



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 28, 2014 – 01:43 PM GMT

PDB ID : 4BI5
Title : CRYSTAL STRUCTURE OF A DOUBLE MUTANT (C202A AND C222D)
OF TRIOSEPHOSPHATE ISOMERASE FROM GIARDIA LAMBLIA.
Authors : Torres-Larios, A.; Enriquez-Flores, S.; Reyes-Vivas, H.; Oria-Hernandez, J.;
Hernandez-Alcantara, G.
Deposited on : 2013-04-09
Resolution : 2.70 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

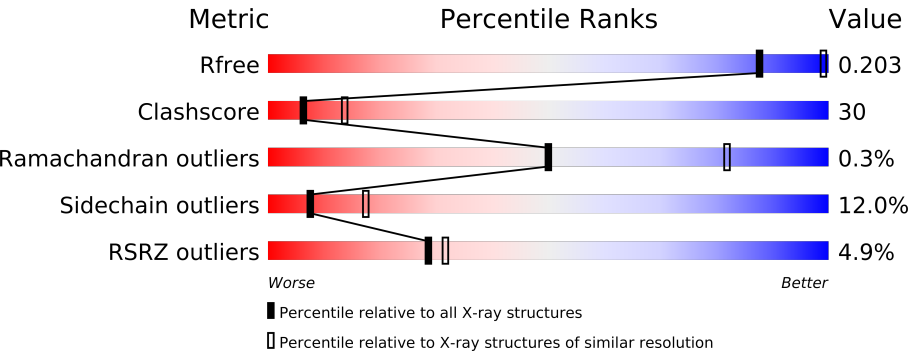
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 2.70 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}	66092	1557 (2.70-2.70)
Clashscore	79885	1939 (2.70-2.70)
Ramachandran outliers	78287	1905 (2.70-2.70)
Sidechain outliers	78261	1905 (2.70-2.70)
RSRZ outliers	66119	1559 (2.70-2.70)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	255	
1	B	255	
1	C	255	
1	D	255	
1	E	255	
1	F	255	
1	G	255	
1	H	255	
1	I	255	
1	J	255	
1	K	255	
1	L	255	
1	M	255	
1	N	255	

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Mol	Chain	Length	Quality of chain
1	O	255	<div><div></div><div></div><div></div></div>
1	P	255	<div><div></div><div></div><div></div></div>
1	Q	255	<div><div></div><div></div><div></div></div>
1	R	255	<div><div></div><div></div><div></div></div>
1	S	255	<div><div></div><div></div><div></div></div>
1	T	255	<div><div></div><div></div><div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 38560 atoms, of which 0 are hydrogen and 0 are deuterium.

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 TRIOSEPHOSPHATE ISOMERASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	B	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	C	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	D	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	E	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	F	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	G	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	H	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	I	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	J	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	K	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	L	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	M	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	N	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	O	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	P	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	Q	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	R	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	S	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			
1	T	254	Total	C	N	O	S	0	0	0
			1928	1212	341	364	11			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
A	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
B	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
B	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
C	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
C	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
D	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
D	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
E	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
E	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
F	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
F	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
G	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
G	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
H	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
H	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
I	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
I	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
J	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
J	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
K	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
K	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
L	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
L	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
M	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
M	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
N	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
N	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
O	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
O	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
P	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186

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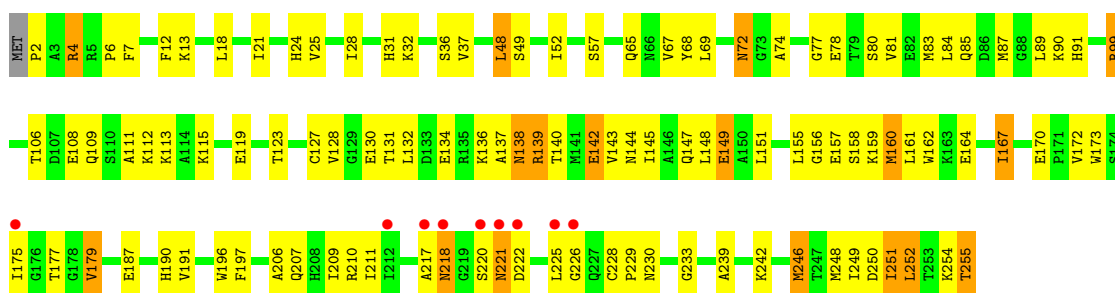
Chain	Residue	Modelled	Actual	Comment	Reference
P	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
Q	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
Q	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
R	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
R	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
S	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
S	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186
T	202	ALA	CYS	ENGINEERED MUTATION	UNP P36186
T	222	ASP	CYS	ENGINEERED MUTATION	UNP P36186

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

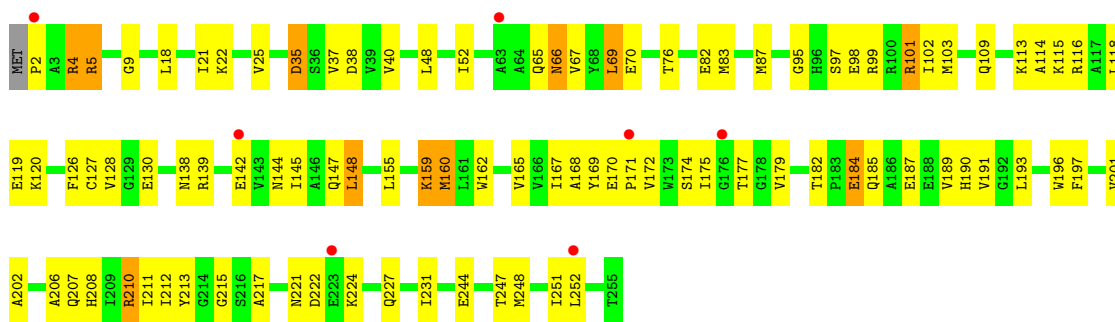
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain A:



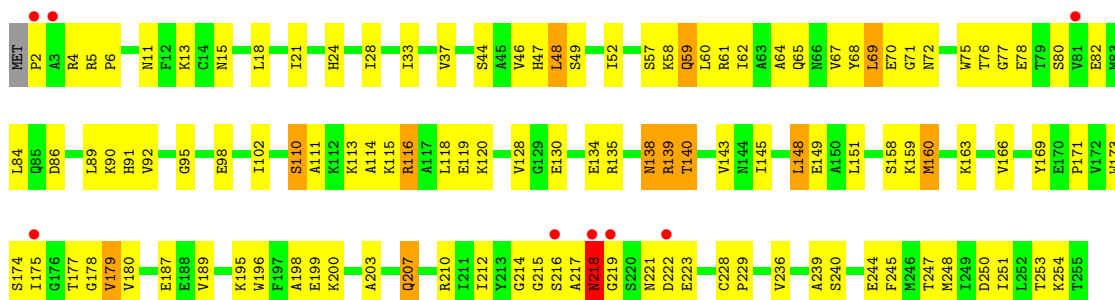
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain B:



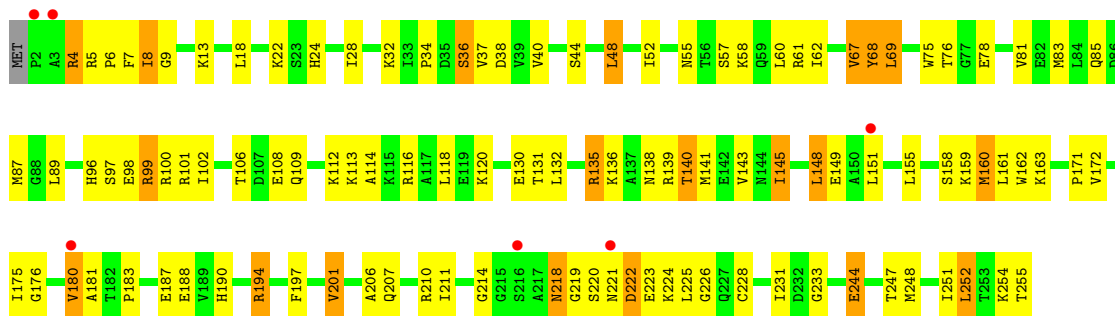
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain C:



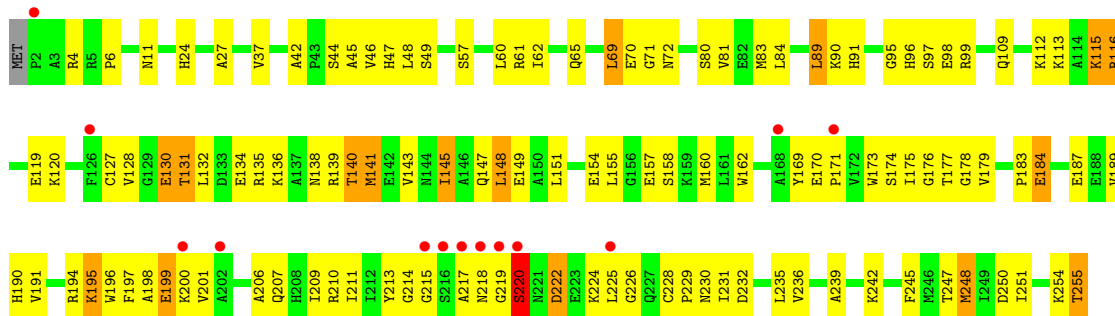
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain D:



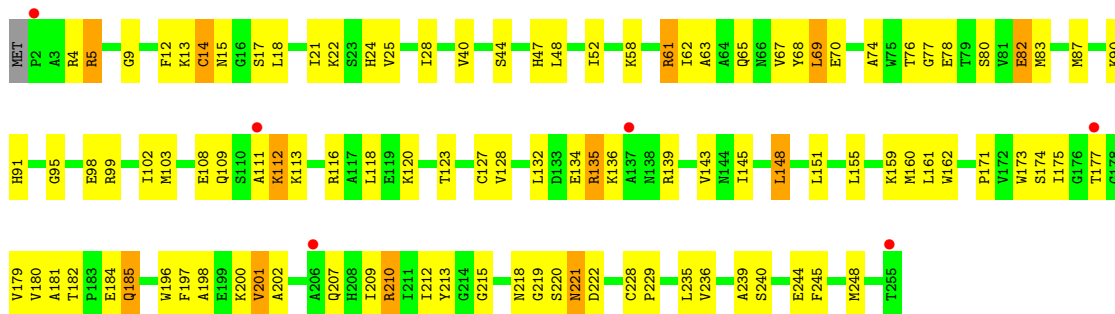
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain E:



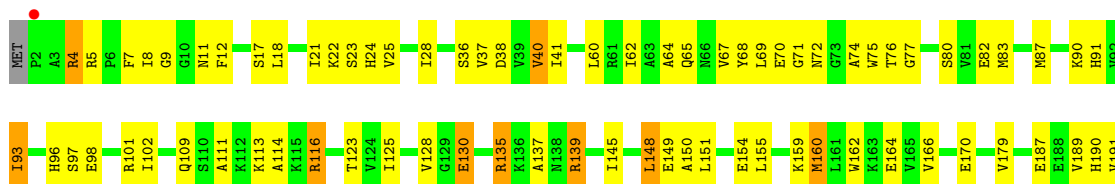
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain F:



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

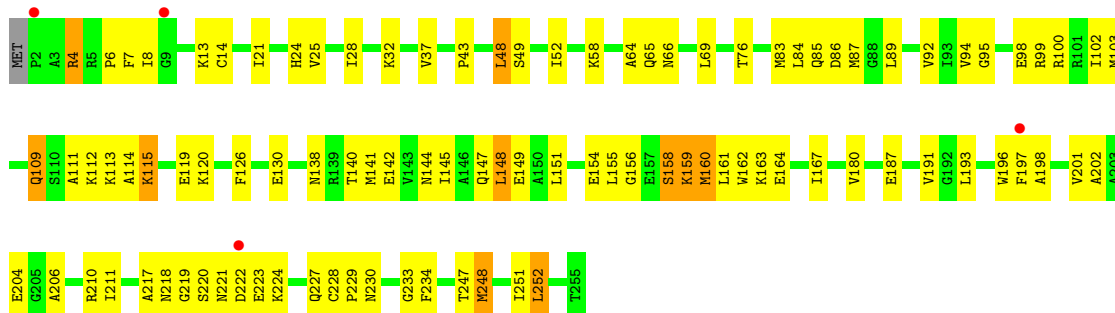
Chain G:





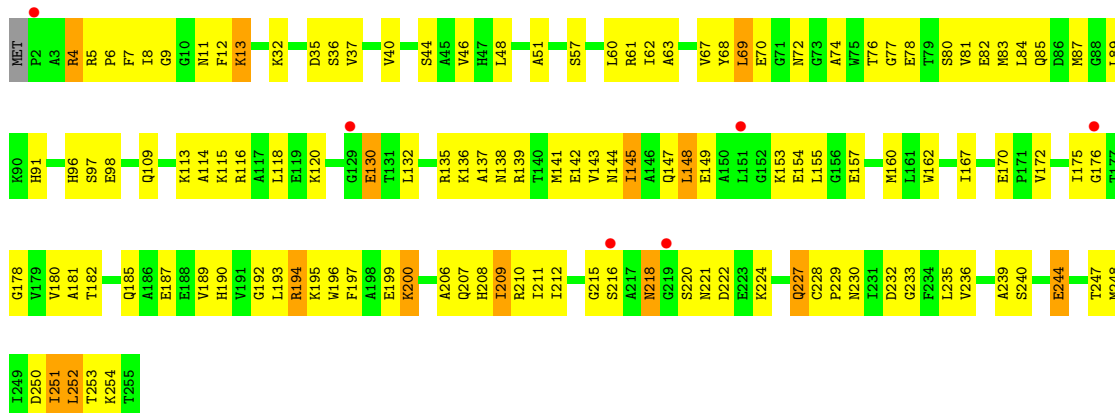
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain H:



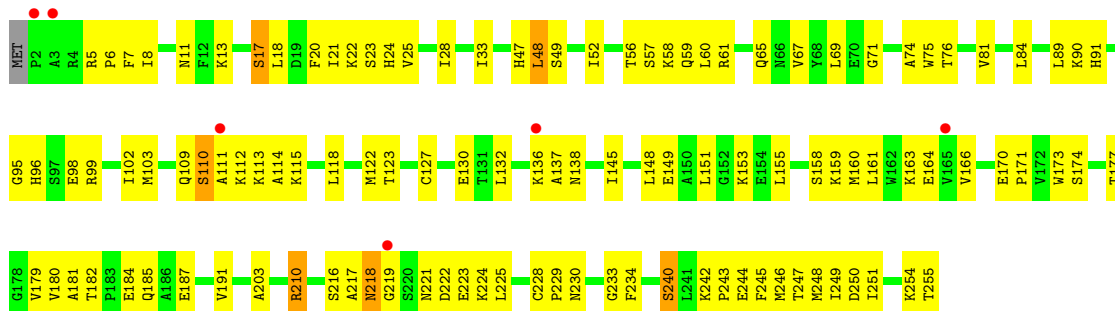
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain I:



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

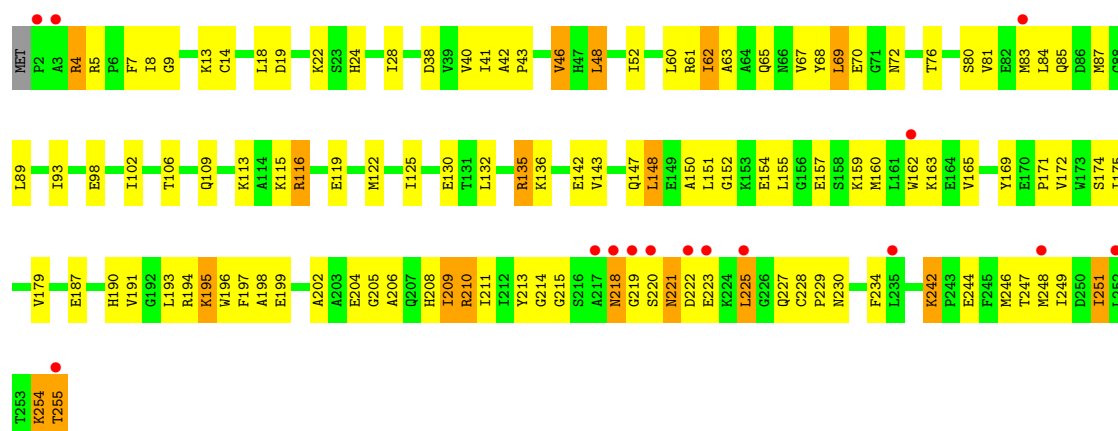
Chain J:



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

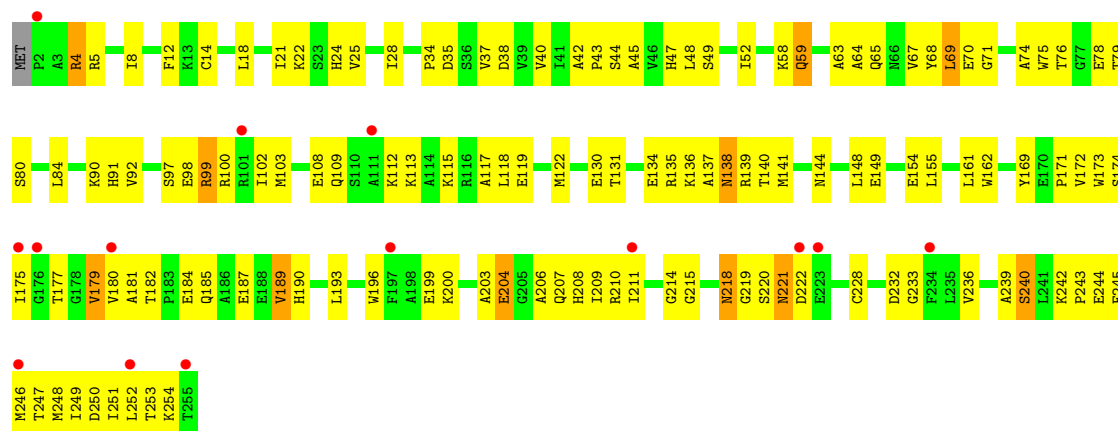
Chain K:





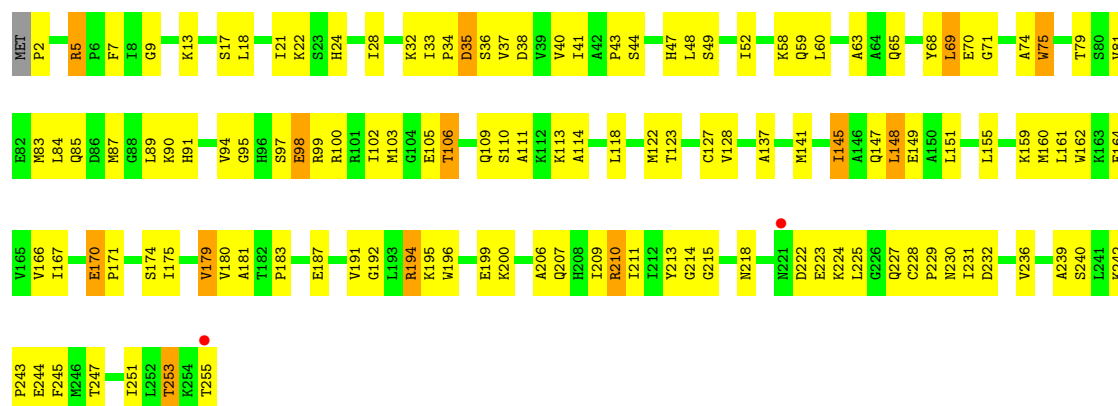
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain L:



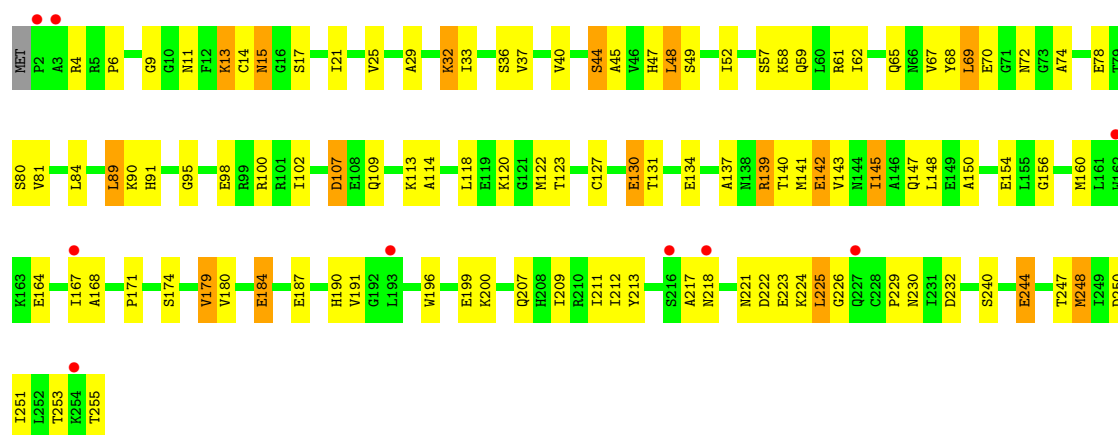
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain M:



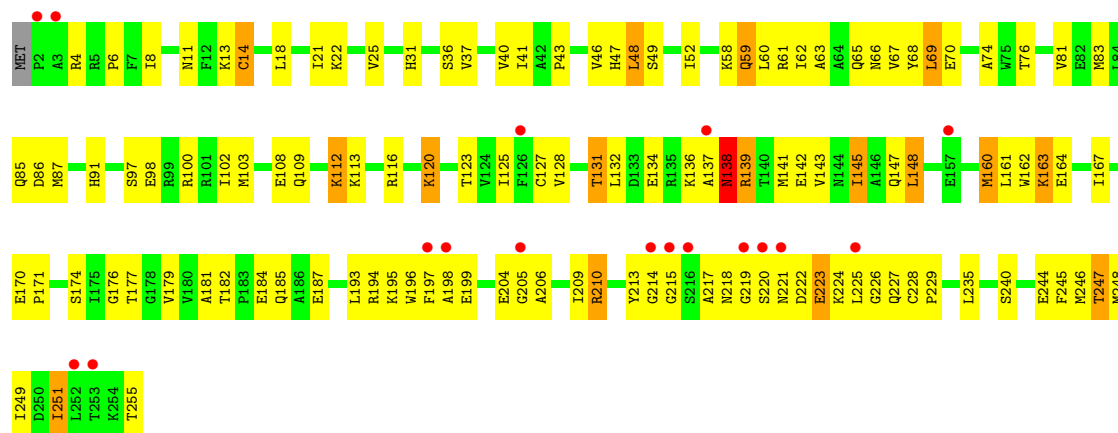
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain N:



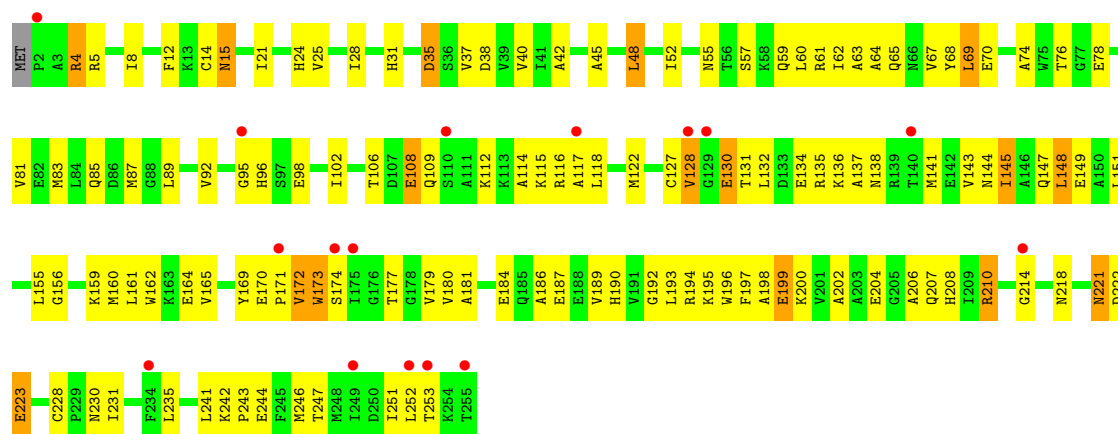
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain O:



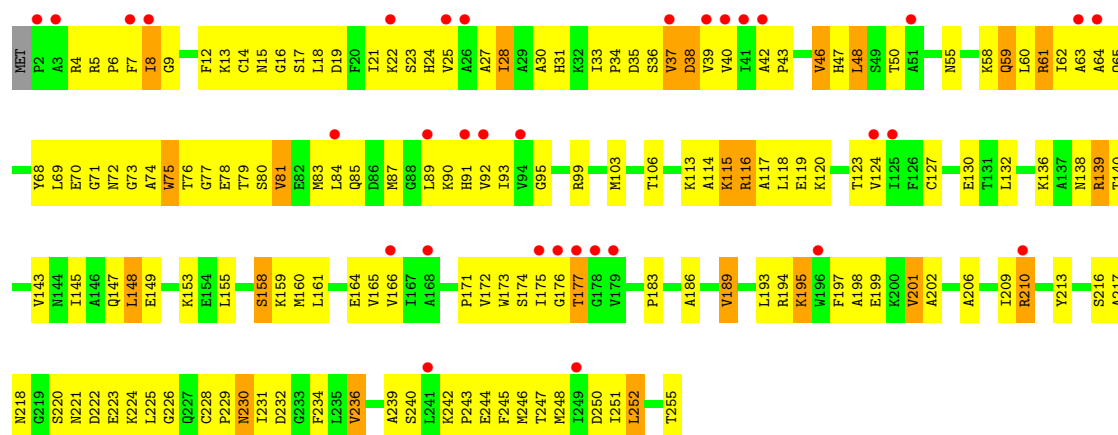
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain P:



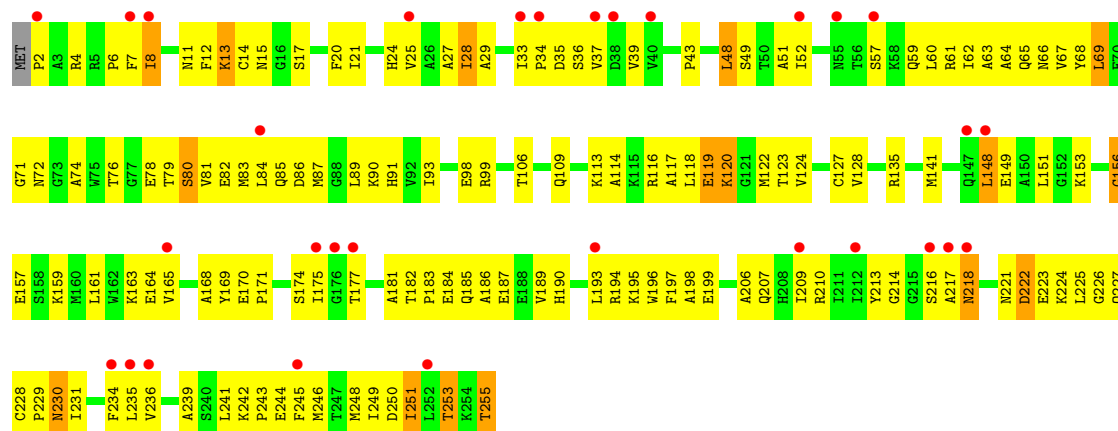
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain Q:



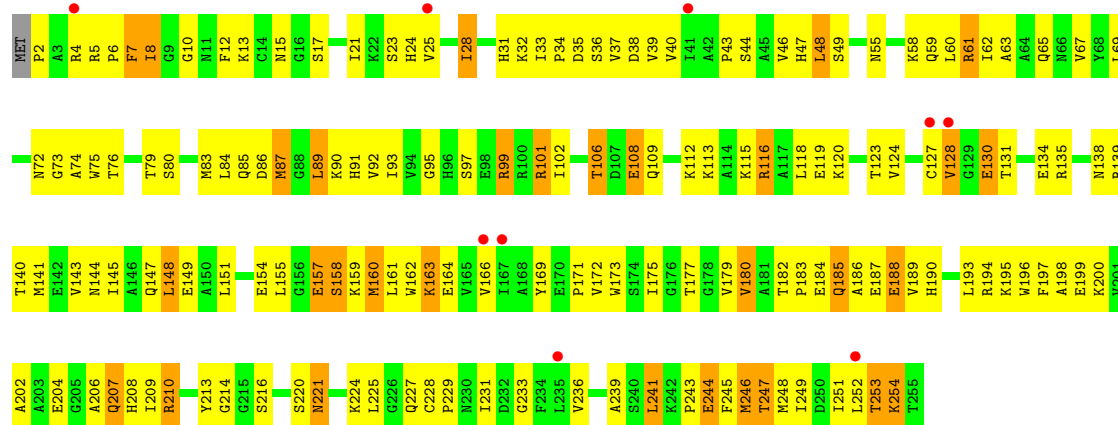
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain R:



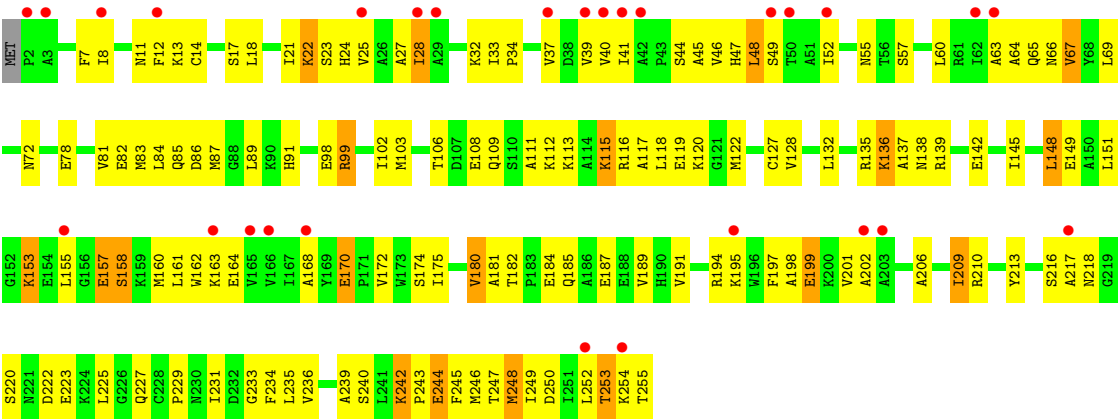
• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain S:



• Molecule 1: TRIOSEPHOSPHATE ISOMERASE

Chain T:



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	105.22Å 131.57Å 132.55Å 115.73° 89.81° 90.24°	Depositor
Resolution (Å)	78.87 – 2.70 78.88 – 2.70	Depositor EDS
% Data completeness (in resolution range)	82.0 (78.87-2.70) 79.8 (78.88-2.70)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.46 (at 2.69Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.239 , 0.272 0.201 , 0.203	Depositor DCC
R_{free} test set	7212 reflections (5.26%)	DCC
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 21.6	EDS
Estimated twinning fraction	0.418 for h,-k,-l 0.197 for -h,-l,-k 0.197 for -h,l,k	Xtriage
L-test for twinning	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Outliers	0 of 144197 reflections	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	38560	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.48	0/1960	0.49	0/2644
1	B	0.58	2/1960 (0.1%)	0.50	0/2644
1	C	0.55	0/1960	0.53	0/2644
1	D	0.40	0/1960	0.48	0/2644
1	E	0.63	0/1960	0.53	0/2644
1	F	0.49	1/1960 (0.1%)	0.52	0/2644
1	G	0.62	2/1960 (0.1%)	0.52	0/2644
1	H	0.58	0/1960	0.52	0/2644
1	I	0.37	0/1960	0.50	0/2644
1	J	0.44	0/1960	0.49	0/2644
1	K	0.34	0/1960	0.51	0/2644
1	L	0.55	0/1960	0.56	0/2644
1	M	0.34	0/1960	0.47	0/2644
1	N	0.27	0/1960	0.46	0/2644
1	O	0.30	0/1960	0.50	0/2644
1	P	0.28	0/1960	0.49	0/2644
1	Q	0.33	0/1960	0.49	0/2644
1	R	0.37	0/1960	0.50	0/2644
1	S	0.32	0/1960	0.50	0/2644
1	T	0.28	0/1960	0.50	0/2644
All	All	0.44	5/39200 (0.0%)	0.50	0/52880

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	F	14	CYS	CB-SG	-5.68	1.72	1.81
1	B	169	TYR	CE2-CZ	-5.38	1.31	1.38
1	G	68	TYR	CD2-CE2	-5.31	1.31	1.39
1	G	68	TYR	CE1-CZ	-5.25	1.31	1.38
1	B	169	TYR	CD2-CE2	-5.00	1.31	1.39

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1928	0	1949	111	0
1	B	1928	0	1949	82	0
1	C	1928	0	1949	95	0
1	D	1928	0	1949	103	0
1	E	1928	0	1949	136	0
1	F	1928	0	1949	93	0
1	G	1928	0	1949	98	0
1	H	1928	0	1949	80	0
1	I	1928	0	1949	137	0
1	J	1928	0	1949	104	0
1	K	1928	0	1949	113	0
1	L	1928	0	1949	141	0
1	M	1928	0	1949	104	0
1	N	1928	0	1949	110	0
1	O	1928	0	1949	141	0
1	P	1928	0	1949	127	0
1	Q	1928	0	1949	195	0
1	R	1928	0	1949	184	0
1	S	1928	0	1949	184	0
1	T	1928	0	1949	130	0
All	All	38560	0	38980	2346	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 30.

All (2346) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:76:THR:CG2	1:D:98:GLU:OE1	1.67	1.42
1:T:115:LYS:HG2	1:T:155:LEU:CD2	1.47	1.41
1:B:66:ASN:HD22	1:B:67:VAL:N	1.25	1.31
1:L:177:THR:HG22	1:L:179:VAL:CG2	1.60	1.30
1:B:66:ASN:ND2	1:B:67:VAL:H	1.30	1.27

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:200:LYS:O	1:L:200:LYS:HD2	1.39	1.19
1:Q:183:PRO:HB3	1:Q:225:LEU:HD23	1.25	1.17
1:P:210:ARG:HG3	1:P:210:ARG:HH11	1.03	1.15
1:N:14:CYS:C	1:N:15:ASN:HD22	1.51	1.14
1:O:58:LYS:HG3	1:O:59:GLN:NE2	1.65	1.12
1:P:14:CYS:C	1:P:15:ASN:HD22	1.52	1.12
1:L:177:THR:HG22	1:L:179:VAL:HG23	1.13	1.12
1:C:217:ALA:O	1:C:218:ASN:HB3	1.46	1.12
1:T:115:LYS:CG	1:T:155:LEU:CD2	2.28	1.11
1:C:178:GLY:HA2	1:R:175:ILE:HD13	1.30	1.10
1:T:115:LYS:HG2	1:T:155:LEU:HD23	1.27	1.10
1:O:58:LYS:HE2	1:O:59:GLN:OE1	1.52	1.10
1:T:115:LYS:CG	1:T:155:LEU:HD23	1.79	1.09
1:E:251:ILE:HA	1:E:254:LYS:HE3	1.32	1.09
1:E:171:PRO:HG2	1:E:215:GLY:HA3	1.16	1.08
1:L:177:THR:CG2	1:L:179:VAL:HG23	1.82	1.08
1:S:210:ARG:HG2	1:S:210:ARG:HH11	0.92	1.08
1:B:66:ASN:ND2	1:B:67:VAL:N	1.91	1.07
1:Q:183:PRO:CB	1:Q:225:LEU:HD23	1.83	1.07
1:G:213:TYR:HB3	1:G:234:PHE:CD1	1.89	1.07
1:E:171:PRO:CG	1:E:215:GLY:HA3	1.85	1.07
1:I:84:LEU:HD22	1:I:89:LEU:HD12	1.31	1.07
1:F:171:PRO:O	1:F:175:ILE:HD13	1.53	1.06
1:E:175:ILE:HA	1:I:176:GLY:HA3	1.33	1.06
1:E:217:ALA:HB3	1:I:178:GLY:CA	1.86	1.06
1:E:217:ALA:HB3	1:I:178:GLY:HA2	1.36	1.06
1:O:226:GLY:HA3	1:O:255:THR:HG21	1.36	1.06
1:Q:61:ARG:HH22	1:Q:90:LYS:HG2	1.19	1.06
1:O:58:LYS:HG3	1:O:59:GLN:CD	1.77	1.05
1:Q:210:ARG:HD3	1:Q:210:ARG:H	1.20	1.05
1:R:225:LEU:HB3	1:R:234:PHE:CE1	1.93	1.04
1:H:218:ASN:O	1:H:222:ASP:HB2	1.58	1.02
1:L:171:PRO:HG2	1:L:174:SER:OG	1.60	1.02
1:Q:197:PHE:O	1:Q:201:VAL:HB	1.58	1.02
1:C:175:ILE:O	1:R:175:ILE:HG21	1.60	1.01
1:T:115:LYS:HG2	1:T:155:LEU:HD21	1.39	1.01
1:O:218:ASN:HD22	1:O:220:SER:H	1.08	1.01
1:Q:75:TRP:CD1	1:R:14:CYS:SG	2.52	1.01
1:L:218:ASN:N	1:L:221:ASN:HD21	1.57	1.01
1:S:158:SER:HB2	1:S:161:LEU:HD23	1.42	1.01
1:O:59:GLN:NE2	1:O:59:GLN:H	1.56	1.01
1:R:225:LEU:HB3	1:R:234:PHE:HE1	1.23	1.00

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:R:195:LYS:O	1:R:199:GLU:HB2	1.62	1.00
1:S:221:ASN:CB	1:S:224:LYS:HE2	1.92	1.00
1:L:177:THR:CG2	1:L:179:VAL:CG2	2.39	0.99
1:C:76:THR:HG23	1:D:98:GLU:CD	1.83	0.98
1:M:2:PRO:HG2	1:M:207:GLN:HB3	1.45	0.98
1:S:6:PRO:HG2	1:S:37:VAL:HA	1.46	0.98
1:P:173:TRP:O	1:P:177:THR:HG21	1.62	0.98
1:B:102:ILE:HG12	1:O:179:VAL:HG22	1.46	0.98
1:L:218:ASN:H	1:L:221:ASN:ND2	1.62	0.98
1:M:191:VAL:HG22	1:M:230:ASN:OD1	1.64	0.97
1:N:226:GLY:C	1:N:255:THR:HG21	1.83	0.97
1:A:172:VAL:HA	1:A:175:ILE:CD1	1.95	0.97
1:O:171:PRO:HD2	1:O:214:GLY:O	1.63	0.96
1:S:210:ARG:HG2	1:S:210:ARG:NH1	1.72	0.96
1:R:251:ILE:O	1:R:255:THR:HB	1.66	0.96
1:K:159:LYS:O	1:K:160:MET:HG2	1.64	0.95
1:S:7:PHE:HE2	1:S:166:VAL:HG21	1.31	0.95
1:C:76:THR:HG23	1:D:98:GLU:OE1	0.77	0.95
1:H:160:MET:O	1:H:163:LYS:HG3	1.65	0.95
1:O:58:LYS:CG	1:O:59:GLN:NE2	2.30	0.94
1:E:190:HIS:HE2	1:E:213:TYR:HB2	1.28	0.94
1:Q:61:ARG:NH2	1:Q:90:LYS:HG2	1.83	0.94
1:G:97:SER:HB3	1:G:170:GLU:OE1	1.66	0.94
1:M:94:VAL:HG11	1:M:114:ALA:HB2	1.49	0.94
1:O:58:LYS:CG	1:O:59:GLN:HE22	1.80	0.94
1:G:236:VAL:CG1	1:G:239:ALA:HB3	1.98	0.93
1:G:69:LEU:HD12	1:G:70:GLU:HG2	1.50	0.93
1:R:228:CYS:CB	1:R:231:ILE:HG13	1.99	0.92
1:G:195:LYS:O	1:G:199:GLU:HG3	1.69	0.92
1:E:169:TYR:CE1	1:E:189:VAL:HG11	2.04	0.92
1:Q:7:PHE:HD1	1:Q:38:ASP:HB2	1.34	0.91
1:Q:89:LEU:HD12	1:Q:90:LYS:H	1.35	0.91
1:S:61:ARG:HG3	1:S:61:ARG:HH11	1.33	0.91
1:T:109:GLN:O	1:T:113:LYS:HG3	1.71	0.91
1:E:171:PRO:HD2	1:E:215:GLY:CA	1.99	0.91
1:E:190:HIS:NE2	1:E:213:TYR:HB2	1.85	0.90
1:H:126:PHE:CZ	1:H:151:LEU:HD11	2.06	0.90
1:E:171:PRO:HD2	1:E:215:GLY:HA2	1.52	0.90
1:L:221:ASN:HD22	1:L:222:ASP:N	1.69	0.89
1:P:210:ARG:HG3	1:P:210:ARG:NH1	1.82	0.89
1:D:4:ARG:HD3	1:D:207:GLN:O	1.72	0.89
1:K:172:VAL:HA	1:K:175:ILE:HD12	1.55	0.89

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:E:4:ARG:HD3	1:E:207:GLN:O	1.72	0.89
1:I:194:ARG:CG	1:I:194:ARG:HH11	1.86	0.89
1:S:210:ARG:HH11	1:S:210:ARG:CG	1.84	0.88
1:J:11:ASN:ND2	1:J:13:LYS:HG3	1.88	0.88
1:T:115:LYS:CD	1:T:155:LEU:HD23	2.04	0.87
1:Q:89:LEU:HD12	1:Q:90:LYS:N	1.89	0.87
1:M:99:ARG:HA	1:M:103:MET:HB2	1.54	0.87
1:Q:7:PHE:CD1	1:Q:38:ASP:HB2	2.09	0.87
1:E:135:ARG:HA	1:E:140:THR:HG22	1.54	0.87
1:R:66:ASN:OD1	1:R:67:VAL:N	2.07	0.87
1:O:218:ASN:ND2	1:O:220:SER:H	1.73	0.86
1:B:224:LYS:O	1:B:227:GLN:HG3	1.74	0.86
1:B:69:LEU:HD23	1:B:70:GLU:HG2	1.58	0.86
1:O:58:LYS:HG2	1:O:59:GLN:HE22	1.39	0.86
1:I:4:ARG:HG2	1:I:4:ARG:HH11	1.41	0.85
1:B:97:SER:HB3	1:B:170:GLU:OE1	1.76	0.85
1:O:59:GLN:HE21	1:O:59:GLN:H	1.19	0.85
1:Q:79:THR:HG21	1:Q:84:LEU:HD21	1.59	0.85
1:P:131:THR:HA	1:P:172:VAL:CG1	2.06	0.85
1:H:217:ALA:HB1	1:H:248:MET:HE1	1.58	0.85
1:G:236:VAL:HG11	1:G:239:ALA:HB3	1.57	0.85
1:R:183:PRO:HG2	1:R:224:LYS:HD3	1.59	0.85
1:K:165:VAL:O	1:K:209:ILE:HD11	1.76	0.85
1:E:130:GLU:OE2	1:E:135:ARG:HB2	1.76	0.84
1:O:171:PRO:HG3	1:O:215:GLY:HA3	1.57	0.84
1:P:131:THR:HA	1:P:172:VAL:HG11	1.59	0.84
1:R:228:CYS:HB2	1:R:231:ILE:HG13	1.58	0.84
1:H:84:LEU:HD22	1:H:89:LEU:HD12	1.59	0.83
1:O:213:TYR:CZ	1:O:215:GLY:HA3	2.13	0.83
1:S:130:GLU:OE2	1:S:140:THR:HG23	1.77	0.83
1:T:155:LEU:HD22	1:T:161:LEU:HD12	1.59	0.83
1:C:69:LEU:HD23	1:C:70:GLU:HG2	1.58	0.83
1:Q:195:LYS:O	1:Q:199:GLU:HB2	1.78	0.83
1:T:115:LYS:HD3	1:T:155:LEU:CD2	2.09	0.83
1:Q:61:ARG:HH22	1:Q:90:LYS:CG	1.92	0.83
1:L:69:LEU:HD23	1:L:70:GLU:HG2	1.61	0.83
1:A:218:ASN:C	1:A:218:ASN:HD22	1.81	0.83
1:G:213:TYR:HB3	1:G:234:PHE:CE1	2.11	0.83
1:T:17:SER:O	1:T:21:ILE:HG12	1.78	0.83
1:F:218:ASN:HB2	1:F:220:SER:OG	1.78	0.83
1:C:175:ILE:O	1:R:175:ILE:CG2	2.26	0.82
1:O:171:PRO:HG3	1:O:215:GLY:CA	2.08	0.82

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:157:GLU:OE1	1:S:157:GLU:HA	1.78	0.82
1:N:14:CYS:C	1:N:15:ASN:ND2	2.30	0.82
1:F:171:PRO:HB3	1:F:173:TRP:NE1	1.93	0.82
1:Q:234:PHE:CD2	1:Q:248:MET:CE	2.61	0.82
1:A:172:VAL:HG13	1:A:175:ILE:HD12	1.59	0.82
1:E:218:ASN:OD1	1:E:219:GLY:N	2.13	0.82
1:S:8:ILE:HD11	1:S:245:PHE:CE1	2.15	0.82
1:D:218:ASN:HD22	1:D:219:GLY:N	1.77	0.82
1:Q:197:PHE:CD2	1:Q:206:ALA:HA	2.14	0.82
1:R:4:ARG:HD3	1:R:207:GLN:O	1.79	0.82
1:R:246:MET:HA	1:R:249:ILE:HD12	1.60	0.82
1:I:194:ARG:HG2	1:I:194:ARG:HH11	1.45	0.81
1:E:219:GLY:O	1:E:220:SER:HB3	1.79	0.81
1:S:183:PRO:HD2	1:S:184:GLU:OE1	1.81	0.81
1:K:218:ASN:HD22	1:K:219:GLY:N	1.78	0.81
1:P:173:TRP:O	1:P:177:THR:CG2	2.29	0.81
1:S:7:PHE:CE2	1:S:166:VAL:HG21	2.15	0.81
1:R:2:PRO:HB3	1:R:207:GLN:HG2	1.62	0.81
1:R:63:ALA:HB2	1:R:91:HIS:HB2	1.60	0.81
1:N:15:ASN:N	1:N:15:ASN:HD22	1.78	0.80
1:J:242:LYS:HB3	1:J:244:GLU:OE1	1.80	0.80
1:A:217:ALA:HB1	1:A:248:MET:HE3	1.62	0.80
1:Q:183:PRO:CB	1:Q:225:LEU:CD2	2.58	0.80
1:I:13:LYS:HG3	1:J:76:THR:CG2	2.11	0.80
1:K:223:GLU:HG3	1:K:254:LYS:HZ1	1.45	0.80
1:H:187:GLU:O	1:H:191:VAL:HG23	1.81	0.80
1:J:222:ASP:HA	1:J:225:LEU:HB2	1.63	0.80
1:N:226:GLY:CA	1:N:255:THR:HG21	2.12	0.80
1:E:247:THR:O	1:E:251:ILE:HD13	1.81	0.80
1:T:115:LYS:HG2	1:T:155:LEU:CG	2.11	0.80
1:T:83:MET:O	1:T:86:ASP:HB3	1.82	0.80
1:P:108:GLU:O	1:P:112:LYS:HG3	1.82	0.80
1:O:226:GLY:CA	1:O:255:THR:HG21	2.12	0.79
1:T:115:LYS:CD	1:T:155:LEU:CD2	2.59	0.79
1:R:69:LEU:H	1:R:69:LEU:HD23	1.45	0.79
1:O:59:GLN:N	1:O:59:GLN:NE2	2.30	0.79
1:N:191:VAL:HG22	1:N:230:ASN:HD22	1.46	0.79
1:P:132:LEU:O	1:P:136:LYS:HG3	1.83	0.79
1:N:6:PRO:HB2	1:N:37:VAL:HG13	1.64	0.79
1:M:228:CYS:HB2	1:M:231:ILE:HD12	1.63	0.78
1:S:221:ASN:HB2	1:S:224:LYS:HE2	1.65	0.78
1:K:159:LYS:O	1:K:160:MET:CG	2.30	0.78

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:11:ASN:HD21	1:J:76:THR:HG21	1.47	0.78
1:I:109:GLN:O	1:I:113:LYS:HG3	1.82	0.78
1:P:5:ARG:O	1:P:210:ARG:HD3	1.82	0.78
1:H:160:MET:O	1:H:163:LYS:CG	2.31	0.78
1:Q:5:ARG:HH12	1:Q:36:SER:HA	1.48	0.78
1:L:108:GLU:O	1:L:112:LYS:HG3	1.83	0.78
1:J:240:SER:HA	1:J:245:PHE:HB2	1.65	0.78
1:R:225:LEU:HA	1:R:228:CYS:SG	2.23	0.78
1:G:69:LEU:CD1	1:G:70:GLU:HG2	2.13	0.78
1:G:225:LEU:HB3	1:G:234:PHE:HZ	1.48	0.78
1:M:225:LEU:O	1:M:231:ILE:HD12	1.83	0.78
1:S:177:THR:HG22	1:S:179:VAL:HG22	1.65	0.78
1:L:204:GLU:CD	1:L:204:GLU:H	1.86	0.78
1:S:61:ARG:HG3	1:S:61:ARG:NH1	1.96	0.78
1:R:217:ALA:O	1:R:218:ASN:C	2.22	0.78
1:O:61:ARG:HE	1:O:62:ILE:H	1.32	0.77
1:P:96:HIS:HD2	1:P:98:GLU:H	1.32	0.77
1:O:58:LYS:CE	1:O:59:GLN:OE1	2.30	0.77
1:H:160:MET:O	1:H:163:LYS:CD	2.32	0.77
1:A:48:LEU:O	1:A:52:ILE:HG13	1.85	0.77
1:R:14:CYS:O	1:R:14:CYS:SG	2.43	0.77
1:K:171:PRO:HG3	1:K:213:TYR:CE1	2.19	0.77
1:R:225:LEU:CB	1:R:234:PHE:CE1	2.65	0.77
1:L:171:PRO:HD2	1:L:214:GLY:O	1.85	0.77
1:F:4:ARG:HD3	1:F:207:GLN:O	1.83	0.77
1:E:45:ALA:HA	1:E:48:LEU:CD2	2.15	0.77
1:B:48:LEU:O	1:B:52:ILE:HG13	1.85	0.77
1:E:217:ALA:HB3	1:I:178:GLY:HA3	1.66	0.77
1:H:160:MET:O	1:H:163:LYS:HD3	1.84	0.77
1:K:195:LYS:HG2	1:K:196:TRP:N	1.99	0.77
1:E:210:ARG:HA	1:E:232:ASP:OD2	1.85	0.77
1:K:171:PRO:HG3	1:K:213:TYR:HE1	1.50	0.77
1:Q:7:PHE:CE2	1:Q:210:ARG:HG3	2.20	0.76
1:A:172:VAL:HA	1:A:175:ILE:HD11	1.66	0.76
1:H:126:PHE:CD1	1:H:151:LEU:HD21	2.20	0.76
1:I:4:ARG:CG	1:I:4:ARG:HH11	1.97	0.76
1:Q:248:MET:O	1:Q:251:ILE:HG22	1.86	0.76
1:N:223:GLU:HA	1:N:223:GLU:OE1	1.84	0.76
1:D:52:ILE:HD11	1:D:89:LEU:HD21	1.67	0.76
1:O:171:PRO:CG	1:O:215:GLY:HA2	2.15	0.76
1:I:11:ASN:HD21	1:J:76:THR:CG2	1.98	0.76
1:Q:85:GLN:HE22	1:Q:120:LYS:HB3	1.48	0.76

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:N:45:ALA:HA	1:N:48:LEU:HD22	1.68	0.76
1:Q:201:VAL:HG12	1:Q:202:ALA:N	2.01	0.76
1:J:98:GLU:O	1:J:102:ILE:HB	1.86	0.76
1:E:132:LEU:O	1:E:136:LYS:HG3	1.86	0.76
1:N:226:GLY:O	1:N:255:THR:HG21	1.86	0.76
1:I:247:THR:O	1:I:251:ILE:HD13	1.86	0.75
1:L:171:PRO:CG	1:L:174:SER:OG	2.33	0.75
1:O:76:THR:HG23	1:P:65:GLN:HB3	1.67	0.75
1:J:182:THR:HG22	1:J:184:GLU:OE1	1.85	0.75
1:N:191:VAL:HG22	1:N:230:ASN:ND2	2.02	0.75
1:R:225:LEU:C	1:R:234:PHE:HZ	1.89	0.75
1:R:250:ASP:HA	1:R:253:THR:CG2	2.16	0.75
1:J:177:THR:HG22	1:J:179:VAL:H	1.52	0.75
1:G:224:LYS:O	1:G:227:GLN:HG3	1.85	0.75
1:L:109:GLN:O	1:L:113:LYS:HG3	1.86	0.75
1:K:218:ASN:O	1:K:222:ASP:HB2	1.87	0.75
1:I:13:LYS:HG3	1:J:76:THR:HG22	1.68	0.75
1:M:2:PRO:HG2	1:M:207:GLN:CB	2.16	0.75
1:R:52:ILE:HD13	1:R:62:ILE:HD12	1.67	0.75
1:C:217:ALA:O	1:C:218:ASN:CB	2.31	0.74
1:T:236:VAL:HG13	1:T:239:ALA:HB3	1.69	0.74
1:A:67:VAL:O	1:A:113:LYS:HD3	1.87	0.74
1:L:219:GLY:H	1:L:222:ASP:CG	1.91	0.74
1:S:7:PHE:HD1	1:S:8:ILE:N	1.85	0.74
1:B:189:VAL:O	1:B:193:LEU:HG	1.86	0.74
1:M:187:GLU:O	1:M:191:VAL:HG23	1.87	0.74
1:B:213:TYR:CZ	1:B:215:GLY:HA3	2.22	0.74
1:R:106:THR:OG1	1:R:109:GLN:HG3	1.87	0.74
1:P:15:ASN:HD22	1:P:15:ASN:N	1.85	0.74
1:F:98:GLU:O	1:F:102:ILE:HB	1.86	0.74
1:J:69:LEU:HD23	1:J:69:LEU:H	1.51	0.74
1:L:98:GLU:HA	1:L:102:ILE:HD12	1.69	0.74
1:C:21:ILE:HG13	1:C:47:HIS:HB3	1.70	0.74
1:A:206:ALA:O	1:A:209:ILE:HG22	1.86	0.74
1:H:198:ALA:HA	1:H:202:ALA:O	1.88	0.74
1:P:177:THR:CG2	1:P:179:VAL:HG22	2.18	0.74
1:J:24:HIS:O	1:J:28:ILE:HG13	1.87	0.74
1:N:69:LEU:HB3	1:N:113:LYS:HG2	1.70	0.74
1:O:69:LEU:HD23	1:O:70:GLU:HG2	1.70	0.73
1:N:139:ARG:HB3	1:N:139:ARG:HH11	1.52	0.73
1:Q:123:THR:HA	1:Q:164:GLU:HG3	1.68	0.73
1:C:76:THR:HG22	1:D:13:LYS:HD3	1.69	0.73

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:175:ILE:HD12	1:F:175:ILE:N	2.02	0.73
1:Q:210:ARG:CD	1:Q:210:ARG:H	2.00	0.73
1:N:217:ALA:HB1	1:N:248:MET:HE1	1.70	0.73
1:R:15:ASN:HD21	1:R:241:LEU:HD11	1.50	0.73
1:O:58:LYS:HG3	1:O:59:GLN:OE1	1.88	0.73
1:R:190:HIS:CE1	1:R:231:ILE:HD13	2.24	0.73
1:N:226:GLY:O	1:N:255:THR:CG2	2.36	0.73
1:S:130:GLU:OE2	1:S:135:ARG:NH2	2.21	0.73
1:I:11:ASN:ND2	1:J:76:THR:HG21	2.03	0.73
1:N:248:MET:O	1:N:251:ILE:HG22	1.89	0.73
1:N:90:LYS:HE3	1:N:91:HIS:CE1	2.24	0.73
1:Q:62:ILE:O	1:Q:89:LEU:CD1	2.37	0.73
1:O:220:SER:O	1:O:221:ASN:HB3	1.88	0.73
1:J:217:ALA:O	1:J:248:MET:HE1	1.89	0.73
1:M:95:GLY:O	1:M:127:CYS:HB2	1.87	0.73
1:Q:4:ARG:HD2	1:Q:232:ASP:OD2	1.87	0.73
1:D:158:SER:OG	1:D:160:MET:HE2	1.89	0.73
1:D:218:ASN:ND2	1:D:220:SER:H	1.86	0.73
1:M:98:GLU:O	1:M:102:ILE:HB	1.88	0.73
1:H:115:LYS:HE2	1:H:119:GLU:OE2	1.88	0.73
1:P:170:GLU:OE2	1:P:235:LEU:HD23	1.89	0.72
1:L:141:MET:HE3	1:L:141:MET:HA	1.71	0.72
1:R:228:CYS:HB2	1:R:231:ILE:CG1	2.19	0.72
1:I:194:ARG:CG	1:I:194:ARG:NH1	2.47	0.72
1:O:143:VAL:O	1:O:147:GLN:HG3	1.88	0.72
1:S:221:ASN:HB3	1:S:224:LYS:HE2	1.69	0.72
1:I:69:LEU:HD23	1:I:70:GLU:HG2	1.71	0.72
1:E:251:ILE:HA	1:E:254:LYS:CE	2.16	0.72
1:H:126:PHE:CE1	1:H:151:LEU:HD21	2.24	0.72
1:P:40:VAL:CG1	1:P:63:ALA:HB2	2.19	0.72
1:C:67:VAL:O	1:C:113:LYS:HD3	1.89	0.72
1:R:175:ILE:O	1:R:175:ILE:HG13	1.88	0.72
1:M:2:PRO:CG	1:M:207:GLN:HB3	2.17	0.72
1:D:247:THR:O	1:D:251:ILE:HD13	1.88	0.72
1:R:175:ILE:HG23	1:R:177:THR:OG1	1.90	0.72
1:F:171:PRO:HB3	1:F:173:TRP:HE1	1.54	0.72
1:S:130:GLU:O	1:S:172:VAL:HB	1.90	0.72
1:I:195:LYS:NZ	1:I:199:GLU:OE2	2.23	0.72
1:T:98:GLU:HA	1:T:102:ILE:HD12	1.69	0.72
1:Q:210:ARG:N	1:Q:210:ARG:HD3	2.01	0.72
1:P:195:LYS:HG3	1:P:199:GLU:OE1	1.89	0.72
1:O:145:ILE:HG23	1:O:196:TRP:CD1	2.25	0.72

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:Q:61:ARG:HH11	1:Q:61:ARG:HG3	1.52	0.72
1:B:69:LEU:CD2	1:B:70:GLU:HG2	2.20	0.72
1:E:171:PRO:CD	1:E:215:GLY:CA	2.67	0.71
1:T:63:ALA:HB2	1:T:91:HIS:HB2	1.70	0.71
1:T:85:GLN:HE22	1:T:120:LYS:HB3	1.55	0.71
1:S:97:SER:O	1:S:101:ARG:HB2	1.90	0.71
1:T:242:LYS:HB2	1:T:243:PRO:HD2	1.72	0.71
1:T:195:LYS:O	1:T:199:GLU:HB2	1.90	0.71
1:T:46:VAL:HG23	1:T:47:HIS:CD2	2.25	0.71
1:O:48:LEU:O	1:O:52:ILE:HG13	1.90	0.71
1:Q:183:PRO:HG3	1:Q:225:LEU:CD2	2.21	0.71
1:G:213:TYR:HD2	1:G:234:PHE:CD1	2.09	0.71
1:J:24:HIS:NE2	1:J:240:SER:O	2.21	0.71
1:R:217:ALA:O	1:R:218:ASN:O	2.08	0.71
1:F:24:HIS:O	1:F:28:ILE:HG13	1.91	0.71
1:S:160:MET:H	1:S:160:MET:HE3	1.56	0.71
1:N:68:TYR:HB2	1:N:78:GLU:HB3	1.73	0.71
1:B:213:TYR:CE2	1:B:215:GLY:HA3	2.25	0.71
1:Q:230:ASN:N	1:Q:230:ASN:HD22	1.88	0.71
1:B:217:ALA:HB1	1:B:222:ASP:OD1	1.90	0.71
1:A:137:ALA:O	1:A:138:ASN:HB3	1.90	0.71
1:G:213:TYR:CD2	1:G:234:PHE:CE1	2.79	0.70
1:P:177:THR:HG23	1:P:179:VAL:HG22	1.72	0.70
1:S:130:GLU:HG2	1:S:144:ASN:HD21	1.55	0.70
1:C:90:LYS:HD3	1:C:91:HIS:CE1	2.26	0.70
1:D:244:GLU:O	1:D:248:MET:HG3	1.91	0.70
1:L:242:LYS:HB3	1:L:243:PRO:HD2	1.72	0.70
1:T:115:LYS:CG	1:T:155:LEU:HD21	2.07	0.70
1:S:155:LEU:HG	1:S:161:LEU:HD11	1.71	0.70
1:A:172:VAL:HA	1:A:175:ILE:CG1	2.20	0.70
1:L:200:LYS:CD	1:L:200:LYS:O	2.30	0.70
1:Q:228:CYS:HB3	1:Q:231:ILE:HG13	1.73	0.70
1:C:98:GLU:O	1:C:102:ILE:HB	1.91	0.70
1:I:145:ILE:HG12	1:I:196:TRP:CD1	2.26	0.70
1:C:69:LEU:H	1:C:69:LEU:HD22	1.54	0.70
1:R:206:ALA:O	1:R:209:ILE:HG22	1.92	0.70
1:C:115:LYS:O	1:C:119:GLU:HG3	1.90	0.70
1:L:218:ASN:H	1:L:221:ASN:HD21	0.80	0.70
1:I:194:ARG:NH2	1:I:232:ASP:OD2	2.24	0.70
1:R:69:LEU:H	1:R:69:LEU:CD2	2.05	0.70
1:C:218:ASN:OD1	1:C:219:GLY:N	2.23	0.70
1:Q:234:PHE:CE2	1:Q:248:MET:CE	2.75	0.70

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:P:170:GLU:HG2	1:P:214:GLY:HA3	1.73	0.70
1:A:132:LEU:O	1:A:136:LYS:HG3	1.92	0.70
1:F:13:LYS:H	1:F:65:GLN:NE2	1.90	0.70
1:Q:46:VAL:HG23	1:Q:47:HIS:CD2	2.26	0.70
1:S:92:VAL:CG1	1:S:124:VAL:HG22	2.22	0.70
1:Q:171:PRO:HB2	1:Q:174:SER:OG	1.92	0.69
1:M:5:ARG:HH11	1:M:5:ARG:HG2	1.54	0.69
1:O:182:THR:H	1:O:185:GLN:HE21	1.37	0.69
1:Q:183:PRO:HA	1:Q:225:LEU:CD2	2.22	0.69
1:O:197:PHE:CD2	1:O:206:ALA:HA	2.27	0.69
1:M:5:ARG:HH11	1:M:5:ARG:CG	2.05	0.69
1:E:171:PRO:CG	1:E:215:GLY:CA	2.68	0.69
1:Q:197:PHE:HD2	1:Q:206:ALA:HA	1.54	0.69
1:Q:234:PHE:CE2	1:Q:248:MET:HE3	2.26	0.69
1:A:217:ALA:CB	1:A:248:MET:HE3	2.23	0.69
1:I:72:ASN:ND2	1:I:80:SER:OG	2.25	0.69
1:I:187:GLU:OE1	1:I:228:CYS:HB3	1.91	0.69
1:D:130:GLU:OE2	1:D:135:ARG:HB2	1.92	0.69
1:Q:7:PHE:CE2	1:Q:210:ARG:NH1	2.61	0.69
1:G:225:LEU:HB3	1:G:234:PHE:CZ	2.26	0.69
1:F:171:PRO:O	1:F:175:ILE:CD1	2.34	0.69
1:H:100:ARG:NH2	1:H:126:PHE:CZ	2.60	0.69
1:Q:17:SER:O	1:Q:21:ILE:HG12	1.92	0.69
1:I:37:VAL:HG21	1:I:253:THR:OG1	1.93	0.69
1:Q:115:LYS:HE2	1:Q:119:GLU:OE2	1.92	0.69
1:Q:183:PRO:CG	1:Q:225:LEU:HD23	2.22	0.69
1:I:194:ARG:HG3	1:I:194:ARG:NH1	2.07	0.69
1:G:18:LEU:O	1:G:22:LYS:HG3	1.92	0.69
1:B:222:ASP:OD2	1:B:248:MET:HE3	1.93	0.69
1:H:220:SER:O	1:H:221:ASN:HB3	1.90	0.69
1:T:115:LYS:HD3	1:T:155:LEU:HD23	1.71	0.69
1:Q:62:ILE:O	1:Q:89:LEU:HD13	1.92	0.69
1:Q:63:ALA:HA	1:Q:89:LEU:HD21	1.75	0.69
1:M:187:GLU:OE1	1:M:228:CYS:HB3	1.92	0.69
1:P:98:GLU:HA	1:P:102:ILE:HD12	1.74	0.69
1:A:158:SER:HB3	1:A:161:LEU:HG	1.73	0.69
1:F:182:THR:OG1	1:F:185:GLN:HB2	1.93	0.69
1:K:143:VAL:O	1:K:147:GLN:HG3	1.93	0.69
1:C:218:ASN:OD1	1:C:218:ASN:C	2.29	0.69
1:R:48:LEU:O	1:R:52:ILE:HG12	1.92	0.69
1:A:187:GLU:O	1:A:191:VAL:HG23	1.92	0.69
1:I:4:ARG:HD2	1:I:208:HIS:C	2.14	0.68

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:172:VAL:HA	1:S:175:ILE:HG12	1.75	0.68
1:N:134:GLU:O	1:N:139:ARG:HB2	1.92	0.68
1:S:197:PHE:CE2	1:S:209:ILE:HD13	2.27	0.68
1:Q:61:ARG:NH1	1:Q:61:ARG:HG3	2.08	0.68
1:J:216:SER:O	1:J:221:ASN:ND2	2.26	0.68
1:C:77:GLY:HA3	1:D:99:ARG:HH11	1.59	0.68
1:G:69:LEU:HD12	1:G:69:LEU:C	2.13	0.68
1:E:195:LYS:O	1:E:199:GLU:HG2	1.93	0.68
1:A:130:GLU:OE2	1:A:140:THR:HG23	1.94	0.68
1:F:69:LEU:HD23	1:F:70:GLU:HG2	1.74	0.68
1:E:98:GLU:OE2	1:F:74:ALA:HB1	1.93	0.68
1:S:63:ALA:HB2	1:S:91:HIS:HB2	1.75	0.68
1:S:118:LEU:HD13	1:S:161:LEU:HD12	1.74	0.68
1:A:145:ILE:O	1:A:149:GLU:HB2	1.93	0.68
1:L:43:PRO:HD2	1:L:48:LEU:CD1	2.23	0.68
1:K:187:GLU:OE1	1:K:228:CYS:HB3	1.93	0.68
1:H:48:LEU:O	1:H:52:ILE:HG13	1.92	0.68
1:O:198:ALA:HB2	1:O:206:ALA:CB	2.24	0.68
1:R:17:SER:O	1:R:21:ILE:HG12	1.93	0.68
1:I:83:MET:O	1:I:87:MET:HG3	1.94	0.68
1:L:177:THR:HG22	1:L:179:VAL:HG21	1.72	0.68
1:K:171:PRO:CG	1:K:213:TYR:CE1	2.77	0.68
1:K:106:THR:OG1	1:K:109:GLN:HG3	1.94	0.68
1:M:109:GLN:O	1:M:113:LYS:HG3	1.94	0.68
1:S:109:GLN:O	1:S:113:LYS:HG3	1.94	0.68
1:K:247:THR:O	1:K:251:ILE:HD13	1.94	0.68
1:J:111:ALA:HB1	1:J:151:LEU:HA	1.76	0.68
1:S:177:THR:CG2	1:S:179:VAL:HG22	2.24	0.68
1:A:134:GLU:HG2	1:A:143:VAL:HG21	1.76	0.68
1:K:41:ILE:HG23	1:K:60:LEU:HD11	1.76	0.68
1:R:29:ALA:HA	1:R:57:SER:OG	1.93	0.68
1:I:84:LEU:HD22	1:I:89:LEU:CD1	2.15	0.67
1:A:218:ASN:ND2	1:A:218:ASN:C	2.48	0.67
1:R:230:ASN:N	1:R:230:ASN:HD22	1.92	0.67
1:I:218:ASN:O	1:I:222:ASP:HB2	1.93	0.67
1:C:130:GLU:OE2	1:C:140:THR:HB	1.94	0.67
1:F:177:THR:O	1:F:177:THR:HG22	1.93	0.67
1:R:156:GLY:O	1:R:159:LYS:HG3	1.94	0.67
1:Q:197:PHE:O	1:Q:201:VAL:CB	2.39	0.67
1:O:221:ASN:HA	1:O:224:LYS:NZ	2.09	0.67
1:A:172:VAL:HA	1:A:175:ILE:HG13	1.74	0.67
1:K:159:LYS:O	1:K:160:MET:CB	2.41	0.67

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:T:69:LEU:HB3	1:T:113:LYS:HG2	1.76	0.67
1:I:4:ARG:HB2	1:I:4:ARG:CZ	2.25	0.67
1:R:194:ARG:HH11	1:R:209:ILE:HG23	1.60	0.67
1:O:171:PRO:CG	1:O:215:GLY:CA	2.73	0.67
1:K:227:GLN:O	1:K:228:CYS:C	2.33	0.67
1:D:109:GLN:O	1:D:113:LYS:HG3	1.95	0.67
1:A:24:HIS:O	1:A:28:ILE:HG13	1.95	0.67
1:K:81:VAL:HG13	1:K:122:MET:SD	2.33	0.67
1:R:194:ARG:HH11	1:R:209:ILE:CG2	2.06	0.67
1:S:65:GLN:O	1:S:93:ILE:HB	1.95	0.67
1:A:218:ASN:HD21	1:A:221:ASN:H	1.43	0.67
1:R:8:ILE:HG22	1:R:39:VAL:HA	1.75	0.67
1:S:171:PRO:HA	1:S:173:TRP:HE1	1.59	0.67
1:M:195:LYS:O	1:M:199:GLU:HG3	1.95	0.67
1:G:130:GLU:OE2	1:G:135:ARG:HB2	1.95	0.67
1:P:210:ARG:CG	1:P:210:ARG:HH11	1.95	0.67
1:C:11:ASN:ND2	1:C:13:LYS:HG2	2.09	0.67
1:R:34:PRO:HB2	1:R:36:SER:OG	1.94	0.67
1:O:18:LEU:O	1:O:22:LYS:HG3	1.94	0.67
1:R:226:GLY:N	1:R:234:PHE:HZ	1.92	0.67
1:R:71:GLY:CA	1:R:116:ARG:NH2	2.58	0.67
1:G:69:LEU:HD12	1:G:70:GLU:CG	2.25	0.67
1:N:187:GLU:OE2	1:N:229:PRO:HG2	1.95	0.67
1:I:218:ASN:HD21	1:I:220:SER:HB3	1.59	0.67
1:N:190:HIS:CE1	1:N:211:ILE:HG22	2.29	0.67
1:Q:183:PRO:CA	1:Q:225:LEU:CD2	2.73	0.66
1:R:12:PHE:O	1:R:13:LYS:HB2	1.95	0.66
1:Q:172:VAL:O	1:Q:175:ILE:HG22	1.95	0.66
1:B:182:THR:OG1	1:B:185:GLN:HG3	1.96	0.66
1:E:115:LYS:HG2	1:E:155:LEU:HD23	1.75	0.66
1:Q:7:PHE:CD2	1:Q:210:ARG:HG3	2.30	0.66
1:Q:177:THR:CG2	1:Q:177:THR:O	2.43	0.66
1:R:114:ALA:O	1:R:118:LEU:HD13	1.95	0.66
1:R:118:LEU:HD23	1:R:161:LEU:HB3	1.76	0.66
1:G:72:ASN:HA	1:H:14:CYS:O	1.95	0.66
1:H:21:ILE:O	1:H:25:VAL:HG23	1.94	0.66
1:H:218:ASN:OD1	1:H:219:GLY:N	2.29	0.66
1:S:67:VAL:O	1:S:113:LYS:HD3	1.94	0.66
1:T:213:TYR:HB2	1:T:231:ILE:HD13	1.76	0.66
1:H:155:LEU:HD12	1:H:162:TRP:NE1	2.10	0.66
1:L:97:SER:OG	1:L:175:ILE:CD1	2.43	0.66
1:R:227:GLN:HA	1:R:227:GLN:HE21	1.59	0.66

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:N:145:ILE:HG23	1:N:196:TRP:CD1	2.30	0.66
1:L:118:LEU:HD13	1:L:161:LEU:O	1.96	0.66
1:N:4:ARG:HD3	1:N:207:GLN:O	1.95	0.66
1:Q:13:LYS:HD3	1:R:74:ALA:HA	1.78	0.66
1:O:223:GLU:O	1:O:227:GLN:HG3	1.95	0.66
1:H:126:PHE:CG	1:H:151:LEU:HD21	2.30	0.66
1:K:4:ARG:HG2	1:K:208:HIS:HA	1.78	0.66
1:L:90:LYS:HE3	1:L:91:HIS:CE1	2.31	0.66
1:Q:225:LEU:O	1:Q:228:CYS:HB2	1.95	0.66
1:R:109:GLN:O	1:R:113:LYS:HG3	1.96	0.66
1:A:138:ASN:O	1:A:138:ASN:ND2	2.29	0.66
1:D:108:GLU:O	1:D:112:LYS:HG3	1.95	0.66
1:P:128:VAL:HG12	1:P:147:GLN:HB2	1.76	0.66
1:A:137:ALA:O	1:A:138:ASN:CB	2.41	0.66
1:M:170:GLU:HB2	1:M:175:ILE:HD11	1.78	0.66
1:K:218:ASN:ND2	1:K:219:GLY:N	2.43	0.66
1:P:98:GLU:O	1:P:102:ILE:HB	1.95	0.66
1:B:18:LEU:O	1:B:22:LYS:HG3	1.96	0.66
1:I:244:GLU:O	1:I:248:MET:HG3	1.94	0.66
1:G:64:ALA:O	1:G:93:ILE:HG23	1.96	0.65
1:F:116:ARG:O	1:F:120:LYS:HG3	1.96	0.65
1:I:74:ALA:HB1	1:J:98:GLU:OE2	1.96	0.65
1:K:132:LEU:O	1:K:136:LYS:HG3	1.97	0.65
1:G:9:GLY:HA2	1:G:40:VAL:O	1.96	0.65
1:Q:165:VAL:O	1:Q:210:ARG:NE	2.28	0.65
1:L:220:SER:OG	1:L:221:ASN:N	2.28	0.65
1:T:236:VAL:CG1	1:T:239:ALA:HB3	2.26	0.65
1:A:160:MET:H	1:A:160:MET:HE3	1.61	0.65
1:L:177:THR:CG2	1:L:179:VAL:HG21	2.24	0.65
1:T:69:LEU:H	1:T:69:LEU:HD23	1.62	0.65
1:R:68:TYR:CD1	1:R:78:GLU:HG3	2.31	0.65
1:N:67:VAL:O	1:N:113:LYS:HD3	1.97	0.65
1:K:109:GLN:O	1:K:113:LYS:HG3	1.97	0.65
1:R:71:GLY:HA2	1:R:116:ARG:NH2	2.12	0.65
1:H:221:ASN:ND2	1:H:221:ASN:O	2.30	0.65
1:S:115:LYS:O	1:S:119:GLU:HG3	1.97	0.65
1:L:130:GLU:O	1:L:172:VAL:HB	1.97	0.65
1:A:84:LEU:HD22	1:A:89:LEU:HD12	1.76	0.65
1:G:17:SER:O	1:G:21:ILE:HG12	1.97	0.65
1:L:40:VAL:CG1	1:L:63:ALA:HB2	2.27	0.65
1:I:4:ARG:HD2	1:I:208:HIS:CA	2.27	0.65
1:I:83:MET:HG2	1:J:47:HIS:CE1	2.32	0.65

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:N:209:ILE:HG23	1:N:211:ILE:HD11	1.79	0.65
1:L:155:LEU:HD12	1:L:162:TRP:CE2	2.32	0.65
1:D:171:PRO:HD2	1:D:214:GLY:O	1.97	0.65
1:L:138:ASN:O	1:L:138:ASN:ND2	2.30	0.65
1:P:14:CYS:O	1:P:15:ASN:ND2	2.30	0.65
1:P:48:LEU:O	1:P:52:ILE:HG13	1.96	0.65
1:O:137:ALA:O	1:O:138:ASN:HB2	1.96	0.65
1:T:206:ALA:O	1:T:209:ILE:HG22	1.97	0.65
1:A:139:ARG:NH1	1:A:142:GLU:OE2	2.30	0.64
1:T:25:VAL:HA	1:T:28:ILE:HG13	1.78	0.64
1:E:155:LEU:HD12	1:E:162:TRP:CE2	2.32	0.64
1:L:134:GLU:O	1:L:139:ARG:N	2.30	0.64
1:S:239:ALA:O	1:S:245:PHE:HB2	1.97	0.64
1:A:217:ALA:HB1	1:A:248:MET:CE	2.27	0.64
1:H:99:ARG:HA	1:H:103:MET:HB2	1.80	0.64
1:Q:158:SER:HB2	1:Q:161:LEU:HD12	1.79	0.64
1:Q:143:VAL:O	1:Q:147:GLN:HG3	1.98	0.64
1:N:14:CYS:O	1:N:15:ASN:ND2	2.30	0.64
1:M:242:LYS:HB3	1:M:243:PRO:HD2	1.79	0.64
1:P:148:LEU:HB3	1:P:196:TRP:CH2	2.33	0.64
1:I:233:GLY:HA2	1:I:252:LEU:CD1	2.28	0.64
1:J:137:ALA:O	1:J:138:ASN:CB	2.43	0.64
1:L:4:ARG:HD2	1:L:207:GLN:O	1.98	0.64
1:M:13:LYS:H	1:M:65:GLN:NE2	1.96	0.64
1:Q:198:ALA:HB2	1:Q:206:ALA:CB	2.27	0.64
1:Q:132:LEU:HG	1:Q:136:LYS:HE2	1.80	0.64
1:L:251:ILE:HD13	1:L:254:LYS:NZ	2.13	0.63
1:F:145:ILE:HG23	1:F:196:TRP:NE1	2.14	0.63
1:H:6:PRO:HB2	1:H:37:VAL:HG13	1.80	0.63
1:Q:239:ALA:O	1:Q:245:PHE:HB2	1.98	0.63
1:L:222:ASP:OD2	1:L:248:MET:HE3	1.98	0.63
1:S:39:VAL:HG12	1:S:60:LEU:HD12	1.79	0.63
1:L:137:ALA:O	1:L:138:ASN:HB3	1.98	0.63
1:Q:244:GLU:O	1:Q:247:THR:HB	1.98	0.63
1:G:65:GLN:O	1:G:93:ILE:HG12	1.98	0.63
1:P:148:LEU:HB3	1:P:196:TRP:CZ3	2.34	0.63
1:S:43:PRO:HG2	1:S:48:LEU:HD12	1.81	0.63
1:S:131:THR:OG1	1:S:134:GLU:HG3	1.98	0.63
1:D:155:LEU:HD12	1:D:162:TRP:NE1	2.14	0.63
1:S:8:ILE:HD11	1:S:245:PHE:CZ	2.33	0.63
1:K:194:ARG:HD3	1:K:206:ALA:O	1.98	0.63
1:B:244:GLU:O	1:B:248:MET:HG3	1.99	0.63

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:48:LEU:O	1:L:52:ILE:HG13	1.98	0.63
1:P:69:LEU:HD23	1:P:70:GLU:HG2	1.80	0.63
1:N:137:ALA:HB3	1:N:139:ARG:HG3	1.80	0.63
1:T:98:GLU:O	1:T:102:ILE:HB	1.99	0.63
1:H:220:SER:O	1:H:221:ASN:CB	2.46	0.63
1:S:173:TRP:CD1	1:S:173:TRP:N	2.56	0.63
1:M:171:PRO:HG2	1:M:174:SER:HB2	1.80	0.63
1:T:34:PRO:HG2	1:T:253:THR:OG1	1.98	0.63
1:J:127:CYS:HB3	1:J:170:GLU:OE2	1.98	0.63
1:B:175:ILE:O	1:O:176:GLY:N	2.32	0.63
1:L:182:THR:OG1	1:L:185:GLN:HG3	1.99	0.63
1:G:67:VAL:O	1:G:113:LYS:HD3	1.99	0.63
1:D:18:LEU:O	1:D:22:LYS:HG3	1.98	0.63
1:L:222:ASP:OD2	1:L:248:MET:CE	2.46	0.62
1:D:57:SER:HB3	1:D:60:LEU:HB3	1.81	0.62
1:L:67:VAL:O	1:L:113:LYS:HD3	1.99	0.62
1:M:106:THR:OG1	1:M:109:GLN:HG3	1.99	0.62
1:P:149:GLU:OE1	1:P:200:LYS:HE3	1.98	0.62
1:O:109:GLN:O	1:O:113:LYS:HG3	1.99	0.62
1:N:171:PRO:HB2	1:N:174:SER:OG	1.98	0.62
1:E:97:SER:HB3	1:E:170:GLU:OE1	1.99	0.62
1:E:190:HIS:CE1	1:E:213:TYR:HB2	2.32	0.62
1:Q:183:PRO:CG	1:Q:225:LEU:CD2	2.77	0.62
1:F:175:ILE:H	1:F:175:ILE:HD12	1.61	0.62
1:I:141:MET:O	1:I:145:ILE:HB	1.99	0.62
1:K:204:GLU:HG2	1:K:205:GLY:N	2.14	0.62
1:R:174:SER:O	1:R:175:ILE:CG2	2.48	0.62
1:O:213:TYR:CE1	1:O:215:GLY:HA3	2.35	0.62
1:Q:222:ASP:OD1	1:Q:223:GLU:N	2.33	0.62
1:N:139:ARG:HH12	1:N:143:VAL:HG22	1.63	0.62
1:F:109:GLN:O	1:F:113:LYS:HG3	1.99	0.62
1:Q:8:ILE:CG2	1:Q:39:VAL:HG22	2.30	0.62
1:E:197:PHE:O	1:E:201:VAL:N	2.33	0.62
1:N:48:LEU:O	1:N:52:ILE:HG13	1.98	0.62
1:D:159:LYS:C	1:D:161:LEU:H	2.03	0.62
1:Q:15:ASN:OD1	1:R:72:ASN:HB3	1.99	0.62
1:T:172:VAL:HA	1:T:175:ILE:HD12	1.80	0.62
1:E:222:ASP:O	1:E:226:GLY:N	2.27	0.62
1:G:213:TYR:HD2	1:G:234:PHE:CE1	2.18	0.62
1:L:218:ASN:HB2	1:L:221:ASN:OD1	1.99	0.62
1:G:9:GLY:O	1:G:235:LEU:HA	2.00	0.62
1:O:83:MET:O	1:O:87:MET:HG3	1.99	0.62

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:R:228:CYS:CB	1:R:231:ILE:CG1	2.77	0.62
1:O:197:PHE:HD2	1:O:206:ALA:HA	1.64	0.62
1:A:139:ARG:NH1	1:A:142:GLU:OE1	2.33	0.62
1:A:144:ASN:O	1:A:148:LEU:HB2	2.00	0.62
1:E:174:SER:O	1:I:176:GLY:HA3	2.00	0.62
1:S:6:PRO:CD	1:S:36:SER:O	2.48	0.61
1:G:69:LEU:O	1:G:116:ARG:HD2	2.00	0.61
1:M:118:LEU:HB3	1:M:161:LEU:HD22	1.82	0.61
1:M:40:VAL:CG1	1:M:63:ALA:HB2	2.29	0.61
1:I:5:ARG:NH2	1:I:35:ASP:O	2.33	0.61
1:S:79:THR:HG21	1:S:84:LEU:HD21	1.82	0.61
1:R:71:GLY:HA2	1:R:116:ARG:HH21	1.65	0.61
1:G:109:GLN:O	1:G:113:LYS:HG3	2.00	0.61
1:L:64:ALA:HB3	1:L:92:VAL:HG23	1.80	0.61
1:G:218:ASN:O	1:G:220:SER:N	2.33	0.61
1:C:178:GLY:CA	1:R:175:ILE:HD13	2.21	0.61
1:E:175:ILE:HA	1:I:176:GLY:CA	2.20	0.61
1:E:171:PRO:CD	1:E:215:GLY:HA3	2.30	0.61
1:O:171:PRO:CD	1:O:214:GLY:O	2.46	0.61
1:G:21:ILE:O	1:G:25:VAL:HG23	2.01	0.61
1:K:98:GLU:O	1:K:102:ILE:HB	2.00	0.61
1:S:246:MET:O	1:S:249:ILE:HB	2.00	0.61
1:J:95:GLY:HA2	1:J:110:SER:OG	2.00	0.61
1:G:213:TYR:CD2	1:G:234:PHE:CD1	2.88	0.61
1:M:228:CYS:HB2	1:M:231:ILE:CD1	2.30	0.61
1:A:145:ILE:HG23	1:A:196:TRP:CD1	2.35	0.61
1:P:95:GLY:O	1:P:127:CYS:HB2	2.00	0.61
1:N:109:GLN:O	1:N:113:LYS:HG3	2.00	0.61
1:M:111:ALA:HB1	1:M:151:LEU:HA	1.81	0.61
1:A:31:HIS:NE2	1:A:250:ASP:OD1	2.31	0.61
1:Q:9:GLY:HA2	1:Q:40:VAL:HG13	1.83	0.61
1:R:225:LEU:CB	1:R:234:PHE:HE1	2.03	0.61
1:R:251:ILE:N	1:R:251:ILE:HD13	2.15	0.61
1:O:98:GLU:OE2	1:P:74:ALA:HB1	2.01	0.61
1:A:177:THR:OG1	1:A:179:VAL:HG13	2.00	0.61
1:C:240:SER:HA	1:C:245:PHE:HB2	1.82	0.61
1:Q:89:LEU:CD1	1:Q:91:HIS:H	2.13	0.61
1:Q:197:PHE:CE1	1:Q:209:ILE:HD13	2.35	0.61
1:H:197:PHE:O	1:H:201:VAL:HB	2.00	0.61
1:J:132:LEU:HD22	1:J:177:THR:HG21	1.83	0.61
1:R:15:ASN:OD1	1:R:15:ASN:N	2.34	0.61
1:R:60:LEU:O	1:R:61:ARG:HD2	2.00	0.61

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:R:61:ARG:HH22	1:R:90:LYS:HD3	1.64	0.61
1:C:72:ASN:ND2	1:C:80:SER:OG	2.33	0.61
1:P:14:CYS:C	1:P:15:ASN:ND2	2.38	0.61
1:S:95:GLY:O	1:S:127:CYS:HB2	1.99	0.61
1:R:174:SER:C	1:R:175:ILE:HG22	2.21	0.61
1:Q:243:PRO:HA	1:Q:246:MET:CE	2.31	0.61
1:E:195:LYS:O	1:E:199:GLU:CG	2.49	0.61
1:R:156:GLY:O	1:R:159:LYS:CG	2.49	0.61
1:J:48:LEU:O	1:J:52:ILE:HG13	2.01	0.61
1:A:123:THR:HA	1:A:164:GLU:HG3	1.81	0.61
1:A:21:ILE:O	1:A:25:VAL:HG23	2.01	0.61
1:E:191:VAL:HG22	1:E:230:ASN:ND2	2.16	0.60
1:F:175:ILE:H	1:F:175:ILE:CD1	2.14	0.60
1:Q:166:VAL:HG22	1:Q:210:ARG:CZ	2.31	0.60
1:N:143:VAL:O	1:N:147:GLN:HG3	2.01	0.60
1:S:83:MET:O	1:S:87:MET:HG3	2.01	0.60
1:C:195:LYS:O	1:C:199:GLU:HG3	2.01	0.60
1:C:6:PRO:HB2	1:C:37:VAL:HG13	1.83	0.60
1:D:194:ARG:HD3	1:D:206:ALA:O	2.01	0.60
1:B:4:ARG:HG2	1:B:208:HIS:O	2.02	0.60
1:H:109:GLN:O	1:H:113:LYS:HG3	2.01	0.60
1:G:213:TYR:CD2	1:G:234:PHE:HE1	2.18	0.60
1:B:98:GLU:O	1:B:102:ILE:HB	2.00	0.60
1:I:4:ARG:NH1	1:I:232:ASP:OD1	2.34	0.60
1:K:251:ILE:O	1:K:255:THR:HB	2.02	0.60
1:S:92:VAL:HG12	1:S:124:VAL:HG22	1.84	0.60
1:E:98:GLU:HB2	1:F:76:THR:HG22	1.83	0.60
1:P:148:LEU:HG	1:P:196:TRP:CZ3	2.36	0.60
1:T:185:GLN:O	1:T:189:VAL:HG23	2.01	0.60
1:K:155:LEU:HD12	1:K:162:TRP:CE2	2.37	0.60
1:P:195:LYS:O	1:P:199:GLU:HB2	2.02	0.60
1:D:81:VAL:O	1:D:85:GLN:HG3	2.02	0.60
1:O:160:MET:O	1:O:163:LYS:HB2	2.00	0.60
1:R:157:GLU:OE1	1:R:157:GLU:HA	2.01	0.60
1:D:8:ILE:HB	1:D:252:LEU:HD22	1.83	0.60
1:C:76:THR:N	1:D:98:GLU:OE1	2.33	0.60
1:I:4:ARG:HD2	1:I:208:HIS:HA	1.83	0.60
1:I:4:ARG:CB	1:I:4:ARG:NH1	2.64	0.60
1:Q:201:VAL:HG12	1:Q:202:ALA:H	1.65	0.60
1:A:218:ASN:ND2	1:A:220:SER:N	2.50	0.60
1:J:130:GLU:OE2	1:J:173:TRP:CD1	2.54	0.60
1:R:225:LEU:HB3	1:R:234:PHE:CZ	2.35	0.60

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:7:PHE:O	1:S:233:GLY:HA3	2.00	0.60
1:R:183:PRO:HB2	1:R:224:LYS:HE2	1.84	0.60
1:D:218:ASN:C	1:D:218:ASN:HD22	2.05	0.60
1:T:243:PRO:HA	1:T:246:MET:CE	2.32	0.60
1:N:4:ARG:HE	1:N:232:ASP:CG	2.05	0.60
1:O:164:GLU:OE1	1:O:164:GLU:HA	2.02	0.60
1:T:11:ASN:ND2	1:T:13:LYS:HG3	2.16	0.60
1:L:236:VAL:HG11	1:L:239:ALA:HB3	1.82	0.60
1:J:123:THR:HG23	1:J:164:GLU:O	2.02	0.60
1:B:155:LEU:HD12	1:B:162:TRP:NE1	2.16	0.60
1:Q:92:VAL:HG12	1:Q:124:VAL:HG22	1.84	0.60
1:T:157:GLU:OE1	1:T:157:GLU:HA	2.00	0.60
1:J:244:GLU:N	1:J:244:GLU:OE1	2.28	0.60
1:R:227:GLN:HA	1:R:227:GLN:NE2	2.15	0.60
1:T:250:ASP:O	1:T:253:THR:HB	2.02	0.60
1:K:151:LEU:O	1:K:155:LEU:HG	2.01	0.60
1:A:83:MET:O	1:A:87:MET:HG3	2.02	0.60
1:F:174:SER:HB2	1:F:179:VAL:HG12	1.82	0.59
1:G:97:SER:CB	1:G:170:GLU:OE1	2.45	0.59
1:K:197:PHE:CD1	1:K:206:ALA:HA	2.37	0.59
1:I:98:GLU:OE1	1:J:76:THR:HG23	2.02	0.59
1:N:199:GLU:C	1:N:200:LYS:HD2	2.22	0.59
1:S:21:ILE:O	1:S:25:VAL:HG23	2.02	0.59
1:C:111:ALA:HB1	1:C:151:LEU:HA	1.84	0.59
1:L:203:ALA:HB3	1:L:204:GLU:OE2	2.03	0.59
1:O:137:ALA:O	1:O:138:ASN:CB	2.49	0.59
1:Q:7:PHE:CE1	1:Q:38:ASP:CG	2.76	0.59
1:I:11:ASN:ND2	1:J:76:THR:CG2	2.63	0.59
1:O:162:TRP:CH2	1:O:196:TRP:HH2	2.21	0.59
1:R:82:GLU:H	1:R:82:GLU:CD	2.06	0.59
1:E:171:PRO:HB2	1:E:174:SER:OG	2.01	0.59
1:H:162:TRP:CE3	1:H:197:PHE:HE2	2.20	0.59
1:E:219:GLY:O	1:E:220:SER:CB	2.50	0.59
1:J:21:ILE:O	1:J:25:VAL:HG23	2.01	0.59
1:Q:69:LEU:O	1:Q:116:ARG:HD2	2.02	0.59
1:I:78:GLU:OE1	1:I:78:GLU:HA	2.02	0.59
1:L:204:GLU:N	1:L:204:GLU:CD	2.55	0.59
1:Q:39:VAL:HG12	1:Q:60:LEU:HD12	1.84	0.59
1:F:155:LEU:HD12	1:F:162:TRP:NE1	2.16	0.59
1:H:141:MET:O	1:H:145:ILE:HG12	2.02	0.59
1:S:151:LEU:O	1:S:155:LEU:HD13	2.03	0.59
1:R:149:GLU:HG2	1:R:196:TRP:HZ2	1.68	0.59

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:171:PRO:HD2	1:C:214:GLY:O	2.02	0.59
1:B:97:SER:O	1:B:101:ARG:HB2	2.03	0.59
1:F:218:ASN:O	1:F:221:ASN:OD1	2.20	0.59
1:F:13:LYS:N	1:F:65:GLN:HE22	2.01	0.59
1:I:250:ASP:O	1:I:254:LYS:HD3	2.03	0.59
1:L:236:VAL:CG1	1:L:239:ALA:HB3	2.33	0.59
1:M:244:GLU:O	1:M:247:THR:HB	2.03	0.59
1:O:222:ASP:OD1	1:O:225:LEU:HD12	2.03	0.59
1:K:222:ASP:OD1	1:K:234:PHE:CZ	2.55	0.59
1:R:250:ASP:HA	1:R:253:THR:HG22	1.85	0.59
1:M:7:PHE:HB2	1:M:210:ARG:HH11	1.68	0.59
1:A:143:VAL:O	1:A:147:GLN:HG3	2.03	0.59
1:R:239:ALA:O	1:R:245:PHE:HB2	2.03	0.59
1:C:187:GLU:OE1	1:C:228:CYS:HB3	2.02	0.59
1:O:218:ASN:HD22	1:O:220:SER:N	1.90	0.59
1:L:177:THR:CB	1:L:179:VAL:HG23	2.33	0.58
1:E:171:PRO:HG2	1:E:215:GLY:CA	2.10	0.58
1:K:218:ASN:ND2	1:K:219:GLY:H	2.00	0.58
1:Q:173:TRP:CZ3	1:Q:174:SER:HB3	2.37	0.58
1:O:14:CYS:SG	1:P:78:GLU:O	2.53	0.58
1:M:81:VAL:HG13	1:M:122:MET:SD	2.43	0.58
1:E:254:LYS:C	1:E:255:THR:OG1	2.36	0.58
1:K:165:VAL:O	1:K:209:ILE:CD1	2.49	0.58
1:K:195:LYS:O	1:K:199:GLU:HG3	2.03	0.58
1:N:21:ILE:O	1:N:25:VAL:HG23	2.02	0.58
1:E:171:PRO:HD2	1:E:214:GLY:O	2.03	0.58
1:P:221:ASN:OD1	1:P:222:ASP:N	2.36	0.58
1:R:228:CYS:SG	1:R:231:ILE:HG13	2.43	0.58
1:Q:173:TRP:CE3	1:Q:174:SER:HB3	2.38	0.58
1:M:13:LYS:N	1:M:65:GLN:HE22	2.01	0.58
1:F:196:TRP:O	1:F:200:LYS:HB2	2.03	0.58
1:P:159:LYS:O	1:P:162:TRP:HD1	1.85	0.58
1:C:76:THR:CG2	1:D:98:GLU:CD	2.57	0.58
1:R:174:SER:O	1:R:175:ILE:HG22	2.04	0.58
1:B:97:SER:CB	1:B:170:GLU:OE1	2.51	0.58
1:B:171:PRO:HG3	1:B:215:GLY:HA2	1.83	0.58
1:M:13:LYS:N	1:M:65:GLN:NE2	2.51	0.58
1:D:37:VAL:CG1	1:D:252:LEU:HD21	2.33	0.58
1:L:8:ILE:HB	1:L:252:LEU:HD22	1.85	0.58
1:F:108:GLU:O	1:F:112:LYS:HG3	2.04	0.58
1:S:221:ASN:O	1:S:224:LYS:HG3	2.02	0.58
1:I:130:GLU:OE2	1:I:135:ARG:NE	2.31	0.58

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:69:LEU:HD23	1:K:70:GLU:HG2	1.86	0.58
1:G:187:GLU:O	1:G:191:VAL:HG23	2.03	0.58
1:D:218:ASN:C	1:D:218:ASN:ND2	2.57	0.58
1:K:221:ASN:H	1:K:221:ASN:ND2	2.01	0.58
1:F:18:LEU:O	1:F:22:LYS:HG3	2.04	0.58
1:E:141:MET:HA	1:E:141:MET:CE	2.34	0.58
1:E:171:PRO:O	1:E:175:ILE:HG13	2.03	0.58
1:Q:7:PHE:HE2	1:Q:210:ARG:HG3	1.67	0.58
1:A:74:ALA:HB1	1:B:98:GLU:OE2	2.04	0.58
1:K:130:GLU:OE1	1:K:169:TYR:HE1	1.85	0.58
1:Q:183:PRO:HG3	1:Q:225:LEU:HD21	1.86	0.58
1:Q:218:ASN:N	1:Q:221:ASN:OD1	2.36	0.58
1:Q:91:HIS:CD2	1:Q:123:THR:HG21	2.39	0.58
1:M:225:LEU:O	1:M:231:ILE:CD1	2.52	0.58
1:L:18:LEU:O	1:L:22:LYS:HG3	2.04	0.58
1:E:190:HIS:ND1	1:E:211:ILE:HG22	2.17	0.58
1:R:225:LEU:CB	1:R:234:PHE:CZ	2.85	0.58
1:J:11:ASN:HD22	1:J:13:LYS:HG3	1.68	0.58
1:F:13:LYS:N	1:F:65:GLN:NE2	2.52	0.58
1:C:187:GLU:OE2	1:C:229:PRO:HG2	2.04	0.58
1:S:34:PRO:HG2	1:S:253:THR:OG1	2.02	0.58
1:M:194:ARG:HD3	1:M:206:ALA:O	2.03	0.58
1:R:66:ASN:ND2	1:R:99:ARG:NE	2.51	0.57
1:M:83:MET:O	1:M:87:MET:HG3	2.04	0.57
1:O:247:THR:O	1:O:251:ILE:HD13	2.04	0.57
1:S:130:GLU:CD	1:S:140:THR:HG23	2.25	0.57
1:Q:248:MET:HA	1:Q:251:ILE:HG22	1.85	0.57
1:R:28:ILE:HG12	1:R:246:MET:HE3	1.85	0.57
1:O:100:ARG:NH1	1:O:128:VAL:HA	2.19	0.57
1:T:246:MET:HA	1:T:249:ILE:CD1	2.34	0.57
1:P:64:ALA:HB3	1:P:92:VAL:HG23	1.84	0.57
1:I:81:VAL:O	1:I:85:GLN:HG3	2.04	0.57
1:E:128:VAL:HG11	1:E:148:LEU:HD13	1.85	0.57
1:R:66:ASN:ND2	1:R:99:ARG:CD	2.67	0.57
1:R:12:PHE:O	1:R:15:ASN:OD1	2.23	0.57
1:I:57:SER:HB3	1:I:60:LEU:HB3	1.86	0.57
1:R:186:ALA:O	1:R:189:VAL:HG22	2.04	0.57
1:O:139:ARG:HD2	1:O:142:GLU:OE2	2.03	0.57
1:S:75:TRP:HD1	1:T:14:CYS:SG	2.28	0.57
1:H:95:GLY:O	1:H:100:ARG:HG3	2.04	0.57
1:K:195:LYS:CG	1:K:196:TRP:N	2.68	0.57
1:R:15:ASN:ND2	1:R:241:LEU:HD11	2.19	0.57

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:251:ILE:HA	1:L:254:LYS:HD2	1.86	0.57
1:O:195:LYS:O	1:O:199:GLU:HG3	2.04	0.57
1:A:7:PHE:O	1:A:233:GLY:HA3	2.05	0.57
1:S:46:VAL:HG23	1:S:47:HIS:CD2	2.38	0.57
1:S:186:ALA:HB2	1:S:213:TYR:CE1	2.40	0.57
1:I:4:ARG:CG	1:I:4:ARG:NH1	2.63	0.57
1:K:251:ILE:HA	1:K:254:LYS:HE3	1.85	0.57
1:J:222:ASP:OD1	1:J:222:ASP:N	2.36	0.57
1:C:135:ARG:HA	1:C:140:THR:HG22	1.87	0.57
1:P:68:TYR:CE2	1:P:70:GLU:HB2	2.39	0.57
1:I:155:LEU:HD12	1:I:162:TRP:CE2	2.39	0.57
1:A:222:ASP:HA	1:A:225:LEU:HB2	1.87	0.57
1:J:182:THR:CG2	1:J:184:GLU:OE1	2.53	0.57
1:N:130:GLU:O	1:N:130:GLU:HG2	2.04	0.57
1:B:5:ARG:NH1	1:B:35:ASP:O	2.32	0.57
1:T:137:ALA:O	1:T:138:ASN:HB3	2.04	0.57
1:I:48:LEU:HD23	1:I:89:LEU:HD11	1.86	0.57
1:Q:177:THR:HG23	1:Q:177:THR:O	2.05	0.57
1:S:6:PRO:HG2	1:S:37:VAL:CA	2.29	0.57
1:Q:61:ARG:CG	1:Q:61:ARG:HH11	2.18	0.57
1:Q:62:ILE:O	1:Q:89:LEU:HD11	2.04	0.57
1:I:4:ARG:CD	1:I:208:HIS:HA	2.34	0.57
1:R:169:TYR:CE2	1:R:189:VAL:HG21	2.40	0.57
1:K:160:MET:HA	1:K:163:LYS:HG2	1.87	0.57
1:R:69:LEU:HD23	1:R:69:LEU:N	2.18	0.57
1:R:51:ALA:HB1	1:R:62:ILE:HD13	1.86	0.57
1:G:9:GLY:O	1:G:235:LEU:HD12	2.05	0.57
1:Q:7:PHE:HE1	1:Q:38:ASP:CG	2.07	0.56
1:S:151:LEU:HD23	1:S:162:TRP:CH2	2.40	0.56
1:P:130:GLU:HG3	1:P:144:ASN:HD21	1.68	0.56
1:S:25:VAL:HA	1:S:28:ILE:HG13	1.87	0.56
1:I:76:THR:HG23	1:J:65:GLN:HB3	1.87	0.56
1:H:126:PHE:CZ	1:H:151:LEU:HD21	2.40	0.56
1:T:239:ALA:O	1:T:245:PHE:HB2	2.05	0.56
1:B:5:ARG:O	1:B:210:ARG:HD2	2.05	0.56
1:I:236:VAL:CG1	1:I:239:ALA:HB3	2.35	0.56
1:E:72:ASN:ND2	1:E:80:SER:OG	2.38	0.56
1:M:105:GLU:HG2	1:M:110:SER:OG	2.04	0.56
1:F:174:SER:OG	1:F:175:ILE:HD12	2.06	0.56
1:I:194:ARG:HD2	1:I:230:ASN:OD1	2.05	0.56
1:R:66:ASN:ND2	1:R:99:ARG:HD2	2.20	0.56
1:D:221:ASN:O	1:D:224:LYS:HG2	2.04	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:M:98:GLU:HG2	1:N:74:ALA:O	2.05	0.56
1:M:210:ARG:HG3	1:M:232:ASP:CB	2.36	0.56
1:R:116:ARG:O	1:R:119:GLU:OE1	2.22	0.56
1:P:145:ILE:O	1:P:149:GLU:HG2	2.05	0.56
1:C:57:SER:HB3	1:C:60:LEU:HB3	1.88	0.56
1:J:223:GLU:OE2	1:J:254:LYS:HE3	2.05	0.56
1:E:143:VAL:O	1:E:147:GLN:HG3	2.05	0.56
1:Q:18:LEU:O	1:Q:22:LYS:HG3	2.05	0.56
1:F:90:LYS:HD3	1:F:91:HIS:CE1	2.39	0.56
1:Q:114:ALA:O	1:Q:118:LEU:HG	2.05	0.56
1:G:217:ALA:HB1	1:G:248:MET:HE1	1.87	0.56
1:S:31:HIS:CB	1:S:246:MET:HG2	2.36	0.56
1:I:155:LEU:HD12	1:I:162:TRP:NE1	2.20	0.56
1:C:64:ALA:HB3	1:C:92:VAL:HG23	1.88	0.56
1:P:198:ALA:HA	1:P:202:ALA:O	2.06	0.56
1:E:90:LYS:HG3	1:E:90:LYS:O	2.05	0.56
1:J:180:VAL:HG22	1:J:181:ALA:N	2.19	0.56
1:O:220:SER:O	1:O:221:ASN:CB	2.52	0.56
1:S:172:VAL:HA	1:S:175:ILE:CG1	2.34	0.56
1:R:63:ALA:CB	1:R:91:HIS:HB2	2.31	0.56
1:N:131:THR:OG1	1:N:134:GLU:HG3	2.06	0.56
1:P:145:ILE:HG13	1:P:196:TRP:CD1	2.41	0.56
1:M:222:ASP:OD1	1:M:223:GLU:N	2.38	0.56
1:C:95:GLY:HA2	1:C:110:SER:OG	2.05	0.56
1:G:189:VAL:O	1:G:193:LEU:HG	2.05	0.56
1:Q:183:PRO:HG3	1:Q:225:LEU:HD23	1.87	0.56
1:R:81:VAL:HG13	1:R:122:MET:SD	2.46	0.56
1:J:114:ALA:O	1:J:118:LEU:HG	2.05	0.56
1:E:95:GLY:C	1:E:127:CYS:HB2	2.26	0.56
1:Q:248:MET:O	1:Q:251:ILE:CG2	2.54	0.56
1:O:69:LEU:H	1:O:69:LEU:HD22	1.69	0.56
1:N:139:ARG:HD2	1:N:142:GLU:OE1	2.03	0.56
1:C:215:GLY:O	1:C:216:SER:C	2.41	0.56
1:I:4:ARG:NH1	1:I:194:ARG:NH2	2.53	0.56
1:D:221:ASN:O	1:D:224:LYS:CG	2.54	0.56
1:O:108:GLU:O	1:O:112:LYS:HB2	2.06	0.56
1:J:191:VAL:HG22	1:J:230:ASN:ND2	2.21	0.56
1:O:148:LEU:HD23	1:O:193:LEU:HD22	1.88	0.56
1:N:15:ASN:N	1:N:15:ASN:ND2	2.50	0.56
1:P:135:ARG:HE	1:P:173:TRP:HZ2	1.52	0.56
1:K:213:TYR:HD2	1:K:234:PHE:HE1	1.53	0.56
1:R:216:SER:O	1:R:217:ALA:HB3	2.06	0.56

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:67:VAL:O	1:D:113:LYS:HD3	2.06	0.56
1:Q:21:ILE:O	1:Q:25:VAL:HG23	2.05	0.56
1:K:42:ALA:HB1	1:K:65:GLN:HG3	1.88	0.56
1:T:222:ASP:HA	1:T:225:LEU:HD12	1.88	0.56
1:D:24:HIS:O	1:D:28:ILE:HG13	2.06	0.56
1:C:128:VAL:HG11	1:C:148:LEU:HD13	1.86	0.56
1:L:169:TYR:CE2	1:L:189:VAL:HG21	2.41	0.55
1:C:215:GLY:O	1:C:217:ALA:N	2.39	0.55
1:A:218:ASN:ND2	1:A:221:ASN:H	2.05	0.55
1:T:242:LYS:CB	1:T:243:PRO:HD2	2.35	0.55
1:K:41:ILE:HG12	1:K:62:ILE:HD12	1.87	0.55
1:P:62:ILE:N	1:P:62:ILE:HD12	2.21	0.55
1:R:127:CYS:HB3	1:R:170:GLU:OE2	2.07	0.55
1:F:17:SER:O	1:F:21:ILE:HG12	2.06	0.55
1:T:99:ARG:HA	1:T:103:MET:HB2	1.88	0.55
1:Q:166:VAL:HG22	1:Q:210:ARG:NE	2.21	0.55
1:D:158:SER:OG	1:D:160:MET:CE	2.54	0.55
1:S:91:HIS:HA	1:S:123:THR:O	2.06	0.55
1:J:155:LEU:HD22	1:J:161:LEU:HB2	1.88	0.55
1:P:197:PHE:HD1	1:P:206:ALA:HB2	1.71	0.55
1:D:40:VAL:HG22	1:D:61:ARG:HB2	1.88	0.55
1:J:90:LYS:HG2	1:J:90:LYS:O	2.04	0.55
1:R:66:ASN:HD22	1:R:99:ARG:CZ	2.19	0.55
1:S:74:ALA:HB1	1:T:98:GLU:OE2	2.06	0.55
1:O:160:MET:HG2	1:O:161:LEU:N	2.21	0.55
1:D:37:VAL:HG11	1:D:252:LEU:CD2	2.37	0.55
1:S:253:THR:HG22	1:S:254:LYS:N	2.20	0.55
1:M:218:ASN:O	1:M:222:ASP:HB3	2.07	0.55
1:F:240:SER:HA	1:F:245:PHE:CD1	2.41	0.55
1:M:74:ALA:HB1	1:N:98:GLU:OE2	2.05	0.55
1:O:65:GLN:HB3	1:P:76:THR:CG2	2.36	0.55
1:J:81:VAL:HG13	1:J:122:MET:SD	2.46	0.55
1:J:187:GLU:OE1	1:J:228:CYS:HB3	2.05	0.55
1:G:225:LEU:O	1:G:228:CYS:HB2	2.05	0.55
1:S:145:ILE:HG23	1:S:196:TRP:CD1	2.42	0.55
1:G:77:GLY:HA3	1:H:99:ARG:HH11	1.70	0.55
1:C:4:ARG:CG	1:C:207:GLN:O	2.53	0.55
1:P:184:GLU:H	1:P:184:GLU:CD	2.10	0.55
1:R:251:ILE:N	1:R:251:ILE:CD1	2.69	0.55
1:A:218:ASN:HD22	1:A:220:SER:N	2.05	0.55
1:L:251:ILE:HD13	1:L:254:LYS:HD2	1.89	0.55
1:E:175:ILE:HG12	1:I:176:GLY:O	2.07	0.55

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:174:SER:O	1:F:179:VAL:HB	2.06	0.55
1:G:236:VAL:HG21	1:G:248:MET:SD	2.46	0.55
1:A:218:ASN:ND2	1:A:220:SER:H	2.05	0.55
1:K:213:TYR:CE2	1:K:215:GLY:HA2	2.41	0.55
1:I:215:GLY:O	1:I:216:SER:C	2.45	0.55
1:P:247:THR:O	1:P:251:ILE:HD13	2.07	0.55
1:S:204:GLU:OE1	1:S:208:HIS:HE1	1.89	0.55
1:L:244:GLU:O	1:L:245:PHE:C	2.43	0.55
1:Q:234:PHE:CD2	1:Q:248:MET:HE2	2.40	0.55
1:Q:248:MET:C	1:Q:251:ILE:HG22	2.27	0.55
1:T:81:VAL:O	1:T:85:GLN:HG3	2.05	0.55
1:S:197:PHE:CD1	1:S:206:ALA:HA	2.42	0.55
1:N:226:GLY:C	1:N:255:THR:CG2	2.66	0.55
1:M:141:MET:O	1:M:145:ILE:HB	2.07	0.55
1:G:229:PRO:HB2	1:G:230:ASN:HD22	1.71	0.55
1:F:9:GLY:HA2	1:F:40:VAL:O	2.07	0.55
1:S:55:ASN:OD1	1:S:60:LEU:HD23	2.07	0.55
1:C:98:GLU:OE1	1:D:76:THR:N	2.34	0.55
1:I:37:VAL:HG11	1:I:252:LEU:HD23	1.88	0.55
1:C:2:PRO:HD2	1:C:207:GLN:HG2	1.87	0.55
1:I:132:LEU:O	1:I:136:LYS:HG3	2.06	0.55
1:R:141:MET:HE1	1:R:193:LEU:HD23	1.89	0.55
1:E:198:ALA:HB2	1:E:206:ALA:CB	2.37	0.55
1:R:228:CYS:HB2	1:R:231:ILE:HB	1.89	0.55
1:H:158:SER:HB2	1:H:161:LEU:HG	1.88	0.55
1:C:244:GLU:O	1:C:247:THR:HB	2.07	0.55
1:P:114:ALA:O	1:P:118:LEU:HG	2.07	0.55
1:C:173:TRP:O	1:C:177:THR:HG21	2.07	0.55
1:R:85:GLN:HE22	1:R:120:LYS:HB3	1.71	0.55
1:I:236:VAL:HG11	1:I:239:ALA:HB3	1.89	0.54
1:T:24:HIS:O	1:T:27:ALA:HB3	2.07	0.54
1:Q:236:VAL:HG12	1:Q:240:SER:HB3	1.89	0.54
1:C:33:ILE:HB	1:C:59:GLN:HE21	1.72	0.54
1:O:58:LYS:CG	1:O:59:GLN:OE1	2.55	0.54
1:C:215:GLY:C	1:C:217:ALA:N	2.56	0.54
1:H:197:PHE:CZ	1:H:201:VAL:HG11	2.42	0.54
1:M:5:ARG:HH12	1:M:36:SER:C	2.11	0.54
1:L:37:VAL:CG1	1:L:252:LEU:HD23	2.38	0.54
1:B:95:GLY:C	1:B:127:CYS:HB2	2.28	0.54
1:Q:27:ALA:O	1:Q:30:ALA:HB3	2.07	0.54
1:P:31:HIS:CE1	1:P:246:MET:HB3	2.42	0.54
1:I:67:VAL:O	1:I:113:LYS:HD3	2.07	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:R:15:ASN:ND2	1:R:241:LEU:CD1	2.70	0.54
1:A:137:ALA:HB3	1:A:139:ARG:HG3	1.90	0.54
1:Q:139:ARG:O	1:Q:143:VAL:HG23	2.07	0.54
1:S:72:ASN:ND2	1:S:80:SER:OG	2.40	0.54
1:E:187:GLU:O	1:E:191:VAL:HG23	2.06	0.54
1:O:98:GLU:O	1:O:102:ILE:HB	2.07	0.54
1:L:244:GLU:O	1:L:247:THR:N	2.40	0.54
1:A:99:ARG:HD2	1:B:76:THR:O	2.08	0.54
1:E:4:ARG:NH2	1:E:229:PRO:O	2.41	0.54
1:D:159:LYS:C	1:D:161:LEU:N	2.61	0.54
1:A:4:ARG:HH22	1:A:230:ASN:HA	1.73	0.54
1:F:40:VAL:HG22	1:F:61:ARG:HB2	1.90	0.54
1:G:137:ALA:HB3	1:G:139:ARG:HG3	1.90	0.54
1:S:5:ARG:HG2	1:S:6:PRO:HD2	1.88	0.54
1:Q:79:THR:CG2	1:Q:84:LEU:HD21	2.36	0.54
1:I:12:PHE:O	1:I:13:LYS:HB2	2.07	0.54
1:B:217:ALA:HB1	1:B:222:ASP:CG	2.28	0.54
1:S:197:PHE:HE2	1:S:209:ILE:HD13	1.72	0.54
1:N:141:MET:O	1:N:145:ILE:CG1	2.56	0.54
1:L:90:LYS:HE3	1:L:91:HIS:HE1	1.73	0.54
1:S:115:LYS:HD2	1:S:154:GLU:O	2.08	0.54
1:T:64:ALA:CB	1:T:84:LEU:HD11	2.38	0.54
1:L:200:LYS:C	1:L:200:LYS:HD2	2.11	0.54
1:Q:83:MET:O	1:Q:87:MET:HG2	2.07	0.54
1:E:169:TYR:CZ	1:E:189:VAL:HG11	2.42	0.54
1:C:47:HIS:CE1	1:D:83:MET:HG2	2.42	0.54
1:A:131:THR:HG22	1:A:132:LEU:N	2.22	0.54
1:D:102:ILE:HD11	1:N:179:VAL:HA	1.88	0.54
1:P:24:HIS:O	1:P:28:ILE:HG13	2.07	0.54
1:Q:7:PHE:CD1	1:Q:38:ASP:CB	2.87	0.54
1:N:226:GLY:HA3	1:N:255:THR:HG21	1.87	0.54
1:D:218:ASN:HD21	1:D:220:SER:H	1.53	0.54
1:Q:175:ILE:O	1:Q:177:THR:HB	2.06	0.54
1:G:93:ILE:HD11	1:G:96:HIS:HB2	1.89	0.54
1:P:162:TRP:HA	1:P:165:VAL:CG2	2.38	0.54
1:O:132:LEU:HD22	1:O:177:THR:HB	1.90	0.54
1:T:44:SER:O	1:T:48:LEU:HD13	2.08	0.54
1:H:144:ASN:HB3	1:H:193:LEU:HD21	1.90	0.54
1:A:108:GLU:OE2	1:A:112:LYS:NZ	2.40	0.54
1:Q:73:GLY:N	1:R:14:CYS:SG	2.81	0.54
1:P:180:VAL:HG22	1:P:181:ALA:N	2.22	0.54
1:P:21:ILE:O	1:P:25:VAL:HG23	2.08	0.54

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:6:PRO:HB2	1:O:37:VAL:HG13	1.90	0.54
1:Q:218:ASN:O	1:Q:221:ASN:OD1	2.26	0.54
1:Q:234:PHE:CD2	1:Q:248:MET:HE3	2.41	0.54
1:N:223:GLU:OE1	1:N:251:ILE:HD11	2.08	0.54
1:A:162:TRP:CE3	1:A:197:PHE:HE2	2.26	0.54
1:M:5:ARG:NH2	1:M:35:ASP:O	2.40	0.54
1:M:170:GLU:CB	1:M:175:ILE:HD11	2.38	0.54
1:O:103:MET:CE	1:P:78:GLU:HG3	2.38	0.54
1:P:162:TRP:HA	1:P:165:VAL:HG23	1.90	0.54
1:M:18:LEU:HD23	1:M:47:HIS:HD2	1.72	0.54
1:C:253:THR:HG22	1:C:254:LYS:N	2.23	0.54
1:G:145:ILE:O	1:G:149:GLU:HG2	2.08	0.54
1:F:219:GLY:HA2	1:F:222:ASP:OD2	2.08	0.54
1:S:5:ARG:CG	1:S:6:PRO:HD2	2.37	0.53
1:D:218:ASN:O	1:D:222:ASP:HB3	2.07	0.53
1:A:111:ALA:HB1	1:A:151:LEU:HA	1.89	0.53
1:S:243:PRO:O	1:S:246:MET:HE3	2.07	0.53
1:D:6:PRO:HB3	1:D:252:LEU:HD11	1.90	0.53
1:G:123:THR:HA	1:G:164:GLU:HB3	1.89	0.53
1:Q:55:ASN:HD22	1:Q:62:ILE:HD13	1.73	0.53
1:A:4:ARG:HD2	1:A:207:GLN:O	2.08	0.53
1:L:233:GLY:HA2	1:L:252:LEU:HD11	1.91	0.53
1:T:48:LEU:O	1:T:52:ILE:HD12	2.09	0.53
1:H:98:GLU:O	1:H:102:ILE:HB	2.08	0.53
1:S:6:PRO:CG	1:S:37:VAL:HG12	2.38	0.53
1:Q:63:ALA:HB2	1:Q:91:HIS:HB2	1.90	0.53
1:T:245:PHE:HA	1:T:248:MET:HG3	1.91	0.53
1:O:66:ASN:ND2	1:O:67:VAL:H	2.07	0.53
1:K:115:LYS:HG3	1:K:155:LEU:HD23	1.90	0.53
1:E:83:MET:HE1	1:F:14:CYS:HA	1.90	0.53
1:H:24:HIS:O	1:H:28:ILE:HG13	2.09	0.53
1:G:213:TYR:CB	1:G:234:PHE:CE1	2.88	0.53
1:S:224:LYS:HG3	1:S:225:LEU:H	1.73	0.53
1:F:145:ILE:HG23	1:F:196:TRP:CD1	2.44	0.53
1:O:46:VAL:HB	1:P:87:MET:SD	2.48	0.53
1:A:72:ASN:N	1:A:72:ASN:HD22	2.06	0.53
1:J:203:ALA:HB3	1:M:200:LYS:HE3	1.91	0.53
1:R:83:MET:O	1:R:86:ASP:HB3	2.07	0.53
1:E:171:PRO:HG3	1:E:213:TYR:CE1	2.44	0.53
1:S:38:ASP:OD2	1:S:210:ARG:NH2	2.40	0.53
1:S:151:LEU:HD23	1:S:162:TRP:CZ3	2.43	0.53
1:L:69:LEU:CD2	1:L:70:GLU:HG2	2.35	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:144:ASN:HD22	1:B:193:LEU:CD2	2.21	0.53
1:S:83:MET:HG2	1:T:46:VAL:HG21	1.91	0.53
1:Q:31:HIS:O	1:Q:33:ILE:HG13	2.09	0.53
1:Q:92:VAL:CG1	1:Q:124:VAL:HG22	2.38	0.53
1:T:82:GLU:CD	1:T:116:ARG:HH12	2.12	0.53
1:N:84:LEU:O	1:N:89:LEU:HB2	2.09	0.53
1:H:85:GLN:HE22	1:H:120:LYS:HB3	1.74	0.53
1:E:187:GLU:OE1	1:E:228:CYS:HB3	2.09	0.53
1:S:158:SER:HB2	1:S:161:LEU:CD2	2.29	0.53
1:O:182:THR:H	1:O:185:GLN:NE2	2.05	0.53
1:F:67:VAL:O	1:F:113:LYS:HD3	2.09	0.53
1:E:96:HIS:HB3	1:F:76:THR:HG21	1.89	0.53
1:J:251:ILE:HD12	1:J:254:LYS:NZ	2.23	0.53
1:C:4:ARG:HG2	1:C:207:GLN:O	2.07	0.53
1:L:24:HIS:O	1:L:28:ILE:HG13	2.09	0.53
1:J:84:LEU:HD22	1:J:89:LEU:HD12	1.90	0.53
1:J:217:ALA:O	1:J:248:MET:CE	2.57	0.53
1:O:197:PHE:HE2	1:O:205:GLY:C	2.12	0.53
1:G:96:HIS:CE1	1:G:98:GLU:HG3	2.44	0.53
1:Q:81:VAL:HG23	1:Q:116:ARG:HH11	1.74	0.53
1:F:95:GLY:O	1:F:127:CYS:HB2	2.09	0.53
1:K:116:ARG:O	1:K:119:GLU:HB2	2.08	0.53
1:M:41:ILE:HG12	1:M:60:LEU:HD11	1.91	0.53
1:P:37:VAL:HG21	1:P:253:THR:OG1	2.09	0.53
1:E:194:ARG:NH1	1:E:211:ILE:HD12	2.24	0.53
1:I:148:LEU:HG	1:I:196:TRP:CZ3	2.43	0.53
1:L:155:LEU:HD22	1:L:161:LEU:HB2	1.91	0.53
1:O:66:ASN:ND2	1:O:67:VAL:N	2.56	0.53
1:C:4:ARG:HD3	1:C:207:GLN:O	2.09	0.53
1:M:18:LEU:O	1:M:22:LYS:HG3	2.07	0.53
1:P:8:ILE:HB	1:P:252:LEU:HD22	1.91	0.53
1:Q:12:PHE:HB2	1:Q:42:ALA:O	2.09	0.53
1:S:2:PRO:HD2	1:S:207:GLN:HB2	1.91	0.53
1:Q:242:LYS:O	1:Q:245:PHE:HB3	2.09	0.53
1:O:139:ARG:CB	1:O:142:GLU:HB3	2.39	0.53
1:L:34:PRO:HG3	1:L:253:THR:OG1	2.08	0.53
1:Q:221:ASN:O	1:Q:225:LEU:HG	2.09	0.53
1:L:174:SER:O	1:L:215:GLY:HA3	2.09	0.53
1:N:255:THR:HG22	1:N:255:THR:O	2.09	0.53
1:E:130:GLU:OE2	1:E:140:THR:HB	2.09	0.53
1:H:187:GLU:OE1	1:H:228:CYS:HB3	2.08	0.53
1:J:69:LEU:HB3	1:J:113:LYS:HG2	1.91	0.53

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:160:MET:H	1:A:160:MET:CE	2.22	0.53
1:S:243:PRO:HA	1:S:246:MET:HE1	1.91	0.53
1:K:69:LEU:CD2	1:K:70:GLU:HG2	2.39	0.53
1:S:99:ARG:NH2	1:T:78:GLU:OE2	2.42	0.53
1:S:139:ARG:O	1:S:143:VAL:HG23	2.09	0.53
1:G:5:ARG:HG3	1:G:36:SER:O	2.09	0.53
1:F:236:VAL:CG1	1:F:239:ALA:HB3	2.39	0.53
1:P:131:THR:HG22	1:P:172:VAL:HG11	1.91	0.52
1:A:109:GLN:O	1:A:113:LYS:HG3	2.08	0.52
1:K:187:GLU:O	1:K:191:VAL:HG23	2.09	0.52
1:L:155:LEU:HD12	1:L:162:TRP:NE1	2.23	0.52
1:T:127:CYS:HA	1:T:168:ALA:O	2.09	0.52
1:O:21:ILE:O	1:O:25:VAL:HG23	2.08	0.52
1:Q:99:ARG:HD3	1:R:76:THR:O	2.09	0.52
1:R:242:LYS:HB3	1:R:243:PRO:HD2	1.91	0.52
1:T:115:LYS:HG2	1:T:155:LEU:HG	1.90	0.52
1:L:221:ASN:HD22	1:L:221:ASN:C	2.11	0.52
1:D:176:GLY:HA3	1:N:174:SER:O	2.09	0.52
1:S:241:LEU:HD23	1:S:241:LEU:N	2.24	0.52
1:A:115:LYS:CE	1:A:119:GLU:OE2	2.57	0.52
1:C:76:THR:CG2	1:D:13:LYS:HD3	2.36	0.52
1:T:217:ALA:HB1	1:T:248:MET:HE1	1.91	0.52
1:B:213:TYR:HB2	1:B:231:ILE:HD13	1.91	0.52
1:T:37:VAL:HG11	1:T:252:LEU:HD23	1.91	0.52
1:S:17:SER:O	1:S:21:ILE:HG12	2.09	0.52
1:E:206:ALA:O	1:E:209:ILE:HG22	2.09	0.52
1:O:217:ALA:HB1	1:O:222:ASP:OD1	2.09	0.52
1:I:13:LYS:HA	1:J:76:THR:HG22	1.90	0.52
1:E:178:GLY:HA3	1:I:172:VAL:CG1	2.39	0.52
1:E:69:LEU:HD23	1:E:70:GLU:HG2	1.91	0.52
1:D:180:VAL:HG13	1:D:181:ALA:N	2.24	0.52
1:Q:183:PRO:HA	1:Q:225:LEU:HD22	1.91	0.52
1:S:6:PRO:CG	1:S:37:VAL:HA	2.31	0.52
1:S:185:GLN:HA	1:S:188:GLU:OE1	2.10	0.52
1:R:11:ASN:OD1	1:R:13:LYS:N	2.42	0.52
1:J:56:THR:HG22	1:K:19:ASP:OD1	2.10	0.52
1:E:236:VAL:CG1	1:E:239:ALA:HB3	2.39	0.52
1:P:171:PRO:HB2	1:P:174:SER:OG	2.09	0.52
1:A:131:THR:HG22	1:A:132:LEU:H	1.74	0.52
1:R:81:VAL:HG21	1:R:116:ARG:HG2	1.92	0.52
1:A:90:LYS:HE2	1:A:123:THR:OG1	2.09	0.52
1:A:115:LYS:HE3	1:A:119:GLU:OE2	2.10	0.52

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:244:GLU:O	1:F:248:MET:HG3	2.09	0.52
1:S:55:ASN:HB2	1:S:62:ILE:HD11	1.89	0.52
1:S:182:THR:OG1	1:S:185:GLN:HB2	2.10	0.52
1:T:213:TYR:CD2	1:T:225:LEU:HD13	2.45	0.52
1:F:236:VAL:HG11	1:F:239:ALA:HB3	1.91	0.52
1:J:7:PHE:O	1:J:233:GLY:HA3	2.10	0.52
1:A:68:TYR:HD1	1:A:78:GLU:OE1	1.93	0.52
1:E:217:ALA:CB	1:I:178:GLY:HA3	2.38	0.52
1:S:118:LEU:HD13	1:S:161:LEU:CD1	2.39	0.52
1:G:69:LEU:CD1	1:G:69:LEU:C	2.77	0.52
1:I:37:VAL:HG11	1:I:252:LEU:CD2	2.40	0.52
1:R:230:ASN:N	1:R:230:ASN:ND2	2.58	0.52
1:B:4:ARG:HD3	1:B:207:GLN:O	2.10	0.52
1:P:194:ARG:HE	1:P:230:ASN:HD22	1.58	0.52
1:L:12:PHE:HB2	1:L:42:ALA:O	2.08	0.52
1:C:84:LEU:HD22	1:C:89:LEU:HD12	1.90	0.52
1:E:222:ASP:HB2	1:E:251:ILE:HG21	1.91	0.52
1:F:179:VAL:HG12	1:F:180:VAL:N	2.24	0.52
1:Q:7:PHE:HD1	1:Q:38:ASP:CB	2.13	0.52
1:G:69:LEU:HD12	1:G:70:GLU:N	2.24	0.52
1:C:68:TYR:HB2	1:C:78:GLU:HB3	1.92	0.52
1:I:13:LYS:HG2	1:J:74:ALA:HA	1.93	0.52
1:I:69:LEU:HB3	1:I:113:LYS:HG2	1.91	0.52
1:T:243:PRO:HA	1:T:246:MET:HE2	1.92	0.52
1:S:171:PRO:HA	1:S:173:TRP:NE1	2.23	0.52
1:J:11:ASN:HD21	1:J:13:LYS:HG3	1.72	0.51
1:O:61:ARG:NE	1:O:62:ILE:H	2.03	0.51
1:F:155:LEU:HD12	1:F:162:TRP:CE2	2.45	0.51
1:A:13:LYS:N	1:A:65:GLN:NE2	2.58	0.51
1:M:41:ILE:O	1:M:43:PRO:HD3	2.09	0.51
1:G:244:GLU:O	1:G:247:THR:HB	2.10	0.51
1:R:175:ILE:O	1:R:177:THR:HG23	2.10	0.51
1:I:4:ARG:HB2	1:I:4:ARG:NH1	2.24	0.51
1:T:13:LYS:H	1:T:65:GLN:NE2	2.08	0.51
1:F:69:LEU:HB3	1:F:113:LYS:HG2	1.91	0.51
1:J:21:ILE:HG13	1:J:47:HIS:HB3	1.92	0.51
1:N:141:MET:O	1:N:145:ILE:HG13	2.10	0.51
1:H:130:GLU:OE2	1:H:140:THR:HG23	2.10	0.51
1:B:139:ARG:HD2	1:B:142:GLU:OE1	2.10	0.51
1:C:134:GLU:O	1:C:139:ARG:HG3	2.09	0.51
1:G:83:MET:O	1:G:87:MET:HG3	2.10	0.51
1:R:175:ILE:CG2	1:R:177:THR:OG1	2.57	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:61:ARG:HH22	1:S:90:LYS:HB2	1.75	0.51
1:A:139:ARG:NH1	1:A:142:GLU:CD	2.63	0.51
1:E:46:VAL:HB	1:F:87:MET:SD	2.51	0.51
1:A:6:PRO:HB2	1:A:37:VAL:HG22	1.92	0.51
1:G:41:ILE:HG23	1:G:60:LEU:HD11	1.91	0.51
1:R:128:VAL:HG11	1:R:148:LEU:HD13	1.92	0.51
1:S:210:ARG:NH1	1:S:210:ARG:CG	2.55	0.51
1:I:194:ARG:HH12	1:I:211:ILE:HG13	1.74	0.51
1:I:4:ARG:CB	1:I:4:ARG:HH11	2.22	0.51
1:R:15:ASN:HD21	1:R:241:LEU:CD1	2.21	0.51
1:G:71:GLY:O	1:G:75:TRP:NE1	2.44	0.51
1:N:141:MET:HE3	1:N:145:ILE:HD11	1.93	0.51
1:C:134:GLU:HG2	1:C:143:VAL:HG21	1.92	0.51
1:A:246:MET:HA	1:A:249:ILE:HD12	1.92	0.51
1:O:58:LYS:CG	1:O:59:GLN:CD	2.66	0.51
1:F:181:ALA:HB3	1:F:213:TYR:OH	2.11	0.51
1:M:228:CYS:CB	1:M:231:ILE:HD12	2.38	0.51
1:R:194:ARG:NH1	1:R:209:ILE:HG23	2.23	0.51
1:S:160:MET:O	1:S:163:LYS:HB3	2.10	0.51
1:M:37:VAL:HG12	1:M:38:ASP:N	2.25	0.51
1:N:199:GLU:O	1:N:200:LYS:HD2	2.11	0.51
1:M:174:SER:HA	1:M:179:VAL:O	2.10	0.51
1:C:24:HIS:NE2	1:C:240:SER:O	2.42	0.51
1:A:239:ALA:HA	1:A:242:LYS:HG2	1.91	0.51
1:A:77:GLY:H	1:B:65:GLN:HE21	1.59	0.51
1:F:134:GLU:OE1	1:F:143:VAL:HG11	2.10	0.51
1:G:213:TYR:CB	1:G:234:PHE:CD1	2.80	0.51
1:T:106:THR:OG1	1:T:109:GLN:HG3	2.11	0.51
1:J:221:ASN:OD1	1:J:222:ASP:N	2.43	0.51
1:S:202:ALA:O	1:S:206:ALA:HB2	2.11	0.51
1:H:145:ILE:HG23	1:H:196:TRP:CD1	2.45	0.51
1:O:139:ARG:HD2	1:O:142:GLU:CD	2.31	0.51
1:B:37:VAL:CG1	1:B:252:LEU:HD23	2.41	0.51
1:P:81:VAL:O	1:P:85:GLN:HG3	2.11	0.51
1:S:112:LYS:O	1:S:116:ARG:HB2	2.11	0.51
1:R:68:TYR:CG	1:R:78:GLU:HG3	2.46	0.51
1:C:24:HIS:O	1:C:28:ILE:HG13	2.10	0.51
1:S:108:GLU:O	1:S:112:LYS:HG3	2.10	0.51
1:B:187:GLU:O	1:B:191:VAL:HG23	2.11	0.51
1:Q:7:PHE:HE2	1:Q:210:ARG:HH11	1.59	0.51
1:P:135:ARG:NE	1:P:173:TRP:CZ2	2.78	0.51
1:A:159:LYS:O	1:A:162:TRP:HB2	2.11	0.51

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:T:158:SER:HB3	1:T:161:LEU:HG	1.93	0.51
1:S:5:ARG:HH22	1:S:35:ASP:C	2.14	0.51
1:E:4:ARG:CD	1:E:207:GLN:O	2.54	0.51
1:K:209:ILE:HD12	1:K:210:ARG:H	1.75	0.51
1:B:171:PRO:HB2	1:B:174:SER:OG	2.10	0.51
1:J:67:VAL:O	1:J:113:LYS:HD3	2.10	0.51
1:A:155:LEU:HD12	1:A:162:TRP:NE1	2.26	0.51
1:K:187:GLU:HB2	1:K:228:CYS:SG	2.51	0.51
1:L:135:ARG:O	1:L:138:ASN:HA	2.11	0.51
1:D:139:ARG:O	1:D:143:VAL:HG23	2.10	0.51
1:Q:197:PHE:HD2	1:Q:206:ALA:CA	2.22	0.51
1:O:76:THR:CG2	1:P:65:GLN:HB3	2.39	0.51
1:Q:175:ILE:O	1:Q:176:GLY:C	2.49	0.51
1:S:31:HIS:HB2	1:S:246:MET:HG2	1.93	0.51
1:C:58:LYS:HB2	1:C:59:GLN:OE1	2.11	0.51
1:M:213:TYR:CE2	1:M:214:GLY:O	2.64	0.51
1:O:184:GLU:CD	1:O:184:GLU:H	2.14	0.51
1:E:190:HIS:CE1	1:E:211:ILE:HG22	2.46	0.50
1:Q:89:LEU:HD12	1:Q:91:HIS:H	1.74	0.50
1:A:172:VAL:CA	1:A:175:ILE:HG13	2.41	0.50
1:R:187:GLU:OE2	1:R:230:ASN:N	2.44	0.50
1:F:128:VAL:HG11	1:F:148:LEU:HD13	1.92	0.50
1:T:187:GLU:OE2	1:T:229:PRO:HG2	2.10	0.50
1:G:150:ALA:O	1:G:154:GLU:HG2	2.11	0.50
1:G:37:VAL:HG12	1:G:38:ASP:N	2.26	0.50
1:L:218:ASN:HB2	1:L:221:ASN:CG	2.31	0.50
1:A:172:VAL:CG1	1:A:175:ILE:HD12	2.37	0.50
1:Q:230:ASN:N	1:Q:230:ASN:ND2	2.58	0.50
1:D:69:LEU:O	1:D:116:ARG:HD2	2.10	0.50
1:B:244:GLU:O	1:B:247:THR:HB	2.11	0.50
1:L:141:MET:CE	1:L:141:MET:HA	2.41	0.50
1:L:137:ALA:O	1:L:138:ASN:CB	2.59	0.50
1:B:2:PRO:HB3	1:B:207:GLN:HG2	1.93	0.50
1:T:108:GLU:OE2	1:T:112:LYS:HE3	2.10	0.50
1:G:82:GLU:OE1	1:G:82:GLU:N	2.44	0.50
1:I:13:LYS:HG3	1:J:76:THR:HG23	1.92	0.50
1:N:222:ASP:O	1:N:223:GLU:C	2.48	0.50
1:T:7:PHE:C	1:T:7:PHE:CD1	2.85	0.50
1:S:173:TRP:HD1	1:S:173:TRP:H	1.49	0.50
1:O:139:ARG:NH1	1:O:142:GLU:OE2	2.44	0.50
1:E:176:GLY:HA3	1:I:132:LEU:HB2	1.93	0.50
1:E:6:PRO:HB2	1:E:37:VAL:HG13	1.92	0.50

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:N:70:GLU:OE1	1:N:70:GLU:HA	2.12	0.50
1:E:190:HIS:HE2	1:E:213:TYR:CB	2.14	0.50
1:R:24:HIS:O	1:R:27:ALA:HB3	2.11	0.50
1:N:196:TRP:O	1:N:200:LYS:HB2	2.11	0.50
1:E:141:MET:HE2	1:E:145:ILE:HD12	1.94	0.50
1:L:180:VAL:HG22	1:L:181:ALA:N	2.26	0.50
1:L:206:ALA:O	1:L:209:ILE:HG22	2.12	0.50
1:E:254:LYS:C	1:E:255:THR:HG1	2.11	0.50
1:O:224:LYS:O	1:O:227:GLN:HB2	2.11	0.50
1:A:138:ASN:HD22	1:A:138:ASN:C	2.11	0.50
1:Q:243:PRO:HA	1:Q:246:MET:HE2	1.94	0.50
1:D:37:VAL:HG13	1:D:252:LEU:HD21	1.94	0.50
1:J:251:ILE:HD12	1:J:254:LYS:HZ1	1.76	0.50
1:I:4:ARG:NE	1:I:207:GLN:O	2.43	0.50
1:R:91:HIS:CD2	1:R:123:THR:CG2	2.94	0.50
1:K:223:GLU:CG	1:K:254:LYS:HZ1	2.18	0.50
1:T:7:PHE:CD1	1:T:8:ILE:N	2.80	0.50
1:I:141:MET:CE	1:I:192:GLY:HA3	2.42	0.50
1:R:227:GLN:CA	1:R:227:GLN:HE21	2.21	0.50
1:Q:39:VAL:HG12	1:Q:60:LEU:CD1	2.41	0.50
1:K:152:GLY:HA2	1:K:162:TRP:HZ2	1.77	0.50
1:T:64:ALA:HB2	1:T:84:LEU:HD11	1.94	0.50
1:M:18:LEU:HD23	1:M:47:HIS:CD2	2.47	0.50
1:K:174:SER:HA	1:K:179:VAL:O	2.11	0.50
1:I:51:ALA:HB1	1:I:62:ILE:HD12	1.94	0.50
1:P:137:ALA:O	1:P:138:ASN:HB3	2.11	0.50
1:E:194:ARG:CZ	1:E:211:ILE:HD12	2.42	0.50
1:F:21:ILE:HG13	1:F:47:HIS:HB3	1.93	0.50
1:T:84:LEU:HB3	1:T:122:MET:HE1	1.93	0.50
1:H:147:GLN:O	1:H:151:LEU:HD13	2.12	0.50
1:K:218:ASN:H	1:K:221:ASN:HD21	1.59	0.50
1:D:158:SER:HA	1:D:160:MET:HE1	1.94	0.50
1:M:9:GLY:HA2	1:M:40:VAL:O	2.12	0.50
1:M:17:SER:O	1:M:21:ILE:HG12	2.12	0.50
1:Q:166:VAL:HG23	1:Q:210:ARG:NH2	2.27	0.49
1:K:42:ALA:O	1:K:65:GLN:NE2	2.44	0.49
1:E:134:GLU:HB3	1:E:143:VAL:HG21	1.94	0.49
1:E:198:ALA:HB2	1:E:206:ALA:HB2	1.93	0.49
1:F:99:ARG:HA	1:F:103:MET:HB2	1.93	0.49
1:O:58:LYS:CD	1:O:59:GLN:OE1	2.60	0.49
1:H:100:ARG:NH2	1:H:126:PHE:CE2	2.80	0.49
1:K:209:ILE:HD12	1:K:210:ARG:N	2.27	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:L:251:ILE:HA	1:L:254:LYS:CD	2.42	0.49
1:J:250:ASP:O	1:J:254:LYS:HG2	2.12	0.49
1:I:40:VAL:HG22	1:I:61:ARG:HB2	1.94	0.49
1:P:106:THR:OG1	1:P:109:GLN:HG3	2.12	0.49
1:H:156:GLY:O	1:H:159:LYS:HG2	2.12	0.49
1:C:46:VAL:HB	1:D:87:MET:SD	2.53	0.49
1:K:213:TYR:O	1:K:215:GLY:N	2.36	0.49
1:P:42:ALA:HB1	1:P:65:GLN:HG2	1.93	0.49
1:M:5:ARG:O	1:M:210:ARG:NH1	2.45	0.49
1:N:190:HIS:ND1	1:N:211:ILE:HG22	2.28	0.49
1:O:67:VAL:HG22	1:O:68:TYR:H	1.77	0.49
1:Q:33:ILE:HB	1:Q:59:GLN:HE21	1.76	0.49
1:D:197:PHE:HD1	1:D:206:ALA:HB2	1.78	0.49
1:H:167:ILE:HB	1:H:211:ILE:HG23	1.94	0.49
1:K:40:VAL:CG1	1:K:63:ALA:HB2	2.42	0.49
1:I:149:GLU:O	1:I:153:LYS:N	2.42	0.49
1:L:169:TYR:CZ	1:L:189:VAL:HG21	2.47	0.49
1:H:126:PHE:CD2	1:H:151:LEU:HD21	2.47	0.49
1:Q:248:MET:CA	1:Q:251:ILE:HG22	2.41	0.49
1:N:218:ASN:HD22	1:N:221:ASN:HD22	1.61	0.49
1:P:141:MET:O	1:P:145:ILE:HB	2.12	0.49
1:S:75:TRP:HD1	1:T:14:CYS:CB	2.25	0.49
1:A:251:ILE:O	1:A:255:THR:HB	2.12	0.49
1:Q:68:TYR:HB2	1:Q:78:GLU:HB3	1.94	0.49
1:K:83:MET:CE	1:L:44:SER:OG	2.61	0.49
1:K:150:ALA:O	1:K:154:GLU:HG2	2.12	0.49
1:P:172:VAL:HG12	1:P:173:TRP:N	2.27	0.49
1:R:24:HIS:O	1:R:28:ILE:HG13	2.12	0.49
1:N:139:ARG:NH1	1:N:143:VAL:CG2	2.76	0.49
1:P:155:LEU:HD22	1:P:161:LEU:HB2	1.94	0.49
1:S:195:LYS:HD3	1:S:199:GLU:OE2	2.13	0.49
1:T:118:LEU:HD13	1:T:155:LEU:HD11	1.94	0.49
1:S:6:PRO:CG	1:S:36:SER:O	2.60	0.49
1:O:218:ASN:HB3	1:O:220:SER:O	2.12	0.49
1:S:7:PHE:CE1	1:S:40:VAL:CG2	2.95	0.49
1:R:246:MET:HA	1:R:249:ILE:CD1	2.35	0.49
1:J:109:GLN:O	1:J:113:LYS:HG3	2.13	0.49
1:R:36:SER:OG	1:R:37:VAL:HG23	2.12	0.49
1:J:180:VAL:CG2	1:J:181:ALA:N	2.75	0.49
1:H:64:ALA:HB3	1:H:92:VAL:HG23	1.93	0.49
1:L:99:ARG:HA	1:L:103:MET:SD	2.53	0.49
1:L:149:GLU:HA	1:L:149:GLU:OE1	2.12	0.49

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:66:ASN:HD22	1:B:67:VAL:H	0.58	0.49
1:F:171:PRO:HG2	1:F:213:TYR:OH	2.11	0.49
1:J:132:LEU:HD22	1:J:177:THR:CG2	2.41	0.49
1:B:128:VAL:HG11	1:B:148:LEU:HD13	1.95	0.49
1:N:98:GLU:O	1:N:102:ILE:HB	2.12	0.49
1:Q:236:VAL:CG1	1:Q:240:SER:N	2.76	0.49
1:P:180:VAL:HG22	1:P:181:ALA:H	1.78	0.49
1:S:2:PRO:HD2	1:S:207:GLN:CB	2.42	0.49
1:O:221:ASN:O	1:O:221:ASN:OD1	2.31	0.49
1:D:218:ASN:ND2	1:D:220:SER:N	2.56	0.49
1:D:222:ASP:HA	1:D:225:LEU:HD12	1.94	0.49
1:I:141:MET:HE1	1:I:192:GLY:HA3	1.94	0.49
1:T:182:THR:OG1	1:T:185:GLN:HG3	2.12	0.49
1:T:227:GLN:NE2	1:T:255:THR:HG22	2.28	0.49
1:S:221:ASN:CA	1:S:224:LYS:HE2	2.43	0.49
1:A:132:LEU:HG	1:A:136:LYS:HE3	1.95	0.49
1:Q:31:HIS:HE2	1:Q:250:ASP:CG	2.16	0.49
1:P:55:ASN:HD22	1:P:62:ILE:CD1	2.25	0.49
1:Q:186:ALA:HB2	1:Q:213:TYR:CE1	2.48	0.49
1:B:167:ILE:O	1:B:211:ILE:HA	2.13	0.49
1:M:79:THR:HG21	1:M:84:LEU:HD21	1.95	0.49
1:T:235:LEU:C	1:T:235:LEU:HD23	2.33	0.49
1:M:164:GLU:OE1	1:M:164:GLU:HA	2.13	0.49
1:E:214:GLY:HA3	1:E:235:LEU:O	2.13	0.49
1:R:228:CYS:HB2	1:R:231:ILE:CB	2.43	0.49
1:Q:198:ALA:HB2	1:Q:206:ALA:HB2	1.95	0.49
1:L:218:ASN:CB	1:L:221:ASN:ND2	2.76	0.49
1:S:228:CYS:CB	1:S:231:ILE:HG13	2.43	0.49
1:J:219:GLY:O	1:J:222:ASP:OD1	2.30	0.49
1:L:137:ALA:HB3	1:L:139:ARG:HG3	1.95	0.49
1:M:240:SER:HA	1:M:245:PHE:HB2	1.95	0.49
1:F:132:LEU:O	1:F:136:LYS:HB2	2.13	0.49
1:O:59:GLN:N	1:O:59:GLN:HE21	1.98	0.48
1:Q:5:ARG:NH2	1:Q:35:ASP:O	2.44	0.48
1:Q:85:GLN:NE2	1:Q:120:LYS:HB3	2.20	0.48
1:M:5:ARG:CG	1:M:5:ARG:NH1	2.69	0.48
1:L:21:ILE:O	1:L:25:VAL:HG23	2.12	0.48
1:E:115:LYS:HE3	1:E:119:GLU:OE2	2.12	0.48
1:P:190:HIS:CE1	1:P:231:ILE:HG12	2.48	0.48
1:E:179:VAL:HG13	1:E:179:VAL:O	2.12	0.48
1:E:99:ARG:HG3	1:F:76:THR:HG23	1.93	0.48
1:N:209:ILE:HG23	1:N:211:ILE:CD1	2.43	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:130:GLU:OE1	1:K:169:TYR:CE1	2.66	0.48
1:E:176:GLY:N	1:I:175:ILE:O	2.43	0.48
1:E:116:ARG:NH2	1:E:120:LYS:HZ1	2.12	0.48
1:E:81:VAL:HG11	1:E:120:LYS:HB2	1.94	0.48
1:Q:80:SER:O	1:Q:83:MET:HB2	2.14	0.48
1:I:194:ARG:HH12	1:I:209:ILE:HG23	1.78	0.48
1:P:40:VAL:HG11	1:P:63:ALA:HB2	1.95	0.48
1:S:145:ILE:O	1:S:149:GLU:HG2	2.13	0.48
1:F:68:TYR:HB2	1:F:78:GLU:HB3	1.96	0.48
1:R:114:ALA:HB3	1:R:151:LEU:HD13	1.94	0.48
1:N:130:GLU:OE1	1:N:140:THR:HG23	2.14	0.48
1:Q:31:HIS:NE2	1:Q:250:ASP:OD1	2.39	0.48
1:O:123:THR:HG23	1:O:164:GLU:O	2.13	0.48
1:M:187:GLU:OE2	1:M:230:ASN:OD1	2.31	0.48
1:N:139:ARG:HH12	1:N:143:VAL:CG2	2.26	0.48
1:K:81:VAL:O	1:K:85:GLN:HG3	2.13	0.48
1:R:236:VAL:CG1	1:R:239:ALA:HB3	2.44	0.48
1:E:141:MET:CE	1:E:145:ILE:HD12	2.43	0.48
1:E:139:ARG:O	1:E:143:VAL:HG23	2.13	0.48
1:H:229:PRO:HG2	1:H:230:ASN:HD22	1.78	0.48
1:T:198:ALA:HA	1:T:202:ALA:O	2.13	0.48
1:D:52:ILE:HA	1:D:62:ILE:HD13	1.95	0.48
1:S:243:PRO:HA	1:S:246:MET:CE	2.42	0.48
1:M:145:ILE:HG13	1:M:196:TRP:CD1	2.48	0.48
1:P:151:LEU:HD12	1:P:151:LEU:O	2.13	0.48
1:A:72:ASN:ND2	1:A:80:SER:OG	2.47	0.48
1:Q:145:ILE:O	1:Q:149:GLU:HG3	2.12	0.48
1:R:20:PHE:CE1	1:R:24:HIS:HB2	2.49	0.48
1:N:90:LYS:HE3	1:N:91:HIS:HE1	1.76	0.48
1:T:244:GLU:O	1:T:247:THR:HB	2.14	0.48
1:L:5:ARG:NH1	1:L:35:ASP:O	2.46	0.48
1:L:79:THR:HG21	1:L:84:LEU:HD21	1.93	0.48
1:R:226:GLY:N	1:R:234:PHE:CZ	2.78	0.48
1:G:236:VAL:HG13	1:G:239:ALA:HB3	1.91	0.48
1:Q:248:MET:HA	1:Q:251:ILE:CG2	2.44	0.48
1:A:250:ASP:O	1:A:254:LYS:HE2	2.12	0.48
1:K:9:GLY:HA2	1:K:40:VAL:O	2.14	0.48
1:J:57:SER:HB3	1:J:60:LEU:HB3	1.95	0.48
1:D:187:GLU:OE1	1:D:228:CYS:HB3	2.14	0.48
1:S:221:ASN:N	1:S:221:ASN:ND2	2.62	0.48
1:S:244:GLU:HG3	1:S:245:PHE:N	2.29	0.48
1:S:196:TRP:CE3	1:S:197:PHE:HA	2.48	0.48

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:103:MET:HE2	1:P:78:GLU:HG3	1.95	0.48
1:O:132:LEU:O	1:O:136:LYS:HG3	2.14	0.48
1:G:24:HIS:O	1:G:28:ILE:HG13	2.14	0.48
1:T:145:ILE:O	1:T:149:GLU:HG3	2.14	0.48
1:K:48:LEU:O	1:K:52:ILE:HG13	2.14	0.48
1:K:14:CYS:SG	1:L:80:SER:HB3	2.54	0.48
1:K:246:MET:O	1:K:249:ILE:HB	2.14	0.48
1:E:251:ILE:HD12	1:E:254:LYS:HE3	1.96	0.48
1:E:171:PRO:CD	1:E:215:GLY:HA2	2.34	0.48
1:D:219:GLY:O	1:D:222:ASP:OD1	2.31	0.48
1:A:4:ARG:NH2	1:A:229:PRO:O	2.46	0.48
1:L:118:LEU:HD23	1:L:122:MET:O	2.14	0.48
1:L:251:ILE:HD13	1:L:254:LYS:HZ2	1.76	0.48
1:S:43:PRO:HG2	1:S:48:LEU:CD1	2.43	0.48
1:B:37:VAL:HG12	1:B:38:ASP:N	2.29	0.48
1:O:184:GLU:N	1:O:184:GLU:CD	2.67	0.48
1:K:18:LEU:O	1:K:22:LYS:HG3	2.13	0.48
1:B:168:ALA:HA	1:B:212:ILE:O	2.14	0.48
1:R:64:ALA:CB	1:R:84:LEU:HD11	2.44	0.48
1:R:171:PRO:HD2	1:R:214:GLY:O	2.13	0.48
1:N:32:LYS:HG3	1:N:32:LYS:O	2.14	0.48
1:F:179:VAL:CG1	1:F:180:VAL:N	2.76	0.48
1:Q:197:PHE:CD2	1:Q:206:ALA:CA	2.94	0.48
1:M:2:PRO:HG2	1:M:207:GLN:CG	2.43	0.48
1:S:7:PHE:CE1	1:S:40:VAL:HG21	2.49	0.48
1:S:7:PHE:CD1	1:S:7:PHE:C	2.87	0.48
1:K:171:PRO:HG2	1:K:213:TYR:CE1	2.48	0.48
1:N:139:ARG:HD2	1:N:142:GLU:CD	2.35	0.48
1:D:226:GLY:O	1:D:255:THR:HG21	2.14	0.48
1:T:55:ASN:OD1	1:T:60:LEU:HD23	2.13	0.48
1:I:72:ASN:HD21	1:I:82:GLU:HB2	1.79	0.48
1:R:39:VAL:O	1:R:60:LEU:HD12	2.14	0.48
1:K:24:HIS:O	1:K:28:ILE:HG13	2.14	0.48
1:S:247:THR:O	1:S:251:ILE:HG12	2.14	0.48
1:B:116:ARG:O	1:B:120:LYS:HG3	2.14	0.48
1:O:131:THR:HG23	1:O:134:GLU:OE1	2.13	0.48
1:M:2:PRO:CB	1:M:207:GLN:HB3	2.43	0.47
1:I:4:ARG:HH12	1:I:194:ARG:NH2	2.12	0.47
1:S:188:GLU:HG2	1:S:189:VAL:N	2.28	0.47
1:B:144:ASN:ND2	1:B:193:LEU:HD21	2.29	0.47
1:O:100:ARG:HH12	1:O:128:VAL:HA	1.78	0.47
1:S:12:PHE:HB2	1:S:43:PRO:HA	1.96	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:S:76:THR:O	1:T:99:ARG:HD2	2.14	0.47
1:D:114:ALA:O	1:D:118:LEU:HG	2.14	0.47
1:N:123:THR:HA	1:N:164:GLU:HB3	1.96	0.47
1:M:69:LEU:HD12	1:M:70:GLU:HG2	1.96	0.47
1:E:190:HIS:CD2	1:E:231:ILE:HG12	2.49	0.47
1:G:97:SER:O	1:G:101:ARG:HG2	2.14	0.47
1:M:99:ARG:CA	1:M:103:MET:HB2	2.37	0.47
1:C:68:TYR:HE2	1:C:70:GLU:HG3	1.79	0.47
1:O:66:ASN:HD22	1:O:67:VAL:H	1.60	0.47
1:J:254:LYS:HG3	1:J:255:THR:H	1.79	0.47
1:F:40:VAL:CG1	1:F:63:ALA:HB2	2.44	0.47
1:A:68:TYR:CD1	1:A:78:GLU:HG3	2.49	0.47
1:H:7:PHE:O	1:H:233:GLY:HA3	2.14	0.47
1:L:187:GLU:OE1	1:L:228:CYS:HB3	2.13	0.47
1:R:250:ASP:HA	1:R:253:THR:HG23	1.96	0.47
1:D:190:HIS:CE1	1:D:211:ILE:O	2.67	0.47
1:E:196:TRP:O	1:E:200:LYS:N	2.38	0.47
1:B:99:ARG:HA	1:B:103:MET:HB2	1.97	0.47
1:Q:183:PRO:HB3	1:Q:225:LEU:CD2	2.15	0.47
1:E:251:ILE:CA	1:E:254:LYS:HE3	2.24	0.47
1:H:151:LEU:O	1:H:155:LEU:HG	2.15	0.47
1:F:218:ASN:C	1:F:220:SER:N	2.65	0.47
1:Q:85:GLN:HE22	1:Q:120:LYS:CB	2.24	0.47
1:L:43:PRO:HB2	1:L:47:HIS:HB2	1.97	0.47
1:G:98:GLU:O	1:G:102:ILE:HB	2.14	0.47
1:G:164:GLU:OE1	1:G:164:GLU:HA	2.12	0.47
1:S:4:ARG:HD3	1:S:207:GLN:O	2.14	0.47
1:G:80:SER:OG	1:G:83:MET:HG3	2.14	0.47
1:M:236:VAL:CG1	1:M:239:ALA:HB3	2.45	0.47
1:E:183:PRO:HG2	1:E:224:LYS:CD	2.45	0.47
1:O:41:ILE:HG23	1:O:60:LEU:HD11	1.96	0.47
1:S:6:PRO:HD2	1:S:36:SER:O	2.14	0.47
1:R:225:LEU:C	1:R:234:PHE:CZ	2.80	0.47
1:Q:73:GLY:O	1:R:14:CYS:SG	2.73	0.47
1:I:4:ARG:HH12	1:I:232:ASP:CG	2.17	0.47
1:R:123:THR:HA	1:R:164:GLU:HB3	1.96	0.47
1:D:254:LYS:HG3	1:D:255:THR:N	2.29	0.47
1:I:7:PHE:O	1:I:233:GLY:HA3	2.14	0.47
1:I:37:VAL:CG1	1:I:252:LEU:CD2	2.92	0.47
1:I:83:MET:HG2	1:J:47:HIS:HE1	1.79	0.47
1:P:221:ASN:OD1	1:P:221:ASN:C	2.53	0.47
1:P:222:ASP:OD1	1:P:223:GLU:N	2.48	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:J:158:SER:HG	1:J:161:LEU:HG	1.80	0.47
1:M:90:LYS:HE3	1:M:123:THR:OG1	2.15	0.47
1:O:174:SER:HA	1:O:179:VAL:O	2.13	0.47
1:O:74:ALA:O	1:P:98:GLU:HG2	2.13	0.47
1:A:128:VAL:HG11	1:A:148:LEU:HD13	1.97	0.47
1:K:67:VAL:O	1:K:113:LYS:HD3	2.14	0.47
1:R:71:GLY:HA3	1:R:116:ARG:NH2	2.29	0.47
1:M:81:VAL:O	1:M:85:GLN:HG3	2.14	0.47
1:Q:216:SER:O	1:Q:221:ASN:ND2	2.46	0.47
1:R:174:SER:C	1:R:175:ILE:CG2	2.83	0.47
1:K:218:ASN:OD1	1:K:244:GLU:OE1	2.32	0.47
1:K:197:PHE:HD1	1:K:206:ALA:HB2	1.80	0.47
1:L:98:GLU:O	1:L:102:ILE:HB	2.15	0.47
1:O:100:ARG:CZ	1:O:127:CYS:O	2.62	0.47
1:R:57:SER:HB2	1:R:60:LEU:HB3	1.97	0.47
1:N:190:HIS:NE2	1:N:213:TYR:HB2	2.30	0.47
1:P:145:ILE:O	1:P:149:GLU:N	2.42	0.47
1:R:85:GLN:HE22	1:R:120:LYS:CB	2.28	0.47
1:T:84:LEU:HD22	1:T:89:LEU:HD12	1.97	0.47
1:A:239:ALA:O	1:A:242:LYS:HG3	2.14	0.47
1:T:132:LEU:O	1:T:136:LYS:HG3	2.15	0.47
1:C:145:ILE:O	1:C:149:GLU:HG2	2.15	0.47
1:E:109:GLN:O	1:E:113:LYS:HG3	2.14	0.47
1:R:117:ALA:HB3	1:R:124:VAL:HG21	1.96	0.47
1:D:132:LEU:O	1:D:136:LYS:HG3	2.15	0.47
1:F:175:ILE:CD1	1:F:175:ILE:N	2.68	0.47
1:R:213:TYR:O	1:R:234:PHE:HA	2.14	0.47
1:L:141:MET:HB3	1:L:141:MET:HE2	1.56	0.47
1:O:198:ALA:CA	1:O:206:ALA:HB2	2.45	0.47
1:Q:115:LYS:HG3	1:Q:155:LEU:HD23	1.96	0.47
1:N:4:ARG:NE	1:N:232:ASP:OD1	2.45	0.47
1:N:100:ARG:NH2	1:N:127:CYS:O	2.45	0.47
1:I:197:PHE:HD2	1:I:206:ALA:HB2	1.80	0.47
1:C:76:THR:O	1:D:99:ARG:HD2	2.15	0.47
1:S:186:ALA:CB	1:S:213:TYR:CE1	2.98	0.47
1:A:222:ASP:O	1:A:226:GLY:N	2.44	0.47
1:R:236:VAL:HG21	1:R:248:MET:SD	2.55	0.47
1:O:11:ASN:OD1	1:O:65:GLN:HG2	2.15	0.47
1:P:37:VAL:HG11	1:P:252:LEU:HD23	1.97	0.47
1:F:134:GLU:OE1	1:F:143:VAL:HG21	2.14	0.47
1:E:116:ARG:CZ	1:E:120:LYS:NZ	2.78	0.47
1:E:173:TRP:O	1:E:177:THR:OG1	2.26	0.47

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:48:LEU:O	1:C:52:ILE:HG13	2.14	0.47
1:P:169:TYR:CE2	1:P:189:VAL:HG21	2.49	0.47
1:Q:165:VAL:C	1:Q:210:ARG:HE	2.18	0.47
1:O:187:GLU:OE1	1:O:228:CYS:HB3	2.15	0.47
1:G:69:LEU:CD1	1:G:70:GLU:CG	2.88	0.47
1:H:126:PHE:CE2	1:H:151:LEU:HD21	2.50	0.47
1:N:191:VAL:CG2	1:N:230:ASN:HD22	2.22	0.47
1:K:148:LEU:CD2	1:K:193:LEU:HD22	2.45	0.47
1:J:17:SER:H	1:J:20:PHE:HB3	1.79	0.47
1:N:167:ILE:O	1:N:212:ILE:N	2.41	0.47
1:N:29:ALA:HB1	1:N:57:SER:HB2	1.97	0.47
1:S:61:ARG:CG	1:S:61:ARG:HH11	2.11	0.46
1:D:222:ASP:OD1	1:D:223:GLU:N	2.48	0.46
1:N:222:ASP:O	1:N:225:LEU:N	2.48	0.46
1:C:15:ASN:N	1:D:83:MET:HE1	2.31	0.46
1:I:196:TRP:CD1	1:I:200:LYS:HG3	2.50	0.46
1:A:2:PRO:HG2	1:A:207:GLN:HB3	1.96	0.46
1:D:148:LEU:O	1:D:151:LEU:HB3	2.15	0.46
1:D:151:LEU:O	1:D:155:LEU:HG	2.15	0.46
1:J:254:LYS:HG3	1:J:255:THR:N	2.31	0.46
1:L:240:SER:HA	1:L:245:PHE:HB2	1.97	0.46
1:K:80:SER:HB3	1:L:14:CYS:SG	2.55	0.46
1:G:4:ARG:HD3	1:G:207:GLN:O	2.15	0.46
1:I:4:ARG:HH12	1:I:194:ARG:HH21	1.63	0.46
1:Q:223:GLU:HB2	1:Q:251:ILE:HD11	1.97	0.46
1:P:192:GLY:O	1:P:195:LYS:HB3	2.16	0.46
1:J:251:ILE:HA	1:J:254:LYS:NZ	2.30	0.46
1:C:198:ALA:HA	1:C:203:ALA:HA	1.97	0.46
1:Q:95:GLY:C	1:Q:127:CYS:HB2	2.36	0.46
1:B:184:GLU:N	1:B:184:GLU:OE1	2.48	0.46
1:S:130:GLU:OE2	1:S:169:TYR:OH	2.30	0.46
1:A:197:PHE:HD1	1:A:206:ALA:HB2	1.81	0.46
1:Q:4:ARG:NH2	1:Q:229:PRO:O	2.47	0.46
1:S:196:TRP:O	1:S:200:LYS:HG2	2.15	0.46
1:D:37:VAL:HG11	1:D:252:LEU:HD21	1.96	0.46
1:Q:69:LEU:HD12	1:Q:113:LYS:HG3	1.98	0.46
1:Q:186:ALA:HB1	1:Q:213:TYR:CD1	2.51	0.46
1:E:183:PRO:HG2	1:E:224:LYS:CE	2.45	0.46
1:T:218:ASN:N	1:T:218:ASN:HD22	2.13	0.46
1:O:221:ASN:HA	1:O:224:LYS:HZ1	1.80	0.46
1:Q:71:GLY:O	1:Q:75:TRP:NE1	2.35	0.46
1:B:128:VAL:HG21	1:B:144:ASN:ND2	2.31	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:41:ILE:O	1:K:43:PRO:HD3	2.15	0.46
1:L:155:LEU:HD23	1:L:155:LEU:HA	1.75	0.46
1:C:171:PRO:CD	1:C:214:GLY:O	2.63	0.46
1:F:197:PHE:CZ	1:F:201:VAL:HG11	2.50	0.46
1:N:9:GLY:HA2	1:N:40:VAL:O	2.15	0.46
1:C:18:LEU:HA	1:C:18:LEU:HD23	1.77	0.46
1:Q:201:VAL:CG1	1:Q:202:ALA:H	2.26	0.46
1:H:111:ALA:HB2	1:H:151:LEU:HD12	1.97	0.46
1:I:4:ARG:NH1	1:I:232:ASP:CG	2.69	0.46
1:A:145:ILE:O	1:A:149:GLU:N	2.42	0.46
1:C:177:THR:OG1	1:C:179:VAL:HG13	2.16	0.46
1:N:81:VAL:HG13	1:N:122:MET:SD	2.56	0.46
1:J:99:ARG:HA	1:J:103:MET:HB2	1.96	0.46
1:F:171:PRO:HB2	1:F:174:SER:OG	2.14	0.46
1:O:222:ASP:HA	1:O:225:LEU:HB2	1.96	0.46
1:S:158:SER:CB	1:S:161:LEU:HD23	2.30	0.46
1:C:69:LEU:H	1:C:69:LEU:CD2	2.26	0.46
1:R:2:PRO:HB3	1:R:207:GLN:CG	2.41	0.46
1:D:48:LEU:O	1:D:52:ILE:HG13	2.15	0.46
1:M:98:GLU:HG3	1:M:102:ILE:HD12	1.97	0.46
1:T:243:PRO:HA	1:T:246:MET:HE1	1.98	0.46
1:S:84:LEU:O	1:S:89:LEU:HB2	2.15	0.46
1:G:135:ARG:HB2	1:G:135:ARG:HE	1.55	0.46
1:Q:186:ALA:CB	1:Q:213:TYR:CE1	2.99	0.46
1:K:72:ASN:HA	1:L:14:CYS:O	2.16	0.46
1:I:224:LYS:O	1:I:227:GLN:HB2	2.16	0.46
1:E:11:ASN:OD1	1:E:65:GLN:HG2	2.15	0.46
1:G:114:ALA:HB3	1:G:151:LEU:HD13	1.97	0.46
1:L:184:GLU:CD	1:L:184:GLU:H	2.19	0.46
1:F:135:ARG:HE	1:F:135:ARG:HB2	1.58	0.46
1:K:76:THR:HG22	1:L:98:GLU:HB2	1.98	0.46
1:D:161:LEU:C	1:D:163:LYS:H	2.19	0.46
1:I:218:ASN:O	1:I:222:ASP:CB	2.61	0.46
1:L:251:ILE:O	1:L:254:LYS:HG2	2.16	0.46
1:R:127:CYS:HA	1:R:168:ALA:O	2.16	0.46
1:N:29:ALA:CB	1:N:57:SER:HB2	2.46	0.46
1:T:180:VAL:CG2	1:T:181:ALA:N	2.78	0.46
1:Q:148:LEU:HA	1:Q:148:LEU:HD13	1.73	0.46
1:T:155:LEU:HD13	1:T:161:LEU:HB2	1.96	0.46
1:Q:210:ARG:CD	1:Q:210:ARG:N	2.67	0.46
1:O:213:TYR:CE2	1:O:215:GLY:O	2.69	0.46
1:L:141:MET:CE	1:L:141:MET:CA	2.94	0.46

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:T:63:ALA:CB	1:T:91:HIS:HB2	2.41	0.46
1:T:39:VAL:HG12	1:T:60:LEU:HD13	1.97	0.46
1:S:164:GLU:OE1	1:S:164:GLU:HA	2.15	0.46
1:T:213:TYR:O	1:T:234:PHE:HA	2.16	0.46
1:E:90:LYS:HE2	1:E:91:HIS:CE1	2.51	0.46
1:A:72:ASN:H	1:A:72:ASN:HD22	1.63	0.46
1:M:137:ALA:HA	1:P:137:ALA:HA	1.97	0.46
1:O:40:VAL:HG11	1:O:63:ALA:HB2	1.97	0.46
1:R:182:THR:OG1	1:R:185:GLN:HG3	2.15	0.46
1:Q:75:TRP:NE1	1:R:14:CYS:SG	2.82	0.46
1:S:61:ARG:NH2	1:S:90:LYS:HB2	2.31	0.46
1:H:111:ALA:HA	1:H:151:LEU:HG	1.97	0.46
1:N:244:GLU:O	1:N:248:MET:CG	2.64	0.46
1:O:198:ALA:HA	1:O:206:ALA:HB2	1.97	0.46
1:R:161:LEU:C	1:R:163:LYS:N	2.68	0.46
1:F:111:ALA:HB1	1:F:151:LEU:HA	1.96	0.46
1:O:21:ILE:HG13	1:O:47:HIS:HB3	1.98	0.46
1:E:236:VAL:HG11	1:E:239:ALA:HB3	1.97	0.46
1:P:187:GLU:OE1	1:P:228:CYS:HB3	2.15	0.46
1:S:213:TYR:HB2	1:S:231:ILE:HD13	1.98	0.46
1:R:250:ASP:O	1:R:253:THR:HG23	2.16	0.46
1:G:224:LYS:HB3	1:G:224:LYS:HE3	1.33	0.46
1:S:198:ALA:HB2	1:S:206:ALA:CB	2.46	0.46
1:N:140:THR:HG22	1:N:141:MET:N	2.29	0.46
1:L:244:GLU:OE1	1:L:244:GLU:HA	2.16	0.46
1:C:244:GLU:O	1:C:248:MET:HG3	2.16	0.46
1:M:181:ALA:HB3	1:M:213:TYR:OH	2.16	0.46
1:T:187:GLU:OE2	1:T:191:VAL:HG23	2.16	0.46
1:C:196:TRP:NE1	1:C:200:LYS:HG3	2.30	0.46
1:P:134:GLU:CD	1:P:143:VAL:HG21	2.37	0.46
1:J:218:ASN:N	1:J:218:ASN:OD1	2.49	0.46
1:B:109:GLN:O	1:B:113:LYS:HG3	2.16	0.45
1:H:197:PHE:HB3	1:H:206:ALA:HB2	1.99	0.45
1:A:218:ASN:H	1:A:222:ASP:CG	2.18	0.45
1:E:136:LYS:HE2	1:E:136:LYS:HB3	1.79	0.45
1:D:158:SER:CB	1:D:160:MET:HE1	2.46	0.45
1:O:196:TRP:CE3	1:O:197:PHE:N	2.84	0.45
1:G:128:VAL:HG11	1:G:148:LEU:HD13	1.98	0.45
1:S:15:ASN:OD1	1:T:72:ASN:HB3	2.15	0.45
1:P:204:GLU:O	1:P:208:HIS:CE1	2.69	0.45
1:G:76:THR:HG22	1:H:65:GLN:HB3	1.96	0.45
1:T:197:PHE:CD1	1:T:201:VAL:HG21	2.50	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:9:GLY:HA2	1:B:40:VAL:O	2.16	0.45
1:N:114:ALA:O	1:N:118:LEU:HG	2.17	0.45
1:T:118:LEU:CD1	1:T:155:LEU:HD11	2.46	0.45
1:K:159:LYS:O	1:K:160:MET:HB3	2.14	0.45
1:Q:251:ILE:HG23	1:Q:252:LEU:N	2.31	0.45
1:K:198:ALA:HB2	1:K:206:ALA:CB	2.46	0.45
1:G:221:ASN:O	1:G:224:LYS:HB2	2.17	0.45
1:M:34:PRO:HB2	1:M:36:SER:OG	2.16	0.45
1:M:34:PRO:HG3	1:M:253:THR:HG21	1.99	0.45
1:J:137:ALA:O	1:J:138:ASN:HB2	2.17	0.45
1:N:72:ASN:ND2	1:N:80:SER:OG	2.50	0.45
1:O:81:VAL:O	1:O:85:GLN:HG3	2.15	0.45
1:O:240:SER:HA	1:O:245:PHE:CD1	2.51	0.45
1:A:81:VAL:O	1:A:85:GLN:HG3	2.16	0.45
1:B:114:ALA:HB2	1:B:126:PHE:CE1	2.51	0.45
1:L:196:TRP:O	1:L:200:LYS:N	2.45	0.45
1:P:5:ARG:NH1	1:P:35:ASP:O	2.43	0.45
1:E:171:PRO:HG3	1:E:213:TYR:HE1	1.80	0.45
1:Q:5:ARG:HA	1:Q:6:PRO:HD2	1.61	0.45
1:N:17:SER:O	1:N:21:ILE:HG12	2.17	0.45
1:P:159:LYS:O	1:P:162:TRP:CD1	2.69	0.45
1:J:158:SER:OG	1:J:161:LEU:HG	2.16	0.45
1:A:13:LYS:HG2	1:B:76:THR:OG1	2.16	0.45
1:P:4:ARG:HD2	1:P:207:GLN:O	2.15	0.45
1:M:24:HIS:O	1:M:28:ILE:HG13	2.15	0.45
1:T:18:LEU:O	1:T:22:LYS:HG3	2.17	0.45
1:G:190:HIS:ND1	1:G:231:ILE:HG12	2.31	0.45
1:F:228:CYS:HA	1:F:229:PRO:HD3	1.83	0.45
1:O:210:ARG:HB2	1:O:210:ARG:HE	1.68	0.45
1:P:164:GLU:OE1	1:P:164:GLU:HA	2.15	0.45
1:Q:218:ASN:N	1:Q:218:ASN:HD22	2.14	0.45
1:E:228:CYS:HB2	1:E:231:ILE:HD12	1.99	0.45
1:K:221:ASN:C	1:K:221:ASN:HD22	2.20	0.45
1:I:233:GLY:HA2	1:I:252:LEU:HD11	1.95	0.45
1:E:151:LEU:O	1:E:155:LEU:HG	2.17	0.45
1:L:37:VAL:HG11	1:L:252:LEU:HD23	1.98	0.45
1:C:71:GLY:O	1:C:75:TRP:NE1	2.49	0.45
1:R:190:HIS:NE2	1:R:231:ILE:HD13	2.31	0.45
1:I:68:TYR:CE2	1:I:70:GLU:HG3	2.51	0.45
1:S:171:PRO:HD3	1:S:214:GLY:O	2.17	0.45
1:L:131:THR:HA	1:L:172:VAL:HB	1.99	0.45
1:T:45:ALA:HA	1:T:48:LEU:HD22	1.98	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:83:MET:O	1:K:87:MET:HG3	2.17	0.45
1:S:141:MET:HE1	1:S:193:LEU:HD23	1.99	0.45
1:F:12:PHE:CD1	1:F:12:PHE:N	2.85	0.45
1:G:155:LEU:HD12	1:G:162:TRP:NE1	2.31	0.45
1:I:139:ARG:NH1	1:I:142:GLU:OE1	2.49	0.45
1:J:171:PRO:HB2	1:J:174:SER:OG	2.17	0.45
1:Q:217:ALA:HA	1:Q:221:ASN:HD21	1.80	0.45
1:M:228:CYS:HB2	1:M:231:ILE:CG1	2.46	0.45
1:S:7:PHE:HD1	1:S:7:PHE:C	2.19	0.45
1:S:194:ARG:HD3	1:S:206:ALA:O	2.16	0.45
1:P:45:ALA:HA	1:P:48:LEU:HD22	1.98	0.45
1:Q:12:PHE:HB2	1:Q:43:PRO:HA	1.99	0.45
1:S:2:PRO:CD	1:S:207:GLN:HB2	2.47	0.45
1:P:194:ARG:NE	1:P:230:ASN:HD22	2.14	0.45
1:C:196:TRP:CD1	1:C:200:LYS:HG3	2.52	0.45
1:J:18:LEU:O	1:J:22:LYS:HG3	2.16	0.45
1:K:13:LYS:HD3	1:L:74:ALA:HA	1.99	0.45
1:R:221:ASN:N	1:R:221:ASN:OD1	2.50	0.45
1:D:96:HIS:CE1	1:D:98:GLU:CD	2.90	0.45
1:Q:91:HIS:HA	1:Q:123:THR:O	2.16	0.45
1:Q:46:VAL:CG2	1:Q:47:HIS:CD2	2.98	0.45
1:S:171:PRO:CD	1:S:214:GLY:O	2.64	0.45
1:E:97:SER:CB	1:E:170:GLU:OE1	2.64	0.45
1:M:155:LEU:HD12	1:M:162:TRP:NE1	2.31	0.45
1:B:5:ARG:NH2	1:B:38:ASP:OD1	2.48	0.45
1:Q:74:ALA:HB1	1:R:98:GLU:OE2	2.17	0.45
1:T:184:GLU:OE1	1:T:184:GLU:N	2.49	0.45
1:L:193:LEU:O	1:L:196:TRP:HB3	2.16	0.45
1:Q:72:ASN:ND2	1:Q:80:SER:OG	2.50	0.45
1:Q:75:TRP:HD1	1:R:14:CYS:SG	2.29	0.45
1:M:228:CYS:HA	1:M:229:PRO:HD3	1.82	0.45
1:D:251:ILE:HA	1:D:254:LYS:HG2	1.98	0.45
1:F:177:THR:CG2	1:F:177:THR:O	2.63	0.45
1:L:136:LYS:C	1:L:138:ASN:N	2.69	0.45
1:G:77:GLY:HA3	1:H:99:ARG:NH1	2.31	0.45
1:T:128:VAL:HG11	1:T:148:LEU:HD13	1.99	0.45
1:H:83:MET:O	1:H:87:MET:HG3	2.17	0.45
1:A:36:SER:HB3	1:G:160:MET:CE	2.47	0.45
1:O:97:SER:CB	1:O:170:GLU:OE1	2.64	0.45
1:F:184:GLU:CD	1:F:184:GLU:H	2.20	0.45
1:S:8:ILE:HG22	1:S:252:LEU:CD2	2.47	0.45
1:R:68:TYR:CZ	1:R:69:LEU:HD21	2.52	0.45

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:217:ALA:HB1	1:B:222:ASP:OD2	2.17	0.45
1:S:101:ARG:N	1:S:101:ARG:HD3	2.31	0.45
1:S:163:LYS:HG2	1:S:164:GLU:HG2	1.98	0.45
1:S:106:THR:HG23	1:S:109:GLN:CD	2.37	0.45
1:A:160:MET:N	1:A:160:MET:HE3	2.32	0.45
1:S:95:GLY:C	1:S:127:CYS:HB2	2.37	0.45
1:A:91:HIS:CD2	1:A:123:THR:HB	2.52	0.45
1:G:166:VAL:HG13	1:G:210:ARG:HB3	1.98	0.45
1:F:175:ILE:HG12	1:F:215:GLY:HA2	1.98	0.45
1:S:190:HIS:CE1	1:S:213:TYR:HB2	2.52	0.45
1:C:68:TYR:CE2	1:C:70:GLU:HG3	2.52	0.45
1:J:243:PRO:HA	1:J:246:MET:CE	2.46	0.45
1:N:244:GLU:O	1:N:248:MET:HG3	2.17	0.45
1:M:210:ARG:HG3	1:M:232:ASP:OD2	2.16	0.45
1:I:6:PRO:HB2	1:I:37:VAL:HG13	1.98	0.45
1:P:67:VAL:HB	1:P:92:VAL:HG21	1.99	0.45
1:I:9:GLY:HA2	1:I:40:VAL:O	2.16	0.45
1:G:90:LYS:HB3	1:G:91:HIS:CE1	2.52	0.45
1:I:180:VAL:HG23	1:I:181:ALA:N	2.30	0.45
1:Q:4:ARG:HD2	1:Q:232:ASP:CG	2.37	0.44
1:Q:171:PRO:HB2	1:Q:174:SER:HG	1.83	0.44
1:P:200:LYS:HG2	1:P:200:LYS:O	2.17	0.44
1:H:145:ILE:O	1:H:149:GLU:HG2	2.17	0.44
1:D:145:ILE:HG23	1:D:149:GLU:OE2	2.17	0.44
1:S:187:GLU:OE2	1:S:229:PRO:HG2	2.17	0.44
1:H:163:LYS:H	1:H:163:LYS:HG3	1.44	0.44
1:H:111:ALA:HB1	1:H:151:LEU:HA	1.98	0.44
1:R:183:PRO:HG2	1:R:224:LYS:CD	2.40	0.44
1:I:68:TYR:HB2	1:I:78:GLU:HB3	2.00	0.44
1:B:190:HIS:ND1	1:B:231:ILE:HG12	2.32	0.44
1:N:139:ARG:HB3	1:N:139:ARG:NH1	2.24	0.44
1:T:227:GLN:N	1:T:227:GLN:OE1	2.50	0.44
1:N:33:ILE:O	1:N:59:GLN:HG2	2.17	0.44
1:L:58:LYS:HD2	1:L:58:LYS:O	2.16	0.44
1:S:245:PHE:HA	1:S:248:MET:HG3	1.99	0.44
1:I:96:HIS:CE1	1:I:98:GLU:OE1	2.70	0.44
1:T:8:ILE:HB	1:T:252:LEU:HD22	1.98	0.44
1:I:200:LYS:HE2	1:I:200:LYS:HB3	1.55	0.44
1:A:187:GLU:HB2	1:A:228:CYS:SG	2.57	0.44
1:R:187:GLU:OE1	1:R:187:GLU:HA	2.17	0.44
1:G:11:ASN:OD1	1:G:65:GLN:HG2	2.18	0.44
1:G:9:GLY:C	1:G:235:LEU:HD12	2.37	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:D:197:PHE:O	1:D:201:VAL:HB	2.17	0.44
1:P:218:ASN:O	1:P:222:ASP:HB3	2.18	0.44
1:O:139:ARG:HB3	1:O:142:GLU:HB3	1.99	0.44
1:O:81:VAL:HG11	1:O:120:LYS:HD3	1.99	0.44
1:C:82:GLU:OE1	1:C:116:ARG:NH1	2.51	0.44
1:H:247:THR:O	1:H:251:ILE:HG13	2.16	0.44
1:K:84:LEU:HD22	1:K:89:LEU:HD12	2.00	0.44
1:N:184:GLU:CD	1:N:184:GLU:H	2.21	0.44
1:N:58:LYS:O	1:N:58:LYS:HG2	2.17	0.44
1:B:201:VAL:O	1:B:202:ALA:HB2	2.17	0.44
1:L:218:ASN:N	1:L:221:ASN:ND2	2.39	0.44
1:R:195:LYS:HB3	1:R:195:LYS:HE3	1.82	0.44
1:T:57:SER:HB3	1:T:60:LEU:HB3	1.99	0.44
1:T:194:ARG:NH1	1:T:206:ALA:O	2.49	0.44
1:O:67:VAL:O	1:O:113:LYS:HD3	2.17	0.44
1:G:4:ARG:HB2	1:G:4:ARG:HE	1.40	0.44
1:P:130:GLU:O	1:P:172:VAL:HB	2.17	0.44
1:I:194:ARG:NH1	1:I:211:ILE:HG13	2.33	0.44
1:D:226:GLY:C	1:D:255:THR:HG21	2.38	0.44
1:M:166:VAL:HG22	1:M:210:ARG:HB3	2.00	0.44
1:O:65:GLN:HB3	1:P:76:THR:HG23	1.99	0.44
1:M:145:ILE:CG1	1:M:196:TRP:CD1	3.01	0.44
1:E:69:LEU:HD12	1:E:112:LYS:CB	2.47	0.44
1:D:140:THR:HG22	1:D:141:MET:N	2.32	0.44
1:P:171:PRO:HD2	1:P:214:GLY:O	2.18	0.44
1:A:140:THR:O	1:A:144:ASN:ND2	2.50	0.44
1:P:149:GLU:OE1	1:P:200:LYS:CE	2.65	0.44
1:D:5:ARG:HA	1:D:6:PRO:HD3	1.86	0.44
1:G:145:ILE:HG23	1:G:196:TRP:NE1	2.32	0.44
1:G:160:MET:H	1:G:160:MET:HG3	1.33	0.44
1:L:140:THR:O	1:L:144:ASN:ND2	2.50	0.44
1:R:222:ASP:OD1	1:R:223:GLU:N	2.50	0.44
1:E:174:SER:O	1:I:176:GLY:CA	2.65	0.44
1:I:190:HIS:CE1	1:I:211:ILE:HG22	2.52	0.44
1:J:173:TRP:HH2	1:J:185:GLN:OE1	2.00	0.44
1:D:106:THR:OG1	1:D:109:GLN:HG3	2.18	0.44
1:A:91:HIS:HA	1:A:123:THR:O	2.17	0.44
1:P:251:ILE:HD12	1:P:251:ILE:N	2.33	0.44
1:O:41:ILE:O	1:O:43:PRO:HD3	2.18	0.44
1:E:24:HIS:O	1:E:27:ALA:HB3	2.17	0.44
1:K:242:LYS:HE2	1:K:242:LYS:HB3	1.68	0.44
1:P:177:THR:HG21	1:P:179:VAL:HG22	1.98	0.44

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:160:MET:HA	1:K:163:LYS:HZ2	1.83	0.44
1:J:246:MET:HA	1:J:249:ILE:HD12	1.99	0.44
1:E:44:SER:O	1:E:48:LEU:HD22	2.18	0.44
1:J:91:HIS:CD2	1:J:123:THR:HB	2.53	0.44
1:M:83:MET:HE2	1:N:44:SER:HB2	2.00	0.44
1:G:74:ALA:HB1	1:H:98:GLU:OE2	2.17	0.44
1:E:116:ARG:NH1	1:E:120:LYS:HZ3	2.16	0.44
1:L:5:ARG:HE	1:L:38:ASP:CG	2.21	0.44
1:G:28:ILE:HD13	1:G:245:PHE:CD2	2.52	0.44
1:D:172:VAL:HA	1:D:175:ILE:HG12	2.00	0.44
1:P:5:ARG:HE	1:P:38:ASP:CG	2.21	0.44
1:H:94:VAL:HG11	1:H:114:ALA:HB2	2.00	0.44
1:E:45:ALA:HA	1:E:48:LEU:HD21	1.95	0.44
1:B:144:ASN:HD22	1:B:193:LEU:HD21	1.83	0.44
1:J:96:HIS:HA	1:J:127:CYS:HB2	2.00	0.44
1:L:37:VAL:HG13	1:L:252:LEU:HD23	2.00	0.44
1:D:9:GLY:HA2	1:D:40:VAL:O	2.18	0.44
1:C:174:SER:HA	1:C:177:THR:HG1	1.83	0.44
1:A:13:LYS:H	1:A:65:GLN:NE2	2.16	0.44
1:H:148:LEU:HD12	1:H:148:LEU:HA	1.80	0.44
1:O:63:ALA:HB2	1:O:91:HIS:HB2	1.99	0.44
1:A:167:ILE:HB	1:A:211:ILE:HG23	1.99	0.44
1:E:184:GLU:N	1:E:184:GLU:OE1	2.51	0.44
1:Q:70:GLU:HB2	1:Q:75:TRP:CE2	2.53	0.43
1:T:66:ASN:HD21	1:T:113:LYS:NZ	2.16	0.43
1:N:218:ASN:ND2	1:N:221:ASN:ND2	2.65	0.43
1:N:45:ALA:HA	1:N:48:LEU:CD2	2.45	0.43
1:Q:229:PRO:HB2	1:Q:230:ASN:HD22	1.82	0.43
1:M:98:GLU:HA	1:M:102:ILE:HD12	2.00	0.43
1:L:180:VAL:CG2	1:L:181:ALA:N	2.81	0.43
1:P:190:HIS:ND1	1:P:231:ILE:HG12	2.33	0.43
1:B:82:GLU:OE2	1:B:116:ARG:NH2	2.45	0.43
1:F:197:PHE:O	1:F:201:VAL:N	2.50	0.43
1:C:222:ASP:OD1	1:C:223:GLU:N	2.51	0.43
1:F:52:ILE:HA	1:F:62:ILE:HD13	2.00	0.43
1:F:212:ILE:CD1	1:F:235:LEU:HB2	2.48	0.43
1:C:221:ASN:HD22	1:C:221:ASN:N	2.14	0.43
1:Q:72:ASN:HA	1:R:14:CYS:O	2.17	0.43
1:D:221:ASN:O	1:D:224:LYS:HG3	2.18	0.43
1:N:218:ASN:HD22	1:N:221:ASN:ND2	2.16	0.43
1:Q:4:ARG:NH1	1:Q:194:ARG:CZ	2.81	0.43
1:T:39:VAL:HG12	1:T:60:LEU:CD1	2.48	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:I:5:ARG:HA	1:I:6:PRO:HD3	1.86	0.43
1:Q:31:HIS:CE1	1:Q:246:MET:HB3	2.52	0.43
1:E:80:SER:HG	1:E:83:MET:H	1.66	0.43
1:M:21:ILE:HG13	1:M:47:HIS:HB3	2.00	0.43
1:E:46:VAL:HG23	1:E:47:HIS:CD2	2.53	0.43
1:P:81:VAL:HG21	1:P:117:ALA:HA	1.99	0.43
1:A:127:CYS:HB3	1:A:170:GLU:OE2	2.18	0.43
1:D:7:PHE:O	1:D:233:GLY:HA3	2.18	0.43
1:Q:183:PRO:HG2	1:Q:224:LYS:HD3	2.00	0.43
1:Q:64:ALA:N	1:Q:89:LEU:HD21	2.33	0.43
1:E:130:GLU:CD	1:E:140:THR:HB	2.39	0.43
1:N:222:ASP:OD2	1:N:248:MET:HE3	2.19	0.43
1:S:67:VAL:HG23	1:S:79:THR:HG22	2.01	0.43
1:B:172:VAL:O	1:O:176:GLY:HA2	2.18	0.43
1:E:239:ALA:HA	1:E:242:LYS:HE3	2.01	0.43
1:P:81:VAL:HG13	1:P:122:MET:SD	2.58	0.43
1:I:77:GLY:HA3	1:J:99:ARG:HH11	1.83	0.43
1:O:40:VAL:CG1	1:O:63:ALA:HB2	2.47	0.43
1:O:97:SER:HB3	1:O:170:GLU:OE1	2.18	0.43
1:M:128:VAL:HG12	1:M:147:GLN:HB2	1.99	0.43
1:I:48:LEU:CD2	1:I:89:LEU:HD11	2.48	0.43
1:O:100:ARG:NH1	1:O:147:GLN:CD	2.72	0.43
1:O:197:PHE:HE2	1:O:205:GLY:O	2.00	0.43
1:O:182:THR:HG23	1:O:185:GLN:NE2	2.33	0.43
1:I:228:CYS:HA	1:I:229:PRO:HD2	1.91	0.43
1:L:40:VAL:HG11	1:L:63:ALA:HB2	1.99	0.43
1:D:151:LEU:HD23	1:D:162:TRP:CH2	2.53	0.43
1:S:143:VAL:O	1:S:147:GLN:HG3	2.18	0.43
1:K:13:LYS:HG2	1:L:76:THR:OG1	2.18	0.43
1:A:252:LEU:HA	1:A:252:LEU:HD12	1.78	0.43
1:Q:166:VAL:CG2	1:Q:210:ARG:NH2	2.81	0.43
1:Q:7:PHE:HE1	1:Q:38:ASP:OD1	2.02	0.43
1:O:181:ALA:HB3	1:O:213:TYR:OH	2.18	0.43
1:J:69:LEU:HD22	1:J:113:LYS:HE2	2.00	0.43
1:A:151:LEU:O	1:A:155:LEU:HG	2.19	0.43
1:M:63:ALA:HB2	1:M:91:HIS:HB2	2.00	0.43
1:K:40:VAL:HA	1:K:61:ARG:O	2.18	0.43
1:R:214:GLY:HA2	1:R:235:LEU:HB3	2.00	0.43
1:E:183:PRO:HG2	1:E:224:LYS:HE2	2.01	0.43
1:I:197:PHE:CD2	1:I:206:ALA:HA	2.53	0.43
1:T:180:VAL:HG22	1:T:181:ALA:N	2.34	0.43
1:M:167:ILE:O	1:M:211:ILE:HA	2.18	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:J:166:VAL:HG13	1:J:210:ARG:HB3	1.99	0.43
1:T:111:ALA:HB1	1:T:151:LEU:HA	2.01	0.43
1:F:118:LEU:HB3	1:F:161:LEU:HD22	2.00	0.43
1:F:80:SER:OG	1:F:83:MET:HG3	2.19	0.43
1:I:182:THR:OG1	1:I:185:GLN:HG3	2.19	0.43
1:E:251:ILE:O	1:E:254:LYS:HG2	2.18	0.43
1:H:94:VAL:HG12	1:H:126:PHE:CD1	2.54	0.43
1:R:184:GLU:OE1	1:R:224:LYS:NZ	2.48	0.43
1:B:144:ASN:HD22	1:B:193:LEU:HD22	1.83	0.43
1:O:100:ARG:HH11	1:O:147:GLN:NE2	2.17	0.43
1:E:155:LEU:HD12	1:E:162:TRP:NE1	2.33	0.43
1:L:117:ALA:O	1:L:122:MET:HB2	2.18	0.43
1:Q:81:VAL:HG11	1:Q:117:ALA:HA	2.01	0.43
1:M:223:GLU:O	1:M:227:GLN:HG3	2.19	0.43
1:P:151:LEU:HD12	1:P:155:LEU:HG	2.01	0.43
1:S:24:HIS:NE2	1:S:241:LEU:HA	2.34	0.43
1:Q:189:VAL:O	1:Q:193:LEU:HG	2.19	0.43
1:B:21:ILE:O	1:B:25:VAL:HG23	2.19	0.43
1:L:246:MET:HA	1:L:249:ILE:HD12	1.99	0.43
1:L:189:VAL:O	1:L:193:LEU:HG	2.19	0.43
1:S:39:VAL:HG12	1:S:60:LEU:CD1	2.47	0.43
1:Q:85:GLN:NE2	1:Q:120:LYS:O	2.52	0.43
1:G:221:ASN:HA	1:G:224:LYS:HG3	2.00	0.43
1:J:69:LEU:H	1:J:69:LEU:CD2	2.27	0.43
1:N:134:GLU:OE1	1:N:143:VAL:HG11	2.19	0.43
1:P:83:MET:O	1:P:87:MET:HG3	2.18	0.43
1:I:115:LYS:HD2	1:I:154:GLU:O	2.18	0.43
1:F:82:GLU:H	1:F:82:GLU:HG2	1.41	0.43
1:B:197:PHE:HD2	1:B:206:ALA:HB2	1.83	0.43
1:A:172:VAL:HA	1:A:175:ILE:HD12	1.95	0.43
1:C:78:GLU:HA	1:C:78:GLU:OE1	2.19	0.43
1:Q:16:GLY:O	1:Q:47:HIS:HE1	2.01	0.43
1:M:210:ARG:HE	1:M:210:ARG:HB2	1.19	0.43
1:L:250:ASP:O	1:L:254:LYS:HE3	2.19	0.43
1:T:99:ARG:HB3	1:T:99:ARG:HE	1.52	0.43
1:T:127:CYS:HB3	1:T:170:GLU:OE2	2.19	0.43
1:Q:14:CYS:SG	1:R:80:SER:HB3	2.59	0.43
1:Q:77:GLY:H	1:R:65:GLN:NE2	2.17	0.43
1:C:160:MET:O	1:C:163:LYS:HB2	2.19	0.43
1:K:135:ARG:HB2	1:K:135:ARG:HE	1.58	0.43
1:N:13:LYS:O	1:N:15:ASN:N	2.51	0.43
1:J:132:LEU:HA	1:J:173:TRP:HB3	2.01	0.43

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:R:187:GLU:OE2	1:R:229:PRO:HB2	2.18	0.43
1:B:130:GLU:O	1:B:172:VAL:HB	2.19	0.43
1:Q:33:ILE:HB	1:Q:59:GLN:NE2	2.34	0.43
1:C:195:LYS:HB2	1:C:195:LYS:HE3	1.76	0.43
1:T:157:GLU:OE1	1:T:157:GLU:CA	2.67	0.43
1:F:151:LEU:HD23	1:F:162:TRP:CH2	2.54	0.43
1:S:2:PRO:HG2	1:S:207:GLN:HB2	2.01	0.43
1:S:10:GLY:HA2	1:S:236:VAL:HB	2.00	0.43
1:N:250:ASP:O	1:N:253:THR:HB	2.19	0.43
1:P:12:PHE:N	1:P:12:PHE:CD1	2.87	0.43
1:M:71:GLY:O	1:M:75:TRP:NE1	2.52	0.43
1:O:4:ARG:HD2	1:O:209:ILE:O	2.18	0.43
1:T:118:LEU:HD13	1:T:155:LEU:CD1	2.49	0.43
1:T:115:LYS:CD	1:T:155:LEU:HD21	2.39	0.43
1:O:83:MET:HE1	1:P:14:CYS:C	2.40	0.43
1:S:155:LEU:CG	1:S:161:LEU:HD11	2.46	0.43
1:R:91:HIS:HA	1:R:123:THR:O	2.18	0.43
1:D:55:ASN:HD22	1:D:62:ILE:HD12	1.84	0.43
1:S:246:MET:H	1:S:246:MET:HE3	1.83	0.43
1:D:37:VAL:HG11	1:D:252:LEU:HD23	2.00	0.43
1:Q:69:LEU:HD12	1:Q:113:LYS:HE2	2.01	0.43
1:F:90:LYS:HE2	1:F:123:THR:OG1	2.19	0.43
1:K:154:GLU:HA	1:K:154:GLU:OE1	2.19	0.43
1:G:4:ARG:HD2	1:G:194:ARG:HH12	1.82	0.43
1:E:42:ALA:O	1:E:65:GLN:NE2	2.45	0.43
1:J:71:GLY:O	1:J:75:TRP:NE1	2.49	0.43
1:F:198:ALA:HA	1:F:202:ALA:O	2.18	0.43
1:K:93:ILE:HG12	1:K:125:ILE:HD12	2.01	0.43
1:P:15:ASN:ND2	1:P:15:ASN:N	2.56	0.42
1:I:4:ARG:NH1	1:I:4:ARG:HG2	2.22	0.42
1:R:66:ASN:ND2	1:R:99:ARG:CZ	2.82	0.42
1:N:221:ASN:O	1:N:223:GLU:N	2.52	0.42
1:N:142:GLU:HG3	1:N:143:VAL:N	2.32	0.42
1:S:13:LYS:O	1:S:65:GLN:NE2	2.50	0.42
1:E:115:LYS:NZ	1:E:154:GLU:O	2.49	0.42
1:D:148:LEU:HA	1:D:148:LEU:HD12	1.72	0.42
1:B:162:TRP:HA	1:B:165:VAL:HG23	2.00	0.42
1:B:37:VAL:HG13	1:B:252:LEU:HD23	2.01	0.42
1:B:37:VAL:HG11	1:B:252:LEU:HD23	2.01	0.42
1:P:118:LEU:HD13	1:P:161:LEU:O	2.19	0.42
1:H:148:LEU:CD2	1:H:193:LEU:HD22	2.49	0.42
1:S:141:MET:CE	1:S:193:LEU:HD23	2.49	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:F:12:PHE:O	1:F:15:ASN:ND2	2.52	0.42
1:L:115:LYS:O	1:L:119:GLU:HG3	2.19	0.42
1:L:71:GLY:O	1:L:75:TRP:NE1	2.52	0.42
1:H:204:GLU:HG3	1:H:204:GLU:O	2.18	0.42
1:K:7:PHE:CD1	1:K:7:PHE:C	2.93	0.42
1:T:115:LYS:O	1:T:119:GLU:HG3	2.19	0.42
1:Q:91:HIS:CD2	1:Q:123:THR:CG2	3.02	0.42
1:P:177:THR:O	1:P:179:VAL:N	2.46	0.42
1:S:8:ILE:HG23	1:S:39:VAL:HG22	2.01	0.42
1:R:197:PHE:CD2	1:R:206:ALA:HA	2.54	0.42
1:N:221:ASN:OD1	1:N:222:ASP:OD1	2.36	0.42
1:T:11:ASN:HD21	1:T:13:LYS:HG3	1.84	0.42
1:T:8:ILE:HG22	1:T:39:VAL:HG22	2.01	0.42
1:S:92:VAL:HG13	1:S:124:VAL:HG22	1.97	0.42
1:S:128:VAL:HG12	1:S:147:GLN:HB2	1.99	0.42
1:A:246:MET:O	1:A:249:ILE:HB	2.19	0.42
1:T:149:GLU:O	1:T:153:LYS:HB3	2.19	0.42
1:R:181:ALA:HA	1:R:185:GLN:OE1	2.19	0.42
1:I:114:ALA:O	1:I:118:LEU:HG	2.19	0.42
1:O:246:MET:O	1:O:249:ILE:HB	2.18	0.42
1:D:97:SER:O	1:D:101:ARG:HB2	2.18	0.42
1:E:84:LEU:HD22	1:E:89:LEU:HD12	2.00	0.42
1:L:177:THR:C	1:L:179:VAL:H	2.20	0.42
1:L:196:TRP:O	1:L:200:LYS:HB3	2.19	0.42
1:O:227:GLN:O	1:O:228:CYS:C	2.56	0.42
1:R:198:ALA:HB2	1:R:206:ALA:CB	2.50	0.42
1:K:76:THR:OG1	1:L:65:GLN:HB3	2.18	0.42
1:R:6:PRO:HD2	1:R:36:SER:O	2.18	0.42
1:R:236:VAL:HG11	1:R:239:ALA:HB3	2.00	0.42
1:S:73:GLY:O	1:T:14:CYS:HB3	2.19	0.42
1:E:71:GLY:O	1:E:72:ASN:C	2.54	0.42
1:L:5:ARG:O	1:L:210:ARG:CD	2.67	0.42
1:T:162:TRP:CD2	1:T:197:PHE:HE1	2.37	0.42
1:T:148:LEU:HD12	1:T:148:LEU:HA	1.87	0.42
1:I:116:ARG:O	1:I:120:LYS:HG3	2.20	0.42
1:T:40:VAL:HG12	1:T:41:ILE:N	2.34	0.42
1:S:58:LYS:N	1:S:58:LYS:HD2	2.34	0.42
1:Q:183:PRO:CG	1:Q:225:LEU:HD21	2.48	0.42
1:L:171:PRO:CG	1:L:174:SER:HG	2.28	0.42
1:R:28:ILE:HG12	1:R:246:MET:CE	2.49	0.42
1:K:251:ILE:CD1	1:K:251:ILE:N	2.83	0.42
1:H:115:LYS:CE	1:H:119:GLU:OE2	2.64	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:141:MET:O	1:O:145:ILE:HG13	2.20	0.42
1:A:139:ARG:HH11	1:A:142:GLU:CD	2.22	0.42
1:E:141:MET:HA	1:E:141:MET:HE3	2.00	0.42
1:F:219:GLY:HA2	1:F:222:ASP:CG	2.39	0.42
1:H:4:ARG:HH22	1:H:230:ASN:HA	1.84	0.42
1:D:190:HIS:CE1	1:D:231:ILE:HG12	2.55	0.42
1:E:57:SER:HB3	1:E:60:LEU:HB3	2.02	0.42
1:S:85:GLN:NE2	1:S:120:LYS:O	2.52	0.42
1:L:218:ASN:HB3	1:L:220:SER:H	1.85	0.42
1:P:131:THR:CA	1:P:172:VAL:HG11	2.41	0.42
1:L:69:LEU:HB3	1:L:113:LYS:HG2	2.02	0.42
1:K:221:ASN:O	1:K:225:LEU:HD12	2.19	0.42
1:J:242:LYS:CB	1:J:244:GLU:OE1	2.59	0.42
1:R:218:ASN:N	1:R:218:ASN:HD22	2.16	0.42
1:N:142:GLU:CG	1:N:143:VAL:N	2.82	0.42
1:E:99:ARG:HH11	1:F:77:GLY:HA3	1.85	0.42
1:I:218:ASN:OD1	1:I:221:ASN:N	2.48	0.42
1:Q:132:LEU:O	1:Q:136:LYS:HG3	2.20	0.42
1:C:5:ARG:HA	1:C:6:PRO:HD3	1.79	0.42
1:P:156:GLY:O	1:P:159:LYS:HG3	2.19	0.42
1:J:118:LEU:HD13	1:J:161:LEU:O	2.20	0.42
1:F:139:ARG:O	1:F:143:VAL:HG23	2.19	0.42
1:J:5:ARG:HA	1:J:6:PRO:HD3	1.80	0.42
1:C:138:ASN:HD22	1:C:138:ASN:HA	1.68	0.42
1:L:78:GLU:OE1	1:L:78:GLU:HA	2.20	0.42
1:O:255:THR:O	1:O:255:THR:HG22	2.19	0.42
1:S:7:PHE:CE1	1:S:40:VAL:HG23	2.55	0.42
1:D:221:ASN:HA	1:D:224:LYS:HG2	2.00	0.42
1:D:161:LEU:HD23	1:D:161:LEU:HA	1.83	0.42
1:A:187:GLU:CD	1:A:229:PRO:HD2	2.40	0.42
1:L:21:ILE:HG13	1:L:47:HIS:HB3	2.01	0.42
1:N:4:ARG:NH2	1:N:232:ASP:OD1	2.52	0.42
1:T:253:THR:HG22	1:T:254:LYS:N	2.33	0.42
1:J:251:ILE:HA	1:J:254:LYS:HZ3	1.83	0.42
1:D:116:ARG:O	1:D:120:LYS:HG3	2.20	0.42
1:Q:76:THR:N	1:R:98:GLU:OE1	2.47	0.42
1:B:67:VAL:O	1:B:113:LYS:HD3	2.19	0.42
1:S:5:ARG:O	1:S:210:ARG:NH1	2.52	0.42
1:D:183:PRO:CG	1:D:224:LYS:HD3	2.50	0.42
1:J:244:GLU:O	1:J:248:MET:HG3	2.19	0.42
1:J:173:TRP:CH2	1:J:185:GLN:OE1	2.73	0.42
1:R:43:PRO:HG2	1:R:51:ALA:CB	2.50	0.42

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:106:THR:OG1	1:A:109:GLN:HG3	2.19	0.42
1:B:215:GLY:O	1:B:217:ALA:N	2.53	0.42
1:D:171:PRO:CD	1:D:214:GLY:O	2.66	0.42
1:P:62:ILE:N	1:P:62:ILE:CD1	2.82	0.42
1:T:197:PHE:CE1	1:T:201:VAL:HG21	2.55	0.42
1:T:139:ARG:HG2	1:T:142:GLU:OE1	2.20	0.42
1:Q:48:LEU:HD12	1:Q:48:LEU:HA	1.70	0.42
1:R:25:VAL:HA	1:R:28:ILE:HG13	2.01	0.42
1:R:12:PHE:CD1	1:R:12:PHE:N	2.88	0.42
1:C:90:LYS:HG2	1:C:90:LYS:O	2.18	0.42
1:S:145:ILE:O	1:S:149:GLU:CG	2.68	0.42
1:H:43:PRO:HG2	1:H:48:LEU:CD1	2.49	0.42
1:G:80:SER:HG	1:G:83:MET:HG3	1.84	0.42
1:N:95:GLY:O	1:N:127:CYS:HB2	2.18	0.42
1:O:116:ARG:O	1:O:120:LYS:HG3	2.19	0.42
1:F:212:ILE:HD11	1:F:235:LEU:HB2	2.01	0.42
1:H:8:ILE:HB	1:H:252:LEU:HD23	2.01	0.42
1:E:245:PHE:HA	1:E:248:MET:HG3	2.02	0.42
1:D:221:ASN:HA	1:D:224:LYS:HE3	2.02	0.42
1:D:218:ASN:OD1	1:D:221:ASN:OD1	2.38	0.42
1:I:144:ASN:O	1:I:148:LEU:HB2	2.19	0.42
1:L:97:SER:OG	1:L:175:ILE:HD11	2.18	0.42
1:B:4:ARG:HB2	1:B:4:ARG:HE	1.43	0.42
1:P:134:GLU:HG2	1:P:143:VAL:HG21	2.00	0.42
1:Q:34:PRO:HG2	1:Q:37:VAL:HG23	2.02	0.42
1:I:212:ILE:CD1	1:I:235:LEU:HB2	2.50	0.42
1:I:87:MET:HE2	1:I:87:MET:HB3	1.92	0.42
1:M:141:MET:HE3	1:M:141:MET:HB3	1.93	0.42
1:Q:236:VAL:HG11	1:Q:240:SER:N	2.35	0.42
1:K:5:ARG:HE	1:K:38:ASP:CG	2.21	0.42
1:L:177:THR:HG21	1:L:179:VAL:HG21	2.00	0.41
1:T:66:ASN:ND2	1:T:67:VAL:H	2.18	0.41
1:K:197:PHE:CD1	1:K:206:ALA:CA	3.02	0.41
1:T:242:LYS:HB2	1:T:243:PRO:CD	2.43	0.41
1:R:116:ARG:NH1	1:R:116:ARG:HG3	2.35	0.41
1:M:151:LEU:HD23	1:M:162:TRP:CH2	2.55	0.41
1:G:196:TRP:O	1:G:200:LYS:HB2	2.20	0.41
1:G:37:VAL:CG1	1:G:38:ASP:N	2.83	0.41
1:N:32:LYS:O	1:N:32:LYS:CG	2.67	0.41
1:D:68:TYR:HB2	1:D:78:GLU:HB3	2.01	0.41
1:S:5:ARG:HE	1:S:38:ASP:CG	2.23	0.41
1:L:219:GLY:HA2	1:L:222:ASP:HB2	2.02	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:R:34:PRO:C	1:R:36:SER:N	2.73	0.41
1:N:141:MET:O	1:N:145:ILE:HG12	2.20	0.41
1:F:145:ILE:HD13	1:F:196:TRP:CD1	2.55	0.41
1:F:148:LEU:HB3	1:F:196:TRP:CH2	2.54	0.41
1:I:76:THR:CG2	1:J:65:GLN:HB3	2.49	0.41
1:F:21:ILE:O	1:F:25:VAL:HG23	2.20	0.41
1:M:145:ILE:O	1:M:149:GLU:HG2	2.20	0.41
1:D:101:ARG:CZ	1:D:131:THR:HG23	2.50	0.41
1:B:83:MET:O	1:B:87:MET:HG3	2.20	0.41
1:Q:65:GLN:O	1:Q:93:ILE:HG22	2.20	0.41
1:R:33:ILE:O	1:R:59:GLN:NE2	2.53	0.41
1:M:148:LEU:HD12	1:M:148:LEU:HA	1.82	0.41
1:Q:138:ASN:ND2	1:Q:138:ASN:O	2.53	0.41
1:S:6:PRO:HG3	1:S:37:VAL:HG12	2.02	0.41
1:O:218:ASN:CG	1:O:219:GLY:N	2.74	0.41
1:S:74:ALA:HA	1:T:13:LYS:HD3	2.02	0.41
1:T:7:PHE:O	1:T:233:GLY:HA3	2.20	0.41
1:T:242:LYS:CB	1:T:243:PRO:CD	2.98	0.41
1:R:34:PRO:C	1:R:36:SER:H	2.22	0.41
1:R:151:LEU:HD12	1:R:151:LEU:O	2.21	0.41
1:J:164:GLU:HA	1:J:164:GLU:OE1	2.20	0.41
1:J:228:CYS:HA	1:J:229:PRO:HD2	1.80	0.41
1:O:116:ARG:HH11	1:O:116:ARG:HG2	1.84	0.41
1:N:11:ASN:OD1	1:N:65:GLN:HG2	2.20	0.41
1:N:61:ARG:HD2	1:N:61:ARG:HA	1.87	0.41
1:S:7:PHE:HE1	1:S:40:VAL:CG2	2.32	0.41
1:B:128:VAL:CG2	1:B:144:ASN:HD21	2.33	0.41
1:E:131:THR:OG1	1:E:134:GLU:HG3	2.21	0.41
1:M:69:LEU:HG	1:M:69:LEU:H	1.71	0.41
1:K:193:LEU:HA	1:K:193:LEU:HD23	1.89	0.41
1:J:5:ARG:O	1:J:210:ARG:HD2	2.21	0.41
1:B:115:LYS:O	1:B:119:GLU:HB2	2.20	0.41
1:S:180:VAL:HG23	1:S:216:SER:HB3	2.01	0.41
1:B:145:ILE:HG12	1:B:196:TRP:CD1	2.55	0.41
1:G:12:PHE:CD1	1:G:12:PHE:N	2.88	0.41
1:A:12:PHE:N	1:A:12:PHE:CD1	2.88	0.41
1:N:107:ASP:OD1	1:N:107:ASP:N	2.53	0.41
1:L:218:ASN:HB3	1:L:220:SER:OG	2.21	0.41
1:A:218:ASN:O	1:A:222:ASP:CG	2.59	0.41
1:S:182:THR:HB	1:S:184:GLU:OE1	2.21	0.41
1:J:217:ALA:HB1	1:J:234:PHE:CD1	2.56	0.41
1:J:243:PRO:HD2	1:J:244:GLU:OE1	2.21	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:197:PHE:HE1	1:K:206:ALA:N	2.18	0.41
1:B:247:THR:O	1:B:251:ILE:HD13	2.21	0.41
1:H:221:ASN:HD22	1:H:224:LYS:HB2	1.85	0.41
1:A:190:HIS:HB3	1:A:230:ASN:O	2.20	0.41
1:R:229:PRO:HB2	1:R:230:ASN:HD22	1.85	0.41
1:S:33:ILE:HA	1:S:34:PRO:HD3	1.91	0.41
1:B:95:GLY:O	1:B:127:CYS:HB2	2.21	0.41
1:A:167:ILE:HG13	1:A:211:ILE:HG12	2.02	0.41
1:D:34:PRO:HB2	1:D:36:SER:OG	2.21	0.41
1:T:217:ALA:O	1:T:248:MET:HE1	2.21	0.41
1:A:137:ALA:HB3	1:A:139:ARG:CG	2.49	0.41
1:K:142:GLU:HG2	1:K:143:VAL:N	2.36	0.41
1:K:67:VAL:HG22	1:K:68:TYR:H	1.85	0.41
1:K:43:PRO:C	1:K:65:GLN:NE2	2.74	0.41
1:R:161:LEU:C	1:R:163:LYS:H	2.22	0.41
1:O:67:VAL:HG22	1:O:68:TYR:N	2.36	0.41
1:K:202:ALA:HB1	1:K:204:GLU:CD	2.41	0.41
1:C:72:ASN:N	1:C:72:ASN:HD22	2.17	0.41
1:C:228:CYS:HA	1:C:229:PRO:HD2	1.90	0.41
1:C:174:SER:HB2	1:C:180:VAL:HA	2.02	0.41
1:K:8:ILE:HG13	1:K:9:GLY:N	2.36	0.41
1:K:229:PRO:HB2	1:K:230:ASN:HD22	1.86	0.41
1:Q:130:GLU:CD	1:Q:140:THR:HG23	2.41	0.41
1:G:213:TYR:CD2	1:G:234:PHE:HD1	2.36	0.41
1:L:221:ASN:HD22	1:L:222:ASP:H	1.61	0.41
1:A:218:ASN:HD22	1:A:220:SER:H	1.64	0.41
1:R:4:ARG:NH2	1:R:194:ARG:NH2	2.68	0.41
1:J:8:ILE:HD13	1:J:245:PHE:CE1	2.55	0.41
1:K:195:LYS:HE3	1:K:195:LYS:HB2	1.70	0.41
1:B:128:VAL:HB	1:B:147:GLN:OE1	2.20	0.41
1:D:161:LEU:C	1:D:163:LYS:N	2.72	0.41
1:I:253:THR:HG22	1:I:254:LYS:HD2	2.02	0.41
1:G:7:PHE:CZ	1:G:40:VAL:HG11	2.56	0.41
1:I:143:VAL:O	1:I:147:GLN:HG3	2.20	0.41
1:B:159:LYS:HG2	1:B:160:MET:N	2.35	0.41
1:K:190:HIS:CE1	1:K:211:ILE:HG22	2.56	0.41
1:J:145:ILE:HG22	1:J:149:GLU:HG2	2.01	0.41
1:I:189:VAL:O	1:I:193:LEU:HG	2.21	0.41
1:C:169:TYR:CE1	1:C:189:VAL:HG11	2.56	0.41
1:R:7:PHE:CD1	1:R:7:PHE:C	2.93	0.41
1:F:171:PRO:HG2	1:F:213:TYR:CZ	2.54	0.41
1:Q:166:VAL:CG2	1:Q:210:ARG:CZ	2.99	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:O:221:ASN:O	1:O:225:LEU:HG	2.21	0.41
1:N:134:GLU:HB3	1:N:143:VAL:HG21	2.01	0.41
1:K:204:GLU:HG2	1:K:205:GLY:H	1.83	0.41
1:P:189:VAL:O	1:P:193:LEU:HG	2.20	0.41
1:T:197:PHE:O	1:T:201:VAL:HB	2.21	0.41
1:E:250:ASP:O	1:E:254:LYS:HG2	2.20	0.41
1:H:163:LYS:HE2	1:H:163:LYS:HB2	1.89	0.41
1:I:194:ARG:NH1	1:I:209:ILE:HG23	2.36	0.41
1:R:67:VAL:HG23	1:R:79:THR:HG22	2.02	0.41
1:A:218:ASN:ND2	1:A:218:ASN:O	2.53	0.41
1:Q:222:ASP:O	1:Q:226:GLY:N	2.49	0.41
1:R:48:LEU:HA	1:R:48:LEU:HD12	1.75	0.41
1:B:128:VAL:HG21	1:B:144:ASN:HD21	1.86	0.41
1:M:95:GLY:O	1:M:100:ARG:NE	2.50	0.41
1:I:72:ASN:HD22	1:I:72:ASN:N	2.18	0.41
1:E:96:HIS:CG	1:F:76:THR:HG21	2.56	0.41
1:I:218:ASN:OD1	1:I:221:ASN:ND2	2.53	0.41
1:R:116:ARG:HG3	1:R:116:ARG:HH11	1.86	0.41
1:R:118:LEU:HD21	1:R:165:VAL:HG23	2.02	0.41
1:P:128:VAL:HG12	1:P:147:GLN:OE1	2.20	0.41
1:K:130:GLU:OE2	1:K:169:TYR:OH	2.34	0.41
1:C:250:ASP:O	1:C:253:THR:HB	2.21	0.41
1:G:74:ALA:HA	1:H:13:LYS:HD3	2.03	0.41
1:E:178:GLY:HA3	1:I:172:VAL:HG13	2.03	0.41
1:S:195:LYS:O	1:S:199:GLU:HG3	2.21	0.41
1:I:137:ALA:HB3	1:I:139:ARG:HG3	2.02	0.41
1:O:31:HIS:HB2	1:O:246:MET:HG2	2.03	0.41
1:C:169:TYR:CZ	1:C:189:VAL:HG11	2.56	0.41
1:C:236:VAL:CG1	1:C:239:ALA:HB3	2.51	0.41
1:C:166:VAL:CG1	1:C:212:ILE:HD13	2.51	0.41
1:H:223:GLU:O	1:H:227:GLN:HG3	2.21	0.41
1:M:180:VAL:HG23	1:M:215:GLY:O	2.21	0.41
1:S:5:ARG:NH1	1:S:35:ASP:O	2.47	0.41
1:Q:61:ARG:HD2	1:Q:61:ARG:HA	1.50	0.41
1:S:224:LYS:O	1:S:227:GLN:HB2	2.21	0.41
1:M:183:PRO:HA	1:M:225:LEU:HD23	2.03	0.41
1:H:155:LEU:HD12	1:H:162:TRP:CE2	2.55	0.41
1:D:224:LYS:HG3	1:D:225:LEU:N	2.36	0.41
1:D:160:MET:O	1:D:163:LYS:HB2	2.21	0.41
1:A:130:GLU:O	1:A:173:TRP:HD1	2.04	0.41
1:C:13:LYS:HA	1:C:65:GLN:OE1	2.21	0.41
1:G:96:HIS:ND1	1:G:98:GLU:HG3	2.36	0.41

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:K:202:ALA:HB1	1:K:204:GLU:OE1	2.20	0.41
1:S:246:MET:CE	1:S:246:MET:H	2.34	0.41
1:H:66:ASN:HD21	1:H:113:LYS:NZ	2.19	0.41
1:J:247:THR:O	1:J:251:ILE:HD13	2.21	0.41
1:I:63:ALA:HB2	1:I:91:HIS:HB2	2.03	0.41
1:P:57:SER:HB3	1:P:60:LEU:HB3	2.03	0.41
1:B:66:ASN:ND2	1:B:67:VAL:O	2.53	0.40
1:E:175:ILE:HG23	1:I:176:GLY:O	2.21	0.40
1:N:187:GLU:O	1:N:191:VAL:HG23	2.21	0.40
1:L:204:GLU:O	1:L:207:GLN:HB2	2.22	0.40
1:O:194:ARG:CG	1:O:206:ALA:O	2.69	0.40
1:G:65:GLN:HB3	1:H:76:THR:HG23	2.03	0.40
1:P:69:LEU:CD2	1:P:70:GLU:HG2	2.50	0.40
1:B:118:LEU:HD12	1:B:155:LEU:HD21	2.03	0.40
1:M:141:MET:HE2	1:M:192:GLY:HA3	2.03	0.40
1:G:111:ALA:HB1	1:G:154:GLU:CG	2.51	0.40
1:C:116:ARG:O	1:C:120:LYS:HG3	2.20	0.40
1:E:184:GLU:CD	1:E:184:GLU:H	2.24	0.40
1:D:68:TYR:CE2	1:D:75:TRP:HB3	2.55	0.40
1:O:125:ILE:HG21	1:O:235:LEU:HD13	2.02	0.40
1:L:59:GLN:HE21	1:L:59:GLN:HB2	1.71	0.40
1:Q:195:LYS:O	1:Q:199:GLU:CB	2.60	0.40
1:R:68:TYR:CE1	1:R:69:LEU:CD2	3.04	0.40
1:F:68:TYR:CE1	1:F:69:LEU:HD22	2.57	0.40
1:I:130:GLU:O	1:I:130:GLU:HG2	2.18	0.40
1:M:83:MET:HG2	1:N:47:HIS:HE1	1.86	0.40
1:A:251:ILE:HA	1:A:251:ILE:HD12	1.80	0.40
1:P:186:ALA:HB1	1:P:231:ILE:HD11	2.03	0.40
1:P:242:LYS:C	1:P:244:GLU:N	2.74	0.40
1:O:226:GLY:C	1:O:255:THR:HG21	2.40	0.40
1:H:222:ASP:OD1	1:H:234:PHE:CZ	2.74	0.40
1:O:218:ASN:ND2	1:O:219:GLY:N	2.70	0.40
1:L:218:ASN:N	1:L:222:ASP:OD1	2.55	0.40
1:L:112:LYS:HE3	1:L:154:GLU:OE2	2.22	0.40
1:T:12:PHE:O	1:T:13:LYS:HB2	2.20	0.40
1:M:5:ARG:HH12	1:M:37:VAL:N	2.19	0.40
1:F:90:LYS:O	1:F:90:LYS:HG2	2.21	0.40
1:T:117:ALA:O	1:T:122:MET:HB2	2.21	0.40
1:M:240:SER:HA	1:M:245:PHE:CD1	2.57	0.40
1:N:168:ALA:HA	1:N:212:ILE:O	2.21	0.40
1:Q:24:HIS:NE2	1:Q:28:ILE:HD11	2.36	0.40
1:N:150:ALA:O	1:N:154:GLU:HG2	2.22	0.40

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Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:M:33:ILE:O	1:M:59:GLN:HG2	2.20	0.40
1:M:52:ILE:HD11	1:M:89:LEU:HD21	2.04	0.40
1:L:190:HIS:CE1	1:L:211:ILE:HG22	2.57	0.40
1:F:5:ARG:O	1:F:210:ARG:HD2	2.21	0.40
1:E:61:ARG:HA	1:E:61:ARG:HD2	1.85	0.40
1:E:187:GLU:HG3	1:E:187:GLU:O	2.21	0.40
1:S:158:SER:O	1:S:161:LEU:HD23	2.22	0.40
1:S:225:LEU:O	1:S:228:CYS:HB2	2.21	0.40
1:L:68:TYR:CE2	1:L:70:GLU:HB2	2.56	0.40
1:S:185:GLN:O	1:S:188:GLU:CD	2.60	0.40
1:K:196:TRP:CE3	1:K:197:PHE:N	2.89	0.40
1:T:249:ILE:O	1:T:252:LEU:HB3	2.21	0.40
1:G:75:TRP:HD1	1:H:14:CYS:HB3	1.86	0.40
1:P:149:GLU:HA	1:P:149:GLU:OE1	2.21	0.40
1:D:37:VAL:HG12	1:D:38:ASP:N	2.36	0.40
1:S:21:ILE:HD13	1:S:21:ILE:N	2.37	0.40
1:R:65:GLN:O	1:R:93:ILE:O	2.40	0.40
1:P:12:PHE:HA	1:P:241:LEU:HD21	2.02	0.40
1:I:97:SER:N	1:I:170:GLU:OE1	2.54	0.40
1:O:228:CYS:HA	1:O:229:PRO:HD3	1.79	0.40
1:S:186:ALA:HB1	1:S:213:TYR:CD1	2.57	0.40
1:S:8:ILE:CG2	1:S:39:VAL:HG22	2.52	0.40
1:J:132:LEU:O	1:J:136:LYS:HB2	2.22	0.40
1:G:93:ILE:HA	1:G:125:ILE:HB	2.04	0.40
1:T:84:LEU:HD23	1:T:84:LEU:HA	1.67	0.40
1:S:128:VAL:HG11	1:S:148:LEU:HD13	2.03	0.40
1:L:12:PHE:N	1:L:12:PHE:CD1	2.90	0.40
1:K:72:ASN:ND2	1:K:80:SER:OG	2.55	0.40
1:C:114:ALA:O	1:C:118:LEU:HG	2.21	0.40
1:K:46:VAL:HG13	1:L:45:ALA:HB1	2.04	0.40
1:J:33:ILE:HB	1:J:59:GLN:HE21	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution. The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	252/255 (99%)	241 (96%)	10 (4%)	1 (0%)	43	76
1	B	252/255 (99%)	247 (98%)	5 (2%)	0	100	100
1	C	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	43	76
1	D	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	43	76
1	E	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	43	76
1	F	252/255 (99%)	244 (97%)	7 (3%)	1 (0%)	43	76
1	G	252/255 (99%)	243 (96%)	8 (3%)	1 (0%)	43	76
1	H	252/255 (99%)	240 (95%)	12 (5%)	0	100	100
1	I	252/255 (99%)	243 (96%)	9 (4%)	0	100	100
1	J	252/255 (99%)	244 (97%)	8 (3%)	0	100	100
1	K	252/255 (99%)	240 (95%)	11 (4%)	1 (0%)	43	76
1	L	252/255 (99%)	239 (95%)	13 (5%)	0	100	100
1	M	252/255 (99%)	244 (97%)	8 (3%)	0	100	100
1	N	252/255 (99%)	239 (95%)	11 (4%)	2 (1%)	27	58
1	O	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	43	76
1	P	252/255 (99%)	233 (92%)	18 (7%)	1 (0%)	43	76
1	Q	252/255 (99%)	237 (94%)	14 (6%)	1 (0%)	43	76
1	R	252/255 (99%)	242 (96%)	7 (3%)	3 (1%)	19	45
1	S	252/255 (99%)	238 (94%)	14 (6%)	0	100	100
1	T	252/255 (99%)	246 (98%)	6 (2%)	0	100	100
All	All	5040/5100 (99%)	4821 (96%)	204 (4%)	15 (0%)	50	82

All (15) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	218	ASN
1	E	220	SER
1	G	219	GLY
1	R	218	ASN
1	Q	201	VAL
1	R	13	LYS
1	K	214	GLY
1	N	13	LYS
1	O	138	ASN
1	R	156	GLY
1	A	156	GLY

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Mol	Chain	Res	Type
1	P	243	PRO
1	D	201	VAL
1	N	156	GLY
1	F	201	VAL

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	202/203 (100%)	178 (88%)	24 (12%)	8	18
1	B	202/203 (100%)	187 (93%)	15 (7%)	20	43
1	C	202/203 (100%)	180 (89%)	22 (11%)	9	21
1	D	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	E	202/203 (100%)	177 (88%)	25 (12%)	7	16
1	F	202/203 (100%)	186 (92%)	16 (8%)	18	39
1	G	202/203 (100%)	181 (90%)	21 (10%)	10	23
1	H	202/203 (100%)	180 (89%)	22 (11%)	9	21
1	I	202/203 (100%)	177 (88%)	25 (12%)	7	16
1	J	202/203 (100%)	184 (91%)	18 (9%)	14	31
1	K	202/203 (100%)	181 (90%)	21 (10%)	10	23
1	L	202/203 (100%)	184 (91%)	18 (9%)	14	31
1	M	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	N	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	O	202/203 (100%)	176 (87%)	26 (13%)	6	15
1	P	202/203 (100%)	180 (89%)	22 (11%)	9	21
1	Q	202/203 (100%)	169 (84%)	33 (16%)	3	9
1	R	202/203 (100%)	181 (90%)	21 (10%)	10	23
1	S	202/203 (100%)	160 (79%)	42 (21%)	2	4
1	T	202/203 (100%)	168 (83%)	34 (17%)	3	8
All	All	4040/4060 (100%)	3557 (88%)	483 (12%)	7	17

All (483) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	4	ARG
1	A	18	LEU
1	A	32	LYS
1	A	48	LEU
1	A	49	SER
1	A	57	SER
1	A	69	LEU
1	A	72	ASN
1	A	99	ARG
1	A	138	ASN
1	A	139	ARG
1	A	142	GLU
1	A	149	GLU
1	A	157	GLU
1	A	160	MET
1	A	167	ILE
1	A	179	VAL
1	A	210	ARG
1	A	218	ASN
1	A	221	ASN
1	A	246	MET
1	A	251	ILE
1	A	252	LEU
1	A	255	THR
1	B	4	ARG
1	B	5	ARG
1	B	35	ASP
1	B	66	ASN
1	B	69	LEU
1	B	101	ARG
1	B	138	ASN
1	B	148	LEU
1	B	159	LYS
1	B	160	MET
1	B	177	THR
1	B	179	VAL
1	B	184	GLU
1	B	210	ARG
1	B	221	ASN
1	C	44	SER
1	C	48	LEU
1	C	49	SER

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Mol	Chain	Res	Type
1	C	59	GLN
1	C	61	ARG
1	C	62	ILE
1	C	69	LEU
1	C	86	ASP
1	C	110	SER
1	C	116	ARG
1	C	138	ASN
1	C	139	ARG
1	C	140	THR
1	C	148	LEU
1	C	158	SER
1	C	159	LYS
1	C	160	MET
1	C	179	VAL
1	C	207	GLN
1	C	210	ARG
1	C	218	ASN
1	C	251	ILE
1	D	4	ARG
1	D	8	ILE
1	D	32	LYS
1	D	36	SER
1	D	44	SER
1	D	48	LEU
1	D	58	LYS
1	D	67	VAL
1	D	68	TYR
1	D	69	LEU
1	D	99	ARG
1	D	100	ARG
1	D	135	ARG
1	D	138	ASN
1	D	140	THR
1	D	145	ILE
1	D	148	LEU
1	D	160	MET
1	D	180	VAL
1	D	188	GLU
1	D	194	ARG
1	D	210	ARG
1	D	218	ASN

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Mol	Chain	Res	Type
1	D	222	ASP
1	D	244	GLU
1	D	252	LEU
1	E	49	SER
1	E	62	ILE
1	E	69	LEU
1	E	89	LEU
1	E	115	LYS
1	E	116	ARG
1	E	130	GLU
1	E	131	THR
1	E	138	ASN
1	E	140	THR
1	E	141	MET
1	E	145	ILE
1	E	148	LEU
1	E	149	GLU
1	E	157	GLU
1	E	158	SER
1	E	160	MET
1	E	184	GLU
1	E	195	LYS
1	E	199	GLU
1	E	220	SER
1	E	222	ASP
1	E	225	LEU
1	E	248	MET
1	E	255	THR
1	F	5	ARG
1	F	44	SER
1	F	48	LEU
1	F	58	LYS
1	F	61	ARG
1	F	69	LEU
1	F	82	GLU
1	F	112	LYS
1	F	135	ARG
1	F	148	LEU
1	F	159	LYS
1	F	160	MET
1	F	185	GLN
1	F	209	ILE

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Mol	Chain	Res	Type
1	F	210	ARG
1	F	221	ASN
1	G	4	ARG
1	G	8	ILE
1	G	23	SER
1	G	40	VAL
1	G	62	ILE
1	G	93	ILE
1	G	116	ARG
1	G	130	GLU
1	G	135	ARG
1	G	139	ARG
1	G	148	LEU
1	G	159	LYS
1	G	160	MET
1	G	179	VAL
1	G	210	ARG
1	G	211	ILE
1	G	224	LYS
1	G	225	LEU
1	G	242	LYS
1	G	252	LEU
1	G	254	LYS
1	H	4	ARG
1	H	32	LYS
1	H	48	LEU
1	H	49	SER
1	H	58	LYS
1	H	69	LEU
1	H	86	ASP
1	H	109	GLN
1	H	112	LYS
1	H	115	LYS
1	H	138	ASN
1	H	142	GLU
1	H	148	LEU
1	H	154	GLU
1	H	158	SER
1	H	159	LYS
1	H	160	MET
1	H	164	GLU
1	H	180	VAL

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Mol	Chain	Res	Type
1	H	210	ARG
1	H	248	MET
1	H	252	LEU
1	I	4	ARG
1	I	8	ILE
1	I	13	LYS
1	I	32	LYS
1	I	36	SER
1	I	44	SER
1	I	46	VAL
1	I	69	LEU
1	I	130	GLU
1	I	138	ASN
1	I	145	ILE
1	I	148	LEU
1	I	157	GLU
1	I	160	MET
1	I	167	ILE
1	I	194	ARG
1	I	200	LYS
1	I	209	ILE
1	I	210	ARG
1	I	218	ASN
1	I	227	GLN
1	I	240	SER
1	I	244	GLU
1	I	251	ILE
1	I	252	LEU
1	J	17	SER
1	J	23	SER
1	J	48	LEU
1	J	49	SER
1	J	58	LYS
1	J	61	ARG
1	J	110	SER
1	J	112	LYS
1	J	115	LYS
1	J	148	LEU
1	J	153	LYS
1	J	159	LYS
1	J	160	MET
1	J	163	LYS

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Mol	Chain	Res	Type
1	J	210	ARG
1	J	218	ASN
1	J	224	LYS
1	J	240	SER
1	K	4	ARG
1	K	46	VAL
1	K	48	LEU
1	K	62	ILE
1	K	69	LEU
1	K	116	ARG
1	K	135	ARG
1	K	148	LEU
1	K	157	GLU
1	K	195	LYS
1	K	209	ILE
1	K	210	ARG
1	K	218	ASN
1	K	220	SER
1	K	221	ASN
1	K	225	LEU
1	K	242	LYS
1	K	248	MET
1	K	251	ILE
1	K	254	LYS
1	K	255	THR
1	L	4	ARG
1	L	49	SER
1	L	59	GLN
1	L	69	LEU
1	L	99	ARG
1	L	100	ARG
1	L	138	ASN
1	L	148	LEU
1	L	173	TRP
1	L	179	VAL
1	L	189	VAL
1	L	199	GLU
1	L	204	GLU
1	L	208	HIS
1	L	218	ASN
1	L	221	ASN
1	L	232	ASP

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Mol	Chain	Res	Type
1	L	240	SER
1	M	5	ARG
1	M	32	LYS
1	M	35	ASP
1	M	44	SER
1	M	48	LEU
1	M	49	SER
1	M	58	LYS
1	M	68	TYR
1	M	69	LEU
1	M	75	TRP
1	M	97	SER
1	M	98	GLU
1	M	106	THR
1	M	145	ILE
1	M	148	LEU
1	M	159	LYS
1	M	160	MET
1	M	170	GLU
1	M	179	VAL
1	M	194	ARG
1	M	209	ILE
1	M	210	ARG
1	M	224	LYS
1	M	251	ILE
1	M	253	THR
1	M	255	THR
1	N	15	ASN
1	N	32	LYS
1	N	36	SER
1	N	44	SER
1	N	48	LEU
1	N	49	SER
1	N	62	ILE
1	N	69	LEU
1	N	89	LEU
1	N	107	ASP
1	N	120	LYS
1	N	130	GLU
1	N	139	ARG
1	N	142	GLU
1	N	145	ILE

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Mol	Chain	Res	Type
1	N	148	LEU
1	N	160	MET
1	N	179	VAL
1	N	180	VAL
1	N	184	GLU
1	N	224	LYS
1	N	225	LEU
1	N	240	SER
1	N	244	GLU
1	N	247	THR
1	N	248	MET
1	O	8	ILE
1	O	13	LYS
1	O	14	CYS
1	O	36	SER
1	O	48	LEU
1	O	49	SER
1	O	59	GLN
1	O	69	LEU
1	O	86	ASP
1	O	112	LYS
1	O	120	LYS
1	O	131	THR
1	O	138	ASN
1	O	139	ARG
1	O	145	ILE
1	O	148	LEU
1	O	160	MET
1	O	163	LYS
1	O	167	ILE
1	O	204	GLU
1	O	210	ARG
1	O	223	GLU
1	O	244	GLU
1	O	247	THR
1	O	248	MET
1	O	251	ILE
1	P	4	ARG
1	P	15	ASN
1	P	35	ASP
1	P	48	LEU
1	P	59	GLN

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Mol	Chain	Res	Type
1	P	61	ARG
1	P	69	LEU
1	P	89	LEU
1	P	108	GLU
1	P	115	LYS
1	P	116	ARG
1	P	128	VAL
1	P	130	GLU
1	P	145	ILE
1	P	148	LEU
1	P	160	MET
1	P	172	VAL
1	P	173	TRP
1	P	199	GLU
1	P	210	ARG
1	P	221	ASN
1	P	223	GLU
1	Q	8	ILE
1	Q	19	ASP
1	Q	23	SER
1	Q	28	ILE
1	Q	37	VAL
1	Q	38	ASP
1	Q	46	VAL
1	Q	48	LEU
1	Q	50	THR
1	Q	58	LYS
1	Q	59	GLN
1	Q	61	ARG
1	Q	75	TRP
1	Q	81	VAL
1	Q	103	MET
1	Q	106	THR
1	Q	115	LYS
1	Q	116	ARG
1	Q	139	ARG
1	Q	148	LEU
1	Q	153	LYS
1	Q	158	SER
1	Q	159	LYS
1	Q	160	MET
1	Q	177	THR

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Mol	Chain	Res	Type
1	Q	189	VAL
1	Q	195	LYS
1	Q	210	ARG
1	Q	220	SER
1	Q	230	ASN
1	Q	236	VAL
1	Q	252	LEU
1	Q	255	THR
1	R	8	ILE
1	R	28	ILE
1	R	35	ASP
1	R	48	LEU
1	R	49	SER
1	R	69	LEU
1	R	80	SER
1	R	87	MET
1	R	89	LEU
1	R	119	GLU
1	R	120	LYS
1	R	135	ARG
1	R	148	LEU
1	R	153	LYS
1	R	210	ARG
1	R	222	ASP
1	R	230	ASN
1	R	244	GLU
1	R	251	ILE
1	R	253	THR
1	R	255	THR
1	S	7	PHE
1	S	8	ILE
1	S	23	SER
1	S	28	ILE
1	S	32	LYS
1	S	44	SER
1	S	48	LEU
1	S	49	SER
1	S	59	GLN
1	S	61	ARG
1	S	69	LEU
1	S	86	ASP
1	S	87	MET

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Mol	Chain	Res	Type
1	S	89	LEU
1	S	99	ARG
1	S	101	ARG
1	S	102	ILE
1	S	106	THR
1	S	108	GLU
1	S	116	ARG
1	S	128	VAL
1	S	130	GLU
1	S	138	ASN
1	S	148	LEU
1	S	157	GLU
1	S	158	SER
1	S	159	LYS
1	S	160	MET
1	S	163	LYS
1	S	180	VAL
1	S	185	GLN
1	S	188	GLU
1	S	207	GLN
1	S	210	ARG
1	S	220	SER
1	S	221	ASN
1	S	241	LEU
1	S	244	GLU
1	S	246	MET
1	S	247	THR
1	S	253	THR
1	S	254	LYS
1	T	22	LYS
1	T	23	SER
1	T	28	ILE
1	T	32	LYS
1	T	33	ILE
1	T	48	LEU
1	T	49	SER
1	T	67	VAL
1	T	87	MET
1	T	99	ARG
1	T	115	LYS
1	T	135	ARG
1	T	136	LYS

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Mol	Chain	Res	Type
1	T	148	LEU
1	T	153	LYS
1	T	157	GLU
1	T	158	SER
1	T	160	MET
1	T	163	LYS
1	T	164	GLU
1	T	170	GLU
1	T	174	SER
1	T	180	VAL
1	T	199	GLU
1	T	209	ILE
1	T	210	ARG
1	T	216	SER
1	T	220	SER
1	T	223	GLU
1	T	240	SER
1	T	242	LYS
1	T	244	GLU
1	T	248	MET
1	T	253	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (112) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	59	GLN
1	A	72	ASN
1	A	91	HIS
1	A	138	ASN
1	A	208	HIS
1	A	218	ASN
1	B	65	GLN
1	B	66	ASN
1	B	72	ASN
1	B	144	ASN
1	C	47	HIS
1	C	72	ASN
1	C	91	HIS
1	C	138	ASN
1	C	221	ASN
1	D	47	HIS
1	D	72	ASN

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Mol	Chain	Res	Type
1	D	144	ASN
1	D	207	GLN
1	D	218	ASN
1	E	66	ASN
1	E	72	ASN
1	E	91	HIS
1	F	47	HIS
1	F	65	GLN
1	F	91	HIS
1	G	66	ASN
1	G	72	ASN
1	G	230	ASN
1	H	47	HIS
1	H	66	ASN
1	H	85	GLN
1	H	221	ASN
1	H	230	ASN
1	I	11	ASN
1	I	72	ASN
1	I	91	HIS
1	I	138	ASN
1	I	221	ASN
1	J	11	ASN
1	J	47	HIS
1	J	72	ASN
1	J	91	HIS
1	J	207	GLN
1	K	59	GLN
1	K	66	ASN
1	K	72	ASN
1	K	218	ASN
1	K	221	ASN
1	K	230	ASN
1	L	47	HIS
1	L	59	GLN
1	L	72	ASN
1	L	91	HIS
1	L	138	ASN
1	L	144	ASN
1	L	221	ASN
1	M	47	HIS
1	M	59	GLN

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Mol	Chain	Res	Type
1	M	65	GLN
1	M	66	ASN
1	M	72	ASN
1	N	15	ASN
1	N	47	HIS
1	N	66	ASN
1	N	72	ASN
1	N	91	HIS
1	N	218	ASN
1	O	59	GLN
1	O	66	ASN
1	O	72	ASN
1	O	185	GLN
1	O	190	HIS
1	O	208	HIS
1	O	218	ASN
1	P	15	ASN
1	P	59	GLN
1	P	66	ASN
1	P	72	ASN
1	P	91	HIS
1	P	96	HIS
1	P	138	ASN
1	P	144	ASN
1	P	230	ASN
1	Q	47	HIS
1	Q	59	GLN
1	Q	66	ASN
1	Q	72	ASN
1	Q	85	GLN
1	Q	91	HIS
1	Q	190	HIS
1	Q	218	ASN
1	Q	230	ASN
1	R	47	HIS
1	R	72	ASN
1	R	85	GLN
1	R	190	HIS
1	R	218	ASN
1	R	230	ASN
1	S	47	HIS
1	S	72	ASN

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Mol	Chain	Res	Type
1	S	144	ASN
1	S	190	HIS
1	S	221	ASN
1	S	230	ASN
1	T	47	HIS
1	T	65	GLN
1	T	66	ASN
1	T	72	ASN
1	T	85	GLN
1	T	190	HIS
1	T	218	ASN

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

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	254/255 (99%)	0.15	9 (3%) 42 47	26, 40, 72, 88	0
1	B	254/255 (99%)	0.16	7 (2%) 50 56	21, 37, 70, 89	0
1	C	254/255 (99%)	0.17	8 (3%) 47 52	22, 39, 72, 93	0
1	D	254/255 (99%)	0.12	6 (2%) 56 62	25, 40, 71, 84	0
1	E	254/255 (99%)	0.23	13 (5%) 27 30	24, 44, 75, 90	0
1	F	254/255 (99%)	0.15	6 (2%) 56 62	23, 39, 71, 88	0
1	G	254/255 (99%)	0.24	10 (3%) 37 42	24, 38, 70, 92	0
1	H	254/255 (99%)	0.12	4 (1%) 68 74	24, 39, 73, 91	0
1	I	254/255 (99%)	0.19	6 (2%) 56 62	25, 40, 70, 85	0
1	J	254/255 (99%)	0.11	6 (2%) 56 62	24, 38, 72, 93	0
1	K	254/255 (99%)	0.32	15 (5%) 22 23	25, 48, 76, 93	0
1	L	254/255 (99%)	0.42	14 (5%) 24 26	27, 52, 79, 90	0
1	M	254/255 (99%)	0.17	2 (0%) 83 87	24, 42, 75, 87	0
1	N	254/255 (99%)	0.20	9 (3%) 42 47	23, 43, 76, 92	0
1	O	254/255 (99%)	0.39	17 (6%) 17 19	24, 45, 77, 93	0
1	P	254/255 (99%)	0.36	16 (6%) 19 21	27, 51, 80, 95	0
1	Q	254/255 (99%)	0.70	33 (12%) 4 4	40, 65, 86, 96	0
1	R	254/255 (99%)	0.60	30 (11%) 5 5	35, 64, 87, 95	0
1	S	254/255 (99%)	0.38	9 (3%) 42 47	41, 64, 85, 96	0
1	T	254/255 (99%)	0.57	28 (11%) 6 6	36, 62, 87, 96	0
All	All	5080/5100 (99%)	0.29	248 (4%) 28 31	21, 46, 79, 96	0

All (248) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	N	2	PRO	11.4
1	R	217	ALA	11.1
1	K	219	GLY	9.6
1	Q	40	VAL	8.2
1	A	217	ALA	7.9
1	C	2	PRO	7.6
1	R	176	GLY	7.6
1	T	2	PRO	7.3
1	L	2	PRO	7.2
1	P	175	ILE	7.0
1	O	2	PRO	7.0
1	A	222	ASP	6.6
1	E	216	SER	6.5
1	O	219	GLY	6.3
1	Q	210	ARG	6.2
1	T	40	VAL	6.0
1	K	218	ASN	5.9
1	R	234	PHE	5.9
1	G	2	PRO	5.8
1	J	2	PRO	5.7
1	Q	25	VAL	5.5
1	Q	176	GLY	5.4
1	L	180	VAL	5.4
1	Q	166	VAL	5.4
1	G	219	GLY	5.3
1	H	222	ASP	5.2
1	O	252	LEU	5.1
1	C	3	ALA	5.1
1	E	215	GLY	5.1
1	K	235	LEU	5.0
1	E	217	ALA	4.9
1	I	176	GLY	4.9
1	S	166	VAL	4.9
1	I	219	GLY	4.8
1	Q	42	ALA	4.7
1	R	33	ILE	4.7
1	E	219	GLY	4.6
1	K	2	PRO	4.4
1	Q	124	VAL	4.4
1	O	225	LEU	4.4
1	I	2	PRO	4.4
1	T	41	ILE	4.4
1	R	2	PRO	4.4

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Mol	Chain	Res	Type	RSRZ
1	Q	63	ALA	4.3
1	T	52	ILE	4.3
1	C	219	GLY	4.2
1	I	216	SER	4.2
1	J	219	GLY	4.1
1	P	253	THR	4.1
1	Q	168	ALA	4.1
1	D	216	SER	4.0
1	L	111	ALA	4.0
1	T	42	ALA	4.0
1	R	40	VAL	4.0
1	C	81	VAL	3.9
1	Q	37	VAL	3.9
1	Q	196	TRP	3.8
1	K	248	MET	3.8
1	R	216	SER	3.8
1	T	29	ALA	3.8
1	A	175	ILE	3.7
1	S	252	LEU	3.7
1	L	175	ILE	3.7
1	T	217	ALA	3.7
1	Q	249	ILE	3.7
1	P	128	VAL	3.7
1	M	255	THR	3.6
1	H	2	PRO	3.6
1	T	166	VAL	3.6
1	Q	125	ILE	3.6
1	R	55	ASN	3.6
1	A	225	LEU	3.6
1	T	63	ALA	3.6
1	N	227	GLN	3.5
1	T	12	PHE	3.5
1	Q	8	ILE	3.5
1	O	198	ALA	3.4
1	T	37	VAL	3.4
1	E	2	PRO	3.3
1	P	2	PRO	3.3
1	K	225	LEU	3.3
1	G	252	LEU	3.3
1	P	95	GLY	3.3
1	R	38	ASP	3.3
1	T	155	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	G	217	ALA	3.2
1	R	148	LEU	3.2
1	G	234	PHE	3.2
1	Q	179	VAL	3.2
1	Q	7	PHE	3.2
1	O	3	ALA	3.2
1	C	175	ILE	3.1
1	L	255	THR	3.1
1	P	110	SER	3.1
1	D	2	PRO	3.1
1	R	25	VAL	3.1
1	R	235	LEU	3.1
1	E	202	ALA	3.1
1	K	83	MET	3.1
1	R	245	PHE	3.1
1	G	220	SER	3.1
1	A	226	GLY	3.0
1	A	220	SER	3.0
1	R	218	ASN	3.0
1	T	252	LEU	3.0
1	T	49	SER	3.0
1	N	3	ALA	2.9
1	N	218	ASN	2.9
1	R	209	ILE	2.9
1	E	225	LEU	2.9
1	Q	89	LEU	2.9
1	B	63	ALA	2.9
1	K	3	ALA	2.9
1	R	177	THR	2.8
1	R	236	VAL	2.8
1	Q	41	ILE	2.8
1	F	177	THR	2.8
1	S	25	VAL	2.8
1	B	176	GLY	2.8
1	T	39	VAL	2.8
1	P	249	ILE	2.8
1	G	236	VAL	2.8
1	Q	94	VAL	2.8
1	F	137	ALA	2.8
1	R	37	VAL	2.7
1	S	128	VAL	2.7
1	K	217	ALA	2.7

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Mol	Chain	Res	Type	RSRZ
1	R	7	PHE	2.7
1	L	222	ASP	2.7
1	O	220	SER	2.7
1	R	52	ILE	2.7
1	Q	51	ALA	2.7
1	D	3	ALA	2.7
1	Q	177	THR	2.7
1	K	220	SER	2.6
1	Q	178	GLY	2.6
1	K	223	GLU	2.6
1	L	101	ARG	2.6
1	Q	39	VAL	2.6
1	L	197	PHE	2.6
1	S	127	CYS	2.6
1	F	206	ALA	2.6
1	L	234	PHE	2.6
1	N	216	SER	2.6
1	B	223	GLU	2.6
1	P	174	SER	2.6
1	T	195	LYS	2.6
1	Q	26	ALA	2.6
1	G	255	THR	2.6
1	T	25	VAL	2.6
1	J	111	ALA	2.5
1	O	197	PHE	2.5
1	T	8	ILE	2.5
1	F	111	ALA	2.5
1	T	168	ALA	2.5
1	I	129	GLY	2.5
1	Q	22	LYS	2.5
1	Q	241	LEU	2.4
1	N	254	LYS	2.4
1	O	205	GLY	2.4
1	B	252	LEU	2.4
1	O	221	ASN	2.4
1	R	252	LEU	2.4
1	E	171	PRO	2.4
1	K	222	ASP	2.4
1	Q	84	LEU	2.4
1	R	175	ILE	2.4
1	T	202	ALA	2.4
1	O	137	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	T	165	VAL	2.3
1	T	203	ALA	2.3
1	B	171	PRO	2.3
1	N	162	TRP	2.3
1	A	221	ASN	2.3
1	K	252	LEU	2.3
1	L	246	MET	2.3
1	I	151	LEU	2.3
1	O	157	GLU	2.3
1	T	163	LYS	2.3
1	G	216	SER	2.3
1	Q	3	ALA	2.3
1	T	28	ILE	2.3
1	E	126	PHE	2.3
1	P	140	THR	2.3
1	N	193	LEU	2.3
1	Q	64	ALA	2.3
1	T	62	ILE	2.3
1	P	129	GLY	2.3
1	S	235	LEU	2.3
1	L	223	GLU	2.2
1	B	2	PRO	2.2
1	R	165	VAL	2.2
1	R	8	ILE	2.2
1	S	4	ARG	2.2
1	C	222	ASP	2.2
1	E	168	ALA	2.2
1	P	117	ALA	2.2
1	O	214	GLY	2.2
1	K	162	TRP	2.2
1	C	218	ASN	2.2
1	C	216	SER	2.2
1	O	126	PHE	2.2
1	R	34	PRO	2.2
1	S	167	ILE	2.2
1	P	234	PHE	2.2
1	L	252	LEU	2.2
1	T	50	THR	2.2
1	J	165	VAL	2.2
1	D	151	LEU	2.2
1	R	84	LEU	2.2
1	L	211	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	218	ASN	2.1
1	L	176	GLY	2.1
1	R	57	SER	2.1
1	P	252	LEU	2.1
1	P	255	THR	2.1
1	M	221	ASN	2.1
1	T	3	ALA	2.1
1	H	9	GLY	2.1
1	O	215	GLY	2.1
1	Q	2	PRO	2.1
1	Q	175	ILE	2.1
1	R	147	GLN	2.1
1	E	218	ASN	2.1
1	A	212	ILE	2.1
1	F	255	THR	2.1
1	D	180	VAL	2.1
1	E	200	LYS	2.1
1	G	222	ASP	2.1
1	T	254	LYS	2.1
1	Q	91	HIS	2.1
1	J	136	LYS	2.1
1	F	2	PRO	2.1
1	P	171	PRO	2.1
1	D	221	ASN	2.1
1	B	142	GLU	2.0
1	K	255	THR	2.0
1	J	3	ALA	2.0
1	R	212	ILE	2.0
1	S	41	ILE	2.0
1	O	253	THR	2.0
1	P	214	GLY	2.0
1	H	197	PHE	2.0
1	N	167	ILE	2.0
1	R	193	LEU	2.0
1	E	220	SER	2.0
1	O	216	SER	2.0
1	Q	92	VAL	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers ⓘ

There are no such residues in this entry.