



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 31, 2016 – 08:18 PM GMT

PDB ID : 1JNB
Title : CONNECTOR PROTEIN FROM BACTERIOPHAGE PHI29
Authors : Simpson, A.A.; Leiman, P.G.; Tao, Y.; He, Y.; Badasso, M.O.; Jardine, P.J.;
Anderson, D.L.; Rossmann, M.G.
Deposited on : 2001-07-23
Resolution : 3.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

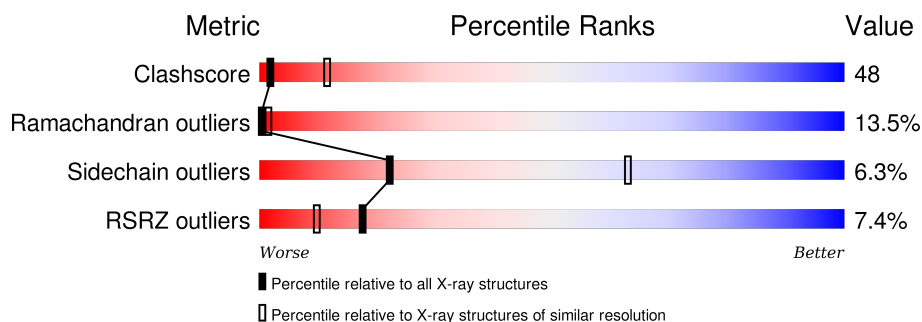
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	309	<div> <div>5%</div> <div> <div>37%</div> <div>32%</div> <div>12%</div> <div>17%</div> </div> </div>
1	B	309	<div> <div>7%</div> <div> <div>36%</div> <div>34%</div> <div>12%</div> <div>17%</div> </div> </div>
1	C	309	<div> <div>6%</div> <div> <div>36%</div> <div>34%</div> <div>12%</div> <div>17%</div> </div> </div>
1	D	309	<div> <div>6%</div> <div> <div>35%</div> <div>34%</div> <div>12%</div> <div>17%</div> </div> </div>
1	E	309	<div> <div>13%</div> <div> <div>37%</div> <div>33%</div> <div>12%</div> <div>17%</div> </div> </div>
1	F	309	<div> <div>5%</div> <div> <div>37%</div> <div>32%</div> <div>12%</div> <div>17%</div> </div> </div>
1	G	309	<div> <div>6%</div> <div> <div>37%</div> <div>33%</div> <div>12%</div> <div>17%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	H	309	<div><div>8%</div><div><div></div><div>35%</div><div>34%</div><div>12%</div><div>•</div><div>17%</div></div></div>
1	I	309	<div><div>6%</div><div><div></div><div>37%</div><div>33%</div><div>12%</div><div>•</div><div>17%</div></div></div>
1	J	309	<div><div>4%</div><div><div></div><div>36%</div><div>33%</div><div>12%</div><div>•</div><div>17%</div></div></div>
1	K	309	<div><div>4%</div><div><div></div><div>37%</div><div>33%</div><div>11%</div><div>•</div><div>17%</div></div></div>
1	L	309	<div><div>5%</div><div><div></div><div>38%</div><div>32%</div><div>12%</div><div>•</div><div>17%</div></div></div>

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 25236 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

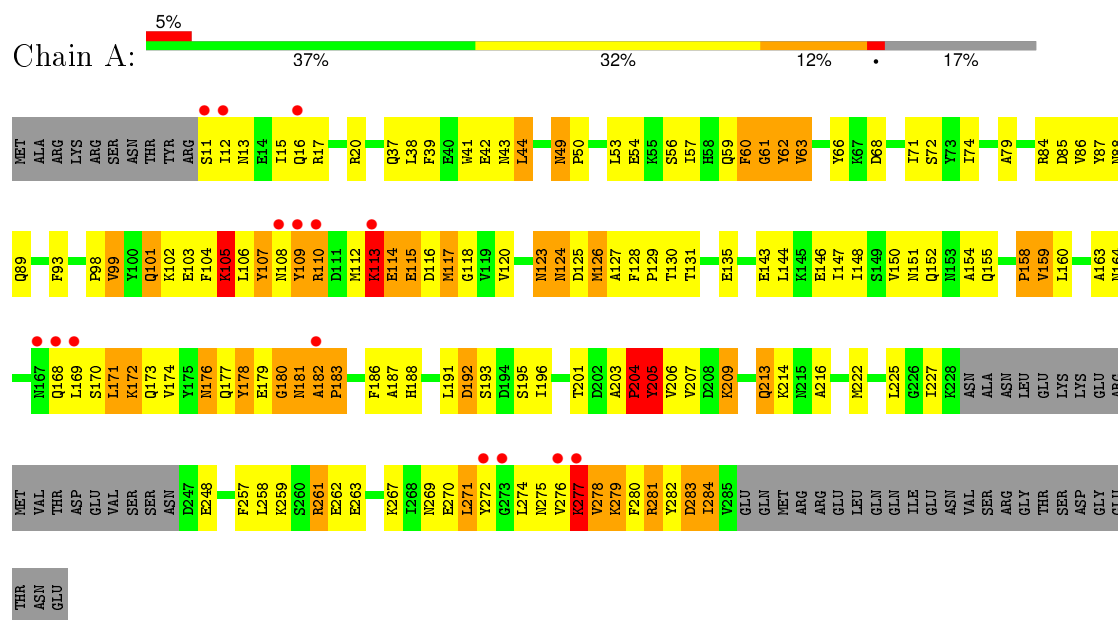
- Molecule 1 is a protein called UPPER COLLAR PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	B	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	C	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	D	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	E	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	F	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	G	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	H	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	I	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	J	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	K	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			
1	L	257	Total	C	N	O	S	0	0	0
			2103	1350	347	399	7			

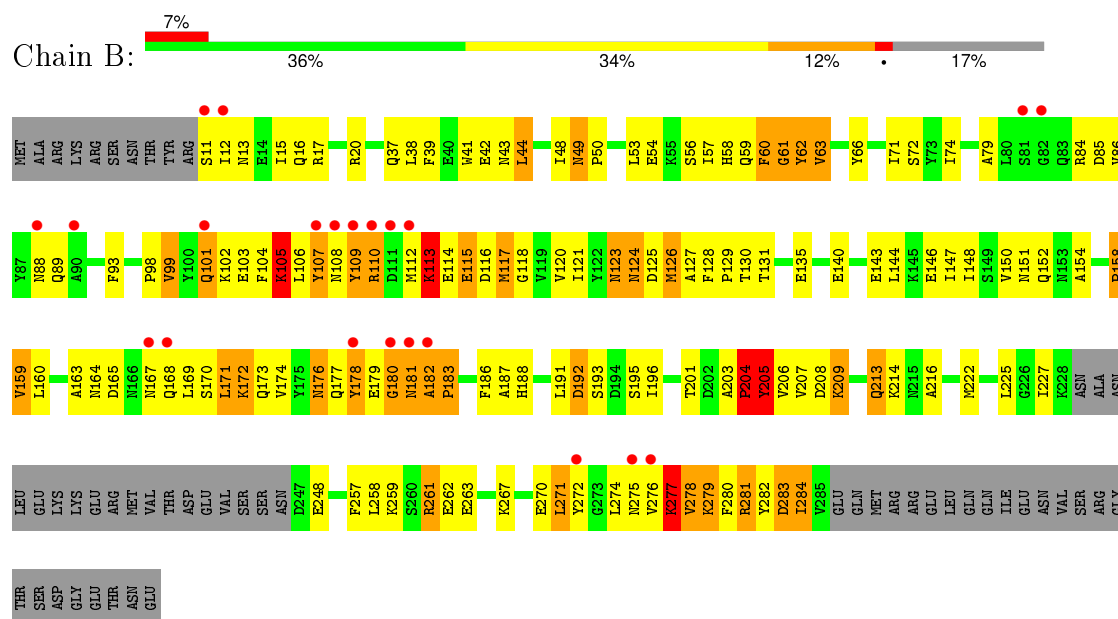
3 Residue-property plots

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.

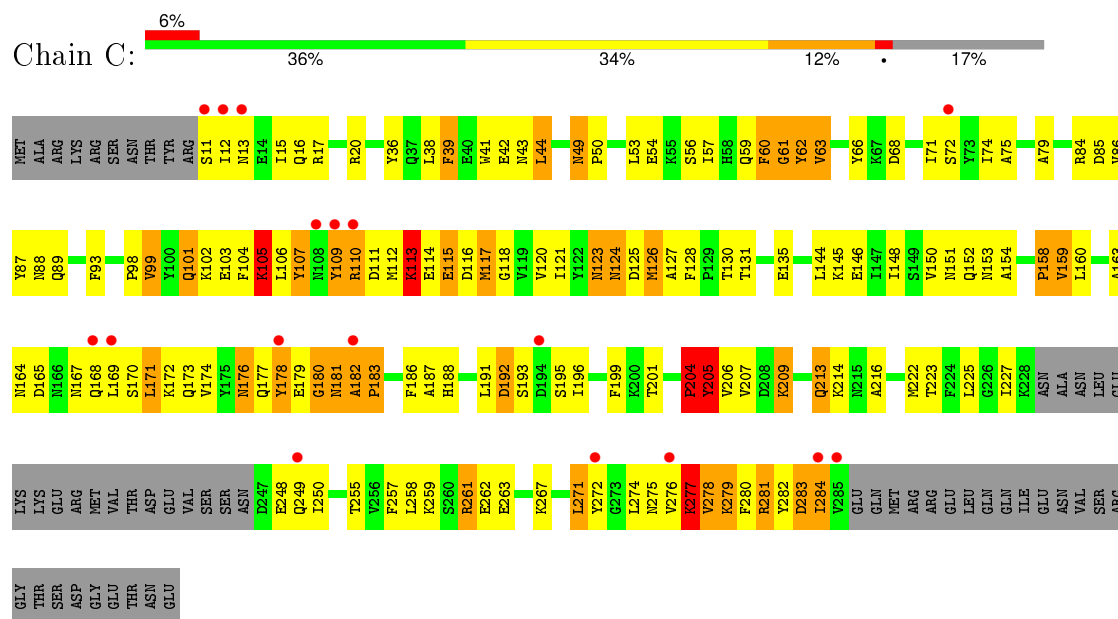
• Molecule 1: UPPER COLLAR PROTEIN



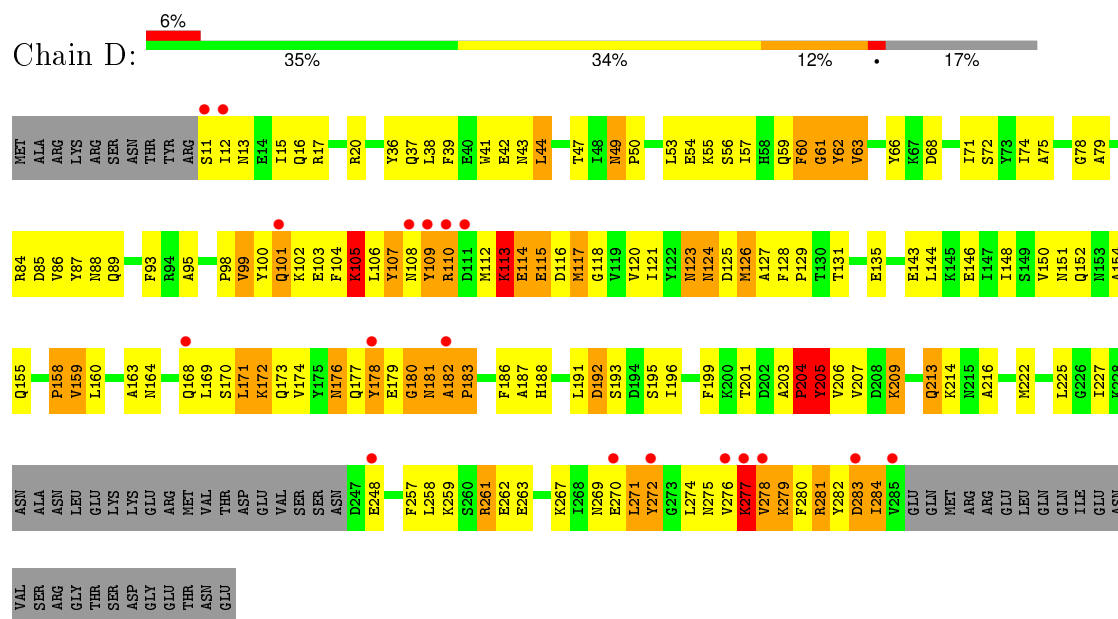
• Molecule 1: UPPER COLLAR PROTEIN



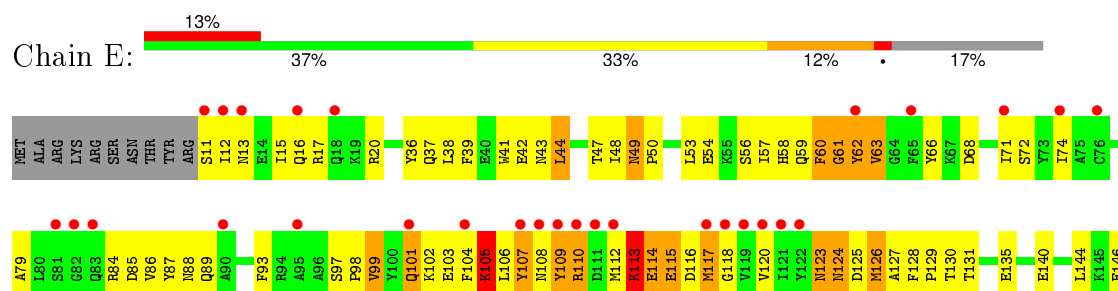
- Molecule 1: UPPER COLLAR PROTEIN

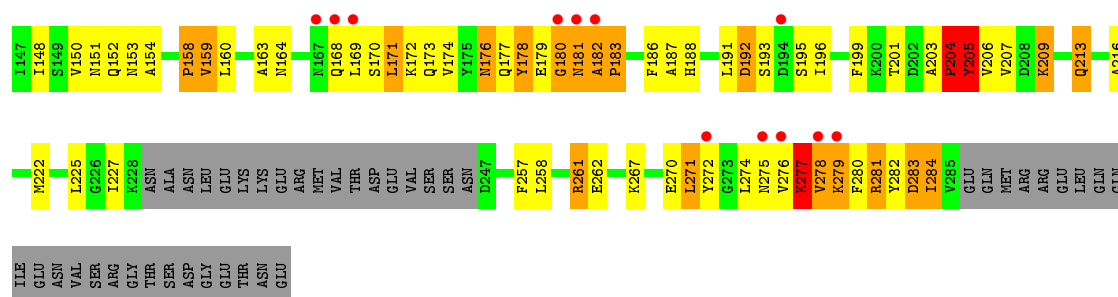


- Molecule 1: UPPER COLLAR PROTEIN

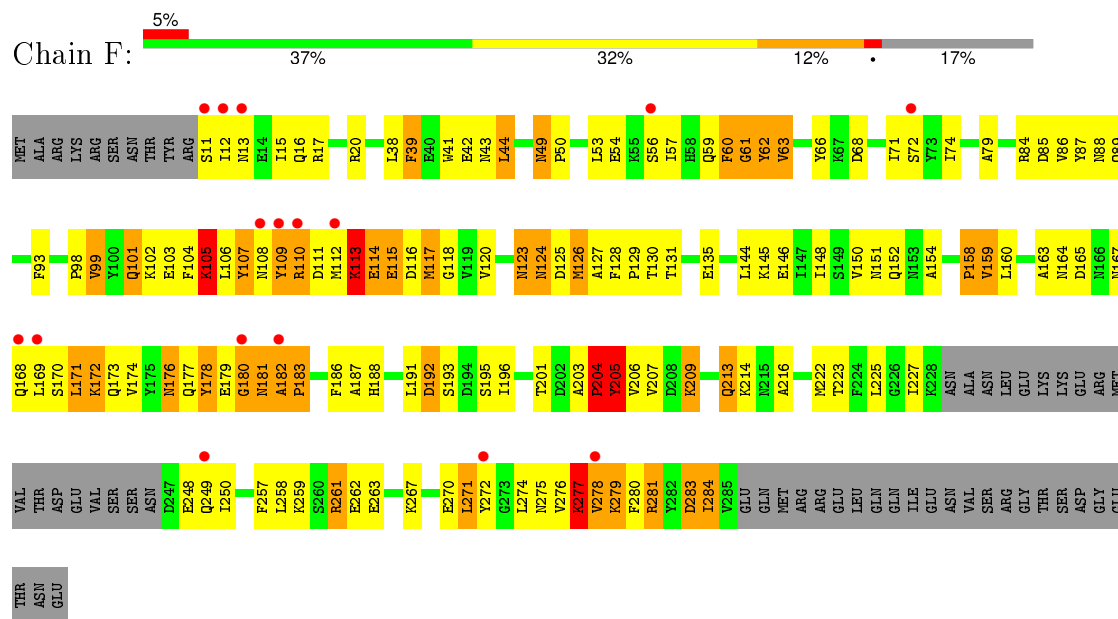


- Molecule 1: UPPER COLLAR PROTEIN

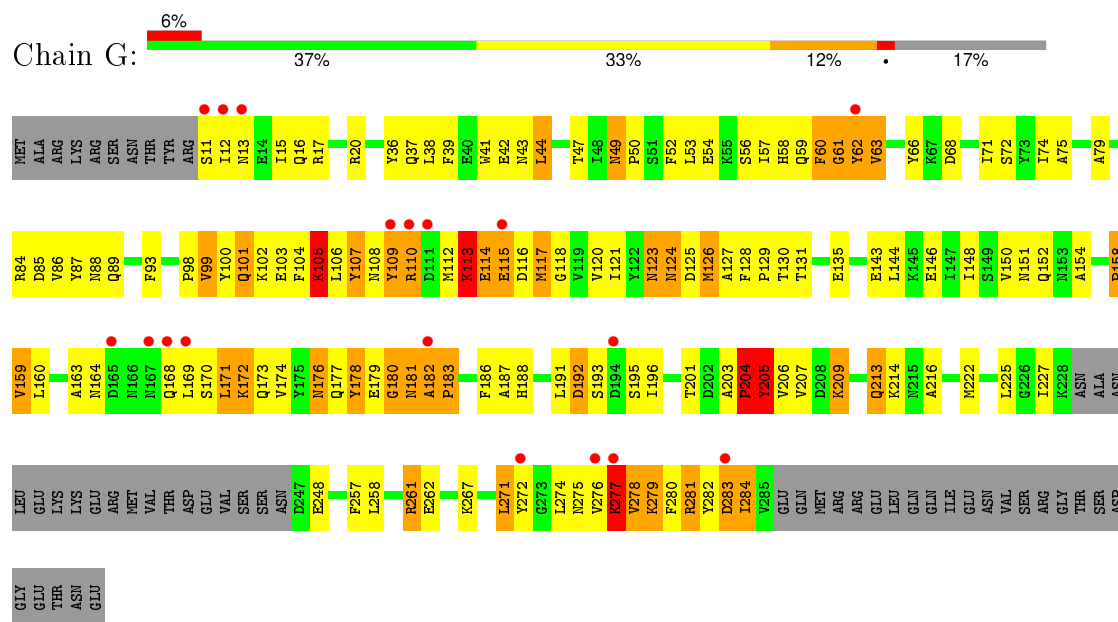




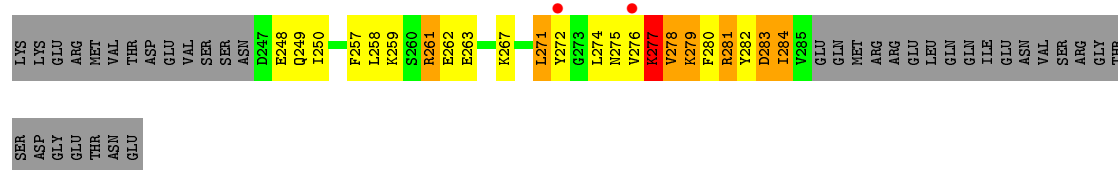
• Molecule 1: UPPER COLLAR PROTEIN



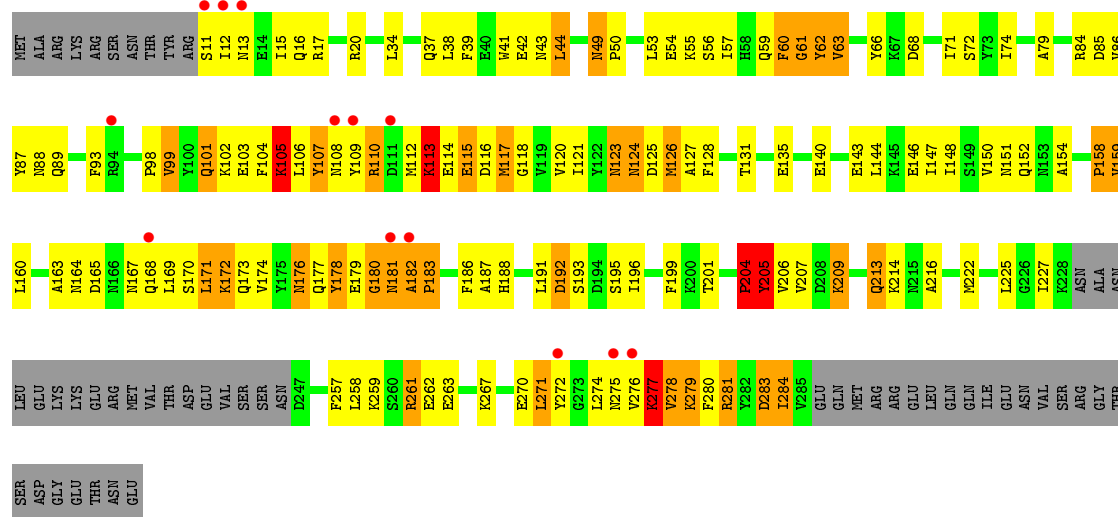
• Molecule 1: UPPER COLLAR PROTEIN



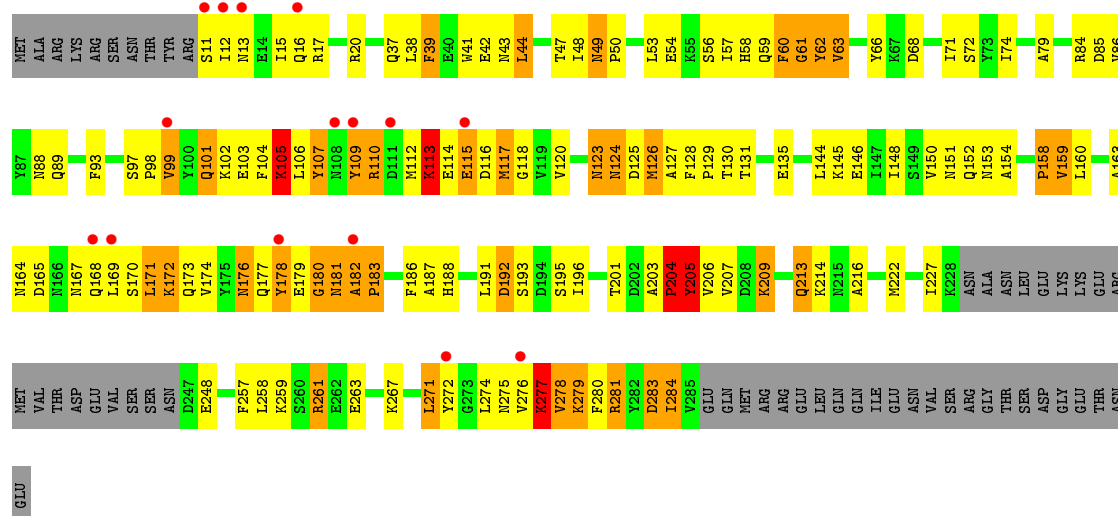
• Molecule 1: UPPER COLLAR PROTEIN



• Molecule 1: UPPER COLLAR PROTEIN



• Molecule 1: UPPER COLLAR PROTEIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.16Å 169.24Å 185.44Å 90.00° 114.10° 90.00°	Depositor
Resolution (Å)	9.00 – 3.20 60.59 – 3.19	Depositor EDS
% Data completeness (in resolution range)	98.5 (9.00-3.20) 98.7 (60.59-3.19)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.81 (at 3.19Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, R_{free}	0.284 , 0.301 0.282 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	DCC
Wilson B-factor (Å ²)	56.0	Xtriage
Anisotropy	0.428	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 56.7	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 81668 reflections	Xtriage
F_o, F_c correlation	0.82	EDS
Total number of atoms	25236	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.95% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.47	0/2150	0.72	2/2913 (0.1%)
1	B	0.46	0/2150	0.71	2/2913 (0.1%)
1	C	0.45	0/2150	0.71	2/2913 (0.1%)
1	D	0.44	0/2150	0.71	2/2913 (0.1%)
1	E	0.42	0/2150	0.70	2/2913 (0.1%)
1	F	0.44	0/2150	0.71	2/2913 (0.1%)
1	G	0.44	0/2150	0.71	2/2913 (0.1%)
1	H	0.44	0/2150	0.70	2/2913 (0.1%)
1	I	0.48	0/2150	0.71	2/2913 (0.1%)
1	J	0.47	0/2150	0.72	3/2913 (0.1%)
1	K	0.46	0/2150	0.71	2/2913 (0.1%)
1	L	0.47	0/2150	0.71	2/2913 (0.1%)
All	All	0.45	0/25800	0.71	25/34956 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	1
1	C	0	1
1	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
1	H	0	1
1	I	0	1
1	J	0	1
1	K	0	1
1	L	0	1
All	All	0	12

There are no bond length outliers.

All (25) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	J	105	LYS	N-CA-C	-5.90	95.08	111.00
1	A	105	LYS	N-CA-C	-5.87	95.16	111.00
1	E	105	LYS	N-CA-C	-5.84	95.22	111.00
1	K	105	LYS	N-CA-C	-5.82	95.29	111.00
1	C	105	LYS	N-CA-C	-5.81	95.31	111.00
1	F	105	LYS	N-CA-C	-5.81	95.31	111.00
1	G	105	LYS	N-CA-C	-5.81	95.32	111.00
1	B	105	LYS	N-CA-C	-5.79	95.36	111.00
1	D	105	LYS	N-CA-C	-5.79	95.36	111.00
1	L	105	LYS	N-CA-C	-5.79	95.38	111.00
1	I	105	LYS	N-CA-C	-5.78	95.39	111.00
1	H	105	LYS	N-CA-C	-5.75	95.47	111.00
1	L	158	PRO	N-CA-C	-5.62	97.49	112.10
1	C	158	PRO	N-CA-C	-5.61	97.52	112.10
1	H	158	PRO	N-CA-C	-5.56	97.64	112.10
1	E	158	PRO	N-CA-C	-5.52	97.76	112.10
1	F	158	PRO	N-CA-C	-5.45	97.93	112.10
1	K	158	PRO	N-CA-C	-5.40	98.05	112.10
1	D	158	PRO	N-CA-C	-5.40	98.06	112.10
1	B	158	PRO	N-CA-C	-5.39	98.09	112.10
1	G	158	PRO	N-CA-C	-5.37	98.13	112.10
1	A	158	PRO	N-CA-C	-5.32	98.28	112.10
1	I	158	PRO	N-CA-C	-5.29	98.34	112.10
1	J	158	PRO	N-CA-C	-5.24	98.46	112.10
1	J	157	THR	N-CA-C	5.05	124.65	111.00

There are no chirality outliers.

All (12) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	205	TYR	Sidechain
1	B	205	TYR	Sidechain
1	C	205	TYR	Sidechain
1	D	205	TYR	Sidechain
1	E	205	TYR	Sidechain
1	F	205	TYR	Sidechain
1	G	205	TYR	Sidechain
1	H	205	TYR	Sidechain
1	I	205	TYR	Sidechain
1	J	205	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	K	205	TYR	Sidechain
1	L	205	TYR	Sidechain

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2103	0	2052	221	0
1	B	2103	0	2052	226	0
1	C	2103	0	2052	250	0
1	D	2103	0	2052	255	1
1	E	2103	0	2052	211	0
1	F	2103	0	2052	219	0
1	G	2103	0	2052	239	0
1	H	2103	0	2052	218	0
1	I	2103	0	2052	220	1
1	J	2103	0	2052	224	0
1	K	2103	0	2052	214	0
1	L	2103	0	2052	209	0
All	All	25236	0	24624	2372	1

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 48.

All (2372) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:VAL:HG11	1:L:201:THR:HG23	1.25	1.18
1:G:87:TYR:OH	1:H:48:ILE:HA	1.43	1.18
1:H:201:THR:HG23	1:I:159:VAL:HG11	1.29	1.12
1:D:87:TYR:OH	1:E:48:ILE:HA	1.50	1.10
1:C:110:ARG:HH22	1:D:72:SER:HB2	1.12	1.09
1:I:201:THR:HG23	1:J:159:VAL:HG11	1.29	1.09
1:C:201:THR:HG23	1:D:159:VAL:HG11	1.31	1.08
1:F:201:THR:HG23	1:G:159:VAL:HG11	1.37	1.07
1:K:201:THR:HG23	1:L:159:VAL:HG11	1.35	1.05

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:163:ALA:HB3	1:G:187:ALA:HB2	1.41	1.03
1:K:11:SER:HB3	1:L:176:ASN:HD22	1.20	1.02
1:B:123:ASN:HD21	1:B:257:PHE:HD2	1.06	1.02
1:G:123:ASN:HD21	1:G:257:PHE:HD2	1.08	1.02
1:A:11:SER:HB3	1:B:176:ASN:HD22	1.20	1.01
1:E:201:THR:HG23	1:F:159:VAL:HG11	1.38	1.00
1:L:123:ASN:HD21	1:L:257:PHE:HD2	1.05	0.99
1:L:169:LEU:HD22	1:L:173:GLN:HE22	1.29	0.98
1:F:110:ARG:HH22	1:G:72:SER:HB2	1.25	0.98
1:D:123:ASN:HD21	1:D:257:PHE:HD2	1.07	0.98
1:K:87:TYR:OH	1:L:48:ILE:HA	1.63	0.98
1:G:169:LEU:HD22	1:G:173:GLN:HE22	1.28	0.97
1:J:123:ASN:HD21	1:J:257:PHE:HD2	1.08	0.97
1:K:11:SER:HB3	1:L:176:ASN:ND2	1.78	0.97
1:C:163:ALA:HB3	1:D:187:ALA:HB2	1.47	0.97
1:K:123:ASN:HD21	1:K:257:PHE:HD2	1.06	0.97
1:B:169:LEU:HD22	1:B:173:GLN:HE22	1.29	0.96
1:D:169:LEU:HD22	1:D:173:GLN:HE22	1.30	0.96
1:I:123:ASN:HD21	1:I:257:PHE:HD2	1.08	0.96
1:I:163:ALA:HB3	1:J:187:ALA:HB2	1.47	0.96
1:H:169:LEU:HD22	1:H:173:GLN:HE22	1.31	0.96
1:C:169:LEU:HD22	1:C:173:GLN:HE22	1.30	0.96
1:E:169:LEU:HD22	1:E:173:GLN:HE22	1.28	0.95
1:H:163:ALA:HB3	1:I:187:ALA:HB2	1.45	0.95
1:A:201:THR:HG23	1:B:159:VAL:HG11	1.46	0.95
1:J:201:THR:HG23	1:K:159:VAL:HG11	1.48	0.95
1:B:201:THR:HG23	1:C:159:VAL:HG11	1.48	0.95
1:A:123:ASN:HD21	1:A:257:PHE:HD2	1.07	0.95
1:D:201:THR:HG23	1:E:159:VAL:HG11	1.46	0.95
1:J:163:ALA:HB3	1:K:187:ALA:HB2	1.44	0.95
1:C:110:ARG:NH2	1:D:72:SER:HB2	1.82	0.95
1:E:123:ASN:HD21	1:E:257:PHE:HD2	1.07	0.94
1:G:163:ALA:HB3	1:H:187:ALA:HB2	1.49	0.94
1:A:187:ALA:HB2	1:L:163:ALA:HB3	1.49	0.94
1:D:163:ALA:HB3	1:E:187:ALA:HB2	1.49	0.93
1:G:201:THR:HG23	1:H:159:VAL:HG11	1.51	0.93
1:K:169:LEU:HD22	1:K:173:GLN:HE22	1.30	0.93
1:C:123:ASN:HD21	1:C:257:PHE:HD2	1.08	0.93
1:J:169:LEU:HD22	1:J:173:GLN:HE22	1.30	0.93
1:H:71:ILE:HB	1:H:74:ILE:HD11	1.50	0.93
1:H:123:ASN:HD21	1:H:257:PHE:HD2	1.07	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:163:ALA:HB3	1:C:187:ALA:HB2	1.47	0.93
1:I:169:LEU:HD22	1:I:173:GLN:HE22	1.33	0.92
1:A:169:LEU:HD22	1:A:173:GLN:HE22	1.31	0.92
1:E:71:ILE:HB	1:E:74:ILE:HD11	1.51	0.92
1:B:71:ILE:HB	1:B:74:ILE:HD11	1.52	0.92
1:F:71:ILE:HB	1:F:74:ILE:HD11	1.52	0.92
1:F:169:LEU:HD22	1:F:173:GLN:HE22	1.34	0.91
1:K:163:ALA:HB3	1:L:187:ALA:HB2	1.49	0.91
1:E:163:ALA:HB3	1:F:187:ALA:HB2	1.49	0.91
1:A:163:ALA:HB3	1:B:187:ALA:HB2	1.52	0.91
1:J:11:SER:HB3	1:K:176:ASN:HD22	1.33	0.91
1:F:123:ASN:HD21	1:F:257:PHE:HD2	1.07	0.91
1:G:71:ILE:HB	1:G:74:ILE:HD11	1.51	0.91
1:C:71:ILE:HB	1:C:74:ILE:HD11	1.50	0.91
1:K:71:ILE:HB	1:K:74:ILE:HD11	1.53	0.91
1:L:71:ILE:HB	1:L:74:ILE:HD11	1.51	0.91
1:A:71:ILE:HB	1:A:74:ILE:HD11	1.50	0.91
1:D:71:ILE:HB	1:D:74:ILE:HD11	1.51	0.89
1:A:11:SER:HB3	1:B:176:ASN:ND2	1.87	0.89
1:B:11:SER:HB3	1:C:176:ASN:ND2	1.88	0.88
1:C:248:GLU:OE2	1:D:227:ILE:HA	1.73	0.88
1:J:71:ILE:HB	1:J:74:ILE:HD11	1.53	0.88
1:I:71:ILE:HB	1:I:74:ILE:HD11	1.54	0.87
1:E:192:ASP:O	1:E:195:SER:HB3	1.75	0.86
1:K:192:ASP:O	1:K:195:SER:HB3	1.76	0.85
1:L:169:LEU:HD22	1:L:173:GLN:NE2	1.92	0.85
1:L:192:ASP:O	1:L:195:SER:HB3	1.77	0.85
1:C:248:GLU:HG3	1:D:227:ILE:CG2	2.06	0.84
1:D:154:ALA:HA	1:F:182:ALA:HB2	1.59	0.84
1:G:169:LEU:HD22	1:G:173:GLN:NE2	1.91	0.84
1:B:11:SER:HB3	1:C:176:ASN:HD22	1.42	0.84
1:A:192:ASP:O	1:A:195:SER:HB3	1.78	0.84
1:E:169:LEU:HD22	1:E:173:GLN:NE2	1.91	0.84
1:B:248:GLU:HB3	1:C:282:TYR:CZ	2.11	0.84
1:F:201:THR:O	1:F:201:THR:HG22	1.78	0.84
1:B:169:LEU:HD22	1:B:173:GLN:NE2	1.92	0.84
1:B:154:ALA:HA	1:D:182:ALA:HB2	1.58	0.84
1:E:201:THR:HG22	1:E:201:THR:O	1.77	0.84
1:G:192:ASP:O	1:G:195:SER:HB3	1.77	0.84
1:B:192:ASP:O	1:B:195:SER:HB3	1.78	0.83
1:C:248:GLU:HG3	1:D:227:ILE:HG23	1.58	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:169:LEU:HD22	1:J:173:GLN:NE2	1.92	0.83
1:H:192:ASP:O	1:H:195:SER:HB3	1.78	0.83
1:C:169:LEU:HD22	1:C:173:GLN:NE2	1.93	0.83
1:H:169:LEU:HD22	1:H:173:GLN:NE2	1.93	0.83
1:A:169:LEU:HD22	1:A:173:GLN:NE2	1.94	0.82
1:K:169:LEU:HD22	1:K:173:GLN:NE2	1.93	0.82
1:I:148:ILE:O	1:I:152:GLN:HG3	1.77	0.82
1:J:192:ASP:O	1:J:195:SER:HB3	1.79	0.82
1:D:192:ASP:O	1:D:195:SER:HB3	1.77	0.82
1:H:201:THR:HG22	1:H:201:THR:O	1.77	0.82
1:C:66:TYR:HB2	1:C:104:PHE:CE2	2.15	0.82
1:D:169:LEU:HD22	1:D:173:GLN:NE2	1.93	0.82
1:J:66:TYR:HB2	1:J:104:PHE:CE2	2.15	0.82
1:F:66:TYR:HB2	1:F:104:PHE:CE2	2.15	0.82
1:H:66:TYR:HB2	1:H:104:PHE:CE2	2.14	0.82
1:C:192:ASP:O	1:C:195:SER:HB3	1.78	0.82
1:L:66:TYR:HB2	1:L:104:PHE:CE2	2.14	0.82
1:G:201:THR:HG22	1:G:201:THR:O	1.79	0.81
1:D:117:MET:HG3	1:D:118:GLY:H	1.45	0.81
1:D:148:ILE:O	1:D:152:GLN:HG3	1.80	0.81
1:A:176:ASN:HD22	1:L:11:SER:HB3	1.43	0.81
1:F:192:ASP:O	1:F:195:SER:HB3	1.79	0.81
1:A:66:TYR:HB2	1:A:104:PHE:CE2	2.15	0.81
1:D:87:TYR:OH	1:E:47:THR:O	1.97	0.81
1:J:117:MET:HG3	1:J:118:GLY:H	1.45	0.81
1:K:66:TYR:HB2	1:K:104:PHE:CE2	2.15	0.81
1:F:148:ILE:O	1:F:152:GLN:HG3	1.79	0.81
1:E:66:TYR:HB2	1:E:104:PHE:CE2	2.15	0.81
1:J:275:ASN:O	1:J:277:LYS:HG3	1.81	0.81
1:D:66:TYR:HB2	1:D:104:PHE:CE2	2.16	0.81
1:L:275:ASN:O	1:L:277:LYS:HG3	1.81	0.81
1:A:117:MET:HG3	1:A:118:GLY:H	1.45	0.81
1:I:192:ASP:O	1:I:195:SER:HB3	1.81	0.80
1:K:201:THR:HG22	1:K:201:THR:O	1.82	0.80
1:B:66:TYR:HB2	1:B:104:PHE:CE2	2.15	0.80
1:I:66:TYR:HB2	1:I:104:PHE:CE2	2.16	0.80
1:I:169:LEU:HD22	1:I:173:GLN:NE2	1.96	0.80
1:D:171:LEU:C	1:D:173:GLN:H	1.85	0.80
1:C:201:THR:HG22	1:C:201:THR:O	1.79	0.80
1:A:126:MET:O	1:A:128:PHE:N	2.15	0.80
1:F:169:LEU:HD22	1:F:173:GLN:NE2	1.96	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:117:MET:HG3	1:G:118:GLY:H	1.46	0.80
1:L:201:THR:O	1:L:201:THR:HG22	1.81	0.80
1:I:275:ASN:O	1:I:277:LYS:HG3	1.82	0.80
1:C:248:GLU:CD	1:D:227:ILE:HG23	2.02	0.79
1:J:171:LEU:C	1:J:173:GLN:H	1.85	0.79
1:K:117:MET:HG3	1:K:118:GLY:H	1.47	0.79
1:G:66:TYR:HB2	1:G:104:PHE:CE2	2.17	0.79
1:G:171:LEU:C	1:G:173:GLN:H	1.84	0.79
1:C:126:MET:O	1:C:128:PHE:N	2.15	0.79
1:I:171:LEU:C	1:I:173:GLN:H	1.86	0.79
1:B:201:THR:HG22	1:B:201:THR:O	1.81	0.79
1:B:148:ILE:O	1:B:152:GLN:HG3	1.82	0.79
1:H:148:ILE:O	1:H:152:GLN:HG3	1.83	0.79
1:C:248:GLU:CG	1:D:227:ILE:HG23	2.12	0.79
1:L:117:MET:HG3	1:L:118:GLY:H	1.47	0.79
1:B:275:ASN:O	1:B:277:LYS:HG3	1.83	0.79
1:K:148:ILE:O	1:K:152:GLN:HG3	1.83	0.79
1:B:117:MET:HG3	1:B:118:GLY:H	1.47	0.79
1:E:171:LEU:C	1:E:173:GLN:H	1.86	0.79
1:J:148:ILE:O	1:J:152:GLN:HG3	1.81	0.79
1:K:277:LYS:HD2	1:K:278:VAL:N	1.98	0.79
1:H:171:LEU:C	1:H:173:GLN:H	1.84	0.78
1:F:248:GLU:HG3	1:G:227:ILE:HG23	1.65	0.78
1:L:125:ASP:O	1:L:126:MET:HE3	1.82	0.78
1:L:148:ILE:O	1:L:152:GLN:HG3	1.82	0.78
1:A:182:ALA:HB2	1:K:154:ALA:HA	1.65	0.78
1:F:171:LEU:C	1:F:173:GLN:H	1.84	0.78
1:L:277:LYS:HD2	1:L:278:VAL:N	1.98	0.78
1:G:277:LYS:HD2	1:G:278:VAL:N	1.98	0.78
1:F:277:LYS:HD2	1:F:278:VAL:N	1.98	0.78
1:I:277:LYS:HD2	1:I:278:VAL:N	1.98	0.78
1:D:277:LYS:HD2	1:D:278:VAL:N	1.98	0.78
1:A:171:LEU:C	1:A:173:GLN:H	1.86	0.78
1:C:117:MET:HG3	1:C:118:GLY:H	1.49	0.78
1:F:126:MET:O	1:F:128:PHE:N	2.17	0.78
1:D:148:ILE:HG23	1:D:207:VAL:HG13	1.66	0.78
1:C:86:VAL:HA	1:D:99:VAL:HG11	1.64	0.78
1:D:11:SER:HB3	1:E:176:ASN:HD22	1.49	0.78
1:G:148:ILE:O	1:G:152:GLN:HG3	1.82	0.78
1:E:117:MET:HG3	1:E:118:GLY:H	1.47	0.78
1:H:117:MET:HG3	1:H:118:GLY:H	1.49	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ILE:O	1:A:152:GLN:HG3	1.84	0.78
1:C:87:TYR:HE1	1:D:75:ALA:O	1.66	0.78
1:F:163:ALA:HB3	1:G:187:ALA:CB	2.14	0.77
1:K:171:LEU:C	1:K:173:GLN:H	1.86	0.77
1:E:275:ASN:O	1:E:277:LYS:HG3	1.85	0.77
1:C:277:LYS:HD2	1:C:278:VAL:N	1.99	0.77
1:G:87:TYR:CD2	1:H:49:ASN:HB2	2.20	0.77
1:E:277:LYS:HD2	1:E:278:VAL:N	1.98	0.77
1:F:275:ASN:O	1:F:277:LYS:HG3	1.84	0.77
1:G:11:SER:HB3	1:H:176:ASN:HD22	1.50	0.77
1:A:275:ASN:O	1:A:277:LYS:HG3	1.84	0.77
1:J:11:SER:HB3	1:K:176:ASN:ND2	1.99	0.77
1:C:275:ASN:O	1:C:277:LYS:HG3	1.84	0.77
1:C:148:ILE:O	1:C:152:GLN:HG3	1.85	0.77
1:I:201:THR:HG22	1:I:201:THR:O	1.84	0.76
1:C:154:ALA:HA	1:E:182:ALA:HB2	1.66	0.76
1:J:201:THR:HG22	1:J:201:THR:O	1.85	0.76
1:D:11:SER:HB3	1:E:176:ASN:ND2	2.01	0.76
1:H:275:ASN:O	1:H:277:LYS:HG3	1.85	0.76
1:F:248:GLU:HG3	1:G:227:ILE:CG2	2.15	0.76
1:B:277:LYS:HD2	1:B:278:VAL:N	2.00	0.76
1:E:148:ILE:O	1:E:152:GLN:HG3	1.84	0.76
1:H:277:LYS:HD2	1:H:278:VAL:N	2.01	0.76
1:F:117:MET:HG3	1:F:118:GLY:H	1.48	0.76
1:B:171:LEU:C	1:B:173:GLN:H	1.85	0.76
1:K:275:ASN:O	1:K:277:LYS:HG3	1.85	0.75
1:A:277:LYS:HD2	1:A:278:VAL:N	2.01	0.75
1:J:37:GLN:O	1:J:281:ARG:HD2	1.87	0.75
1:C:171:LEU:C	1:C:173:GLN:H	1.84	0.75
1:H:125:ASP:O	1:H:126:MET:HE3	1.85	0.75
1:A:201:THR:O	1:A:201:THR:HG22	1.85	0.75
1:D:275:ASN:O	1:D:277:LYS:HG3	1.87	0.75
1:C:163:ALA:HB3	1:D:187:ALA:CB	2.17	0.75
1:D:201:THR:O	1:D:201:THR:HG22	1.85	0.75
1:H:148:ILE:HG23	1:H:207:VAL:HG13	1.69	0.75
1:I:150:VAL:HG13	1:K:180:GLY:HA2	1.69	0.75
1:E:125:ASP:O	1:E:126:MET:HE3	1.86	0.74
1:A:154:ALA:HA	1:C:182:ALA:HB2	1.69	0.74
1:I:117:MET:HG3	1:I:118:GLY:H	1.51	0.74
1:F:110:ARG:NH2	1:G:72:SER:HB2	2.02	0.74
1:G:148:ILE:HG23	1:G:207:VAL:HG13	1.68	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:11:SER:HB3	1:H:176:ASN:ND2	2.03	0.74
1:I:148:ILE:HG23	1:I:207:VAL:HG13	1.68	0.74
1:H:163:ALA:HB3	1:I:187:ALA:CB	2.18	0.74
1:F:124:ASN:HD21	1:F:128:PHE:HB2	1.52	0.74
1:G:275:ASN:O	1:G:277:LYS:HG3	1.87	0.74
1:L:171:LEU:C	1:L:173:GLN:H	1.86	0.73
1:G:154:ALA:HA	1:I:182:ALA:HB2	1.70	0.73
1:B:37:GLN:O	1:B:281:ARG:HD2	1.87	0.73
1:J:277:LYS:HD2	1:J:278:VAL:N	2.04	0.73
1:C:150:VAL:HG13	1:E:180:GLY:HA2	1.70	0.73
1:B:148:ILE:HG23	1:B:207:VAL:HG13	1.69	0.73
1:E:163:ALA:HB3	1:F:187:ALA:CB	2.19	0.73
1:A:148:ILE:HG23	1:A:207:VAL:HG13	1.71	0.73
1:L:126:MET:O	1:L:128:PHE:N	2.21	0.73
1:H:171:LEU:O	1:H:173:GLN:N	2.22	0.73
1:F:248:GLU:OE2	1:G:227:ILE:HA	1.89	0.72
1:J:150:VAL:HG13	1:L:180:GLY:HA2	1.70	0.72
1:D:87:TYR:CD2	1:E:49:ASN:HB2	2.24	0.72
1:D:213:GLN:HG3	1:E:207:VAL:HG11	1.70	0.72
1:L:276:VAL:O	1:L:278:VAL:HG23	1.88	0.72
1:L:148:ILE:HG23	1:L:207:VAL:HG13	1.70	0.72
1:A:159:VAL:CG1	1:L:201:THR:HG23	2.14	0.72
1:B:182:ALA:HB2	1:L:154:ALA:HA	1.71	0.72
1:C:171:LEU:O	1:C:173:GLN:N	2.22	0.72
1:D:171:LEU:O	1:D:173:GLN:N	2.23	0.72
1:C:124:ASN:HD21	1:C:128:PHE:HB2	1.53	0.72
1:A:276:VAL:O	1:A:278:VAL:HG23	1.90	0.72
1:F:87:TYR:HE1	1:G:75:ALA:O	1.73	0.72
1:K:276:VAL:O	1:K:278:VAL:HG23	1.91	0.71
1:F:171:LEU:O	1:F:173:GLN:N	2.22	0.71
1:J:148:ILE:HG23	1:J:207:VAL:HG13	1.72	0.71
1:D:163:ALA:HB3	1:E:187:ALA:CB	2.19	0.71
1:G:87:TYR:OH	1:H:47:THR:O	2.07	0.71
1:A:125:ASP:O	1:A:126:MET:HB2	1.91	0.71
1:J:163:ALA:HB3	1:K:187:ALA:CB	2.21	0.71
1:J:276:VAL:O	1:J:278:VAL:HG23	1.90	0.71
1:B:180:GLY:HA2	1:L:150:VAL:HG13	1.71	0.71
1:C:144:LEU:HD21	1:D:152:GLN:NE2	2.06	0.71
1:I:276:VAL:O	1:I:278:VAL:HG23	1.90	0.71
1:K:148:ILE:HG23	1:K:207:VAL:HG13	1.70	0.71
1:G:276:VAL:O	1:G:278:VAL:HG23	1.91	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:159:VAL:HG11	1:L:201:THR:CG2	2.15	0.70
1:G:171:LEU:O	1:G:173:GLN:N	2.23	0.70
1:A:213:GLN:HG3	1:B:207:VAL:HG11	1.73	0.70
1:D:276:VAL:O	1:D:278:VAL:HG23	1.91	0.70
1:E:148:ILE:HG23	1:E:207:VAL:HG13	1.71	0.70
1:C:125:ASP:O	1:C:126:MET:HB2	1.91	0.70
1:D:125:ASP:O	1:D:126:MET:HB2	1.91	0.70
1:K:87:TYR:OH	1:L:47:THR:O	2.07	0.70
1:F:57:ILE:CG2	1:F:123:ASN:HB2	2.22	0.70
1:C:263:GLU:OE1	1:D:50:PRO:HG2	1.92	0.70
1:A:124:ASN:HD21	1:A:128:PHE:HB2	1.56	0.70
1:F:86:VAL:HA	1:G:99:VAL:HG11	1.73	0.70
1:A:57:ILE:CG2	1:A:123:ASN:HB2	2.22	0.70
1:F:276:VAL:O	1:F:278:VAL:HG23	1.92	0.70
1:C:276:VAL:O	1:C:278:VAL:HG23	1.91	0.70
1:G:213:GLN:HG3	1:H:207:VAL:HG11	1.73	0.69
1:G:37:GLN:O	1:G:281:ARG:HD2	1.91	0.69
1:L:171:LEU:O	1:L:173:GLN:N	2.26	0.69
1:A:71:ILE:CB	1:A:74:ILE:HD11	2.23	0.69
1:D:154:ALA:CA	1:F:182:ALA:HB2	2.23	0.69
1:B:276:VAL:O	1:B:278:VAL:HG23	1.93	0.69
1:H:276:VAL:O	1:H:278:VAL:HG23	1.91	0.69
1:H:201:THR:CG2	1:I:159:VAL:HG11	2.17	0.69
1:B:171:LEU:O	1:B:173:GLN:N	2.25	0.69
1:F:148:ILE:HG23	1:F:207:VAL:HG13	1.73	0.69
1:J:213:GLN:HG3	1:K:207:VAL:HG11	1.75	0.69
1:I:171:LEU:O	1:I:173:GLN:N	2.25	0.69
1:D:71:ILE:CB	1:D:74:ILE:HD11	2.23	0.69
1:G:163:ALA:HB3	1:H:187:ALA:CB	2.22	0.69
1:E:276:VAL:O	1:E:278:VAL:HG23	1.92	0.69
1:E:171:LEU:O	1:E:173:GLN:N	2.25	0.69
1:C:66:TYR:HB2	1:C:104:PHE:CZ	2.28	0.69
1:G:125:ASP:O	1:G:126:MET:HB2	1.93	0.69
1:I:163:ALA:HB3	1:J:187:ALA:CB	2.23	0.69
1:J:71:ILE:CB	1:J:74:ILE:HD11	2.23	0.69
1:L:125:ASP:O	1:L:126:MET:HB2	1.92	0.69
1:C:57:ILE:CG2	1:C:123:ASN:HB2	2.22	0.69
1:H:150:VAL:HG13	1:J:180:GLY:HA2	1.74	0.69
1:K:66:TYR:HB2	1:K:104:PHE:CZ	2.29	0.68
1:I:125:ASP:O	1:I:126:MET:HB2	1.91	0.68
1:C:71:ILE:CB	1:C:74:ILE:HD11	2.23	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:66:TYR:HB2	1:E:104:PHE:CZ	2.29	0.68
1:A:171:LEU:O	1:A:173:GLN:N	2.27	0.68
1:F:125:ASP:O	1:F:126:MET:HB2	1.91	0.68
1:B:125:ASP:O	1:B:126:MET:HB2	1.92	0.68
1:F:248:GLU:CG	1:G:227:ILE:HG23	2.23	0.68
1:G:71:ILE:CB	1:G:74:ILE:HD11	2.23	0.68
1:L:71:ILE:CB	1:L:74:ILE:HD11	2.23	0.68
1:K:201:THR:HG23	1:L:159:VAL:CG1	2.19	0.68
1:H:57:ILE:CG2	1:H:123:ASN:HB2	2.23	0.68
1:H:125:ASP:O	1:H:126:MET:HB2	1.94	0.68
1:B:107:TYR:HB3	1:B:267:LYS:HD3	1.76	0.68
1:C:107:TYR:HB3	1:C:267:LYS:HD3	1.75	0.68
1:J:126:MET:O	1:J:128:PHE:N	2.24	0.68
1:K:171:LEU:O	1:K:173:GLN:N	2.27	0.68
1:H:66:TYR:HB2	1:H:104:PHE:CZ	2.28	0.68
1:G:16:GLN:O	1:G:20:ARG:HG3	1.94	0.68
1:G:107:TYR:HB3	1:G:267:LYS:HD3	1.76	0.68
1:J:274:LEU:O	1:J:274:LEU:HD13	1.94	0.68
1:L:57:ILE:CG2	1:L:123:ASN:HB2	2.23	0.68
1:J:57:ILE:CG2	1:J:123:ASN:HB2	2.24	0.68
1:E:125:ASP:O	1:E:126:MET:HB2	1.93	0.68
1:C:56:SER:HB3	1:C:63:VAL:HG22	1.76	0.68
1:J:66:TYR:HB2	1:J:104:PHE:CZ	2.29	0.68
1:H:71:ILE:CB	1:H:74:ILE:HD11	2.24	0.68
1:D:154:ALA:CB	1:F:182:ALA:HB2	2.24	0.68
1:F:66:TYR:HB2	1:F:104:PHE:CZ	2.29	0.68
1:C:148:ILE:HG23	1:C:207:VAL:HG13	1.76	0.68
1:H:201:THR:HG23	1:I:159:VAL:CG1	2.16	0.67
1:K:57:ILE:CG2	1:K:123:ASN:HB2	2.24	0.67
1:I:57:ILE:CG2	1:I:123:ASN:HB2	2.25	0.67
1:J:125:ASP:O	1:J:126:MET:HE2	1.94	0.67
1:E:57:ILE:CG2	1:E:123:ASN:HB2	2.24	0.67
1:J:171:LEU:O	1:J:173:GLN:N	2.26	0.67
1:E:71:ILE:CB	1:E:74:ILE:HD11	2.23	0.67
1:F:56:SER:HB3	1:F:63:VAL:HG22	1.76	0.67
1:F:107:TYR:HB3	1:F:267:LYS:HD3	1.75	0.67
1:F:248:GLU:CD	1:G:227:ILE:HG23	2.15	0.67
1:A:176:ASN:ND2	1:L:11:SER:HB3	2.08	0.67
1:I:107:TYR:HB3	1:I:267:LYS:HD3	1.76	0.67
1:D:38:LEU:O	1:D:39:PHE:HB2	1.91	0.67
1:G:57:ILE:CG2	1:G:123:ASN:HB2	2.24	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:66:TYR:HB2	1:D:104:PHE:CZ	2.30	0.67
1:G:66:TYR:HB2	1:G:104:PHE:CZ	2.29	0.67
1:A:207:VAL:HG11	1:L:213:GLN:HG3	1.77	0.67
1:L:179:GLU:O	1:L:181:ASN:OD1	2.13	0.67
1:K:201:THR:CG2	1:L:159:VAL:HG11	2.20	0.67
1:D:107:TYR:HB3	1:D:267:LYS:HD3	1.75	0.67
1:B:16:GLN:O	1:B:20:ARG:HG3	1.94	0.67
1:K:125:ASP:O	1:K:126:MET:HB2	1.93	0.67
1:D:57:ILE:CG2	1:D:123:ASN:HB2	2.24	0.67
1:B:163:ALA:HB3	1:C:187:ALA:CB	2.21	0.67
1:E:107:TYR:HB3	1:E:267:LYS:HD3	1.77	0.67
1:A:163:ALA:HB3	1:B:187:ALA:CB	2.24	0.67
1:I:144:LEU:HD21	1:J:152:GLN:NE2	2.10	0.67
1:B:57:ILE:CG2	1:B:123:ASN:HB2	2.25	0.67
1:J:125:ASP:O	1:J:126:MET:HB2	1.93	0.67
1:C:179:GLU:O	1:C:181:ASN:N	2.28	0.67
1:J:117:MET:HG3	1:J:118:GLY:N	2.10	0.66
1:I:66:TYR:HB2	1:I:104:PHE:CZ	2.29	0.66
1:F:144:LEU:HD21	1:G:152:GLN:NE2	2.09	0.66
1:J:107:TYR:HB3	1:J:267:LYS:HD3	1.77	0.66
1:D:62:TYR:HE2	1:D:79:ALA:HA	1.61	0.66
1:A:187:ALA:CB	1:L:163:ALA:HB3	2.25	0.66
1:D:179:GLU:O	1:D:181:ASN:OD1	2.13	0.66
1:B:66:TYR:HB2	1:B:104:PHE:CZ	2.29	0.66
1:G:117:MET:HG3	1:G:118:GLY:N	2.10	0.66
1:F:16:GLN:O	1:F:20:ARG:HG3	1.95	0.66
1:A:152:GLN:NE2	1:L:144:LEU:HD21	2.11	0.66
1:C:11:SER:HB3	1:D:176:ASN:HD22	1.61	0.66
1:B:62:TYR:HE2	1:B:79:ALA:HA	1.61	0.66
1:I:126:MET:O	1:I:128:PHE:N	2.28	0.66
1:A:56:SER:HB3	1:A:63:VAL:HG22	1.77	0.66
1:E:179:GLU:O	1:E:181:ASN:OD1	2.13	0.66
1:K:107:TYR:HB3	1:K:267:LYS:HD3	1.76	0.66
1:B:154:ALA:CA	1:D:182:ALA:HB2	2.25	0.66
1:A:66:TYR:HB2	1:A:104:PHE:CZ	2.30	0.66
1:I:179:GLU:O	1:I:181:ASN:OD1	2.14	0.66
1:B:125:ASP:O	1:B:126:MET:HE3	1.95	0.66
1:H:16:GLN:O	1:H:20:ARG:HG3	1.95	0.66
1:L:107:TYR:HB3	1:L:267:LYS:HD3	1.76	0.66
1:A:179:GLU:O	1:A:181:ASN:N	2.29	0.66
1:F:71:ILE:CB	1:F:74:ILE:HD11	2.25	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:117:MET:HG3	1:A:118:GLY:N	2.11	0.66
1:E:201:THR:HG23	1:F:159:VAL:CG1	2.22	0.66
1:L:66:TYR:HB2	1:L:104:PHE:CZ	2.30	0.66
1:K:151:ASN:HD22	1:K:207:VAL:HG23	1.61	0.66
1:H:179:GLU:O	1:H:181:ASN:N	2.29	0.66
1:C:16:GLN:O	1:C:20:ARG:HG3	1.96	0.66
1:K:16:GLN:O	1:K:20:ARG:HG3	1.95	0.66
1:B:49:ASN:C	1:B:49:ASN:HD22	1.97	0.66
1:C:179:GLU:O	1:C:181:ASN:OD1	2.14	0.66
1:J:154:ALA:HA	1:L:182:ALA:HB2	1.78	0.65
1:D:16:GLN:O	1:D:20:ARG:HG3	1.96	0.65
1:I:158:PRO:O	1:I:159:VAL:HB	1.96	0.65
1:A:16:GLN:O	1:A:20:ARG:HG3	1.95	0.65
1:J:56:SER:HB3	1:J:63:VAL:HG22	1.78	0.65
1:I:71:ILE:CB	1:I:74:ILE:HD11	2.25	0.65
1:E:213:GLN:HG3	1:F:207:VAL:HG11	1.79	0.65
1:I:277:LYS:CD	1:I:278:VAL:H	2.10	0.65
1:I:16:GLN:O	1:I:20:ARG:HG3	1.97	0.65
1:B:151:ASN:HD22	1:B:207:VAL:HG23	1.62	0.65
1:G:56:SER:HB3	1:G:63:VAL:HG22	1.79	0.65
1:G:179:GLU:O	1:G:181:ASN:OD1	2.14	0.65
1:A:107:TYR:HB3	1:A:267:LYS:HD3	1.77	0.65
1:I:49:ASN:HD22	1:I:49:ASN:C	2.00	0.65
1:E:117:MET:HG3	1:E:118:GLY:N	2.11	0.65
1:E:16:GLN:O	1:E:20:ARG:HG3	1.96	0.65
1:C:125:ASP:O	1:C:126:MET:HE2	1.96	0.65
1:H:126:MET:O	1:H:128:PHE:N	2.29	0.65
1:B:71:ILE:CB	1:B:74:ILE:HD11	2.24	0.65
1:K:163:ALA:HB3	1:L:187:ALA:CB	2.24	0.65
1:E:179:GLU:O	1:E:181:ASN:N	2.30	0.65
1:B:274:LEU:O	1:B:274:LEU:HD13	1.96	0.65
1:H:107:TYR:HB3	1:H:267:LYS:HD3	1.76	0.65
1:B:179:GLU:O	1:B:181:ASN:OD1	2.15	0.65
1:J:179:GLU:O	1:J:181:ASN:OD1	2.15	0.65
1:D:179:GLU:O	1:D:181:ASN:N	2.28	0.65
1:J:49:ASN:C	1:J:49:ASN:HD22	2.00	0.65
1:B:56:SER:HB3	1:B:63:VAL:HG22	1.77	0.65
1:K:56:SER:HB3	1:K:63:VAL:HG22	1.79	0.65
1:E:151:ASN:HD22	1:E:207:VAL:HG23	1.61	0.65
1:J:16:GLN:O	1:J:20:ARG:HG3	1.97	0.65
1:K:71:ILE:CB	1:K:74:ILE:HD11	2.25	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:182:ALA:H	1:D:183:PRO:CD	2.10	0.65
1:K:277:LYS:CD	1:K:278:VAL:H	2.10	0.65
1:D:117:MET:HG3	1:D:118:GLY:N	2.11	0.64
1:D:277:LYS:CD	1:D:278:VAL:H	2.10	0.64
1:C:182:ALA:H	1:C:183:PRO:CD	2.10	0.64
1:H:179:GLU:O	1:H:181:ASN:OD1	2.15	0.64
1:H:62:TYR:HE2	1:H:79:ALA:HA	1.61	0.64
1:J:151:ASN:HD22	1:J:207:VAL:HG23	1.62	0.64
1:E:277:LYS:CD	1:E:278:VAL:H	2.11	0.64
1:E:182:ALA:H	1:E:183:PRO:CD	2.10	0.64
1:I:182:ALA:H	1:I:183:PRO:CD	2.10	0.64
1:C:39:PHE:HA	1:C:280:PHE:O	1.98	0.64
1:L:277:LYS:CD	1:L:278:VAL:H	2.10	0.64
1:L:16:GLN:O	1:L:20:ARG:HG3	1.97	0.64
1:I:56:SER:HB3	1:I:63:VAL:HG22	1.78	0.64
1:E:62:TYR:HE2	1:E:79:ALA:HA	1.62	0.64
1:D:151:ASN:HD22	1:D:207:VAL:HG23	1.63	0.64
1:F:151:ASN:HD22	1:F:207:VAL:HG23	1.62	0.64
1:B:179:GLU:O	1:B:181:ASN:N	2.30	0.64
1:G:179:GLU:O	1:G:181:ASN:N	2.31	0.64
1:F:179:GLU:O	1:F:181:ASN:N	2.31	0.64
1:G:62:TYR:HE2	1:G:79:ALA:HA	1.63	0.64
1:A:151:ASN:HD22	1:A:207:VAL:HG23	1.62	0.64
1:A:179:GLU:O	1:A:181:ASN:OD1	2.15	0.64
1:K:62:TYR:HE2	1:K:79:ALA:HA	1.62	0.64
1:K:158:PRO:O	1:K:159:VAL:HB	1.97	0.64
1:H:144:LEU:HD21	1:I:152:GLN:NE2	2.12	0.64
1:F:150:VAL:HG13	1:H:180:GLY:HA2	1.79	0.64
1:B:158:PRO:O	1:B:159:VAL:HB	1.98	0.64
1:H:56:SER:HB3	1:H:63:VAL:HG22	1.79	0.64
1:B:277:LYS:CD	1:B:278:VAL:H	2.11	0.64
1:C:154:ALA:CA	1:E:182:ALA:HB2	2.27	0.64
1:C:248:GLU:CD	1:D:227:ILE:HA	2.18	0.64
1:L:179:GLU:O	1:L:181:ASN:N	2.29	0.64
1:A:49:ASN:HD22	1:A:49:ASN:C	1.99	0.64
1:F:117:MET:HG3	1:F:118:GLY:N	2.13	0.64
1:F:179:GLU:O	1:F:181:ASN:OD1	2.15	0.64
1:I:11:SER:HB3	1:J:176:ASN:HD22	1.63	0.64
1:I:277:LYS:CD	1:I:278:VAL:N	2.62	0.63
1:K:117:MET:HG3	1:K:118:GLY:N	2.11	0.63
1:G:38:LEU:O	1:G:39:PHE:HB2	1.98	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:62:TYR:HE2	1:L:79:ALA:HA	1.63	0.63
1:J:62:TYR:HE2	1:J:79:ALA:HA	1.63	0.63
1:F:62:TYR:HE2	1:F:79:ALA:HA	1.63	0.63
1:G:277:LYS:CD	1:G:278:VAL:H	2.11	0.63
1:I:179:GLU:O	1:I:181:ASN:N	2.31	0.63
1:F:179:GLU:C	1:F:181:ASN:H	2.02	0.63
1:K:213:GLN:HG3	1:L:207:VAL:HG11	1.79	0.63
1:C:117:MET:HG3	1:C:118:GLY:N	2.14	0.63
1:H:182:ALA:H	1:H:183:PRO:CD	2.10	0.63
1:A:62:TYR:HE2	1:A:79:ALA:HA	1.62	0.63
1:K:144:LEU:HD21	1:L:152:GLN:NE2	2.12	0.63
1:D:49:ASN:HD22	1:D:49:ASN:C	2.00	0.63
1:L:49:ASN:C	1:L:49:ASN:HD22	2.00	0.63
1:E:126:MET:O	1:E:128:PHE:N	2.31	0.63
1:F:182:ALA:H	1:F:183:PRO:CD	2.11	0.63
1:J:179:GLU:O	1:J:181:ASN:N	2.31	0.63
1:E:154:ALA:HA	1:G:182:ALA:HB2	1.79	0.63
1:I:62:TYR:HE2	1:I:79:ALA:HA	1.63	0.63
1:F:277:LYS:CD	1:F:278:VAL:H	2.11	0.63
1:D:248:GLU:HB3	1:E:282:TYR:CZ	2.34	0.63
1:F:277:LYS:CD	1:F:278:VAL:N	2.62	0.63
1:H:49:ASN:C	1:H:49:ASN:HD22	2.01	0.63
1:C:249:GLN:HB3	1:D:222:MET:HE2	1.81	0.63
1:H:179:GLU:C	1:H:181:ASN:H	2.02	0.63
1:L:182:ALA:H	1:L:183:PRO:CD	2.11	0.63
1:A:158:PRO:O	1:A:159:VAL:HB	1.97	0.63
1:I:125:ASP:O	1:I:126:MET:HE2	1.98	0.63
1:E:56:SER:HB3	1:E:63:VAL:HG22	1.79	0.63
1:H:57:ILE:HG22	1:H:123:ASN:HB2	1.81	0.63
1:I:213:GLN:HG3	1:J:207:VAL:HG11	1.81	0.63
1:A:179:GLU:C	1:A:181:ASN:H	2.02	0.63
1:I:274:LEU:HD13	1:I:274:LEU:O	1.98	0.63
1:D:213:GLN:HG3	1:E:207:VAL:CG1	2.29	0.62
1:G:125:ASP:O	1:G:126:MET:HE2	1.98	0.62
1:J:179:GLU:C	1:J:181:ASN:H	2.02	0.62
1:A:274:LEU:HD13	1:A:274:LEU:O	1.98	0.62
1:F:249:GLN:HB3	1:G:222:MET:HE2	1.79	0.62
1:G:277:LYS:CD	1:G:278:VAL:N	2.62	0.62
1:K:179:GLU:C	1:K:181:ASN:H	2.03	0.62
1:L:179:GLU:C	1:L:181:ASN:H	2.01	0.62
1:E:274:LEU:HD13	1:E:274:LEU:O	1.99	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:277:LYS:CD	1:C:278:VAL:H	2.11	0.62
1:H:277:LYS:CD	1:H:278:VAL:H	2.12	0.62
1:C:179:GLU:C	1:C:181:ASN:H	2.01	0.62
1:G:179:GLU:C	1:G:181:ASN:H	2.03	0.62
1:G:274:LEU:O	1:G:274:LEU:HD13	1.99	0.62
1:C:57:ILE:HG22	1:C:123:ASN:HB2	1.80	0.62
1:F:93:PHE:HB3	1:F:104:PHE:CG	2.35	0.62
1:L:277:LYS:CD	1:L:278:VAL:N	2.62	0.62
1:F:213:GLN:HG3	1:G:207:VAL:HG11	1.80	0.62
1:H:117:MET:HG3	1:H:118:GLY:N	2.13	0.62
1:D:179:GLU:C	1:D:181:ASN:H	2.02	0.62
1:K:87:TYR:CD2	1:L:49:ASN:HB2	2.34	0.62
1:K:123:ASN:ND2	1:K:261:ARG:NH2	2.48	0.62
1:K:277:LYS:CD	1:K:278:VAL:N	2.62	0.62
1:B:179:GLU:C	1:B:181:ASN:H	2.02	0.62
1:K:179:GLU:O	1:K:181:ASN:N	2.31	0.62
1:D:274:LEU:HD13	1:D:274:LEU:O	2.00	0.62
1:L:151:ASN:HD22	1:L:207:VAL:HG23	1.64	0.62
1:G:151:ASN:HD22	1:G:207:VAL:HG23	1.64	0.62
1:L:117:MET:HG3	1:L:118:GLY:N	2.13	0.62
1:C:277:LYS:CD	1:C:278:VAL:N	2.62	0.62
1:C:151:ASN:HD22	1:C:207:VAL:HG23	1.64	0.62
1:F:49:ASN:C	1:F:49:ASN:HD22	2.03	0.62
1:H:274:LEU:HD13	1:H:274:LEU:O	1.99	0.62
1:A:182:ALA:H	1:A:183:PRO:CD	2.12	0.62
1:E:179:GLU:C	1:E:181:ASN:H	2.02	0.62
1:E:115:GLU:O	1:E:116:ASP:HB3	2.00	0.62
1:I:57:ILE:HG22	1:I:123:ASN:HB2	1.82	0.62
1:B:182:ALA:H	1:B:183:PRO:CD	2.12	0.62
1:K:179:GLU:O	1:K:181:ASN:OD1	2.18	0.62
1:K:182:ALA:H	1:K:183:PRO:CD	2.12	0.62
1:G:49:ASN:HD22	1:G:49:ASN:C	2.01	0.62
1:D:56:SER:HB3	1:D:63:VAL:HG22	1.81	0.62
1:I:37:GLN:O	1:I:281:ARG:HD2	2.00	0.62
1:H:37:GLN:O	1:H:281:ARG:HD2	1.99	0.62
1:D:277:LYS:CD	1:D:278:VAL:N	2.62	0.62
1:F:158:PRO:O	1:F:159:VAL:HB	2.00	0.61
1:C:171:LEU:C	1:C:173:GLN:N	2.53	0.61
1:E:93:PHE:HB3	1:E:104:PHE:CG	2.35	0.61
1:G:158:PRO:O	1:G:159:VAL:HB	2.00	0.61
1:D:123:ASN:ND2	1:D:261:ARG:NH2	2.48	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:39:PHE:HA	1:F:280:PHE:O	2.00	0.61
1:C:213:GLN:HG3	1:D:207:VAL:HG11	1.82	0.61
1:J:277:LYS:CD	1:J:278:VAL:H	2.13	0.61
1:J:182:ALA:H	1:J:183:PRO:CD	2.12	0.61
1:D:158:PRO:O	1:D:159:VAL:HB	1.99	0.61
1:C:62:TYR:HE2	1:C:79:ALA:HA	1.65	0.61
1:B:117:MET:HG3	1:B:118:GLY:N	2.12	0.61
1:C:49:ASN:C	1:C:49:ASN:HD22	2.02	0.61
1:H:277:LYS:CD	1:H:278:VAL:N	2.64	0.61
1:J:115:GLU:O	1:J:116:ASP:HB3	2.00	0.61
1:C:274:LEU:O	1:C:274:LEU:HD13	2.00	0.61
1:I:201:THR:HG23	1:J:159:VAL:CG1	2.20	0.61
1:G:171:LEU:C	1:G:173:GLN:N	2.53	0.61
1:E:123:ASN:ND2	1:E:261:ARG:NH2	2.48	0.61
1:G:93:PHE:HB3	1:G:104:PHE:CG	2.36	0.61
1:A:277:LYS:CD	1:A:278:VAL:H	2.13	0.61
1:K:274:LEU:O	1:K:274:LEU:HD13	2.00	0.61
1:F:57:ILE:HG22	1:F:123:ASN:HB2	1.80	0.61
1:C:106:LEU:HD22	1:C:120:VAL:HG23	1.83	0.61
1:A:93:PHE:HB3	1:A:104:PHE:CG	2.35	0.61
1:L:56:SER:HB3	1:L:63:VAL:HG22	1.81	0.61
1:J:123:ASN:ND2	1:J:261:ARG:NH2	2.48	0.61
1:H:168:GLN:NE2	1:H:169:LEU:HG	2.15	0.61
1:K:168:GLN:NE2	1:K:169:LEU:HG	2.16	0.61
1:H:213:GLN:HG3	1:I:207:VAL:HG11	1.81	0.61
1:H:93:PHE:HB3	1:H:104:PHE:CG	2.36	0.61
1:E:144:LEU:HD21	1:F:152:GLN:NE2	2.15	0.61
1:E:277:LYS:CD	1:E:278:VAL:N	2.62	0.61
1:H:171:LEU:C	1:H:173:GLN:N	2.53	0.61
1:A:277:LYS:CD	1:A:278:VAL:N	2.64	0.61
1:I:179:GLU:C	1:I:181:ASN:H	2.03	0.61
1:E:12:ILE:HG21	1:E:15:ILE:HB	1.83	0.61
1:H:158:PRO:O	1:H:159:VAL:HB	2.00	0.61
1:K:171:LEU:C	1:K:173:GLN:N	2.54	0.61
1:J:168:GLN:NE2	1:J:169:LEU:HG	2.16	0.61
1:I:93:PHE:HB3	1:I:104:PHE:CG	2.36	0.61
1:K:49:ASN:HD22	1:K:49:ASN:C	2.01	0.61
1:H:115:GLU:O	1:H:116:ASP:HB3	2.01	0.61
1:C:158:PRO:O	1:C:159:VAL:HB	2.01	0.61
1:B:277:LYS:CD	1:B:278:VAL:N	2.63	0.61
1:H:154:ALA:HA	1:J:182:ALA:HB2	1.83	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:12:ILE:HG21	1:B:15:ILE:HB	1.83	0.60
1:H:12:ILE:HG21	1:H:15:ILE:HB	1.83	0.60
1:G:123:ASN:ND2	1:G:261:ARG:NH2	2.48	0.60
1:I:151:ASN:HD21	1:I:206:VAL:H	1.49	0.60
1:B:213:GLN:HG3	1:C:207:VAL:HG11	1.82	0.60
1:I:117:MET:HG3	1:I:118:GLY:N	2.16	0.60
1:K:12:ILE:HG21	1:K:15:ILE:HB	1.83	0.60
1:D:12:ILE:HG21	1:D:15:ILE:HB	1.84	0.60
1:E:49:ASN:C	1:E:49:ASN:HD22	2.03	0.60
1:C:125:ASP:O	1:C:126:MET:CB	2.49	0.60
1:G:182:ALA:H	1:G:183:PRO:CD	2.14	0.60
1:D:168:GLN:NE2	1:D:169:LEU:HG	2.16	0.60
1:A:37:GLN:O	1:A:281:ARG:HD2	2.00	0.60
1:F:168:GLN:NE2	1:F:169:LEU:HG	2.16	0.60
1:D:125:ASP:O	1:D:126:MET:CB	2.50	0.60
1:L:124:ASN:HD21	1:L:128:PHE:HB2	1.65	0.60
1:F:171:LEU:C	1:F:173:GLN:N	2.53	0.60
1:H:151:ASN:HD22	1:H:207:VAL:HG23	1.66	0.60
1:J:144:LEU:HD21	1:K:152:GLN:NE2	2.17	0.60
1:F:12:ILE:HG21	1:F:15:ILE:HB	1.84	0.60
1:B:123:ASN:ND2	1:B:261:ARG:NH2	2.50	0.60
1:L:57:ILE:HG22	1:L:123:ASN:HB2	1.82	0.60
1:K:123:ASN:ND2	1:K:257:PHE:HD2	1.89	0.60
1:C:168:GLN:NE2	1:C:169:LEU:HG	2.16	0.60
1:H:123:ASN:ND2	1:H:261:ARG:NH2	2.49	0.60
1:A:171:LEU:C	1:A:173:GLN:N	2.55	0.60
1:A:144:LEU:HD21	1:B:152:GLN:NE2	2.16	0.60
1:E:150:VAL:HG13	1:G:180:GLY:HA2	1.83	0.60
1:A:115:GLU:O	1:A:116:ASP:HB3	2.01	0.60
1:L:168:GLN:NE2	1:L:169:LEU:HG	2.17	0.60
1:J:171:LEU:C	1:J:173:GLN:N	2.54	0.60
1:C:151:ASN:HD21	1:C:206:VAL:H	1.50	0.60
1:C:154:ALA:CB	1:E:182:ALA:HB2	2.32	0.60
1:L:60:PHE:HA	1:L:129:PRO:HG3	1.83	0.60
1:J:277:LYS:CD	1:J:278:VAL:N	2.65	0.60
1:D:93:PHE:HB3	1:D:104:PHE:CG	2.37	0.60
1:G:154:ALA:CA	1:I:182:ALA:HB2	2.32	0.60
1:G:12:ILE:HG21	1:G:15:ILE:HB	1.84	0.60
1:A:57:ILE:HG22	1:A:123:ASN:HB2	1.84	0.60
1:G:106:LEU:HD22	1:G:120:VAL:HG23	1.84	0.60
1:G:115:GLU:O	1:G:116:ASP:HB3	2.02	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:37:GLN:O	1:L:281:ARG:HD2	2.01	0.60
1:I:125:ASP:O	1:I:126:MET:CB	2.49	0.60
1:I:123:ASN:ND2	1:I:261:ARG:NH2	2.48	0.60
1:E:57:ILE:HG22	1:E:123:ASN:HB2	1.84	0.60
1:D:57:ILE:HG22	1:D:123:ASN:HB2	1.82	0.59
1:D:171:LEU:C	1:D:173:GLN:N	2.53	0.59
1:L:274:LEU:HD13	1:L:274:LEU:O	2.01	0.59
1:C:201:THR:HG23	1:D:159:VAL:CG1	2.20	0.59
1:J:60:PHE:HD1	1:J:60:PHE:O	1.85	0.59
1:H:39:PHE:HA	1:H:280:PHE:O	2.02	0.59
1:B:115:GLU:O	1:B:116:ASP:HB3	2.02	0.59
1:L:171:LEU:C	1:L:173:GLN:N	2.55	0.59
1:C:209:LYS:HD3	1:D:205:TYR:CE2	2.36	0.59
1:A:12:ILE:HG21	1:A:15:ILE:HB	1.84	0.59
1:L:12:ILE:HG21	1:L:15:ILE:HB	1.84	0.59
1:J:158:PRO:O	1:J:159:VAL:HB	2.01	0.59
1:F:151:ASN:HD21	1:F:206:VAL:H	1.49	0.59
1:B:106:LEU:HD22	1:B:120:VAL:HG23	1.84	0.59
1:K:126:MET:O	1:K:128:PHE:N	2.31	0.59
1:A:43:ASN:O	1:A:44:LEU:HB3	2.01	0.59
1:E:171:LEU:C	1:E:173:GLN:N	2.54	0.59
1:I:168:GLN:NE2	1:I:169:LEU:HG	2.17	0.59
1:A:213:GLN:HG3	1:B:207:VAL:CG1	2.32	0.59
1:C:93:PHE:HB3	1:C:104:PHE:CG	2.37	0.59
1:A:182:ALA:HB2	1:K:154:ALA:CA	2.32	0.59
1:G:154:ALA:CB	1:I:182:ALA:HB2	2.32	0.59
1:E:201:THR:CG2	1:E:201:THR:O	2.49	0.59
1:L:125:ASP:O	1:L:126:MET:CB	2.50	0.59
1:D:201:THR:HG23	1:E:159:VAL:CG1	2.28	0.59
1:F:123:ASN:O	1:F:124:ASN:CG	2.41	0.59
1:I:151:ASN:HD22	1:I:207:VAL:HG23	1.66	0.59
1:J:117:MET:HB2	1:J:271:LEU:CD1	2.33	0.59
1:C:115:GLU:O	1:C:116:ASP:HB3	2.02	0.59
1:K:115:GLU:O	1:K:116:ASP:HB3	2.01	0.59
1:C:12:ILE:HG21	1:C:15:ILE:HB	1.84	0.59
1:J:57:ILE:CG1	1:J:63:VAL:HG21	2.33	0.59
1:I:123:ASN:O	1:I:124:ASN:CG	2.40	0.59
1:F:125:ASP:O	1:F:126:MET:CB	2.49	0.59
1:L:123:ASN:O	1:L:124:ASN:CG	2.40	0.59
1:E:158:PRO:O	1:E:159:VAL:HB	2.02	0.59
1:A:106:LEU:HD22	1:A:120:VAL:HG23	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:93:PHE:HB3	1:B:104:PHE:CG	2.37	0.59
1:I:115:GLU:O	1:I:116:ASP:HB3	2.03	0.59
1:E:201:THR:CG2	1:F:159:VAL:HG11	2.24	0.59
1:C:248:GLU:CG	1:D:227:ILE:CG2	2.76	0.59
1:G:168:GLN:NE2	1:G:169:LEU:HG	2.18	0.59
1:B:168:GLN:NE2	1:B:169:LEU:HG	2.18	0.59
1:E:168:GLN:NE2	1:E:169:LEU:HG	2.18	0.59
1:B:151:ASN:HD21	1:B:206:VAL:H	1.49	0.59
1:L:93:PHE:HB3	1:L:104:PHE:CG	2.37	0.59
1:F:117:MET:CG	1:F:118:GLY:H	2.13	0.59
1:F:274:LEU:O	1:F:274:LEU:HD13	2.02	0.59
1:J:43:ASN:O	1:J:44:LEU:HB3	2.03	0.59
1:C:110:ARG:HB3	1:D:47:THR:HG22	1.84	0.59
1:L:158:PRO:O	1:L:159:VAL:HB	2.02	0.59
1:G:123:ASN:O	1:G:124:ASN:CG	2.41	0.59
1:G:57:ILE:HG22	1:G:123:ASN:HB2	1.83	0.59
1:A:168:GLN:NE2	1:A:169:LEU:HG	2.17	0.59
1:F:106:LEU:HD22	1:F:120:VAL:HG23	1.84	0.59
1:K:93:PHE:HB3	1:K:104:PHE:CG	2.38	0.59
1:D:117:MET:HB2	1:D:271:LEU:CD1	2.33	0.58
1:C:182:ALA:N	1:C:183:PRO:HD3	2.18	0.58
1:L:39:PHE:HA	1:L:280:PHE:O	2.03	0.58
1:B:117:MET:HB2	1:B:271:LEU:CD1	2.33	0.58
1:F:115:GLU:O	1:F:116:ASP:HB3	2.02	0.58
1:J:125:ASP:O	1:J:126:MET:CB	2.50	0.58
1:A:125:ASP:O	1:A:126:MET:CB	2.50	0.58
1:E:37:GLN:O	1:E:281:ARG:HD2	2.03	0.58
1:H:106:LEU:HD22	1:H:120:VAL:HG23	1.85	0.58
1:K:117:MET:HB2	1:K:271:LEU:CD1	2.33	0.58
1:K:182:ALA:N	1:K:183:PRO:HD3	2.19	0.58
1:L:115:GLU:O	1:L:116:ASP:HB3	2.02	0.58
1:L:123:ASN:ND2	1:L:257:PHE:HD2	1.90	0.58
1:C:85:ASP:OD1	1:C:86:VAL:N	2.37	0.58
1:J:12:ILE:HG21	1:J:15:ILE:HB	1.83	0.58
1:D:248:GLU:HB3	1:E:282:TYR:CE2	2.39	0.58
1:D:115:GLU:O	1:D:116:ASP:HB3	2.02	0.58
1:B:57:ILE:HG22	1:B:123:ASN:HB2	1.86	0.58
1:I:39:PHE:HA	1:I:280:PHE:O	2.03	0.58
1:D:106:LEU:HD22	1:D:120:VAL:HG23	1.85	0.58
1:E:117:MET:HB2	1:E:271:LEU:CD1	2.34	0.58
1:J:154:ALA:CB	1:L:182:ALA:HB2	2.34	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:201:THR:CG2	1:H:201:THR:O	2.50	0.58
1:C:201:THR:CG2	1:C:201:THR:O	2.51	0.58
1:D:57:ILE:CG1	1:D:63:VAL:HG21	2.33	0.58
1:C:123:ASN:O	1:C:124:ASN:CG	2.42	0.58
1:H:60:PHE:HA	1:H:129:PRO:HG3	1.86	0.58
1:J:93:PHE:HB3	1:J:104:PHE:CG	2.38	0.58
1:L:151:ASN:HD21	1:L:206:VAL:H	1.51	0.58
1:G:126:MET:O	1:G:128:PHE:N	2.36	0.58
1:K:151:ASN:HD21	1:K:206:VAL:H	1.52	0.58
1:F:154:ALA:HA	1:H:182:ALA:HB2	1.85	0.58
1:B:43:ASN:O	1:B:44:LEU:HB3	2.03	0.58
1:G:213:GLN:HG3	1:H:207:VAL:CG1	2.32	0.58
1:L:117:MET:CG	1:L:118:GLY:H	2.13	0.58
1:F:213:GLN:HG3	1:G:207:VAL:CG1	2.33	0.58
1:C:278:VAL:HG12	1:C:279:LYS:N	2.19	0.58
1:I:182:ALA:N	1:I:183:PRO:HD3	2.19	0.58
1:F:123:ASN:ND2	1:F:257:PHE:HD2	1.91	0.58
1:B:154:ALA:CB	1:D:182:ALA:HB2	2.33	0.58
1:I:12:ILE:HG21	1:I:15:ILE:HB	1.84	0.58
1:D:123:ASN:O	1:D:124:ASN:CG	2.43	0.57
1:L:117:MET:HB2	1:L:271:LEU:CD1	2.34	0.57
1:I:117:MET:HB2	1:I:271:LEU:CD1	2.33	0.57
1:B:126:MET:O	1:B:128:PHE:N	2.35	0.57
1:D:107:TYR:CB	1:D:267:LYS:HD3	2.34	0.57
1:A:123:ASN:ND2	1:A:261:ARG:NH2	2.52	0.57
1:L:182:ALA:N	1:L:183:PRO:HD3	2.20	0.57
1:G:43:ASN:O	1:G:44:LEU:HB3	2.04	0.57
1:D:222:MET:CE	1:D:227:ILE:HG21	2.34	0.57
1:J:124:ASN:HD21	1:J:128:PHE:HB2	1.70	0.57
1:E:213:GLN:HG3	1:F:207:VAL:CG1	2.34	0.57
1:C:86:VAL:HA	1:D:99:VAL:CG1	2.34	0.57
1:G:107:TYR:CB	1:G:267:LYS:HD3	2.34	0.57
1:K:107:TYR:CB	1:K:267:LYS:HD3	2.34	0.57
1:K:123:ASN:O	1:K:124:ASN:CG	2.41	0.57
1:A:123:ASN:O	1:A:124:ASN:CG	2.42	0.57
1:C:57:ILE:CG1	1:C:63:VAL:HG21	2.34	0.57
1:F:123:ASN:ND2	1:F:261:ARG:NH2	2.53	0.57
1:F:182:ALA:N	1:F:183:PRO:HD3	2.19	0.57
1:K:278:VAL:HG12	1:K:279:LYS:N	2.19	0.57
1:B:182:ALA:N	1:B:183:PRO:HD3	2.20	0.57
1:H:117:MET:HB2	1:H:271:LEU:CD1	2.34	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:85:ASP:OD1	1:F:86:VAL:N	2.37	0.57
1:B:125:ASP:O	1:B:126:MET:CB	2.52	0.57
1:J:57:ILE:HG22	1:J:123:ASN:HB2	1.84	0.57
1:B:171:LEU:C	1:B:173:GLN:N	2.53	0.57
1:E:39:PHE:HA	1:E:280:PHE:O	2.03	0.57
1:E:60:PHE:O	1:E:60:PHE:HD1	1.87	0.57
1:C:277:LYS:O	1:C:278:VAL:HB	2.05	0.57
1:K:125:ASP:O	1:K:126:MET:CB	2.52	0.57
1:H:11:SER:HB3	1:I:176:ASN:HD22	1.69	0.57
1:H:125:ASP:O	1:H:126:MET:CB	2.52	0.57
1:A:117:MET:HB2	1:A:271:LEU:CD1	2.34	0.57
1:J:213:GLN:HG3	1:K:207:VAL:CG1	2.34	0.57
1:G:151:ASN:HD21	1:G:206:VAL:H	1.53	0.57
1:C:107:TYR:CB	1:C:267:LYS:HD3	2.34	0.57
1:F:107:TYR:CB	1:F:267:LYS:HD3	2.34	0.57
1:F:112:MET:O	1:F:113:LYS:HB2	2.05	0.57
1:E:106:LEU:HD22	1:E:120:VAL:HG23	1.85	0.57
1:B:277:LYS:O	1:B:278:VAL:HB	2.05	0.57
1:C:117:MET:HB2	1:C:271:LEU:CD1	2.35	0.57
1:C:117:MET:CG	1:C:118:GLY:H	2.13	0.57
1:A:151:ASN:HD21	1:A:206:VAL:H	1.52	0.57
1:F:117:MET:HB2	1:F:271:LEU:CD1	2.34	0.57
1:G:150:VAL:HG13	1:I:180:GLY:HA2	1.86	0.57
1:C:201:THR:CG2	1:D:159:VAL:HG11	2.21	0.57
1:D:37:GLN:O	1:D:281:ARG:HD2	2.04	0.57
1:E:125:ASP:O	1:E:126:MET:CB	2.52	0.57
1:G:117:MET:HB2	1:G:271:LEU:CD1	2.35	0.57
1:B:182:ALA:HB2	1:L:154:ALA:CA	2.34	0.57
1:A:154:ALA:CB	1:C:182:ALA:HB2	2.35	0.57
1:E:182:ALA:N	1:E:183:PRO:HD3	2.19	0.57
1:C:249:GLN:NE2	1:D:222:MET:HG3	2.20	0.57
1:D:182:ALA:N	1:D:183:PRO:HD3	2.19	0.57
1:F:278:VAL:HG12	1:F:279:LYS:N	2.20	0.57
1:L:106:LEU:HD22	1:L:120:VAL:HG23	1.87	0.57
1:I:277:LYS:O	1:I:278:VAL:HB	2.05	0.57
1:H:278:VAL:HG12	1:H:279:LYS:N	2.20	0.57
1:H:182:ALA:N	1:H:183:PRO:HD3	2.19	0.57
1:B:85:ASP:OD1	1:B:86:VAL:N	2.38	0.57
1:I:123:ASN:ND2	1:I:257:PHE:HD2	1.92	0.56
1:E:42:GLU:HG3	1:E:279:LYS:HE2	1.87	0.56
1:J:123:ASN:ND2	1:J:261:ARG:HH21	2.03	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:57:ILE:HG22	1:K:123:ASN:HB2	1.87	0.56
1:F:209:LYS:HD3	1:G:205:TYR:CE2	2.41	0.56
1:H:42:GLU:HG3	1:H:279:LYS:HE2	1.87	0.56
1:L:112:MET:O	1:L:113:LYS:HB2	2.05	0.56
1:B:60:PHE:HD1	1:B:60:PHE:O	1.88	0.56
1:A:60:PHE:HD1	1:A:60:PHE:O	1.88	0.56
1:E:123:ASN:O	1:E:124:ASN:CG	2.43	0.56
1:H:57:ILE:CG1	1:H:63:VAL:HG21	2.35	0.56
1:L:278:VAL:HG12	1:L:279:LYS:N	2.20	0.56
1:I:106:LEU:HD22	1:I:120:VAL:HG23	1.87	0.56
1:I:278:VAL:HG12	1:I:279:LYS:N	2.19	0.56
1:A:207:VAL:CG1	1:L:213:GLN:HG3	2.35	0.56
1:E:151:ASN:HD22	1:E:207:VAL:CG2	2.18	0.56
1:G:125:ASP:O	1:G:126:MET:CB	2.52	0.56
1:E:107:TYR:CB	1:E:267:LYS:HD3	2.35	0.56
1:L:43:ASN:O	1:L:44:LEU:HB3	2.06	0.56
1:L:85:ASP:OD1	1:L:86:VAL:N	2.38	0.56
1:K:201:THR:CG2	1:K:201:THR:O	2.53	0.56
1:E:57:ILE:CG1	1:E:63:VAL:HG21	2.35	0.56
1:B:182:ALA:HB2	1:L:154:ALA:CB	2.36	0.56
1:J:107:TYR:CB	1:J:267:LYS:HD3	2.35	0.56
1:L:107:TYR:CB	1:L:267:LYS:HD3	2.35	0.56
1:B:123:ASN:O	1:B:124:ASN:CG	2.44	0.56
1:L:60:PHE:HD1	1:L:60:PHE:O	1.89	0.56
1:K:39:PHE:HA	1:K:280:PHE:O	2.05	0.56
1:H:123:ASN:O	1:H:124:ASN:CG	2.43	0.56
1:I:151:ASN:ND2	1:I:206:VAL:H	2.03	0.56
1:J:106:LEU:HD22	1:J:120:VAL:HG23	1.87	0.56
1:A:277:LYS:O	1:A:278:VAL:HB	2.05	0.56
1:K:43:ASN:O	1:K:44:LEU:HB3	2.06	0.56
1:J:123:ASN:O	1:J:124:ASN:CG	2.44	0.56
1:G:201:THR:O	1:G:201:THR:CG2	2.52	0.56
1:C:60:PHE:O	1:C:60:PHE:HD1	1.88	0.56
1:H:60:PHE:HD1	1:H:60:PHE:O	1.87	0.56
1:F:57:ILE:CG1	1:F:63:VAL:HG21	2.36	0.56
1:F:151:ASN:ND2	1:F:206:VAL:H	2.03	0.56
1:B:107:TYR:CB	1:B:267:LYS:HD3	2.35	0.56
1:I:107:TYR:CB	1:I:267:LYS:HD3	2.35	0.56
1:B:172:LYS:HG3	1:C:179:GLU:OE1	2.06	0.56
1:C:123:ASN:ND2	1:C:261:ARG:NH2	2.53	0.56
1:I:171:LEU:C	1:I:173:GLN:N	2.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:151:ASN:HD21	1:D:206:VAL:H	1.53	0.56
1:H:151:ASN:HD21	1:H:206:VAL:H	1.54	0.56
1:E:43:ASN:O	1:E:44:LEU:HB3	2.05	0.56
1:H:85:ASP:OD1	1:H:86:VAL:N	2.39	0.56
1:G:57:ILE:CG1	1:G:63:VAL:HG21	2.36	0.56
1:D:38:LEU:O	1:D:39:PHE:CB	2.53	0.56
1:H:123:ASN:ND2	1:H:257:PHE:HD2	1.91	0.56
1:L:277:LYS:O	1:L:278:VAL:HB	2.06	0.56
1:F:277:LYS:O	1:F:278:VAL:HB	2.06	0.56
1:A:180:GLY:HA2	1:K:150:VAL:HG13	1.88	0.56
1:G:38:LEU:HD21	1:G:227:ILE:HD11	1.88	0.56
1:G:60:PHE:O	1:G:60:PHE:HD1	1.88	0.56
1:F:123:ASN:O	1:F:124:ASN:OD1	2.24	0.56
1:K:106:LEU:HD22	1:K:120:VAL:HG23	1.86	0.56
1:B:117:MET:HB2	1:B:271:LEU:HD13	1.88	0.56
1:E:278:VAL:HG12	1:E:279:LYS:N	2.21	0.56
1:H:277:LYS:O	1:H:278:VAL:HB	2.06	0.56
1:A:107:TYR:CB	1:A:267:LYS:HD3	2.36	0.56
1:C:50:PRO:O	1:C:54:GLU:HG3	2.06	0.56
1:C:112:MET:O	1:C:113:LYS:HB2	2.05	0.56
1:B:201:THR:O	1:B:201:THR:CG2	2.53	0.56
1:B:151:ASN:ND2	1:B:206:VAL:H	2.04	0.56
1:G:151:ASN:HD22	1:G:207:VAL:CG2	2.19	0.56
1:I:43:ASN:O	1:I:44:LEU:HB3	2.06	0.56
1:H:43:ASN:O	1:H:44:LEU:HB3	2.06	0.56
1:D:43:ASN:O	1:D:44:LEU:HB3	2.06	0.56
1:A:182:ALA:N	1:A:183:PRO:HD3	2.20	0.55
1:E:277:LYS:O	1:E:278:VAL:HB	2.06	0.55
1:C:151:ASN:ND2	1:C:206:VAL:H	2.03	0.55
1:D:144:LEU:HD21	1:E:152:GLN:NE2	2.21	0.55
1:J:182:ALA:N	1:J:183:PRO:HD3	2.20	0.55
1:F:111:ASP:OD1	1:G:71:ILE:HG23	2.07	0.55
1:K:57:ILE:CG1	1:K:63:VAL:HG21	2.36	0.55
1:A:39:PHE:HA	1:A:280:PHE:O	2.06	0.55
1:J:117:MET:HB2	1:J:271:LEU:HD13	1.88	0.55
1:B:42:GLU:HG3	1:B:279:LYS:HE2	1.89	0.55
1:F:43:ASN:O	1:F:44:LEU:HB3	2.05	0.55
1:C:186:PHE:CD2	1:C:196:ILE:HD11	2.41	0.55
1:G:117:MET:CG	1:G:118:GLY:H	2.11	0.55
1:J:151:ASN:HD22	1:J:207:VAL:CG2	2.19	0.55
1:A:151:ASN:HD22	1:A:207:VAL:CG2	2.20	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:ALA:CA	1:C:182:ALA:HB2	2.34	0.55
1:A:278:VAL:HG12	1:A:279:LYS:N	2.22	0.55
1:B:57:ILE:CG1	1:B:63:VAL:HG21	2.36	0.55
1:D:60:PHE:HD1	1:D:60:PHE:O	1.89	0.55
1:F:42:GLU:HG3	1:F:279:LYS:HE2	1.89	0.55
1:H:107:TYR:CB	1:H:267:LYS:HD3	2.35	0.55
1:D:112:MET:O	1:D:113:LYS:HB2	2.07	0.55
1:B:123:ASN:ND2	1:B:257:PHE:HD2	1.90	0.55
1:C:209:LYS:HB3	1:C:209:LYS:NZ	2.22	0.55
1:K:277:LYS:O	1:K:278:VAL:HB	2.06	0.55
1:H:178:TYR:C	1:H:180:GLY:H	2.09	0.55
1:B:43:ASN:O	1:B:44:LEU:CB	2.55	0.55
1:E:85:ASP:OD1	1:E:86:VAL:N	2.40	0.55
1:D:123:ASN:ND2	1:D:257:PHE:HD2	1.90	0.55
1:E:38:LEU:HD21	1:E:227:ILE:HD11	1.89	0.55
1:J:42:GLU:HG3	1:J:279:LYS:HE2	1.88	0.55
1:E:117:MET:HB2	1:E:271:LEU:HD13	1.89	0.55
1:A:205:TYR:CE2	1:L:209:LYS:HD3	2.42	0.55
1:C:43:ASN:O	1:C:44:LEU:HB3	2.06	0.55
1:B:60:PHE:HA	1:B:129:PRO:HG3	1.87	0.55
1:B:39:PHE:HA	1:B:280:PHE:O	2.07	0.55
1:J:56:SER:O	1:J:59:GLN:O	2.25	0.55
1:A:117:MET:HB2	1:A:271:LEU:HD13	1.88	0.55
1:K:151:ASN:ND2	1:K:206:VAL:H	2.05	0.55
1:K:213:GLN:HG3	1:L:207:VAL:CG1	2.37	0.55
1:L:151:ASN:ND2	1:L:206:VAL:H	2.05	0.55
1:G:123:ASN:ND2	1:G:257:PHE:HD2	1.91	0.55
1:F:60:PHE:HD1	1:F:60:PHE:O	1.90	0.55
1:L:117:MET:HB2	1:L:271:LEU:HD13	1.89	0.55
1:C:110:ARG:CB	1:D:47:THR:HG22	2.37	0.54
1:B:56:SER:O	1:B:59:GLN:O	2.26	0.54
1:L:123:ASN:O	1:L:124:ASN:OD1	2.25	0.54
1:K:123:ASN:ND2	1:K:261:ARG:HH21	2.05	0.54
1:E:123:ASN:ND2	1:E:261:ARG:HH21	2.05	0.54
1:J:277:LYS:O	1:J:278:VAL:HB	2.06	0.54
1:K:117:MET:HB2	1:K:271:LEU:HD13	1.89	0.54
1:L:209:LYS:HB3	1:L:209:LYS:NZ	2.22	0.54
1:I:154:ALA:HA	1:K:182:ALA:HB2	1.89	0.54
1:J:43:ASN:O	1:J:44:LEU:CB	2.55	0.54
1:K:50:PRO:O	1:K:54:GLU:HG3	2.06	0.54
1:I:50:PRO:O	1:I:54:GLU:HG3	2.07	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:112:MET:O	1:I:113:LYS:HB2	2.07	0.54
1:F:248:GLU:CD	1:G:227:ILE:HA	2.27	0.54
1:K:37:GLN:O	1:K:281:ARG:HD2	2.07	0.54
1:G:144:LEU:HD21	1:H:152:GLN:NE2	2.21	0.54
1:B:278:VAL:HG12	1:B:279:LYS:N	2.22	0.54
1:D:278:VAL:HG12	1:D:279:LYS:N	2.22	0.54
1:G:182:ALA:N	1:G:183:PRO:HD3	2.22	0.54
1:D:150:VAL:HG13	1:F:180:GLY:HA2	1.88	0.54
1:C:111:ASP:OD1	1:D:71:ILE:HA	2.08	0.54
1:B:38:LEU:O	1:B:39:PHE:HB2	2.06	0.54
1:I:57:ILE:CG1	1:I:63:VAL:HG21	2.37	0.54
1:C:42:GLU:HG3	1:C:279:LYS:HE2	1.88	0.54
1:I:117:MET:HB2	1:I:271:LEU:HD13	1.89	0.54
1:L:186:PHE:CD2	1:L:196:ILE:HD11	2.43	0.54
1:K:112:MET:O	1:K:113:LYS:HB2	2.07	0.54
1:F:263:GLU:OE1	1:G:50:PRO:HG2	2.08	0.54
1:J:57:ILE:HG13	1:J:63:VAL:HG21	1.89	0.54
1:K:60:PHE:O	1:K:60:PHE:HD1	1.90	0.54
1:G:278:VAL:HG12	1:G:279:LYS:N	2.21	0.54
1:D:42:GLU:HG3	1:D:279:LYS:HE2	1.87	0.54
1:A:151:ASN:ND2	1:A:206:VAL:H	2.06	0.54
1:D:178:TYR:C	1:D:180:GLY:H	2.09	0.54
1:C:111:ASP:OD1	1:D:71:ILE:HG23	2.07	0.54
1:G:201:THR:CG2	1:H:159:VAL:HG11	2.33	0.54
1:C:213:GLN:HG3	1:D:207:VAL:CG1	2.37	0.54
1:I:42:GLU:HG3	1:I:279:LYS:HE2	1.89	0.54
1:I:213:GLN:HG3	1:J:207:VAL:CG1	2.37	0.54
1:F:117:MET:HB2	1:F:271:LEU:HD13	1.89	0.54
1:I:178:TYR:C	1:I:180:GLY:H	2.11	0.54
1:J:50:PRO:O	1:J:54:GLU:HG3	2.07	0.54
1:L:123:ASN:ND2	1:L:261:ARG:NH2	2.55	0.54
1:C:248:GLU:HG3	1:D:227:ILE:HG22	1.85	0.54
1:D:39:PHE:HA	1:D:280:PHE:O	2.08	0.54
1:D:169:LEU:HD13	1:D:173:GLN:OE1	2.07	0.54
1:L:42:GLU:HG3	1:L:279:LYS:HE2	1.89	0.54
1:H:151:ASN:HD22	1:H:207:VAL:CG2	2.21	0.54
1:G:277:LYS:O	1:G:278:VAL:HB	2.07	0.54
1:J:178:TYR:C	1:J:180:GLY:H	2.10	0.54
1:E:112:MET:O	1:E:113:LYS:HB2	2.06	0.54
1:C:182:ALA:N	1:C:183:PRO:CD	2.71	0.54
1:G:17:ARG:HG2	1:G:20:ARG:NH2	2.23	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:49:ASN:C	1:B:49:ASN:ND2	2.61	0.54
1:L:17:ARG:HG2	1:L:20:ARG:NH2	2.23	0.54
1:K:85:ASP:OD1	1:K:86:VAL:N	2.41	0.54
1:G:112:MET:O	1:G:113:LYS:HB2	2.07	0.54
1:G:50:PRO:O	1:G:54:GLU:HG3	2.08	0.54
1:E:123:ASN:ND2	1:E:257:PHE:HD2	1.90	0.54
1:D:117:MET:HB2	1:D:271:LEU:HD13	1.89	0.54
1:D:277:LYS:O	1:D:278:VAL:HB	2.07	0.54
1:B:213:GLN:HG3	1:C:207:VAL:CG1	2.38	0.54
1:E:178:TYR:C	1:E:180:GLY:H	2.10	0.54
1:J:174:VAL:O	1:J:177:GLN:HG3	2.07	0.54
1:C:17:ARG:HG2	1:C:20:ARG:NH2	2.23	0.54
1:A:50:PRO:O	1:A:54:GLU:HG3	2.08	0.54
1:C:248:GLU:OE1	1:D:227:ILE:HG23	2.08	0.54
1:I:123:ASN:O	1:I:124:ASN:OD1	2.25	0.54
1:H:56:SER:O	1:H:59:GLN:O	2.26	0.54
1:I:209:LYS:HD3	1:J:205:TYR:CE2	2.43	0.54
1:J:151:ASN:HD21	1:J:206:VAL:H	1.54	0.54
1:G:42:GLU:HG3	1:G:279:LYS:HE2	1.89	0.54
1:G:178:TYR:C	1:G:180:GLY:H	2.11	0.54
1:D:117:MET:CG	1:D:118:GLY:H	2.11	0.54
1:F:151:ASN:HD22	1:F:207:VAL:CG2	2.20	0.54
1:K:178:TYR:C	1:K:180:GLY:H	2.11	0.54
1:B:17:ARG:HG2	1:B:20:ARG:NH2	2.23	0.54
1:G:43:ASN:O	1:G:44:LEU:CB	2.56	0.54
1:B:98:PRO:O	1:B:99:VAL:HB	2.08	0.54
1:B:38:LEU:HD21	1:B:227:ILE:HD11	1.90	0.53
1:J:38:LEU:HD21	1:J:227:ILE:HD11	1.90	0.53
1:A:56:SER:O	1:A:59:GLN:O	2.25	0.53
1:C:209:LYS:HB2	1:D:205:TYR:OH	2.08	0.53
1:H:209:LYS:HB3	1:H:209:LYS:NZ	2.22	0.53
1:G:151:ASN:ND2	1:G:206:VAL:H	2.06	0.53
1:H:117:MET:CG	1:H:118:GLY:H	2.14	0.53
1:A:43:ASN:O	1:A:44:LEU:CB	2.54	0.53
1:D:71:ILE:HG22	1:D:71:ILE:O	2.08	0.53
1:J:39:PHE:HA	1:J:280:PHE:O	2.07	0.53
1:D:151:ASN:HD22	1:D:207:VAL:CG2	2.21	0.53
1:K:151:ASN:HD22	1:K:207:VAL:CG2	2.20	0.53
1:B:178:TYR:C	1:B:180:GLY:H	2.10	0.53
1:E:182:ALA:N	1:E:183:PRO:CD	2.72	0.53
1:E:186:PHE:CD2	1:E:196:ILE:HD11	2.42	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:186:PHE:CD2	1:G:196:ILE:HD11	2.43	0.53
1:K:169:LEU:HD13	1:K:173:GLN:OE1	2.08	0.53
1:F:71:ILE:HG22	1:F:71:ILE:O	2.08	0.53
1:J:117:MET:CG	1:J:118:GLY:H	2.10	0.53
1:H:117:MET:HB2	1:H:271:LEU:HD13	1.89	0.53
1:J:172:LYS:HG3	1:K:179:GLU:OE1	2.08	0.53
1:A:17:ARG:HG2	1:A:20:ARG:NH2	2.24	0.53
1:D:123:ASN:ND2	1:D:261:ARG:HH21	2.06	0.53
1:I:60:PHE:O	1:I:60:PHE:HD1	1.90	0.53
1:A:123:ASN:ND2	1:A:261:ARG:HH21	2.07	0.53
1:H:123:ASN:ND2	1:H:261:ARG:HH21	2.07	0.53
1:F:56:SER:O	1:F:59:GLN:O	2.26	0.53
1:G:117:MET:HB2	1:G:271:LEU:HD13	1.90	0.53
1:K:42:GLU:HG3	1:K:279:LYS:HE2	1.90	0.53
1:A:42:GLU:HG3	1:A:279:LYS:HE2	1.90	0.53
1:H:154:ALA:CB	1:J:182:ALA:HB2	2.38	0.53
1:L:182:ALA:N	1:L:183:PRO:CD	2.72	0.53
1:A:11:SER:CB	1:B:176:ASN:HD22	2.08	0.53
1:B:151:ASN:HD22	1:B:207:VAL:CG2	2.20	0.53
1:E:151:ASN:HD21	1:E:206:VAL:H	1.56	0.53
1:H:182:ALA:N	1:H:183:PRO:CD	2.72	0.53
1:H:112:MET:O	1:H:113:LYS:HB2	2.09	0.53
1:F:201:THR:O	1:F:201:THR:CG2	2.51	0.53
1:B:71:ILE:HG22	1:B:71:ILE:O	2.08	0.53
1:F:60:PHE:O	1:F:61:GLY:C	2.47	0.53
1:K:117:MET:CG	1:K:118:GLY:H	2.12	0.53
1:A:182:ALA:HB2	1:K:154:ALA:CB	2.38	0.53
1:L:174:VAL:O	1:L:177:GLN:HG3	2.08	0.53
1:I:98:PRO:O	1:I:99:VAL:HB	2.09	0.53
1:J:86:VAL:HA	1:K:99:VAL:HG11	1.89	0.53
1:I:85:ASP:OD1	1:I:86:VAL:N	2.41	0.53
1:B:112:MET:O	1:B:113:LYS:HB2	2.08	0.53
1:I:123:ASN:ND2	1:I:261:ARG:HH21	2.05	0.53
1:H:59:GLN:O	1:H:60:PHE:CD1	2.62	0.53
1:A:169:LEU:HD13	1:A:173:GLN:OE1	2.09	0.53
1:A:49:ASN:ND2	1:A:49:ASN:C	2.62	0.53
1:J:85:ASP:OD1	1:J:86:VAL:N	2.41	0.53
1:G:85:ASP:OD1	1:G:86:VAL:N	2.41	0.53
1:G:71:ILE:HG22	1:G:71:ILE:O	2.08	0.53
1:E:56:SER:O	1:E:59:GLN:O	2.26	0.53
1:F:125:ASP:O	1:F:126:MET:HE2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:151:ASN:ND2	1:D:206:VAL:H	2.07	0.53
1:B:144:LEU:HD21	1:C:152:GLN:NE2	2.23	0.53
1:K:102:LYS:HG3	1:K:103:GLU:N	2.24	0.53
1:L:222:MET:HE3	1:L:227:ILE:HG21	1.91	0.53
1:J:41:TRP:HA	1:J:277:LYS:HD3	1.91	0.53
1:F:209:LYS:NZ	1:F:209:LYS:HB3	2.23	0.53
1:C:178:TYR:C	1:C:180:GLY:H	2.11	0.53
1:J:186:PHE:CD2	1:J:196:ILE:HD11	2.44	0.53
1:K:209:LYS:NZ	1:K:209:LYS:HB3	2.24	0.53
1:B:123:ASN:ND2	1:B:261:ARG:HH21	2.07	0.53
1:E:123:ASN:O	1:E:124:ASN:OD1	2.27	0.53
1:D:98:PRO:O	1:D:99:VAL:HB	2.09	0.53
1:I:177:GLN:O	1:I:178:TYR:C	2.46	0.53
1:L:38:LEU:HD21	1:L:227:ILE:HD11	1.91	0.53
1:D:38:LEU:HD21	1:D:227:ILE:HD11	1.91	0.52
1:F:169:LEU:HD13	1:F:173:GLN:OE1	2.08	0.52
1:F:182:ALA:N	1:F:183:PRO:CD	2.72	0.52
1:D:182:ALA:N	1:D:183:PRO:CD	2.72	0.52
1:J:278:VAL:HG12	1:J:279:LYS:N	2.23	0.52
1:K:182:ALA:N	1:K:183:PRO:CD	2.72	0.52
1:I:182:ALA:N	1:I:183:PRO:CD	2.72	0.52
1:A:179:GLU:OE1	1:L:172:LYS:HG3	2.09	0.52
1:K:17:ARG:HG2	1:K:20:ARG:NH2	2.23	0.52
1:A:186:PHE:CD2	1:A:196:ILE:HD11	2.45	0.52
1:C:102:LYS:HG3	1:C:103:GLU:N	2.24	0.52
1:K:71:ILE:O	1:K:72:SER:HB3	2.09	0.52
1:J:71:ILE:O	1:J:72:SER:HB3	2.08	0.52
1:B:182:ALA:N	1:B:183:PRO:CD	2.72	0.52
1:L:151:ASN:HD22	1:L:207:VAL:CG2	2.22	0.52
1:E:177:GLN:O	1:E:178:TYR:C	2.48	0.52
1:K:177:GLN:O	1:K:178:TYR:C	2.47	0.52
1:D:201:THR:CG2	1:E:159:VAL:HG11	2.28	0.52
1:C:123:ASN:O	1:C:124:ASN:OD1	2.28	0.52
1:D:85:ASP:OD1	1:D:86:VAL:N	2.42	0.52
1:L:50:PRO:O	1:L:53:LEU:HB3	2.09	0.52
1:A:112:MET:O	1:A:113:LYS:HB2	2.08	0.52
1:H:50:PRO:O	1:H:54:GLU:HG3	2.09	0.52
1:D:186:PHE:CD2	1:D:196:ILE:HD11	2.44	0.52
1:L:56:SER:O	1:L:59:GLN:O	2.26	0.52
1:E:169:LEU:HD13	1:E:173:GLN:OE1	2.09	0.52
1:I:209:LYS:HB3	1:I:209:LYS:NZ	2.23	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:151:ASN:ND2	1:J:206:VAL:H	2.07	0.52
1:A:41:TRP:HA	1:A:277:LYS:HD3	1.92	0.52
1:L:177:GLN:O	1:L:178:TYR:C	2.48	0.52
1:L:178:TYR:C	1:L:180:GLY:H	2.11	0.52
1:C:177:GLN:O	1:C:178:TYR:C	2.47	0.52
1:B:150:VAL:HG13	1:D:180:GLY:HA2	1.92	0.52
1:G:177:GLN:O	1:G:178:TYR:C	2.48	0.52
1:C:98:PRO:O	1:C:99:VAL:HB	2.09	0.52
1:E:98:PRO:O	1:E:99:VAL:HB	2.09	0.52
1:C:123:ASN:ND2	1:C:257:PHE:HD2	1.92	0.52
1:K:71:ILE:HG22	1:K:71:ILE:O	2.09	0.52
1:A:182:ALA:N	1:A:183:PRO:CD	2.73	0.52
1:C:117:MET:HB2	1:C:271:LEU:HD13	1.91	0.52
1:D:174:VAL:O	1:D:177:GLN:HG3	2.09	0.52
1:E:17:ARG:HG2	1:E:20:ARG:NH2	2.24	0.52
1:A:57:ILE:CG1	1:A:63:VAL:HG21	2.39	0.52
1:F:41:TRP:HA	1:F:277:LYS:HD3	1.92	0.52
1:J:182:ALA:N	1:J:183:PRO:CD	2.72	0.52
1:I:17:ARG:HG2	1:I:20:ARG:NH2	2.24	0.52
1:K:43:ASN:O	1:K:44:LEU:CB	2.58	0.52
1:J:98:PRO:O	1:J:99:VAL:HB	2.09	0.52
1:F:102:LYS:HG3	1:F:103:GLU:N	2.25	0.52
1:G:123:ASN:ND2	1:G:261:ARG:HH21	2.06	0.52
1:L:57:ILE:CG1	1:L:63:VAL:HG21	2.39	0.52
1:B:169:LEU:HD13	1:B:173:GLN:OE1	2.09	0.52
1:C:93:PHE:HB2	1:C:106:LEU:HD21	1.92	0.52
1:F:154:ALA:CB	1:H:182:ALA:HB2	2.40	0.52
1:A:282:TYR:CE2	1:L:248:GLU:HB3	2.44	0.52
1:L:98:PRO:O	1:L:99:VAL:HB	2.09	0.52
1:J:249:GLN:HB3	1:K:222:MET:HE2	1.92	0.52
1:E:71:ILE:O	1:E:71:ILE:HG22	2.10	0.52
1:L:93:PHE:HB2	1:L:106:LEU:HD21	1.92	0.52
1:B:117:MET:CG	1:B:118:GLY:H	2.13	0.52
1:J:17:ARG:HG2	1:J:20:ARG:NH2	2.24	0.52
1:D:49:ASN:ND2	1:D:49:ASN:C	2.63	0.52
1:A:98:PRO:O	1:A:99:VAL:HB	2.10	0.52
1:G:102:LYS:HG3	1:G:103:GLU:N	2.24	0.52
1:I:186:PHE:CD2	1:I:196:ILE:HD11	2.45	0.52
1:G:123:ASN:O	1:G:124:ASN:OD1	2.28	0.52
1:K:38:LEU:HD21	1:K:227:ILE:HD11	1.92	0.52
1:K:38:LEU:O	1:K:39:PHE:HB2	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:60:PHE:O	1:K:61:GLY:C	2.49	0.52
1:I:169:LEU:HD13	1:I:173:GLN:OE1	2.10	0.52
1:G:98:PRO:O	1:G:99:VAL:HB	2.10	0.52
1:H:17:ARG:HG2	1:H:20:ARG:NH2	2.25	0.52
1:D:17:ARG:HG2	1:D:20:ARG:NH2	2.24	0.52
1:D:123:ASN:O	1:D:124:ASN:OD1	2.27	0.52
1:B:50:PRO:O	1:B:54:GLU:HG3	2.10	0.52
1:G:209:LYS:HB3	1:G:209:LYS:NZ	2.25	0.52
1:A:85:ASP:OD1	1:A:86:VAL:N	2.43	0.52
1:A:209:LYS:NZ	1:A:209:LYS:HB3	2.25	0.52
1:H:49:ASN:ND2	1:H:49:ASN:C	2.63	0.51
1:I:201:THR:CG2	1:J:159:VAL:HG11	2.20	0.51
1:I:56:SER:O	1:I:59:GLN:O	2.27	0.51
1:A:123:ASN:O	1:A:124:ASN:OD1	2.28	0.51
1:A:93:PHE:HB2	1:A:106:LEU:HD21	1.92	0.51
1:A:117:MET:CG	1:A:118:GLY:H	2.10	0.51
1:I:93:PHE:HB2	1:I:106:LEU:HD21	1.92	0.51
1:F:177:GLN:O	1:F:178:TYR:C	2.48	0.51
1:F:50:PRO:O	1:F:54:GLU:HG3	2.10	0.51
1:G:39:PHE:HA	1:G:280:PHE:O	2.10	0.51
1:I:60:PHE:HA	1:I:129:PRO:HG3	1.91	0.51
1:H:71:ILE:O	1:H:72:SER:HB3	2.09	0.51
1:I:151:ASN:HD22	1:I:207:VAL:CG2	2.23	0.51
1:D:115:GLU:CD	1:D:116:ASP:H	2.11	0.51
1:L:201:THR:O	1:L:201:THR:CG2	2.53	0.51
1:L:49:ASN:C	1:L:49:ASN:ND2	2.63	0.51
1:H:93:PHE:HB2	1:H:106:LEU:HD21	1.92	0.51
1:H:151:ASN:ND2	1:H:206:VAL:H	2.07	0.51
1:K:98:PRO:O	1:K:99:VAL:HB	2.10	0.51
1:E:11:SER:HB3	1:F:176:ASN:HD22	1.75	0.51
1:D:209:LYS:NZ	1:D:209:LYS:HB3	2.25	0.51
1:I:71:ILE:HG22	1:I:71:ILE:O	2.10	0.51
1:I:41:TRP:CE3	1:I:277:LYS:HE2	2.46	0.51
1:C:86:VAL:HG13	1:D:100:TYR:HB2	1.93	0.51
1:J:154:ALA:CA	1:L:182:ALA:HB2	2.39	0.51
1:J:102:LYS:HG3	1:J:103:GLU:N	2.25	0.51
1:C:283:ASP:CG	1:C:284:ILE:H	2.14	0.51
1:J:222:MET:CE	1:J:227:ILE:HG21	2.40	0.51
1:L:41:TRP:CE3	1:L:277:LYS:HE2	2.45	0.51
1:B:93:PHE:HB2	1:B:106:LEU:HD21	1.92	0.51
1:K:174:VAL:O	1:K:177:GLN:HG3	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:283:ASP:CG	1:L:284:ILE:H	2.14	0.51
1:F:38:LEU:HD21	1:F:227:ILE:HD11	1.92	0.51
1:G:38:LEU:O	1:G:39:PHE:CB	2.58	0.51
1:G:169:LEU:HD13	1:G:173:GLN:OE1	2.10	0.51
1:B:248:GLU:HB3	1:C:282:TYR:CE2	2.44	0.51
1:I:277:LYS:CE	1:I:278:VAL:H	2.24	0.51
1:E:174:VAL:O	1:E:177:GLN:HG3	2.10	0.51
1:H:41:TRP:HA	1:H:277:LYS:HD3	1.92	0.51
1:A:178:TYR:C	1:A:180:GLY:H	2.12	0.51
1:G:182:ALA:N	1:G:183:PRO:CD	2.74	0.51
1:B:115:GLU:CD	1:B:116:ASP:H	2.14	0.51
1:K:50:PRO:O	1:K:53:LEU:HB3	2.11	0.51
1:I:86:VAL:HA	1:J:99:VAL:HG11	1.92	0.51
1:J:112:MET:O	1:J:113:LYS:HB2	2.09	0.51
1:B:143:GLU:OE2	1:C:153:ASN:ND2	2.40	0.51
1:F:186:PHE:CD2	1:F:196:ILE:HD11	2.45	0.51
1:G:93:PHE:HB2	1:G:106:LEU:HD21	1.93	0.51
1:B:41:TRP:HA	1:B:277:LYS:HD3	1.93	0.51
1:F:41:TRP:CE3	1:F:277:LYS:HE2	2.45	0.51
1:A:177:GLN:O	1:A:178:TYR:C	2.47	0.51
1:L:12:ILE:HG22	1:L:13:ASN:N	2.26	0.51
1:F:178:TYR:C	1:F:180:GLY:H	2.12	0.51
1:A:102:LYS:HG3	1:A:103:GLU:N	2.25	0.51
1:G:222:MET:CE	1:G:227:ILE:HG21	2.40	0.51
1:A:201:THR:HG23	1:B:159:VAL:CG1	2.32	0.51
1:K:277:LYS:CE	1:K:278:VAL:H	2.24	0.51
1:C:41:TRP:HA	1:C:277:LYS:HD3	1.92	0.51
1:F:110:ARG:HB3	1:G:47:THR:HG22	1.92	0.51
1:J:38:LEU:O	1:J:39:PHE:HB2	2.11	0.51
1:H:168:GLN:HE22	1:H:169:LEU:HG	1.75	0.51
1:C:56:SER:O	1:C:59:GLN:O	2.29	0.51
1:J:169:LEU:HD13	1:J:173:GLN:OE1	2.11	0.51
1:F:168:GLN:HE22	1:F:169:LEU:HG	1.76	0.51
1:L:71:ILE:HG22	1:L:71:ILE:O	2.11	0.51
1:G:12:ILE:HG22	1:G:13:ASN:N	2.26	0.51
1:K:186:PHE:CD2	1:K:196:ILE:HD11	2.45	0.51
1:I:201:THR:CG2	1:I:201:THR:O	2.55	0.51
1:G:60:PHE:HA	1:G:129:PRO:HG3	1.93	0.51
1:K:222:MET:CE	1:K:227:ILE:HG21	2.41	0.51
1:K:158:PRO:O	1:K:159:VAL:CB	2.59	0.51
1:H:71:ILE:HG22	1:H:71:ILE:O	2.11	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:71:ILE:HG22	1:J:71:ILE:O	2.10	0.51
1:D:277:LYS:CE	1:D:278:VAL:H	2.24	0.51
1:F:17:ARG:HG2	1:F:20:ARG:NH2	2.26	0.51
1:C:11:SER:HB3	1:D:176:ASN:ND2	2.24	0.51
1:D:12:ILE:HG22	1:D:13:ASN:N	2.26	0.51
1:K:115:GLU:CD	1:K:116:ASP:H	2.14	0.51
1:E:43:ASN:O	1:E:44:LEU:CB	2.59	0.51
1:E:49:ASN:ND2	1:E:49:ASN:C	2.65	0.50
1:H:123:ASN:O	1:H:124:ASN:OD1	2.29	0.50
1:A:71:ILE:O	1:A:71:ILE:HG22	2.11	0.50
1:B:177:GLN:O	1:B:178:TYR:C	2.49	0.50
1:C:151:ASN:HD22	1:C:207:VAL:CG2	2.23	0.50
1:D:176:ASN:OD1	1:D:176:ASN:N	2.44	0.50
1:L:20:ARG:HG2	1:L:146:GLU:OE1	2.11	0.50
1:G:115:GLU:CD	1:G:116:ASP:H	2.14	0.50
1:D:43:ASN:O	1:D:44:LEU:CB	2.59	0.50
1:E:50:PRO:O	1:E:54:GLU:HG3	2.10	0.50
1:J:283:ASP:CG	1:J:284:ILE:H	2.14	0.50
1:K:222:MET:HE1	1:K:227:ILE:HG21	1.93	0.50
1:I:124:ASN:HD21	1:I:128:PHE:HB2	1.75	0.50
1:A:59:GLN:O	1:A:60:PHE:CD1	2.63	0.50
1:B:174:VAL:O	1:B:177:GLN:HG3	2.11	0.50
1:G:41:TRP:HA	1:G:277:LYS:HD3	1.93	0.50
1:C:182:ALA:H	1:C:183:PRO:HD3	1.76	0.50
1:I:178:TYR:H	1:I:178:TYR:HD2	1.59	0.50
1:J:283:ASP:CG	1:J:284:ILE:N	2.65	0.50
1:H:38:LEU:HD21	1:H:227:ILE:HD11	1.91	0.50
1:A:158:PRO:O	1:A:159:VAL:CB	2.60	0.50
1:C:71:ILE:O	1:C:71:ILE:HG22	2.10	0.50
1:H:213:GLN:HG3	1:I:207:VAL:CG1	2.40	0.50
1:D:178:TYR:C	1:D:180:GLY:N	2.65	0.50
1:I:49:ASN:ND2	1:I:49:ASN:C	2.63	0.50
1:I:50:PRO:O	1:I:53:LEU:HB3	2.11	0.50
1:G:283:ASP:CG	1:G:284:ILE:H	2.14	0.50
1:C:169:LEU:HD13	1:C:173:GLN:OE1	2.12	0.50
1:G:201:THR:HG23	1:H:159:VAL:CG1	2.32	0.50
1:B:41:TRP:CE3	1:B:277:LYS:HE2	2.47	0.50
1:C:41:TRP:CE3	1:C:277:LYS:HE2	2.47	0.50
1:C:277:LYS:CE	1:C:278:VAL:H	2.23	0.50
1:D:126:MET:O	1:D:128:PHE:N	2.39	0.50
1:G:126:MET:HG3	1:H:55:LYS:NZ	2.26	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:178:TYR:C	1:H:180:GLY:N	2.65	0.50
1:K:49:ASN:C	1:K:49:ASN:ND2	2.64	0.50
1:I:158:PRO:O	1:I:159:VAL:CB	2.57	0.50
1:L:169:LEU:HD13	1:L:173:GLN:OE1	2.11	0.50
1:D:168:GLN:HE22	1:D:169:LEU:HG	1.76	0.50
1:C:168:GLN:HE22	1:C:169:LEU:HG	1.76	0.50
1:A:123:ASN:ND2	1:A:257:PHE:HD2	1.91	0.50
1:J:168:GLN:HE22	1:J:169:LEU:HG	1.77	0.50
1:J:93:PHE:HB2	1:J:106:LEU:HD21	1.93	0.50
1:F:93:PHE:HB2	1:F:106:LEU:HD21	1.92	0.50
1:E:41:TRP:CE3	1:E:277:LYS:HE2	2.47	0.50
1:H:41:TRP:CE3	1:H:277:LYS:HE2	2.47	0.50
1:I:174:VAL:O	1:I:177:GLN:HG3	2.11	0.50
1:B:12:ILE:HG22	1:B:13:ASN:N	2.26	0.50
1:J:12:ILE:HG22	1:J:13:ASN:N	2.26	0.50
1:L:43:ASN:O	1:L:44:LEU:CB	2.59	0.50
1:D:102:LYS:HG3	1:D:103:GLU:N	2.26	0.50
1:L:84:ARG:HD2	1:L:88:ASN:O	2.12	0.50
1:D:71:ILE:O	1:D:72:SER:HB3	2.12	0.50
1:J:123:ASN:O	1:J:124:ASN:OD1	2.30	0.50
1:K:168:GLN:HE22	1:K:169:LEU:HG	1.77	0.50
1:C:71:ILE:O	1:C:72:SER:HB3	2.11	0.50
1:L:71:ILE:O	1:L:72:SER:HB3	2.11	0.50
1:J:209:LYS:HB3	1:J:209:LYS:NZ	2.27	0.50
1:E:41:TRP:HA	1:E:277:LYS:HD3	1.94	0.50
1:B:126:MET:HE2	1:C:36:TYR:CE1	2.46	0.50
1:H:174:VAL:O	1:H:177:GLN:HG3	2.12	0.50
1:H:177:GLN:O	1:H:178:TYR:C	2.50	0.50
1:E:154:ALA:CA	1:G:182:ALA:HB2	2.42	0.50
1:C:49:ASN:C	1:C:49:ASN:ND2	2.65	0.50
1:F:98:PRO:O	1:F:99:VAL:HB	2.11	0.50
1:E:93:PHE:HB2	1:E:106:LEU:HD21	1.94	0.50
1:L:178:TYR:H	1:L:178:TYR:HD2	1.59	0.50
1:D:177:GLN:O	1:D:178:TYR:C	2.50	0.50
1:F:201:THR:HG23	1:G:159:VAL:CG1	2.27	0.50
1:D:60:PHE:HA	1:D:129:PRO:HG3	1.93	0.50
1:J:201:THR:CG2	1:J:201:THR:O	2.57	0.50
1:F:123:ASN:ND2	1:F:261:ARG:HH21	2.10	0.50
1:B:178:TYR:C	1:B:180:GLY:N	2.65	0.50
1:I:43:ASN:O	1:I:44:LEU:CB	2.60	0.50
1:H:248:GLU:HB3	1:I:282:TYR:CZ	2.47	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:102:LYS:HG3	1:E:103:GLU:N	2.26	0.50
1:F:283:ASP:CG	1:F:284:ILE:H	2.15	0.50
1:H:283:ASP:CG	1:H:284:ILE:H	2.15	0.50
1:B:283:ASP:CG	1:B:284:ILE:H	2.15	0.50
1:I:249:GLN:HB3	1:J:222:MET:HE2	1.94	0.50
1:A:71:ILE:O	1:A:72:SER:HB3	2.11	0.50
1:C:213:GLN:O	1:C:216:ALA:HB3	2.12	0.50
1:B:248:GLU:CB	1:C:282:TYR:CZ	2.91	0.50
1:C:104:PHE:O	1:C:105:LYS:HB2	2.12	0.50
1:B:104:PHE:O	1:B:105:LYS:HB2	2.12	0.50
1:I:104:PHE:O	1:I:105:LYS:HB2	2.12	0.50
1:D:41:TRP:HA	1:D:277:LYS:HD3	1.94	0.50
1:E:151:ASN:ND2	1:E:206:VAL:H	2.10	0.50
1:L:283:ASP:CG	1:L:284:ILE:N	2.66	0.50
1:H:248:GLU:HB3	1:I:282:TYR:CE2	2.47	0.50
1:G:50:PRO:O	1:G:53:LEU:HB3	2.12	0.49
1:G:56:SER:O	1:G:59:GLN:O	2.30	0.49
1:K:57:ILE:HG13	1:K:63:VAL:HG21	1.94	0.49
1:E:57:ILE:HG13	1:E:63:VAL:HG21	1.94	0.49
1:B:248:GLU:CB	1:C:282:TYR:CE1	2.95	0.49
1:L:104:PHE:O	1:L:105:LYS:HB2	2.11	0.49
1:I:182:ALA:H	1:I:183:PRO:HD3	1.76	0.49
1:K:172:LYS:HG3	1:L:179:GLU:OE1	2.11	0.49
1:J:178:TYR:C	1:J:180:GLY:N	2.66	0.49
1:B:126:MET:HE2	1:C:36:TYR:CD1	2.47	0.49
1:G:283:ASP:CG	1:G:284:ILE:N	2.65	0.49
1:H:186:PHE:CD2	1:H:196:ILE:HD11	2.46	0.49
1:I:283:ASP:CG	1:I:284:ILE:H	2.15	0.49
1:B:71:ILE:O	1:B:72:SER:HB3	2.12	0.49
1:I:71:ILE:O	1:I:72:SER:HB3	2.12	0.49
1:B:277:LYS:CE	1:B:278:VAL:H	2.25	0.49
1:H:277:LYS:CE	1:H:278:VAL:H	2.25	0.49
1:A:150:VAL:HG13	1:C:180:GLY:HA2	1.93	0.49
1:J:49:ASN:C	1:J:49:ASN:ND2	2.63	0.49
1:E:115:GLU:CD	1:E:116:ASP:H	2.15	0.49
1:H:115:GLU:CD	1:H:116:ASP:H	2.16	0.49
1:F:12:ILE:HG22	1:F:13:ASN:N	2.27	0.49
1:C:283:ASP:CG	1:C:284:ILE:N	2.65	0.49
1:E:50:PRO:O	1:E:53:LEU:HB3	2.11	0.49
1:H:98:PRO:O	1:H:99:VAL:HB	2.11	0.49
1:H:102:LYS:HG3	1:H:103:GLU:N	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:176:ASN:OD1	1:B:176:ASN:N	2.44	0.49
1:J:60:PHE:CD1	1:J:60:PHE:O	2.64	0.49
1:K:123:ASN:O	1:K:124:ASN:OD1	2.30	0.49
1:A:222:MET:CE	1:A:227:ILE:HG21	2.42	0.49
1:C:123:ASN:ND2	1:C:261:ARG:HH21	2.09	0.49
1:C:178:TYR:H	1:C:178:TYR:HD2	1.58	0.49
1:H:12:ILE:HG22	1:H:13:ASN:N	2.28	0.49
1:C:12:ILE:HG22	1:C:13:ASN:N	2.27	0.49
1:C:43:ASN:O	1:C:44:LEU:CB	2.60	0.49
1:F:283:ASP:CG	1:F:284:ILE:N	2.66	0.49
1:B:140:GLU:CD	1:C:145:LYS:HE2	2.32	0.49
1:A:283:ASP:CG	1:A:284:ILE:H	2.15	0.49
1:I:60:PHE:O	1:I:61:GLY:C	2.51	0.49
1:A:130:THR:HG22	1:A:257:PHE:HE2	1.76	0.49
1:L:277:LYS:CE	1:L:278:VAL:H	2.25	0.49
1:C:277:LYS:NZ	1:C:278:VAL:O	2.38	0.49
1:E:178:TYR:H	1:E:178:TYR:HD2	1.60	0.49
1:K:178:TYR:C	1:K:180:GLY:N	2.66	0.49
1:D:178:TYR:HD2	1:D:178:TYR:H	1.61	0.49
1:A:178:TYR:HD2	1:A:178:TYR:H	1.60	0.49
1:E:12:ILE:HG22	1:E:13:ASN:N	2.27	0.49
1:A:115:GLU:CD	1:A:116:ASP:H	2.16	0.49
1:C:38:LEU:HD21	1:C:227:ILE:HD11	1.94	0.49
1:F:59:GLN:O	1:F:60:PHE:CD1	2.66	0.49
1:F:277:LYS:CE	1:F:278:VAL:H	2.26	0.49
1:D:50:PRO:O	1:D:54:GLU:HG3	2.12	0.49
1:C:174:VAL:O	1:C:177:GLN:HG3	2.12	0.49
1:F:178:TYR:H	1:F:178:TYR:HD2	1.61	0.49
1:B:186:PHE:CD2	1:B:196:ILE:HD11	2.46	0.49
1:I:102:LYS:HG3	1:I:103:GLU:N	2.27	0.49
1:D:50:PRO:O	1:D:53:LEU:HB3	2.13	0.49
1:K:12:ILE:HG22	1:K:13:ASN:N	2.27	0.49
1:F:174:VAL:O	1:F:177:GLN:HG3	2.11	0.49
1:H:11:SER:HB3	1:I:176:ASN:ND2	2.27	0.49
1:I:283:ASP:CG	1:I:284:ILE:N	2.66	0.49
1:E:283:ASP:CG	1:E:284:ILE:H	2.15	0.49
1:B:209:LYS:HB3	1:B:209:LYS:NZ	2.27	0.49
1:A:201:THR:O	1:A:201:THR:CG2	2.57	0.49
1:F:126:MET:HE1	1:G:36:TYR:HE1	1.77	0.49
1:G:104:PHE:O	1:G:105:LYS:HB2	2.13	0.49
1:A:151:ASN:ND2	1:A:207:VAL:HG23	2.27	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:12:ILE:HG22	1:I:13:ASN:N	2.28	0.49
1:L:115:GLU:CD	1:L:116:ASP:H	2.16	0.49
1:B:102:LYS:HG3	1:B:103:GLU:N	2.27	0.49
1:J:84:ARG:HD2	1:J:88:ASN:O	2.13	0.49
1:D:222:MET:HE3	1:D:227:ILE:HG21	1.94	0.49
1:K:59:GLN:O	1:K:60:PHE:CD1	2.66	0.49
1:F:71:ILE:O	1:F:72:SER:HB3	2.12	0.49
1:D:117:MET:CG	1:D:118:GLY:N	2.75	0.49
1:K:93:PHE:HB2	1:K:106:LEU:HD21	1.93	0.49
1:I:93:PHE:H	1:I:104:PHE:HB2	1.78	0.49
1:K:117:MET:CG	1:K:118:GLY:N	2.75	0.49
1:E:277:LYS:CE	1:E:278:VAL:H	2.26	0.49
1:J:177:GLN:O	1:J:178:TYR:C	2.50	0.49
1:K:20:ARG:HG2	1:K:146:GLU:OE1	2.12	0.49
1:C:115:GLU:CD	1:C:116:ASP:H	2.16	0.49
1:B:283:ASP:CG	1:B:284:ILE:N	2.66	0.49
1:L:176:ASN:OD1	1:L:176:ASN:N	2.46	0.49
1:D:60:PHE:O	1:D:61:GLY:C	2.52	0.49
1:A:41:TRP:CE3	1:A:277:LYS:HE2	2.48	0.49
1:E:178:TYR:C	1:E:180:GLY:N	2.66	0.49
1:A:174:VAL:O	1:A:177:GLN:HG3	2.12	0.49
1:A:12:ILE:HG22	1:A:13:ASN:N	2.27	0.49
1:H:86:VAL:HA	1:I:99:VAL:HG11	1.93	0.49
1:C:222:MET:CE	1:C:227:ILE:HG21	2.43	0.49
1:I:38:LEU:HD21	1:I:227:ILE:HD11	1.93	0.49
1:B:168:GLN:HE22	1:B:169:LEU:HG	1.78	0.49
1:B:201:THR:HG23	1:C:159:VAL:CG1	2.32	0.49
1:D:41:TRP:CE3	1:D:277:LYS:HE2	2.48	0.49
1:C:154:ALA:HA	1:E:181:ASN:O	2.12	0.49
1:J:115:GLU:CD	1:J:116:ASP:H	2.15	0.49
1:H:43:ASN:O	1:H:44:LEU:CB	2.60	0.49
1:H:50:PRO:O	1:H:53:LEU:HB3	2.13	0.49
1:G:71:ILE:O	1:G:72:SER:HB3	2.12	0.48
1:J:130:THR:HG22	1:J:257:PHE:HE2	1.78	0.48
1:D:20:ARG:HG2	1:D:146:GLU:OE1	2.13	0.48
1:F:49:ASN:ND2	1:F:49:ASN:C	2.65	0.48
1:A:283:ASP:CG	1:A:284:ILE:N	2.66	0.48
1:K:283:ASP:CG	1:K:284:ILE:N	2.67	0.48
1:D:283:ASP:CG	1:D:284:ILE:N	2.67	0.48
1:D:283:ASP:CG	1:D:284:ILE:H	2.16	0.48
1:F:248:GLU:HG3	1:G:227:ILE:HG22	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:L:123:ASN:ND2	1:L:261:ARG:HH21	2.11	0.48
1:H:169:LEU:HD13	1:H:173:GLN:OE1	2.13	0.48
1:A:125:ASP:O	1:A:126:MET:HE2	2.13	0.48
1:A:38:LEU:HD21	1:A:227:ILE:HD11	1.94	0.48
1:B:248:GLU:HB2	1:C:282:TYR:CE1	2.48	0.48
1:B:178:TYR:H	1:B:178:TYR:HD2	1.61	0.48
1:G:277:LYS:CE	1:G:278:VAL:H	2.26	0.48
1:A:277:LYS:CE	1:A:278:VAL:H	2.26	0.48
1:I:178:TYR:C	1:I:180:GLY:N	2.66	0.48
1:H:178:TYR:H	1:H:178:TYR:HD2	1.61	0.48
1:E:154:ALA:HA	1:G:181:ASN:O	2.13	0.48
1:A:50:PRO:O	1:A:53:LEU:HB3	2.13	0.48
1:B:101:GLN:O	1:B:102:LYS:HB2	2.13	0.48
1:G:59:GLN:O	1:G:60:PHE:CD1	2.66	0.48
1:H:60:PHE:O	1:H:61:GLY:C	2.51	0.48
1:E:71:ILE:O	1:E:72:SER:HB3	2.12	0.48
1:K:41:TRP:HA	1:K:277:LYS:HD3	1.95	0.48
1:I:222:MET:HE3	1:I:227:ILE:HG21	1.96	0.48
1:C:110:ARG:CB	1:D:47:THR:CG2	2.91	0.48
1:A:11:SER:CB	1:B:176:ASN:ND2	2.70	0.48
1:J:248:GLU:HG3	1:K:227:ILE:HG23	1.94	0.48
1:K:277:LYS:HE3	1:K:278:VAL:H	1.78	0.48
1:B:181:ASN:O	1:L:154:ALA:HA	2.14	0.48
1:G:178:TYR:H	1:G:178:TYR:HD2	1.60	0.48
1:I:115:GLU:CD	1:I:116:ASP:H	2.15	0.48
1:F:283:ASP:O	1:F:284:ILE:CB	2.62	0.48
1:L:102:LYS:HG3	1:L:103:GLU:N	2.28	0.48
1:G:57:ILE:HG13	1:G:63:VAL:HG21	1.95	0.48
1:D:182:ALA:H	1:D:183:PRO:HD3	1.76	0.48
1:H:104:PHE:O	1:H:105:LYS:HB2	2.14	0.48
1:L:41:TRP:HA	1:L:277:LYS:HD3	1.94	0.48
1:F:115:GLU:CD	1:F:116:ASP:H	2.16	0.48
1:A:99:VAL:HG11	1:L:86:VAL:HA	1.95	0.48
1:L:222:MET:CE	1:L:227:ILE:HG21	2.44	0.48
1:E:209:LYS:NZ	1:E:209:LYS:HB3	2.28	0.48
1:D:56:SER:O	1:D:59:GLN:O	2.31	0.48
1:J:59:GLN:O	1:J:60:PHE:CD1	2.67	0.48
1:K:56:SER:O	1:K:59:GLN:O	2.30	0.48
1:E:59:GLN:O	1:E:60:PHE:CD1	2.66	0.48
1:B:93:PHE:H	1:B:104:PHE:HB2	1.79	0.48
1:H:176:ASN:N	1:H:176:ASN:OD1	2.47	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:50:PRO:O	1:F:53:LEU:HB3	2.14	0.48
1:K:283:ASP:CG	1:K:284:ILE:H	2.16	0.48
1:I:248:GLU:HB3	1:J:282:TYR:CE2	2.48	0.48
1:E:60:PHE:O	1:E:61:GLY:C	2.51	0.48
1:A:168:GLN:HE22	1:A:169:LEU:HG	1.77	0.48
1:J:41:TRP:CE3	1:J:277:LYS:HE2	2.48	0.48
1:J:151:ASN:ND2	1:J:207:VAL:HG23	2.28	0.48
1:A:262:GLU:OE2	1:A:278:VAL:HG13	2.14	0.48
1:E:84:ARG:HD2	1:E:88:ASN:O	2.14	0.48
1:F:248:GLU:CG	1:G:227:ILE:CG2	2.87	0.48
1:H:57:ILE:HG13	1:H:63:VAL:HG21	1.94	0.48
1:I:168:GLN:HE22	1:I:169:LEU:HG	1.77	0.48
1:G:41:TRP:CE3	1:G:277:LYS:HE2	2.49	0.48
1:L:178:TYR:C	1:L:180:GLY:N	2.66	0.48
1:G:172:LYS:HG3	1:H:179:GLU:OE1	2.14	0.48
1:L:60:PHE:O	1:L:61:GLY:C	2.52	0.48
1:C:59:GLN:O	1:C:60:PHE:CD1	2.67	0.48
1:F:93:PHE:H	1:F:104:PHE:HB2	1.79	0.48
1:I:277:LYS:HE3	1:I:278:VAL:H	1.79	0.48
1:C:178:TYR:C	1:C:180:GLY:N	2.66	0.48
1:A:178:TYR:C	1:A:180:GLY:N	2.66	0.48
1:E:154:ALA:CB	1:G:182:ALA:HB2	2.44	0.48
1:I:176:ASN:N	1:I:176:ASN:OD1	2.47	0.48
1:D:131:THR:O	1:D:135:GLU:HG3	2.14	0.48
1:B:123:ASN:O	1:B:124:ASN:OD1	2.32	0.48
1:B:62:TYR:HB3	1:B:63:VAL:H	1.31	0.48
1:E:168:GLN:HE22	1:E:169:LEU:HG	1.78	0.48
1:H:60:PHE:O	1:H:60:PHE:CD1	2.67	0.48
1:H:93:PHE:H	1:H:104:PHE:HB2	1.79	0.48
1:A:176:ASN:OD1	1:A:176:ASN:N	2.46	0.48
1:D:93:PHE:HB2	1:D:106:LEU:HD21	1.94	0.48
1:I:154:ALA:HA	1:K:181:ASN:O	2.14	0.48
1:B:20:ARG:HG2	1:B:146:GLU:OE1	2.14	0.48
1:C:283:ASP:O	1:C:284:ILE:CB	2.62	0.48
1:H:283:ASP:CG	1:H:284:ILE:N	2.67	0.48
1:A:248:GLU:HG3	1:B:227:ILE:HG23	1.95	0.47
1:B:72:SER:O	1:B:74:ILE:HG13	2.14	0.47
1:K:93:PHE:H	1:K:104:PHE:HB2	1.79	0.47
1:D:104:PHE:O	1:D:105:LYS:HB2	2.14	0.47
1:I:154:ALA:CB	1:K:182:ALA:HB2	2.44	0.47
1:B:12:ILE:CG2	1:B:15:ILE:HB	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:222:MET:CE	1:F:227:ILE:HG21	2.44	0.47
1:C:84:ARG:HD2	1:C:88:ASN:O	2.14	0.47
1:F:84:ARG:HD2	1:F:88:ASN:O	2.13	0.47
1:C:57:ILE:HG13	1:C:63:VAL:HG21	1.95	0.47
1:H:124:ASN:HD21	1:H:128:PHE:HB2	1.79	0.47
1:F:57:ILE:HG13	1:F:63:VAL:HG21	1.95	0.47
1:H:277:LYS:HE3	1:H:278:VAL:H	1.79	0.47
1:J:178:TYR:H	1:J:178:TYR:HD2	1.61	0.47
1:F:283:ASP:O	1:F:284:ILE:CG1	2.62	0.47
1:E:283:ASP:O	1:E:284:ILE:CB	2.62	0.47
1:G:176:ASN:OD1	1:G:176:ASN:N	2.48	0.47
1:B:222:MET:CE	1:B:227:ILE:HG21	2.43	0.47
1:G:60:PHE:O	1:G:61:GLY:C	2.52	0.47
1:G:62:TYR:HB3	1:G:63:VAL:H	1.31	0.47
1:J:104:PHE:O	1:J:105:LYS:HB2	2.15	0.47
1:F:151:ASN:ND2	1:F:207:VAL:HG23	2.27	0.47
1:E:104:PHE:O	1:E:105:LYS:HB2	2.13	0.47
1:C:277:LYS:HE3	1:C:278:VAL:H	1.77	0.47
1:K:182:ALA:H	1:K:183:PRO:HD3	1.77	0.47
1:E:283:ASP:CG	1:E:284:ILE:N	2.67	0.47
1:B:59:GLN:O	1:B:60:PHE:CD1	2.67	0.47
1:G:38:LEU:HD11	1:G:225:LEU:HB3	1.96	0.47
1:K:176:ASN:OD1	1:K:176:ASN:N	2.48	0.47
1:J:262:GLU:OE2	1:J:278:VAL:HG13	2.14	0.47
1:A:150:VAL:HG22	1:C:180:GLY:HA2	1.95	0.47
1:C:179:GLU:C	1:C:181:ASN:N	2.67	0.47
1:G:283:ASP:O	1:G:284:ILE:CB	2.63	0.47
1:A:131:THR:O	1:A:135:GLU:HG3	2.15	0.47
1:D:38:LEU:HD11	1:D:225:LEU:HB3	1.96	0.47
1:D:60:PHE:CD1	1:D:60:PHE:O	2.68	0.47
1:E:93:PHE:H	1:E:104:PHE:HB2	1.78	0.47
1:G:93:PHE:H	1:G:104:PHE:HB2	1.79	0.47
1:B:277:LYS:HE3	1:B:278:VAL:H	1.80	0.47
1:D:277:LYS:HE3	1:D:278:VAL:H	1.79	0.47
1:H:12:ILE:CG2	1:H:15:ILE:HB	2.44	0.47
1:I:12:ILE:CG2	1:I:15:ILE:HB	2.44	0.47
1:G:49:ASN:ND2	1:G:49:ASN:C	2.64	0.47
1:D:283:ASP:O	1:D:284:ILE:CB	2.62	0.47
1:B:60:PHE:O	1:B:61:GLY:C	2.52	0.47
1:G:60:PHE:O	1:G:60:PHE:CD1	2.67	0.47
1:D:168:GLN:HB2	1:D:188:HIS:CE1	2.50	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:154:ALA:CA	1:J:182:ALA:HB2	2.44	0.47
1:H:20:ARG:HG2	1:H:146:GLU:OE1	2.15	0.47
1:J:12:ILE:CG2	1:J:15:ILE:HB	2.45	0.47
1:A:209:LYS:HD3	1:B:205:TYR:CE2	2.49	0.47
1:J:283:ASP:O	1:J:284:ILE:HG13	2.15	0.47
1:I:58:HIS:ND1	1:I:130:THR:HG21	2.29	0.47
1:B:60:PHE:CD1	1:B:60:PHE:O	2.68	0.47
1:B:57:ILE:HG13	1:B:63:VAL:HG21	1.97	0.47
1:D:57:ILE:HG12	1:D:63:VAL:HG21	1.96	0.47
1:D:62:TYR:HB3	1:D:63:VAL:H	1.31	0.47
1:I:248:GLU:HG3	1:J:227:ILE:HG23	1.97	0.47
1:I:59:GLN:O	1:I:60:PHE:CD1	2.67	0.47
1:C:60:PHE:O	1:C:61:GLY:C	2.52	0.47
1:L:191:LEU:O	1:L:192:ASP:HB3	2.15	0.47
1:I:209:LYS:H	1:I:209:LYS:HG2	1.38	0.47
1:L:204:PRO:O	1:L:205:TYR:CB	2.63	0.47
1:E:176:ASN:N	1:E:176:ASN:OD1	2.47	0.47
1:K:178:TYR:HD2	1:K:178:TYR:H	1.60	0.47
1:A:12:ILE:CG2	1:A:15:ILE:HB	2.44	0.47
1:G:174:VAL:O	1:G:177:GLN:HG3	2.14	0.47
1:G:178:TYR:C	1:G:180:GLY:N	2.67	0.47
1:E:12:ILE:CG2	1:E:15:ILE:HB	2.44	0.47
1:J:50:PRO:O	1:J:53:LEU:HB3	2.14	0.47
1:F:178:TYR:C	1:F:180:GLY:N	2.67	0.47
1:C:12:ILE:CG2	1:C:15:ILE:HB	2.44	0.47
1:L:50:PRO:O	1:L:54:GLU:HG3	2.14	0.47
1:A:283:ASP:O	1:A:284:ILE:CB	2.63	0.47
1:C:60:PHE:O	1:C:60:PHE:CD1	2.67	0.47
1:D:93:PHE:H	1:D:104:PHE:HB2	1.79	0.47
1:K:41:TRP:CE3	1:K:277:LYS:HE2	2.50	0.47
1:C:204:PRO:O	1:C:205:TYR:CB	2.63	0.47
1:F:117:MET:CG	1:F:118:GLY:N	2.76	0.47
1:I:11:SER:HB3	1:J:176:ASN:ND2	2.27	0.47
1:A:85:ASP:HB3	1:A:89:GLN:H	1.80	0.47
1:C:283:ASP:O	1:C:284:ILE:CG1	2.63	0.47
1:B:163:ALA:O	1:C:187:ALA:HA	2.15	0.47
1:K:191:LEU:O	1:K:192:ASP:HB3	2.15	0.47
1:L:104:PHE:O	1:L:105:LYS:CB	2.63	0.47
1:A:104:PHE:O	1:A:105:LYS:HB2	2.14	0.47
1:K:204:PRO:O	1:K:205:TYR:CB	2.62	0.47
1:A:204:PRO:O	1:A:205:TYR:CB	2.63	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:277:LYS:HE3	1:A:278:VAL:H	1.79	0.47
1:J:179:GLU:C	1:J:181:ASN:N	2.68	0.47
1:F:179:GLU:C	1:F:181:ASN:N	2.68	0.47
1:C:50:PRO:O	1:C:53:LEU:HB3	2.15	0.47
1:E:222:MET:CE	1:E:227:ILE:HG21	2.45	0.47
1:E:60:PHE:O	1:E:60:PHE:CD1	2.67	0.47
1:A:93:PHE:H	1:A:104:PHE:HB2	1.79	0.47
1:J:277:LYS:CE	1:J:278:VAL:H	2.26	0.47
1:I:41:TRP:HA	1:I:277:LYS:HD3	1.95	0.47
1:A:155:GLN:HG3	1:L:206:VAL:HG21	1.97	0.47
1:I:172:LYS:HG3	1:J:179:GLU:OE1	2.15	0.47
1:F:283:ASP:O	1:F:284:ILE:HG13	2.14	0.47
1:C:222:MET:HE3	1:C:227:ILE:HG21	1.96	0.47
1:C:176:ASN:N	1:C:176:ASN:OD1	2.48	0.46
1:C:93:PHE:H	1:C:104:PHE:HB2	1.79	0.46
1:J:93:PHE:H	1:J:104:PHE:HB2	1.80	0.46
1:B:179:GLU:C	1:B:181:ASN:N	2.68	0.46
1:E:151:ASN:ND2	1:E:207:VAL:HG23	2.26	0.46
1:G:20:ARG:HG2	1:G:146:GLU:OE1	2.15	0.46
1:G:283:ASP:O	1:G:284:ILE:HG13	2.15	0.46
1:B:283:ASP:O	1:B:284:ILE:CB	2.63	0.46
1:D:84:ARG:HD2	1:D:88:ASN:O	2.15	0.46
1:F:158:PRO:O	1:F:159:VAL:CB	2.62	0.46
1:L:168:GLN:HE22	1:L:169:LEU:HG	1.78	0.46
1:K:87:TYR:CE2	1:L:49:ASN:HB2	2.50	0.46
1:F:104:PHE:O	1:F:105:LYS:HB2	2.14	0.46
1:I:209:LYS:HB2	1:J:205:TYR:OH	2.15	0.46
1:F:20:ARG:HG2	1:F:146:GLU:OE1	2.16	0.46
1:K:12:ILE:CG2	1:K:15:ILE:HB	2.44	0.46
1:C:283:ASP:O	1:C:284:ILE:HG13	2.15	0.46
1:J:283:ASP:O	1:J:284:ILE:CB	2.64	0.46
1:H:283:ASP:O	1:H:284:ILE:CB	2.62	0.46
1:H:62:TYR:O	1:H:63:VAL:HB	2.15	0.46
1:B:104:PHE:O	1:B:105:LYS:CB	2.64	0.46
1:L:151:ASN:ND2	1:L:207:VAL:HG23	2.30	0.46
1:C:20:ARG:HG2	1:C:146:GLU:OE1	2.16	0.46
1:I:283:ASP:O	1:I:284:ILE:HG13	2.16	0.46
1:I:222:MET:CE	1:I:227:ILE:HG21	2.45	0.46
1:J:223:THR:HG23	1:J:250:ILE:HG12	1.97	0.46
1:L:58:HIS:ND1	1:L:130:THR:HG21	2.31	0.46
1:B:84:ARG:HD2	1:B:88:ASN:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:222:MET:HE1	1:J:227:ILE:HG21	1.96	0.46
1:C:57:ILE:N	1:C:63:VAL:HG21	2.31	0.46
1:H:39:PHE:HE1	1:H:258:LEU:HB2	1.80	0.46
1:K:179:GLU:C	1:K:181:ASN:N	2.69	0.46
1:L:179:GLU:C	1:L:181:ASN:N	2.67	0.46
1:J:274:LEU:HD13	1:J:274:LEU:C	2.35	0.46
1:F:43:ASN:O	1:F:44:LEU:CB	2.60	0.46
1:L:59:GLN:O	1:L:60:PHE:CD1	2.68	0.46
1:K:62:TYR:HB3	1:K:63:VAL:H	1.31	0.46
1:D:151:ASN:ND2	1:D:207:VAL:HG23	2.29	0.46
1:C:104:PHE:O	1:C:105:LYS:CB	2.64	0.46
1:H:204:PRO:O	1:H:205:TYR:CB	2.63	0.46
1:G:151:ASN:ND2	1:G:207:VAL:HG23	2.30	0.46
1:C:151:ASN:ND2	1:C:207:VAL:HG23	2.31	0.46
1:A:20:ARG:HG2	1:A:146:GLU:OE1	2.14	0.46
1:H:84:ARG:HD2	1:H:88:ASN:O	2.14	0.46
1:L:60:PHE:CD1	1:L:60:PHE:O	2.68	0.46
1:C:255:THR:HG21	1:D:281:ARG:HD3	1.98	0.46
1:A:60:PHE:O	1:A:60:PHE:CD1	2.67	0.46
1:A:60:PHE:O	1:A:61:GLY:C	2.53	0.46
1:C:209:LYS:HG2	1:C:209:LYS:H	1.38	0.46
1:L:93:PHE:H	1:L:104:PHE:HB2	1.80	0.46
1:J:209:LYS:H	1:J:209:LYS:HG2	1.36	0.46
1:G:277:LYS:HE3	1:G:278:VAL:H	1.80	0.46
1:D:125:ASP:O	1:D:126:MET:HE2	2.16	0.46
1:H:222:MET:CE	1:H:227:ILE:HG21	2.46	0.46
1:K:283:ASP:O	1:K:284:ILE:CB	2.63	0.46
1:D:222:MET:HE1	1:D:227:ILE:HG21	1.98	0.46
1:E:60:PHE:HA	1:E:129:PRO:HG3	1.97	0.46
1:A:182:ALA:H	1:A:183:PRO:HD3	1.79	0.46
1:D:179:GLU:C	1:D:181:ASN:N	2.68	0.46
1:H:38:LEU:HD11	1:H:225:LEU:HB3	1.98	0.46
1:I:283:ASP:O	1:I:284:ILE:CG1	2.64	0.46
1:K:283:ASP:O	1:K:284:ILE:CG1	2.64	0.46
1:G:84:ARG:HD2	1:G:88:ASN:O	2.15	0.46
1:I:126:MET:HG3	1:J:55:LYS:NZ	2.31	0.46
1:C:168:GLN:HB2	1:C:188:HIS:CE1	2.50	0.46
1:E:62:TYR:O	1:E:63:VAL:HB	2.16	0.46
1:F:204:PRO:O	1:F:205:TYR:CB	2.64	0.46
1:H:151:ASN:ND2	1:H:207:VAL:HG23	2.31	0.46
1:B:172:LYS:NZ	1:C:177:GLN:HE22	2.13	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:PRO:O	1:B:205:TYR:CB	2.63	0.46
1:J:101:GLN:O	1:J:102:LYS:HB2	2.15	0.46
1:G:283:ASP:O	1:G:284:ILE:CG1	2.63	0.46
1:C:223:THR:HG23	1:C:250:ILE:HG12	1.97	0.46
1:D:158:PRO:O	1:D:159:VAL:CB	2.59	0.46
1:B:39:PHE:CA	1:B:280:PHE:O	2.64	0.46
1:B:38:LEU:O	1:B:39:PHE:CB	2.63	0.46
1:J:277:LYS:HE3	1:J:278:VAL:H	1.80	0.46
1:F:262:GLU:OE2	1:F:278:VAL:HG13	2.16	0.46
1:I:179:GLU:C	1:I:181:ASN:N	2.70	0.46
1:I:20:ARG:HG2	1:I:146:GLU:OE1	2.16	0.46
1:F:154:ALA:CA	1:H:182:ALA:HB2	2.46	0.46
1:G:12:ILE:CG2	1:G:15:ILE:HB	2.45	0.46
1:F:176:ASN:OD1	1:F:176:ASN:N	2.48	0.46
1:J:283:ASP:O	1:J:284:ILE:CG1	2.64	0.46
1:G:143:GLU:OE2	1:H:153:ASN:ND2	2.44	0.46
1:F:248:GLU:OE1	1:G:227:ILE:HG23	2.16	0.46
1:D:59:GLN:O	1:D:60:PHE:CD1	2.69	0.46
1:H:170:SER:C	1:H:171:LEU:O	2.54	0.46
1:B:151:ASN:ND2	1:B:207:VAL:HG23	2.29	0.46
1:F:191:LEU:O	1:F:192:ASP:HB3	2.15	0.46
1:D:12:ILE:CG2	1:D:15:ILE:HB	2.45	0.46
1:J:176:ASN:OD1	1:J:176:ASN:N	2.47	0.46
1:D:248:GLU:CB	1:E:282:TYR:CZ	2.99	0.46
1:F:12:ILE:CG2	1:F:15:ILE:HB	2.44	0.46
1:I:85:ASP:HB3	1:I:89:GLN:H	1.80	0.46
1:L:283:ASP:O	1:L:284:ILE:CB	2.63	0.46
1:K:283:ASP:O	1:K:284:ILE:HG13	2.15	0.46
1:H:58:HIS:ND1	1:H:130:THR:HG21	2.31	0.46
1:G:168:GLN:HE22	1:G:169:LEU:HG	1.79	0.45
1:J:123:ASN:ND2	1:J:257:PHE:HD2	1.92	0.45
1:A:39:PHE:CZ	1:A:257:PHE:HB2	2.51	0.45
1:K:151:ASN:ND2	1:K:207:VAL:HG23	2.28	0.45
1:D:144:LEU:HD13	1:D:214:LYS:HA	1.98	0.45
1:E:204:PRO:O	1:E:205:TYR:CB	2.63	0.45
1:L:177:GLN:O	1:L:179:GLU:N	2.50	0.45
1:L:60:PHE:N	1:L:129:PRO:HB3	2.31	0.45
1:J:57:ILE:N	1:J:63:VAL:HG21	2.31	0.45
1:I:39:PHE:HE1	1:I:258:LEU:HB2	1.80	0.45
1:I:163:ALA:O	1:J:187:ALA:HA	2.16	0.45
1:B:105:LYS:HE2	1:B:114:GLU:OE1	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:154:ALA:HA	1:I:181:ASN:O	2.16	0.45
1:I:177:GLN:O	1:I:179:GLU:N	2.49	0.45
1:L:12:ILE:CG2	1:L:15:ILE:HB	2.45	0.45
1:G:85:ASP:HB3	1:G:89:GLN:H	1.81	0.45
1:F:101:GLN:O	1:F:102:LYS:HB2	2.16	0.45
1:A:84:ARG:HD2	1:A:88:ASN:O	2.16	0.45
1:H:72:SER:O	1:H:74:ILE:HG13	2.16	0.45
1:A:191:LEU:O	1:A:192:ASP:HB3	2.16	0.45
1:J:71:ILE:CG2	1:J:74:ILE:HD11	2.45	0.45
1:L:277:LYS:HE3	1:L:278:VAL:H	1.81	0.45
1:L:209:LYS:H	1:L:209:LYS:HG2	1.39	0.45
1:B:50:PRO:O	1:B:53:LEU:HB3	2.16	0.45
1:F:284:ILE:HG22	1:F:284:ILE:O	2.16	0.45
1:L:101:GLN:O	1:L:102:LYS:HB2	2.16	0.45
1:H:131:THR:O	1:H:135:GLU:HG3	2.17	0.45
1:K:84:ARG:HD2	1:K:88:ASN:O	2.16	0.45
1:G:62:TYR:O	1:G:63:VAL:HB	2.17	0.45
1:D:280:PHE:O	1:D:281:ARG:HB2	2.17	0.45
1:D:57:ILE:N	1:D:63:VAL:HG21	2.31	0.45
1:J:39:PHE:HE1	1:J:258:LEU:HB2	1.82	0.45
1:J:62:TYR:HB3	1:J:63:VAL:H	1.31	0.45
1:K:60:PHE:O	1:K:60:PHE:CD1	2.69	0.45
1:K:159:VAL:HA	1:K:199:PHE:O	2.16	0.45
1:C:159:VAL:HA	1:C:199:PHE:O	2.16	0.45
1:A:193:SER:O	1:A:195:SER:N	2.50	0.45
1:I:117:MET:CG	1:I:118:GLY:N	2.78	0.45
1:J:85:ASP:HB3	1:J:89:GLN:H	1.81	0.45
1:D:87:TYR:CE2	1:E:49:ASN:HB2	2.51	0.45
1:B:57:ILE:N	1:B:63:VAL:HG21	2.32	0.45
1:J:60:PHE:O	1:J:61:GLY:C	2.55	0.45
1:A:201:THR:CG2	1:B:159:VAL:HG11	2.33	0.45
1:J:191:LEU:O	1:J:192:ASP:HB3	2.15	0.45
1:I:191:LEU:O	1:I:192:ASP:HB3	2.17	0.45
1:D:262:GLU:OE2	1:D:278:VAL:HG13	2.16	0.45
1:A:204:PRO:O	1:A:205:TYR:HB3	2.16	0.45
1:K:177:GLN:O	1:K:179:GLU:N	2.49	0.45
1:F:86:VAL:HA	1:G:99:VAL:CG1	2.45	0.45
1:K:101:GLN:O	1:K:102:LYS:HB2	2.17	0.45
1:B:284:ILE:O	1:B:284:ILE:HG22	2.16	0.45
1:E:283:ASP:O	1:E:284:ILE:CG1	2.65	0.45
1:D:283:ASP:O	1:D:284:ILE:CG1	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:62:TYR:O	1:D:63:VAL:HB	2.17	0.45
1:C:191:LEU:O	1:C:192:ASP:HB3	2.17	0.45
1:E:38:LEU:HD11	1:E:225:LEU:HB3	1.99	0.45
1:I:170:SER:C	1:I:171:LEU:O	2.55	0.45
1:F:170:SER:C	1:F:171:LEU:O	2.54	0.45
1:F:168:GLN:HB2	1:F:188:HIS:CE1	2.51	0.45
1:F:277:LYS:HE3	1:F:278:VAL:H	1.82	0.45
1:J:150:VAL:HG13	1:L:180:GLY:CA	2.43	0.45
1:B:283:ASP:O	1:B:284:ILE:HG13	2.17	0.45
1:C:110:ARG:HB3	1:D:47:THR:CG2	2.45	0.45
1:I:280:PHE:O	1:I:281:ARG:HB2	2.17	0.45
1:C:170:SER:C	1:C:171:LEU:O	2.55	0.45
1:A:222:MET:HE3	1:A:227:ILE:HG21	1.98	0.45
1:E:39:PHE:CZ	1:E:257:PHE:HB2	2.52	0.45
1:K:204:PRO:O	1:K:205:TYR:HB3	2.17	0.45
1:C:206:VAL:HG21	1:D:155:GLN:HG3	1.98	0.45
1:A:177:GLN:HE22	1:L:172:LYS:NZ	2.14	0.45
1:E:11:SER:HB3	1:F:176:ASN:ND2	2.32	0.45
1:J:38:LEU:HD11	1:J:225:LEU:HB3	1.98	0.45
1:I:168:GLN:HB2	1:I:188:HIS:CE1	2.52	0.45
1:E:191:LEU:O	1:E:192:ASP:HB3	2.16	0.45
1:C:262:GLU:OE2	1:C:278:VAL:HG13	2.17	0.45
1:L:222:MET:HE3	1:L:227:ILE:CG2	2.47	0.45
1:C:101:GLN:O	1:C:102:LYS:HB2	2.15	0.45
1:J:113:LYS:HD2	1:J:113:LYS:O	2.17	0.45
1:I:283:ASP:O	1:I:284:ILE:CB	2.63	0.45
1:H:191:LEU:O	1:H:192:ASP:HB3	2.17	0.45
1:H:39:PHE:CZ	1:H:257:PHE:HB2	2.51	0.45
1:B:151:ASN:O	1:B:154:ALA:HB3	2.17	0.45
1:H:213:GLN:O	1:H:216:ALA:HB3	2.17	0.45
1:K:104:PHE:O	1:K:105:LYS:HB2	2.16	0.45
1:L:204:PRO:O	1:L:205:TYR:HB3	2.17	0.45
1:K:85:ASP:HB3	1:K:89:GLN:H	1.82	0.45
1:A:283:ASP:O	1:A:284:ILE:CG1	2.65	0.45
1:E:158:PRO:O	1:E:159:VAL:CB	2.65	0.45
1:K:170:SER:C	1:K:171:LEU:O	2.55	0.45
1:G:284:ILE:O	1:G:284:ILE:HG22	2.17	0.45
1:G:87:TYR:CE2	1:H:49:ASN:HB2	2.52	0.44
1:E:170:SER:C	1:E:171:LEU:O	2.55	0.44
1:A:170:SER:C	1:A:171:LEU:O	2.55	0.44
1:L:71:ILE:CG2	1:L:74:ILE:HD11	2.47	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:GLN:O	1:A:216:ALA:HB3	2.17	0.44
1:K:213:GLN:O	1:K:216:ALA:HB3	2.18	0.44
1:F:213:GLN:O	1:F:216:ALA:HB3	2.17	0.44
1:E:204:PRO:O	1:E:205:TYR:HB3	2.17	0.44
1:B:283:ASP:O	1:B:284:ILE:CG1	2.65	0.44
1:I:284:ILE:HG22	1:I:284:ILE:O	2.16	0.44
1:B:280:PHE:O	1:B:281:ARG:HB2	2.17	0.44
1:G:280:PHE:O	1:G:281:ARG:HB2	2.17	0.44
1:F:110:ARG:CB	1:G:47:THR:HG22	2.47	0.44
1:G:72:SER:O	1:G:74:ILE:HG13	2.17	0.44
1:G:168:GLN:HB2	1:G:188:HIS:CE1	2.52	0.44
1:C:158:PRO:O	1:C:159:VAL:CB	2.63	0.44
1:A:280:PHE:O	1:A:281:ARG:HB2	2.17	0.44
1:F:209:LYS:HB2	1:G:205:TYR:OH	2.16	0.44
1:E:277:LYS:HE3	1:E:278:VAL:H	1.81	0.44
1:B:150:VAL:HG22	1:D:180:GLY:HA2	1.99	0.44
1:A:283:ASP:O	1:A:284:ILE:HG13	2.17	0.44
1:E:283:ASP:O	1:E:284:ILE:HG13	2.17	0.44
1:J:259:LYS:O	1:J:263:GLU:HG3	2.17	0.44
1:A:57:ILE:HG13	1:A:63:VAL:HG21	1.99	0.44
1:A:187:ALA:HA	1:L:163:ALA:O	2.18	0.44
1:E:177:GLN:O	1:E:179:GLU:N	2.51	0.44
1:C:259:LYS:O	1:C:263:GLU:HG3	2.17	0.44
1:C:178:TYR:N	1:C:178:TYR:CD2	2.85	0.44
1:A:101:GLN:O	1:A:102:LYS:HB2	2.17	0.44
1:E:284:ILE:O	1:E:284:ILE:HG22	2.18	0.44
1:G:39:PHE:CZ	1:G:257:PHE:HB2	2.53	0.44
1:G:57:ILE:N	1:G:63:VAL:HG21	2.32	0.44
1:L:39:PHE:CZ	1:L:257:PHE:HB2	2.53	0.44
1:K:280:PHE:O	1:K:281:ARG:HB2	2.18	0.44
1:B:168:GLN:HB2	1:B:188:HIS:CE1	2.53	0.44
1:I:62:TYR:O	1:I:63:VAL:HB	2.18	0.44
1:A:57:ILE:N	1:A:63:VAL:HG21	2.32	0.44
1:C:57:ILE:HG12	1:C:63:VAL:HG21	1.99	0.44
1:A:168:GLN:HB2	1:A:188:HIS:CE1	2.52	0.44
1:F:130:THR:HG22	1:F:257:PHE:HE2	1.82	0.44
1:F:203:ALA:O	1:F:205:TYR:N	2.50	0.44
1:J:172:LYS:NZ	1:K:177:GLN:HE22	2.15	0.44
1:G:58:HIS:ND1	1:G:130:THR:HG21	2.32	0.44
1:D:159:VAL:HA	1:D:199:PHE:O	2.17	0.44
1:D:57:ILE:HG13	1:D:63:VAL:HG21	1.98	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:57:ILE:HG12	1:I:63:VAL:HG21	1.99	0.44
1:E:39:PHE:HE1	1:E:258:LEU:HB2	1.82	0.44
1:L:72:SER:O	1:L:74:ILE:HG13	2.17	0.44
1:I:72:SER:O	1:I:74:ILE:HG13	2.18	0.44
1:J:151:ASN:HD21	1:J:205:TYR:HA	1.83	0.44
1:C:284:ILE:HG22	1:C:284:ILE:O	2.17	0.44
1:I:101:GLN:O	1:I:102:LYS:HB2	2.18	0.44
1:K:38:LEU:HD11	1:K:225:LEU:HB3	1.98	0.44
1:J:170:SER:C	1:J:171:LEU:O	2.55	0.44
1:J:193:SER:O	1:J:195:SER:N	2.50	0.44
1:G:144:LEU:HD13	1:G:214:LYS:HA	1.99	0.44
1:E:168:GLN:HB2	1:E:188:HIS:CE1	2.53	0.44
1:C:280:PHE:O	1:C:281:ARG:HB2	2.18	0.44
1:H:60:PHE:N	1:H:129:PRO:HB3	2.33	0.44
1:D:204:PRO:O	1:D:205:TYR:CB	2.65	0.44
1:D:191:LEU:O	1:D:192:ASP:HB3	2.18	0.44
1:G:262:GLU:OE2	1:G:278:VAL:HG13	2.16	0.44
1:G:179:GLU:C	1:G:181:ASN:N	2.69	0.44
1:K:113:LYS:HD2	1:K:113:LYS:O	2.18	0.44
1:H:283:ASP:O	1:H:284:ILE:CG1	2.66	0.44
1:C:38:LEU:HD11	1:C:225:LEU:HB3	2.00	0.44
1:C:113:LYS:HD2	1:C:113:LYS:O	2.18	0.44
1:L:280:PHE:O	1:L:281:ARG:HB2	2.18	0.44
1:K:62:TYR:O	1:K:63:VAL:HB	2.18	0.44
1:A:62:TYR:HB3	1:A:63:VAL:H	1.31	0.44
1:J:163:ALA:O	1:K:187:ALA:HA	2.17	0.44
1:H:204:PRO:O	1:H:205:TYR:HB3	2.18	0.44
1:G:204:PRO:O	1:G:205:TYR:CB	2.66	0.44
1:C:204:PRO:O	1:C:205:TYR:HB3	2.18	0.44
1:F:85:ASP:HB3	1:F:89:GLN:H	1.83	0.44
1:E:87:TYR:CE2	1:F:49:ASN:HB2	2.52	0.44
1:D:283:ASP:O	1:D:284:ILE:HG13	2.18	0.44
1:I:84:ARG:HD2	1:I:88:ASN:O	2.17	0.44
1:L:131:THR:O	1:L:135:GLU:HG3	2.18	0.44
1:I:108:ASN:CG	1:I:108:ASN:O	2.55	0.44
1:G:158:PRO:O	1:G:159:VAL:CB	2.62	0.44
1:J:39:PHE:CA	1:J:280:PHE:O	2.65	0.44
1:E:57:ILE:N	1:E:63:VAL:HG21	2.33	0.44
1:K:168:GLN:HB2	1:K:188:HIS:CE1	2.53	0.44
1:H:57:ILE:N	1:H:63:VAL:HG21	2.32	0.44
1:L:85:ASP:HB3	1:L:89:GLN:H	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:284:ILE:HG22	1:H:284:ILE:O	2.17	0.44
1:H:140:GLU:CD	1:I:145:LYS:HE2	2.38	0.44
1:L:170:SER:C	1:L:171:LEU:O	2.56	0.43
1:G:170:SER:C	1:G:171:LEU:O	2.55	0.43
1:H:62:TYR:HB3	1:H:63:VAL:H	1.30	0.43
1:F:57:ILE:N	1:F:63:VAL:HG21	2.33	0.43
1:C:105:LYS:HE2	1:C:114:GLU:OE1	2.18	0.43
1:H:104:PHE:O	1:H:105:LYS:CB	2.66	0.43
1:A:104:PHE:O	1:A:105:LYS:CB	2.65	0.43
1:K:104:PHE:O	1:K:105:LYS:CB	2.66	0.43
1:D:105:LYS:HE2	1:D:114:GLU:OE1	2.18	0.43
1:B:262:GLU:OE2	1:B:278:VAL:HG13	2.18	0.43
1:E:179:GLU:C	1:E:181:ASN:N	2.68	0.43
1:F:178:TYR:N	1:F:178:TYR:CD2	2.86	0.43
1:I:113:LYS:O	1:I:113:LYS:HD2	2.18	0.43
1:B:203:ALA:O	1:B:205:TYR:N	2.51	0.43
1:F:39:PHE:HE1	1:F:258:LEU:HB2	1.81	0.43
1:F:104:PHE:O	1:F:105:LYS:CB	2.65	0.43
1:G:104:PHE:O	1:G:105:LYS:CB	2.66	0.43
1:L:213:GLN:O	1:L:216:ALA:HB3	2.18	0.43
1:C:150:VAL:HG13	1:E:180:GLY:CA	2.45	0.43
1:I:178:TYR:CD2	1:I:178:TYR:N	2.86	0.43
1:G:126:MET:HE1	1:H:36:TYR:CE1	2.53	0.43
1:B:53:LEU:HD11	1:B:121:ILE:HD12	2.00	0.43
1:I:110:ARG:C	1:I:112:MET:H	2.22	0.43
1:D:85:ASP:HB3	1:D:89:GLN:H	1.82	0.43
1:D:284:ILE:HG22	1:D:284:ILE:O	2.17	0.43
1:G:131:THR:O	1:G:135:GLU:HG3	2.18	0.43
1:B:62:TYR:O	1:B:63:VAL:HB	2.18	0.43
1:G:222:MET:HE3	1:G:227:ILE:HG21	1.99	0.43
1:L:57:ILE:HG12	1:L:63:VAL:HG21	1.99	0.43
1:I:39:PHE:CZ	1:I:257:PHE:HB2	2.53	0.43
1:I:60:PHE:O	1:I:60:PHE:CD1	2.69	0.43
1:H:168:GLN:HB2	1:H:188:HIS:CE1	2.53	0.43
1:F:62:TYR:O	1:F:63:VAL:HB	2.18	0.43
1:E:104:PHE:O	1:E:105:LYS:CB	2.66	0.43
1:I:262:GLU:OE2	1:I:278:VAL:HG13	2.18	0.43
1:G:213:GLN:O	1:G:216:ALA:HB3	2.19	0.43
1:D:213:GLN:O	1:D:216:ALA:HB3	2.18	0.43
1:A:177:GLN:O	1:A:179:GLU:N	2.51	0.43
1:E:20:ARG:HG2	1:E:146:GLU:OE1	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:101:GLN:O	1:D:102:LYS:HB2	2.18	0.43
1:J:62:TYR:O	1:J:63:VAL:HB	2.19	0.43
1:A:60:PHE:HA	1:A:129:PRO:HG3	2.00	0.43
1:G:163:ALA:O	1:H:187:ALA:HA	2.18	0.43
1:C:39:PHE:CZ	1:C:257:PHE:HB2	2.53	0.43
1:F:39:PHE:CZ	1:F:257:PHE:HB2	2.53	0.43
1:I:71:ILE:CG2	1:I:74:ILE:HD11	2.48	0.43
1:I:105:LYS:HE2	1:I:114:GLU:OE1	2.17	0.43
1:H:262:GLU:OE2	1:H:278:VAL:HG13	2.18	0.43
1:D:178:TYR:N	1:D:178:TYR:CD2	2.87	0.43
1:D:113:LYS:O	1:D:113:LYS:HD2	2.19	0.43
1:L:283:ASP:O	1:L:284:ILE:CG1	2.66	0.43
1:D:72:SER:O	1:D:74:ILE:HG13	2.19	0.43
1:D:71:ILE:CG2	1:D:74:ILE:HD11	2.48	0.43
1:I:57:ILE:N	1:I:63:VAL:HG21	2.32	0.43
1:D:201:THR:CG2	1:D:201:THR:O	2.57	0.43
1:F:72:SER:O	1:F:74:ILE:HG13	2.18	0.43
1:F:280:PHE:O	1:F:281:ARG:HB2	2.18	0.43
1:B:193:SER:O	1:B:195:SER:N	2.51	0.43
1:I:206:VAL:HG21	1:J:155:GLN:HG3	1.99	0.43
1:J:193:SER:C	1:J:195:SER:N	2.72	0.43
1:C:66:TYR:CE2	1:C:68:ASP:HA	2.54	0.43
1:H:105:LYS:HE2	1:H:114:GLU:OE1	2.18	0.43
1:E:213:GLN:O	1:E:216:ALA:HB3	2.19	0.43
1:G:105:LYS:HE2	1:G:114:GLU:OE1	2.19	0.43
1:G:151:ASN:HD21	1:G:205:TYR:HA	1.84	0.43
1:C:277:LYS:O	1:C:278:VAL:CB	2.67	0.43
1:E:178:TYR:N	1:E:178:TYR:CD2	2.86	0.43
1:A:178:TYR:N	1:A:178:TYR:CD2	2.87	0.43
1:G:177:GLN:O	1:G:179:GLU:N	2.51	0.43
1:H:274:LEU:HD13	1:H:274:LEU:C	2.39	0.43
1:B:85:ASP:HB3	1:B:89:GLN:HB2	2.00	0.43
1:G:110:ARG:C	1:G:112:MET:H	2.22	0.43
1:J:126:MET:HG3	1:K:55:LYS:NZ	2.34	0.43
1:I:126:MET:HE1	1:J:36:TYR:HE1	1.83	0.43
1:I:126:MET:HE1	1:J:36:TYR:CE1	2.54	0.43
1:C:62:TYR:O	1:C:63:VAL:HB	2.17	0.43
1:H:144:LEU:HD13	1:H:214:LYS:HA	2.00	0.43
1:I:204:PRO:O	1:I:205:TYR:CB	2.66	0.43
1:F:204:PRO:O	1:F:205:TYR:HB3	2.18	0.43
1:I:144:LEU:HD13	1:I:214:LYS:HA	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:203:ALA:O	1:J:205:TYR:N	2.51	0.43
1:L:284:ILE:HG22	1:L:284:ILE:O	2.16	0.43
1:B:259:LYS:O	1:B:263:GLU:HG3	2.18	0.43
1:I:259:LYS:O	1:I:263:GLU:HG3	2.19	0.43
1:F:131:THR:O	1:F:135:GLU:HG3	2.19	0.43
1:I:51:SER:O	1:I:55:LYS:HG3	2.19	0.43
1:L:62:TYR:O	1:L:63:VAL:HB	2.18	0.43
1:D:222:MET:HE3	1:D:227:ILE:CG2	2.49	0.43
1:C:130:THR:HG22	1:C:257:PHE:HE2	1.84	0.43
1:H:280:PHE:O	1:H:281:ARG:HB2	2.19	0.43
1:E:72:SER:O	1:E:74:ILE:HG13	2.17	0.43
1:A:71:ILE:CG2	1:A:74:ILE:HD11	2.49	0.43
1:G:191:LEU:O	1:G:192:ASP:HB3	2.18	0.43
1:D:104:PHE:O	1:D:105:LYS:CB	2.66	0.43
1:K:144:LEU:HD13	1:K:214:LYS:HA	2.00	0.43
1:B:204:PRO:O	1:B:205:TYR:HB3	2.18	0.43
1:C:283:ASP:O	1:C:284:ILE:HB	2.19	0.43
1:D:36:TYR:CD1	1:D:55:LYS:HD2	2.54	0.43
1:C:131:THR:O	1:C:135:GLU:HG3	2.18	0.43
1:G:39:PHE:CA	1:G:280:PHE:O	2.67	0.43
1:L:168:GLN:HB2	1:L:188:HIS:CE1	2.54	0.43
1:J:280:PHE:O	1:J:281:ARG:HB2	2.18	0.43
1:A:39:PHE:HE1	1:A:258:LEU:HB2	1.84	0.43
1:F:60:PHE:CD1	1:F:60:PHE:O	2.70	0.43
1:J:104:PHE:O	1:J:105:LYS:CB	2.67	0.43
1:J:105:LYS:HE2	1:J:114:GLU:OE1	2.19	0.43
1:H:151:ASN:HD21	1:H:205:TYR:HA	1.84	0.43
1:J:209:LYS:HD3	1:K:205:TYR:CE2	2.54	0.43
1:L:203:ALA:O	1:L:205:TYR:N	2.52	0.43
1:A:205:TYR:OH	1:L:209:LYS:HB2	2.19	0.43
1:B:274:LEU:HD13	1:B:274:LEU:C	2.39	0.43
1:H:85:ASP:HB3	1:H:89:GLN:HB2	2.01	0.43
1:K:110:ARG:C	1:K:112:MET:N	2.72	0.43
1:K:85:ASP:HB3	1:K:89:GLN:HB2	2.01	0.43
1:K:284:ILE:HG22	1:K:284:ILE:O	2.17	0.43
1:J:131:THR:O	1:J:135:GLU:HG3	2.18	0.43
1:L:259:LYS:O	1:L:263:GLU:HG3	2.19	0.43
1:B:222:MET:HE1	1:B:227:ILE:HG21	2.00	0.43
1:K:57:ILE:N	1:K:63:VAL:HG21	2.33	0.43
1:E:280:PHE:O	1:E:281:ARG:HB2	2.18	0.43
1:I:104:PHE:O	1:I:105:LYS:CB	2.66	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:277:LYS:O	1:I:278:VAL:CB	2.67	0.43
1:I:274:LEU:C	1:I:274:LEU:HD13	2.39	0.43
1:F:38:LEU:HD11	1:F:225:LEU:HB3	2.00	0.43
1:J:284:ILE:O	1:J:284:ILE:HG22	2.18	0.43
1:G:248:GLU:HB3	1:H:282:TYR:CZ	2.54	0.43
1:C:193:SER:O	1:C:195:SER:N	2.52	0.43
1:B:158:PRO:O	1:B:159:VAL:CB	2.60	0.43
1:E:62:TYR:HB3	1:E:63:VAL:H	1.31	0.43
1:C:39:PHE:HE1	1:C:258:LEU:HB2	1.83	0.43
1:A:72:SER:O	1:A:74:ILE:HG13	2.18	0.43
1:D:151:ASN:HD21	1:D:205:TYR:HA	1.84	0.43
1:K:105:LYS:HE2	1:K:114:GLU:OE1	2.19	0.43
1:J:182:ALA:H	1:J:183:PRO:HD3	1.79	0.43
1:K:209:LYS:HZ3	1:K:209:LYS:HB3	1.82	0.43
1:D:143:GLU:OE2	1:E:153:ASN:ND2	2.49	0.43
1:D:39:PHE:HE1	1:D:258:LEU:HB2	1.83	0.42
1:A:62:TYR:O	1:A:63:VAL:HB	2.19	0.42
1:L:105:LYS:HE2	1:L:114:GLU:OE1	2.19	0.42
1:B:277:LYS:O	1:B:278:VAL:CB	2.67	0.42
1:K:151:ASN:HD21	1:K:205:TYR:HA	1.84	0.42
1:G:277:LYS:NZ	1:G:278:VAL:O	2.36	0.42
1:F:42:GLU:HB2	1:F:277:LYS:HB3	2.01	0.42
1:C:86:VAL:CA	1:D:99:VAL:HG11	2.43	0.42
1:B:144:LEU:HD13	1:B:214:LYS:HA	2.00	0.42
1:A:209:LYS:HG2	1:A:209:LYS:H	1.40	0.42
1:E:101:GLN:O	1:E:102:LYS:HB2	2.19	0.42
1:E:283:ASP:O	1:E:284:ILE:HB	2.18	0.42
1:C:110:ARG:C	1:C:112:MET:N	2.72	0.42
1:G:71:ILE:CG2	1:G:74:ILE:HD11	2.49	0.42
1:I:57:ILE:HG13	1:I:63:VAL:HG21	2.01	0.42
1:K:72:SER:O	1:K:74:ILE:HG13	2.19	0.42
1:J:66:TYR:CE2	1:J:68:ASP:HA	2.54	0.42
1:A:105:LYS:HE2	1:A:114:GLU:OE1	2.19	0.42
1:J:277:LYS:O	1:J:278:VAL:CB	2.67	0.42
1:A:151:ASN:O	1:A:154:ALA:HB3	2.19	0.42
1:E:277:LYS:O	1:E:278:VAL:CB	2.68	0.42
1:E:131:THR:O	1:E:135:GLU:HG3	2.19	0.42
1:F:223:THR:HG23	1:F:250:ILE:HG12	2.01	0.42
1:J:60:PHE:HA	1:J:129:PRO:HG3	2.00	0.42
1:C:59:GLN:O	1:C:60:PHE:C	2.57	0.42
1:C:62:TYR:HB3	1:C:63:VAL:H	1.32	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:168:GLN:HB2	1:J:188:HIS:CE1	2.54	0.42
1:C:209:LYS:HB2	1:D:205:TYR:CZ	2.54	0.42
1:D:205:TYR:CD2	1:D:205:TYR:C	2.92	0.42
1:F:193:SER:C	1:F:195:SER:N	2.73	0.42
1:K:277:LYS:NZ	1:K:278:VAL:O	2.36	0.42
1:A:203:ALA:O	1:A:205:TYR:N	2.52	0.42
1:E:262:GLU:OE2	1:E:278:VAL:HG13	2.18	0.42
1:K:178:TYR:CD2	1:K:178:TYR:N	2.87	0.42
1:C:177:GLN:O	1:C:179:GLU:N	2.52	0.42
1:H:177:GLN:O	1:H:179:GLU:N	2.52	0.42
1:G:178:TYR:CD2	1:G:178:TYR:N	2.86	0.42
1:G:101:GLN:O	1:G:102:LYS:HB2	2.19	0.42
1:H:283:ASP:O	1:H:284:ILE:HG13	2.18	0.42
1:I:131:THR:O	1:I:135:GLU:HG3	2.19	0.42
1:K:39:PHE:HE1	1:K:258:LEU:HB2	1.83	0.42
1:B:170:SER:C	1:B:171:LEU:O	2.58	0.42
1:B:201:THR:CG2	1:C:159:VAL:HG11	2.33	0.42
1:E:71:ILE:CG2	1:E:74:ILE:HD11	2.49	0.42
1:I:151:ASN:ND2	1:I:207:VAL:HG23	2.32	0.42
1:F:193:SER:O	1:F:195:SER:N	2.52	0.42
1:B:178:TYR:CD2	1:B:178:TYR:N	2.87	0.42
1:J:178:TYR:N	1:J:178:TYR:CD2	2.87	0.42
1:B:85:ASP:HB3	1:B:89:GLN:H	1.84	0.42
1:H:85:ASP:HB3	1:H:89:GLN:H	1.85	0.42
1:I:109:TYR:O	1:I:110:ARG:HB2	2.18	0.42
1:G:85:ASP:HB3	1:G:89:GLN:HB2	2.01	0.42
1:L:283:ASP:O	1:L:284:ILE:HG13	2.18	0.42
1:H:283:ASP:O	1:H:284:ILE:HB	2.19	0.42
1:A:284:ILE:O	1:A:284:ILE:HG22	2.19	0.42
1:K:39:PHE:CZ	1:K:257:PHE:HB2	2.54	0.42
1:I:39:PHE:CE1	1:I:258:LEU:HB2	2.54	0.42
1:A:193:SER:C	1:A:195:SER:H	2.22	0.42
1:B:191:LEU:O	1:B:192:ASP:HB3	2.18	0.42
1:D:193:SER:O	1:D:195:SER:N	2.53	0.42
1:L:277:LYS:O	1:L:278:VAL:CB	2.68	0.42
1:J:213:GLN:O	1:J:216:ALA:HB3	2.20	0.42
1:J:204:PRO:O	1:J:205:TYR:CB	2.66	0.42
1:C:42:GLU:HB2	1:C:277:LYS:HB3	2.00	0.42
1:H:172:LYS:HG3	1:I:179:GLU:OE1	2.19	0.42
1:I:172:LYS:NZ	1:J:177:GLN:HE22	2.17	0.42
1:J:109:TYR:O	1:J:110:ARG:HB2	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:283:ASP:O	1:F:284:ILE:HB	2.20	0.42
1:A:248:GLU:CD	1:B:227:ILE:HG23	2.40	0.42
1:L:39:PHE:HE1	1:L:258:LEU:HB2	1.84	0.42
1:D:39:PHE:CZ	1:D:257:PHE:HB2	2.54	0.42
1:A:193:SER:C	1:A:195:SER:N	2.71	0.42
1:K:193:SER:C	1:K:195:SER:H	2.23	0.42
1:B:248:GLU:HB2	1:C:282:TYR:CD1	2.55	0.42
1:B:193:SER:C	1:B:195:SER:N	2.73	0.42
1:E:105:LYS:HE2	1:E:114:GLU:OE1	2.19	0.42
1:J:42:GLU:HB2	1:J:277:LYS:HB3	2.02	0.42
1:C:151:ASN:O	1:C:154:ALA:HB3	2.19	0.42
1:C:154:ALA:HB1	1:E:182:ALA:HB2	2.01	0.42
1:D:126:MET:HE1	1:E:36:TYR:CE1	2.54	0.42
1:J:20:ARG:HG2	1:J:146:GLU:OE1	2.19	0.42
1:E:85:ASP:HB3	1:E:89:GLN:H	1.85	0.42
1:E:113:LYS:O	1:E:113:LYS:HD2	2.20	0.42
1:H:113:LYS:HD2	1:H:113:LYS:O	2.19	0.42
1:A:113:LYS:HD2	1:A:113:LYS:O	2.18	0.42
1:C:110:ARG:C	1:C:112:MET:H	2.21	0.42
1:F:201:THR:CG2	1:G:159:VAL:HG11	2.27	0.42
1:E:38:LEU:O	1:E:39:PHE:HB2	2.20	0.42
1:K:163:ALA:O	1:L:187:ALA:HA	2.20	0.42
1:A:66:TYR:CE2	1:A:68:ASP:HA	2.55	0.42
1:J:144:LEU:HD13	1:J:214:LYS:HA	2.01	0.42
1:A:172:LYS:HG3	1:B:179:GLU:OE1	2.20	0.42
1:J:15:ILE:C	1:J:17:ARG:H	2.22	0.42
1:E:274:LEU:C	1:E:274:LEU:HD13	2.40	0.42
1:E:110:ARG:C	1:E:112:MET:N	2.73	0.42
1:A:259:LYS:O	1:A:263:GLU:HG3	2.19	0.42
1:E:140:GLU:CD	1:F:145:LYS:HE2	2.40	0.42
1:K:131:THR:O	1:K:135:GLU:HG3	2.20	0.42
1:B:58:HIS:ND1	1:B:130:THR:HG21	2.34	0.42
1:B:38:LEU:HD11	1:B:225:LEU:HB3	2.01	0.42
1:G:53:LEU:HD11	1:G:121:ILE:HD12	2.02	0.42
1:E:193:SER:C	1:E:195:SER:N	2.73	0.42
1:K:193:SER:C	1:K:195:SER:N	2.73	0.42
1:J:117:MET:HB2	1:J:271:LEU:HD11	2.02	0.42
1:F:151:ASN:HD21	1:F:205:TYR:HA	1.84	0.42
1:L:144:LEU:HD13	1:L:214:LYS:HA	2.02	0.42
1:D:172:LYS:HG3	1:E:179:GLU:OE1	2.19	0.42
1:H:42:GLU:HB2	1:H:277:LYS:HB3	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:110:ARG:C	1:H:112:MET:N	2.73	0.42
1:J:110:ARG:C	1:J:112:MET:H	2.23	0.42
1:B:131:THR:O	1:B:135:GLU:HG3	2.19	0.42
1:K:143:GLU:OE2	1:L:153:ASN:ND2	2.51	0.42
1:H:193:SER:C	1:H:195:SER:N	2.73	0.42
1:C:193:SER:C	1:C:195:SER:N	2.73	0.42
1:E:39:PHE:CA	1:E:280:PHE:O	2.68	0.42
1:H:39:PHE:CA	1:H:280:PHE:O	2.66	0.42
1:K:193:SER:O	1:K:195:SER:N	2.52	0.42
1:G:193:SER:O	1:G:195:SER:N	2.53	0.42
1:D:193:SER:C	1:D:195:SER:N	2.73	0.42
1:G:66:TYR:CE2	1:G:68:ASP:HA	2.54	0.42
1:K:262:GLU:OE2	1:K:278:VAL:HG13	2.20	0.42
1:C:85:ASP:HB3	1:C:89:GLN:H	1.85	0.42
1:A:151:ASN:HD21	1:A:205:TYR:HA	1.85	0.42
1:A:205:TYR:C	1:A:205:TYR:CD2	2.93	0.42
1:F:172:LYS:HG3	1:G:179:GLU:OE1	2.20	0.42
1:J:15:ILE:C	1:J:17:ARG:N	2.73	0.42
1:I:38:LEU:HD11	1:I:225:LEU:HB3	2.01	0.42
1:D:259:LYS:O	1:D:263:GLU:HG3	2.20	0.42
1:F:259:LYS:HD2	1:G:281:ARG:NH1	2.35	0.42
1:G:39:PHE:HE1	1:G:258:LEU:HB2	1.84	0.42
1:F:110:ARG:C	1:F:112:MET:H	2.22	0.42
1:I:66:TYR:CE2	1:I:68:ASP:HA	2.55	0.42
1:I:213:GLN:O	1:I:216:ALA:HB3	2.20	0.42
1:A:277:LYS:O	1:A:278:VAL:CB	2.66	0.42
1:B:213:GLN:O	1:B:216:ALA:HB3	2.19	0.42
1:H:178:TYR:N	1:H:178:TYR:CD2	2.88	0.42
1:F:177:GLN:O	1:F:179:GLU:N	2.53	0.42
1:B:86:VAL:HA	1:C:99:VAL:HG11	2.01	0.42
1:C:102:LYS:HG3	1:C:103:GLU:H	1.85	0.42
1:D:283:ASP:O	1:D:284:ILE:HB	2.19	0.42
1:I:108:ASN:ND2	1:I:270:GLU:HB3	2.35	0.42
1:E:58:HIS:ND1	1:E:130:THR:HG21	2.35	0.42
1:K:165:ASP:HB3	1:K:167:ASN:ND2	2.35	0.42
1:A:143:GLU:O	1:A:147:ILE:HG13	2.20	0.42
1:B:39:PHE:HE1	1:B:258:LEU:HB2	1.85	0.41
1:F:110:ARG:C	1:F:112:MET:N	2.72	0.41
1:C:72:SER:O	1:C:74:ILE:HG13	2.19	0.41
1:F:66:TYR:CE2	1:F:68:ASP:HA	2.55	0.41
1:F:193:SER:C	1:F:195:SER:H	2.24	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:104:PHE:HB3	1:A:105:LYS:H	1.54	0.41
1:B:177:GLN:O	1:B:179:GLU:N	2.53	0.41
1:L:205:TYR:CD2	1:L:205:TYR:C	2.93	0.41
1:A:274:LEU:C	1:A:274:LEU:HD13	2.40	0.41
1:A:109:TYR:O	1:A:110:ARG:HB2	2.20	0.41
1:H:259:LYS:O	1:H:263:GLU:HG3	2.20	0.41
1:C:109:TYR:O	1:C:110:ARG:HB2	2.20	0.41
1:C:110:ARG:NH2	1:D:72:SER:CB	2.67	0.41
1:B:39:PHE:CZ	1:B:257:PHE:HB2	2.55	0.41
1:B:57:ILE:HG12	1:B:63:VAL:HG21	2.02	0.41
1:I:39:PHE:CA	1:I:280:PHE:O	2.68	0.41
1:A:57:ILE:HG23	1:A:123:ASN:HB2	2.01	0.41
1:B:71:ILE:CG2	1:B:74:ILE:HD11	2.49	0.41
1:I:193:SER:O	1:I:195:SER:N	2.53	0.41
1:D:42:GLU:HB2	1:D:277:LYS:HB3	2.02	0.41
1:C:85:ASP:HB3	1:C:89:GLN:HB2	2.02	0.41
1:G:204:PRO:O	1:G:205:TYR:HB3	2.20	0.41
1:A:150:VAL:HG13	1:C:180:GLY:O	2.20	0.41
1:J:49:ASN:HD22	1:J:50:PRO:N	2.18	0.41
1:C:53:LEU:HD11	1:C:121:ILE:HD12	2.02	0.41
1:D:110:ARG:C	1:D:112:MET:H	2.23	0.41
1:D:110:ARG:C	1:D:112:MET:N	2.73	0.41
1:E:110:ARG:C	1:E:112:MET:H	2.23	0.41
1:G:113:LYS:HD2	1:G:113:LYS:O	2.19	0.41
1:B:98:PRO:O	1:B:99:VAL:CB	2.68	0.41
1:B:113:LYS:O	1:B:113:LYS:HD2	2.20	0.41
1:B:143:GLU:O	1:B:147:ILE:HG13	2.20	0.41
1:K:283:ASP:O	1:K:284:ILE:HB	2.20	0.41
1:E:209:LYS:H	1:E:209:LYS:HG2	1.38	0.41
1:G:87:TYR:CZ	1:H:49:ASN:N	2.82	0.41
1:D:87:TYR:CZ	1:E:49:ASN:N	2.85	0.41
1:L:39:PHE:CA	1:L:280:PHE:O	2.67	0.41
1:D:57:ILE:HG12	1:D:63:VAL:CG2	2.50	0.41
1:K:38:LEU:O	1:K:39:PHE:CB	2.68	0.41
1:H:57:ILE:HG12	1:H:63:VAL:HG21	2.01	0.41
1:E:193:SER:O	1:E:195:SER:N	2.53	0.41
1:G:193:SER:C	1:G:195:SER:N	2.73	0.41
1:B:117:MET:HB2	1:B:271:LEU:HD11	2.02	0.41
1:F:277:LYS:O	1:F:278:VAL:CB	2.68	0.41
1:E:151:ASN:HD21	1:E:205:TYR:HA	1.84	0.41
1:L:178:TYR:N	1:L:178:TYR:CD2	2.86	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:53:LEU:HD11	1:D:121:ILE:HD12	2.03	0.41
1:L:113:LYS:O	1:L:113:LYS:HD2	2.20	0.41
1:E:108:ASN:O	1:E:109:TYR:C	2.59	0.41
1:K:108:ASN:ND2	1:K:270:GLU:HB3	2.35	0.41
1:F:249:GLN:NE2	1:G:222:MET:HG3	2.34	0.41
1:F:259:LYS:O	1:F:263:GLU:HG3	2.19	0.41
1:G:57:ILE:HG12	1:G:63:VAL:HG21	2.02	0.41
1:D:39:PHE:CA	1:D:280:PHE:O	2.68	0.41
1:C:193:SER:C	1:C:195:SER:H	2.23	0.41
1:E:159:VAL:HA	1:E:199:PHE:O	2.21	0.41
1:K:71:ILE:CG2	1:K:74:ILE:HD11	2.51	0.41
1:J:204:PRO:O	1:J:205:TYR:HB3	2.21	0.41
1:E:203:ALA:O	1:E:205:TYR:N	2.53	0.41
1:D:274:LEU:HD13	1:D:274:LEU:C	2.41	0.41
1:E:85:ASP:HB3	1:E:89:GLN:HB2	2.01	0.41
1:H:108:ASN:O	1:H:109:TYR:C	2.59	0.41
1:D:85:ASP:HB3	1:D:89:GLN:HB2	2.01	0.41
1:K:259:LYS:O	1:K:263:GLU:HG3	2.20	0.41
1:K:39:PHE:CA	1:K:280:PHE:O	2.67	0.41
1:H:170:SER:O	1:H:171:LEU:O	2.38	0.41
1:H:163:ALA:O	1:I:187:ALA:HA	2.21	0.41
1:A:280:PHE:O	1:A:281:ARG:CB	2.68	0.41
1:A:61:GLY:O	1:A:62:TYR:O	2.38	0.41
1:C:144:LEU:HD13	1:C:214:LYS:HA	2.02	0.41
1:F:105:LYS:HE2	1:F:114:GLU:OE1	2.20	0.41
1:G:42:GLU:HB2	1:G:277:LYS:HB3	2.02	0.41
1:F:87:TYR:HB3	1:G:52:PHE:CD1	2.55	0.41
1:H:154:ALA:HB1	1:J:182:ALA:HB2	2.03	0.41
1:A:180:GLY:HA2	1:K:150:VAL:HG22	2.01	0.41
1:G:274:LEU:C	1:G:274:LEU:HD13	2.41	0.41
1:K:274:LEU:C	1:K:274:LEU:HD13	2.40	0.41
1:K:143:GLU:O	1:K:147:ILE:HG13	2.21	0.41
1:J:165:ASP:HB3	1:J:167:ASN:ND2	2.35	0.41
1:F:165:ASP:HB3	1:F:167:ASN:ND2	2.35	0.41
1:D:87:TYR:OH	1:E:48:ILE:CA	2.43	0.41
1:G:280:PHE:O	1:G:281:ARG:CB	2.69	0.41
1:J:39:PHE:CZ	1:J:257:PHE:HB2	2.55	0.41
1:D:170:SER:C	1:D:171:LEU:O	2.55	0.41
1:A:39:PHE:CA	1:A:280:PHE:O	2.67	0.41
1:G:193:SER:C	1:G:195:SER:H	2.24	0.41
1:H:209:LYS:HD3	1:I:205:TYR:CE2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:193:SER:C	1:J:195:SER:H	2.23	0.41
1:K:66:TYR:CE2	1:K:68:ASP:HA	2.56	0.41
1:D:66:TYR:CE2	1:D:68:ASP:HA	2.56	0.41
1:I:193:SER:C	1:I:195:SER:H	2.24	0.41
1:I:193:SER:C	1:I:195:SER:N	2.73	0.41
1:H:154:ALA:HA	1:J:181:ASN:O	2.20	0.41
1:B:49:ASN:HD22	1:B:50:PRO:N	2.18	0.41
1:L:85:ASP:HB3	1:L:89:GLN:HB2	2.02	0.41
1:G:102:LYS:HG3	1:G:103:GLU:H	1.85	0.41
1:F:113:LYS:HD2	1:F:113:LYS:O	2.21	0.41
1:J:38:LEU:O	1:J:39:PHE:CB	2.69	0.41
1:H:188:HIS:HB3	1:H:191:LEU:HG	2.03	0.41
1:H:74:ILE:HG22	1:H:75:ALA:N	2.36	0.41
1:I:151:ASN:HD21	1:I:205:TYR:HA	1.85	0.41
1:H:205:TYR:C	1:H:205:TYR:CD2	2.94	0.41
1:K:15:ILE:C	1:K:17:ARG:N	2.74	0.41
1:J:154:ALA:HB1	1:L:182:ALA:HB2	2.01	0.41
1:L:15:ILE:C	1:L:17:ARG:N	2.74	0.41
1:K:53:LEU:HD11	1:K:121:ILE:HD12	2.02	0.41
1:K:110:ARG:C	1:K:112:MET:H	2.22	0.41
1:B:110:ARG:C	1:B:112:MET:N	2.73	0.41
1:J:110:ARG:C	1:J:112:MET:N	2.74	0.41
1:B:283:ASP:O	1:B:284:ILE:HB	2.20	0.41
1:D:282:TYR:CG	1:D:283:ASP:N	2.89	0.41
1:F:11:SER:HB3	1:G:176:ASN:HD22	1.85	0.41
1:H:165:ASP:HB3	1:H:167:ASN:ND2	2.36	0.41
1:A:108:ASN:ND2	1:A:270:GLU:HB3	2.35	0.41
1:L:57:ILE:N	1:L:63:VAL:HG21	2.35	0.41
1:D:280:PHE:O	1:D:281:ARG:CB	2.69	0.41
1:A:38:LEU:O	1:A:39:PHE:HB2	2.21	0.41
1:B:193:SER:C	1:B:195:SER:H	2.24	0.41
1:L:66:TYR:CE2	1:L:68:ASP:HA	2.55	0.41
1:D:117:MET:HB2	1:D:271:LEU:HD11	2.03	0.41
1:E:66:TYR:CE2	1:E:68:ASP:HA	2.55	0.41
1:I:209:LYS:HB3	1:I:209:LYS:HZ2	1.85	0.41
1:A:49:ASN:HA	1:A:50:PRO:HD2	1.95	0.41
1:I:85:ASP:HB3	1:I:89:GLN:HB2	2.03	0.41
1:K:209:LYS:HG2	1:K:209:LYS:H	1.36	0.41
1:L:283:ASP:O	1:L:284:ILE:HB	2.20	0.41
1:B:108:ASN:O	1:B:109:TYR:C	2.59	0.41
1:D:60:PHE:N	1:D:129:PRO:HB3	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:K:57:ILE:HG23	1:K:123:ASN:HB2	2.00	0.41
1:I:280:PHE:O	1:I:281:ARG:CB	2.69	0.41
1:H:193:SER:C	1:H:195:SER:H	2.24	0.41
1:H:193:SER:O	1:H:195:SER:N	2.54	0.41
1:C:188:HIS:HB3	1:C:191:LEU:HG	2.03	0.41
1:E:124:ASN:HD21	1:E:128:PHE:HB2	1.86	0.41
1:H:71:ILE:CG2	1:H:74:ILE:HD11	2.51	0.41
1:C:71:ILE:CG2	1:C:74:ILE:HD11	2.50	0.41
1:J:72:SER:O	1:J:74:ILE:HG13	2.20	0.41
1:E:193:SER:C	1:E:195:SER:H	2.24	0.41
1:H:209:LYS:O	1:H:212:ALA:HB3	2.21	0.41
1:I:204:PRO:O	1:I:205:TYR:HB3	2.20	0.41
1:H:104:PHE:HB3	1:H:105:LYS:H	1.56	0.41
1:J:205:TYR:C	1:J:205:TYR:CD2	2.93	0.41
1:L:151:ASN:O	1:L:154:ALA:HB3	2.20	0.41
1:D:269:ASN:ND2	1:D:275:ASN:H	2.19	0.41
1:G:203:ALA:O	1:G:205:TYR:N	2.53	0.41
1:A:269:ASN:ND2	1:A:275:ASN:H	2.18	0.41
1:I:154:ALA:CA	1:K:182:ALA:HB2	2.49	0.41
1:F:86:VAL:HG13	1:G:100:TYR:HB2	2.03	0.41
1:J:177:GLN:O	1:J:179:GLU:N	2.54	0.41
1:D:177:GLN:O	1:D:179:GLU:N	2.54	0.41
1:L:110:ARG:C	1:L:112:MET:H	2.24	0.41
1:D:108:ASN:ND2	1:D:270:GLU:HB3	2.36	0.41
1:D:108:ASN:O	1:D:109:TYR:C	2.59	0.41
1:G:108:ASN:O	1:G:109:TYR:C	2.59	0.41
1:H:109:TYR:O	1:H:110:ARG:HB2	2.21	0.41
1:B:110:ARG:C	1:B:112:MET:H	2.23	0.41
1:A:85:ASP:HB3	1:A:89:GLN:HB2	2.02	0.41
1:G:283:ASP:O	1:G:284:ILE:HB	2.20	0.41
1:B:282:TYR:CG	1:B:283:ASP:N	2.89	0.41
1:A:87:TYR:OH	1:B:48:ILE:HA	2.21	0.41
1:K:34:LEU:HA	1:K:34:LEU:HD23	1.97	0.41
1:G:57:ILE:HA	1:G:61:GLY:O	2.21	0.41
1:E:57:ILE:HG12	1:E:63:VAL:HG21	2.02	0.41
1:C:57:ILE:HG12	1:C:63:VAL:CG2	2.52	0.41
1:I:205:TYR:C	1:I:205:TYR:CD2	2.94	0.41
1:F:209:LYS:HB2	1:G:205:TYR:CZ	2.55	0.41
1:C:151:ASN:HD21	1:C:205:TYR:HA	1.85	0.41
1:K:15:ILE:C	1:K:17:ARG:H	2.23	0.41
1:D:15:ILE:C	1:D:17:ARG:N	2.74	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:I:15:ILE:C	1:I:17:ARG:N	2.75	0.41
1:H:108:ASN:ND2	1:H:270:GLU:HB3	2.36	0.41
1:B:108:ASN:ND2	1:B:270:GLU:HB3	2.36	0.41
1:A:42:GLU:HB2	1:A:277:LYS:HB3	2.02	0.40
1:H:15:ILE:C	1:H:17:ARG:N	2.74	0.40
1:D:15:ILE:C	1:D:17:ARG:H	2.24	0.40
1:L:109:TYR:O	1:L:110:ARG:HB2	2.21	0.40
1:K:102:LYS:HG3	1:K:103:GLU:H	1.85	0.40
1:A:110:ARG:C	1:A:112:MET:N	2.74	0.40
1:A:283:ASP:O	1:A:284:ILE:HB	2.20	0.40
1:K:140:GLU:CD	1:L:145:LYS:HE2	2.42	0.40
1:L:165:ASP:HB3	1:L:167:ASN:ND2	2.36	0.40
1:B:280:PHE:O	1:B:281:ARG:CB	2.69	0.40
1:F:109:TYR:O	1:F:110:ARG:HB2	2.22	0.40
1:A:188:HIS:HB3	1:A:191:LEU:HG	2.03	0.40
1:L:193:SER:C	1:L:195:SER:N	2.74	0.40
1:H:66:TYR:CE2	1:H:68:ASP:HA	2.56	0.40
1:H:172:LYS:NZ	1:I:177:GLN:HE22	2.19	0.40
1:D:126:MET:HE1	1:E:36:TYR:CD1	2.56	0.40
1:A:15:ILE:C	1:A:17:ARG:N	2.74	0.40
1:E:15:ILE:C	1:E:17:ARG:H	2.24	0.40
1:J:53:LEU:HD11	1:J:121:ILE:HD12	2.02	0.40
1:C:274:LEU:C	1:C:274:LEU:HD13	2.40	0.40
1:G:110:ARG:C	1:G:112:MET:N	2.72	0.40
1:G:282:TYR:CG	1:G:283:ASP:N	2.88	0.40
1:H:101:GLN:O	1:H:102:LYS:HB2	2.19	0.40
1:D:78:GLY:HA3	1:D:95:ALA:HA	2.04	0.40
1:L:158:PRO:O	1:L:159:VAL:CB	2.64	0.40
1:B:61:GLY:O	1:B:62:TYR:O	2.39	0.40
1:A:38:LEU:HD11	1:A:225:LEU:HB3	2.02	0.40
1:E:39:PHE:CE1	1:E:258:LEU:HB2	2.57	0.40
1:D:203:ALA:O	1:D:205:TYR:N	2.55	0.40
1:A:144:LEU:HD13	1:A:214:LYS:HA	2.03	0.40
1:D:193:SER:C	1:D:195:SER:H	2.23	0.40
1:E:15:ILE:C	1:E:17:ARG:N	2.74	0.40
1:F:274:LEU:HD13	1:F:274:LEU:C	2.41	0.40
1:D:109:TYR:O	1:D:110:ARG:HB2	2.21	0.40
1:L:98:PRO:O	1:L:99:VAL:CB	2.69	0.40
1:F:71:ILE:CG2	1:F:74:ILE:HD11	2.51	0.40
1:F:128:PHE:HA	1:F:129:PRO:HD3	1.97	0.40
1:C:74:ILE:HG22	1:C:75:ALA:N	2.37	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:151:ASN:O	1:D:154:ALA:HB3	2.22	0.40
1:B:42:GLU:HB2	1:B:277:LYS:HB3	2.04	0.40
1:D:277:LYS:O	1:D:278:VAL:CB	2.69	0.40
1:F:209:LYS:HZ2	1:F:209:LYS:HB3	1.86	0.40
1:G:205:TYR:C	1:G:205:TYR:CD2	2.95	0.40
1:H:277:LYS:O	1:H:278:VAL:CB	2.68	0.40
1:F:172:LYS:NZ	1:G:177:GLN:HE22	2.19	0.40
1:J:102:LYS:HG3	1:J:103:GLU:H	1.86	0.40
1:J:283:ASP:O	1:J:284:ILE:HB	2.22	0.40
1:B:165:ASP:HB3	1:B:167:ASN:ND2	2.36	0.40
1:C:165:ASP:HB3	1:C:167:ASN:ND2	2.36	0.40
1:J:61:GLY:O	1:J:62:TYR:O	2.39	0.40
1:D:204:PRO:O	1:D:205:TYR:HB3	2.21	0.40
1:B:180:GLY:CA	1:L:150:VAL:HG13	2.47	0.40
1:L:151:ASN:HD21	1:L:205:TYR:HA	1.86	0.40
1:C:117:MET:HB2	1:C:271:LEU:HD11	2.04	0.40
1:F:144:LEU:HD13	1:F:214:LYS:HA	2.02	0.40
1:G:154:ALA:HB1	1:I:182:ALA:HB2	2.02	0.40
1:B:15:ILE:C	1:B:17:ARG:H	2.25	0.40
1:B:15:ILE:C	1:B:17:ARG:N	2.75	0.40
1:A:15:ILE:C	1:A:17:ARG:H	2.24	0.40
1:I:15:ILE:C	1:I:17:ARG:H	2.24	0.40
1:G:109:TYR:O	1:G:110:ARG:HB2	2.21	0.40
1:H:222:MET:HE3	1:H:227:ILE:HG21	2.02	0.40
1:E:108:ASN:ND2	1:E:270:GLU:HB3	2.36	0.40
1:F:108:ASN:ND2	1:F:270:GLU:HB3	2.37	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:272:TYR:OH	1:I:62:TYR:OH[3_445]	2.12	0.08

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	B	253/309 (82%)	182 (72%)	37 (15%)	34 (13%)	0	1
1	C	253/309 (82%)	179 (71%)	40 (16%)	34 (13%)	0	1
1	D	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	E	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	F	253/309 (82%)	180 (71%)	38 (15%)	35 (14%)	0	1
1	G	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
1	H	253/309 (82%)	180 (71%)	38 (15%)	35 (14%)	0	1
1	I	253/309 (82%)	181 (72%)	37 (15%)	35 (14%)	0	1
1	J	253/309 (82%)	182 (72%)	37 (15%)	34 (13%)	0	1
1	K	253/309 (82%)	181 (72%)	39 (15%)	33 (13%)	0	2
1	L	253/309 (82%)	181 (72%)	38 (15%)	34 (13%)	0	1
All	All	3036/3708 (82%)	2170 (72%)	456 (15%)	410 (14%)	0	1

All (410) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	62	TYR
1	A	105	LYS
1	A	107	TYR
1	A	113	LYS
1	A	117	MET
1	A	127	ALA
1	A	181	ASN
1	A	182	ALA
1	A	279	LYS
1	A	281	ARG
1	A	284	ILE
1	B	61	GLY
1	B	62	TYR
1	B	105	LYS
1	B	107	TYR
1	B	113	LYS
1	B	117	MET
1	B	127	ALA
1	B	181	ASN

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Mol	Chain	Res	Type
1	B	182	ALA
1	B	183	PRO
1	B	279	LYS
1	B	281	ARG
1	B	284	ILE
1	C	62	TYR
1	C	105	LYS
1	C	107	TYR
1	C	113	LYS
1	C	117	MET
1	C	127	ALA
1	C	181	ASN
1	C	182	ALA
1	C	183	PRO
1	C	279	LYS
1	C	281	ARG
1	C	284	ILE
1	D	61	GLY
1	D	62	TYR
1	D	105	LYS
1	D	107	TYR
1	D	113	LYS
1	D	117	MET
1	D	127	ALA
1	D	181	ASN
1	D	182	ALA
1	D	183	PRO
1	D	279	LYS
1	D	281	ARG
1	D	284	ILE
1	E	61	GLY
1	E	62	TYR
1	E	105	LYS
1	E	107	TYR
1	E	113	LYS
1	E	117	MET
1	E	127	ALA
1	E	181	ASN
1	E	182	ALA
1	E	279	LYS
1	E	281	ARG
1	E	284	ILE

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Mol	Chain	Res	Type
1	F	61	GLY
1	F	62	TYR
1	F	105	LYS
1	F	107	TYR
1	F	113	LYS
1	F	117	MET
1	F	127	ALA
1	F	181	ASN
1	F	182	ALA
1	F	183	PRO
1	F	279	LYS
1	F	281	ARG
1	F	284	ILE
1	G	61	GLY
1	G	62	TYR
1	G	105	LYS
1	G	107	TYR
1	G	113	LYS
1	G	117	MET
1	G	127	ALA
1	G	181	ASN
1	G	182	ALA
1	G	183	PRO
1	G	279	LYS
1	G	281	ARG
1	G	284	ILE
1	H	61	GLY
1	H	62	TYR
1	H	105	LYS
1	H	107	TYR
1	H	113	LYS
1	H	117	MET
1	H	127	ALA
1	H	181	ASN
1	H	182	ALA
1	H	279	LYS
1	H	281	ARG
1	H	284	ILE
1	I	61	GLY
1	I	62	TYR
1	I	105	LYS
1	I	107	TYR

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Mol	Chain	Res	Type
1	I	113	LYS
1	I	117	MET
1	I	127	ALA
1	I	181	ASN
1	I	182	ALA
1	I	279	LYS
1	I	281	ARG
1	I	284	ILE
1	J	61	GLY
1	J	62	TYR
1	J	105	LYS
1	J	107	TYR
1	J	113	LYS
1	J	117	MET
1	J	127	ALA
1	J	181	ASN
1	J	182	ALA
1	J	277	LYS
1	J	279	LYS
1	J	281	ARG
1	J	284	ILE
1	K	61	GLY
1	K	62	TYR
1	K	105	LYS
1	K	107	TYR
1	K	113	LYS
1	K	117	MET
1	K	127	ALA
1	K	181	ASN
1	K	182	ALA
1	K	279	LYS
1	K	281	ARG
1	K	284	ILE
1	L	61	GLY
1	L	62	TYR
1	L	105	LYS
1	L	107	TYR
1	L	113	LYS
1	L	117	MET
1	L	127	ALA
1	L	181	ASN
1	L	182	ALA

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Mol	Chain	Res	Type
1	L	279	LYS
1	L	281	ARG
1	L	284	ILE
1	A	60	PHE
1	A	61	GLY
1	A	63	VAL
1	A	109	TYR
1	A	110	ARG
1	A	126	MET
1	A	171	LEU
1	A	178	TYR
1	A	180	GLY
1	A	183	PRO
1	A	204	PRO
1	A	277	LYS
1	A	278	VAL
1	B	60	PHE
1	B	63	VAL
1	B	109	TYR
1	B	110	ARG
1	B	124	ASN
1	B	126	MET
1	B	171	LEU
1	B	178	TYR
1	B	180	GLY
1	B	204	PRO
1	B	277	LYS
1	B	278	VAL
1	C	60	PHE
1	C	61	GLY
1	C	63	VAL
1	C	109	TYR
1	C	110	ARG
1	C	124	ASN
1	C	126	MET
1	C	171	LEU
1	C	178	TYR
1	C	180	GLY
1	C	204	PRO
1	C	277	LYS
1	C	278	VAL
1	D	60	PHE

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Mol	Chain	Res	Type
1	D	63	VAL
1	D	109	TYR
1	D	110	ARG
1	D	124	ASN
1	D	126	MET
1	D	171	LEU
1	D	178	TYR
1	D	180	GLY
1	D	204	PRO
1	D	277	LYS
1	D	278	VAL
1	E	60	PHE
1	E	63	VAL
1	E	109	TYR
1	E	110	ARG
1	E	124	ASN
1	E	126	MET
1	E	171	LEU
1	E	178	TYR
1	E	180	GLY
1	E	183	PRO
1	E	204	PRO
1	E	277	LYS
1	E	278	VAL
1	F	60	PHE
1	F	63	VAL
1	F	109	TYR
1	F	110	ARG
1	F	124	ASN
1	F	126	MET
1	F	171	LEU
1	F	178	TYR
1	F	180	GLY
1	F	204	PRO
1	F	277	LYS
1	F	278	VAL
1	G	60	PHE
1	G	63	VAL
1	G	109	TYR
1	G	110	ARG
1	G	124	ASN
1	G	126	MET

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Mol	Chain	Res	Type
1	G	171	LEU
1	G	178	TYR
1	G	180	GLY
1	G	204	PRO
1	G	277	LYS
1	G	278	VAL
1	H	60	PHE
1	H	63	VAL
1	H	109	TYR
1	H	110	ARG
1	H	124	ASN
1	H	126	MET
1	H	171	LEU
1	H	178	TYR
1	H	180	GLY
1	H	183	PRO
1	H	204	PRO
1	H	277	LYS
1	H	278	VAL
1	I	60	PHE
1	I	63	VAL
1	I	109	TYR
1	I	110	ARG
1	I	124	ASN
1	I	126	MET
1	I	171	LEU
1	I	178	TYR
1	I	180	GLY
1	I	183	PRO
1	I	204	PRO
1	I	277	LYS
1	I	278	VAL
1	J	60	PHE
1	J	63	VAL
1	J	109	TYR
1	J	110	ARG
1	J	124	ASN
1	J	126	MET
1	J	171	LEU
1	J	178	TYR
1	J	180	GLY
1	J	183	PRO

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Mol	Chain	Res	Type
1	J	204	PRO
1	J	278	VAL
1	K	60	PHE
1	K	63	VAL
1	K	109	TYR
1	K	110	ARG
1	K	124	ASN
1	K	126	MET
1	K	171	LEU
1	K	178	TYR
1	K	180	GLY
1	K	183	PRO
1	K	204	PRO
1	K	277	LYS
1	K	278	VAL
1	L	60	PHE
1	L	63	VAL
1	L	109	TYR
1	L	110	ARG
1	L	126	MET
1	L	171	LEU
1	L	178	TYR
1	L	180	GLY
1	L	183	PRO
1	L	204	PRO
1	L	277	LYS
1	L	278	VAL
1	A	124	ASN
1	A	272	TYR
1	B	283	ASP
1	C	172	LYS
1	C	272	TYR
1	C	283	ASP
1	D	172	LYS
1	D	272	TYR
1	D	283	ASP
1	E	172	LYS
1	F	172	LYS
1	F	272	TYR
1	F	283	ASP
1	G	172	LYS
1	G	283	ASP

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Mol	Chain	Res	Type
1	H	172	LYS
1	H	272	TYR
1	I	172	LYS
1	I	272	TYR
1	I	283	ASP
1	J	172	LYS
1	J	272	TYR
1	J	283	ASP
1	K	272	TYR
1	K	283	ASP
1	L	124	ASN
1	A	44	LEU
1	A	172	LYS
1	A	192	ASP
1	A	205	TYR
1	A	283	ASP
1	B	44	LEU
1	B	172	LYS
1	B	192	ASP
1	B	205	TYR
1	B	272	TYR
1	C	39	PHE
1	C	44	LEU
1	C	159	VAL
1	C	192	ASP
1	C	205	TYR
1	D	44	LEU
1	D	159	VAL
1	D	192	ASP
1	D	205	TYR
1	E	44	LEU
1	E	159	VAL
1	E	192	ASP
1	E	205	TYR
1	E	272	TYR
1	E	283	ASP
1	F	44	LEU
1	F	192	ASP
1	G	44	LEU
1	G	192	ASP
1	G	205	TYR
1	G	272	TYR

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Mol	Chain	Res	Type
1	H	44	LEU
1	H	159	VAL
1	H	192	ASP
1	H	205	TYR
1	H	283	ASP
1	I	44	LEU
1	I	192	ASP
1	I	205	TYR
1	J	44	LEU
1	J	192	ASP
1	J	205	TYR
1	K	44	LEU
1	K	172	LYS
1	K	192	ASP
1	K	205	TYR
1	L	44	LEU
1	L	172	LYS
1	L	192	ASP
1	L	205	TYR
1	L	272	TYR
1	L	283	ASP
1	A	114	GLU
1	A	159	VAL
1	B	159	VAL
1	D	114	GLU
1	E	114	GLU
1	F	39	PHE
1	F	159	VAL
1	F	205	TYR
1	G	114	GLU
1	G	159	VAL
1	I	159	VAL
1	J	159	VAL
1	K	159	VAL
1	L	159	VAL
1	A	99	VAL
1	B	208	ASP
1	C	99	VAL
1	E	99	VAL
1	F	99	VAL
1	F	114	GLU
1	G	99	VAL

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Mol	Chain	Res	Type
1	H	99	VAL
1	H	114	GLU
1	H	208	ASP
1	I	39	PHE
1	I	99	VAL
1	I	208	ASP
1	J	114	GLU
1	K	99	VAL
1	L	39	PHE
1	L	99	VAL
1	B	99	VAL
1	D	99	VAL
1	J	99	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	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	B	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	C	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	D	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	E	229/277 (83%)	214 (93%)	15 (7%)	21	61
1	F	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	G	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	H	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	I	229/277 (83%)	213 (93%)	16 (7%)	19	58
1	J	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	K	229/277 (83%)	215 (94%)	14 (6%)	23	64
1	L	229/277 (83%)	214 (93%)	15 (7%)	21	61
All	All	2748/3324 (83%)	2576 (94%)	172 (6%)	22	63

All (172) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	49	ASN
1	A	101	GLN
1	A	113	LYS
1	A	115	GLU
1	A	123	ASN
1	A	160	LEU
1	A	164	ASN
1	A	176	ASN
1	A	204	PRO
1	A	209	LYS
1	A	213	GLN
1	A	261	ARG
1	A	271	LEU
1	A	277	LYS
1	B	49	ASN
1	B	101	GLN
1	B	113	LYS
1	B	115	GLU
1	B	123	ASN
1	B	160	LEU
1	B	164	ASN
1	B	176	ASN
1	B	204	PRO
1	B	209	LYS
1	B	213	GLN
1	B	261	ARG
1	B	271	LEU
1	B	277	LYS
1	C	49	ASN
1	C	101	GLN
1	C	113	LYS
1	C	115	GLU
1	C	123	ASN
1	C	160	LEU
1	C	164	ASN
1	C	176	ASN
1	C	204	PRO
1	C	209	LYS
1	C	213	GLN
1	C	261	ARG
1	C	271	LEU
1	C	277	LYS

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Mol	Chain	Res	Type
1	D	49	ASN
1	D	101	GLN
1	D	113	LYS
1	D	115	GLU
1	D	123	ASN
1	D	160	LEU
1	D	164	ASN
1	D	176	ASN
1	D	204	PRO
1	D	209	LYS
1	D	213	GLN
1	D	261	ARG
1	D	271	LEU
1	D	277	LYS
1	E	49	ASN
1	E	97	SER
1	E	101	GLN
1	E	113	LYS
1	E	115	GLU
1	E	123	ASN
1	E	160	LEU
1	E	164	ASN
1	E	176	ASN
1	E	204	PRO
1	E	209	LYS
1	E	213	GLN
1	E	261	ARG
1	E	271	LEU
1	E	277	LYS
1	F	49	ASN
1	F	101	GLN
1	F	113	LYS
1	F	115	GLU
1	F	123	ASN
1	F	160	LEU
1	F	164	ASN
1	F	176	ASN
1	F	204	PRO
1	F	209	LYS
1	F	213	GLN
1	F	261	ARG
1	F	271	LEU

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Mol	Chain	Res	Type
1	F	277	LYS
1	G	49	ASN
1	G	101	GLN
1	G	113	LYS
1	G	115	GLU
1	G	123	ASN
1	G	160	LEU
1	G	164	ASN
1	G	176	ASN
1	G	204	PRO
1	G	209	LYS
1	G	213	GLN
1	G	261	ARG
1	G	271	LEU
1	G	277	LYS
1	H	49	ASN
1	H	101	GLN
1	H	113	LYS
1	H	115	GLU
1	H	123	ASN
1	H	160	LEU
1	H	164	ASN
1	H	176	ASN
1	H	204	PRO
1	H	209	LYS
1	H	213	GLN
1	H	261	ARG
1	H	271	LEU
1	H	277	LYS
1	I	49	ASN
1	I	62	TYR
1	I	97	SER
1	I	101	GLN
1	I	113	LYS
1	I	115	GLU
1	I	123	ASN
1	I	160	LEU
1	I	164	ASN
1	I	176	ASN
1	I	204	PRO
1	I	209	LYS
1	I	213	GLN

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Mol	Chain	Res	Type
1	I	261	ARG
1	I	271	LEU
1	I	277	LYS
1	J	49	ASN
1	J	101	GLN
1	J	113	LYS
1	J	115	GLU
1	J	123	ASN
1	J	160	LEU
1	J	164	ASN
1	J	176	ASN
1	J	204	PRO
1	J	209	LYS
1	J	213	GLN
1	J	261	ARG
1	J	271	LEU
1	J	277	LYS
1	K	49	ASN
1	K	101	GLN
1	K	113	LYS
1	K	115	GLU
1	K	123	ASN
1	K	160	LEU
1	K	164	ASN
1	K	176	ASN
1	K	204	PRO
1	K	209	LYS
1	K	213	GLN
1	K	261	ARG
1	K	271	LEU
1	K	277	LYS
1	L	49	ASN
1	L	97	SER
1	L	101	GLN
1	L	113	LYS
1	L	115	GLU
1	L	123	ASN
1	L	160	LEU
1	L	164	ASN
1	L	176	ASN
1	L	204	PRO
1	L	209	LYS

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Mol	Chain	Res	Type
1	L	213	GLN
1	L	261	ARG
1	L	271	LEU
1	L	277	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (198) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	ASN
1	A	29	ASN
1	A	32	GLN
1	A	43	ASN
1	A	49	ASN
1	A	123	ASN
1	A	124	ASN
1	A	151	ASN
1	A	152	GLN
1	A	155	GLN
1	A	166	ASN
1	A	167	ASN
1	A	168	GLN
1	A	173	GLN
1	A	177	GLN
1	A	188	HIS
1	A	213	GLN
1	B	21	ASN
1	B	29	ASN
1	B	32	GLN
1	B	43	ASN
1	B	49	ASN
1	B	123	ASN
1	B	151	ASN
1	B	152	GLN
1	B	155	GLN
1	B	166	ASN
1	B	167	ASN
1	B	168	GLN
1	B	173	GLN
1	B	177	GLN
1	B	188	HIS
1	B	213	GLN
1	C	21	ASN

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Mol	Chain	Res	Type
1	C	29	ASN
1	C	32	GLN
1	C	43	ASN
1	C	49	ASN
1	C	123	ASN
1	C	124	ASN
1	C	151	ASN
1	C	152	GLN
1	C	155	GLN
1	C	166	ASN
1	C	167	ASN
1	C	168	GLN
1	C	173	GLN
1	C	177	GLN
1	C	188	HIS
1	C	213	GLN
1	D	21	ASN
1	D	29	ASN
1	D	32	GLN
1	D	43	ASN
1	D	49	ASN
1	D	59	GLN
1	D	123	ASN
1	D	151	ASN
1	D	152	GLN
1	D	155	GLN
1	D	166	ASN
1	D	167	ASN
1	D	168	GLN
1	D	173	GLN
1	D	177	GLN
1	D	188	HIS
1	E	21	ASN
1	E	29	ASN
1	E	32	GLN
1	E	43	ASN
1	E	49	ASN
1	E	123	ASN
1	E	124	ASN
1	E	151	ASN
1	E	152	GLN
1	E	155	GLN

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Mol	Chain	Res	Type
1	E	166	ASN
1	E	167	ASN
1	E	168	GLN
1	E	173	GLN
1	E	177	GLN
1	E	188	HIS
1	E	213	GLN
1	F	21	ASN
1	F	29	ASN
1	F	32	GLN
1	F	43	ASN
1	F	49	ASN
1	F	123	ASN
1	F	124	ASN
1	F	151	ASN
1	F	152	GLN
1	F	155	GLN
1	F	166	ASN
1	F	167	ASN
1	F	168	GLN
1	F	173	GLN
1	F	177	GLN
1	F	188	HIS
1	F	213	GLN
1	G	21	ASN
1	G	29	ASN
1	G	32	GLN
1	G	43	ASN
1	G	49	ASN
1	G	123	ASN
1	G	124	ASN
1	G	151	ASN
1	G	152	GLN
1	G	155	GLN
1	G	166	ASN
1	G	167	ASN
1	G	168	GLN
1	G	173	GLN
1	G	177	GLN
1	G	188	HIS
1	H	21	ASN
1	H	29	ASN

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Mol	Chain	Res	Type
1	H	32	GLN
1	H	43	ASN
1	H	49	ASN
1	H	123	ASN
1	H	124	ASN
1	H	151	ASN
1	H	152	GLN
1	H	155	GLN
1	H	166	ASN
1	H	167	ASN
1	H	168	GLN
1	H	173	GLN
1	H	177	GLN
1	H	188	HIS
1	I	21	ASN
1	I	29	ASN
1	I	32	GLN
1	I	43	ASN
1	I	49	ASN
1	I	123	ASN
1	I	124	ASN
1	I	151	ASN
1	I	152	GLN
1	I	155	GLN
1	I	166	ASN
1	I	167	ASN
1	I	168	GLN
1	I	173	GLN
1	I	177	GLN
1	I	188	HIS
1	I	213	GLN
1	J	21	ASN
1	J	29	ASN
1	J	32	GLN
1	J	43	ASN
1	J	49	ASN
1	J	123	ASN
1	J	124	ASN
1	J	151	ASN
1	J	152	GLN
1	J	155	GLN
1	J	166	ASN

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Mol	Chain	Res	Type
1	J	167	ASN
1	J	168	GLN
1	J	173	GLN
1	J	177	GLN
1	J	188	HIS
1	K	21	ASN
1	K	29	ASN
1	K	32	GLN
1	K	43	ASN
1	K	49	ASN
1	K	123	ASN
1	K	124	ASN
1	K	151	ASN
1	K	152	GLN
1	K	155	GLN
1	K	166	ASN
1	K	167	ASN
1	K	168	GLN
1	K	173	GLN
1	K	177	GLN
1	K	188	HIS
1	L	21	ASN
1	L	29	ASN
1	L	32	GLN
1	L	43	ASN
1	L	49	ASN
1	L	59	GLN
1	L	123	ASN
1	L	124	ASN
1	L	151	ASN
1	L	152	GLN
1	L	155	GLN
1	L	166	ASN
1	L	167	ASN
1	L	168	GLN
1	L	173	GLN
1	L	177	GLN
1	L	188	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	257/309 (83%)	0.22	15 (5%)	26 15	18, 45, 98, 120	0
1	B	257/309 (83%)	0.44	22 (8%)	13 7	18, 52, 97, 121	0
1	C	257/309 (83%)	0.53	17 (6%)	22 12	21, 55, 100, 124	0
1	D	257/309 (83%)	0.39	18 (7%)	19 11	20, 58, 109, 127	0
1	E	257/309 (83%)	0.77	41 (15%)	3 2	23, 72, 113, 123	0
1	F	257/309 (83%)	0.42	16 (6%)	24 13	19, 61, 104, 120	0
1	G	257/309 (83%)	0.38	18 (7%)	19 11	21, 57, 102, 127	0
1	H	257/309 (83%)	0.54	24 (9%)	11 6	17, 64, 111, 124	0
1	I	257/309 (83%)	0.34	18 (7%)	19 11	19, 46, 90, 116	0
1	J	257/309 (83%)	0.16	11 (4%)	39 25	22, 43, 87, 115	0
1	K	257/309 (83%)	0.34	13 (5%)	32 18	17, 53, 96, 127	0
1	L	257/309 (83%)	0.31	15 (5%)	26 15	19, 48, 98, 116	0
All	All	3084/3708 (83%)	0.40	228 (7%)	17 10	17, 53, 106, 127	0

All (228) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	11	SER	13.5
1	F	11	SER	12.2
1	I	11	SER	11.2
1	C	11	SER	11.2
1	A	11	SER	11.1
1	B	11	SER	10.8
1	G	11	SER	10.2
1	B	12	ILE	10.0
1	E	111	ASP	9.8
1	K	111	ASP	9.4
1	K	11	SER	9.4

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Mol	Chain	Res	Type	RSRZ
1	D	11	SER	9.3
1	C	12	ILE	9.1
1	L	12	ILE	9.1
1	L	11	SER	8.8
1	G	12	ILE	8.6
1	H	12	ILE	8.5
1	E	11	SER	8.4
1	A	12	ILE	8.3
1	D	12	ILE	8.2
1	K	12	ILE	8.1
1	K	182	ALA	7.3
1	J	12	ILE	7.3
1	H	111	ASP	7.1
1	E	118	GLY	7.0
1	I	111	ASP	7.0
1	E	12	ILE	6.3
1	K	168	GLN	6.2
1	C	109	TYR	6.2
1	J	11	SER	6.1
1	B	111	ASP	6.0
1	I	109	TYR	5.9
1	G	276	VAL	5.9
1	D	168	GLN	5.8
1	F	168	GLN	5.8
1	G	182	ALA	5.7
1	B	182	ALA	5.6
1	E	108	ASN	5.5
1	H	108	ASN	5.4
1	L	182	ALA	5.4
1	J	182	ALA	5.3
1	F	109	TYR	5.3
1	G	168	GLN	5.2
1	B	168	GLN	5.1
1	L	108	ASN	5.1
1	I	272	TYR	5.1
1	D	111	ASP	5.0
1	J	111	ASP	4.9
1	C	168	GLN	4.9
1	I	12	ILE	4.8
1	C	276	VAL	4.7
1	L	168	GLN	4.7
1	H	276	VAL	4.7

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Mol	Chain	Res	Type	RSRZ
1	I	276	VAL	4.6
1	D	276	VAL	4.5
1	B	108	ASN	4.5
1	K	109	TYR	4.5
1	C	182	ALA	4.4
1	E	182	ALA	4.4
1	E	272	TYR	4.4
1	E	168	GLN	4.3
1	I	182	ALA	4.3
1	H	182	ALA	4.3
1	F	108	ASN	4.2
1	A	182	ALA	4.2
1	E	109	TYR	4.2
1	A	276	VAL	4.2
1	E	120	VAL	4.1
1	A	168	GLN	4.1
1	I	168	GLN	4.1
1	I	108	ASN	4.1
1	K	276	VAL	4.1
1	F	12	ILE	4.1
1	I	112	MET	4.0
1	D	182	ALA	3.9
1	F	169	LEU	3.9
1	H	272	TYR	3.9
1	G	110	ARG	3.9
1	J	108	ASN	3.9
1	D	270	GLU	3.8
1	H	118	GLY	3.8
1	D	285	VAL	3.7
1	G	165	ASP	3.7
1	K	108	ASN	3.7
1	J	276	VAL	3.6
1	L	109	TYR	3.6
1	B	167	ASN	3.6
1	D	283	ASP	3.6
1	H	99	VAL	3.5
1	A	108	ASN	3.5
1	G	283	ASP	3.5
1	E	110	ARG	3.5
1	E	95	ALA	3.4
1	E	119	VAL	3.4
1	C	169	LEU	3.4

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Mol	Chain	Res	Type	RSRZ
1	G	111	ASP	3.4
1	C	285	VAL	3.4
1	F	182	ALA	3.3
1	J	109	TYR	3.3
1	J	168	GLN	3.3
1	I	110	ARG	3.3
1	D	109	TYR	3.3
1	I	99	VAL	3.2
1	H	95	ALA	3.2
1	H	168	GLN	3.2
1	D	101	GLN	3.2
1	D	110	ARG	3.2
1	A	110	ARG	3.1
1	G	272	TYR	3.1
1	F	13	ASN	3.1
1	B	272	TYR	3.1
1	L	272	TYR	3.1
1	J	112	MET	3.1
1	A	272	TYR	3.1
1	H	110	ARG	3.1
1	A	109	TYR	3.1
1	L	111	ASP	3.0
1	E	276	VAL	3.0
1	H	278	VAL	3.0
1	C	110	ARG	2.9
1	C	272	TYR	2.9
1	L	169	LEU	2.9
1	E	90	ALA	2.9
1	F	110	ARG	2.9
1	E	107	TYR	2.9
1	E	169	LEU	2.9
1	B	181	ASN	2.8
1	K	181	ASN	2.8
1	L	276	VAL	2.8
1	D	272	TYR	2.8
1	B	109	TYR	2.8
1	H	13	ASN	2.8
1	B	101	GLN	2.8
1	E	71	ILE	2.8
1	G	169	LEU	2.8
1	J	272	TYR	2.8
1	I	13	ASN	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	276	VAL	2.7
1	E	117	MET	2.7
1	A	113	LYS	2.7
1	B	88	ASN	2.7
1	H	109	TYR	2.7
1	C	108	ASN	2.7
1	E	18	GLN	2.7
1	E	101	GLN	2.6
1	L	16	GLN	2.6
1	D	278	VAL	2.6
1	E	275	ASN	2.6
1	G	167	ASN	2.6
1	H	119	VAL	2.5
1	G	109	TYR	2.5
1	A	169	LEU	2.5
1	H	112	MET	2.5
1	E	13	ASN	2.5
1	A	16	GLN	2.5
1	E	83	GLN	2.5
1	L	99	VAL	2.5
1	D	277	LYS	2.5
1	H	270	GLU	2.5
1	D	178	TYR	2.5
1	I	18	GLN	2.5
1	C	72	SER	2.5
1	F	180	GLY	2.5
1	E	278	VAL	2.5
1	G	194	ASP	2.4
1	H	194	ASP	2.4
1	D	108	ASN	2.4
1	E	279	LYS	2.4
1	G	115	GLU	2.4
1	E	81	SER	2.4
1	K	275	ASN	2.4
1	F	112	MET	2.4
1	C	194	ASP	2.4
1	E	82	GLY	2.4
1	E	181	ASN	2.4
1	E	16	GLN	2.3
1	F	72	SER	2.3
1	I	169	LEU	2.3
1	E	74	ILE	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	277	LYS	2.3
1	E	194	ASP	2.3
1	C	284	ILE	2.3
1	C	13	ASN	2.3
1	H	181	ASN	2.3
1	L	115	GLU	2.3
1	K	272	TYR	2.3
1	B	180	GLY	2.2
1	F	278	VAL	2.2
1	E	167	ASN	2.2
1	H	117	MET	2.2
1	I	194	ASP	2.2
1	K	13	ASN	2.2
1	E	65	PHE	2.2
1	B	178	TYR	2.2
1	C	178	TYR	2.2
1	D	248	GLU	2.2
1	L	13	ASN	2.2
1	B	110	ARG	2.2
1	C	249	GLN	2.2
1	E	76	CYS	2.2
1	B	275	ASN	2.2
1	E	104	PHE	2.1
1	H	97	SER	2.1
1	A	167	ASN	2.1
1	F	56	SER	2.1
1	H	180	GLY	2.1
1	E	112	MET	2.1
1	B	82	GLY	2.1
1	L	178	TYR	2.1
1	I	181	ASN	2.1
1	E	62	TYR	2.1
1	B	112	MET	2.1
1	K	94	ARG	2.1
1	B	107	TYR	2.1
1	B	90	ALA	2.1
1	E	121	ILE	2.1
1	A	273	GLY	2.1
1	F	249	GLN	2.1
1	G	277	LYS	2.1
1	G	62	TYR	2.0
1	B	81	SER	2.0

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Mol	Chain	Res	Type	RSRZ
1	F	272	TYR	2.0
1	G	13	ASN	2.0
1	I	178	TYR	2.0
1	J	228	LYS	2.0
1	E	180	GLY	2.0
1	E	122	TYR	2.0
1	H	169	LEU	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.