN:O	1:P:23:PRO:HD3	2.12	0.50
1:T:105:VAL:HG22	1:T:137:ALA:HB3	1.93	0.50
1:T:58:HIS:CD2	1:T:58:HIS:H	2.28	0.50
1:A:184:GLN:NE2	1:A:185:ARG:HA	2.26	0.50
1:E:189:LEU:O	1:E:193:ILE:HG13	2.11	0.50
1:G:254:ARG:O	1:G:258:GLN:HB2	2.12	0.50
1:L:254:ARG:O	1:L:258:GLN:HB2	2.11	0.50
1:N:191:THR:HG22	1:N:202:ILE:CG2	2.41	0.50
1:Q:207:VAL:CG1	1:Q:209:LYS:O	2.59	0.50
1:R:261:HIS:ND1	1:R:290:LYS:HG2	2.27	0.50
1:D:110:GLY:O	1:D:111:ALA:HB3	2.12	0.50
1:E:273:VAL:HG12	1:E:274:HIS:HD2	1.77	0.50
1:H:65:THR:HG22	1:H:68:LEU:HD12	1.94	0.50
1:J:50:LYS:HA	1:J:248:SER:O	2.11	0.50
1:N:56:PHE:CD2	1:N:56:PHE:N	2.79	0.50
1:O:144:ILE:HA	1:O:149:GLU:HG3	1.94	0.50
1:Q:76:ALA:HA	1:Q:79:PHE:CE2	2.47	0.50
1:E:79:PHE:CD2	1:E:100:THR:HG21	2.47	0.50
1:H:79:PHE:CD2	1:H:100:THR:HG21	2.47	0.50
1:H:58:HIS:O	1:H:62:GLN:HB2	2.12	0.50
1:I:239:CYS:HG	1:I:252:MET:CE	2.17	0.50
1:I:285:LEU:CD2	1:I:285:LEU:O	2.58	0.50
1:L:102:ARG:HG3	1:L:103:PRO:CD	2.41	0.50
1:L:79:PHE:CD2	1:L:100:THR:HG21	2.46	0.50
1:N:14:ARG:O	1:N:14:ARG:HG3	2.12	0.50
1:Q:253:GLY:O	1:Q:257:PHE:CD2	2.65	0.50
1:A:142:VAL:HA	1:A:152:SER:HB2	1.94	0.49
1:A:70:ARG:NH2	1:A:73:ILE:CD1	2.75	0.49
1:B:196:GLU:OE2	1:A:91:ILE:HG13	2.11	0.49
1:E:73:ILE:HG22	1:E:74:ASN:N	2.26	0.49
1:I:79:PHE:CD2	1:I:100:THR:HG21	2.46	0.49
1:S:103:PRO:HB3	1:S:136:CYS:SG	2.51	0.49
1:T:184:GLN:NE2	1:T:185:ARG:HA	2.27	0.49
1:A:189:LEU:O	1:A:193:ILE:HG13	2.11	0.49
1:B:52:VAL:N	1:B:83:ASP:OD2	2.38	0.49
1:C:144:ILE:HA	1:C:149:GLU:HG3	1.94	0.49
1:H:88:THR:HG21	1:G:196:GLU:HG3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:261:HIS:CG	1:G:290:LYS:HG2	2.46	0.49
1:I:113:SER:OG	1:H:149:GLU:CD	2.50	0.49
1:I:88:THR:HG21	1:H:196:GLU:HG3	1.94	0.49
1:K:53:MET:HG3	1:K:84:VAL:HG13	1.95	0.49
1:B:185:ARG:CG	1:B:186:TYR:N	2.74	0.49
1:B:56:PHE:CD2	1:B:56:PHE:N	2.80	0.49
1:I:33:ASP:OD1	1:D:93:ARG:NH1	2.45	0.49
1:G:56:PHE:CD2	1:G:56:PHE:N	2.79	0.49
1:N:70:ARG:NH2	1:N:73:ILE:CD1	2.74	0.49
1:O:261:HIS:ND1	1:O:290:LYS:HG2	2.27	0.49
1:R:191:THR:HG22	1:R:202:ILE:CG2	2.42	0.49
1:R:263:VAL:O	1:R:267:LYS:HG3	2.11	0.49
1:A:285:LEU:CD2	1:A:285:LEU:O	2.58	0.49
1:B:81:HIS:HB2	1:B:266:MET:HE2	1.94	0.49
1:C:204:THR:O	1:C:224:ILE:HA	2.12	0.49
1:G:142:VAL:HA	1:G:152:SER:HB2	1.94	0.49
1:H:14:ARG:O	1:H:14:ARG:HG3	2.12	0.49
1:I:21:ASN:O	1:I:23:PRO:HD3	2.12	0.49
1:J:164:MET:HE2	1:J:200:GLN:NE2	2.26	0.49
1:R:110:GLY:O	1:R:111:ALA:HB3	2.12	0.49
1:S:79:PHE:CD2	1:S:100:THR:HG21	2.47	0.49
1:B:189:LEU:O	1:B:193:ILE:HG13	2.13	0.49
1:D:182:ARG:NH1	1:D:182:ARG:HG2	2.26	0.49
1:D:283:TYR:O	1:D:286:TYR:CB	2.44	0.49
1:F:113:SER:OG	1:J:149:GLU:CD	2.51	0.49
1:F:189:LEU:O	1:F:193:ILE:HG13	2.12	0.49
1:F:283:TYR:C	1:F:283:TYR:HD2	2.12	0.49
1:G:125:LEU:CD1	1:G:125:LEU:O	2.45	0.49
1:G:45:ASN:OD1	1:G:47:LYS:N	2.45	0.49
1:N:105:VAL:HG22	1:N:137:ALA:HB3	1.94	0.49
1:N:142:VAL:HA	1:N:152:SER:HB2	1.94	0.49
1:O:109:SER:HB2	1:O:121:GLU:OE1	2.13	0.49
1:P:185:ARG:HG2	1:P:186:TYR:N	2.26	0.49
1:R:14:ARG:HG3	1:R:14:ARG:O	2.12	0.49
1:S:126:SER:HB2	2:S:299:HOH:O	2.11	0.49
1:S:251:ASP:OD1	1:S:251:ASP:C	2.48	0.49
1:A:185:ARG:HG2	1:A:186:TYR:N	2.28	0.49
1:H:45:ASN:O	1:H:49:GLY:N	2.38	0.49
1:L:82:ALA:O	1:L:102:ARG:HD3	2.13	0.49
1:Q:239:CYS:SG	1:Q:252:MET:HE1	2.41	0.49
1:F:132:ARG:O	1:A:35:GLY:HA3	2.13	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:91:ILE:HG13	1:D:196:GLU:OE2	2.12	0.49
1:I:58:HIS:CD2	1:I:58:HIS:H	2.29	0.49
1:J:191:THR:HG22	1:J:202:ILE:CG2	2.43	0.49
1:O:184:GLN:HE21	1:O:185:ARG:HA	1.77	0.49
1:R:144:ILE:HA	1:R:149:GLU:HG3	1.95	0.49
1:R:287:LEU:HA	1:R:290:LYS:HD3	1.94	0.49
1:S:111:ALA:H	1:T:197:MET:HE2	1.78	0.49
1:T:261:HIS:ND1	1:T:290:LYS:HG2	2.27	0.49
1:T:56:PHE:N	1:T:56:PHE:CD2	2.81	0.49
1:H:273:VAL:HG12	1:H:274:HIS:HD2	1.78	0.49
1:H:70:ARG:NH2	1:H:73:ILE:CD1	2.75	0.49
1:H:99:ALA:HB1	1:C:46:PRO:HB3	1.94	0.49
1:I:65:THR:HG22	1:I:68:LEU:HD12	1.95	0.49
1:K:73:ILE:HG22	1:K:74:ASN:N	2.27	0.49
1:M:141:GLN:OE1	1:M:173:VAL:CB	2.57	0.49
1:N:283:TYR:OH	1:G:275:HIS:HB3	2.12	0.49
1:P:185:ARG:HD2	2:P:295:HOH:O	2.12	0.49
1:Q:107:ARG:HH12	1:Q:141:GLN:CG	2.06	0.49
1:Q:273:VAL:HG12	1:Q:274:HIS:HD2	1.76	0.49
1:E:82:ALA:O	1:E:102:ARG:HD3	2.12	0.49
1:E:185:ARG:CG	1:E:186:TYR:N	2.74	0.49
1:H:136:CYS:O	1:H:169:PRO:HD2	2.13	0.49
1:I:144:ILE:HA	1:I:149:GLU:HG3	1.94	0.49
1:J:251:ASP:OD1	1:J:251:ASP:C	2.51	0.49
1:L:197:MET:HE1	1:K:111:ALA:H	1.77	0.49
1:K:56:PHE:N	1:K:56:PHE:CD2	2.81	0.49
1:L:156:ILE:O	1:L:160:VAL:HG23	2.13	0.49
1:P:261:HIS:ND1	1:P:290:LYS:HG2	2.28	0.49
1:P:110:GLY:HA3	1:Q:197:MET:HE3	1.95	0.49
1:R:135:SER:HB2	1:R:168:MET:CE	2.43	0.49
1:S:14:ARG:HG3	1:S:14:ARG:O	2.12	0.49
1:A:105:VAL:HG22	1:A:137:ALA:HB3	1.94	0.49
1:D:185:ARG:CG	1:D:186:TYR:N	2.75	0.49
1:G:253:GLY:CA	1:G:257:PHE:CE2	2.89	0.49
1:L:111:ALA:H	1:M:197:MET:HE1	1.78	0.49
1:E:102:ARG:HG3	1:E:103:PRO:CD	2.41	0.48
1:J:35:GLY:HA3	1:E:132:ARG:O	2.12	0.48
1:F:285:LEU:O	1:F:285:LEU:CD2	2.58	0.48
1:I:164:MET:HE1	1:I:200:GLN:NE2	2.26	0.48
1:L:93:ARG:CZ	1:L:133:LEU:HD21	2.43	0.48
1:O:42:ARG:HD3	1:O:136:CYS:SG	2.53	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:287:LEU:HA	1:O:290:LYS:HD3	1.95	0.48
1:S:144:ILE:HA	1:S:149:GLU:HG3	1.94	0.48
1:T:144:ILE:HG13	1:T:190:ALA:HA	1.95	0.48
1:B:273:VAL:HG12	1:B:274:HIS:HD2	1.79	0.48
1:F:82:ALA:O	1:F:102:ARG:HD3	2.13	0.48
1:O:273:VAL:HG12	1:O:274:HIS:HD2	1.78	0.48
1:O:283:TYR:HD2	1:O:283:TYR:C	2.13	0.48
1:Q:143:TYR:HB3	1:Q:146:SER:HB2	1.96	0.48
1:A:14:ARG:O	1:A:14:ARG:HG3	2.11	0.48
1:E:58:HIS:O	1:E:62:GLN:HB2	2.13	0.48
1:I:164:MET:HE2	1:I:200:GLN:NE2	2.23	0.48
1:M:45:ASN:OD1	1:M:47:LYS:N	2.46	0.48
1:P:164:MET:HE1	1:P:200:GLN:NE2	2.29	0.48
1:R:45:ASN:O	1:R:49:GLY:N	2.39	0.48
1:R:65:THR:CG2	1:R:68:LEU:CD1	2.91	0.48
1:T:45:ASN:OD1	1:T:47:LYS:N	2.46	0.48
1:H:164:MET:HE1	1:H:200:GLN:HE22	1.77	0.48
1:J:56:PHE:CD2	1:J:56:PHE:N	2.81	0.48
1:M:65:THR:CG2	1:M:66:THR:N	2.75	0.48
1:N:261:HIS:ND1	1:N:290:LYS:HG2	2.28	0.48
1:O:191:THR:HG22	1:O:202:ILE:CG2	2.44	0.48
1:A:125:LEU:HD13	1:A:125:LEU:C	2.32	0.48
1:B:187:PHE:HB2	1:B:214:ILE:CD1	2.43	0.48
1:C:82:ALA:O	1:C:102:ARG:HD3	2.13	0.48
1:F:185:ARG:CG	1:F:186:TYR:N	2.74	0.48
1:H:21:ASN:O	1:H:23:PRO:HD3	2.13	0.48
1:H:65:THR:CG2	1:H:68:LEU:CD1	2.91	0.48
1:J:45:ASN:O	1:J:49:GLY:N	2.43	0.48
1:L:196:GLU:HG3	1:K:88:THR:HG21	1.94	0.48
1:L:65:THR:HB	1:L:68:LEU:CD1	2.36	0.48
1:M:82:ALA:O	1:M:102:ARG:HD3	2.13	0.48
1:M:185:ARG:HG2	1:M:186:TYR:N	2.29	0.48
1:Q:185:ARG:HG2	1:Q:186:TYR:N	2.28	0.48
1:Q:287:LEU:HA	1:Q:290:LYS:HD3	1.96	0.48
1:Q:58:HIS:H	1:Q:58:HIS:CD2	2.29	0.48
1:T:143:TYR:HB3	1:T:146:SER:HB2	1.96	0.48
1:B:254:ARG:O	1:B:258:GLN:HB2	2.13	0.48
1:C:42:ARG:HD3	1:C:136:CYS:SG	2.53	0.48
1:C:251:ASP:C	1:C:251:ASP:OD1	2.51	0.48
1:E:263:VAL:O	1:E:267:LYS:HG3	2.13	0.48
1:F:251:ASP:C	1:F:251:ASP:OD1	2.51	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:164:MET:HE1	1:G:200:GLN:NE2	2.28	0.48
1:I:14:ARG:O	1:I:14:ARG:HG3	2.14	0.48
1:L:184:GLN:NE2	1:L:185:ARG:HA	2.28	0.48
1:N:279:ALA:O	1:N:282:ALA:HB3	2.14	0.48
1:N:287:LEU:CD2	1:G:275:HIS:NE2	2.62	0.48
1:R:283:TYR:HD2	1:R:283:TYR:C	2.17	0.48
1:S:277:GLU:OE1	1:S:281:ARG:HD2	2.13	0.48
1:S:285:LEU:HD22	1:S:286:TYR:N	2.26	0.48
1:A:285:LEU:CA	1:A:288:SER:HB3	2.34	0.48
1:C:265:MET:O	1:C:268:ALA:HB3	2.13	0.48
1:D:263:VAL:O	1:D:267:LYS:HG3	2.14	0.48
1:I:132:ARG:O	1:D:35:GLY:HA3	2.13	0.48
1:I:45:ASN:OD1	1:I:47:LYS:N	2.47	0.48
1:J:261:HIS:CG	1:J:290:LYS:HG2	2.49	0.48
1:O:88:THR:HG21	1:K:196:GLU:HG3	1.96	0.48
1:K:261:HIS:CG	1:K:290:LYS:HG2	2.48	0.48
1:L:113:SER:HB2	1:L:115:LEU:H	1.79	0.48
1:N:81:HIS:O	1:N:266:MET:HE2	2.14	0.48
1:O:285:LEU:O	1:O:285:LEU:CD2	2.56	0.48
1:S:110:GLY:HA3	1:T:197:MET:CE	2.43	0.48
1:M:251:ASP:OD1	1:M:251:ASP:C	2.52	0.48
1:O:283:TYR:O	1:O:283:TYR:CD2	2.66	0.48
1:R:142:VAL:HA	1:R:152:SER:HB2	1.95	0.48
1:P:197:MET:HE1	1:T:111:ALA:H	1.79	0.48
1:A:261:HIS:ND1	1:A:290:LYS:HG2	2.29	0.48
1:D:14:ARG:O	1:D:14:ARG:HG3	2.14	0.48
1:D:224:ILE:O	1:D:224:ILE:HG13	2.13	0.48
1:H:109:SER:HB2	1:H:121:GLU:OE1	2.13	0.48
1:H:143:TYR:HB3	1:H:146:SER:HB2	1.96	0.48
1:H:261:HIS:CG	1:H:290:LYS:HG2	2.48	0.48
1:I:143:TYR:HB3	1:I:146:SER:HB2	1.95	0.48
1:J:185:ARG:HG2	1:J:186:TYR:N	2.29	0.48
1:J:81:HIS:HB2	1:J:266:MET:HE2	1.96	0.48
1:P:110:GLY:HA3	1:Q:197:MET:HE1	1.96	0.48
1:K:143:TYR:HB3	1:K:146:SER:HB2	1.95	0.48
1:K:266:MET:O	1:K:270:GLN:HG2	2.14	0.48
1:N:79:PHE:CD2	1:N:100:THR:HG21	2.49	0.48
1:P:70:ARG:NH2	1:P:73:ILE:CD1	2.75	0.48
1:Q:82:ALA:O	1:Q:102:ARG:HD3	2.14	0.48
1:T:263:VAL:O	1:T:267:LYS:HG3	2.13	0.48
1:C:273:VAL:HG12	1:C:274:HIS:HD2	1.78	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:197:MET:HE3	1:G:110:GLY:HA3	1.95	0.47
1:G:129:ASP:HA	1:G:132:ARG:NH1	2.29	0.47
1:G:14:ARG:HG3	1:G:14:ARG:O	2.14	0.47
1:I:185:ARG:HG2	1:I:186:TYR:N	2.29	0.47
1:K:185:ARG:HG2	1:K:186:TYR:N	2.29	0.47
1:N:109:SER:HB2	1:N:121:GLU:OE1	2.14	0.47
1:A:56:PHE:N	1:A:56:PHE:CD2	2.82	0.47
1:B:184:GLN:NE2	1:B:185:ARG:HA	2.29	0.47
1:B:111:ALA:H	1:C:197:MET:HE2	1.77	0.47
1:D:254:ARG:O	1:D:258:GLN:HB2	2.13	0.47
1:G:102:ARG:HG3	1:G:103:PRO:CD	2.43	0.47
1:G:185:ARG:HG2	1:G:186:TYR:N	2.29	0.47
1:H:14:ARG:HE	1:H:14:ARG:HB2	1.35	0.47
1:H:254:ARG:O	1:H:258:GLN:HB2	2.14	0.47
1:J:187:PHE:HB2	1:J:214:ILE:CD1	2.44	0.47
1:J:277:GLU:OE1	1:J:281:ARG:HD2	2.14	0.47
1:L:197:MET:HE3	1:K:110:GLY:HA3	1.96	0.47
1:P:185:ARG:CG	1:P:186:TYR:N	2.77	0.47
1:P:65:THR:HG22	1:P:68:LEU:HD12	1.93	0.47
1:A:67:GLY:H	1:A:69:GLU:CD	2.17	0.47
1:B:283:TYR:HD2	1:B:283:TYR:C	2.13	0.47
1:C:164:MET:HE2	1:C:200:GLN:NE2	2.28	0.47
1:K:45:ASN:OD1	1:K:47:LYS:N	2.47	0.47
1:N:67:GLY:H	1:N:69:GLU:CD	2.18	0.47
1:Q:93:ARG:CZ	1:Q:133:LEU:HD21	2.44	0.47
1:S:149:GLU:CD	1:R:113:SER:HG	2.18	0.47
1:S:285:LEU:CD2	1:S:285:LEU:O	2.59	0.47
1:A:164:MET:HE1	1:A:200:GLN:NE2	2.29	0.47
1:B:45:ASN:OD1	1:B:47:LYS:N	2.47	0.47
1:E:14:ARG:HE	1:E:14:ARG:HB2	1.36	0.47
1:E:266:MET:O	1:E:270:GLN:HG2	2.14	0.47
1:F:73:ILE:HG22	1:F:74:ASN:N	2.29	0.47
1:R:184:GLN:NE2	1:R:185:ARG:HA	2.29	0.47
1:R:45:ASN:OD1	1:R:47:LYS:N	2.48	0.47
1:B:14:ARG:HG3	1:B:14:ARG:O	2.14	0.47
1:B:285:LEU:CD2	1:B:285:LEU:O	2.61	0.47
1:C:79:PHE:CD2	1:C:100:THR:HG21	2.49	0.47
1:B:88:THR:HG21	1:C:196:GLU:HG3	1.95	0.47
1:D:45:ASN:O	1:D:49:GLY:N	2.42	0.47
1:G:136:CYS:O	1:G:169:PRO:HD2	2.14	0.47
1:I:113:SER:HG	1:H:149:GLU:CD	2.18	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:273:VAL:HG12	1:I:274:HIS:HD2	1.78	0.47
1:F:110:GLY:HA3	1:J:197:MET:CE	2.44	0.47
1:L:277:GLU:OE1	1:L:281:ARG:HD2	2.12	0.47
1:A:79:PHE:CD2	1:A:100:THR:HG21	2.49	0.47
1:B:82:ALA:O	1:B:102:ARG:HD3	2.14	0.47
1:E:261:HIS:ND1	1:E:290:LYS:HG2	2.29	0.47
1:J:144:ILE:HG13	1:J:190:ALA:HA	1.97	0.47
1:L:58:HIS:O	1:L:62:GLN:HB2	2.13	0.47
1:O:115:LEU:HD12	1:K:144:ILE:HG22	1.96	0.47
1:P:144:ILE:HA	1:P:149:GLU:HG3	1.97	0.47
1:S:263:VAL:O	1:S:267:LYS:HG3	2.14	0.47
1:S:56:PHE:N	1:S:56:PHE:CD2	2.81	0.47
1:E:111:ALA:H	1:A:197:MET:HE1	1.79	0.47
1:C:109:SER:HB2	1:C:121:GLU:OE1	2.14	0.47
1:C:261:HIS:CG	1:C:290:LYS:HG2	2.50	0.47
1:E:144:ILE:HG13	1:E:190:ALA:HA	1.95	0.47
1:F:67:GLY:N	1:F:69:GLU:OE1	2.46	0.47
1:J:185:ARG:CG	1:J:186:TYR:N	2.76	0.47
1:K:253:GLY:O	1:K:257:PHE:CD2	2.68	0.47
1:M:253:GLY:CA	1:M:257:PHE:CE2	2.86	0.47
1:O:144:ILE:HG13	1:O:190:ALA:HA	1.96	0.47
1:P:253:GLY:CA	1:P:257:PHE:CE2	2.86	0.47
1:T:144:ILE:HA	1:T:149:GLU:HG3	1.96	0.47
1:A:251:ASP:OD1	1:A:251:ASP:C	2.52	0.47
1:D:81:HIS:HB2	1:D:266:MET:HE2	1.96	0.47
1:I:92:LEU:HD11	1:D:34:TRP:CZ2	2.50	0.47
1:D:73:ILE:HG22	1:D:74:ASN:N	2.30	0.47
1:F:115:LEU:HD12	1:J:144:ILE:HG22	1.96	0.47
1:F:143:TYR:HB3	1:F:146:SER:HB2	1.95	0.47
1:H:115:LEU:HD12	1:G:144:ILE:HG22	1.97	0.47
1:J:81:HIS:O	1:J:266:MET:HE2	2.14	0.47
1:O:21:ASN:O	1:O:23:PRO:HD3	2.14	0.47
1:Q:105:VAL:HG22	1:Q:137:ALA:HB3	1.97	0.47
1:S:113:SER:HG	1:T:149:GLU:CD	2.17	0.47
1:A:53:MET:HG3	1:A:84:VAL:HG13	1.97	0.47
1:G:132:ARG:O	1:B:35:GLY:HA3	2.15	0.47
1:E:45:ASN:OD1	1:E:47:LYS:N	2.48	0.47
1:H:189:LEU:O	1:H:193:ILE:HG13	2.14	0.47
1:K:189:LEU:O	1:K:193:ILE:HG13	2.15	0.47
1:M:273:VAL:HG12	1:M:274:HIS:HD2	1.80	0.47
1:O:182:ARG:NH1	1:O:182:ARG:HG2	2.27	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:102:ARG:HG3	1:Q:103:PRO:CD	2.44	0.47
1:Q:263:VAL:O	1:Q:267:LYS:HG3	2.15	0.47
1:Q:285:LEU:CA	1:Q:288:SER:HB3	2.34	0.47
1:Q:73:ILE:HG22	1:Q:74:ASN:N	2.30	0.47
1:Q:93:ARG:NH2	1:Q:129:ASP:OD1	2.45	0.47
1:S:144:ILE:HG13	1:S:190:ALA:HA	1.97	0.47
1:A:254:ARG:N	1:A:257:PHE:CE2	2.82	0.47
1:H:277:GLU:OE1	1:H:281:ARG:HD2	2.15	0.47
1:I:253:GLY:CA	1:I:257:PHE:CE2	2.93	0.47
1:K:58:HIS:O	1:K:62:GLN:HB2	2.15	0.47
1:P:142:VAL:HA	1:P:152:SER:HB2	1.96	0.47
1:P:277:GLU:OE1	1:P:281:ARG:HD2	2.13	0.47
1:P:285:LEU:CA	1:P:288:SER:HB3	2.35	0.47
1:T:185:ARG:CG	1:T:186:TYR:N	2.78	0.47
1:T:251:ASP:C	1:T:251:ASP:OD1	2.52	0.47
1:T:82:ALA:O	1:T:102:ARG:HD3	2.15	0.47
1:B:285:LEU:CA	1:B:288:SER:HB3	2.38	0.47
1:B:83:ASP:O	1:B:103:PRO:HD2	2.15	0.47
1:E:196:GLU:HG3	1:D:88:THR:HG21	1.96	0.47
1:E:266:MET:O	1:E:270:GLN:CG	2.63	0.47
1:E:67:GLY:H	1:E:69:GLU:CD	2.18	0.47
1:I:141:GLN:OE1	1:I:173:VAL:CB	2.57	0.47
1:O:197:MET:HE1	1:N:110:GLY:HA3	1.96	0.47
1:T:67:GLY:N	1:T:69:GLU:OE1	2.47	0.47
1:D:285:LEU:CA	1:D:288:SER:HB3	2.38	0.46
1:G:184:GLN:NE2	1:G:185:ARG:HA	2.30	0.46
1:I:143:TYR:O	1:I:149:GLU:HB2	2.15	0.46
1:J:263:VAL:O	1:J:267:LYS:HG3	2.15	0.46
1:O:144:ILE:HG21	1:O:189:LEU:HD23	1.97	0.46
1:S:197:MET:HE3	1:R:110:GLY:HA3	1.96	0.46
1:T:273:VAL:HG12	1:T:274:HIS:HD2	1.81	0.46
1:P:196:GLU:HG3	1:T:88:THR:OG1	2.15	0.46
1:A:207:VAL:CG1	1:A:209:LYS:O	2.63	0.46
1:E:191:THR:HG22	1:E:202:ILE:CG2	2.44	0.46
1:G:65:THR:CG2	1:G:66:THR:N	2.78	0.46
1:K:268:ALA:HA	1:K:285:LEU:HD11	1.98	0.46
1:M:79:PHE:CD2	1:M:100:THR:HG21	2.50	0.46
1:Q:142:VAL:HA	1:Q:152:SER:HB2	1.97	0.46
1:S:58:HIS:O	1:S:62:GLN:HB2	2.15	0.46
1:T:287:LEU:HA	1:T:290:LYS:HD3	1.97	0.46
1:B:261:HIS:CG	1:B:290:LYS:HG2	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:277:GLU:OE1	1:E:281:ARG:HD2	2.14	0.46
1:I:102:ARG:HG3	1:I:103:PRO:CD	2.44	0.46
1:M:261:HIS:CG	1:M:290:LYS:HG2	2.51	0.46
1:P:143:TYR:O	1:P:149:GLU:HB2	2.14	0.46
1:P:136:CYS:O	1:P:169:PRO:HD2	2.15	0.46
1:P:111:ALA:H	1:Q:197:MET:HE1	1.81	0.46
1:S:82:ALA:O	1:S:102:ARG:HD3	2.14	0.46
1:S:45:ASN:HA	1:S:46:PRO:HD3	1.81	0.46
1:T:102:ARG:HG3	1:T:103:PRO:CD	2.43	0.46
1:A:113:SER:HB2	1:A:115:LEU:H	1.81	0.46
1:A:45:ASN:OD1	1:A:47:LYS:N	2.48	0.46
1:C:143:TYR:HB3	1:C:146:SER:HB2	1.96	0.46
1:D:65:THR:CG2	1:D:66:THR:N	2.78	0.46
1:H:88:THR:OG1	1:G:196:GLU:HG3	2.15	0.46
1:H:253:GLY:CA	1:H:257:PHE:CE2	2.91	0.46
1:K:144:ILE:HG13	1:K:190:ALA:HA	1.98	0.46
1:K:21:ASN:O	1:K:23:PRO:HD3	2.15	0.46
1:K:273:VAL:HG12	1:K:274:HIS:HD2	1.80	0.46
1:L:109:SER:HB2	1:L:121:GLU:OE1	2.15	0.46
1:M:88:THR:HG21	1:N:196:GLU:HG3	1.97	0.46
1:M:110:GLY:HA3	1:N:197:MET:HE3	1.98	0.46
1:N:55:ALA:HB3	1:N:251:ASP:OD2	2.14	0.46
1:N:76:ALA:HA	1:N:79:PHE:CE2	2.51	0.46
1:P:285:LEU:O	1:P:285:LEU:CD2	2.62	0.46
1:P:73:ILE:HG22	1:P:74:ASN:N	2.30	0.46
1:Q:52:VAL:N	1:Q:83:ASP:OD2	2.41	0.46
1:T:65:THR:CG2	1:T:68:LEU:CD1	2.93	0.46
1:C:253:GLY:CA	1:C:257:PHE:CE2	2.95	0.46
1:C:253:GLY:O	1:C:257:PHE:CE2	2.69	0.46
1:D:82:ALA:O	1:D:102:ARG:HD3	2.15	0.46
1:F:196:GLU:OE2	1:G:91:ILE:HG13	2.16	0.46
1:G:173:VAL:HG13	1:G:203:LYS:HB3	1.98	0.46
1:G:34:TRP:CZ2	1:B:92:LEU:HD11	2.51	0.46
1:I:124:ALA:HA	1:H:157:ILE:HD13	1.98	0.46
1:I:266:MET:O	1:I:270:GLN:HG2	2.15	0.46
1:I:93:ARG:CZ	1:I:133:LEU:HD21	2.45	0.46
1:J:65:THR:CG2	1:J:66:THR:N	2.79	0.46
1:L:141:GLN:OE1	1:L:173:VAL:CB	2.59	0.46
1:O:136:CYS:O	1:O:169:PRO:HD2	2.15	0.46
1:P:14:ARG:HE	1:P:14:ARG:HB2	1.36	0.46
1:T:67:GLY:H	1:T:69:GLU:CD	2.19	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:277:GLU:OE1	1:D:281:ARG:HD2	2.10	0.46
1:D:45:ASN:HA	1:D:46:PRO:HD3	1.83	0.46
1:F:165:LYS:HB3	2:F:294:HOH:O	2.16	0.46
1:I:185:ARG:CG	1:I:186:TYR:N	2.78	0.46
1:I:253:GLY:O	1:I:257:PHE:CD2	2.68	0.46
1:K:110:GLY:O	1:K:111:ALA:CB	2.64	0.46
1:L:239:CYS:HG	1:L:252:MET:HE3	1.74	0.46
1:M:266:MET:O	1:M:270:GLN:HG2	2.16	0.46
1:M:287:LEU:HA	1:M:290:LYS:HD3	1.98	0.46
1:R:65:THR:CG2	1:R:66:THR:N	2.79	0.46
1:T:73:ILE:HG22	1:T:74:ASN:N	2.28	0.46
1:F:67:GLY:H	1:F:69:GLU:CD	2.17	0.46
1:H:182:ARG:HG2	1:H:182:ARG:NH1	2.30	0.46
1:H:56:PHE:N	1:H:56:PHE:CD2	2.84	0.46
1:K:14:ARG:O	1:K:14:ARG:HG3	2.15	0.46
1:O:124:ALA:HA	1:K:157:ILE:HD13	1.96	0.46
1:L:14:ARG:HB2	1:L:14:ARG:HE	1.31	0.46
1:Q:191:THR:HG22	1:Q:202:ILE:CG2	2.42	0.46
1:Q:79:PHE:CD2	1:Q:100:THR:HG21	2.51	0.46
1:S:164:MET:HE1	1:S:200:GLN:HE22	1.77	0.46
1:B:136:CYS:O	1:B:169:PRO:HD2	2.15	0.46
1:B:70:ARG:NH2	1:B:73:ILE:CD1	2.79	0.46
1:C:171:MET:HA	1:C:201:ILE:O	2.16	0.46
1:D:103:PRO:HB3	1:D:136:CYS:SG	2.56	0.46
1:G:212:GLU:CB	1:C:15:THR:CG2	2.72	0.46
1:H:185:ARG:CG	1:H:186:TYR:N	2.77	0.46
1:H:191:THR:CG2	1:H:202:ILE:HG21	2.39	0.46
1:I:261:HIS:CG	1:I:290:LYS:HG2	2.50	0.46
1:L:191:THR:HG22	1:L:202:ILE:CG2	2.42	0.46
1:L:285:LEU:CD2	1:L:285:LEU:O	2.62	0.46
1:L:65:THR:CG2	1:L:68:LEU:HD12	2.45	0.46
1:O:135:SER:HB2	1:O:168:MET:CE	2.45	0.46
1:Q:144:ILE:HG13	1:Q:190:ALA:HA	1.98	0.46
1:R:70:ARG:NH2	1:R:73:ILE:CD1	2.78	0.46
1:E:21:ASN:O	1:E:23:PRO:HD3	2.16	0.46
1:I:157:ILE:HG22	1:I:158:GLN:N	2.30	0.46
1:J:65:THR:CG2	1:J:68:LEU:CD1	2.93	0.46
1:L:185:ARG:HG2	1:L:186:TYR:N	2.30	0.46
1:N:184:GLN:HE21	1:N:185:ARG:HA	1.79	0.46
1:N:82:ALA:O	1:N:102:ARG:HD3	2.16	0.46
1:R:65:THR:HG22	1:R:68:LEU:HD12	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:65:THR:HG22	1:T:68:LEU:HD12	1.97	0.46
1:C:14:ARG:HG3	1:C:14:ARG:O	2.15	0.46
1:C:207:VAL:CG1	1:C:209:LYS:O	2.64	0.46
1:D:81:HIS:O	1:D:266:MET:HE2	2.16	0.46
1:F:14:ARG:CG	1:F:14:ARG:O	2.63	0.46
1:F:21:ASN:O	1:F:23:PRO:HD3	2.15	0.46
1:H:65:THR:CG2	1:H:66:THR:N	2.79	0.46
1:I:76:ALA:HA	1:I:79:PHE:CE2	2.51	0.46
1:K:185:ARG:CG	1:K:186:TYR:N	2.78	0.46
1:K:266:MET:O	1:K:270:GLN:CG	2.64	0.46
1:L:144:ILE:HA	1:L:149:GLU:HG3	1.97	0.46
1:P:82:ALA:O	1:P:102:ARG:HD3	2.15	0.46
1:Q:110:GLY:O	1:Q:111:ALA:HB3	2.16	0.46
1:S:65:THR:CG2	1:S:68:LEU:CD1	2.92	0.46
1:A:109:SER:CB	1:A:121:GLU:OE1	2.64	0.45
1:A:185:ARG:CG	1:A:186:TYR:N	2.79	0.45
1:D:287:LEU:HA	1:D:290:LYS:HD3	1.98	0.45
1:D:56:PHE:CD2	1:D:56:PHE:N	2.83	0.45
1:E:285:LEU:O	1:E:285:LEU:CD2	2.62	0.45
1:J:184:GLN:NE2	1:J:185:ARG:HA	2.31	0.45
1:L:144:ILE:HG22	1:K:115:LEU:HD12	1.97	0.45
1:M:14:ARG:HB2	1:M:14:ARG:HE	1.30	0.45
1:O:254:ARG:N	1:O:257:PHE:CE2	2.84	0.45
1:O:56:PHE:CD2	1:O:56:PHE:N	2.84	0.45
1:Q:65:THR:CG2	1:Q:66:THR:N	2.77	0.45
1:A:81:HIS:O	1:A:266:MET:HE2	2.17	0.45
1:E:254:ARG:N	1:E:257:PHE:CE2	2.84	0.45
1:F:196:GLU:HG3	1:G:88:THR:HG21	1.98	0.45
1:L:251:ASP:C	1:L:251:ASP:OD1	2.54	0.45
1:O:82:ALA:O	1:O:102:ARG:HD3	2.15	0.45
1:Q:182:ARG:NH1	1:Q:182:ARG:HG2	2.25	0.45
1:R:173:VAL:HG13	1:R:203:LYS:HB3	1.98	0.45
1:S:261:HIS:ND1	1:S:290:LYS:HG2	2.32	0.45
1:S:65:THR:HG22	1:S:68:LEU:HD12	1.98	0.45
1:T:187:PHE:HB2	1:T:214:ILE:CD1	2.46	0.45
1:B:65:THR:HG23	1:B:66:THR:N	2.31	0.45
1:E:76:ALA:HA	1:E:79:PHE:CE2	2.50	0.45
1:F:283:TYR:O	1:F:286:TYR:CB	2.49	0.45
1:H:141:GLN:OE1	1:H:173:VAL:CB	2.61	0.45
1:I:142:VAL:HA	1:I:152:SER:HB2	1.98	0.45
1:L:171:MET:HA	1:L:201:ILE:O	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:261:HIS:ND1	1:L:290:LYS:HG2	2.31	0.45
1:M:184:GLN:NE2	1:M:185:ARG:HA	2.31	0.45
1:N:285:LEU:CD2	1:N:285:LEU:O	2.61	0.45
1:N:67:GLY:N	1:N:69:GLU:OE1	2.48	0.45
1:O:32:LEU:HD13	1:O:36:MET:SD	2.56	0.45
1:A:52:VAL:N	1:A:83:ASP:OD2	2.47	0.45
1:B:143:TYR:HB3	1:B:146:SER:HB2	1.98	0.45
1:B:65:THR:HG22	1:B:68:LEU:HD12	1.98	0.45
1:C:56:PHE:N	1:C:56:PHE:CD2	2.84	0.45
1:G:285:LEU:O	1:G:285:LEU:CD2	2.64	0.45
1:H:266:MET:O	1:H:270:GLN:CG	2.64	0.45
1:L:182:ARG:NH1	1:L:182:ARG:HG2	2.32	0.45
1:M:109:SER:HB2	1:M:121:GLU:OE1	2.16	0.45
1:N:83:ASP:O	1:N:103:PRO:HD2	2.16	0.45
1:A:21:ASN:O	1:A:23:PRO:HD3	2.16	0.45
1:A:266:MET:O	1:A:270:GLN:HG2	2.16	0.45
1:A:76:ALA:HA	1:A:79:PHE:CE2	2.52	0.45
1:B:144:ILE:HA	1:B:149:GLU:HG3	1.96	0.45
1:C:14:ARG:HB2	1:C:14:ARG:HE	1.34	0.45
1:I:166:VAL:HG22	1:D:131:VAL:HG12	1.98	0.45
1:F:56:PHE:CE1	1:F:87:CYS:HB3	2.51	0.45
1:I:184:GLN:NE2	1:I:185:ARG:HA	2.31	0.45
1:I:65:THR:CG2	1:I:68:LEU:CD1	2.93	0.45
1:J:14:ARG:CG	1:J:14:ARG:O	2.63	0.45
1:J:182:ARG:HG2	1:J:182:ARG:NH1	2.31	0.45
1:J:73:ILE:HG22	1:J:74:ASN:N	2.31	0.45
1:K:164:MET:HE2	1:K:200:GLN:NE2	2.32	0.45
1:M:45:ASN:HA	1:M:46:PRO:HD3	1.78	0.45
1:Q:81:HIS:O	1:Q:266:MET:HE2	2.17	0.45
1:R:185:ARG:HG2	1:R:186:TYR:N	2.32	0.45
1:R:207:VAL:CG1	1:R:209:LYS:O	2.64	0.45
1:S:171:MET:HA	1:S:201:ILE:O	2.17	0.45
1:T:81:HIS:O	1:T:266:MET:HE2	2.16	0.45
1:B:65:THR:CG2	1:B:68:LEU:CD1	2.95	0.45
1:D:14:ARG:HE	1:D:14:ARG:HB2	1.31	0.45
1:F:250:VAL:HG23	1:F:250:VAL:O	2.16	0.45
1:H:45:ASN:HA	1:H:46:PRO:HD3	1.78	0.45
1:N:207:VAL:CG1	1:N:209:LYS:O	2.64	0.45
1:P:115:LEU:HD12	1:Q:144:ILE:HG22	1.99	0.45
1:P:144:ILE:HG21	1:P:189:LEU:HD23	1.99	0.45
1:P:207:VAL:CG1	1:P:209:LYS:O	2.64	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:T:21:ASN:O	1:T:23:PRO:HD3	2.16	0.45
1:T:79:PHE:CD2	1:T:100:THR:HG21	2.52	0.45
1:A:32:LEU:HD13	1:A:36:MET:SD	2.57	0.45
1:F:143:TYR:O	1:F:149:GLU:HB2	2.16	0.45
1:F:33:ASP:CG	1:A:93:ARG:NH1	2.70	0.45
1:G:233:ARG:HB2	1:G:283:TYR:CE1	2.52	0.45
1:G:21:ASN:O	1:G:23:PRO:HD3	2.16	0.45
1:G:58:HIS:O	1:G:62:GLN:HB2	2.16	0.45
1:H:82:ALA:O	1:H:102:ARG:HD3	2.15	0.45
1:H:93:ARG:CZ	1:H:133:LEU:HD21	2.47	0.45
1:O:110:GLY:O	1:O:111:ALA:HB3	2.16	0.45
1:O:14:ARG:HG3	1:O:14:ARG:O	2.17	0.45
1:O:237:GLU:O	1:O:241:GLN:HG2	2.17	0.45
1:A:14:ARG:HB2	1:A:14:ARG:HE	1.29	0.45
1:B:196:GLU:HG3	1:A:88:THR:HG21	1.99	0.45
1:G:82:ALA:O	1:G:102:ARG:HD3	2.16	0.45
1:H:164:MET:HE1	1:H:200:GLN:NE2	2.32	0.45
1:J:92:LEU:HA	1:J:96:VAL:CG2	2.47	0.45
1:M:185:ARG:CG	1:M:186:TYR:N	2.78	0.45
1:N:144:ILE:HG13	1:N:190:ALA:HA	1.98	0.45
1:O:251:ASP:OD1	1:O:251:ASP:C	2.55	0.45
1:P:61:PHE:CD2	1:P:61:PHE:N	2.85	0.45
1:Q:45:ASN:OD1	1:Q:47:LYS:N	2.50	0.45
1:Q:70:ARG:NH2	1:Q:73:ILE:CD1	2.80	0.45
1:E:144:ILE:HG22	1:D:115:LEU:HD12	1.99	0.45
1:E:81:HIS:HB2	1:E:266:MET:HE2	1.98	0.45
1:E:56:PHE:CD2	1:E:56:PHE:N	2.85	0.45
1:E:67:GLY:N	1:E:69:GLU:OE1	2.48	0.45
1:F:197:MET:HE1	1:G:110:GLY:HA3	1.98	0.45
1:M:14:ARG:HG3	1:M:14:ARG:O	2.15	0.45
1:M:52:VAL:N	1:M:83:ASP:OD2	2.44	0.45
1:Q:21:ASN:O	1:Q:23:PRO:HD3	2.17	0.45
1:A:266:MET:O	1:A:270:GLN:CG	2.64	0.45
1:C:32:LEU:HD13	1:C:36:MET:SD	2.57	0.45
1:F:273:VAL:HG12	1:F:274:HIS:HD2	1.82	0.45
1:F:277:GLU:OE1	1:F:281:ARG:HD2	2.14	0.45
1:F:45:ASN:OD1	1:F:47:LYS:N	2.50	0.45
1:G:144:ILE:HG13	1:G:190:ALA:HA	1.99	0.45
1:I:277:GLU:OE1	1:I:281:ARG:HD2	2.17	0.45
1:K:109:SER:HB2	1:K:121:GLU:OE1	2.17	0.45
1:M:164:MET:HE2	1:M:200:GLN:HE22	1.80	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:144:ILE:HA	1:N:149:GLU:HG3	1.99	0.45
1:O:187:PHE:HB2	1:O:214:ILE:CD1	2.46	0.45
1:S:164:MET:HE1	1:S:200:GLN:NE2	2.32	0.45
1:T:182:ARG:NH1	1:T:182:ARG:HG2	2.31	0.45
1:T:191:THR:HG22	1:T:202:ILE:CG2	2.43	0.45
1:F:237:GLU:O	1:F:241:GLN:HG2	2.17	0.44
1:H:184:GLN:NE2	1:H:185:ARG:HA	2.32	0.44
1:K:207:VAL:CG1	1:K:209:LYS:O	2.65	0.44
1:K:92:LEU:HA	1:K:96:VAL:CG2	2.47	0.44
1:L:285:LEU:HD22	1:L:286:TYR:N	2.32	0.44
1:L:76:ALA:HA	1:L:79:PHE:CE2	2.52	0.44
1:R:82:ALA:O	1:R:102:ARG:HD3	2.18	0.44
1:Q:88:THR:HG21	1:R:196:GLU:HG3	1.97	0.44
1:A:283:TYR:O	1:A:286:TYR:CB	2.48	0.44
1:C:65:THR:CG2	1:C:66:THR:N	2.80	0.44
1:I:46:PRO:HB3	1:D:99:ALA:HB1	1.98	0.44
1:E:65:THR:CG2	1:E:66:THR:N	2.79	0.44
1:F:144:ILE:HG22	1:G:115:LEU:HD12	1.99	0.44
1:H:266:MET:O	1:H:270:GLN:HG2	2.17	0.44
1:I:144:ILE:HG13	1:I:190:ALA:HA	2.00	0.44
1:L:144:ILE:HG13	1:L:190:ALA:HA	1.98	0.44
1:L:185:ARG:CG	1:L:186:TYR:N	2.79	0.44
1:L:81:HIS:HB2	1:L:266:MET:HE2	1.99	0.44
1:M:76:ALA:HA	1:M:79:PHE:CE2	2.53	0.44
1:O:171:MET:HA	1:O:201:ILE:O	2.17	0.44
1:P:250:VAL:O	1:P:250:VAL:HG23	2.18	0.44
1:Q:56:PHE:CE1	1:Q:87:CYS:HB3	2.52	0.44
1:R:81:HIS:HB2	1:R:266:MET:HE2	1.99	0.44
1:S:21:ASN:O	1:S:23:PRO:HD3	2.17	0.44
1:T:109:SER:HB2	1:T:121:GLU:OE1	2.17	0.44
1:B:171:MET:CE	1:B:173:VAL:HG22	2.47	0.44
1:B:203:LYS:HA	1:B:223:VAL:O	2.18	0.44
1:C:285:LEU:CA	1:C:288:SER:HB3	2.40	0.44
1:D:93:ARG:NH2	1:D:129:ASP:OD1	2.51	0.44
1:G:182:ARG:NH1	1:G:182:ARG:HG2	2.32	0.44
1:K:45:ASN:HA	1:K:46:PRO:HD3	1.85	0.44
1:L:14:ARG:CG	1:L:14:ARG:O	2.64	0.44
1:N:185:ARG:CG	1:N:186:TYR:N	2.75	0.44
1:O:141:GLN:OE1	1:O:173:VAL:CB	2.58	0.44
1:O:55:ALA:HB3	1:O:251:ASP:OD2	2.16	0.44
1:P:42:ARG:HD3	1:P:136:CYS:SG	2.58	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:14:ARG:HG3	1:Q:14:ARG:O	2.17	0.44
1:B:55:ALA:HB3	1:B:251:ASP:OD2	2.17	0.44
1:C:185:ARG:HG3	2:C:322:HOH:O	2.18	0.44
1:J:21:ASN:O	1:J:23:PRO:HD3	2.17	0.44
1:L:73:ILE:HG22	1:L:74:ASN:N	2.33	0.44
1:M:164:MET:HE2	1:M:200:GLN:NE2	2.33	0.44
1:M:285:LEU:CA	1:M:288:SER:HB3	2.37	0.44
1:M:67:GLY:N	1:M:69:GLU:OE1	2.47	0.44
1:M:113:SER:OG	1:N:149:GLU:OE1	2.35	0.44
1:O:75:ILE:O	1:O:78:LEU:HB2	2.18	0.44
1:Q:185:ARG:CG	1:Q:186:TYR:N	2.78	0.44
1:S:110:GLY:O	1:S:111:ALA:CB	2.65	0.44
1:A:287:LEU:HA	1:A:290:LYS:HD3	1.98	0.44
1:E:109:SER:HB2	1:E:121:GLU:OE1	2.18	0.44
1:H:91:ILE:HG13	1:G:196:GLU:OE2	2.17	0.44
1:I:52:VAL:N	1:I:83:ASP:OD2	2.48	0.44
1:J:82:ALA:O	1:J:102:ARG:HD3	2.18	0.44
1:K:187:PHE:HB2	1:K:214:ILE:CD1	2.47	0.44
1:K:285:LEU:HD22	1:K:286:TYR:N	2.30	0.44
1:L:110:GLY:O	1:L:111:ALA:CB	2.63	0.44
1:N:45:ASN:HA	1:N:46:PRO:HD3	1.85	0.44
1:N:76:ALA:N	1:N:77:PRO:HD2	2.32	0.44
1:O:67:GLY:H	1:O:69:GLU:CD	2.20	0.44
1:S:67:GLY:H	1:S:69:GLU:CD	2.20	0.44
1:S:67:GLY:N	1:S:69:GLU:OE1	2.48	0.44
1:H:46:PRO:HB3	1:C:99:ALA:HB1	1.99	0.44
1:E:139:ALA:HA	1:E:171:MET:O	2.18	0.44
1:H:142:VAL:HA	1:H:152:SER:HB2	1.98	0.44
1:K:93:ARG:CZ	1:K:133:LEU:HD21	2.47	0.44
1:L:45:ASN:HA	1:L:46:PRO:HD3	1.84	0.44
1:M:143:TYR:HB3	1:M:146:SER:HB2	2.00	0.44
1:L:113:SER:HG	1:M:149:GLU:CD	2.19	0.44
1:N:126:SER:HB2	2:N:299:HOH:O	2.17	0.44
1:O:254:ARG:HA	1:O:257:PHE:CZ	2.52	0.44
1:Q:261:HIS:CG	1:Q:290:LYS:HG2	2.52	0.44
1:B:277:GLU:OE1	1:B:281:ARG:HD2	2.14	0.44
1:D:173:VAL:HG13	1:D:203:LYS:HB3	1.99	0.44
1:I:187:PHE:HB2	1:I:214:ILE:CD1	2.48	0.44
1:J:136:CYS:O	1:J:169:PRO:HD2	2.18	0.44
1:J:285:LEU:CA	1:J:288:SER:HB3	2.40	0.44
1:K:263:VAL:O	1:K:267:LYS:HG3	2.17	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:285:LEU:HA	1:N:288:SER:CB	2.33	0.44
1:O:149:GLU:CD	1:N:113:SER:HG	2.19	0.44
1:O:67:GLY:N	1:O:69:GLU:OE1	2.48	0.44
1:P:152:SER:O	1:P:155:ASN:HB2	2.18	0.44
1:P:184:GLN:HE21	1:P:185:ARG:HA	1.82	0.44
1:Q:109:SER:CB	1:Q:121:GLU:OE1	2.66	0.44
1:B:144:ILE:HG22	1:A:115:LEU:HD12	1.99	0.44
1:B:32:LEU:HD13	1:B:36:MET:SD	2.58	0.44
1:C:277:GLU:OE1	1:C:281:ARG:HD2	2.16	0.44
1:D:144:ILE:HG13	1:D:190:ALA:HA	2.00	0.44
1:D:55:ALA:HB3	1:D:251:ASP:OD2	2.17	0.44
1:G:39:ARG:O	1:G:42:ARG:HB2	2.17	0.44
1:G:75:ILE:O	1:G:78:LEU:HB2	2.16	0.44
1:H:285:LEU:O	1:H:285:LEU:CD2	2.61	0.44
1:J:187:PHE:HB2	1:J:214:ILE:HD13	1.98	0.44
1:J:65:THR:HG22	1:J:68:LEU:HD12	1.98	0.44
1:O:277:GLU:OE1	1:O:281:ARG:HD2	2.14	0.44
1:P:58:HIS:C	1:P:60:TYR:H	2.21	0.44
1:Q:58:HIS:C	1:Q:60:TYR:N	2.71	0.44
1:S:65:THR:CG2	1:S:66:THR:N	2.81	0.44
1:B:56:PHE:CE1	1:B:87:CYS:HB3	2.53	0.44
1:E:285:LEU:HD22	1:E:286:TYR:N	2.30	0.44
1:H:212:GLU:HB3	1:D:15:THR:HG22	1.99	0.44
1:N:277:GLU:OE1	1:N:281:ARG:HD2	2.14	0.44
1:N:73:ILE:HG22	1:N:74:ASN:N	2.32	0.44
1:R:79:PHE:CD2	1:R:100:THR:HG21	2.53	0.44
1:S:196:GLU:OE2	1:R:91:ILE:HG13	2.18	0.44
1:S:253:GLY:CA	1:S:257:PHE:CE2	2.87	0.44
1:C:182:ARG:NH1	1:C:182:ARG:HG2	2.32	0.43
1:C:144:ILE:HG13	1:C:190:ALA:HA	2.01	0.43
1:C:73:ILE:HG22	1:C:74:ASN:N	2.32	0.43
1:C:52:VAL:N	1:C:83:ASP:OD2	2.44	0.43
1:F:207:VAL:CG1	1:F:209:LYS:O	2.65	0.43
1:I:251:ASP:C	1:I:251:ASP:OD1	2.56	0.43
1:L:279:ALA:O	1:L:282:ALA:HB3	2.18	0.43
1:O:285:LEU:CA	1:O:288:SER:HB3	2.37	0.43
1:R:109:SER:HB2	1:R:121:GLU:OE1	2.18	0.43
1:R:93:ARG:NH2	1:R:129:ASP:OD1	2.49	0.43
1:R:20:LYS:HE3	1:R:20:LYS:HB2	1.82	0.43
1:S:196:GLU:HG3	1:R:88:THR:HG21	1.99	0.43
1:A:14:ARG:CG	1:A:14:ARG:O	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:21:ASN:O	1:B:23:PRO:HD3	2.18	0.43
1:B:253:GLY:O	1:B:257:PHE:CD2	2.71	0.43
1:D:143:TYR:O	1:D:149:GLU:HB2	2.17	0.43
1:F:164:MET:HE2	1:F:200:GLN:HE22	1.83	0.43
1:G:106:LEU:HD23	1:G:106:LEU:HA	1.89	0.43
1:G:56:PHE:CE1	1:G:87:CYS:HB3	2.52	0.43
1:H:45:ASN:OD1	1:H:47:LYS:N	2.51	0.43
1:M:81:HIS:O	1:M:266:MET:HE2	2.18	0.43
1:N:21:ASN:O	1:N:23:PRO:HD3	2.18	0.43
1:B:144:ILE:HG13	1:B:190:ALA:HA	1.99	0.43
1:C:107:ARG:NH1	1:C:109:SER:OG	2.49	0.43
1:D:143:TYR:HB3	1:D:146:SER:HB2	1.99	0.43
1:H:52:VAL:N	1:H:83:ASP:OD2	2.44	0.43
1:I:14:ARG:HE	1:I:14:ARG:HB2	1.35	0.43
1:I:266:MET:O	1:I:270:GLN:CG	2.67	0.43
1:I:93:ARG:NH1	1:D:33:ASP:CG	2.71	0.43
1:F:110:GLY:HA3	1:J:197:MET:HE3	2.00	0.43
1:J:261:HIS:ND1	1:J:290:LYS:HG2	2.33	0.43
1:L:56:PHE:CE1	1:L:87:CYS:HB3	2.53	0.43
1:L:70:ARG:NH2	1:L:73:ILE:CD1	2.79	0.43
1:O:144:ILE:HG22	1:N:115:LEU:HD12	2.00	0.43
1:A:73:ILE:HG22	1:A:74:ASN:N	2.33	0.43
1:D:109:SER:CB	1:D:121:GLU:OE1	2.66	0.43
1:E:144:ILE:HG21	1:E:189:LEU:HD23	2.00	0.43
1:G:277:GLU:OE1	1:G:281:ARG:HD2	2.14	0.43
1:H:107:ARG:O	1:H:107:ARG:HG3	2.18	0.43
1:H:93:ARG:NH2	1:H:129:ASP:OD1	2.50	0.43
1:H:56:PHE:CE1	1:H:87:CYS:HB3	2.52	0.43
1:J:250:VAL:HG23	1:J:250:VAL:O	2.17	0.43
1:M:265:MET:O	1:M:269:VAL:HG23	2.18	0.43
1:O:260:ASP:C	1:O:262:PRO:HD3	2.39	0.43
1:Q:129:ASP:HA	1:Q:132:ARG:NH1	2.33	0.43
1:Q:184:GLN:HE21	1:Q:185:ARG:HA	1.82	0.43
1:Q:115:LEU:HD12	1:R:144:ILE:HG22	2.00	0.43
1:R:185:ARG:CG	1:R:186:TYR:N	2.80	0.43
1:B:197:MET:HE1	1:A:110:GLY:HA3	2.00	0.43
1:A:76:ALA:HB3	1:A:77:PRO:CD	2.48	0.43
1:A:78:LEU:HD23	1:A:78:LEU:HA	1.68	0.43
1:D:164:MET:HE1	1:D:200:GLN:NE2	2.33	0.43
1:E:115:LEU:HD12	1:A:144:ILE:HG22	2.00	0.43
1:E:279:ALA:O	1:E:282:ALA:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:78:LEU:HD23	1:I:78:LEU:HA	1.70	0.43
1:L:283:TYR:O	1:L:286:TYR:CB	2.52	0.43
1:M:283:TYR:CZ	1:M:287:LEU:HD11	2.50	0.43
1:P:143:TYR:HB3	1:P:146:SER:HB2	2.01	0.43
1:P:182:ARG:NH1	1:P:182:ARG:HG2	2.31	0.43
1:R:73:ILE:HG22	1:R:74:ASN:N	2.33	0.43
1:S:268:ALA:HA	1:S:285:LEU:HD11	2.01	0.43
1:C:61:PHE:CD2	1:C:61:PHE:N	2.86	0.43
1:E:197:MET:CE	1:D:111:ALA:H	2.31	0.43
1:F:144:ILE:HG21	1:F:189:LEU:HD23	2.00	0.43
1:I:91:ILE:HG13	1:H:196:GLU:OE2	2.18	0.43
1:J:142:VAL:HA	1:J:152:SER:HB2	2.00	0.43
1:N:164:MET:HE1	1:N:200:GLN:NE2	2.32	0.43
1:O:70:ARG:CZ	1:O:73:ILE:HD12	2.49	0.43
1:P:251:ASP:C	1:P:251:ASP:OD1	2.56	0.43
1:R:143:TYR:HB3	1:R:146:SER:HB2	1.99	0.43
1:R:76:ALA:HA	1:R:79:PHE:CE2	2.54	0.43
1:C:185:ARG:CG	1:C:186:TYR:N	2.79	0.43
1:C:83:ASP:O	1:C:103:PRO:HD2	2.19	0.43
1:G:81:HIS:O	1:G:266:MET:HE2	2.18	0.43
1:J:20:LYS:HB2	1:J:20:LYS:HE3	1.72	0.43
1:J:287:LEU:HA	1:J:290:LYS:HD3	2.01	0.43
1:K:14:ARG:HB2	1:K:14:ARG:HE	1.36	0.43
1:K:279:ALA:O	1:K:282:ALA:HB3	2.19	0.43
1:L:65:THR:CG2	1:L:66:THR:N	2.81	0.43
1:L:110:GLY:HA3	1:M:197:MET:HE3	2.00	0.43
1:M:88:THR:OG1	1:N:196:GLU:HG3	2.18	0.43
1:P:58:HIS:C	1:P:60:TYR:N	2.71	0.43
1:C:124:ALA:HA	1:D:157:ILE:HD13	2.00	0.43
1:C:93:ARG:NH2	1:C:129:ASP:OD1	2.49	0.43
1:H:15:THR:HG22	1:D:212:GLU:HB3	2.00	0.43
1:D:65:THR:HG22	1:D:68:LEU:HD12	2.01	0.43
1:I:110:GLY:HA3	1:H:197:MET:HE1	1.98	0.43
1:I:283:TYR:O	1:I:286:TYR:CB	2.47	0.43
1:M:200:GLN:O	1:M:220:VAL:HB	2.19	0.43
1:M:67:GLY:H	1:M:69:GLU:CD	2.21	0.43
1:N:273:VAL:HG12	1:N:274:HIS:HD2	1.84	0.43
1:O:164:MET:HE2	1:O:200:GLN:NE2	2.31	0.43
1:A:191:THR:HG22	1:A:202:ILE:CG2	2.45	0.43
1:E:182:ARG:HG2	1:E:182:ARG:NH1	2.31	0.43
1:F:279:ALA:O	1:F:282:ALA:HB3	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:266:MET:O	1:P:270:GLN:HG2	2.19	0.43
1:R:14:ARG:O	1:R:14:ARG:CG	2.66	0.43
1:S:184:GLN:HE21	1:S:185:ARG:HA	1.84	0.43
1:T:254:ARG:N	1:T:257:PHE:CE2	2.86	0.43
1:T:70:ARG:NH2	1:T:73:ILE:CD1	2.81	0.43
1:B:156:ILE:O	1:B:160:VAL:HG23	2.18	0.43
1:B:159:LEU:HD23	1:B:159:LEU:HA	1.90	0.43
1:C:253:GLY:O	1:C:257:PHE:CD2	2.72	0.43
1:D:203:LYS:HA	1:D:223:VAL:O	2.18	0.43
1:G:261:HIS:ND1	1:G:290:LYS:HG2	2.33	0.43
1:H:239:CYS:HG	1:H:252:MET:CE	2.22	0.43
1:O:93:ARG:NH2	1:O:129:ASP:OD1	2.51	0.43
1:Q:14:ARG:HE	1:Q:14:ARG:HB2	1.32	0.43
1:Q:228:LYS:HZ2	1:Q:230:LEU:HD23	1.84	0.43
1:Q:67:GLY:H	1:Q:69:GLU:CD	2.22	0.43
1:S:127:MET:SD	1:S:168:MET:HG2	2.59	0.43
1:S:273:VAL:HG12	1:S:274:HIS:HD2	1.83	0.43
1:S:283:TYR:CZ	1:S:287:LEU:HD11	2.51	0.43
1:T:185:ARG:HG2	1:T:186:TYR:N	2.33	0.43
1:A:61:PHE:N	1:A:61:PHE:CD2	2.87	0.42
1:C:184:GLN:HE21	1:C:185:ARG:HA	1.82	0.42
1:C:65:THR:HG22	1:C:68:LEU:HD12	2.01	0.42
1:E:65:THR:HG22	1:E:68:LEU:HD12	2.01	0.42
1:G:185:ARG:CG	1:G:186:TYR:N	2.81	0.42
1:G:93:ARG:CZ	1:G:133:LEU:HD21	2.48	0.42
1:I:81:HIS:HB2	1:I:266:MET:HE2	2.00	0.42
1:K:191:THR:HG22	1:K:202:ILE:CG2	2.46	0.42
1:N:263:VAL:O	1:N:267:LYS:HG3	2.19	0.42
1:Q:285:LEU:O	1:Q:285:LEU:CD2	2.66	0.42
1:S:81:HIS:O	1:S:266:MET:HE2	2.19	0.42
1:T:207:VAL:CG1	1:T:209:LYS:O	2.67	0.42
1:T:266:MET:HE2	1:T:266:MET:HB3	1.93	0.42
1:C:127:MET:HE3	1:C:162:ALA:HB3	2.01	0.42
1:E:65:THR:CG2	1:E:68:LEU:CD1	2.96	0.42
1:E:93:ARG:CZ	1:E:133:LEU:HD21	2.49	0.42
1:G:159:LEU:HD23	1:G:159:LEU:HA	1.91	0.42
1:G:279:ALA:O	1:G:282:ALA:HB3	2.19	0.42
1:I:263:VAL:O	1:I:267:LYS:HG3	2.19	0.42
1:L:83:ASP:O	1:L:103:PRO:HD2	2.19	0.42
1:O:185:ARG:HG2	1:O:186:TYR:N	2.34	0.42
1:P:52:VAL:N	1:P:83:ASP:OD2	2.42	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:Q:184:GLN:O	1:Q:185:ARG:C	2.55	0.42
1:Q:88:THR:CA	2:Q:300:HOH:O	2.67	0.42
1:R:156:ILE:HD13	1:R:156:ILE:HA	1.89	0.42
1:R:182:ARG:HG2	1:R:182:ARG:NH1	2.33	0.42
1:A:144:ILE:HG13	1:A:190:ALA:HA	2.01	0.42
1:C:106:LEU:HD23	1:C:106:LEU:HA	1.85	0.42
1:D:285:LEU:HA	1:D:288:SER:CB	2.40	0.42
1:G:171:MET:HA	1:G:201:ILE:O	2.18	0.42
1:G:187:PHE:HB2	1:G:214:ILE:CD1	2.50	0.42
1:N:287:LEU:HD23	1:G:275:HIS:HE1	1.75	0.42
1:I:45:ASN:HA	1:I:46:PRO:HD3	1.81	0.42
1:K:20:LYS:HB2	1:K:20:LYS:HE3	1.78	0.42
1:M:254:ARG:N	1:M:257:PHE:CE2	2.87	0.42
1:O:185:ARG:CG	1:O:186:TYR:N	2.83	0.42
1:O:266:MET:O	1:O:270:GLN:HG2	2.19	0.42
1:S:156:ILE:O	1:S:160:VAL:HG23	2.19	0.42
1:P:197:MET:HE3	1:T:110:GLY:HA3	2.00	0.42
1:T:93:ARG:CZ	1:T:133:LEU:HD21	2.48	0.42
1:B:110:GLY:O	1:B:111:ALA:HB3	2.19	0.42
1:F:109:SER:CB	1:F:121:GLU:OE1	2.68	0.42
1:K:159:LEU:HD23	1:K:159:LEU:HA	1.91	0.42
1:Q:58:HIS:O	1:Q:62:GLN:HB2	2.18	0.42
1:R:250:VAL:O	1:R:250:VAL:HG23	2.18	0.42
1:R:81:HIS:O	1:R:266:MET:CE	2.67	0.42
1:T:252:MET:CB	1:T:256:ILE:HG13	2.45	0.42
1:A:65:THR:CG2	1:A:66:THR:N	2.81	0.42
1:B:182:ARG:HG2	1:B:182:ARG:NH1	2.32	0.42
1:C:266:MET:O	1:C:270:GLN:HG2	2.19	0.42
1:D:187:PHE:HB2	1:D:214:ILE:CD1	2.49	0.42
1:I:212:GLU:HB2	1:E:15:THR:HG21	1.96	0.42
1:E:20:LYS:HE3	1:E:20:LYS:HB2	1.82	0.42
1:H:55:ALA:HB3	1:H:251:ASP:OD2	2.19	0.42
1:K:19:GLN:NE2	2:K:297:HOH:O	2.52	0.42
1:K:232:GLU:O	1:K:233:ARG:C	2.55	0.42
1:N:143:TYR:HB3	1:N:146:SER:HB2	2.01	0.42
1:N:61:PHE:N	1:N:61:PHE:CD2	2.88	0.42
1:O:200:GLN:O	1:O:220:VAL:HB	2.18	0.42
1:O:250:VAL:O	1:O:250:VAL:HG23	2.20	0.42
1:O:252:MET:O	1:O:256:ILE:HG13	2.19	0.42
1:O:65:THR:CG2	1:O:68:LEU:CD1	2.96	0.42
1:Q:67:GLY:N	1:Q:69:GLU:OE1	2.52	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:ARG:HD3	1:A:136:CYS:SG	2.60	0.42
1:E:110:GLY:HA3	1:A:197:MET:HE1	2.00	0.42
1:E:171:MET:HG3	1:E:201:ILE:CB	2.40	0.42
1:F:184:GLN:HE21	1:F:185:ARG:HA	1.83	0.42
1:F:250:VAL:O	1:F:250:VAL:CG2	2.66	0.42
1:G:14:ARG:CG	1:G:14:ARG:O	2.68	0.42
1:J:76:ALA:HA	1:J:79:PHE:CE2	2.55	0.42
1:N:14:ARG:CG	1:N:14:ARG:O	2.66	0.42
1:O:143:TYR:O	1:O:149:GLU:HB2	2.19	0.42
1:R:144:ILE:HG13	1:R:190:ALA:HA	2.01	0.42
1:B:266:MET:O	1:B:270:GLN:HG2	2.20	0.42
1:C:110:GLY:HA3	1:D:197:MET:HE2	2.01	0.42
1:C:55:ALA:HB3	1:C:251:ASP:OD2	2.20	0.42
1:I:93:ARG:NH1	1:D:33:ASP:OD2	2.53	0.42
1:G:216:ALA:HB3	1:C:13:PHE:HB3	2.01	0.42
1:H:102:ARG:HG3	1:H:103:PRO:CD	2.49	0.42
1:H:156:ILE:HA	1:H:156:ILE:HD13	1.87	0.42
1:H:279:ALA:O	1:H:282:ALA:HB3	2.20	0.42
1:J:99:ALA:HB1	1:E:46:PRO:HB3	2.00	0.42
1:K:83:ASP:O	1:K:103:PRO:HD2	2.20	0.42
1:L:52:VAL:N	1:L:83:ASP:OD2	2.48	0.42
1:L:88:THR:HG21	1:M:196:GLU:HG3	2.01	0.42
1:M:277:GLU:OE1	1:M:281:ARG:HD2	2.15	0.42
1:N:250:VAL:O	1:N:250:VAL:HG23	2.20	0.42
1:Q:156:ILE:HD13	1:Q:156:ILE:HA	1.88	0.42
1:A:20:LYS:HB2	1:A:20:LYS:HE3	1.74	0.42
1:C:171:MET:CE	1:C:173:VAL:HG22	2.49	0.42
1:E:285:LEU:CA	1:E:288:SER:HB3	2.37	0.42
1:F:136:CYS:O	1:F:169:PRO:HD2	2.19	0.42
1:G:33:ASP:OD2	1:B:93:ARG:NH1	2.52	0.42
1:N:14:ARG:HE	1:N:14:ARG:HB2	1.30	0.42
1:P:14:ARG:O	1:P:14:ARG:HG3	2.19	0.42
1:P:20:LYS:HE3	1:P:20:LYS:HB2	1.70	0.42
1:P:76:ALA:HA	1:P:79:PHE:CE2	2.54	0.42
1:A:93:ARG:CZ	1:A:133:LEU:HD21	2.50	0.42
1:D:136:CYS:O	1:D:169:PRO:HD2	2.19	0.42
1:D:65:THR:CG2	1:D:68:LEU:CD1	2.98	0.42
1:E:14:ARG:CG	1:E:14:ARG:O	2.66	0.42
1:E:156:ILE:O	1:E:160:VAL:HG23	2.20	0.42
1:J:45:ASN:HA	1:J:46:PRO:HD3	1.85	0.42
1:M:263:VAL:O	1:M:267:LYS:HG3	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:79:PHE:CD2	1:O:100:THR:CG2	3.03	0.42
1:Q:58:HIS:C	1:Q:60:TYR:H	2.22	0.42
1:R:106:LEU:HA	1:R:106:LEU:HD23	1.85	0.42
1:S:196:GLU:HG3	1:R:88:THR:OG1	2.20	0.42
1:T:92:LEU:HA	1:T:96:VAL:CG2	2.50	0.42
1:A:184:GLN:O	1:A:185:ARG:C	2.58	0.42
1:B:207:VAL:CG1	1:B:209:LYS:O	2.68	0.42
1:C:266:MET:HB3	1:C:266:MET:HE2	1.91	0.42
1:C:81:HIS:HB2	1:C:266:MET:HE2	2.01	0.42
1:E:124:ALA:HA	1:A:157:ILE:HD13	2.00	0.42
1:J:132:ARG:O	1:E:35:GLY:HA3	2.20	0.42
1:H:73:ILE:HG22	1:H:74:ASN:N	2.33	0.42
1:I:182:ARG:HG2	1:I:182:ARG:NH1	2.32	0.42
1:K:283:TYR:O	1:K:286:TYR:CB	2.48	0.42
1:N:171:MET:HA	1:N:201:ILE:O	2.20	0.42
1:P:263:VAL:O	1:P:267:LYS:HG3	2.20	0.42
1:R:52:VAL:N	1:R:83:ASP:OD2	2.47	0.42
1:S:14:ARG:HB2	1:S:14:ARG:HE	1.35	0.42
1:S:184:GLN:O	1:S:185:ARG:C	2.58	0.42
1:T:232:GLU:O	1:T:233:ARG:C	2.56	0.42
1:T:55:ALA:HB3	1:T:251:ASP:OD2	2.20	0.42
1:A:182:ARG:HG2	1:A:182:ARG:NH1	2.33	0.41
1:C:70:ARG:NH2	1:C:73:ILE:CD1	2.79	0.41
1:D:56:PHE:CE1	1:D:87:CYS:HB3	2.55	0.41
1:D:70:ARG:CZ	1:D:73:ILE:HD12	2.49	0.41
1:E:127:MET:SD	1:E:168:MET:HG2	2.60	0.41
1:I:13:PHE:CD2	1:E:213:ARG:HG2	2.54	0.41
1:G:110:GLY:O	1:G:111:ALA:CB	2.68	0.41
1:H:33:ASP:CG	1:C:93:ARG:NH1	2.73	0.41
1:I:156:ILE:HA	1:I:156:ILE:HD13	1.91	0.41
1:I:207:VAL:CG1	1:I:209:LYS:O	2.67	0.41
1:K:58:HIS:C	1:K:60:TYR:N	2.73	0.41
1:L:273:VAL:HG12	1:L:274:HIS:HD2	1.85	0.41
1:P:144:ILE:HG13	1:P:190:ALA:HA	2.00	0.41
1:R:164:MET:HE1	1:R:200:GLN:NE2	2.34	0.41
1:T:171:MET:CE	1:T:173:VAL:HG22	2.50	0.41
1:B:14:ARG:HE	1:B:14:ARG:HB2	1.33	0.41
1:H:35:GLY:HA3	1:C:132:ARG:O	2.20	0.41
1:C:143:TYR:O	1:C:149:GLU:HB2	2.20	0.41
1:C:65:THR:CG2	1:C:68:LEU:CD1	2.97	0.41
1:E:39:ARG:HD2	1:E:167:GLY:O	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:70:ARG:CZ	1:E:73:ILE:HD12	2.50	0.41
1:G:45:ASN:HA	1:G:46:PRO:HD3	1.81	0.41
1:L:81:HIS:O	1:L:266:MET:HE2	2.20	0.41
1:Q:110:GLY:HA3	1:R:197:MET:HE1	2.02	0.41
1:Q:229:LYS:HD2	1:Q:255:ASN:HA	2.02	0.41
1:R:251:ASP:C	1:R:251:ASP:OD1	2.56	0.41
1:S:73:ILE:HG22	1:S:74:ASN:N	2.34	0.41
1:T:81:HIS:HB2	1:T:266:MET:HE2	2.01	0.41
1:A:285:LEU:HA	1:A:288:SER:CB	2.38	0.41
1:E:88:THR:HG21	1:A:196:GLU:HG3	2.03	0.41
1:F:261:HIS:ND1	1:F:290:LYS:HG2	2.36	0.41
1:H:144:ILE:HG13	1:H:190:ALA:HA	2.01	0.41
1:I:152:SER:O	1:I:155:ASN:HB2	2.20	0.41
1:J:283:TYR:CZ	1:J:287:LEU:HD11	2.48	0.41
1:O:73:ILE:HG22	1:O:74:ASN:N	2.36	0.41
1:P:129:ASP:HA	1:P:132:ARG:NH1	2.34	0.41
1:P:67:GLY:H	1:P:69:GLU:CD	2.23	0.41
1:P:91:ILE:HG13	1:Q:196:GLU:OE2	2.20	0.41
1:T:171:MET:HA	1:T:201:ILE:O	2.20	0.41
1:T:253:GLY:HA2	1:T:257:PHE:HE2	1.83	0.41
1:T:75:ILE:O	1:T:78:LEU:HB2	2.20	0.41
1:E:164:MET:HE3	1:E:200:GLN:NE2	2.36	0.41
1:L:39:ARG:O	1:L:42:ARG:HB2	2.20	0.41
1:M:73:ILE:HG22	1:M:74:ASN:N	2.36	0.41
1:N:268:ALA:HA	1:N:285:LEU:HD11	2.03	0.41
1:O:20:LYS:HB2	1:O:20:LYS:HE3	1.74	0.41
1:P:159:LEU:HD23	1:P:159:LEU:HA	1.91	0.41
1:P:171:MET:CE	1:P:173:VAL:HG22	2.50	0.41
1:R:279:ALA:O	1:R:282:ALA:HB3	2.21	0.41
1:T:65:THR:CG2	1:T:66:THR:N	2.84	0.41
1:B:93:ARG:NH2	1:B:129:ASP:OD1	2.53	0.41
1:B:143:TYR:O	1:B:149:GLU:HB2	2.20	0.41
1:B:88:THR:HG21	1:C:196:GLU:CG	2.51	0.41
1:C:76:ALA:HA	1:C:79:PHE:CE2	2.55	0.41
1:D:251:ASP:OD1	1:D:251:ASP:C	2.56	0.41
1:D:52:VAL:N	1:D:83:ASP:OD2	2.49	0.41
1:G:220:VAL:HB	1:G:221:PRO:HD2	2.01	0.41
1:G:53:MET:HG3	1:G:84:VAL:HG13	2.03	0.41
1:J:171:MET:HA	1:J:201:ILE:O	2.20	0.41
1:L:136:CYS:O	1:L:169:PRO:HD2	2.20	0.41
1:N:159:LEU:HD23	1:N:159:LEU:HA	1.90	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:196:GLU:HG3	1:T:88:THR:HG21	2.02	0.41
1:Q:276:ASN:O	1:Q:277:GLU:C	2.59	0.41
1:R:125:LEU:C	1:R:125:LEU:HD13	2.37	0.41
1:R:228:LYS:HZ2	1:R:230:LEU:HD23	1.85	0.41
1:S:252:MET:CB	1:S:256:ILE:HG13	2.46	0.41
1:T:78:LEU:HA	1:T:78:LEU:HD23	1.75	0.41
1:C:281:ARG:HB3	2:C:316:HOH:O	2.20	0.41
1:E:196:GLU:OE2	1:D:91:ILE:HG13	2.20	0.41
1:F:52:VAL:N	1:F:83:ASP:OD2	2.45	0.41
1:F:99:ALA:HB1	1:A:46:PRO:HB3	2.02	0.41
1:H:58:HIS:C	1:H:60:TYR:N	2.73	0.41
1:I:191:THR:HG22	1:I:202:ILE:CG2	2.47	0.41
1:J:230:LEU:HB3	1:J:231:PRO:HD2	2.02	0.41
1:K:182:ARG:HG2	1:K:182:ARG:NH1	2.34	0.41
1:L:61:PHE:N	1:L:61:PHE:CD2	2.89	0.41
1:Q:56:PHE:N	1:Q:56:PHE:CD2	2.89	0.41
1:S:285:LEU:HD23	1:S:289:GLU:HG2	2.02	0.41
1:T:14:ARG:CG	1:T:14:ARG:O	2.66	0.41
1:A:273:VAL:HG12	1:A:274:HIS:HD2	1.85	0.41
1:B:42:ARG:HD3	1:B:136:CYS:SG	2.61	0.41
1:C:233:ARG:NH1	1:C:233:ARG:CG	2.47	0.41
1:D:232:GLU:O	1:D:233:ARG:C	2.59	0.41
1:G:251:ASP:OD1	1:G:251:ASP:C	2.59	0.41
1:G:70:ARG:CZ	1:G:73:ILE:HD12	2.50	0.41
1:I:65:THR:CG2	1:I:66:THR:N	2.83	0.41
1:M:106:LEU:HA	1:M:106:LEU:HD23	1.84	0.41
1:N:173:VAL:HG13	1:N:203:LYS:HB3	2.03	0.41
1:O:81:HIS:HB2	1:O:266:MET:HE2	2.03	0.41
1:Q:213:ARG:NH1	2:Q:293:HOH:O	2.54	0.41
1:R:58:HIS:O	1:R:62:GLN:HB2	2.21	0.41
1:A:253:GLY:CA	1:A:257:PHE:CE2	2.84	0.41
1:B:61:PHE:CD2	1:B:61:PHE:N	2.89	0.41
1:C:21:ASN:O	1:C:23:PRO:HD3	2.20	0.41
1:D:254:ARG:N	1:D:257:PHE:CE2	2.88	0.41
1:G:143:TYR:HB3	1:G:146:SER:HB2	2.02	0.41
1:I:287:LEU:HA	1:I:290:LYS:HD3	2.02	0.41
1:I:56:PHE:CE1	1:I:87:CYS:HB3	2.56	0.41
1:I:73:ILE:HG22	1:I:74:ASN:N	2.35	0.41
1:K:127:MET:SD	1:K:168:MET:HG2	2.61	0.41
1:K:171:MET:HE3	1:K:173:VAL:HG22	2.02	0.41
1:K:164:MET:HE2	1:K:200:GLN:HE22	1.81	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:81:HIS:O	1:K:266:MET:HE2	2.20	0.41
1:K:61:PHE:CD2	1:K:61:PHE:N	2.89	0.41
1:K:65:THR:CG2	1:K:66:THR:N	2.83	0.41
1:K:76:ALA:HB3	1:K:77:PRO:CD	2.50	0.41
1:L:127:MET:SD	1:L:168:MET:HG2	2.61	0.41
1:L:187:PHE:HB2	1:L:214:ILE:CD1	2.50	0.41
1:L:237:GLU:O	1:L:241:GLN:HG2	2.21	0.41
1:P:89:ARG:HG2	2:Q:295:HOH:O	2.19	0.41
1:Q:141:GLN:OE1	1:Q:173:VAL:CB	2.60	0.41
1:Q:65:THR:CG2	1:Q:68:LEU:CD1	2.97	0.41
1:S:135:SER:HB2	1:S:168:MET:CE	2.50	0.41
1:T:265:MET:O	1:T:269:VAL:HG23	2.20	0.41
1:C:88:THR:OG1	1:D:196:GLU:HG3	2.21	0.41
1:F:254:ARG:HA	1:F:257:PHE:CZ	2.56	0.41
1:I:106:LEU:HA	1:I:106:LEU:HD23	1.87	0.41
1:I:67:GLY:H	1:I:69:GLU:CD	2.24	0.41
1:J:103:PRO:HB3	1:J:136:CYS:SG	2.61	0.41
1:L:184:GLN:HE21	1:L:185:ARG:HA	1.85	0.41
1:L:285:LEU:HA	1:L:288:SER:CB	2.36	0.41
1:O:65:THR:HG22	1:O:68:LEU:HD12	2.03	0.41
1:P:237:GLU:O	1:P:241:GLN:HG2	2.21	0.41
1:R:14:ARG:HE	1:R:14:ARG:HB2	1.32	0.41
1:R:156:ILE:O	1:R:160:VAL:HG23	2.20	0.41
1:R:283:TYR:O	1:R:286:TYR:CB	2.52	0.41
1:T:122:ALA:CA	2:T:298:HOH:O	2.64	0.41
1:A:159:LEU:HD23	1:A:159:LEU:HA	1.89	0.41
1:B:110:GLY:HA3	1:C:197:MET:HE1	2.02	0.41
1:B:45:ASN:HA	1:B:46:PRO:HD3	1.79	0.41
1:C:237:GLU:O	1:C:241:GLN:HG2	2.21	0.41
1:C:287:LEU:HA	1:C:290:LYS:HD3	2.02	0.41
1:H:132:ARG:O	1:C:35:GLY:HA3	2.20	0.41
1:E:106:LEU:HD23	1:E:106:LEU:HA	1.83	0.41
1:J:39:ARG:O	1:J:42:ARG:HB2	2.20	0.41
1:L:266:MET:HE2	1:L:266:MET:HB3	1.90	0.41
1:M:65:THR:HG23	1:M:66:THR:N	2.36	0.41
1:O:184:GLN:O	1:O:185:ARG:C	2.59	0.41
1:P:93:ARG:NH2	1:P:129:ASP:OD1	2.54	0.41
1:P:65:THR:CG2	1:P:66:THR:N	2.84	0.41
1:Q:14:ARG:O	1:Q:14:ARG:CG	2.69	0.41
1:R:184:GLN:O	1:R:185:ARG:C	2.59	0.41
1:R:58:HIS:C	1:R:60:TYR:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:266:MET:HE2	1:A:266:MET:HB3	1.89	0.41
1:A:99:ALA:C	1:A:101:ASN:N	2.73	0.41
1:G:35:GLY:HA3	1:B:132:ARG:O	2.20	0.41
1:B:250:VAL:HG23	1:B:250:VAL:O	2.19	0.41
1:B:53:MET:HG3	1:B:84:VAL:HG13	2.02	0.41
1:G:46:PRO:HB3	1:B:99:ALA:HB1	2.03	0.41
1:C:39:ARG:O	1:C:42:ARG:HB2	2.21	0.41
1:E:103:PRO:HB3	1:E:136:CYS:SG	2.61	0.41
1:E:283:TYR:CZ	1:E:287:LEU:HD11	2.54	0.41
1:G:164:MET:HE1	1:G:200:GLN:HE22	1.84	0.41
1:I:14:ARG:O	1:I:14:ARG:CG	2.68	0.41
1:I:196:GLU:HG3	1:J:88:THR:OG1	2.21	0.41
1:M:61:PHE:CD2	1:M:61:PHE:N	2.89	0.41
1:M:70:ARG:NH2	1:M:73:ILE:CD1	2.81	0.41
1:N:136:CYS:O	1:N:169:PRO:HD2	2.20	0.41
1:N:58:HIS:O	1:N:62:GLN:HB2	2.20	0.41
1:O:207:VAL:CG1	1:O:209:LYS:O	2.68	0.41
1:O:78:LEU:HD23	1:O:78:LEU:HA	1.73	0.41
1:P:254:ARG:HA	1:P:257:PHE:CZ	2.56	0.41
1:S:144:ILE:HG21	1:S:189:LEU:HD23	2.03	0.41
1:T:279:ALA:O	1:T:282:ALA:HB3	2.21	0.41
1:B:187:PHE:HB2	1:B:214:ILE:HD13	2.03	0.40
1:B:268:ALA:HA	1:B:285:LEU:HD11	2.03	0.40
1:G:15:THR:HG22	1:C:212:GLU:HB3	2.01	0.40
1:C:283:TYR:O	1:C:286:TYR:CB	2.52	0.40
1:E:220:VAL:HB	1:E:221:PRO:HD2	2.03	0.40
1:F:15:THR:HG21	1:B:212:GLU:HB2	1.96	0.40
1:F:266:MET:O	1:F:270:GLN:HG2	2.21	0.40
1:G:156:ILE:O	1:G:160:VAL:HG23	2.21	0.40
1:I:109:SER:CB	1:I:121:GLU:OE1	2.69	0.40
1:J:46:PRO:HB3	1:E:99:ALA:HB1	2.02	0.40
1:K:254:ARG:HA	1:K:257:PHE:CZ	2.56	0.40
1:L:103:PRO:HB3	1:L:136:CYS:SG	2.61	0.40
1:L:45:ASN:OD1	1:L:47:LYS:N	2.54	0.40
1:M:232:GLU:O	1:M:233:ARG:C	2.60	0.40
1:O:106:LEU:HD23	1:O:106:LEU:HA	1.85	0.40
1:O:232:GLU:O	1:O:233:ARG:C	2.59	0.40
1:P:203:LYS:HA	1:P:223:VAL:O	2.20	0.40
1:Q:111:ALA:H	1:R:197:MET:CE	2.29	0.40
1:Q:20:LYS:HE3	1:Q:20:LYS:HB2	1.81	0.40
1:Q:32:LEU:HD13	1:Q:36:MET:SD	2.61	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:R:103:PRO:HB3	1:R:136:CYS:SG	2.62	0.40
1:B:191:THR:HG22	1:B:202:ILE:CG2	2.50	0.40
1:D:14:ARG:O	1:D:14:ARG:CG	2.70	0.40
1:D:20:LYS:HB2	1:D:20:LYS:HE3	1.80	0.40
1:D:67:GLY:H	1:D:69:GLU:CD	2.25	0.40
1:E:143:TYR:HB3	1:E:146:SER:HB2	2.02	0.40
1:E:157:ILE:HG22	1:E:158:GLN:N	2.36	0.40
1:E:237:GLU:O	1:E:241:GLN:HG2	2.21	0.40
1:E:251:ASP:C	1:E:251:ASP:OD1	2.58	0.40
1:F:14:ARG:HB2	1:F:14:ARG:HE	1.33	0.40
1:F:76:ALA:HA	1:F:79:PHE:CE2	2.56	0.40
1:F:53:MET:HG3	1:F:84:VAL:HG13	2.04	0.40
1:J:67:GLY:N	1:J:69:GLU:OE1	2.54	0.40
1:J:78:LEU:HD23	1:J:78:LEU:HA	1.78	0.40
1:K:203:LYS:HA	1:K:223:VAL:O	2.21	0.40
1:K:32:LEU:HD13	1:K:36:MET:SD	2.61	0.40
1:M:110:GLY:O	1:M:111:ALA:HB3	2.21	0.40
1:M:228:LYS:HZ2	1:M:230:LEU:HD23	1.87	0.40
1:M:70:ARG:CZ	1:M:73:ILE:HD12	2.51	0.40
1:N:58:HIS:C	1:N:60:TYR:N	2.74	0.40
1:N:65:THR:HG23	1:N:66:THR:N	2.36	0.40
1:O:14:ARG:CG	1:O:14:ARG:O	2.69	0.40
1:O:45:ASN:HA	1:O:46:PRO:HD3	1.88	0.40
1:P:56:PHE:CE1	1:P:87:CYS:HB3	2.55	0.40
1:Q:253:GLY:HA2	1:Q:257:PHE:HE2	1.83	0.40
1:Q:266:MET:HE2	1:Q:266:MET:HB3	1.93	0.40
1:T:184:GLN:O	1:T:185:ARG:C	2.59	0.40
1:B:113:SER:HG	1:C:149:GLU:CD	2.23	0.40
1:B:261:HIS:ND1	1:B:290:LYS:HG2	2.37	0.40
1:D:252:MET:O	1:D:256:ILE:HG13	2.21	0.40
1:D:266:MET:O	1:D:270:GLN:HG2	2.21	0.40
1:D:39:ARG:O	1:D:42:ARG:HB2	2.22	0.40
1:F:110:GLY:O	1:F:111:ALA:CB	2.62	0.40
1:F:55:ALA:HB3	1:F:251:ASP:OD2	2.22	0.40
1:H:207:VAL:CG1	1:H:209:LYS:O	2.69	0.40
1:I:20:LYS:HE3	1:I:20:LYS:HB2	1.76	0.40
1:I:285:LEU:CA	1:I:288:SER:HB3	2.39	0.40
1:J:254:ARG:HA	1:J:257:PHE:CZ	2.57	0.40
1:J:61:PHE:CD2	1:J:61:PHE:N	2.89	0.40
1:N:230:LEU:HB3	1:N:231:PRO:HD2	2.03	0.40
1:N:252:MET:CB	1:N:256:ILE:HG13	2.48	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:N:253:GLY:CA	1:N:257:PHE:CE2	2.92	0.40
1:P:114:ILE:HD11	1:Q:189:LEU:HD13	2.03	0.40
1:R:200:GLN:O	1:R:220:VAL:HB	2.21	0.40
1:T:14:ARG:HE	1:T:14:ARG:HB2	1.32	0.40
1:T:187:PHE:HB2	1:T:214:ILE:HD13	2.04	0.40
1:A:184:GLN:HE21	1:A:185:ARG:HA	1.86	0.40
1:A:67:GLY:N	1:A:69:GLU:OE1	2.49	0.40
1:B:283:TYR:O	1:B:286:TYR:CB	2.45	0.40
1:G:156:ILE:HD13	1:G:156:ILE:HA	1.89	0.40
1:G:276:ASN:O	1:G:277:GLU:C	2.56	0.40
1:M:53:MET:HG3	1:M:84:VAL:HG13	2.03	0.40
1:O:229:LYS:HD2	1:O:255:ASN:HA	2.03	0.40
1:R:159:LEU:HD23	1:R:159:LEU:HA	1.83	0.40
1:T:110:GLY:O	1:T:111:ALA:CB	2.70	0.40
1:A:107:ARG:O	1:A:107:ARG:HG3	2.19	0.40
1:A:82:ALA:O	1:A:102:ARG:CD	2.69	0.40
1:B:196:GLU:HG3	1:A:88:THR:OG1	2.22	0.40
1:B:73:ILE:HG22	1:B:74:ASN:N	2.36	0.40
1:C:141:GLN:OE1	1:C:173:VAL:CB	2.57	0.40
1:C:265:MET:O	1:C:269:VAL:HG23	2.22	0.40
1:D:207:VAL:CG1	1:D:209:LYS:O	2.69	0.40
1:E:266:MET:HB3	1:E:266:MET:HE2	1.90	0.40
1:G:266:MET:O	1:G:270:GLN:HG2	2.22	0.40
1:H:99:ALA:C	1:H:101:ASN:N	2.74	0.40
1:J:266:MET:O	1:J:270:GLN:HG2	2.22	0.40
1:K:14:ARG:CG	1:K:14:ARG:O	2.68	0.40
1:L:143:TYR:HB3	1:L:146:SER:HB2	2.04	0.40
1:L:159:LEU:HD23	1:L:159:LEU:HA	1.87	0.40
1:M:14:ARG:O	1:M:14:ARG:CG	2.70	0.40
1:N:32:LEU:HD13	1:N:36:MET:SD	2.61	0.40
1:N:42:ARG:HD3	1:N:136:CYS:SG	2.62	0.40
1:O:92:LEU:HA	1:O:96:VAL:CG2	2.51	0.40
1:P:13:PHE:O	1:P:14:ARG:C	2.58	0.40
1:P:232:GLU:O	1:P:233:ARG:C	2.59	0.40
1:R:220:VAL:HB	1:R:221:PRO:HD2	2.03	0.40
1:R:285:LEU:HA	1:R:288:SER:CB	2.36	0.40
1:T:105:VAL:HG12	1:T:105:VAL:O	2.21	0.40
1:T:136:CYS:O	1:T:169:PRO:HD2	2.22	0.40

All (8) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:O:287:LEU:CD2	1:M:275:HIS:CE1[1_565]	1.57	0.63
1:O:287:LEU:CD2	1:M:275:HIS:ND1[1_565]	1.83	0.37
1:L:233:ARG:NH2	1:E:234:GLU:OE2[1_546]	1.89	0.31
1:N:281:ARG:NH2	1:D:276:ASN:ND2[1_545]	1.91	0.29
1:O:287:LEU:CD2	1:M:275:HIS:NE2[1_565]	2.00	0.20
1:L:275:HIS:NE2	1:J:287:LEU:CD2[1_446]	2.11	0.09
1:B:277:GLU:OE2	1:D:233:ARG:CD[1_545]	2.13	0.07
1:L:275:HIS:CE1	1:J:287:LEU:CD2[1_446]	2.15	0.05

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	272/293 (93%)	264 (97%)	8 (3%)	0	100	100
1	B	272/293 (93%)	265 (97%)	7 (3%)	0	100	100
1	C	272/293 (93%)	265 (97%)	7 (3%)	0	100	100
1	D	272/293 (93%)	262 (96%)	10 (4%)	0	100	100
1	E	272/293 (93%)	265 (97%)	7 (3%)	0	100	100
1	F	272/293 (93%)	262 (96%)	10 (4%)	0	100	100
1	G	272/293 (93%)	262 (96%)	10 (4%)	0	100	100
1	H	272/293 (93%)	263 (97%)	9 (3%)	0	100	100
1	I	272/293 (93%)	263 (97%)	9 (3%)	0	100	100
1	J	272/293 (93%)	264 (97%)	8 (3%)	0	100	100
1	K	272/293 (93%)	263 (97%)	9 (3%)	0	100	100
1	L	272/293 (93%)	264 (97%)	8 (3%)	0	100	100
1	M	272/293 (93%)	263 (97%)	9 (3%)	0	100	100
1	N	272/293 (93%)	261 (96%)	11 (4%)	0	100	100
1	O	272/293 (93%)	263 (97%)	9 (3%)	0	100	100
1	P	272/293 (93%)	262 (96%)	10 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	Q	272/293 (93%)	261 (96%)	11 (4%)	0	100	100
1	R	272/293 (93%)	260 (96%)	12 (4%)	0	100	100
1	S	272/293 (93%)	262 (96%)	10 (4%)	0	100	100
1	T	272/293 (93%)	263 (97%)	9 (3%)	0	100	100
All	All	5440/5860 (93%)	5257 (97%)	183 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	224/238 (94%)	202 (90%)	22 (10%)	8	24
1	B	224/238 (94%)	204 (91%)	20 (9%)	9	29
1	C	224/238 (94%)	202 (90%)	22 (10%)	8	24
1	D	224/238 (94%)	203 (91%)	21 (9%)	8	26
1	E	224/238 (94%)	203 (91%)	21 (9%)	8	26
1	F	224/238 (94%)	204 (91%)	20 (9%)	9	29
1	G	224/238 (94%)	201 (90%)	23 (10%)	7	22
1	H	224/238 (94%)	204 (91%)	20 (9%)	9	29
1	I	224/238 (94%)	203 (91%)	21 (9%)	8	26
1	J	224/238 (94%)	204 (91%)	20 (9%)	9	29
1	K	224/238 (94%)	203 (91%)	21 (9%)	8	26
1	L	224/238 (94%)	204 (91%)	20 (9%)	9	29
1	M	224/238 (94%)	202 (90%)	22 (10%)	8	24
1	N	224/238 (94%)	204 (91%)	20 (9%)	9	29
1	O	224/238 (94%)	205 (92%)	19 (8%)	10	31
1	P	224/238 (94%)	203 (91%)	21 (9%)	8	26
1	Q	224/238 (94%)	203 (91%)	21 (9%)	8	26

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	R	224/238 (94%)	203 (91%)	21 (9%)	8	26
1	S	224/238 (94%)	203 (91%)	21 (9%)	8	26
1	T	224/238 (94%)	204 (91%)	20 (9%)	9	29
All	All	4480/4760 (94%)	4064 (91%)	416 (9%)	9	27

All (416) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	O	14	ARG
1	O	15	THR
1	O	20	LYS
1	O	65	THR
1	O	80	GLU
1	O	100	THR
1	O	102	ARG
1	O	113	SER
1	O	125	LEU
1	O	166	VAL
1	O	184	GLN
1	O	197	MET
1	O	207	VAL
1	O	233	ARG
1	O	254	ARG
1	O	270	GLN
1	O	278	THR
1	O	285	LEU
1	O	287	LEU
1	L	14	ARG
1	L	15	THR
1	L	20	LYS
1	L	60	TYR
1	L	65	THR
1	L	80	GLU
1	L	100	THR
1	L	102	ARG
1	L	113	SER
1	L	125	LEU
1	L	166	VAL
1	L	184	GLN
1	L	197	MET
1	L	207	VAL

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Mol	Chain	Res	Type
1	L	233	ARG
1	L	254	ARG
1	L	270	GLN
1	L	278	THR
1	L	285	LEU
1	L	287	LEU
1	M	14	ARG
1	M	15	THR
1	M	20	LYS
1	M	60	TYR
1	M	65	THR
1	M	80	GLU
1	M	102	ARG
1	M	104	VAL
1	M	113	SER
1	M	125	LEU
1	M	166	VAL
1	M	184	GLN
1	M	197	MET
1	M	207	VAL
1	M	208	GLU
1	M	233	ARG
1	M	254	ARG
1	M	270	GLN
1	M	278	THR
1	M	283	TYR
1	M	285	LEU
1	M	287	LEU
1	N	14	ARG
1	N	15	THR
1	N	20	LYS
1	N	65	THR
1	N	80	GLU
1	N	102	ARG
1	N	104	VAL
1	N	113	SER
1	N	125	LEU
1	N	166	VAL
1	N	184	GLN
1	N	185	ARG
1	N	197	MET
1	N	207	VAL

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Mol	Chain	Res	Type
1	N	233	ARG
1	N	254	ARG
1	N	270	GLN
1	N	278	THR
1	N	285	LEU
1	N	287	LEU
1	K	14	ARG
1	K	15	THR
1	K	20	LYS
1	K	60	TYR
1	K	65	THR
1	K	80	GLU
1	K	100	THR
1	K	102	ARG
1	K	104	VAL
1	K	113	SER
1	K	125	LEU
1	K	166	VAL
1	K	197	MET
1	K	207	VAL
1	K	233	ARG
1	K	254	ARG
1	K	270	GLN
1	K	278	THR
1	K	283	TYR
1	K	285	LEU
1	K	287	LEU
1	F	14	ARG
1	F	15	THR
1	F	20	LYS
1	F	60	TYR
1	F	65	THR
1	F	80	GLU
1	F	102	ARG
1	F	104	VAL
1	F	113	SER
1	F	125	LEU
1	F	166	VAL
1	F	184	GLN
1	F	197	MET
1	F	207	VAL
1	F	233	ARG

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Mol	Chain	Res	Type
1	F	254	ARG
1	F	270	GLN
1	F	278	THR
1	F	285	LEU
1	F	287	LEU
1	I	14	ARG
1	I	15	THR
1	I	20	LYS
1	I	56	PHE
1	I	65	THR
1	I	80	GLU
1	I	102	ARG
1	I	104	VAL
1	I	113	SER
1	I	125	LEU
1	I	166	VAL
1	I	197	MET
1	I	207	VAL
1	I	208	GLU
1	I	233	ARG
1	I	254	ARG
1	I	267	LYS
1	I	270	GLN
1	I	278	THR
1	I	285	LEU
1	I	287	LEU
1	H	14	ARG
1	H	15	THR
1	H	20	LYS
1	H	60	TYR
1	H	65	THR
1	H	80	GLU
1	H	102	ARG
1	H	104	VAL
1	H	113	SER
1	H	125	LEU
1	H	166	VAL
1	H	197	MET
1	H	207	VAL
1	H	233	ARG
1	H	254	ARG
1	H	270	GLN

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Mol	Chain	Res	Type
1	H	278	THR
1	H	283	TYR
1	H	285	LEU
1	H	287	LEU
1	G	14	ARG
1	G	15	THR
1	G	20	LYS
1	G	60	TYR
1	G	65	THR
1	G	68	LEU
1	G	80	GLU
1	G	102	ARG
1	G	104	VAL
1	G	113	SER
1	G	125	LEU
1	G	166	VAL
1	G	184	GLN
1	G	185	ARG
1	G	197	MET
1	G	207	VAL
1	G	233	ARG
1	G	254	ARG
1	G	270	GLN
1	G	278	THR
1	G	283	TYR
1	G	285	LEU
1	G	287	LEU
1	J	14	ARG
1	J	15	THR
1	J	20	LYS
1	J	60	TYR
1	J	65	THR
1	J	80	GLU
1	J	102	ARG
1	J	104	VAL
1	J	113	SER
1	J	125	LEU
1	J	166	VAL
1	J	184	GLN
1	J	197	MET
1	J	207	VAL
1	J	233	ARG

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Mol	Chain	Res	Type
1	J	254	ARG
1	J	270	GLN
1	J	278	THR
1	J	285	LEU
1	J	287	LEU
1	S	14	ARG
1	S	15	THR
1	S	20	LYS
1	S	60	TYR
1	S	65	THR
1	S	80	GLU
1	S	102	ARG
1	S	104	VAL
1	S	113	SER
1	S	125	LEU
1	S	166	VAL
1	S	184	GLN
1	S	197	MET
1	S	207	VAL
1	S	233	ARG
1	S	254	ARG
1	S	270	GLN
1	S	278	THR
1	S	283	TYR
1	S	285	LEU
1	S	287	LEU
1	P	14	ARG
1	P	15	THR
1	P	20	LYS
1	P	60	TYR
1	P	65	THR
1	P	80	GLU
1	P	102	ARG
1	P	104	VAL
1	P	113	SER
1	P	125	LEU
1	P	166	VAL
1	P	184	GLN
1	P	197	MET
1	P	207	VAL
1	P	233	ARG
1	P	254	ARG

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Mol	Chain	Res	Type
1	P	270	GLN
1	P	278	THR
1	P	283	TYR
1	P	285	LEU
1	P	287	LEU
1	Q	14	ARG
1	Q	15	THR
1	Q	20	LYS
1	Q	60	TYR
1	Q	65	THR
1	Q	80	GLU
1	Q	102	ARG
1	Q	104	VAL
1	Q	113	SER
1	Q	125	LEU
1	Q	166	VAL
1	Q	184	GLN
1	Q	197	MET
1	Q	207	VAL
1	Q	233	ARG
1	Q	254	ARG
1	Q	270	GLN
1	Q	278	THR
1	Q	283	TYR
1	Q	285	LEU
1	Q	287	LEU
1	R	14	ARG
1	R	15	THR
1	R	20	LYS
1	R	56	PHE
1	R	60	TYR
1	R	65	THR
1	R	80	GLU
1	R	102	ARG
1	R	104	VAL
1	R	113	SER
1	R	125	LEU
1	R	166	VAL
1	R	184	GLN
1	R	197	MET
1	R	207	VAL
1	R	233	ARG

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Mol	Chain	Res	Type
1	R	254	ARG
1	R	270	GLN
1	R	278	THR
1	R	285	LEU
1	R	287	LEU
1	T	14	ARG
1	T	15	THR
1	T	20	LYS
1	T	60	TYR
1	T	65	THR
1	T	80	GLU
1	T	102	ARG
1	T	113	SER
1	T	125	LEU
1	T	166	VAL
1	T	184	GLN
1	T	197	MET
1	T	207	VAL
1	T	233	ARG
1	T	254	ARG
1	T	270	GLN
1	T	278	THR
1	T	283	TYR
1	T	285	LEU
1	T	287	LEU
1	E	14	ARG
1	E	15	THR
1	E	20	LYS
1	E	60	TYR
1	E	65	THR
1	E	80	GLU
1	E	102	ARG
1	E	104	VAL
1	E	113	SER
1	E	125	LEU
1	E	166	VAL
1	E	184	GLN
1	E	197	MET
1	E	207	VAL
1	E	233	ARG
1	E	254	ARG
1	E	270	GLN

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Mol	Chain	Res	Type
1	E	278	THR
1	E	283	TYR
1	E	285	LEU
1	E	287	LEU
1	B	14	ARG
1	B	15	THR
1	B	20	LYS
1	B	60	TYR
1	B	65	THR
1	B	80	GLU
1	B	102	ARG
1	B	104	VAL
1	B	113	SER
1	B	125	LEU
1	B	166	VAL
1	B	184	GLN
1	B	197	MET
1	B	207	VAL
1	B	233	ARG
1	B	254	ARG
1	B	270	GLN
1	B	278	THR
1	B	285	LEU
1	B	287	LEU
1	C	14	ARG
1	C	15	THR
1	C	20	LYS
1	C	60	TYR
1	C	65	THR
1	C	68	LEU
1	C	80	GLU
1	C	102	ARG
1	C	104	VAL
1	C	113	SER
1	C	125	LEU
1	C	166	VAL
1	C	184	GLN
1	C	197	MET
1	C	207	VAL
1	C	233	ARG
1	C	254	ARG
1	C	270	GLN

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Mol	Chain	Res	Type
1	C	278	THR
1	C	283	TYR
1	C	285	LEU
1	C	287	LEU
1	D	14	ARG
1	D	15	THR
1	D	20	LYS
1	D	60	TYR
1	D	65	THR
1	D	80	GLU
1	D	100	THR
1	D	102	ARG
1	D	104	VAL
1	D	113	SER
1	D	125	LEU
1	D	166	VAL
1	D	184	GLN
1	D	197	MET
1	D	207	VAL
1	D	233	ARG
1	D	254	ARG
1	D	270	GLN
1	D	278	THR
1	D	285	LEU
1	D	287	LEU
1	A	14	ARG
1	A	15	THR
1	A	20	LYS
1	A	60	TYR
1	A	65	THR
1	A	68	LEU
1	A	80	GLU
1	A	102	ARG
1	A	113	SER
1	A	125	LEU
1	A	166	VAL
1	A	184	GLN
1	A	185	ARG
1	A	197	MET
1	A	207	VAL
1	A	233	ARG
1	A	254	ARG

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Mol	Chain	Res	Type
1	A	270	GLN
1	A	278	THR
1	A	283	TYR
1	A	285	LEU
1	A	287	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (64) such sidechains are listed below:

Mol	Chain	Res	Type
1	O	58	HIS
1	O	200	GLN
1	O	274	HIS
1	L	58	HIS
1	L	200	GLN
1	L	274	HIS
1	M	58	HIS
1	M	200	GLN
1	M	274	HIS
1	N	58	HIS
1	N	200	GLN
1	N	241	GLN
1	K	58	HIS
1	K	200	GLN
1	K	274	HIS
1	F	200	GLN
1	F	274	HIS
1	I	58	HIS
1	I	200	GLN
1	I	241	GLN
1	I	274	HIS
1	H	58	HIS
1	H	200	GLN
1	H	274	HIS
1	G	58	HIS
1	G	200	GLN
1	G	274	HIS
1	G	275	HIS
1	J	58	HIS
1	J	200	GLN
1	S	58	HIS
1	S	200	GLN
1	S	274	HIS

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Mol	Chain	Res	Type
1	P	58	HIS
1	P	200	GLN
1	P	241	GLN
1	P	274	HIS
1	Q	58	HIS
1	Q	200	GLN
1	Q	274	HIS
1	R	58	HIS
1	R	200	GLN
1	R	274	HIS
1	T	58	HIS
1	T	200	GLN
1	T	241	GLN
1	T	274	HIS
1	E	58	HIS
1	E	200	GLN
1	E	274	HIS
1	B	58	HIS
1	B	200	GLN
1	B	241	GLN
1	B	274	HIS
1	C	58	HIS
1	C	200	GLN
1	C	241	GLN
1	C	274	HIS
1	D	58	HIS
1	D	200	GLN
1	D	274	HIS
1	A	58	HIS
1	A	200	GLN
1	A	274	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	276/293 (94%)	0.07	12 (4%) 35 31	19, 32, 60, 81	0
1	B	276/293 (94%)	-0.11	2 (0%) 87 87	19, 32, 60, 81	0
1	C	276/293 (94%)	-0.01	3 (1%) 80 80	19, 32, 60, 81	0
1	D	276/293 (94%)	0.01	4 (1%) 75 75	19, 32, 60, 81	0
1	E	276/293 (94%)	0.10	11 (3%) 38 33	19, 32, 60, 81	0
1	F	276/293 (94%)	-0.06	4 (1%) 75 75	19, 32, 60, 81	0
1	G	276/293 (94%)	-0.15	1 (0%) 92 93	19, 32, 60, 81	0
1	H	276/293 (94%)	0.06	3 (1%) 80 80	19, 32, 60, 81	0
1	I	276/293 (94%)	-0.03	3 (1%) 80 80	19, 32, 60, 81	0
1	J	276/293 (94%)	-0.09	5 (1%) 68 67	19, 32, 60, 81	0
1	K	276/293 (94%)	-0.03	11 (3%) 38 33	19, 32, 60, 81	0
1	L	276/293 (94%)	-0.07	7 (2%) 57 55	19, 32, 60, 81	0
1	M	276/293 (94%)	-0.07	4 (1%) 75 75	19, 32, 60, 81	0
1	N	276/293 (94%)	-0.02	6 (2%) 62 59	19, 32, 60, 81	0
1	O	276/293 (94%)	-0.08	5 (1%) 68 67	19, 32, 60, 81	0
1	P	276/293 (94%)	0.03	11 (3%) 38 33	19, 32, 60, 81	0
1	Q	276/293 (94%)	-0.04	3 (1%) 80 80	19, 32, 60, 81	0
1	R	276/293 (94%)	0.05	5 (1%) 68 67	19, 32, 60, 81	0
1	S	276/293 (94%)	-0.06	6 (2%) 62 59	19, 32, 60, 81	0
1	T	276/293 (94%)	0.01	12 (4%) 35 31	19, 32, 60, 81	0
All	All	5520/5860 (94%)	-0.02	118 (2%) 63 61	19, 32, 61, 81	0

All (118) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	10	GLY	7.0
1	E	289	GLU	6.6
1	E	288	SER	6.0
1	N	288	SER	5.4
1	E	286	TYR	5.2
1	M	10	GLY	4.9
1	S	288	SER	4.8
1	K	288	SER	4.5
1	S	289	GLU	4.3
1	K	289	GLU	4.1
1	N	289	GLU	3.9
1	L	289	GLU	3.9
1	F	287	LEU	3.7
1	K	10	GLY	3.7
1	A	286	TYR	3.6
1	P	286	TYR	3.5
1	T	10	GLY	3.5
1	K	286	TYR	3.5
1	A	284	GLU	3.4
1	N	10	GLY	3.4
1	E	290	LYS	3.3
1	L	286	TYR	3.2
1	D	289	GLU	3.1
1	D	287	LEU	3.1
1	A	261	HIS	3.0
1	A	234	GLU	3.0
1	E	66	THR	3.0
1	L	10	GLY	2.9
1	R	145	GLY	2.9
1	A	289	GLU	2.9
1	J	11	LYS	2.8
1	S	286	TYR	2.8
1	L	16	ASP	2.8
1	O	10	GLY	2.7
1	K	285	LEU	2.7
1	E	281	ARG	2.7
1	H	288	SER	2.7
1	A	281	ARG	2.7
1	N	290	LYS	2.7
1	P	275	HIS	2.7
1	P	278	THR	2.6
1	C	10	GLY	2.6
1	E	261	HIS	2.6

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Mol	Chain	Res	Type	RSRZ
1	R	287	LEU	2.6
1	D	228	LYS	2.6
1	G	233	ARG	2.6
1	T	11	LYS	2.6
1	P	260	ASP	2.6
1	J	182	ARG	2.5
1	T	17	GLN	2.5
1	P	208	GLU	2.5
1	S	287	LEU	2.5
1	S	176	VAL	2.5
1	D	11	LYS	2.5
1	R	208	GLU	2.5
1	M	286	TYR	2.5
1	K	233	ARG	2.4
1	E	260	ASP	2.4
1	Q	288	SER	2.4
1	L	290	LYS	2.4
1	T	228	LYS	2.4
1	N	286	TYR	2.4
1	I	280	ASP	2.4
1	A	287	LEU	2.4
1	J	10	GLY	2.4
1	I	11	LYS	2.3
1	A	209	LYS	2.3
1	O	17	GLN	2.3
1	O	47	LYS	2.3
1	T	288	SER	2.3
1	K	16	ASP	2.3
1	C	17	GLN	2.3
1	T	47	LYS	2.3
1	I	278	THR	2.3
1	T	289	GLU	2.3
1	S	280	ASP	2.3
1	B	228	LYS	2.2
1	P	207	VAL	2.2
1	B	47	LYS	2.2
1	H	202	ILE	2.2
1	K	47	LYS	2.2
1	T	280	ASP	2.2
1	M	289	GLU	2.2
1	M	288	SER	2.2
1	A	288	SER	2.2

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Mol	Chain	Res	Type	RSRZ
1	J	228	LYS	2.2
1	P	240	TRP	2.2
1	A	48	THR	2.2
1	Q	209	LYS	2.1
1	R	289	GLU	2.1
1	F	10	GLY	2.1
1	T	176	VAL	2.1
1	P	288	SER	2.1
1	E	283	TYR	2.1
1	O	228	LYS	2.1
1	P	187	PHE	2.1
1	F	233	ARG	2.1
1	J	18	PRO	2.1
1	T	281	ARG	2.1
1	F	176	VAL	2.1
1	N	261	HIS	2.1
1	C	47	LYS	2.1
1	L	11	LYS	2.1
1	T	209	LYS	2.1
1	E	25	THR	2.1
1	H	185	ARG	2.1
1	Q	207	VAL	2.1
1	T	261	HIS	2.1
1	R	286	TYR	2.1
1	L	185	ARG	2.1
1	K	11	LYS	2.1
1	P	209	LYS	2.1
1	K	290	LYS	2.0
1	A	207	VAL	2.0
1	P	228	LYS	2.0
1	K	283	TYR	2.0
1	O	233	ARG	2.0
1	E	285	LEU	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.