



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 4, 2026 – 10:36 PM UTC

PDB ID : 4XEI / pdb_00004xei
Title : Orthorhombic isomorph of bovine Arp2/3 complex
Authors : Jurgenson, C.J.; Pollard, T.P.
Deposited on : 2014-12-23
Resolution : 3.87 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

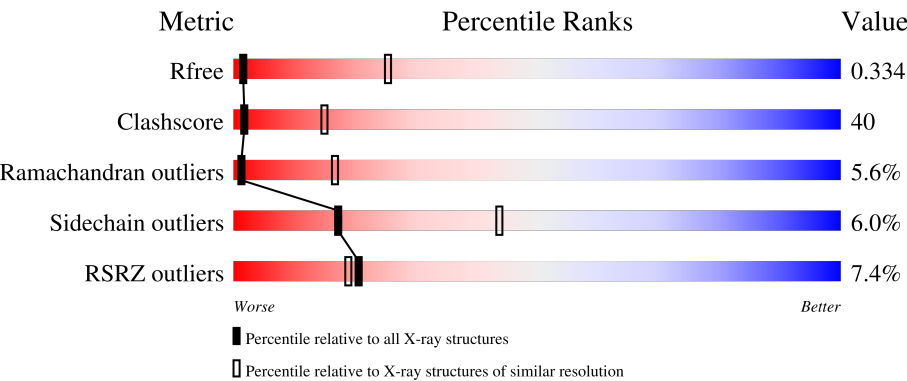
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.87 Å.

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



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	1186 (4.06-3.70)
Clashscore	190562	1012 (4.04-3.72)
Ramachandran outliers	187476	1167 (4.06-3.70)
Sidechain outliers	187428	1160 (4.06-3.70)
RSRZ outliers	180081	1185 (4.06-3.70)

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

Mol	Chain	Length	Quality of chain
1	A	418	
2	B	394	
3	C	372	
4	D	300	
5	E	178	

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Mol	Chain	Length	Quality of chain
6	F	168	6% 54% 40% 5%
7	G	151	5% 53% 31% 5% 11%

2 Entry composition [i](#)

There are 8 unique types of molecules in this entry. The entry contains 13731 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 Actin-related protein 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	400	Total	C	N	O	S	0	0	0
			3185	2045	533	592	15			

- Molecule 2 is a protein called Actin-related protein 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	218	Total	C	N	O	S	0	0	0
			1759	1133	301	319	6			

- Molecule 3 is a protein called Actin-related protein 2/3 complex subunit 1B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	344	Total	C	N	O	S	0	0	0
			2661	1688	467	487	19			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	58	VAL	ILE	conflict	UNP Q58CQ2

- Molecule 4 is a protein called Actin-related protein 2/3 complex subunit 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	282	Total	C	N	O	S	0	0	0
			2272	1443	394	427	8			

- Molecule 5 is a protein called Actin-related protein 2/3 complex subunit 3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	E	174	Total	C	N	O	S	0	0	0
			1414	908	236	261	9			

- Molecule 6 is a protein called Actin-related protein 2/3 complex subunit 4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
6	F	168	Total	C	N	O	S	0	0	0
			1378	880	240	248	10			

- Molecule 7 is a protein called Actin-related protein 2/3 complex subunit 5.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
7	G	135	Total	C	N	O	S	0	0	0
			1014	636	171	204	3			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	17	ASP	GLY	conflict	UNP Q3SYX9
G	28	ASP	GLU	conflict	UNP Q3SYX9

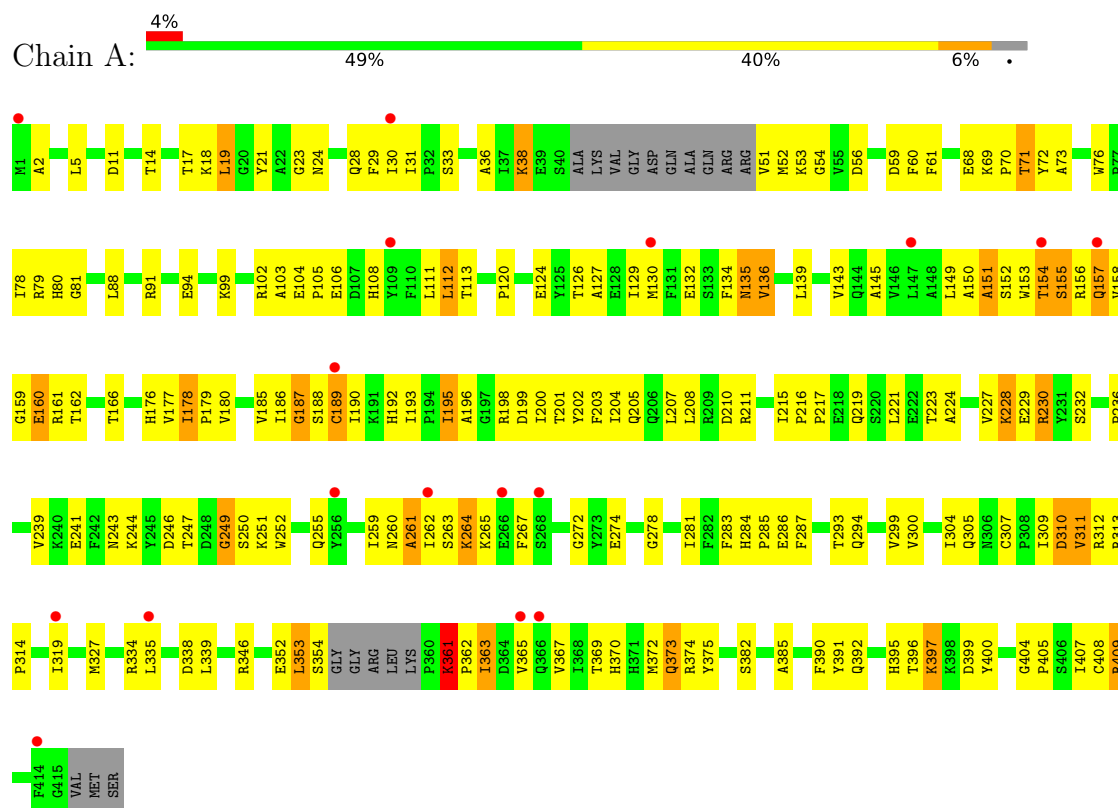
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	8	Total	O	0	0
			8	8		
8	B	5	Total	O	0	0
			5	5		
8	C	10	Total	O	0	0
			10	10		
8	D	8	Total	O	0	0
			8	8		
8	E	9	Total	O	0	0
			9	9		
8	F	3	Total	O	0	0
			3	3		
8	G	5	Total	O	0	0
			5	5		

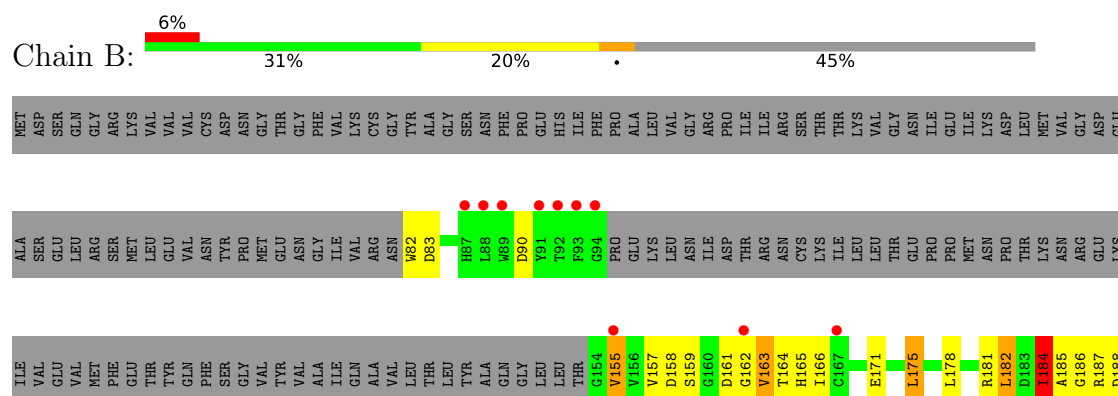
3 Residue-property plots

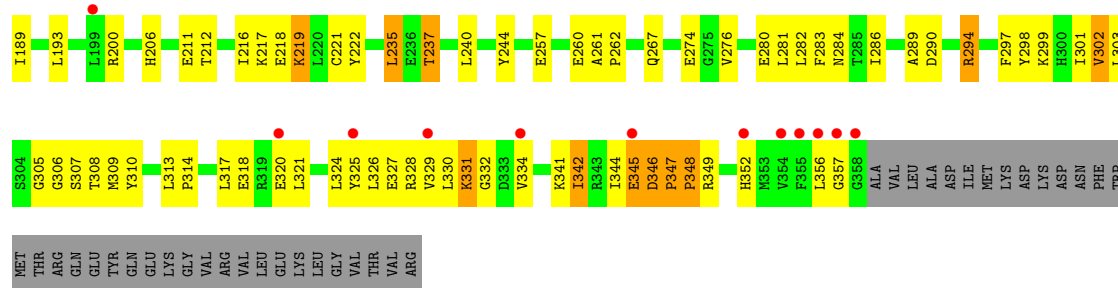
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: Actin-related protein 3

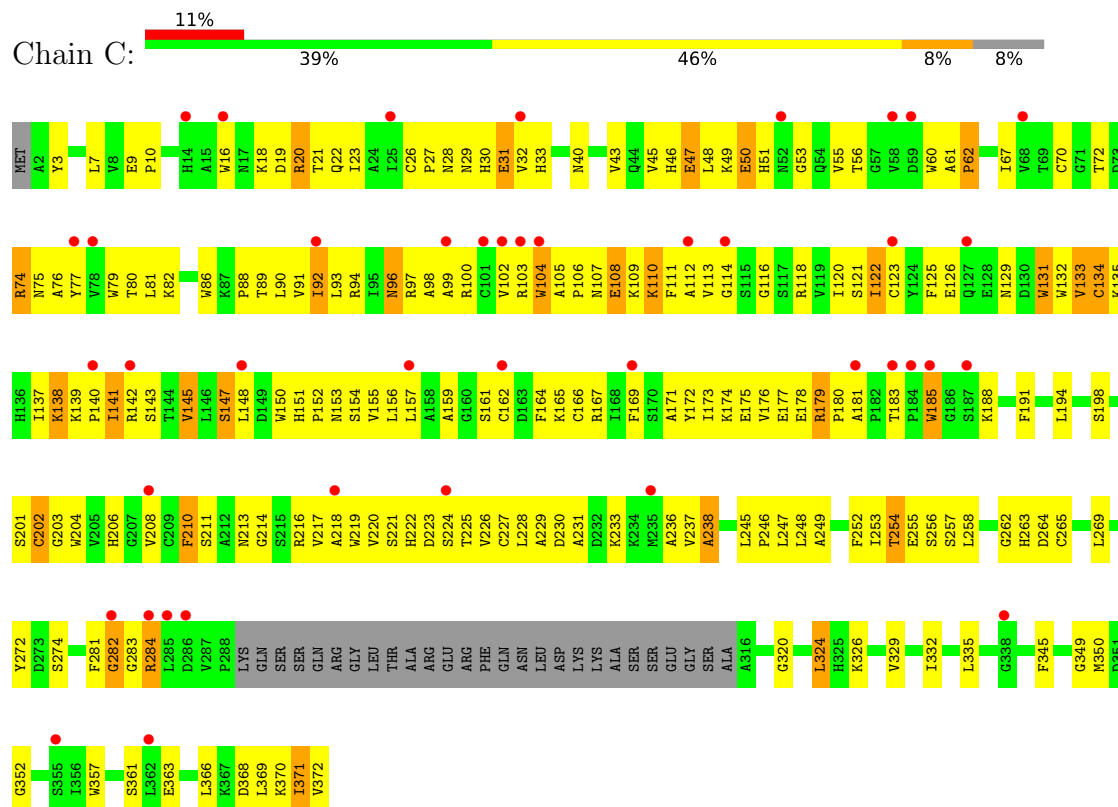


• Molecule 2: Actin-related protein 2

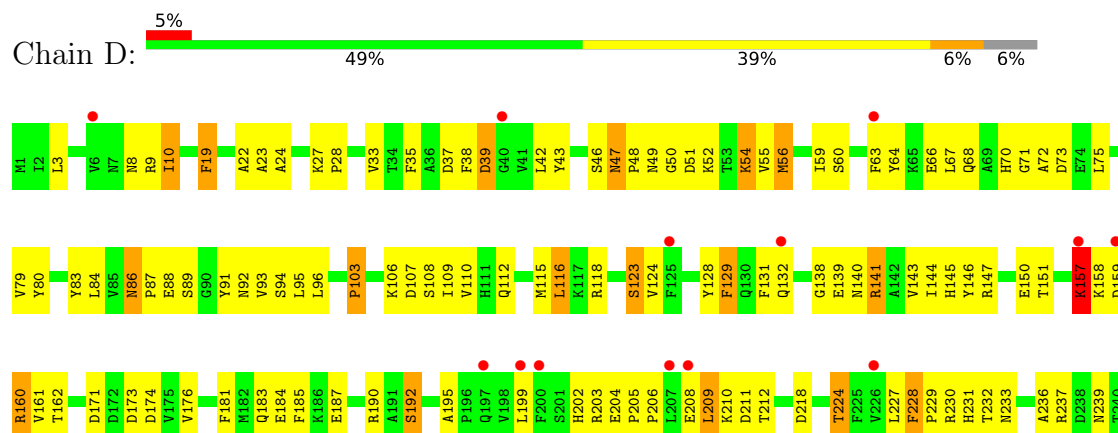




• Molecule 3: Actin-related protein 2/3 complex subunit 1B

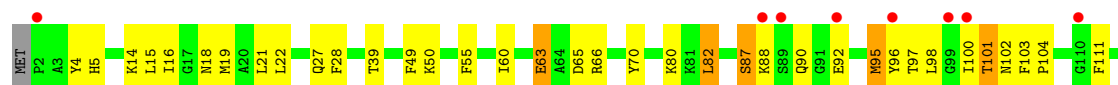


• Molecule 4: Actin-related protein 2/3 complex subunit 2





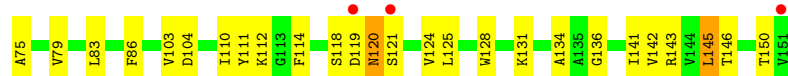
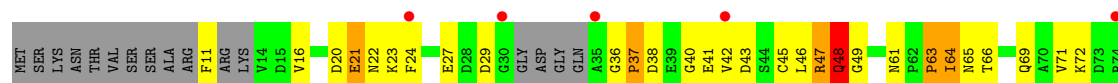
- Molecule 5: Actin-related protein 2/3 complex subunit 3



- Molecule 6: Actin-related protein 2/3 complex subunit 4



- Molecule 7: Actin-related protein 2/3 complex subunit 5



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	105.57Å 156.98Å 178.09Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.41 – 3.87 45.41 – 3.87	Depositor EDS
% Data completeness (in resolution range)	95.6 (45.41-3.87) 95.5 (45.41-3.87)	Depositor EDS
R_{merge}	0.19	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 3.88Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.279 , 0.329 0.305 , 0.334	Depositor DCC
R_{free} test set	1344 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	104.5	Xtriage
Anisotropy	0.056	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 82.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.83	EDS
Total number of atoms	13731	wwPDB-VP
Average B, all atoms (Å ²)	95.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.73% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

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	0.38	0/3266	0.93	13/4432 (0.3%)
2	B	0.41	0/1797	0.99	7/2426 (0.3%)
3	C	0.31	0/2730	0.79	2/3707 (0.1%)
4	D	0.33	0/2321	0.84	6/3135 (0.2%)
5	E	0.37	0/1448	0.80	2/1953 (0.1%)
6	F	0.34	0/1400	0.86	0/1878
7	G	0.37	0/1025	0.99	3/1382 (0.2%)
All	All	0.36	0/13987	0.88	33/18913 (0.2%)

There are no bond length outliers.

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	206	HIS	N-CA-C	9.33	121.14	110.97
1	A	404	GLY	CA-C-N	8.12	127.84	119.56
1	A	404	GLY	C-N-CA	8.12	127.84	119.56
1	A	215	ILE	CA-C-N	7.80	128.41	120.38
1	A	215	ILE	C-N-CA	7.80	128.41	120.38
2	B	175	LEU	CA-C-N	7.57	127.11	119.24
2	B	175	LEU	C-N-CA	7.57	127.11	119.24
3	C	145	VAL	N-CA-C	7.16	119.18	108.23
7	G	61	ASN	CA-C-N	6.53	127.11	120.38
7	G	61	ASN	C-N-CA	6.53	127.11	120.38
1	A	76	TRP	CA-C-N	6.44	126.06	119.56
1	A	76	TRP	C-N-CA	6.44	126.06	119.56
1	A	361	LYS	CA-C-N	6.43	126.38	119.76
1	A	361	LYS	C-N-CA	6.43	126.38	119.76
4	D	129	PHE	N-CA-C	-6.24	104.56	111.36
5	E	49	PHE	N-CA-C	6.19	118.54	111.11
3	C	43	VAL	N-CA-C	6.03	117.45	108.46
2	B	267	GLN	CA-C-N	5.96	125.83	119.28
2	B	267	GLN	C-N-CA	5.96	125.83	119.28
5	E	141	GLY	N-CA-C	5.80	119.23	112.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	184	ILE	N-CA-C	5.76	116.58	108.17
4	D	19	PHE	N-CA-C	5.73	117.60	111.36
1	A	136	VAL	CA-C-N	5.46	125.16	119.64
1	A	136	VAL	C-N-CA	5.46	125.16	119.64
4	D	55	VAL	N-CA-C	5.34	115.84	111.62
1	A	397	LYS	N-CA-C	-5.33	105.58	111.71
7	G	61	ASN	CB-CA-C	-5.32	107.42	111.20
4	D	123	SER	N-CA-C	5.30	117.05	111.28
1	A	311	VAL	N-CA-C	-5.27	107.84	112.90
2	B	302	VAL	N-CA-C	5.08	116.03	108.46
1	A	338	ASP	N-CA-C	5.07	116.49	111.07
4	D	47	ASN	CA-C-N	5.02	126.12	119.84
4	D	47	ASN	C-N-CA	5.02	126.12	119.84

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	3185	0	3113	253	2
2	B	1759	0	1772	118	0
3	C	2661	0	2613	370	0
4	D	2272	0	2228	144	6
5	E	1414	0	1416	80	6
6	F	1378	0	1422	134	0
7	G	1014	0	1007	60	2
8	A	8	0	0	0	0
8	B	5	0	0	0	0
8	C	10	0	0	0	0
8	D	8	0	0	0	0
8	E	9	0	0	6	0
8	F	3	0	0	1	0
8	G	5	0	0	0	0
All	All	13731	0	13571	1101	8

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 40.

All (1101) 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)
3:C:140:PRO:HD2	3:C:169:PHE:CZ	1.27	1.59
1:A:178:ILE:HG23	1:A:190:ILE:CD1	1.23	1.57
1:A:200:ILE:CD1	1:A:281:ILE:HD11	1.34	1.52
1:A:178:ILE:CG2	1:A:190:ILE:CD1	2.05	1.33
1:A:200:ILE:HD13	1:A:281:ILE:CD1	1.57	1.33
3:C:72:THR:HA	3:C:98:ALA:CB	1.57	1.32
3:C:122:ILE:CD1	3:C:137:ILE:HD11	1.59	1.31
3:C:122:ILE:HD13	3:C:137:ILE:CD1	1.59	1.31
3:C:165:LYS:HG2	3:C:198:SER:OG	1.25	1.26
1:A:178:ILE:CG2	1:A:190:ILE:HD11	1.65	1.24
3:C:118:ARG:CB	3:C:142:ARG:O	1.84	1.24
3:C:118:ARG:CG	3:C:142:ARG:O	1.85	1.24
3:C:140:PRO:CD	3:C:169:PHE:CZ	2.20	1.24
3:C:118:ARG:HB3	3:C:142:ARG:O	1.34	1.23
3:C:151:HIS:CG	3:C:152:PRO:HD2	1.75	1.22
3:C:62:PRO:HD2	3:C:108:GLU:CD	1.67	1.20
1:A:178:ILE:CG2	1:A:185:VAL:HG11	1.73	1.18
2:B:302:VAL:HA	2:B:345:GLU:CB	1.72	1.18
3:C:140:PRO:HG2	3:C:167:ARG:HD3	1.25	1.18
1:A:178:ILE:HG22	1:A:185:VAL:CG1	1.72	1.17
3:C:72:THR:CA	3:C:98:ALA:HB1	1.73	1.17
1:A:205:GLN:OE1	1:A:221:LEU:HD23	1.43	1.17
1:A:178:ILE:HG23	1:A:190:ILE:HD12	1.18	1.15
1:A:153:TRP:NE1	1:A:161:ARG:HA	1.61	1.14
6:F:9:LEU:HB3	6:F:136:ILE:HD11	1.29	1.14
1:A:178:ILE:CG2	1:A:185:VAL:CG1	2.25	1.13
1:A:21:TYR:OH	1:A:103:ALA:HB2	1.48	1.13
6:F:54:SER:HB3	6:F:60:LYS:CB	1.78	1.13
1:A:205:GLN:CD	1:A:221:LEU:HD23	1.72	1.12
3:C:140:PRO:HD2	3:C:169:PHE:CE1	1.83	1.12
4:D:205:PRO:HB2	4:D:208:GLU:HB2	1.32	1.11
5:E:18:ASN:HB3	5:E:118:ALA:HB3	1.11	1.10
2:B:302:VAL:CA	2:B:345:GLU:HB2	1.81	1.10
3:C:125:PHE:HD1	3:C:132:TRP:CE2	1.70	1.10
4:D:210:LYS:HA	4:D:211:ASP:HB3	1.31	1.10
2:B:158:ASP:C	2:B:164:THR:HG23	1.76	1.09
3:C:179:ARG:HG3	3:C:180:PRO:HD2	1.32	1.09

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:162:CYS:HG	3:C:204:TRP:CD1	1.70	1.08
3:C:140:PRO:CD	3:C:169:PHE:CE1	2.36	1.08
6:F:45:GLU:HB3	7:G:24:PHE:CD2	1.89	1.08
1:A:30:ILE:HD13	1:A:375:TYR:CE2	1.89	1.07
4:D:281:ARG:HB3	4:D:282:PRO:CD	1.83	1.07
6:F:45:GLU:HB3	7:G:24:PHE:CE2	1.90	1.07
3:C:118:ARG:HG2	3:C:142:ARG:O	1.51	1.07
3:C:62:PRO:HD2	3:C:108:GLU:OE2	1.53	1.07
1:A:178:ILE:HG22	1:A:185:VAL:HG13	1.28	1.06
4:D:228:PHE:HB3	4:D:229:PRO:HD2	1.32	1.06
4:D:281:ARG:HB3	4:D:282:PRO:HD2	1.37	1.06
4:D:103:PRO:HG3	4:D:109:ILE:HD12	1.08	1.06
1:A:178:ILE:CB	1:A:190:ILE:HD12	1.85	1.06
6:F:54:SER:HB3	6:F:60:LYS:HB3	1.31	1.06
3:C:252:PHE:CE2	3:C:258:LEU:HD21	1.90	1.06
1:A:153:TRP:CD1	1:A:161:ARG:HA	1.90	1.05
1:A:178:ILE:HG21	1:A:185:VAL:HG11	1.33	1.05
3:C:79:TRP:CH2	3:C:88:PRO:HG3	1.91	1.05
1:A:178:ILE:CG2	1:A:190:ILE:HD12	1.73	1.04
3:C:150:TRP:CZ2	3:C:157:LEU:HD21	1.91	1.04
2:B:341:LYS:O	2:B:342:ILE:HG13	1.55	1.03
5:E:18:ASN:HB3	5:E:118:ALA:CB	1.87	1.03
3:C:79:TRP:CZ3	3:C:88:PRO:HD3	1.93	1.03
4:D:147:ARG:HB2	4:D:150:GLU:HB2	1.04	1.03
3:C:18:LYS:HB2	3:C:62:PRO:HA	1.40	1.03
2:B:163:VAL:HA	2:B:185:ALA:CB	1.87	1.03
6:F:51:VAL:HG21	7:G:145:LEU:CD2	1.89	1.02
3:C:140:PRO:CD	3:C:169:PHE:HZ	1.63	1.02
1:A:153:TRP:HE1	1:A:161:ARG:HA	1.23	1.02
1:A:179:PRO:HD2	1:A:190:ILE:HD13	1.36	1.02
2:B:302:VAL:HA	2:B:345:GLU:HB2	1.02	1.02
2:B:314:PRO:HA	2:B:344:ILE:HG21	1.39	1.02
2:B:303:LEU:HB2	2:B:346:ASP:HB2	1.04	1.01
1:A:153:TRP:HE1	1:A:161:ARG:CA	1.73	1.01
3:C:133:VAL:HG12	3:C:134:CYS:H	1.23	1.01
5:E:18:ASN:ND2	5:E:118:ALA:H	1.58	1.01
1:A:200:ILE:CD1	1:A:281:ILE:CD1	2.28	1.00
2:B:301:ILE:O	2:B:345:GLU:HB2	1.59	1.00
1:A:178:ILE:HA	1:A:190:ILE:CD1	1.90	1.00
3:C:79:TRP:CE3	3:C:88:PRO:HD3	1.97	0.99
3:C:129:ASN:HB2	3:C:131:TRP:CE3	1.97	0.99

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:68:GLU:O	1:A:70:PRO:HD3	1.62	0.99
3:C:140:PRO:HG2	3:C:167:ARG:CD	1.93	0.99
3:C:283:GLY:HA3	3:C:284:ARG:HB2	1.45	0.98
4:D:37:ASP:HB2	4:D:43:TYR:HE2	1.27	0.98
5:E:138:GLN:O	8:E:201:HOH:O	1.81	0.98
2:B:302:VAL:HB	2:B:345:GLU:CD	1.88	0.98
5:E:150:ASP:CG	5:E:151:PRO:HD2	1.88	0.98
4:D:103:PRO:HG3	4:D:109:ILE:CD1	1.93	0.97
3:C:252:PHE:CZ	3:C:258:LEU:HD21	1.98	0.96
4:D:205:PRO:CB	4:D:208:GLU:HB2	1.94	0.96
1:A:186:ILE:HD12	1:A:307:CYS:SG	2.05	0.96
4:D:239:ASN:HA	4:D:242:ASN:ND2	1.81	0.96
1:A:150:ALA:HA	1:A:153:TRP:CZ3	2.01	0.95
3:C:31:GLU:HG2	3:C:49:LYS:HB3	1.46	0.95
3:C:80:THR:HG22	3:C:81:LEU:H	1.31	0.95
3:C:131:TRP:HE3	3:C:131:TRP:H	1.09	0.95
2:B:163:VAL:HA	2:B:185:ALA:HB3	1.48	0.94
3:C:79:TRP:CD2	3:C:88:PRO:HB3	2.02	0.94
2:B:314:PRO:O	2:B:344:ILE:HG13	1.67	0.94
3:C:125:PHE:CD1	3:C:132:TRP:CE2	2.54	0.94
1:A:205:GLN:NE2	1:A:221:LEU:HD23	1.81	0.94
3:C:151:HIS:CD2	3:C:152:PRO:HD2	2.02	0.94
2:B:302:VAL:HG23	2:B:345:GLU:HB3	1.46	0.94
1:A:205:GLN:OE1	1:A:221:LEU:CD2	2.16	0.94
5:E:87:SER:C	5:E:149:PHE:CE1	2.46	0.94
6:F:51:VAL:HG12	6:F:52:THR:H	1.27	0.94
6:F:138:PHE:CZ	6:F:142:ILE:HG21	2.01	0.93
3:C:165:LYS:CG	3:C:198:SER:OG	2.17	0.93
5:E:18:ASN:ND2	5:E:117:TYR:HA	1.84	0.93
4:D:228:PHE:HB3	4:D:229:PRO:CD	1.99	0.93
4:D:147:ARG:CB	4:D:150:GLU:HB2	1.98	0.93
2:B:303:LEU:HB2	2:B:346:ASP:CB	1.98	0.92
3:C:60:TRP:CZ2	3:C:67:ILE:HD11	2.04	0.92
6:F:101:PHE:CD2	6:F:104:LEU:HD12	2.03	0.92
2:B:330:LEU:O	2:B:332:GLY:N	2.01	0.92
6:F:54:SER:CB	6:F:60:LYS:HB3	1.98	0.92
1:A:153:TRP:NE1	1:A:161:ARG:CA	2.31	0.92
3:C:366:LEU:HD23	3:C:369:LEU:HD22	1.48	0.92
4:D:147:ARG:HB2	4:D:150:GLU:CB	1.97	0.92
2:B:158:ASP:O	2:B:164:THR:HG23	1.70	0.91
3:C:218:ALA:HB2	3:C:228:LEU:HD12	1.53	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:ILE:CA	1:A:190:ILE:HD12	2.00	0.91
3:C:80:THR:O	3:C:86:TRP:CE3	2.23	0.91
6:F:51:VAL:CG2	7:G:145:LEU:CD2	2.47	0.91
1:A:178:ILE:HG23	1:A:190:ILE:HD11	0.93	0.90
1:A:178:ILE:HA	1:A:190:ILE:HD12	1.53	0.90
2:B:314:PRO:CA	2:B:344:ILE:HG21	2.01	0.90
3:C:129:ASN:HB2	3:C:131:TRP:CZ3	2.07	0.89
4:D:103:PRO:CG	4:D:109:ILE:HD12	1.98	0.89
2:B:301:ILE:O	2:B:345:GLU:CB	2.19	0.89
4:D:132:GLN:HE21	4:D:159:ASP:HA	1.34	0.89
3:C:79:TRP:CZ3	3:C:88:PRO:HG3	2.07	0.89
4:D:8:ASN:ND2	4:D:37:ASP:OD2	2.05	0.89
1:A:69:LYS:HD2	1:A:72:TYR:CE2	2.07	0.88
2:B:341:LYS:C	2:B:342:ILE:HG13	1.97	0.88
4:D:239:ASN:HA	4:D:242:ASN:HD21	1.37	0.88
5:E:87:SER:O	5:E:149:PHE:CZ	2.26	0.88
3:C:253:ILE:HD11	3:C:257:SER:CB	2.02	0.88
5:E:18:ASN:HD21	5:E:117:TYR:HA	1.38	0.88
1:A:159:GLY:O	1:A:160:GLU:HB2	1.74	0.87
4:D:75:LEU:O	4:D:79:VAL:HG23	1.74	0.87
3:C:10:PRO:HB3	3:C:350:MET:O	1.75	0.87
6:F:138:PHE:CE1	6:F:142:ILE:HG21	2.10	0.86
1:A:30:ILE:HD13	1:A:375:TYR:CZ	2.10	0.86
3:C:72:THR:CA	3:C:98:ALA:CB	2.42	0.86
3:C:97:ARG:HG3	3:C:116:GLY:C	2.01	0.86
3:C:140:PRO:HD3	3:C:169:PHE:HE1	1.40	0.86
3:C:77:TYR:HB3	3:C:89:THR:O	1.75	0.85
3:C:151:HIS:HB2	3:C:156:LEU:HB2	1.58	0.85
3:C:138:LYS:O	3:C:141:ILE:HG12	1.75	0.85
3:C:216:ARG:HD3	3:C:230:ASP:OD1	1.75	0.85
3:C:60:TRP:CE2	3:C:67:ILE:HD11	2.12	0.84
3:C:140:PRO:CG	3:C:167:ARG:HD3	2.06	0.84
5:E:18:ASN:CG	5:E:118:ALA:H	1.84	0.84
2:B:341:LYS:O	2:B:342:ILE:CG1	2.25	0.84
4:D:210:LYS:HA	4:D:211:ASP:CB	2.04	0.84
3:C:216:ARG:HD3	3:C:230:ASP:CG	2.01	0.84
3:C:30:HIS:HB3	3:C:51:HIS:O	1.77	0.84
3:C:245:LEU:HB2	3:C:264:ASP:OD1	1.77	0.84
3:C:247:LEU:O	3:C:248:LEU:HD13	1.76	0.84
3:C:151:HIS:ND1	3:C:152:PRO:HD2	1.91	0.84
1:A:216:PRO:HB2	1:A:219:GLN:O	1.77	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:95:MET:SD	6:F:108:PRO:HD3	2.18	0.83
1:A:111:LEU:HD12	1:A:390:PHE:CE1	2.13	0.83
3:C:19:ASP:O	3:C:21:THR:N	2.11	0.83
3:C:257:SER:O	3:C:258:LEU:HG	1.78	0.83
2:B:163:VAL:HA	2:B:185:ALA:HB2	1.60	0.83
3:C:79:TRP:CZ3	3:C:88:PRO:CD	2.61	0.83
6:F:101:PHE:CB	6:F:104:LEU:HB2	2.08	0.83
3:C:62:PRO:CD	3:C:108:GLU:CD	2.49	0.82
3:C:72:THR:HA	3:C:98:ALA:HB1	0.83	0.82
5:E:18:ASN:CB	5:E:118:ALA:HB3	2.04	0.82
3:C:252:PHE:CD2	3:C:258:LEU:HD21	2.13	0.82
1:A:112:LEU:HD12	1:A:126:THR:CG2	2.09	0.82
3:C:140:PRO:HG3	3:C:194:LEU:HD13	1.60	0.82
3:C:179:ARG:CG	3:C:180:PRO:HD2	2.09	0.82
4:D:132:GLN:NE2	4:D:159:ASP:HA	1.95	0.82
1:A:178:ILE:HA	1:A:190:ILE:HD13	1.60	0.81
3:C:125:PHE:CD1	3:C:132:TRP:NE1	2.48	0.81
3:C:140:PRO:HD3	3:C:169:PHE:CE1	2.11	0.81
3:C:253:ILE:HD11	3:C:257:SER:HB2	1.62	0.81
4:D:86:ASN:HB3	4:D:87:PRO:HD2	1.62	0.81
3:C:145:VAL:HG11	3:C:148:LEU:HD21	1.61	0.81
3:C:164:PHE:HB3	3:C:202:CYS:O	1.80	0.81
6:F:138:PHE:CE1	6:F:142:ILE:HD13	2.16	0.81
1:A:186:ILE:CG2	1:A:189:CYS:HB2	2.11	0.81
6:F:22:LEU:HD21	6:F:70:VAL:HG23	1.63	0.81
3:C:31:GLU:CG	3:C:49:LYS:HB3	2.11	0.81
3:C:7:LEU:HD23	3:C:7:LEU:H	1.46	0.80
3:C:77:TYR:CB	3:C:89:THR:O	2.29	0.80
2:B:303:LEU:CB	2:B:346:ASP:HB2	2.00	0.80
3:C:366:LEU:CD2	3:C:369:LEU:HD22	2.11	0.80
1:A:112:LEU:HD12	1:A:126:THR:HG23	1.62	0.80
6:F:4:THR:CG2	6:F:55:ARG:HE	1.95	0.80
2:B:298:TYR:HB3	2:B:342:ILE:HG12	1.62	0.79
4:D:37:ASP:HB2	4:D:43:TYR:CE2	2.16	0.79
7:G:46:LEU:HA	7:G:47:ARG:CB	2.12	0.79
3:C:233:LYS:NZ	3:C:274:SER:O	2.15	0.79
1:A:21:TYR:OH	1:A:103:ALA:CB	2.28	0.79
3:C:9:GLU:HB3	3:C:10:PRO:HD2	1.65	0.78
3:C:126:GLU:OE2	3:C:133:VAL:HG21	1.83	0.78
3:C:150:TRP:CH2	3:C:157:LEU:HD11	2.18	0.78
1:A:186:ILE:HG21	1:A:189:CYS:SG	2.23	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:54:SER:HB2	6:F:59:GLU:O	1.83	0.78
1:A:30:ILE:CD1	1:A:375:TYR:CE2	2.66	0.78
3:C:96:ASN:HD22	3:C:96:ASN:H	1.32	0.78
3:C:176:VAL:HG23	3:C:177:GLU:H	1.48	0.78
1:A:17:THR:HG1	1:A:33:SER:HG	1.26	0.78
1:A:200:ILE:HD12	1:A:281:ILE:HD11	1.57	0.78
1:A:178:ILE:CA	1:A:190:ILE:CD1	2.61	0.78
1:A:105:PRO:O	1:A:136:VAL:HG12	1.83	0.78
2:B:302:VAL:CA	2:B:345:GLU:CB	2.50	0.78
6:F:45:GLU:CB	7:G:24:PHE:CE2	2.67	0.78
6:F:101:PHE:HB3	6:F:104:LEU:HB2	1.66	0.78
1:A:153:TRP:CD1	1:A:161:ARG:HG2	2.19	0.77
3:C:151:HIS:CG	3:C:152:PRO:CD	2.62	0.77
1:A:179:PRO:O	1:A:186:ILE:HG13	1.85	0.77
1:A:179:PRO:CG	1:A:189:CYS:HB3	2.14	0.77
3:C:79:TRP:CZ3	3:C:88:PRO:CG	2.68	0.77
6:F:9:LEU:HB3	6:F:136:ILE:CD1	2.12	0.77
2:B:163:VAL:CA	2:B:185:ALA:HB3	2.15	0.77
3:C:224:SER:HA	3:C:246:PRO:HA	1.67	0.77
5:E:66:ARG:O	8:E:202:HOH:O	2.01	0.76
6:F:54:SER:HB3	6:F:60:LYS:HB2	1.67	0.76
3:C:150:TRP:CE2	3:C:157:LEU:HD21	2.20	0.76
6:F:51:VAL:CG1	7:G:111:TYR:CD1	2.68	0.76
4:D:147:ARG:HD3	4:D:150:GLU:CD	2.10	0.76
3:C:118:ARG:HB3	3:C:142:ARG:C	2.11	0.76
5:E:18:ASN:ND2	5:E:118:ALA:N	2.33	0.76
3:C:228:LEU:HD11	3:C:252:PHE:HZ	1.51	0.75
5:E:126:ASP:OD2	5:E:130:ARG:NH1	2.19	0.75
3:C:10:PRO:HB3	3:C:350:MET:CA	2.17	0.75
3:C:10:PRO:CB	3:C:350:MET:HA	2.16	0.75
3:C:107:ASN:C	3:C:108:GLU:HG2	2.12	0.75
3:C:253:ILE:HD11	3:C:257:SER:HB3	1.68	0.75
3:C:208:VAL:HG12	3:C:219:TRP:HB2	1.69	0.74
2:B:163:VAL:HG13	2:B:165:HIS:HE2	1.52	0.74
6:F:138:PHE:O	6:F:142:ILE:HG12	1.87	0.74
3:C:60:TRP:CD1	3:C:67:ILE:HG12	2.23	0.74
3:C:74:ARG:CZ	6:F:31:GLU:OE2	2.35	0.74
2:B:314:PRO:HB3	2:B:344:ILE:CG2	2.17	0.74
6:F:51:VAL:O	6:F:62:LEU:HD12	1.88	0.74
6:F:86:LEU:HD23	6:F:146:ILE:HG23	1.68	0.74
2:B:163:VAL:CA	2:B:185:ALA:CB	2.65	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:51:VAL:CG2	7:G:145:LEU:HD23	2.18	0.74
6:F:78:GLN:NE2	6:F:113:ASP:OD2	2.21	0.74
3:C:106:PRO:HG2	3:C:151:HIS:O	1.88	0.73
3:C:185:TRP:CE2	3:C:231:ALA:HB2	2.23	0.73
6:F:51:VAL:HG12	6:F:52:THR:N	2.02	0.73
3:C:122:ILE:HD13	3:C:137:ILE:HD11	0.80	0.72
5:E:142:LEU:N	8:E:201:HOH:O	1.85	0.72
1:A:150:ALA:CA	1:A:153:TRP:CZ3	2.72	0.72
1:A:179:PRO:HG3	1:A:189:CYS:HB3	1.71	0.72
2:B:298:TYR:HD2	2:B:342:ILE:CD1	2.01	0.72
3:C:62:PRO:CD	3:C:108:GLU:OE1	2.38	0.72
1:A:179:PRO:HD2	1:A:190:ILE:CD1	2.18	0.72
4:D:228:PHE:CB	4:D:229:PRO:HD2	2.16	0.72
3:C:79:TRP:CE3	3:C:88:PRO:CD	2.69	0.72
3:C:109:LYS:C	3:C:110:LYS:HG3	2.13	0.72
3:C:164:PHE:CE1	3:C:204:TRP:CD1	2.77	0.72
5:E:88:LYS:HA	5:E:149:PHE:CE1	2.25	0.72
1:A:186:ILE:CD1	1:A:307:CYS:SG	2.77	0.71
2:B:302:VAL:HB	2:B:345:GLU:OE2	1.90	0.71
5:E:88:LYS:HA	5:E:149:PHE:CD1	2.24	0.71
1:A:205:GLN:HE22	1:A:221:LEU:HD23	1.55	0.71
3:C:256:SER:O	3:C:272:TYR:N	2.23	0.71
4:D:281:ARG:CB	4:D:282:PRO:CD	2.61	0.71
3:C:245:LEU:HD13	6:F:21:CYS:SG	2.30	0.71
2:B:302:VAL:CG2	2:B:345:GLU:HB3	2.21	0.71
6:F:39:GLU:OE2	6:F:105:ARG:NH2	2.23	0.71
2:B:280:GLU:CD	2:B:328:ARG:HH22	1.98	0.71
3:C:171:ALA:O	3:C:173:ILE:HG12	1.89	0.71
6:F:51:VAL:HG21	7:G:145:LEU:HD21	1.71	0.70
3:C:133:VAL:HG12	3:C:134:CYS:N	2.03	0.70
1:A:18:LYS:HG3	1:A:30:ILE:HG12	1.72	0.70
1:A:29:PHE:CZ	4:D:10:ILE:HG23	2.26	0.70
4:D:202:HIS:HD1	4:D:203:ARG:HG3	1.55	0.70
5:E:50:LYS:NZ	5:E:159:TRP:O	2.24	0.70
7:G:38:ASP:O	7:G:42:VAL:HG23	1.90	0.70
2:B:301:ILE:C	2:B:345:GLU:HB2	2.15	0.70
6:F:4:THR:HG23	6:F:55:ARG:HE	1.55	0.70
1:A:111:LEU:HD23	1:A:111:LEU:O	1.90	0.70
3:C:151:HIS:CE1	3:C:152:PRO:HD2	2.25	0.70
3:C:254:THR:OG1	3:C:255:GLU:N	2.21	0.70
7:G:72:LYS:HZ3	7:G:150:THR:HG21	1.57	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:150:ASP:CG	5:E:151:PRO:CD	2.63	0.70
2:B:163:VAL:HG13	2:B:165:HIS:NE2	2.06	0.69
3:C:96:ASN:H	3:C:96:ASN:ND2	1.90	0.69
1:A:223:THR:O	1:A:227:VAL:HG23	1.92	0.69
3:C:109:LYS:HD3	3:C:176:VAL:HG12	1.74	0.69
4:D:228:PHE:CB	4:D:229:PRO:CD	2.71	0.69
1:A:111:LEU:HD13	1:A:385:ALA:HB2	1.73	0.69
3:C:145:VAL:HA	3:C:161:SER:HA	1.74	0.69
1:A:104:GLU:HG3	1:A:106:GLU:H	1.58	0.69
1:A:153:TRP:NE1	1:A:161:ARG:HG2	2.08	0.69
2:B:301:ILE:O	2:B:345:GLU:HG3	1.93	0.69
3:C:10:PRO:HB3	3:C:350:MET:C	2.18	0.69
4:D:147:ARG:HD3	4:D:150:GLU:CG	2.23	0.69
2:B:163:VAL:CG2	2:B:182:LEU:O	2.41	0.69
1:A:105:PRO:O	1:A:136:VAL:HA	1.94	0.69
3:C:103:ARG:HG3	3:C:148:LEU:O	1.93	0.69
5:E:88:LYS:HA	5:E:149:PHE:CG	2.28	0.69
3:C:220:VAL:HG11	3:C:247:LEU:HB2	1.75	0.68
1:A:205:GLN:HE22	1:A:221:LEU:CD2	2.06	0.68
3:C:253:ILE:CD1	3:C:257:SER:HB2	2.21	0.68
1:A:260:ASN:CG	1:A:263:SER:HB3	2.18	0.68
3:C:125:PHE:CE1	3:C:132:TRP:NE1	2.62	0.68
3:C:140:PRO:CD	3:C:169:PHE:HE1	1.97	0.68
4:D:209:LEU:HA	4:D:210:LYS:O	1.92	0.68
5:E:88:LYS:HA	5:E:149:PHE:CZ	2.28	0.68
1:A:38:LYS:HB2	1:A:38:LYS:NZ	2.07	0.68
1:A:106:GLU:HG2	1:A:106:GLU:O	1.93	0.68
1:A:159:GLY:O	1:A:160:GLU:CB	2.40	0.68
1:A:200:ILE:O	1:A:204:ILE:HG12	1.93	0.68
3:C:150:TRP:CZ3	3:C:157:LEU:HD11	2.28	0.68
3:C:252:PHE:CE1	3:C:258:LEU:HD21	2.28	0.68
5:E:87:SER:O	5:E:149:PHE:CE1	2.44	0.68
1:A:278:GLY:O	1:A:281:ILE:HG12	1.94	0.68
1:A:201:THR:HA	1:A:204:ILE:HD11	1.76	0.67
3:C:363:GLU:HG3	3:C:369:LEU:HD23	1.76	0.67
6:F:51:VAL:HG11	7:G:111:TYR:CD1	2.29	0.67
6:F:27:SER:N	6:F:33:HIS:O	2.20	0.67
3:C:283:GLY:HA3	3:C:284:ARG:CB	2.14	0.67
6:F:55:ARG:O	6:F:55:ARG:HG2	1.93	0.67
3:C:155:VAL:O	3:C:157:LEU:HD12	1.93	0.67
3:C:9:GLU:O	3:C:352:GLY:HA3	1.95	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:219:TRP:CE2	3:C:227:CYS:HB2	2.30	0.67
3:C:79:TRP:CZ2	3:C:88:PRO:HG3	2.30	0.67
6:F:27:SER:HB3	6:F:30:VAL:HG23	1.76	0.67
2:B:314:PRO:CB	2:B:344:ILE:HG21	2.25	0.67
3:C:97:ARG:NE	6:F:28:GLN:O	2.27	0.67
6:F:54:SER:CB	6:F:60:LYS:CB	2.64	0.67
7:G:124:VAL:HG22	7:G:128:TRP:HD1	1.60	0.67
3:C:151:HIS:HB3	3:C:153:ASN:OD1	1.94	0.67
7:G:72:LYS:NZ	7:G:150:THR:HG21	2.09	0.67
5:E:88:LYS:HA	5:E:149:PHE:CD2	2.30	0.66
6:F:51:VAL:HG11	7:G:111:TYR:CE1	2.30	0.66
7:G:124:VAL:HG22	7:G:128:TRP:CD1	2.31	0.66
3:C:223:ASP:OD1	3:C:225:THR:OG1	2.10	0.66
1:A:111:LEU:HD12	1:A:390:PHE:CZ	2.30	0.66
3:C:153:ASN:HD21	3:C:155:VAL:HB	1.60	0.66
1:A:153:TRP:NE1	1:A:161:ARG:CB	2.59	0.66
1:A:200:ILE:HD13	1:A:281:ILE:HD11	0.66	0.66
3:C:129:ASN:H	3:C:131:TRP:HZ3	1.43	0.66
3:C:228:LEU:HD11	3:C:252:PHE:CZ	2.31	0.66
2:B:314:PRO:O	2:B:344:ILE:CG1	2.44	0.66
6:F:137:HIS:CD2	6:F:141:GLU:HG2	2.32	0.65
5:E:96:TYR:O	5:E:100:ILE:HG12	1.96	0.65
6:F:22:LEU:HD21	6:F:70:VAL:CG2	2.26	0.65
2:B:164:THR:O	2:B:165:HIS:ND1	2.30	0.65
3:C:114:GLY:HA3	3:C:148:LEU:HD11	1.79	0.65
1:A:396:THR:HG23	1:A:399:ASP:H	1.61	0.65
5:E:88:LYS:HA	5:E:149:PHE:CE2	2.30	0.65
1:A:186:ILE:HG22	1:A:189:CYS:HB2	1.78	0.65
3:C:249:ALA:HB1	3:C:332:ILE:HG22	1.78	0.65
5:E:88:LYS:N	5:E:149:PHE:CE1	2.64	0.65
5:E:152:GLN:HB2	5:E:155:LYS:HD2	1.77	0.65
3:C:62:PRO:CG	3:C:108:GLU:OE1	2.45	0.65
3:C:269:LEU:HB3	3:C:283:GLY:O	1.97	0.65
6:F:138:PHE:O	6:F:142:ILE:HG23	1.97	0.65
1:A:38:LYS:HB2	1:A:38:LYS:HZ2	1.60	0.65
3:C:345:PHE:CZ	3:C:357:TRP:HB2	2.32	0.65
4:D:159:ASP:O	4:D:160:ARG:HB3	1.96	0.65
6:F:51:VAL:CG2	7:G:145:LEU:HD22	2.26	0.65
1:A:361:LYS:HG2	1:A:362:PRO:HD2	1.79	0.65
2:B:189:ILE:HD12	2:B:262:PRO:HA	1.79	0.65
4:D:128:TYR:OH	4:D:141:ARG:O	2.14	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:179:PRO:CD	1:A:190:ILE:HD13	2.18	0.65
2:B:318:GLU:HB2	2:B:344:ILE:HG12	1.79	0.64
3:C:94:ARG:NH2	3:C:134:CYS:O	2.30	0.64
6:F:101:PHE:O	6:F:102:PHE:HB2	1.97	0.64
2:B:301:ILE:O	2:B:345:GLU:CG	2.45	0.64
2:B:329:VAL:C	2:B:330:LEU:HG	2.22	0.64
1:A:134:PHE:O	1:A:136:VAL:N	2.27	0.64
3:C:185:TRP:CZ2	3:C:231:ALA:HB2	2.33	0.64
3:C:206:HIS:CG	3:C:248:LEU:HD12	2.33	0.64
5:E:154:ASP:O	5:E:155:LYS:HG3	1.98	0.64
1:A:178:ILE:CG1	1:A:190:ILE:HD12	2.26	0.64
2:B:163:VAL:CG1	2:B:165:HIS:HE2	2.11	0.64
2:B:345:GLU:O	2:B:346:ASP:HB3	1.98	0.64
3:C:111:PHE:CZ	3:C:123:CYS:CB	2.81	0.64
3:C:157:LEU:CD1	3:C:171:ALA:HB2	2.27	0.64
6:F:51:VAL:CG1	7:G:111:TYR:HD1	2.10	0.64
2:B:347:PRO:HB2	2:B:348:PRO:CD	2.28	0.64
2:B:298:TYR:CD2	2:B:342:ILE:HD11	2.33	0.64
3:C:111:PHE:CZ	3:C:123:CYS:HB2	2.32	0.64
3:C:283:GLY:CA	3:C:284:ARG:HB2	2.24	0.64
1:A:69:LYS:HB3	1:A:72:TYR:CD2	2.33	0.63
3:C:97:ARG:HG3	3:C:116:GLY:O	1.99	0.63
3:C:248:LEU:HD23	3:C:262:GLY:CA	2.28	0.63
1:A:179:PRO:HG2	1:A:186:ILE:HB	1.81	0.63
3:C:162:CYS:SG	3:C:204:TRP:CD1	2.87	0.63
3:C:208:VAL:HG12	3:C:219:TRP:CB	2.29	0.63
3:C:366:LEU:HD23	3:C:369:LEU:CD2	2.24	0.63
6:F:142:ILE:HG13	6:F:143:ASP:N	2.14	0.63
1:A:196:ALA:O	1:A:200:ILE:HG12	1.99	0.63
3:C:18:LYS:HD2	3:C:62:PRO:O	1.99	0.63
1:A:180:VAL:HG22	1:A:185:VAL:HG22	1.81	0.63
1:A:153:TRP:CE2	1:A:161:ARG:HG2	2.34	0.63
6:F:133:ASP:O	6:F:136:ILE:HG22	1.98	0.63
3:C:211:SER:OG	3:C:213:ASN:OD1	2.16	0.62
5:E:102:ASN:O	5:E:102:ASN:ND2	2.32	0.62
6:F:101:PHE:CE2	6:F:104:LEU:HD12	2.34	0.62
2:B:163:VAL:HG22	2:B:165:HIS:CE1	2.34	0.62
3:C:60:TRP:CG	3:C:67:ILE:HG12	2.34	0.62
3:C:151:HIS:NE2	3:C:214:GLY:HA3	2.14	0.62
3:C:164:PHE:HE1	3:C:204:TRP:CD1	2.16	0.62
4:D:75:LEU:HD23	4:D:79:VAL:CG2	2.29	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:216:ILE:HG12	2:B:244:TYR:CE1	2.35	0.62
4:D:80:TYR:CZ	4:D:95:LEU:HD21	2.35	0.62
1:A:239:VAL:HG13	5:E:4:TYR:CE1	2.35	0.62
3:C:10:PRO:HG3	6:F:124:GLU:HG2	1.82	0.62
3:C:151:HIS:ND1	3:C:152:PRO:CD	2.63	0.62
3:C:113:VAL:HG23	3:C:121:SER:HB2	1.81	0.62
3:C:125:PHE:HD1	3:C:132:TRP:NE1	1.89	0.62
1:A:283:PHE:CZ	1:A:334:ARG:HG2	2.35	0.62
4:D:146:TYR:OH	4:D:150:GLU:OE2	2.18	0.62
2:B:237:THR:HB	6:F:117:LEU:HD23	1.82	0.62
4:D:230:ARG:HG3	4:D:231:HIS:CE1	2.34	0.62
4:D:80:TYR:CE2	4:D:95:LEU:HD21	2.34	0.61
3:C:245:LEU:N	3:C:264:ASP:OD1	2.32	0.61
1:A:150:ALA:HB1	1:A:153:TRP:HZ3	1.64	0.61
3:C:248:LEU:HD23	3:C:262:GLY:HA2	1.82	0.61
1:A:102:ARG:O	4:D:37:ASP:HA	1.99	0.61
1:A:178:ILE:HG13	1:A:190:ILE:HG23	1.83	0.61
3:C:18:LYS:HB2	3:C:62:PRO:CA	2.25	0.61
3:C:173:ILE:C	3:C:175:GLU:H	2.09	0.61
6:F:153:VAL:O	6:F:156:ARG:HG2	2.00	0.61
2:B:327:GLU:HG2	7:G:11:PHE:HB3	1.83	0.61
4:D:109:ILE:HG22	4:D:109:ILE:O	2.01	0.61
6:F:50:PRO:HB3	6:F:64:GLU:HG2	1.83	0.61
5:E:88:LYS:CA	5:E:149:PHE:CD1	2.84	0.61
3:C:222:HIS:O	3:C:246:PRO:CG	2.49	0.61
3:C:257:SER:HB3	3:C:269:LEU:HD11	1.81	0.61
5:E:95:MET:HE3	5:E:95:MET:HA	1.82	0.60
1:A:69:LYS:HD2	1:A:72:TYR:CD2	2.36	0.60
2:B:182:LEU:HG	2:B:281:LEU:HD12	1.83	0.60
4:D:281:ARG:HB3	4:D:282:PRO:HD3	1.80	0.60
5:E:18:ASN:ND2	5:E:117:TYR:CA	2.63	0.60
3:C:16:TRP:CE2	3:C:23:ILE:HG22	2.37	0.60
3:C:80:THR:HG22	3:C:81:LEU:N	2.11	0.60
7:G:42:VAL:HG12	7:G:42:VAL:O	2.00	0.60
1:A:60:PHE:C	1:A:61:PHE:HD1	2.10	0.60
3:C:77:TYR:CD2	3:C:89:THR:O	2.54	0.60
4:D:147:ARG:HD3	4:D:150:GLU:HG3	1.84	0.60
7:G:104:ASP:CG	7:G:143:ARG:HE	2.10	0.60
3:C:140:PRO:HG2	3:C:167:ARG:NE	2.17	0.60
4:D:237:ARG:O	4:D:241:ILE:HG13	2.02	0.60
1:A:69:LYS:HB3	1:A:72:TYR:HB2	1.83	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:150:ASP:OD1	5:E:151:PRO:HD2	2.01	0.59
3:C:252:PHE:CD1	3:C:258:LEU:CD2	2.86	0.59
4:D:143:VAL:HG12	4:D:145:HIS:CE1	2.37	0.59
1:A:69:LYS:CG	1:A:72:TYR:CD2	2.86	0.59
1:A:229:GLU:O	1:A:230:ARG:HB2	2.01	0.59
2:B:314:PRO:HB3	2:B:344:ILE:HG21	1.82	0.59
4:D:181:PHE:O	4:D:185:PHE:HD2	1.85	0.59
6:F:30:VAL:HG23	6:F:33:HIS:HB2	1.85	0.59
3:C:31:GLU:HB3	3:C:49:LYS:HG2	1.85	0.59
3:C:31:GLU:HB3	3:C:49:LYS:HA	1.84	0.59
3:C:89:THR:HG22	3:C:90:LEU:N	2.18	0.59
3:C:157:LEU:HD13	3:C:171:ALA:HB2	1.83	0.59
6:F:53:ILE:HD11	7:G:111:TYR:CE1	2.38	0.59
2:B:218:GLU:O	2:B:219:LYS:HG2	2.03	0.59
3:C:79:TRP:CE2	3:C:88:PRO:HB3	2.38	0.59
4:D:86:ASN:HB3	4:D:87:PRO:CD	2.31	0.59
4:D:230:ARG:CG	4:D:231:HIS:CE1	2.86	0.59
3:C:153:ASN:ND2	3:C:155:VAL:HB	2.17	0.59
7:G:72:LYS:HZ3	7:G:150:THR:CG2	2.16	0.59
6:F:76:VAL:HG12	6:F:77:LYS:N	2.17	0.59
6:F:4:THR:HG23	6:F:55:ARG:NE	2.18	0.59
7:G:121:SER:O	7:G:125:LEU:HG	2.03	0.59
1:A:69:LYS:CB	1:A:72:TYR:CD2	2.86	0.58
3:C:30:HIS:CE1	3:C:53:GLY:C	2.81	0.58
3:C:210:PHE:CE1	3:C:217:VAL:HB	2.38	0.58
3:C:206:HIS:NE2	6:F:23:GLU:OE1	2.36	0.58
1:A:187:GLY:C	1:A:189:CYS:H	2.11	0.58
2:B:155:VAL:HG12	2:B:166:ILE:CG2	2.33	0.58
2:B:302:VAL:CB	2:B:345:GLU:CD	2.73	0.58
3:C:122:ILE:CD1	3:C:137:ILE:CD1	2.44	0.58
3:C:252:PHE:CE1	3:C:258:LEU:CD2	2.86	0.58
3:C:252:PHE:CG	3:C:258:LEU:CD2	2.87	0.58
2:B:163:VAL:CG2	2:B:165:HIS:CE1	2.86	0.58
3:C:80:THR:O	3:C:86:TRP:CD2	2.56	0.58
3:C:137:ILE:HG22	3:C:137:ILE:O	2.02	0.58
4:D:106:LYS:C	4:D:108:SER:H	2.11	0.58
1:A:187:GLY:O	1:A:189:CYS:N	2.35	0.58
3:C:10:PRO:CB	3:C:350:MET:CA	2.80	0.58
6:F:4:THR:HG22	6:F:55:ARG:HH21	1.67	0.58
7:G:118:SER:O	7:G:121:SER:HB3	2.02	0.58
1:A:124:GLU:OE2	1:A:409:ARG:NH1	2.36	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:10:PRO:HB2	3:C:350:MET:HA	1.84	0.58
1:A:150:ALA:O	1:A:153:TRP:CE3	2.56	0.58
4:D:161:VAL:HG12	4:D:162:THR:N	2.18	0.58
1:A:195:ILE:HD13	1:A:285:PRO:HB3	1.86	0.58
1:A:286:GLU:HB3	1:A:293:THR:HB	1.86	0.58
5:E:95:MET:HA	5:E:95:MET:CE	2.34	0.58
1:A:176:HIS:NE2	1:A:192:HIS:NE2	2.52	0.58
4:D:106:LYS:O	4:D:110:VAL:HG23	2.04	0.58
6:F:94:MET:HE1	6:F:138:PHE:HE2	1.68	0.58
1:A:153:TRP:HE1	1:A:162:THR:N	2.00	0.58
3:C:60:TRP:HD1	3:C:61:ALA:H	1.52	0.58
3:C:166:CYS:H	3:C:198:SER:HB3	1.69	0.58
1:A:69:LYS:CG	1:A:72:TYR:HD2	2.16	0.57
3:C:31:GLU:HB3	3:C:49:LYS:CA	2.34	0.57
1:A:180:VAL:HA	1:A:185:VAL:HA	1.86	0.57
3:C:120:ILE:HG13	3:C:141:ILE:CD1	2.34	0.57
5:E:88:LYS:CA	5:E:149:PHE:CE1	2.87	0.57
7:G:72:LYS:NZ	7:G:150:THR:CG2	2.68	0.57
1:A:69:LYS:CB	1:A:72:TYR:HD2	2.16	0.57
1:A:176:HIS:CE1	1:A:192:HIS:CD2	2.91	0.57
3:C:228:LEU:CD1	3:C:252:PHE:HZ	2.17	0.57
2:B:302:VAL:HG23	2:B:346:ASP:H	1.69	0.57
5:E:150:ASP:OD2	5:E:151:PRO:HD2	2.04	0.57
1:A:207:LEU:O	1:A:207:LEU:HD23	2.04	0.57
2:B:163:VAL:N	2:B:185:ALA:HB3	2.20	0.57
1:A:176:HIS:NE2	1:A:192:HIS:CD2	2.72	0.57
3:C:77:TYR:CD2	3:C:90:LEU:HA	2.39	0.57
3:C:138:LYS:NZ	7:G:22:ASN:OD1	2.36	0.57
3:C:172:TYR:HB3	3:C:191:PHE:HB2	1.87	0.57
4:D:233:ASN:OD1	4:D:236:ALA:N	2.36	0.57
3:C:9:GLU:HB3	3:C:10:PRO:CD	2.34	0.57
3:C:185:TRP:CD2	3:C:231:ALA:HB2	2.39	0.57
4:D:281:ARG:CB	4:D:282:PRO:HD2	2.21	0.57
3:C:60:TRP:CE2	3:C:67:ILE:CD1	2.85	0.57
3:C:104:TRP:O	3:C:105:ALA:HB2	2.05	0.57
2:B:298:TYR:CD2	2:B:342:ILE:CD1	2.86	0.57
2:B:302:VAL:HA	2:B:345:GLU:HB3	1.77	0.57
4:D:187:GLU:HB3	4:D:190:ARG:HD3	1.86	0.57
1:A:150:ALA:CB	1:A:153:TRP:HZ3	2.18	0.56
3:C:56:THR:OG1	3:C:99:ALA:O	2.19	0.56
3:C:252:PHE:CD2	3:C:258:LEU:CD2	2.86	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:G:47:ARG:C	7:G:49:GLY:H	2.13	0.56
3:C:263:HIS:CG	6:F:21:CYS:HB3	2.39	0.56
6:F:27:SER:CB	6:F:30:VAL:HG23	2.35	0.56
3:C:77:TYR:HA	3:C:89:THR:O	2.03	0.56
4:D:75:LEU:HD23	4:D:79:VAL:HG21	1.87	0.56
5:E:98:LEU:O	5:E:101:THR:OG1	2.23	0.56
6:F:76:VAL:HG13	6:F:143:ASP:OD1	2.05	0.56
2:B:280:GLU:OE1	2:B:328:ARG:NH2	2.36	0.56
3:C:125:PHE:CD1	3:C:132:TRP:CZ2	2.94	0.56
4:D:56:MET:HE3	4:D:96:LEU:HD13	1.88	0.56
4:D:68:GLN:HA	4:D:72:ALA:HB3	1.87	0.56
6:F:51:VAL:CG1	6:F:52:THR:H	2.09	0.56
2:B:261:ALA:HB3	2:B:262:PRO:HD3	1.88	0.56
3:C:247:LEU:C	3:C:248:LEU:HD22	2.31	0.56
1:A:352:GLU:O	1:A:354:SER:N	2.35	0.56
3:C:219:TRP:CZ2	3:C:227:CYS:HB2	2.41	0.56
4:D:86:ASN:O	4:D:94:SER:HB3	2.04	0.56
1:A:24:ASN:OD1	4:D:33:VAL:HA	2.06	0.56
3:C:79:TRP:CE3	3:C:88:PRO:CG	2.88	0.56
3:C:120:ILE:HG13	3:C:141:ILE:HD13	1.86	0.56
3:C:140:PRO:CG	3:C:194:LEU:HD13	2.33	0.56
1:A:11:ASP:HA	1:A:113:THR:CG2	2.36	0.56
2:B:157:VAL:HB	2:B:303:LEU:HD13	1.88	0.56
1:A:52:MET:SD	4:D:261:TYR:HE1	2.29	0.55
5:E:97:THR:O	5:E:101:THR:HG23	2.06	0.55
2:B:212:THR:O	2:B:216:ILE:HG13	2.07	0.55
3:C:165:LYS:HA	3:C:198:SER:OG	2.06	0.55
1:A:54:GLY:O	6:F:156:ARG:NH1	2.39	0.55
4:D:173:ASP:OD1	6:F:85:ILE:HD12	2.07	0.55
1:A:70:PRO:C	1:A:72:TYR:H	2.15	0.55
2:B:329:VAL:O	2:B:330:LEU:HG	2.06	0.55
3:C:131:TRP:CE3	3:C:131:TRP:N	2.73	0.55
4:D:51:ASP:HB3	4:D:54:LYS:HD3	1.88	0.55
3:C:97:ARG:CG	3:C:116:GLY:C	2.76	0.55
3:C:151:HIS:CE1	3:C:152:PRO:HG2	2.42	0.55
4:D:161:VAL:N	4:D:227:LEU:O	2.40	0.55
1:A:153:TRP:HE1	1:A:161:ARG:C	2.15	0.55
1:A:201:THR:O	1:A:204:ILE:HG13	2.07	0.55
1:A:310:ASP:OD1	1:A:310:ASP:N	2.40	0.55
4:D:71:GLY:O	4:D:123:SER:HB2	2.07	0.55
5:E:18:ASN:HD21	5:E:117:TYR:CA	2.15	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:E:88:LYS:O	5:E:92:GLU:HG3	2.07	0.55
5:E:101:THR:OG1	5:E:103:PHE:CE2	2.60	0.55
2:B:280:GLU:HG3	2:B:328:ARG:HH22	1.72	0.55
3:C:151:HIS:CD2	3:C:214:GLY:HA3	2.42	0.55
3:C:164:PHE:HE1	3:C:204:TRP:NE1	2.05	0.55
1:A:36:ALA:HB1	1:A:72:TYR:HB3	1.89	0.55
2:B:185:ALA:O	2:B:187:ARG:N	2.40	0.55
4:D:48:PRO:O	4:D:50:GLY:N	2.39	0.55
7:G:119:ASP:C	7:G:121:SER:H	2.14	0.55
1:A:186:ILE:HB	1:A:189:CYS:HB2	1.87	0.54
2:B:302:VAL:CB	2:B:345:GLU:CB	2.85	0.54
2:B:347:PRO:CB	2:B:348:PRO:CD	2.83	0.54
1:A:203:PHE:CD2	1:A:281:ILE:HG21	2.43	0.54
2:B:159:SER:HB2	2:B:308:THR:HG23	1.89	0.54
1:A:30:ILE:HG21	1:A:375:TYR:CE1	2.42	0.54
1:A:178:ILE:HG22	1:A:190:ILE:HD11	1.77	0.54
3:C:129:ASN:HB2	3:C:131:TRP:CD2	2.42	0.54
3:C:366:LEU:C	3:C:368:ASP:H	2.15	0.54
4:D:64:TYR:OH	4:D:73:ASP:OD1	2.21	0.54
6:F:138:PHE:CZ	6:F:142:ILE:CG2	2.86	0.54
3:C:72:THR:CA	3:C:98:ALA:HB2	2.35	0.54
3:C:217:VAL:HG12	3:C:229:ALA:O	2.07	0.54
6:F:54:SER:HA	6:F:60:LYS:HA	1.88	0.54
3:C:218:ALA:HB3	3:C:252:PHE:HE1	1.73	0.54
3:C:366:LEU:HD23	3:C:369:LEU:HD13	1.89	0.54
2:B:280:GLU:CG	2:B:328:ARG:HH22	2.20	0.54
3:C:230:ASP:H	3:C:236:ALA:HB3	1.71	0.54
5:E:168:PHE:CE2	5:E:169:MET:HE2	2.43	0.54
2:B:257:GLU:HA	2:B:260:GLU:HB2	1.89	0.54
5:E:16:ILE:O	5:E:16:ILE:HG13	2.06	0.54
4:D:75:LEU:HD23	4:D:75:LEU:C	2.32	0.54
3:C:77:TYR:CA	3:C:89:THR:O	2.55	0.54
3:C:111:PHE:CE2	3:C:123:CYS:HB2	2.43	0.54
3:C:252:PHE:CG	3:C:258:LEU:HD21	2.42	0.54
4:D:209:LEU:CA	4:D:210:LYS:CB	2.85	0.54
6:F:27:SER:HB2	6:F:33:HIS:O	2.07	0.54
1:A:104:GLU:O	1:A:108:HIS:HB2	2.08	0.54
5:E:28:PHE:HZ	5:E:96:TYR:HE1	1.55	0.54
3:C:109:LYS:HD3	3:C:176:VAL:CG1	2.38	0.53
1:A:284:HIS:O	1:A:287:PHE:HB2	2.08	0.53
7:G:111:TYR:OH	7:G:141:ILE:HD12	2.07	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:186:ILE:CB	1:A:189:CYS:HB2	2.38	0.53
3:C:102:VAL:HA	3:C:112:ALA:O	2.09	0.53
3:C:222:HIS:O	3:C:246:PRO:HB3	2.09	0.53
4:D:22:ALA:C	4:D:24:ALA:H	2.15	0.53
5:E:18:ASN:CB	5:E:118:ALA:CB	2.74	0.53
1:A:79:ARG:C	1:A:81:GLY:H	2.17	0.53
3:C:16:TRP:CD2	3:C:23:ILE:HG22	2.42	0.53
4:D:171:ASP:O	4:D:174:ASP:HB2	2.09	0.53
4:D:230:ARG:HG3	4:D:231:HIS:ND1	2.22	0.53
6:F:94:MET:CE	6:F:138:PHE:HE2	2.21	0.53
1:A:153:TRP:NE1	1:A:161:ARG:CG	2.71	0.53
1:A:166:THR:OG1	1:A:319:ILE:HG12	2.09	0.53
2:B:283:PHE:CE2	2:B:328:ARG:HD2	2.44	0.53
3:C:77:TYR:HE2	3:C:90:LEU:HD23	1.74	0.53
1:A:203:PHE:CD2	1:A:281:ILE:CG2	2.92	0.53
1:A:219:GLN:CD	1:A:261:ALA:CB	2.81	0.53
3:C:9:GLU:O	3:C:352:GLY:CA	2.57	0.53
5:E:19:MET:HE3	8:E:202:HOH:O	2.08	0.53
3:C:118:ARG:CD	3:C:142:ARG:O	2.55	0.53
3:C:151:HIS:CB	3:C:156:LEU:HB2	2.36	0.53
3:C:281:PHE:CG	3:C:282:GLY:N	2.77	0.53
1:A:153:TRP:CD1	1:A:161:ARG:CG	2.91	0.53
4:D:59:ILE:HB	4:D:116:LEU:HD13	1.91	0.53
3:C:26:CYS:SG	3:C:55:VAL:HB	2.50	0.52
6:F:139:MET:HA	6:F:142:ILE:CD1	2.39	0.52
7:G:64:ILE:O	7:G:65:ASN:HB2	2.08	0.52
1:A:166:THR:HG21	1:A:304:ILE:CD1	2.40	0.52
1:A:216:PRO:CB	1:A:219:GLN:O	2.53	0.52
3:C:111:PHE:CE2	3:C:123:CYS:SG	3.03	0.52
4:D:35:PHE:O	4:D:43:TYR:HB2	2.09	0.52
6:F:139:MET:HA	6:F:142:ILE:HD11	1.92	0.52
3:C:173:ILE:O	3:C:175:GLU:N	2.39	0.52
3:C:218:ALA:HB3	3:C:252:PHE:CE1	2.44	0.52
6:F:41:ARG:NH2	8:F:201:HOH:O	2.42	0.52
1:A:153:TRP:CD1	1:A:161:ARG:CA	2.79	0.52
4:D:158:LYS:O	4:D:158:LYS:HD3	2.08	0.52
6:F:51:VAL:HG13	7:G:111:TYR:CD1	2.45	0.52
1:A:69:LYS:CD	1:A:72:TYR:CD2	2.92	0.52
6:F:4:THR:CG2	6:F:55:ARG:HH21	2.23	0.52
2:B:163:VAL:CA	2:B:185:ALA:HB2	2.34	0.52
3:C:74:ARG:HG2	3:C:97:ARG:O	2.10	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:209:LEU:N	4:D:210:LYS:CB	2.73	0.52
5:E:16:ILE:O	5:E:129:MET:HE2	2.10	0.52
1:A:178:ILE:HG23	1:A:190:ILE:CG1	2.25	0.52
1:A:195:ILE:CD1	1:A:285:PRO:HB3	2.40	0.52
1:A:305:GLN:CD	1:A:346:ARG:HH12	2.18	0.52
2:B:217:LYS:HD2	2:B:310:TYR:OH	2.10	0.52
3:C:77:TYR:HD2	3:C:89:THR:O	1.93	0.52
1:A:395:HIS:HB3	1:A:407:ILE:HD12	1.91	0.52
3:C:162:CYS:HG	3:C:204:TRP:CG	2.22	0.52
3:C:245:LEU:CB	3:C:264:ASP:OD1	2.54	0.52
6:F:108:PRO:HB3	6:F:114:ILE:HA	1.92	0.52
7:G:125:LEU:HA	7:G:128:TRP:HB2	1.92	0.52
1:A:186:ILE:CG2	1:A:189:CYS:CB	2.86	0.51
5:E:70:TYR:HB2	8:E:202:HOH:O	2.10	0.51
1:A:14:THR:HG22	1:A:78:ILE:HG22	1.91	0.51
3:C:211:SER:HB3	3:C:216:ARG:HB2	1.92	0.51
3:C:253:ILE:CG1	3:C:257:SER:HB2	2.40	0.51
4:D:43:TYR:CE1	4:D:59:ILE:HG13	2.46	0.51
2:B:158:ASP:O	2:B:164:THR:HA	2.10	0.51
3:C:226:VAL:HG13	3:C:226:VAL:O	2.10	0.51
3:C:252:PHE:CG	3:C:258:LEU:HD23	2.46	0.51
4:D:63:PHE:HB3	4:D:145:HIS:O	2.09	0.51
3:C:216:ARG:NH1	3:C:230:ASP:OD2	2.43	0.51
6:F:22:LEU:CD2	6:F:70:VAL:HG23	2.36	0.51
1:A:260:ASN:OD1	1:A:263:SER:HB3	2.11	0.51
7:G:46:LEU:CA	7:G:47:ARG:CB	2.87	0.51
2:B:331:LYS:HG3	2:B:331:LYS:O	2.10	0.51
3:C:20:ARG:HE	3:C:335:LEU:HA	1.75	0.51
2:B:164:THR:C	2:B:165:HIS:CG	2.88	0.51
3:C:150:TRP:CE2	3:C:157:LEU:CD2	2.93	0.51
3:C:248:LEU:HD21	3:C:263:HIS:CD2	2.46	0.51
3:C:257:SER:C	3:C:258:LEU:HG	2.35	0.51
4:D:203:ARG:NH2	4:D:218:ASP:HB3	2.26	0.51
2:B:301:ILE:O	2:B:345:GLU:N	2.43	0.51
1:A:370:HIS:NE2	1:A:372:MET:O	2.44	0.51
3:C:74:ARG:NE	6:F:31:GLU:OE2	2.44	0.51
3:C:329:VAL:HA	3:C:349:GLY:CA	2.41	0.51
1:A:132:GLU:OE2	6:F:92:ARG:NH2	2.43	0.50
2:B:165:HIS:ND1	2:B:181:ARG:HB3	2.27	0.50
3:C:138:LYS:HE3	7:G:22:ASN:HD21	1.75	0.50
3:C:248:LEU:CD2	3:C:262:GLY:CA	2.89	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:101:PHE:HB2	6:F:104:LEU:HB2	1.91	0.50
1:A:99:LYS:HE2	4:D:9:ARG:NH2	2.25	0.50
2:B:155:VAL:HG21	2:B:286:ILE:HD11	1.92	0.50
6:F:51:VAL:HG23	7:G:145:LEU:HD22	1.93	0.50
1:A:11:ASP:HA	1:A:113:THR:HG21	1.92	0.50
1:A:186:ILE:HD12	1:A:307:CYS:HG	1.72	0.50
3:C:202:CYS:HB2	3:C:221:SER:CB	2.41	0.50
4:D:80:TYR:HB3	4:D:83:TYR:HB2	1.93	0.50
6:F:13:ARG:NH2	6:F:136:ILE:HG21	2.25	0.50
1:A:38:LYS:HD3	1:A:59:ASP:HB3	1.92	0.50
1:A:186:ILE:HB	1:A:189:CYS:CB	2.41	0.50
3:C:79:TRP:CG	3:C:88:PRO:HB3	2.44	0.50
5:E:14:LYS:C	5:E:15:LEU:HG	2.36	0.50
6:F:142:ILE:HG13	6:F:143:ASP:H	1.77	0.50
1:A:283:PHE:CZ	1:A:334:ARG:CG	2.94	0.50
3:C:133:VAL:O	3:C:134:CYS:HB3	2.12	0.50
3:C:165:LYS:HA	3:C:198:SER:CB	2.42	0.50
2:B:302:VAL:N	2:B:345:GLU:HB2	2.25	0.50
4:D:143:VAL:CG1	4:D:145:HIS:CE1	2.95	0.50
1:A:228:LYS:O	1:A:232:SER:HB2	2.12	0.50
6:F:53:ILE:O	6:F:61:VAL:N	2.33	0.50
1:A:193:ILE:HD11	1:A:299:VAL:HG11	1.93	0.49
3:C:151:HIS:ND1	3:C:153:ASN:OD1	2.45	0.49
3:C:80:THR:CG2	3:C:81:LEU:H	2.12	0.49
3:C:179:ARG:HH21	3:C:188:LYS:HZ1	1.58	0.49
1:A:112:LEU:HG	1:A:139:LEU:HD11	1.94	0.49
5:E:15:LEU:HD21	5:E:63:GLU:HG3	1.92	0.49
6:F:30:VAL:HG23	6:F:33:HIS:CB	2.42	0.49
6:F:54:SER:CB	6:F:59:GLU:O	2.57	0.49
6:F:139:MET:HA	6:F:142:ILE:HG12	1.93	0.49
1:A:149:LEU:HD11	1:A:180:VAL:HB	1.94	0.49
4:D:27:LYS:HD3	4:D:28:PRO:HD2	1.94	0.49
6:F:52:THR:O	7:G:114:PHE:HB3	2.13	0.49
2:B:294:ARG:O	2:B:297:PHE:HB2	2.12	0.49
3:C:30:HIS:CB	3:C:51:HIS:O	2.56	0.49
3:C:79:TRP:HA	3:C:88:PRO:HA	1.93	0.49
7:G:20:ASP:OD1	7:G:21:GLU:N	2.46	0.49
1:A:53:LYS:H	1:A:56:ASP:HB2	1.77	0.49
1:A:106:GLU:HA	1:A:135:ASN:O	2.13	0.49
3:C:31:GLU:HB3	3:C:48:LEU:O	2.12	0.49
6:F:72:VAL:O	6:F:116:PHE:N	2.40	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:216:ILE:HG12	2:B:244:TYR:CZ	2.47	0.49
5:E:14:LYS:O	5:E:15:LEU:HG	2.13	0.49
5:E:95:MET:HE3	5:E:95:MET:CA	2.42	0.49
6:F:20:LEU:O	6:F:21:CYS:HB2	2.13	0.49
1:A:211:ARG:HH12	1:A:274:GLU:CD	2.19	0.49
3:C:107:ASN:HD21	3:C:109:LYS:HB2	1.78	0.49
6:F:76:VAL:CG1	6:F:77:LYS:N	2.76	0.49
1:A:153:TRP:HE1	1:A:162:THR:H	1.61	0.49
2:B:303:LEU:HD12	2:B:308:THR:HB	1.95	0.49
7:G:75:ALA:O	7:G:79:VAL:HG23	2.13	0.49
1:A:105:PRO:O	1:A:136:VAL:CG1	2.58	0.49
3:C:223:ASP:O	3:C:225:THR:HG23	2.13	0.49
4:D:27:LYS:CD	4:D:28:PRO:HD2	2.42	0.49
4:D:209:LEU:HA	4:D:210:LYS:C	2.35	0.49
6:F:72:VAL:O	6:F:115:SER:HA	2.13	0.49
1:A:18:LYS:HG2	1:A:375:TYR:CD1	2.48	0.48
1:A:300:VAL:O	1:A:304:ILE:HG12	2.13	0.48
6:F:101:PHE:CG	6:F:104:LEU:HD12	2.44	0.48
1:A:239:VAL:HG13	5:E:4:TYR:CZ	2.48	0.48
2:B:348:PRO:HG2	3:C:75:ASN:OD1	2.12	0.48
3:C:252:PHE:CD1	3:C:258:LEU:HD21	2.48	0.48
4:D:210:LYS:CB	4:D:211:ASP:C	2.86	0.48
1:A:204:ILE:HD12	1:A:224:ALA:O	2.13	0.48
3:C:208:VAL:HG23	3:C:208:VAL:O	2.12	0.48
3:C:224:SER:CA	3:C:246:PRO:HA	2.40	0.48
6:F:103:ILE:O	6:F:116:PHE:HD1	1.96	0.48
3:C:49:LYS:O	3:C:50:GLU:HB2	2.13	0.48
6:F:141:GLU:OE2	6:F:141:GLU:HA	2.14	0.48
3:C:107:ASN:ND2	3:C:109:LYS:HB2	2.29	0.48
3:C:222:HIS:O	3:C:246:PRO:CB	2.61	0.48
4:D:184:GLU:HB3	6:F:158:ARG:HA	1.96	0.48
3:C:60:TRP:CE2	3:C:67:ILE:CG1	2.97	0.48
3:C:246:PRO:CG	7:G:142:VAL:HG11	2.44	0.48
7:G:63:PRO:C	7:G:64:ILE:HG12	2.39	0.48
7:G:71:VAL:HG13	7:G:72:LYS:N	2.28	0.48
1:A:353:LEU:HD12	1:A:353:LEU:HA	1.71	0.48
6:F:75:ALA:O	6:F:76:VAL:HB	2.13	0.48
4:D:211:ASP:N	4:D:212:THR:CA	2.77	0.47
6:F:43:SER:HB2	6:F:46:LEU:HD12	1.96	0.47
1:A:36:ALA:O	1:A:60:PHE:HB2	2.14	0.47
1:A:69:LYS:HG3	1:A:72:TYR:HD2	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:105:PRO:O	1:A:136:VAL:CA	2.61	0.47
1:A:179:PRO:HG2	1:A:189:CYS:HB3	1.94	0.47
1:A:150:ALA:HA	1:A:153:TRP:CH2	2.47	0.47
1:A:189:CYS:HG	1:A:307:CYS:HG	1.31	0.47
1:A:243:ASN:O	1:A:247:THR:HG22	2.13	0.47
1:A:246:ASP:OD2	5:E:50:LYS:HE3	2.14	0.47
1:A:249:GLY:C	1:A:251:LYS:H	2.23	0.47
1:A:264:LYS:O	1:A:265:LYS:HG3	2.14	0.47
2:B:302:VAL:CB	2:B:345:GLU:HB3	2.43	0.47
3:C:165:LYS:HG2	3:C:198:SER:HG	1.66	0.47
4:D:19:PHE:HB3	4:D:106:LYS:HG2	1.97	0.47
3:C:222:HIS:C	3:C:224:SER:H	2.22	0.47
4:D:67:LEU:HD23	4:D:144:ILE:HD13	1.96	0.47
6:F:27:SER:OG	6:F:30:VAL:HG22	2.14	0.47
1:A:52:MET:SD	4:D:261:TYR:CE1	3.08	0.47
1:A:196:ALA:H	1:A:199:ASP:HB2	1.80	0.47
2:B:163:VAL:CG1	2:B:165:HIS:NE2	2.73	0.47
3:C:31:GLU:HB3	3:C:49:LYS:CB	2.44	0.47
3:C:60:TRP:NE1	3:C:67:ILE:CG1	2.78	0.47
3:C:272:TYR:HE1	3:C:274:SER:HA	1.79	0.47
5:E:87:SER:OG	5:E:90:GLN:CB	2.63	0.47
1:A:219:GLN:CD	1:A:261:ALA:HB3	2.40	0.47
3:C:122:ILE:CD1	3:C:137:ILE:CG1	2.93	0.47
3:C:153:ASN:HD22	3:C:181:ALA:HB3	1.80	0.47
3:C:263:HIS:ND1	6:F:21:CYS:HB3	2.30	0.47
4:D:63:PHE:CB	4:D:145:HIS:O	2.63	0.47
4:D:205:PRO:HB2	4:D:208:GLU:CB	2.24	0.47
2:B:159:SER:HG	2:B:164:THR:CB	2.12	0.47
3:C:16:TRP:CZ2	3:C:23:ILE:HG21	2.49	0.47
3:C:272:TYR:CE1	3:C:274:SER:HA	2.50	0.47
4:D:59:ILE:HG22	4:D:93:VAL:HB	1.96	0.47
6:F:54:SER:HB2	6:F:60:LYS:HB3	1.92	0.47
4:D:145:HIS:CD2	4:D:151:THR:HG22	2.50	0.47
3:C:31:GLU:CB	3:C:49:LYS:HG2	2.46	0.46
3:C:118:ARG:HG2	3:C:143:SER:HA	1.96	0.46
3:C:179:ARG:HH21	3:C:188:LYS:NZ	2.13	0.46
3:C:253:ILE:C	3:C:254:THR:CG2	2.88	0.46
3:C:254:THR:HG1	3:C:255:GLU:H	1.58	0.46
4:D:112:GLN:OE1	4:D:112:GLN:HA	2.15	0.46
4:D:228:PHE:O	4:D:232:THR:HG23	2.15	0.46
1:A:150:ALA:CB	1:A:153:TRP:CZ3	2.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:31:GLU:CG	3:C:49:LYS:CB	2.89	0.46
5:E:98:LEU:HD13	5:E:98:LEU:C	2.40	0.46
7:G:23:LYS:HG2	7:G:24:PHE:H	1.81	0.46
1:A:152:SER:C	1:A:154:THR:N	2.71	0.46
1:A:157:GLN:HA	1:A:158:VAL:HA	1.62	0.46
1:A:313:ARG:HG2	1:A:363:ILE:HG23	1.97	0.46
3:C:185:TRP:CH2	3:C:231:ALA:HB2	2.50	0.46
4:D:158:LYS:HD3	4:D:158:LYS:C	2.41	0.46
5:E:139:GLU:C	8:E:201:HOH:O	2.57	0.46
1:A:151:ALA:O	1:A:370:HIS:NE2	2.49	0.46
2:B:306:GLY:HA2	2:B:309:MET:HE2	1.98	0.46
3:C:46:HIS:HD2	3:C:48:LEU:HD11	1.80	0.46
3:C:153:ASN:O	3:C:154:SER:HB2	2.15	0.46
4:D:106:LYS:C	4:D:108:SER:N	2.73	0.46
5:E:150:ASP:C	5:E:152:GLN:N	2.73	0.46
7:G:36:GLY:HA2	7:G:63:PRO:HG3	1.98	0.46
1:A:216:PRO:HB2	1:A:219:GLN:C	2.37	0.46
4:D:208:GLU:OE2	4:D:208:GLU:N	2.49	0.46
5:E:14:LYS:O	5:E:15:LEU:HD23	2.15	0.46
1:A:23:GLY:N	1:A:382:SER:OG	2.48	0.46
1:A:60:PHE:O	1:A:61:PHE:HD1	1.98	0.46
1:A:187:GLY:C	1:A:189:CYS:N	2.73	0.46
3:C:173:ILE:C	3:C:175:GLU:N	2.73	0.46
3:C:248:LEU:CD2	3:C:262:GLY:HA3	2.45	0.46
1:A:112:LEU:CD1	1:A:126:THR:HG23	2.39	0.46
1:A:307:CYS:O	1:A:312:ARG:NH2	2.37	0.46
4:D:42:LEU:HB3	4:D:60:SER:HB3	1.97	0.46
4:D:129:PHE:HD2	4:D:237:ARG:HG3	1.80	0.46
1:A:36:ALA:HA	1:A:73:ALA:O	2.15	0.46
1:A:390:PHE:C	1:A:392:GLN:H	2.23	0.46
3:C:72:THR:CB	3:C:98:ALA:CB	2.93	0.46
4:D:75:LEU:CD2	4:D:79:VAL:HG21	2.46	0.46
1:A:18:LYS:CG	1:A:375:TYR:CD1	3.00	0.46
1:A:204:ILE:O	1:A:208:LEU:HG	2.16	0.46
2:B:330:LEU:C	2:B:332:GLY:N	2.73	0.46
3:C:45:VAL:HG23	3:C:46:HIS:ND1	2.30	0.46
1:A:69:LYS:CB	1:A:72:TYR:HB2	2.45	0.45
1:A:91:ARG:O	1:A:94:GLU:HB2	2.16	0.45
1:A:111:LEU:CD1	1:A:390:PHE:CE1	2.94	0.45
3:C:46:HIS:CD2	3:C:86:TRP:CD1	3.03	0.45
3:C:89:THR:CG2	3:C:90:LEU:N	2.79	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:96:ASN:HD22	3:C:96:ASN:N	2.06	0.45
3:C:129:ASN:CB	3:C:131:TRP:CZ3	2.91	0.45
5:E:116:ILE:HG22	5:E:117:TYR:CD1	2.51	0.45
6:F:126:MET:SD	6:F:131:LEU:HD21	2.55	0.45
2:B:313:LEU:HB3	2:B:314:PRO:HD3	1.98	0.45
3:C:79:TRP:CD2	3:C:88:PRO:CB	2.88	0.45
3:C:248:LEU:HD22	3:C:262:GLY:HA3	1.97	0.45
4:D:199:LEU:HB2	4:D:224:THR:OG1	2.16	0.45
5:E:18:ASN:CG	5:E:118:ALA:N	2.65	0.45
6:F:48:LEU:HD22	7:G:146:THR:HG22	1.98	0.45
1:A:287:PHE:HZ	5:E:55:PHE:CE1	2.35	0.45
2:B:307:SER:O	2:B:307:SER:OG	2.32	0.45
3:C:179:ARG:CG	3:C:180:PRO:CD	2.89	0.45
4:D:146:TYR:CZ	4:D:150:GLU:HB3	2.51	0.45
1:A:260:ASN:HB3	1:A:264:LYS:N	2.32	0.45
3:C:92:ILE:HG22	3:C:94:ARG:HG3	1.98	0.45
3:C:138:LYS:CE	7:G:22:ASN:HD21	2.30	0.45
3:C:371:ILE:O	3:C:372:VAL:HB	2.17	0.45
6:F:138:PHE:CE2	6:F:142:ILE:HG21	2.49	0.45
1:A:283:PHE:CE2	1:A:334:ARG:HG2	2.51	0.45
4:D:161:VAL:CG1	4:D:162:THR:N	2.80	0.45
1:A:153:TRP:CG	1:A:161:ARG:HG2	2.51	0.45
3:C:329:VAL:HA	3:C:349:GLY:HA2	1.99	0.45
6:F:138:PHE:CE2	6:F:142:ILE:CG2	2.99	0.45
1:A:405:PRO:HG3	6:F:96:MET:SD	2.57	0.45
3:C:179:ARG:CB	3:C:180:PRO:HD2	2.47	0.45
3:C:366:LEU:C	3:C:368:ASP:N	2.73	0.45
5:E:95:MET:HG2	5:E:141:GLY:CA	2.47	0.45
5:E:132:TYR:CE2	5:E:136:LEU:HD11	2.52	0.45
1:A:205:GLN:NE2	1:A:221:LEU:CD2	2.59	0.45
3:C:60:TRP:CD1	3:C:67:ILE:CG1	2.97	0.45
3:C:165:LYS:HA	3:C:198:SER:HB3	1.99	0.45
4:D:247:PHE:O	4:D:250:TYR:HB3	2.17	0.45
6:F:139:MET:CA	6:F:142:ILE:HG12	2.47	0.45
1:A:285:PRO:C	1:A:287:PHE:H	2.24	0.45
2:B:329:VAL:HG12	2:B:330:LEU:HG	1.98	0.45
3:C:30:HIS:O	3:C:51:HIS:HB2	2.17	0.45
3:C:31:GLU:CB	3:C:49:LYS:HA	2.46	0.45
3:C:18:LYS:HG3	3:C:62:PRO:CB	2.46	0.44
3:C:254:THR:O	3:C:255:GLU:HG2	2.16	0.44
4:D:43:TYR:HE1	4:D:59:ILE:HD12	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:F:136:ILE:HG23	6:F:137:HIS:N	2.31	0.44
1:A:29:PHE:HZ	4:D:10:ILE:HA	1.82	0.44
2:B:163:VAL:HG22	2:B:164:THR:N	2.32	0.44
4:D:10:ILE:H	4:D:10:ILE:HG13	1.55	0.44
4:D:271:SER:O	4:D:275:LYS:HG3	2.16	0.44
5:E:14:LYS:HA	5:E:14:LYS:HD3	1.64	0.44
7:G:119:ASP:C	7:G:121:SER:N	2.73	0.44
1:A:150:ALA:CA	1:A:153:TRP:HZ3	2.28	0.44
1:A:272:GLY:H	1:A:274:GLU:CD	2.25	0.44
5:E:150:ASP:C	5:E:152:GLN:H	2.25	0.44
6:F:20:LEU:HD12	6:F:132:VAL:CG2	2.47	0.44
7:G:103:VAL:HG11	7:G:136:GLY:HA3	2.00	0.44
2:B:317:LEU:O	2:B:321:LEU:HG	2.17	0.44
5:E:92:GLU:O	5:E:96:TYR:CD2	2.70	0.44
1:A:339:LEU:HD23	1:A:365:VAL:HG11	2.00	0.44
3:C:31:GLU:HB3	3:C:49:LYS:CG	2.47	0.44
3:C:97:ARG:NH2	6:F:29:VAL:O	2.51	0.44
3:C:164:PHE:CE1	3:C:204:TRP:NE1	2.84	0.44
4:D:129:PHE:CG	4:D:232:THR:HB	2.53	0.44
1:A:198:ARG:O	1:A:202:TYR:HD1	2.00	0.44
1:A:219:GLN:NE2	1:A:261:ALA:HB1	2.33	0.44
3:C:147:SER:C	3:C:148:LEU:HG	2.43	0.44
3:C:148:LEU:HD23	3:C:159:ALA:HA	2.00	0.44
7:G:131:LYS:O	7:G:134:ALA:HB3	2.18	0.44
1:A:38:LYS:NZ	1:A:38:LYS:CB	2.78	0.44
1:A:156:ARG:HD2	1:A:156:ARG:HA	1.74	0.44
2:B:314:PRO:HB3	2:B:344:ILE:HG22	1.98	0.44
2:B:324:LEU:C	2:B:326:LEU:H	2.25	0.44
3:C:151:HIS:NE2	3:C:152:PRO:HD2	2.30	0.44
3:C:324:LEU:HA	3:C:324:LEU:HD23	1.69	0.44
4:D:56:MET:HA	4:D:95:LEU:O	2.18	0.44
2:B:164:THR:O	2:B:165:HIS:CG	2.71	0.43
2:B:222:TYR:O	2:B:262:PRO:HG2	2.18	0.43
3:C:100:ARG:HD2	3:C:100:ARG:O	2.17	0.43
3:C:253:ILE:HG13	3:C:257:SER:HB2	1.99	0.43
4:D:161:VAL:HB	4:D:227:LEU:HB2	2.00	0.43
4:D:202:HIS:O	4:D:204:GLU:N	2.49	0.43
4:D:262:ILE:HG23	6:F:149:MET:HE2	1.99	0.43
1:A:153:TRP:HE1	1:A:161:ARG:CB	2.24	0.43
2:B:158:ASP:O	2:B:164:THR:CG2	2.55	0.43
2:B:325:TYR:O	2:B:325:TYR:CD2	2.72	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:3:TYR:HB2	3:C:324:LEU:HD13	2.00	0.43
3:C:70:CYS:SG	3:C:99:ALA:HB1	2.58	0.43
3:C:140:PRO:HD2	3:C:169:PHE:HZ	0.71	0.43
5:E:15:LEU:CD2	5:E:63:GLU:HG3	2.47	0.43
5:E:16:ILE:O	5:E:16:ILE:HG23	2.18	0.43
5:E:87:SER:C	5:E:149:PHE:HE1	2.16	0.43
5:E:139:GLU:O	5:E:143:ARG:HB2	2.18	0.43
6:F:51:VAL:O	6:F:52:THR:OG1	2.26	0.43
3:C:33:HIS:ND1	3:C:47:GLU:HB3	2.33	0.43
6:F:4:THR:HG21	6:F:55:ARG:HE	1.78	0.43
1:A:327:MET:SD	1:A:373:GLN:HB2	2.59	0.43
2:B:184:ILE:HG13	2:B:188:ASP:HB2	2.01	0.43
4:D:145:HIS:CD2	4:D:151:THR:CG2	3.01	0.43
6:F:48:LEU:O	6:F:50:PRO:HD3	2.19	0.43
7:G:79:VAL:O	7:G:83:LEU:HG	2.19	0.43
7:G:110:ILE:HG23	7:G:125:LEU:HD22	2.00	0.43
1:A:361:LYS:HG2	1:A:362:PRO:CD	2.47	0.43
2:B:175:LEU:HD13	2:B:178:LEU:HD12	2.01	0.43
4:D:52:LYS:C	4:D:54:LYS:H	2.25	0.43
4:D:68:GLN:C	4:D:70:HIS:H	2.25	0.43
7:G:47:ARG:C	7:G:49:GLY:N	2.77	0.43
2:B:302:VAL:CA	2:B:345:GLU:HB3	2.40	0.43
3:C:129:ASN:N	3:C:131:TRP:CZ3	2.82	0.43
3:C:366:LEU:HD23	3:C:369:LEU:CG	2.48	0.43
5:E:82:LEU:HD23	5:E:148:VAL:HG21	2.00	0.43
6:F:139:MET:HA	6:F:142:ILE:CG1	2.48	0.43
1:A:153:TRP:O	1:A:155:SER:N	2.49	0.43
1:A:244:LYS:HD3	1:A:252:TRP:CZ2	2.53	0.43
2:B:193:LEU:HD22	2:B:221:CYS:SG	2.59	0.43
3:C:114:GLY:CA	3:C:148:LEU:HD11	2.46	0.43
4:D:37:ASP:CB	4:D:43:TYR:HE2	2.14	0.43
4:D:60:SER:HB2	4:D:91:TYR:HA	2.01	0.43
4:D:131:PHE:CZ	4:D:139:GLU:HG3	2.54	0.43
4:D:205:PRO:CG	4:D:208:GLU:HB2	2.45	0.43
1:A:200:ILE:CD1	1:A:281:ILE:CG1	2.94	0.43
3:C:126:GLU:CD	3:C:133:VAL:HG21	2.44	0.43
3:C:129:ASN:CB	3:C:131:TRP:CE3	2.86	0.43
6:F:9:LEU:CB	6:F:136:ILE:HD11	2.22	0.43
7:G:48:GLN:H	7:G:48:GLN:HG3	1.60	0.43
1:A:150:ALA:O	1:A:152:SER:N	2.45	0.43
3:C:18:LYS:HD2	3:C:62:PRO:C	2.44	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:11:ASP:HA	1:A:113:THR:HG22	2.01	0.43
1:A:11:ASP:OD1	1:A:113:THR:HG21	2.19	0.43
1:A:369:THR:O	1:A:369:THR:OG1	2.36	0.43
5:E:95:MET:HG2	5:E:141:GLY:HA3	2.01	0.43
2:B:284:ASN:OD1	2:B:328:ARG:NH1	2.52	0.42
3:C:139:LYS:HA	3:C:140:PRO:HA	1.72	0.42
3:C:176:VAL:HG23	3:C:177:GLU:N	2.26	0.42
1:A:120:PRO:HB3	1:A:409:ARG:HG2	2.01	0.42
1:A:335:LEU:HD12	1:A:335:LEU:HA	1.74	0.42
3:C:32:VAL:N	3:C:48:LEU:O	2.52	0.42
3:C:16:TRP:CZ2	3:C:23:ILE:CG2	3.03	0.42
3:C:107:ASN:OD1	3:C:108:GLU:N	2.52	0.42
3:C:188:LYS:HD3	3:C:188:LYS:HA	1.84	0.42
5:E:87:SER:OG	5:E:90:GLN:HB3	2.19	0.42
3:C:110:LYS:HB2	3:C:110:LYS:HE3	1.74	0.42
3:C:173:ILE:HG22	3:C:175:GLU:HB2	2.02	0.42
2:B:159:SER:O	2:B:305:GLY:HA3	2.19	0.42
2:B:163:VAL:HG21	2:B:182:LEU:O	2.18	0.42
3:C:107:ASN:C	3:C:108:GLU:CG	2.86	0.42
3:C:164:PHE:CZ	6:F:45:GLU:HB2	2.55	0.42
6:F:4:THR:CG2	6:F:55:ARG:NE	2.73	0.42
1:A:178:ILE:CB	1:A:190:ILE:CD1	2.65	0.42
1:A:30:ILE:HG21	1:A:375:TYR:CZ	2.55	0.42
1:A:216:PRO:HG3	1:A:267:PHE:CZ	2.54	0.42
1:A:311:VAL:C	1:A:314:PRO:HD2	2.45	0.42
1:A:319:ILE:CG2	1:A:367:VAL:HG22	2.50	0.42
2:B:283:PHE:HE2	2:B:328:ARG:HD2	1.82	0.42
3:C:10:PRO:CB	3:C:350:MET:O	2.57	0.42
3:C:72:THR:CB	3:C:98:ALA:HB1	2.42	0.42
5:E:104:PRO:HB2	5:E:111:PHE:HB2	2.00	0.42
6:F:27:SER:CB	6:F:30:VAL:CG2	2.96	0.42
1:A:177:VAL:O	1:A:177:VAL:HG12	2.19	0.42
2:B:162:GLY:O	2:B:163:VAL:HB	2.19	0.42
3:C:203:GLY:HA3	3:C:222:HIS:HB3	2.02	0.42
3:C:218:ALA:HB2	3:C:228:LEU:CD1	2.36	0.42
4:D:211:ASP:N	4:D:212:THR:C	2.77	0.42
4:D:263:HIS:O	4:D:267:ARG:HG3	2.20	0.42
6:F:138:PHE:CD1	6:F:142:ILE:HD13	2.54	0.42
7:G:40:GLY:O	7:G:43:ASP:N	2.50	0.42
1:A:286:GLU:HB3	1:A:293:THR:CB	2.50	0.42
4:D:47:ASN:HA	4:D:48:PRO:HD2	1.81	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:259:ILE:HD12	1:A:259:ILE:N	2.35	0.42
2:B:159:SER:CB	2:B:164:THR:OG1	2.64	0.42
3:C:31:GLU:HG2	3:C:49:LYS:CB	2.31	0.42
4:D:143:VAL:CG1	4:D:145:HIS:HE1	2.32	0.42
1:A:285:PRO:HG2	1:A:294:GLN:O	2.20	0.41
1:A:327:MET:HE3	1:A:327:MET:HB3	1.99	0.41
3:C:76:ALA:O	3:C:91:VAL:HB	2.20	0.41
4:D:176:VAL:HG11	6:F:85:ILE:CD1	2.50	0.41
1:A:28:GLN:HB3	1:A:29:PHE:CE2	2.55	0.41
2:B:347:PRO:HA	2:B:348:PRO:HD3	1.85	0.41
3:C:228:LEU:HD21	3:C:230:ASP:OD1	2.20	0.41
7:G:43:ASP:O	7:G:46:LEU:N	2.47	0.41
1:A:5:LEU:HD13	1:A:108:HIS:CE1	2.55	0.41
3:C:32:VAL:HG12	3:C:33:HIS:N	2.34	0.41
3:C:60:TRP:CD2	3:C:67:ILE:HG12	2.55	0.41
3:C:111:PHE:CE2	3:C:123:CYS:CB	3.03	0.41
3:C:370:LYS:O	3:C:371:ILE:HB	2.21	0.41
1:A:19:LEU:HD23	1:A:19:LEU:N	2.36	0.41
4:D:75:LEU:CD2	4:D:79:VAL:CG2	2.98	0.41
5:E:173:LEU:HD23	5:E:173:LEU:HA	1.91	0.41
6:F:86:LEU:HD21	6:F:149:MET:HB2	2.02	0.41
6:F:103:ILE:HG22	6:F:122:HIS:CE1	2.55	0.41
1:A:28:GLN:C	1:A:29:PHE:CG	2.98	0.41
3:C:151:HIS:CE1	3:C:152:PRO:CD	2.98	0.41
3:C:218:ALA:CB	3:C:252:PHE:CE1	3.03	0.41
4:D:277:LEU:HD11	6:F:103:ILE:HD11	2.02	0.41
4:D:278:ASN:C	4:D:280:ALA:H	2.28	0.41
1:A:132:GLU:HG3	1:A:400:TYR:OH	2.21	0.41
1:A:166:THR:HG21	1:A:304:ILE:HD11	2.03	0.41
1:A:205:GLN:HE22	1:A:221:LEU:CG	2.32	0.41
2:B:211:GLU:OE1	2:B:211:GLU:HA	2.21	0.41
3:C:253:ILE:O	3:C:254:THR:HG22	2.20	0.41
4:D:115:MET:HE2	4:D:118:ARG:HD2	2.02	0.41
4:D:185:PHE:CE1	6:F:161:ALA:HA	2.56	0.41
6:F:59:GLU:CD	6:F:77:LYS:HB2	2.45	0.41
1:A:71:THR:O	1:A:72:TYR:CD1	2.73	0.41
7:G:37:PRO:HD3	7:G:75:ALA:HB2	2.03	0.41
7:G:64:ILE:C	7:G:66:THR:H	2.28	0.41
3:C:237:VAL:O	3:C:238:ALA:C	2.64	0.41
4:D:66:GLU:OE2	4:D:145:HIS:N	2.47	0.41
1:A:127:ALA:HB2	1:A:408:CYS:SG	2.61	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:166:ILE:HD13	2:B:282:LEU:HA	2.03	0.41
3:C:27:PRO:O	3:C:28:ASN:C	2.63	0.41
3:C:217:VAL:O	3:C:228:LEU:HG	2.21	0.41
3:C:219:TRP:CZ2	3:C:227:CYS:CB	3.03	0.41
4:D:192:SER:HB3	4:D:195:ALA:HB2	2.02	0.41
5:E:156:PRO:O	5:E:158:LYS:N	2.53	0.41
6:F:82:ILE:HD12	6:F:85:ILE:HD11	2.03	0.41
6:F:104:LEU:HD23	6:F:104:LEU:HA	1.77	0.41
1:A:130:MET:O	1:A:134:PHE:HB2	2.21	0.41
3:C:135:LYS:HB3	3:C:191:PHE:HZ	1.86	0.41
4:D:38:PHE:C	4:D:39:ASP:CG	2.88	0.41
4:D:42:LEU:O	4:D:43:TYR:CD1	2.74	0.41
7:G:21:GLU:C	7:G:23:LYS:H	2.29	0.41
1:A:29:PHE:HZ	4:D:10:ILE:HG23	1.81	0.40
2:B:299:LYS:O	2:B:299:LYS:HG2	2.21	0.40
3:C:77:TYR:CG	3:C:89:THR:O	2.74	0.40
3:C:138:LYS:NZ	7:G:22:ASN:HD21	2.19	0.40
4:D:230:ARG:O	4:D:233:ASN:ND2	2.54	0.40
6:F:161:ALA:O	6:F:165:LEU:HB2	2.21	0.40
1:A:129:ILE:HD11	4:D:267:ARG:HH21	1.87	0.40
1:A:145:ALA:HB2	1:A:178:ILE:HD13	2.04	0.40
2:B:235:LEU:HD13	2:B:235:LEU:HA	1.91	0.40
4:D:176:VAL:HG11	6:F:85:ILE:HD11	2.03	0.40
5:E:5:HIS:HD2	5:E:65:ASP:OD2	2.03	0.40
5:E:144:LEU:O	5:E:148:VAL:HG23	2.21	0.40
6:F:98:ALA:HB1	6:F:104:LEU:O	2.21	0.40
3:C:27:PRO:HG2	3:C:29:ASN:OD1	2.22	0.40
3:C:185:TRP:CD2	3:C:231:ALA:CB	3.05	0.40
4:D:43:TYR:CE1	4:D:59:ILE:HD12	2.56	0.40
4:D:46:SER:OG	4:D:88:GLU:OE1	2.39	0.40
4:D:124:VAL:O	4:D:128:TYR:HD1	2.03	0.40
7:G:63:PRO:HB2	7:G:64:ILE:H	1.69	0.40
1:A:241:GLU:OE1	1:A:244:LYS:HD2	2.21	0.40
3:C:93:LEU:O	3:C:94:ARG:HB2	2.22	0.40
4:D:42:LEU:O	4:D:43:TYR:CG	2.75	0.40
6:F:82:ILE:O	6:F:86:LEU:HB2	2.20	0.40
1:A:370:HIS:CD2	1:A:372:MET:O	2.75	0.40
4:D:209:LEU:HA	4:D:210:LYS:CB	2.51	0.40
6:F:101:PHE:C	6:F:103:ILE:H	2.30	0.40

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

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:157:LYS:CB	5:E:27:GLN:NE2[3_555]	1.39	0.81
4:D:157:LYS:CD	5:E:27:GLN:OE1[3_555]	1.79	0.41
1:A:265:LYS:N	7:G:120:ASN:ND2[3_545]	1.83	0.37
4:D:183:GLN:NE2	5:E:151:PRO:CG[3_555]	2.02	0.18
4:D:157:LYS:CG	5:E:27:GLN:OE1[3_555]	2.08	0.12
4:D:157:LYS:CG	5:E:27:GLN:CD[3_555]	2.11	0.09
1:A:264:LYS:C	7:G:120:ASN:ND2[3_545]	2.13	0.07
4:D:157:LYS:CB	5:E:27:GLN:CD[3_555]	2.16	0.04

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	394/418 (94%)	322 (82%)	47 (12%)	25 (6%)	1	15
2	B	214/394 (54%)	173 (81%)	26 (12%)	15 (7%)	1	13
3	C	340/372 (91%)	270 (79%)	49 (14%)	21 (6%)	1	15
4	D	280/300 (93%)	228 (81%)	35 (12%)	17 (6%)	1	15
5	E	172/178 (97%)	150 (87%)	16 (9%)	6 (4%)	3	23
6	F	166/168 (99%)	148 (89%)	14 (8%)	4 (2%)	4	30
7	G	130/151 (86%)	108 (83%)	15 (12%)	7 (5%)	1	17
All	All	1696/1981 (86%)	1399 (82%)	202 (12%)	95 (6%)	1	17

All (95) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	ASN
1	A	151	ALA
1	A	160	GLU
1	A	217	PRO
1	A	230	ARG
2	B	186	GLY

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Mol	Chain	Res	Type
2	B	289	ALA
2	B	331	LYS
2	B	348	PRO
3	C	20	ARG
3	C	50	GLU
3	C	238	ALA
3	C	284	ARG
4	D	49	ASN
4	D	56	MET
5	E	87	SER
6	F	4	THR
6	F	65	GLY
6	F	76	VAL
7	G	64	ILE
1	A	80	HIS
1	A	112	LEU
1	A	188	SER
1	A	228	LYS
1	A	309	ILE
1	A	353	LEU
2	B	161	ASP
2	B	219	LYS
3	C	104	TRP
3	C	147	SER
3	C	174	LYS
3	C	178	GLU
3	C	185	TRP
3	C	324	LEU
4	D	92	ASN
4	D	140	ASN
4	D	157	LYS
4	D	160	ARG
5	E	21	LEU
5	E	157	SER
7	G	63	PRO
1	A	157	GLN
1	A	187	GLY
1	A	236	PRO
1	A	261	ALA
1	A	391	TYR
2	B	347	PRO
2	B	356	LEU

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Mol	Chain	Res	Type
3	C	62	PRO
3	C	82	LYS
3	C	141	ILE
4	D	89	SER
4	D	103	PRO
4	D	141	ARG
4	D	209	LEU
4	D	228	PHE
5	E	154	ASP
7	G	29	ASP
7	G	37	PRO
7	G	120	ASN
1	A	71	THR
1	A	154	THR
1	A	264	LYS
2	B	171	GLU
2	B	334	VAL
3	C	282	GLY
4	D	23	ALA
4	D	138	GLY
5	E	101	THR
7	G	48	GLN
1	A	250	SER
1	A	262	ILE
1	A	374	ARG
2	B	163	VAL
2	B	346	ASP
3	C	134	CYS
3	C	138	LYS
3	C	254	THR
3	C	265	CYS
3	C	371	ILE
4	D	86	ASN
4	D	107	ASP
4	D	206	PRO
5	E	156	PRO
6	F	79	ALA
1	A	2	ALA
2	B	345	GLU
2	B	357	GLY
3	C	320	GLY
4	D	281	ARG

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Mol	Chain	Res	Type
7	G	47	ARG
1	A	361	LYS
3	C	133	VAL
2	B	342	ILE
1	A	249	GLY

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	343/363 (94%)	326 (95%)	17 (5%)	22	47
2	B	190/345 (55%)	173 (91%)	17 (9%)	9	32
3	C	290/313 (93%)	272 (94%)	18 (6%)	16	43
4	D	246/264 (93%)	237 (96%)	9 (4%)	30	53
5	E	156/159 (98%)	144 (92%)	12 (8%)	12	37
6	F	155/155 (100%)	148 (96%)	7 (4%)	24	49
7	G	109/124 (88%)	99 (91%)	10 (9%)	8	30
All	All	1489/1723 (86%)	1399 (94%)	90 (6%)	17	44

All (90) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	19	LEU
1	A	31	ILE
1	A	38	LYS
1	A	51	VAL
1	A	88	LEU
1	A	143	VAL
1	A	155	SER
1	A	178	ILE
1	A	189	CYS
1	A	195	ILE
1	A	210	ASP
1	A	255	GLN

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Mol	Chain	Res	Type
1	A	310	ASP
1	A	363	ILE
1	A	373	GLN
1	A	397	LYS
1	A	409	ARG
2	B	82	TRP
2	B	83	ASP
2	B	90	ASP
2	B	155	VAL
2	B	182	LEU
2	B	184	ILE
2	B	200	ARG
2	B	235	LEU
2	B	237	THR
2	B	240	LEU
2	B	274	GLU
2	B	276	VAL
2	B	290	ASP
2	B	294	ARG
2	B	320	GLU
2	B	349	ARG
2	B	352	HIS
3	C	22	GLN
3	C	31	GLU
3	C	40	ASN
3	C	47	GLU
3	C	74	ARG
3	C	92	ILE
3	C	96	ASN
3	C	108	GLU
3	C	110	LYS
3	C	122	ILE
3	C	131	TRP
3	C	179	ARG
3	C	183	THR
3	C	201	SER
3	C	202	CYS
3	C	210	PHE
3	C	326	LYS
3	C	361	SER
4	D	3	LEU
4	D	10	ILE

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Mol	Chain	Res	Type
4	D	39	ASP
4	D	54	LYS
4	D	84	LEU
4	D	116	LEU
4	D	157	LYS
4	D	192	SER
4	D	224	THR
5	E	22	LEU
5	E	39	THR
5	E	60	ILE
5	E	63	GLU
5	E	80	LYS
5	E	82	LEU
5	E	95	MET
5	E	116	ILE
5	E	142	LEU
5	E	144	LEU
5	E	146	GLU
5	E	161	THR
6	F	22	LEU
6	F	33	HIS
6	F	55	ARG
6	F	77	LYS
6	F	104	LEU
6	F	141	GLU
6	F	165	LEU
7	G	16	VAL
7	G	21	GLU
7	G	27	GLU
7	G	41	GLU
7	G	45	CYS
7	G	48	GLN
7	G	69	GLN
7	G	86	PHE
7	G	112	LYS
7	G	145	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	HIS
1	A	306	ASN

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Mol	Chain	Res	Type
1	A	373	GLN
1	A	410	HIS
2	B	205	ASN
2	B	231	GLN
2	B	267	GLN
3	C	96	ASN
3	C	136	HIS
4	D	132	GLN
4	D	145	HIS
4	D	231	HIS
5	E	18	ASN
6	F	33	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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	400/418 (95%)	0.47	17 (4%) 40 29	30, 83, 125, 158	0
2	B	218/394 (55%)	0.69	22 (10%) 12 15	62, 97, 143, 178	0
3	C	344/372 (92%)	1.02	42 (12%) 8 12	84, 120, 145, 165	0
4	D	282/300 (94%)	0.55	15 (5%) 32 25	56, 82, 113, 165	0
5	E	174/178 (97%)	0.63	13 (7%) 20 19	57, 91, 119, 134	0
6	F	168/168 (100%)	0.39	10 (5%) 27 23	55, 77, 101, 289	0
7	G	135/151 (89%)	0.66	8 (5%) 28 23	66, 102, 150, 161	0
All	All	1721/1981 (86%)	0.65	127 (7%) 20 19	30, 91, 138, 289	0

All (127) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	88	LEU	5.5
2	B	87	HIS	5.3
2	B	92	THR	5.1
4	D	40	GLY	4.9
3	C	148	LEU	4.8
6	F	1	MET	4.6
5	E	88	LYS	4.4
3	C	101	CYS	4.4
2	B	352	HIS	4.3
3	C	218	ALA	4.2
2	B	354	VAL	4.2
1	A	268	SER	4.2
5	E	96	TYR	4.1
2	B	89	TRP	4.0
2	B	345	GLU	4.0
7	G	119	ASP	3.8
5	E	100	ILE	3.7

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Mol	Chain	Res	Type	RSRZ
7	G	121	SER	3.6
2	B	94	GLY	3.5
5	E	92	GLU	3.3
3	C	208	VAL	3.2
3	C	78	VAL	3.1
3	C	140	PRO	3.1
4	D	159	ASP	3.1
3	C	92	ILE	3.0
1	A	157	GLN	3.0
3	C	169	PHE	3.0
5	E	146	GLU	3.0
5	E	153	ASN	2.9
6	F	31	GLU	2.9
3	C	362	LEU	2.9
3	C	162	CYS	2.9
4	D	197	GLN	2.8
2	B	167	CYS	2.8
1	A	256	TYR	2.8
2	B	334	VAL	2.7
3	C	104	TRP	2.7
5	E	154	ASP	2.7
4	D	199	LEU	2.7
2	B	320	GLU	2.7
4	D	6	VAL	2.6
3	C	103	ARG	2.6
3	C	181	ALA	2.6
5	E	110	GLY	2.6
3	C	282	GLY	2.6
2	B	93	PHE	2.6
3	C	142	ARG	2.6
2	B	356	LEU	2.6
3	C	102	VAL	2.6
7	G	42	VAL	2.6
2	B	357	GLY	2.5
6	F	89	LYS	2.5
3	C	157	LEU	2.5
2	B	162	GLY	2.5
4	D	132	GLN	2.4
1	A	414	PHE	2.4
1	A	262	ILE	2.4
2	B	91	TYR	2.4
6	F	32	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	266	GLU	2.4
4	D	208	GLU	2.4
3	C	123	CYS	2.4
6	F	54	SER	2.4
7	G	24	PHE	2.4
3	C	25	ILE	2.4
6	F	2	THR	2.4
5	E	175	GLY	2.3
4	D	226	VAL	2.3
7	G	151	VAL	2.3
3	C	77	TYR	2.3
2	B	199	LEU	2.3
3	C	184	PRO	2.3
4	D	282	PRO	2.3
3	C	185	TRP	2.3
3	C	68	VAL	2.3
7	G	35	ALA	2.3
3	C	32	VAL	2.3
5	E	2	PRO	2.3
1	A	130	MET	2.3
3	C	183	THR	2.3
3	C	16	TRP	2.3
1	A	189	CYS	2.3
4	D	63	PHE	2.2
4	D	200	PHE	2.2
3	C	127	GLN	2.2
5	E	89	SER	2.2
2	B	329	VAL	2.2
3	C	14	HIS	2.2
2	B	355	PHE	2.2
1	A	366	GLN	2.2
1	A	1	MET	2.2
2	B	325	TYR	2.2
3	C	285	LEU	2.2
4	D	125	PHE	2.2
3	C	59	ASP	2.2
1	A	109	TYR	2.2
4	D	272	ASP	2.1
5	E	99	GLY	2.1
7	G	30	GLY	2.1
3	C	112	ALA	2.1
3	C	284	ARG	2.1

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Mol	Chain	Res	Type	RSRZ
3	C	286	ASP	2.1
1	A	365	VAL	2.1
6	F	4	THR	2.1
3	C	52	ASN	2.1
4	D	207	LEU	2.1
3	C	187	SER	2.1
4	D	157	LYS	2.1
6	F	17	GLN	2.1
3	C	58	VAL	2.1
1	A	335	LEU	2.1
3	C	235	MET	2.1
1	A	319	ILE	2.1
6	F	85	ILE	2.1
1	A	147	LEU	2.1
2	B	155	VAL	2.1
2	B	358	GLY	2.0
3	C	224	SER	2.0
3	C	355	SER	2.0
6	F	14	ALA	2.0
3	C	114	GLY	2.0
3	C	99	ALA	2.0
5	E	136	LEU	2.0
3	C	338	GLY	2.0
1	A	30	ILE	2.0
7	G	74	ARG	2.0
1	A	154	THR	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.