



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 04:29 AM UTC

PDB ID : 6RIP / pdb_00006rip
EMDB ID : EMD-4893
Title : Cryo-EM structure of E. coli RNA polymerase backtracked elongation complex in swiveled state
Authors : Abdelkareem, M.; Saint-Andre, C.; Takacs, M.; Papai, G.; Crucifix, C.; Guo, X.; Ortiz, J.; Weixlbaumer, A.
Deposited on : 2019-04-24
Resolution : 3.40 Å (reported)
Based on initial model : 6ALH

This is a Full wwPDB EM 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/EMValidationReportHelp>

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:

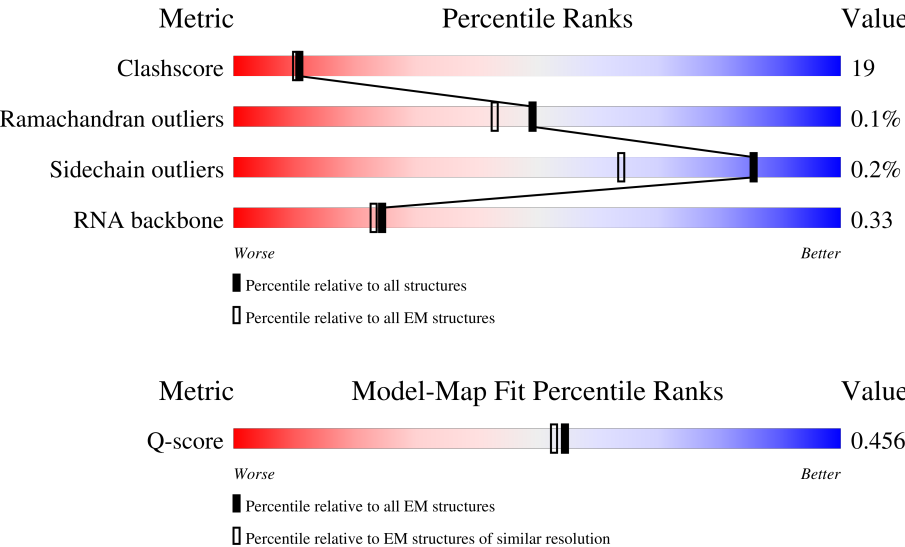
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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 EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	N	39	18% 26% 36% 38%
2	T	39	18% 23% 56% 18%
3	A	329	50% 19% 31%

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Mol	Chain	Length	Quality of chain
3	B	329	
4	C	1342	
5	D	1407	
6	E	91	
7	R	14	

2 Entry composition [i](#)

There are 9 unique types of molecules in this entry. The entry contains 26346 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, 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 DNA chain called Non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	N	24	Total	C	N	O	P	0	0
			489	232	89	144	24		

- Molecule 2 is a DNA chain called Template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	T	32	Total	C	N	O	P	0	0
			655	311	124	189	31		

- Molecule 3 is a protein called DNA-directed RNA polymerase subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	A	228	Total	C	N	O	S	0	0
			1768	1102	312	348	6		
3	B	229	Total	C	N	O	S	0	0
			1772	1104	313	349	6		

- Molecule 4 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	1319	Total	C	N	O	S	0	0
			10407	6530	1814	2020	43		

- Molecule 5 is a protein called DNA-directed RNA polymerase subunit beta'.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	1336	Total	C	N	O	S	0	0
			10397	6533	1854	1960	50		

- Molecule 6 is a protein called DNA-directed RNA polymerase subunit omega.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	73	Total	C	N	O	S	0	0
			582	355	111	115	1		

- Molecule 7 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	R	13	Total	C	N	O	P	0	0
			273	123	46	92	12		

- Molecule 8 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
8	D	2	Total	Zn	0
			2	2	

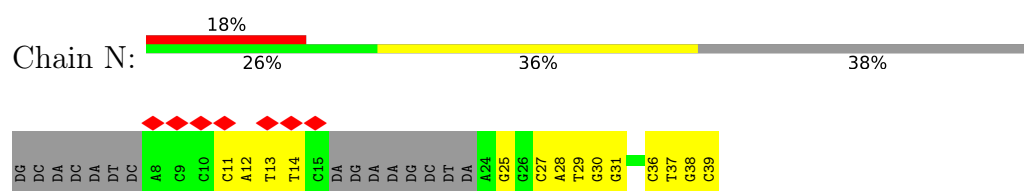
- Molecule 9 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
9	D	1	Total	Mg	0
			1	1	

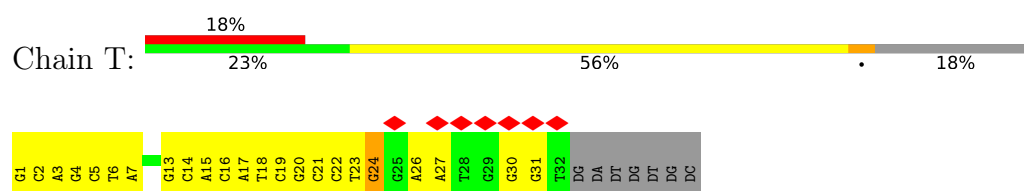
3 Residue-property plots

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 atom inclusion in map 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 diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). 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.

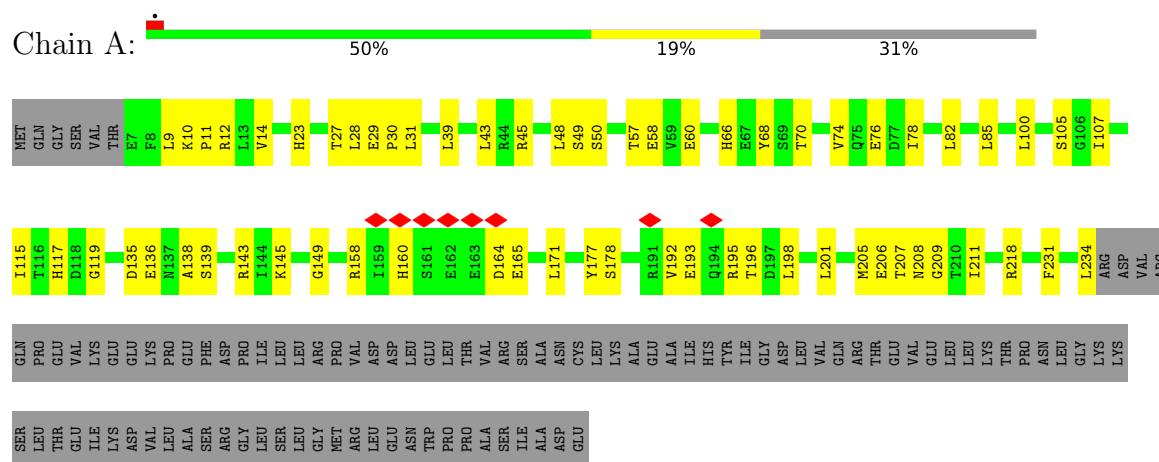
• Molecule 1: Non-template DNA



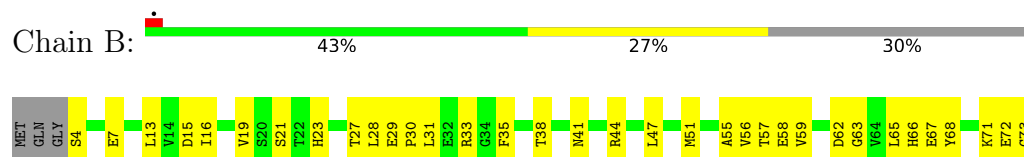
• Molecule 2: Template DNA



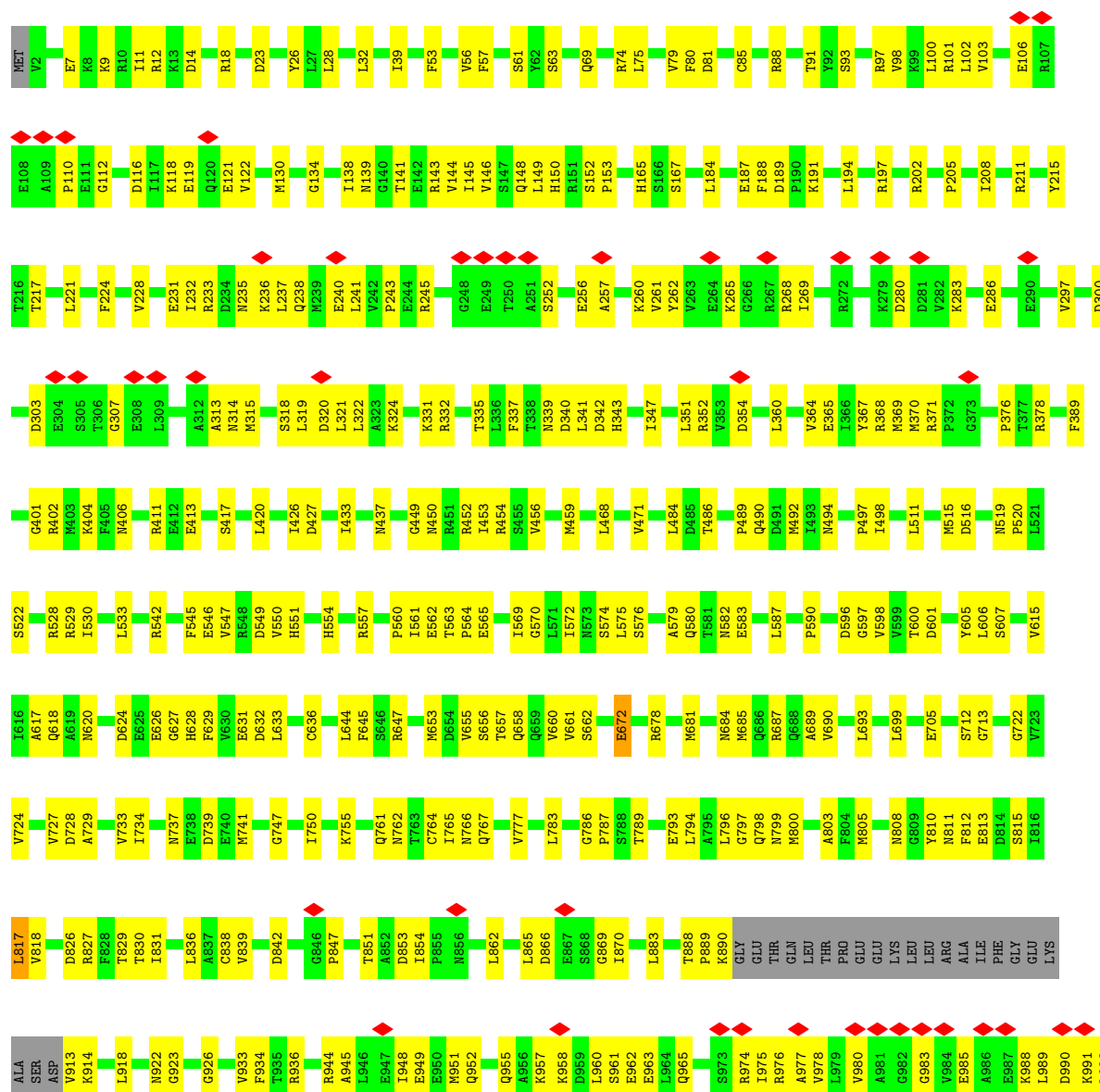
• Molecule 3: DNA-directed RNA polymerase subunit alpha

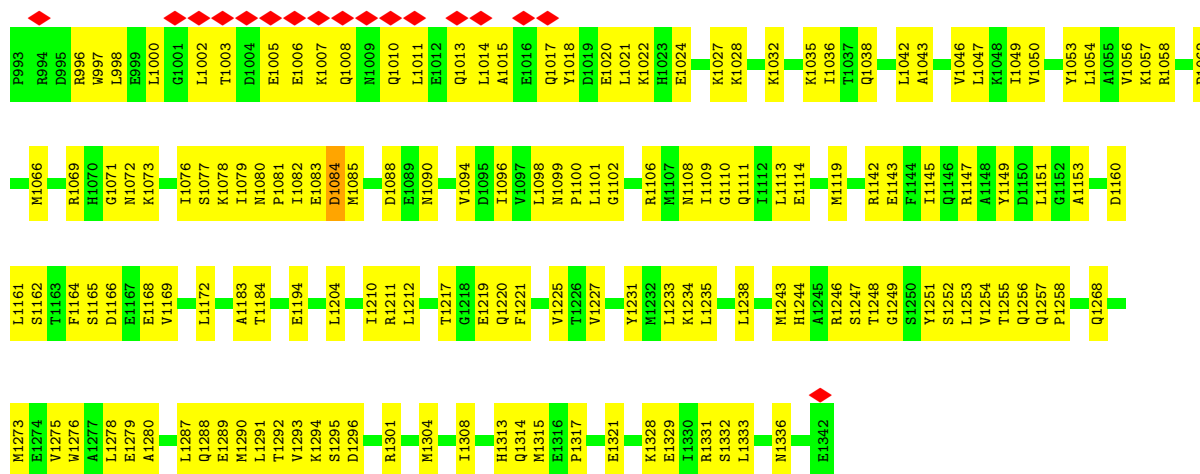


• Molecule 3: DNA-directed RNA polymerase subunit alpha

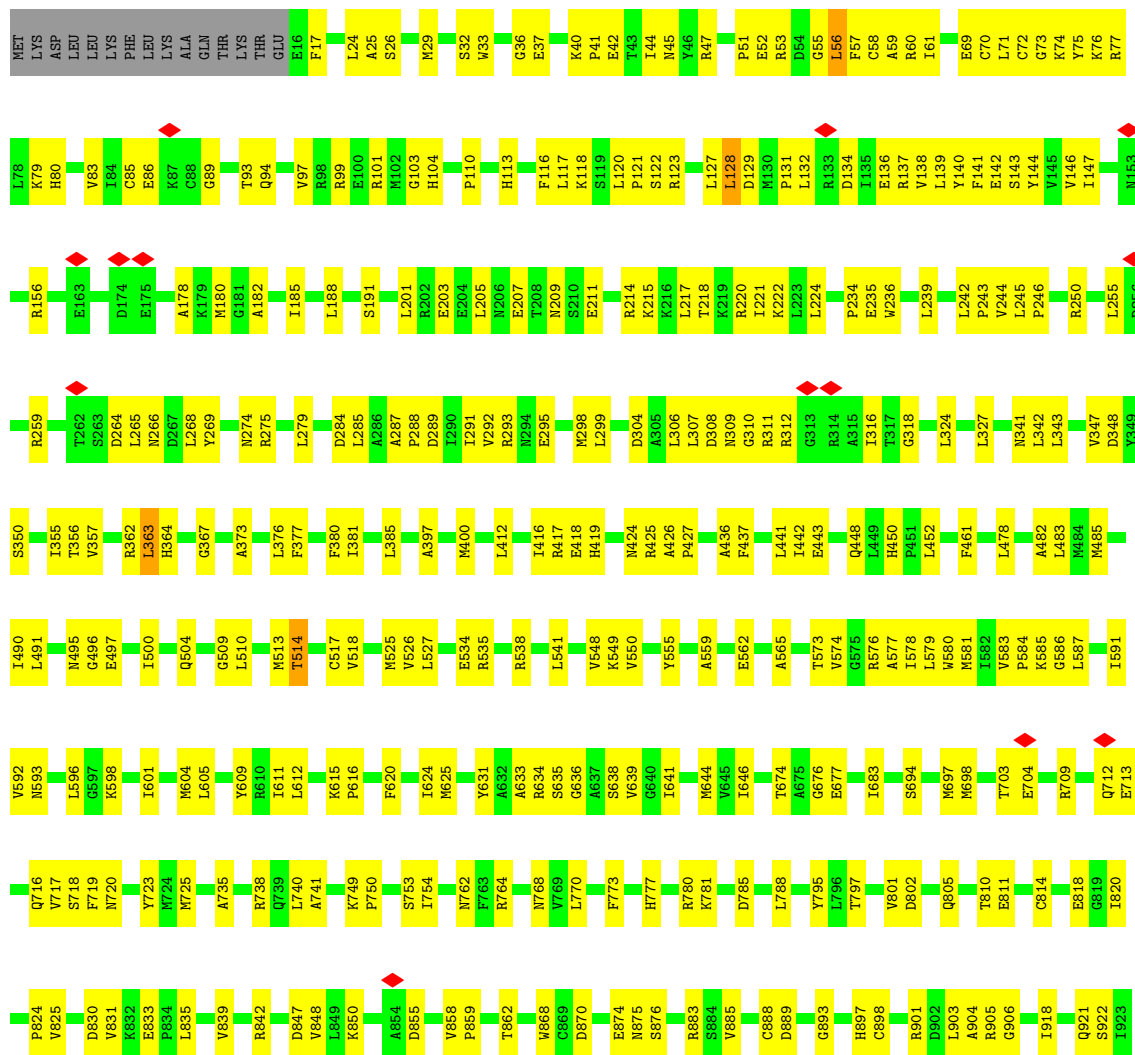


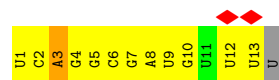
- Molecule 4: DNA-directed RNA polymerase subunit beta





• Molecule 5: DNA-directed RNA polymerase subunit beta'





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	102899	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	49	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	4.193	Depositor
Minimum map value	-2.058	Depositor
Average map value	0.014	Depositor
Map value standard deviation	0.129	Depositor
Recommended contour level	0.6	Depositor
Map size (Å)	307.29602, 307.29602, 307.29602	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.067, 1.067, 1.067	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	N	0.38	0/546	0.44	0/837
2	T	0.52	0/735	0.63	2/1133 (0.2%)
3	A	0.74	0/1790	0.77	2/2426 (0.1%)
3	B	0.65	0/1794	0.77	2/2432 (0.1%)
4	C	0.76	3/10573 (0.0%)	0.74	4/14265 (0.0%)
5	D	0.69	2/10554 (0.0%)	0.76	7/14248 (0.0%)
6	E	0.66	0/584	0.75	0/786
7	R	0.49	0/304	0.46	0/472
All	All	0.71	5/26880 (0.0%)	0.74	17/36599 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	810	TYR	CA-C	-7.73	1.39	1.52
4	C	672	GLU	CA-C	-7.58	1.39	1.52
4	C	1084	ASP	C-N	-6.60	1.23	1.33
5	D	363	LEU	CA-C	-5.66	1.42	1.52
5	D	514	THR	CA-CB	-5.02	1.37	1.53

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	T	24	DG	OP1-P-O3'	-8.92	81.24	108.00
2	T	24	DG	OP2-P-O3'	-8.20	83.39	108.00
3	B	152	TYR	CA-C-N	-7.37	116.44	122.85
3	B	152	TYR	C-N-CA	-7.37	116.44	122.85
5	D	500	ILE	N-CA-C	-6.29	106.31	111.91
5	D	897	HIS	CA-C-N	-5.84	110.62	122.31
5	D	897	HIS	C-N-CA	-5.84	110.62	122.31
4	C	1084	ASP	CA-C-N	-5.83	112.59	121.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	1084	ASP	C-N-CA	-5.83	112.59	121.92
5	D	362	ARG	CA-C-N	-5.81	110.69	122.31
5	D	362	ARG	C-N-CA	-5.81	110.69	122.31
4	C	1295	SER	CA-C-N	-5.70	113.11	122.79
4	C	1295	SER	C-N-CA	-5.70	113.11	122.79
5	D	1326	GLN	CB-CA-C	-5.66	101.49	110.04
5	D	1344	LEU	CA-CB-CG	-5.32	97.69	116.30
3	A	9	LEU	CA-C-N	-5.17	107.38	122.21
3	A	9	LEU	C-N-CA	-5.17	107.38	122.21

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	N	489	0	271	23	0
2	T	655	0	360	30	0
3	A	1768	0	1793	55	0
3	B	1772	0	1799	89	0
4	C	10407	0	10420	386	0
5	D	10397	0	10618	412	0
6	E	582	0	593	18	0
7	R	273	0	140	15	0
8	D	2	0	0	0	0
9	D	1	0	0	0	0
All	All	26346	0	25994	968	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 19.

All (968) 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:B:166:ARG:HD3	3:B:170:ARG:NH1	1.70	1.06

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:166:ARG:HD3	3:B:170:ARG:CZ	1.88	1.04
3:B:166:ARG:CD	3:B:170:ARG:NH1	2.21	1.03
5:D:1049:GLN:O	5:D:1058:SER:HB2	1.62	0.98
1:N:39:DC:O2	2:T:1:DG:N2	1.98	0.96
5:D:1179:PRO:HD2	5:D:1184:ASP:HA	1.49	0.92
3:A:207:THR:HG22	3:A:209:GLY:H	1.35	0.91
1:N:39:DC:N3	2:T:1:DG:N1	2.20	0.89
1:N:36:DC:N3	2:T:4:DG:N1	2.22	0.88
4:C:1072:ASN:ND2	4:C:1111:GLN:OE1	2.08	0.87
5:D:318:GLY:HA2	5:D:324:LEU:HD23	1.57	0.86
4:C:69:GLN:HE21	4:C:101:ARG:HD2	1.40	0.85
4:C:231:GLU:O	4:C:237:LEU:HA	1.76	0.83
4:C:404:LYS:NZ	4:C:450:ASN:OD1	2.13	0.82
5:D:805:GLN:HE22	5:D:1348:LYS:HB2	1.45	0.81
5:D:576:ARG:HD3	5:D:593:ASN:HA	1.61	0.81
5:D:709:ARG:NH2	5:D:712:GLN:OE1	2.14	0.81
5:D:1164:SER:HA	5:D:1200:GLU:HG2	1.63	0.81
1:N:36:DC:O2	2:T:4:DG:N2	2.11	0.81
4:C:549:ASP:OD1	4:C:550:VAL:N	2.13	0.80
5:D:144:TYR:OH	5:D:293:ARG:NH2	2.14	0.80
4:C:1314:GLN:HB2	6:E:28:ARG:HH12	1.47	0.80
7:R:7:G:H2'	7:R:8:A:H8	1.47	0.80
3:A:12:ARG:H	3:A:29:GLU:HB2	1.48	0.79
5:D:1173:ARG:HG3	5:D:1174:ARG:H	1.47	0.79
3:B:192:VAL:HG12	3:B:193:GLU:H	1.48	0.78
3:B:93:GLN:HG3	3:B:94:GLY:H	1.48	0.78
4:C:1002:LEU:HD23	4:C:1003:THR:H	1.50	0.77
7:R:7:G:H2'	7:R:8:A:C8	2.19	0.77
4:C:985:GLU:O	4:C:989:LEU:HB3	1.85	0.77
4:C:97:ARG:HB3	4:C:121:GLU:HB2	1.65	0.77
4:C:256:GLU:HA	4:C:261:VAL:HA	1.65	0.76
4:C:985:GLU:HB3	4:C:988:LYS:HB2	1.66	0.76
2:T:21:DC:O2	7:R:5:G:N2	2.15	0.76
2:T:21:DC:H2'	2:T:22:DC:H6	1.51	0.76
4:C:728:ASP:OD1	4:C:729:ALA:N	2.19	0.75
4:C:842:ASP:HB2	4:C:1047:LEU:HD11	1.69	0.75
4:C:1142:ARG:NH2	4:C:1166:ASP:OD1	2.20	0.75
4:C:838:CYS:HB2	4:C:918:LEU:HD22	1.69	0.74
3:B:196:THR:HG23	5:D:443:GLU:HG3	1.69	0.74
3:B:44:ARG:HA	3:B:183:ILE:HD11	1.67	0.74
4:C:300:ASP:OD1	4:C:313:ALA:N	2.21	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1000:LEU:O	4:C:1008:GLN:NE2	2.20	0.74
5:D:1029:THR:H	5:D:1118:GLY:HA2	1.53	0.74
4:C:582:ASN:OD1	4:C:583:GLU:N	2.19	0.74
4:C:1106:ARG:O	4:C:1108:ASN:N	2.21	0.74
5:D:1038:THR:HB	5:D:1081:VAL:HG11	1.70	0.74
5:D:1360:GLY:O	5:D:1363:TYR:N	2.21	0.73
3:B:23:HIS:ND1	3:B:206:GLU:OE2	2.20	0.73
4:C:297:VAL:HG12	4:C:315:MET:H	1.52	0.73
5:D:452:LEU:HG	5:D:625:MET:HE3	1.68	0.73
5:D:246:PRO:O	5:D:250:ARG:NH1	2.22	0.73
3:A:192:VAL:HG12	3:A:193:GLU:H	1.54	0.73
3:A:195:ARG:HG2	3:A:196:THR:H	1.52	0.73
4:C:590:PRO:HB2	4:C:655:VAL:HG21	1.70	0.72
5:D:1024:THR:HG23	5:D:1124:ILE:H	1.55	0.72
4:C:303:ASP:HB3	4:C:307:GLY:H	1.52	0.71
4:C:1254:VAL:HG13	4:C:1255:THR:HG23	1.71	0.71
5:D:1039:ASP:HB2	5:D:1079:LYS:HE2	1.70	0.71
4:C:933:VAL:HG22	4:C:1050:VAL:HG22	1.73	0.71
4:C:985:GLU:O	4:C:989:LEU:CB	2.38	0.71
5:D:342:LEU:HD23	5:D:1352:ILE:HG23	1.72	0.71
5:D:850:LYS:NZ	5:D:875:ASN:OD1	2.24	0.71
5:D:903:LEU:H	5:D:903:LEU:HD12	1.55	0.71
3:A:135:ASP:OD1	3:A:136:GLU:N	2.24	0.71
4:C:1073:LYS:NZ	7:R:10:G:OP1	2.23	0.71
5:D:638:SER:OG	5:D:639:VAL:N	2.24	0.71
7:R:6:C:H2'	7:R:7:G:C8	2.25	0.71
3:A:28:LEU:HD12	3:A:201:LEU:HD23	1.73	0.70
5:D:495:ASN:O	5:D:497:GLU:N	2.23	0.70
5:D:514:THR:HG21	5:D:596:LEU:HD12	1.72	0.70
4:C:1032:LYS:HE2	4:C:1036:ILE:HD11	1.73	0.70
5:D:824:PRO:HD3	5:D:835:LEU:HD12	1.72	0.70
5:D:901:ARG:HH21	5:D:906:GLY:HA2	1.56	0.70
4:C:766:ASN:OD1	4:C:767:GLN:N	2.25	0.70
4:C:339:ASN:OD1	4:C:340:ASP:N	2.25	0.69
3:B:51:MET:HE1	3:B:219:ARG:HD2	1.74	0.69
5:D:805:GLN:NE2	5:D:1348:LYS:HB2	2.07	0.69
5:D:93:THR:HG22	5:D:94:GLN:H	1.58	0.69
4:C:1255:THR:O	4:C:1257:GLN:N	2.24	0.69
3:B:35:PHE:HA	3:B:38:THR:HG22	1.73	0.68
4:C:232:ILE:HA	4:C:237:LEU:HG	1.73	0.68
5:D:55:GLY:H	5:D:58:CYS:HB2	1.56	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:591:ILE:HG23	5:D:592:VAL:HG13	1.73	0.68
2:T:19:DC:H2'	2:T:20:DG:C8	2.28	0.68
5:D:85:CYS:SG	5:D:86:GLU:N	2.61	0.68
2:T:21:DC:H2'	2:T:22:DC:C6	2.28	0.68
4:C:741:MET:SD	4:C:974:ARG:NH1	2.66	0.68
5:D:674:THR:N	5:D:677:GLU:OE2	2.26	0.68
5:D:1029:THR:HG21	5:D:1080:ILE:HD11	1.76	0.68
4:C:817:LEU:HD21	4:C:1085:MET:HE1	1.76	0.67
4:C:101:ARG:HE	4:C:118:LYS:HD3	1.57	0.67
4:C:998:LEU:HG	4:C:1015:ALA:HB1	1.77	0.67
4:C:404:LYS:NZ	4:C:449:GLY:O	2.26	0.67
3:B:166:ARG:NE	3:B:170:ARG:HH12	1.91	0.67
3:A:117:HIS:HD2	3:A:119:GLY:H	1.41	0.67
3:B:23:HIS:HA	3:B:206:GLU:HG2	1.76	0.66
3:B:166:ARG:CZ	3:B:170:ARG:HH12	2.09	0.66
5:D:964:LYS:O	5:D:976:THR:OG1	2.10	0.66
5:D:255:LEU:HD11	5:D:259:ARG:HB2	1.76	0.66
5:D:797:THR:HG22	5:D:924:GLY:HA3	1.77	0.66
4:C:926:GLY:HA3	4:C:1054:LEU:HD23	1.77	0.66
5:D:70:CYS:SG	5:D:71:LEU:N	2.69	0.66
4:C:238:GLN:HG2	4:C:286:GLU:HA	1.77	0.65
4:C:303:ASP:HB3	4:C:307:GLY:N	2.10	0.65
4:C:951:MET:O	4:C:955:GLN:HG2	1.95	0.65
4:C:826:ASP:OD1	4:C:829:THR:OG1	2.12	0.65
4:C:747:GLY:O	4:C:974:ARG:NH2	2.30	0.65
4:C:1257:GLN:OE1	5:D:341:ASN:ND2	2.29	0.65
5:D:1036:ARG:NH2	5:D:1082:ASP:O	2.28	0.65
5:D:201:LEU:HD11	5:D:220:ARG:HH11	1.62	0.65
5:D:381:ILE:HD11	5:D:412:LEU:HD13	1.78	0.65
5:D:156:ARG:NH2	5:D:191:SER:O	2.30	0.64
4:C:685:MET:SD	4:C:1073:LYS:HG2	2.37	0.64
4:C:811:ASN:ND2	4:C:1098:LEU:O	2.29	0.64
4:C:870:ILE:HB	4:C:944:ARG:HD3	1.79	0.64
5:D:718:SER:OG	5:D:719:PHE:N	2.29	0.64
4:C:224:PHE:CD2	4:C:347:ILE:HG13	2.33	0.64
5:D:1049:GLN:O	5:D:1058:SER:CB	2.44	0.64
5:D:1166:GLY:HA3	5:D:1174:ARG:HD2	1.79	0.64
4:C:18:ARG:HH21	4:C:620:ASN:HB2	1.62	0.64
4:C:318:SER:OG	4:C:320:ASP:OD1	2.10	0.64
5:D:44:ILE:HG22	5:D:51:PRO:HA	1.80	0.64
5:D:129:ASP:OD1	5:D:220:ARG:NE	2.31	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:491:LEU:HB2	5:D:904:ALA:HA	1.80	0.64
3:B:15:ASP:OD1	3:B:16:ILE:N	2.31	0.64
5:D:364:HIS:O	5:D:364:HIS:ND1	2.31	0.64
5:D:1173:ARG:HD3	5:D:1192:LYS:HD2	1.79	0.64
3:A:207:THR:HG22	3:A:209:GLY:N	2.11	0.64
1:N:25:DG:OP1	4:C:542:ARG:NH1	2.31	0.63
4:C:550:VAL:CG1	5:D:777:HIS:HB3	2.28	0.63
4:C:1101:LEU:HD13	5:D:504:GLN:HB2	1.80	0.63
5:D:1076:PRO:HB2	5:D:1101:LEU:HD12	1.81	0.63
3:B:41:ASN:ND2	4:C:1217:THR:HA	2.13	0.63
4:C:12:ARG:NH2	4:C:793:GLU:OE1	2.27	0.63
4:C:360:LEU:HD11	4:C:378:ARG:HG3	1.80	0.63
4:C:976:ARG:HB2	4:C:997:TRP:CZ2	2.33	0.63
5:D:1027:VAL:HG21	5:D:1122:ALA:HB3	1.81	0.63
4:C:1212:LEU:HD22	4:C:1225:VAL:HG21	1.79	0.63
3:A:57:THR:HG23	3:A:158:ARG:NH1	2.14	0.62
3:A:218:ARG:NH1	3:B:231:PHE:O	2.33	0.62
3:B:208:ASN:OD1	3:B:209:GLY:N	2.31	0.62
4:C:805:MET:HE1	4:C:1221:PHE:CZ	2.34	0.62
5:D:77:ARG:HG3	5:D:79:LYS:H	1.64	0.62
5:D:1045:THR:HB	5:D:1076:PRO:HB3	1.81	0.62
3:B:166:ARG:NE	3:B:170:ARG:NH1	2.47	0.62
4:C:618:GLN:NE2	5:D:770:LEU:H	1.96	0.62
5:D:1078:LEU:O	5:D:1098:GLN:HA	2.00	0.62
1:N:36:DC:H2"	1:N:37:DT:C5	2.35	0.62
5:D:1038:THR:HG21	5:D:1081:VAL:HG21	1.79	0.62
4:C:106:GLU:N	4:C:112:GLY:O	2.33	0.62
5:D:235:GLU:OE1	5:D:235:GLU:N	2.31	0.62
5:D:1322:ALA:O	5:D:1325:PHE:N	2.33	0.62
4:C:1275:VAL:HG13	4:C:1287:LEU:HD11	1.80	0.62
4:C:1069:ARG:NH2	4:C:1114:GLU:OE2	2.26	0.61
4:C:812:PHE:CD2	4:C:813:GLU:HG2	2.35	0.61
5:D:749:LYS:HD3	5:D:753:SER:HB2	1.81	0.61
3:B:65:LEU:HB2	3:B:168:ILE:HG22	1.82	0.61
4:C:866:ASP:OD1	4:C:869:GLY:N	2.33	0.61
4:C:550:VAL:HG13	5:D:777:HIS:HB3	1.82	0.61
4:C:808:ASN:H	5:D:633:ALA:HB2	1.64	0.61
4:C:546:GLU:OE1	4:C:546:GLU:N	2.34	0.61
4:C:992:LEU:HD13	4:C:996:ARG:HB2	1.83	0.61
4:C:705:GLU:HB3	4:C:794:LEU:H	1.65	0.61
4:C:320:ASP:OD1	4:C:321:LEU:N	2.33	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:380:PHE:HE2	5:D:419:HIS:HE1	1.47	0.61
1:N:29:DT:H5''	5:D:1148:ARG:NE	2.16	0.61
4:C:976:ARG:NH2	4:C:989:LEU:O	2.32	0.60
5:D:591:ILE:HD11	5:D:604:MET:HA	1.83	0.60
5:D:1186:TYR:OH	5:D:1188:GLU:OE1	2.19	0.60
5:D:709:ARG:HH12	5:D:713:GLU:H	1.49	0.60
5:D:1141:VAL:HG22	5:D:1237:VAL:HG23	1.84	0.60
1:N:30:DG:H2''	1:N:31:DG:H8	1.66	0.60
5:D:1143:ASP:OD1	5:D:1148:ARG:NH1	2.28	0.60
4:C:56:VAL:HG11	4:C:468:LEU:HD13	1.83	0.60
5:D:1179:PRO:HG2	5:D:1185:PRO:HD2	1.84	0.60
3:A:82:LEU:HD11	3:A:171:LEU:HD23	1.84	0.60
4:C:624:ASP:O	4:C:626:GLU:N	2.34	0.60
5:D:577:ALA:O	5:D:580:TRP:N	2.34	0.60
3:A:195:ARG:HD2	3:A:198:LEU:HD21	1.83	0.60
3:B:107:ILE:HG23	3:B:134:THR:HA	1.83	0.60
4:C:812:PHE:HD2	4:C:813:GLU:HG2	1.67	0.60
5:D:859:PRO:HD2	5:D:862:THR:HG21	1.84	0.60
3:A:57:THR:HG22	3:A:58:GLU:HG3	1.83	0.59
5:D:1036:ARG:O	5:D:1038:THR:N	2.33	0.59
5:D:1322:ALA:HB1	5:D:1331:VAL:HG21	1.84	0.59
4:C:243:PRO:HD3	4:C:283:LYS:HE2	1.84	0.59
4:C:1043:ALA:O	4:C:1046:VAL:HG12	2.02	0.59
5:D:289:ASP:HA	5:D:292:VAL:HG22	1.83	0.59
4:C:119:GLU:HB2	4:C:489:PRO:HD2	1.83	0.59
4:C:632:ASP:OD1	4:C:647:ARG:NH1	2.34	0.59
5:D:1208:ASP:OD1	5:D:1209:VAL:N	2.34	0.59
6:E:42:GLU:HG2	6:E:52:ARG:HH22	1.65	0.59
7:R:8:A:H2'	7:R:9:U:C6	2.38	0.59
4:C:590:PRO:HG3	4:C:605:TYR:CE1	2.37	0.59
5:D:984:LEU:HB3	5:D:993:GLU:HB2	1.84	0.59
3:B:103:ASN:HA	3:B:140:ILE:O	2.03	0.59
4:C:1119:MET:HE1	4:C:1227:VAL:HG23	1.84	0.59
5:D:424:ASN:OD1	5:D:425:ARG:N	2.36	0.59
5:D:674:THR:HG22	5:D:676:GLY:H	1.68	0.59
5:D:1368:ASP:OD1	5:D:1371:ARG:NH2	2.36	0.59
4:C:712:SER:OG	4:C:713:GLY:N	2.36	0.59
4:C:764:CYS:SG	4:C:765:ILE:N	2.76	0.59
5:D:442:ILE:HG22	5:D:443:GLU:O	2.02	0.59
5:D:820:ILE:HG22	5:D:1227:HIS:ND1	2.18	0.59
5:D:951:GLN:OE1	5:D:1016:THR:OG1	2.20	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:660:VAL:HG13	4:C:661:VAL:HG13	1.85	0.59
2:T:26:DA:H2''	2:T:27:DA:H5'	1.85	0.58
5:D:833:GLU:OE2	5:D:1242:ARG:NH1	2.36	0.58
3:B:47:LEU:HD23	3:B:183:ILE:HD13	1.84	0.58
7:R:8:A:H2'	7:R:9:U:H6	1.67	0.58
4:C:14:ASP:HA	4:C:1183:ALA:HB3	1.85	0.58
4:C:1143:GLU:OE2	4:C:1147:ARG:NH2	2.35	0.58
5:D:674:THR:HB	5:D:677:GLU:OE1	2.02	0.58
4:C:890:LYS:O	4:C:913:VAL:N	2.37	0.58
4:C:1313:HIS:CD2	6:E:31:GLN:HE22	2.22	0.58
5:D:1064:SER:OG	5:D:1067:ARG:NH2	2.31	0.58
4:C:977:ALA:HA	4:C:980:VAL:HB	1.86	0.58
5:D:1275:LEU:HG	5:D:1276:GLU:H	1.69	0.58
5:D:85:CYS:HB3	5:D:89:GLY:H	1.69	0.58
3:B:66:HIS:CG	3:B:67:GLU:H	2.21	0.57
4:C:321:LEU:HD23	4:C:324:LYS:HD2	1.86	0.57
5:D:1075:ARG:HB3	5:D:1100:PHE:HE1	1.68	0.57
1:N:25:DG:H22	4:C:547:VAL:CG1	2.17	0.57
3:A:74:VAL:HG22	3:A:76:GLU:H	1.69	0.57
4:C:489:PRO:HA	4:C:492:MET:HE2	1.86	0.57
5:D:513:MET:SD	5:D:631:TYR:HD2	2.27	0.57
5:D:1077:ALA:HB1	5:D:1098:GLN:HB2	1.85	0.57
5:D:495:ASN:HD22	5:D:1247:LYS:HB2	1.69	0.57
4:C:98:VAL:O	4:C:121:GLU:HA	2.03	0.57
4:C:1210:ILE:HG22	4:C:1211:ARG:N	2.18	0.57
4:C:1289:GLU:HA	4:C:1315:MET:HE1	1.85	0.57
5:D:29:MET:O	5:D:32:SER:OG	2.17	0.57
5:D:644:MET:SD	5:D:740:LEU:HD23	2.44	0.57
4:C:765:ILE:HG13	4:C:787:PRO:HG3	1.87	0.57
5:D:1326:GLN:O	5:D:1327:GLU:HB3	2.03	0.57
1:N:30:DG:H2''	1:N:31:DG:C8	2.39	0.57
5:D:357:VAL:HG22	5:D:461:PHE:CD2	2.40	0.57
5:D:559:ALA:HB3	5:D:562:GLU:HB3	1.87	0.57
3:A:58:GLU:HB2	3:A:145:LYS:HB3	1.86	0.57
2:T:21:DC:N3	7:R:5:G:N1	2.39	0.56
4:C:811:ASN:O	4:C:1099:ASN:ND2	2.38	0.56
5:D:77:ARG:HB3	5:D:80:HIS:ND1	2.20	0.56
5:D:137:ARG:NH2	5:D:143:SER:OG	2.38	0.56
5:D:510:LEU:O	5:D:514:THR:HG22	2.05	0.56
4:C:1066:MET:HE2	4:C:1076:ILE:HB	1.88	0.56
5:D:309:ASN:OD1	5:D:310:GLY:N	2.38	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:187:GLU:OE2	4:C:197:ARG:NH2	2.39	0.56
4:C:798:GLN:OE1	4:C:827:ARG:HB2	2.06	0.56
5:D:245:LEU:O	5:D:250:ARG:NH1	2.38	0.56
5:D:526:VAL:HG12	5:D:549:LYS:HB2	1.86	0.56
3:A:10:LYS:HE3	3:B:226:GLU:HB3	1.88	0.56
5:D:58:CYS:SG	5:D:60:ARG:HG2	2.46	0.56
4:C:549:ASP:OD2	5:D:750:PRO:HB3	2.04	0.56
4:C:1101:LEU:HD23	5:D:725:MET:SD	2.45	0.56
3:A:12:ARG:HB2	3:A:29:GLU:CD	2.30	0.56
4:C:961:SER:O	4:C:965:GLN:HG3	2.05	0.56
5:D:140:TYR:OH	5:D:304:ASP:OD2	2.21	0.56
5:D:377:PHE:HE2	5:D:416:ILE:HD13	1.71	0.56
4:C:1035:LYS:O	4:C:1038:GLN:HG2	2.06	0.56
5:D:611:ILE:HG22	5:D:612:LEU:HD12	1.88	0.56
5:D:888:CYS:SG	5:D:889:ASP:N	2.79	0.56
5:D:889:ASP:OD1	5:D:1286:LYS:NZ	2.26	0.56
3:A:29:GLU:HB3	3:A:30:PRO:CD	2.36	0.56
4:C:617:ALA:HB3	4:C:653:MET:HA	1.87	0.56
5:D:136:GLU:OE2	5:D:312:ARG:NE	2.37	0.56
5:D:1249:ASN:OD1	5:D:1250:ASP:N	2.39	0.56
4:C:339:ASN:ND2	4:C:342:ASP:H	2.02	0.55
4:C:989:LEU:HD12	4:C:992:LEU:HD11	1.88	0.55
5:D:1046:ILE:HA	5:D:1068:THR:HG21	1.88	0.55
5:D:1029:THR:N	5:D:1118:GLY:HA2	2.20	0.55
5:D:1275:LEU:HB3	5:D:1278:GLU:HB2	1.89	0.55
3:B:59:VAL:HG22	3:B:144:ILE:HA	1.87	0.55
5:D:56:LEU:HD21	5:D:269:TYR:HB3	1.88	0.55
5:D:635:SER:OG	5:D:636:GLY:N	2.40	0.55
5:D:904:ALA:C	5:D:905:ARG:HD2	2.32	0.55
5:D:955:LYS:HG3	5:D:1011:VAL:O	2.07	0.55
7:R:6:C:H2'	7:R:7:G:H8	1.69	0.55
3:A:23:HIS:HB2	3:A:205:MET:O	2.06	0.55
4:C:957:LYS:O	4:C:961:SER:OG	2.15	0.55
5:D:1064:SER:HG	5:D:1067:ARG:HH21	1.54	0.55
7:R:2:C:H2'	7:R:3:A:C8	2.42	0.55
4:C:11:ILE:HG23	4:C:1149:TYR:OH	2.07	0.55
4:C:215:TYR:HE2	4:C:426:ILE:HD11	1.71	0.55
4:C:1276:TRP:CE2	5:D:801:VAL:HG21	2.42	0.55
5:D:513:MET:HE1	5:D:579:LEU:HD13	1.88	0.55
3:B:166:ARG:HD3	3:B:170:ARG:NH2	2.21	0.55
6:E:13:ILE:O	6:E:15:ASN:N	2.36	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1280:ALA:HB1	5:D:918:ILE:HG22	1.88	0.54
5:D:883:ARG:NH2	5:D:898:CYS:SG	2.80	0.54
3:A:208:ASN:OD1	3:A:209:GLY:N	2.40	0.54
3:B:102:LEU:HB3	3:B:142:MET:HG2	1.89	0.54
5:D:72:CYS:SG	5:D:73:GLY:N	2.81	0.54
5:D:1111:ASP:OD1	5:D:1112:GLY:N	2.41	0.54
5:D:42:GLU:HB2	5:D:52:GLU:HG2	1.90	0.54
4:C:590:PRO:HG3	4:C:605:TYR:HE1	1.72	0.54
5:D:58:CYS:SG	5:D:59:ALA:N	2.80	0.54
5:D:1322:ALA:HB3	5:D:1331:VAL:HG11	1.88	0.54
6:E:4:VAL:HG13	6:E:5:THR:HG23	1.88	0.54
4:C:596:ASP:OD1	4:C:597:GLY:N	2.39	0.54
4:C:750:ILE:HD13	4:C:963:GLU:HG3	1.88	0.54
5:D:244:VAL:HG12	5:D:269:TYR:CE1	2.43	0.54
5:D:357:VAL:HG22	5:D:461:PHE:CE2	2.43	0.54
5:D:1181:ASP:OD1	5:D:1182:GLY:N	2.40	0.54
4:C:490:GLN:OE1	4:C:490:GLN:N	2.33	0.53
4:C:786:GLY:N	4:C:789:THR:OG1	2.38	0.53
4:C:1081:PRO:HB2	4:C:1083:GLU:OE1	2.08	0.53
1:N:36:DC:H2"	1:N:37:DT:C6	2.43	0.53
3:B:67:GLU:N	3:B:67:GLU:OE1	2.41	0.53
4:C:150:HIS:CE1	4:C:454:ARG:NE	2.77	0.53
5:D:830:ASP:OD1	5:D:831:VAL:N	2.41	0.53
4:C:1080:ASN:HD22	4:C:1085:MET:CE	2.21	0.53
4:C:1153:ALA:N	4:C:1194:GLU:OE2	2.24	0.53
5:D:134:ASP:O	5:D:138:VAL:HG23	2.09	0.53
5:D:785:ASP:OD1	5:D:932:MET:HB3	2.08	0.53
5:D:1036:ARG:HG2	5:D:1112:GLY:HA2	1.90	0.53
5:D:347:VAL:HG12	5:D:348:ASP:O	2.07	0.53
3:A:23:HIS:HB2	3:A:206:GLU:HA	1.90	0.53
3:A:70:THR:HG21	4:C:755:LYS:HE2	1.90	0.53
3:B:166:ARG:CD	3:B:170:ARG:HH12	2.09	0.53
5:D:55:GLY:O	5:D:57:PHE:N	2.42	0.53
6:E:25:ARG:HH21	6:E:68:GLU:CD	2.17	0.53
4:C:39:ILE:HD11	4:C:75:LEU:HD22	1.90	0.53
4:C:605:TYR:C	4:C:606:LEU:HD12	2.33	0.53
5:D:709:ARG:NH1	5:D:712:GLN:H	2.06	0.53
4:C:777:VAL:HG11	4:C:783:LEU:HD21	1.90	0.53
5:D:1327:GLU:OE1	5:D:1327:GLU:N	2.41	0.53
3:A:29:GLU:HB3	3:A:30:PRO:HD2	1.91	0.53
5:D:1062:LEU:HB2	5:D:1067:ARG:HA	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1075:ARG:HB3	5:D:1100:PHE:CE1	2.44	0.52
4:C:231:GLU:O	4:C:237:LEU:CA	2.52	0.52
4:C:1169:VAL:O	4:C:1172:LEU:N	2.42	0.52
5:D:1018:ALA:HB1	5:D:1020:TRP:HZ3	1.74	0.52
4:C:975:ILE:O	4:C:978:VAL:HB	2.09	0.52
5:D:85:CYS:HB3	5:D:89:GLY:N	2.24	0.52
5:D:380:PHE:CE2	5:D:419:HIS:HE1	2.25	0.52
1:N:36:DC:N4	2:T:4:DG:O6	2.22	0.52
3:B:192:VAL:HG12	3:B:193:GLU:N	2.22	0.52
3:B:203:ILE:HG21	3:B:217:ILE:HD11	1.92	0.52
4:C:364:VAL:HG13	4:C:376:PRO:HG3	1.91	0.52
5:D:977:SER:O	5:D:980:THR:OG1	2.20	0.52
3:A:31:LEU:O	3:A:198:LEU:HA	2.10	0.52
3:B:47:LEU:HG	3:B:180:VAL:HG11	1.92	0.52
3:B:182:ARG:NE	5:D:581:MET:HE1	2.25	0.52
4:C:149:LEU:HD12	4:C:452:ARG:O	2.10	0.52
5:D:956:GLY:HA3	5:D:985:ILE:O	2.09	0.52
5:D:978:ARG:NE	5:D:1197:ASN:O	2.42	0.52
4:C:91:THR:HG22	4:C:138:ILE:O	2.09	0.52
5:D:36:GLY:O	5:D:104:HIS:ND1	2.43	0.52
1:N:25:DG:N2	4:C:547:VAL:CG1	2.73	0.52
4:C:26:TYR:HE2	4:C:32:LEU:HD12	1.74	0.52
4:C:1078:LYS:HG2	4:C:1079:ILE:N	2.25	0.52
5:D:1045:THR:HA	5:D:1071:GLY:HA3	1.92	0.52
4:C:79:VAL:HG23	4:C:80:PHE:CD2	2.44	0.51
4:C:678:ARG:NH1	4:C:681:MET:SD	2.84	0.51
4:C:983:GLY:H	4:C:1007:LYS:HZ3	1.55	0.51
5:D:141:PHE:HD1	5:D:180:MET:HE2	1.75	0.51
3:B:62:ASP:OD1	3:B:71:LYS:NZ	2.35	0.51
4:C:103:VAL:HG12	4:C:116:ASP:HB3	1.92	0.51
4:C:796:LEU:N	4:C:1231:TYR:OH	2.43	0.51
5:D:367:GLY:N	5:D:448:GLN:O	2.42	0.51
3:A:45:ARG:NH1	4:C:1084:ASP:OD1	2.23	0.51
4:C:797:GLY:N	4:C:1231:TYR:OH	2.37	0.51
5:D:930:LEU:HD23	5:D:1244:GLN:HG3	1.92	0.51
3:B:102:LEU:O	3:B:141:SER:HA	2.10	0.51
4:C:314:ASN:OD1	4:C:352:ARG:NH2	2.43	0.51
5:D:1034:PHE:HD2	5:D:1036:ARG:HE	1.58	0.51
3:A:117:HIS:CD2	3:A:119:GLY:H	2.24	0.51
4:C:81:ASP:O	4:C:85:CYS:HB2	2.10	0.51
4:C:976:ARG:HB2	4:C:997:TRP:HZ2	1.72	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:128:LEU:HD13	5:D:128:LEU:O	2.11	0.51
5:D:1067:ARG:HD2	5:D:1072:LYS:HA	1.91	0.51
4:C:519:ASN:O	4:C:522:SER:N	2.43	0.51
5:D:1138:LEU:HB3	5:D:1139:PRO:HD3	1.92	0.51
3:B:57:THR:HG23	3:B:158:ARG:NH2	2.25	0.51
4:C:990:ASP:OD1	4:C:991:LYS:N	2.44	0.51
5:D:1064:SER:O	5:D:1067:ARG:NH2	2.44	0.51
4:C:803:ALA:HB2	4:C:1094:VAL:HG21	1.93	0.51
4:C:1082:ILE:H	4:C:1082:ILE:HD12	1.76	0.51
5:D:925:GLU:HB3	5:D:926:PRO:HD3	1.93	0.51
4:C:224:PHE:HD2	4:C:347:ILE:HG13	1.72	0.51
4:C:402:ARG:HH21	4:C:417:SER:C	2.19	0.51
4:C:1056:VAL:HG11	4:C:1058:ARG:HE	1.76	0.51
2:T:20:DG:C4	2:T:21:DC:C5	2.98	0.50
5:D:716:GLN:HG3	5:D:717:VAL:O	2.11	0.50
6:E:46:THR:HA	6:E:49:ILE:HD12	1.92	0.50
2:T:20:DG:H2'	2:T:21:DC:C6	2.47	0.50
4:C:830:THR:OG1	4:C:831:ILE:N	2.43	0.50
4:C:245:ARG:HB3	4:C:337:PHE:CE1	2.46	0.50
4:C:468:LEU:O	4:C:471:VAL:HG12	2.12	0.50
5:D:510:LEU:HD22	5:D:601:ILE:HD12	1.92	0.50
5:D:974:VAL:HG12	5:D:1002:VAL:HG22	1.94	0.50
4:C:997:TRP:HA	4:C:1000:LEU:HD11	1.93	0.50
4:C:1161:LEU:HD12	4:C:1164:PHE:CE2	2.46	0.50
5:D:26:SER:HB2	5:D:236:TRP:CE3	2.45	0.50
5:D:287:ALA:HB1	5:D:288:PRO:HD2	1.93	0.50
2:T:17:DA:H5''	2:T:17:DA:H8	1.77	0.50
3:A:12:ARG:N	3:A:29:GLU:HB2	2.21	0.50
5:D:275:ARG:CZ	5:D:298:MET:HB3	2.41	0.50
3:B:62:ASP:OD1	3:B:63:GLY:N	2.43	0.50
4:C:936:ARG:HB2	4:C:1042:LEU:HD12	1.93	0.50
2:T:13:DG:H2''	2:T:14:DC:O5'	2.11	0.50
4:C:484:LEU:O	4:C:486:THR:N	2.44	0.50
4:C:922:ASN:OD1	4:C:923:GLY:N	2.45	0.50
4:C:1109:ILE:HG12	5:D:644:MET:HE1	1.94	0.50
4:C:1252:SER:OG	4:C:1253:LEU:N	2.41	0.50
5:D:218:THR:HA	5:D:221:ILE:HG22	1.94	0.50
5:D:586:GLY:C	5:D:587:LEU:HD12	2.37	0.50
4:C:367:TYR:OH	4:C:371:ARG:NH1	2.41	0.49
5:D:1325:PHE:CE1	5:D:1326:GLN:HG3	2.47	0.49
3:A:66:HIS:CE1	3:A:68:TYR:HB2	2.47	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:656:SER:OG	4:C:657:THR:N	2.44	0.49
5:D:137:ARG:HG2	5:D:142:GLU:OE2	2.11	0.49
3:A:11:PRO:HA	3:A:29:GLU:HB2	1.95	0.49
4:C:1161:LEU:HD12	4:C:1164:PHE:CD2	2.46	0.49
5:D:517:CYS:SG	5:D:518:VAL:N	2.84	0.49
5:D:1081:VAL:HG12	5:D:1087:ASP:HA	1.93	0.49
4:C:56:VAL:HG13	4:C:57:PHE:CD1	2.48	0.49
4:C:528:ARG:NH2	4:C:576:SER:O	2.46	0.49
5:D:1005:LYS:HE3	5:D:1011:VAL:HG12	1.94	0.49
5:D:1215:GLU:HG2	5:D:1220:ILE:HD11	1.94	0.49
4:C:545:PHE:CE2	5:D:933:ARG:HD2	2.47	0.49
4:C:1183:ALA:O	4:C:1184:THR:OG1	2.26	0.49
4:C:1217:THR:OG1	4:C:1219:GLU:HG2	2.12	0.49
5:D:986:ASP:OD1	5:D:990:ARG:N	2.37	0.49
4:C:1017:GLN:O	4:C:1020:GLU:HB3	2.12	0.49
4:C:1018:TYR:OH	4:C:1022:LYS:HD3	2.12	0.49
5:D:367:GLY:HA3	5:D:448:GLN:HB2	1.95	0.49
5:D:416:ILE:O	5:D:418:GLU:N	2.46	0.49
5:D:573:THR:OG1	5:D:576:ARG:NH1	2.45	0.49
5:D:1172:LYS:HA	5:D:1191:PRO:HA	1.95	0.49
3:B:15:ASP:HB3	3:B:27:THR:OG1	2.11	0.49
4:C:139:ASN:C	4:C:141:THR:H	2.21	0.49
4:C:257:ALA:N	4:C:260:LYS:O	2.46	0.49
5:D:1168:GLU:HG3	5:D:1173:ARG:HB2	1.94	0.49
3:B:4:SER:HB2	3:B:7:GLU:HB3	1.95	0.49
3:B:181:GLU:HA	5:D:535:ARG:NH1	2.28	0.49
3:B:183:ILE:HG22	3:B:205:MET:HG3	1.93	0.49
4:C:389:PHE:HD2	4:C:420:LEU:HD12	1.78	0.49
4:C:600:THR:HG22	4:C:601:ASP:N	2.28	0.49
4:C:693:LEU:HB2	4:C:829:THR:O	2.12	0.49
4:C:1234:LYS:HE2	4:C:1238:LEU:HD11	1.95	0.49
4:C:268:ARG:NH2	4:C:269:ILE:O	2.46	0.49
4:C:319:LEU:HA	4:C:322:LEU:HD12	1.93	0.49
5:D:209:ASN:HA	5:D:214:ARG:HH21	1.78	0.49
5:D:264:ASP:CG	5:D:324:LEU:HB2	2.38	0.49
5:D:1059:LEU:HB2	5:D:1107:VAL:HB	1.93	0.49
3:A:193:GLU:O	3:A:195:ARG:N	2.45	0.49
4:C:565:GLU:HA	4:C:569:ILE:HG12	1.94	0.49
4:C:851:THR:HG23	4:C:853:ASP:H	1.78	0.49
5:D:203:GLU:O	5:D:207:GLU:HG2	2.13	0.49
4:C:233:ARG:HD3	4:C:238:GLN:HB2	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:815:SER:HB3	4:C:1077:SER:HB3	1.94	0.48
5:D:41:PRO:HG3	5:D:274:ASN:OD1	2.13	0.48
5:D:697:MET:HG3	5:D:698:MET:N	2.27	0.48
4:C:101:ARG:NE	4:C:118:LYS:HD3	2.27	0.48
5:D:26:SER:O	5:D:29:MET:N	2.46	0.48
5:D:842:ARG:HH21	5:D:1251:LYS:HG2	1.79	0.48
3:A:49:SER:OG	3:A:50:SER:N	2.45	0.48
3:A:192:VAL:HG12	3:A:193:GLU:N	2.25	0.48
3:B:100:LEU:HD23	3:B:115:ILE:HG21	1.96	0.48
4:C:620:ASN:HD21	5:D:768:ASN:HB2	1.79	0.48
5:D:478:LEU:HG	6:E:47:THR:HG23	1.95	0.48
5:D:583:VAL:HA	5:D:620:PHE:CE1	2.48	0.48
5:D:697:MET:SD	5:D:741:ALA:HB3	2.53	0.48
2:T:18:DT:H3'	2:T:19:DC:H6	1.77	0.48
4:C:53:PHE:CE1	4:C:468:LEU:HD11	2.49	0.48
4:C:545:PHE:HE1	5:D:788:LEU:HD12	1.78	0.48
5:D:205:LEU:HD21	5:D:217:LEU:HB2	1.96	0.48
5:D:436:ALA:HB3	5:D:485:MET:HA	1.95	0.48
3:B:57:THR:O	3:B:173:VAL:HB	2.13	0.48
4:C:983:GLY:H	4:C:1007:LYS:NZ	2.12	0.48
5:D:957:SER:O	5:D:984:LEU:HD12	2.13	0.48
3:B:13:LEU:H	3:B:13:LEU:HD23	1.79	0.48
4:C:189:ASP:O	4:C:191:LYS:N	2.47	0.48
4:C:402:ARG:HD2	4:C:406:ASN:HD21	1.79	0.48
4:C:562:GLU:OE1	4:C:662:SER:OG	2.25	0.48
4:C:870:ILE:HD12	4:C:870:ILE:H	1.78	0.48
5:D:52:GLU:HG3	5:D:53:ARG:O	2.14	0.48
5:D:265:LEU:O	5:D:266:ASN:C	2.57	0.48
5:D:275:ARG:HG2	5:D:299:LEU:HA	1.96	0.48
5:D:1043:GLY:H	5:D:1046:ILE:HG12	1.79	0.48
3:B:99:ILE:C	3:B:100:LEU:HD12	2.38	0.48
4:C:351:LEU:HD12	4:C:354:ASP:OD2	2.14	0.48
4:C:1056:VAL:HG12	4:C:1057:LYS:N	2.29	0.48
4:C:1253:LEU:HB2	7:R:1:U:H5'	1.94	0.48
5:D:452:LEU:HG	5:D:625:MET:CE	2.42	0.48
2:T:22:DC:H2'	2:T:23:DT:H71	1.95	0.48
4:C:557:ARG:NH2	4:C:607:SER:O	2.47	0.48
4:C:888:THR:OG1	4:C:914:LYS:HB3	2.13	0.48
1:N:27:DC:P	1:N:27:DC:H3'	2.54	0.47
2:T:2:DC:H2''	2:T:3:DA:C8	2.49	0.47
3:B:29:GLU:OE1	3:B:200:LYS:NZ	2.37	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:184:LEU:HD13	4:C:389:PHE:CZ	2.49	0.47
5:D:948:SER:OG	5:D:949:SER:N	2.40	0.47
5:D:1038:THR:CB	5:D:1081:VAL:HG11	2.42	0.47
4:C:339:ASN:CG	4:C:341:LEU:H	2.22	0.47
4:C:1220:GLN:HG2	4:C:1221:PHE:O	2.13	0.47
5:D:17:PHE:HZ	5:D:1353:VAL:HG21	1.79	0.47
5:D:122:SER:HB2	5:D:132:LEU:HD12	1.96	0.47
5:D:847:ASP:N	5:D:847:ASP:OD1	2.46	0.47
5:D:1178:THR:HG23	5:D:1184:ASP:HB3	1.96	0.47
4:C:1268:GLN:HG2	5:D:350:SER:OG	2.14	0.47
4:C:519:ASN:O	4:C:520:PRO:C	2.55	0.47
5:D:110:PRO:HB2	5:D:182:ALA:HB1	1.95	0.47
5:D:968:ASN:ND2	5:D:970:SER:HB2	2.30	0.47
5:D:976:THR:HA	5:D:999:TYR:CE1	2.49	0.47
3:B:47:LEU:HD21	3:B:205:MET:SD	2.54	0.47
3:B:66:HIS:CD2	3:B:67:GLU:H	2.31	0.47
4:C:232:ILE:HB	4:C:331:LYS:HD3	1.96	0.47
4:C:240:GLU:C	4:C:241:LEU:HD12	2.40	0.47
4:C:705:GLU:H	4:C:705:GLU:CD	2.21	0.47
4:C:733:VAL:HG22	4:C:750:ILE:HG12	1.95	0.47
2:T:15:DA:H2'	2:T:16:DC:H6	1.80	0.47
3:A:231:PHE:CE2	3:B:28:LEU:HD11	2.49	0.47
4:C:796:LEU:N	4:C:796:LEU:HD12	2.30	0.47
3:B:58:GLU:CD	3:B:170:ARG:HD2	2.39	0.47
4:C:39:ILE:HD11	4:C:75:LEU:CD2	2.45	0.47
4:C:1024:GLU:HA	4:C:1027:LYS:HG2	1.96	0.47
4:C:1243:MET:HG2	4:C:1244:HIS:N	2.30	0.47
5:D:412:LEU:HA	5:D:412:LEU:HD12	1.65	0.47
5:D:641:ILE:HD11	5:D:764:ARG:HG3	1.96	0.47
5:D:1140:ARG:HH21	5:D:1236:GLU:CD	2.23	0.47
5:D:1261:LEU:CD1	5:D:1304:ARG:HH21	2.28	0.47
4:C:960:LEU:HD13	4:C:1032:LYS:HG2	1.96	0.47
3:A:39:LEU:HA	3:A:39:LEU:HD23	1.64	0.47
3:A:60:GLU:CD	3:A:143:ARG:HH21	2.23	0.47
4:C:148:GLN:OE1	4:C:459:MET:HE1	2.15	0.47
4:C:235:ASN:OD1	4:C:236:LYS:N	2.46	0.47
4:C:560:PRO:HG3	5:D:773:PHE:HE1	1.80	0.47
4:C:818:VAL:HG21	4:C:1066:MET:HE1	1.96	0.47
4:C:1013:GLN:O	4:C:1017:GLN:HG2	2.15	0.47
4:C:1331:ARG:HG3	5:D:33:TRP:CH2	2.50	0.47
5:D:436:ALA:O	5:D:437:PHE:CG	2.68	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:858:VAL:HG12	5:D:868:TRP:HZ3	1.80	0.47
5:D:1011:VAL:HB	5:D:1015:GLU:OE1	2.15	0.47
4:C:339:ASN:HB3	4:C:343:HIS:H	1.80	0.47
4:C:617:ALA:HA	4:C:636:CYS:SG	2.55	0.47
4:C:739:ASP:OD1	4:C:739:ASP:N	2.47	0.47
5:D:74:LYS:HG2	5:D:75:TYR:CD1	2.50	0.47
5:D:215:LYS:O	5:D:218:THR:HG22	2.15	0.47
1:N:12:DA:H2'	1:N:13:DT:H71	1.97	0.46
3:A:105:SER:HB3	3:A:139:SER:HB2	1.96	0.46
3:B:41:ASN:HD21	4:C:1217:THR:HA	1.79	0.46
5:D:1289:ASN:OD1	5:D:1290:ARG:N	2.49	0.46
1:N:11:DC:H2''	1:N:12:DA:N7	2.30	0.46
5:D:1146:GLU:HG2	5:D:1148:ARG:CZ	2.45	0.46
3:B:55:ALA:O	3:B:146:VAL:HA	2.15	0.46
3:B:66:HIS:CG	3:B:67:GLU:N	2.83	0.46
4:C:515:MET:HG2	4:C:516:ASP:O	2.14	0.46
5:D:205:LEU:HD11	5:D:217:LEU:HB3	1.96	0.46
5:D:1173:ARG:HG3	5:D:1174:ARG:N	2.24	0.46
1:N:28:DA:H1'	1:N:29:DT:O4'	2.16	0.46
4:C:74:ARG:C	4:C:75:LEU:HD12	2.40	0.46
4:C:314:ASN:HD22	4:C:351:LEU:HD23	1.80	0.46
4:C:574:SER:OG	4:C:575:LEU:N	2.43	0.46
5:D:525:MET:O	5:D:548:VAL:HG23	2.16	0.46
4:C:575:LEU:HD21	4:C:579:ALA:HB3	1.98	0.46
5:D:284:ASP:C	5:D:285:LEU:HD12	2.41	0.46
5:D:513:MET:SD	5:D:631:TYR:CD2	3.07	0.46
5:D:584:PRO:HD3	5:D:620:PHE:CD1	2.50	0.46
4:C:262:TYR:OH	4:C:280:ASP:OD2	2.16	0.46
4:C:948:ILE:O	4:C:952:GLN:HG3	2.16	0.46
4:C:1210:ILE:HD12	4:C:1227:VAL:HG21	1.97	0.46
3:A:164:ASP:OD1	3:A:165:GLU:N	2.45	0.46
4:C:1160:ASP:O	4:C:1162:SER:N	2.49	0.46
4:C:1290:MET:HG2	4:C:1294:LYS:HD2	1.97	0.46
4:C:1291:LEU:HD23	4:C:1291:LEU:HA	1.70	0.46
5:D:306:LEU:HD23	5:D:307:LEU:HD23	1.98	0.46
5:D:694:SER:CB	5:D:738:ARG:HE	2.29	0.46
5:D:839:VAL:HG12	5:D:839:VAL:O	2.16	0.46
6:E:33:GLY:O	6:E:35:LYS:NZ	2.27	0.46
4:C:624:ASP:C	4:C:626:GLU:H	2.23	0.46
4:C:1288:GLN:NE2	4:C:1317:PRO:HB3	2.31	0.46
5:D:69:GLU:HG2	5:D:76:LYS:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:185:ILE:HD13	5:D:188:LEU:HD12	1.97	0.46
5:D:201:LEU:HD11	5:D:220:ARG:NH1	2.27	0.46
5:D:1316:THR:HG22	5:D:1317:GLU:N	2.30	0.46
2:T:19:DC:C2	2:T:20:DG:C8	3.03	0.46
4:C:1256:GLN:HE21	5:D:99:ARG:HH22	1.64	0.46
5:D:244:VAL:HG12	5:D:269:TYR:HE1	1.79	0.46
5:D:958:ILE:HG23	5:D:982:LEU:HD11	1.96	0.46
5:D:1097:ALA:HB1	5:D:1099:TYR:CZ	2.51	0.46
5:D:1357:ILE:HG22	5:D:1359:ALA:H	1.81	0.46
4:C:839:VAL:HG12	4:C:1049:ILE:HG12	1.98	0.45
4:C:958:LYS:O	4:C:962:GLU:HB3	2.16	0.45
4:C:996:ARG:O	4:C:997:TRP:HD1	1.99	0.45
4:C:1279:GLU:HG2	5:D:1357:ILE:HD13	1.99	0.45
5:D:45:ASN:C	5:D:47:ARG:H	2.24	0.45
5:D:1046:ILE:HD12	5:D:1059:LEU:HB3	1.98	0.45
5:D:1226:VAL:O	5:D:1229:VAL:HG12	2.16	0.45
3:B:166:ARG:HB3	3:B:167:PRO:HD2	1.99	0.45
4:C:413:GLU:OE1	4:C:413:GLU:N	2.49	0.45
4:C:453:ILE:HD12	4:C:587:LEU:HD21	1.99	0.45
5:D:810:THR:HG23	5:D:811:GLU:N	2.31	0.45
6:E:15:ASN:HD22	6:E:18:ASP:CG	2.24	0.45
4:C:165:HIS:O	4:C:167:SER:N	2.49	0.45
4:C:690:VAL:HG12	4:C:1234:LYS:O	2.16	0.45
4:C:1024:GLU:O	4:C:1028:LYS:HG3	2.17	0.45
5:D:113:HIS:HB3	5:D:116:PHE:HD2	1.81	0.45
4:C:138:ILE:HG13	4:C:143:ARG:HD3	1.98	0.45
4:C:1018:TYR:CZ	4:C:1022:LYS:HD3	2.51	0.45
5:D:1144:LEU:HD23	5:D:1144:LEU:HA	1.73	0.45
2:T:6:DT:H2''	2:T:7:DA:C8	2.50	0.45
3:B:181:GLU:HA	5:D:535:ARG:HH11	1.82	0.45
4:C:145:ILE:HB	4:C:456:VAL:HG22	1.99	0.45
4:C:672:GLU:OE1	4:C:672:GLU:N	2.41	0.45
4:C:1018:TYR:HA	4:C:1021:LEU:HD12	1.98	0.45
4:C:1108:ASN:C	4:C:1110:GLY:H	2.24	0.45
4:C:1165:SER:O	4:C:1168:GLU:N	2.49	0.45
5:D:1144:LEU:HD11	5:D:1236:GLU:CG	2.47	0.45
2:T:15:DA:H2'	2:T:16:DC:C6	2.52	0.45
4:C:598:VAL:HA	4:C:627:GLY:O	2.16	0.45
5:D:683:ILE:HD11	5:D:754:ILE:HD13	1.99	0.45
3:B:78:ILE:O	3:B:82:LEU:HD13	2.17	0.45
4:C:144:VAL:HG23	4:C:515:MET:HB2	1.97	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:217:THR:HG23	4:C:351:LEU:HD21	1.97	0.45
4:C:854:ILE:HD12	4:C:862:LEU:HD21	1.98	0.45
4:C:976:ARG:NH2	4:C:989:LEU:HG	2.32	0.45
4:C:1005:GLU:HB3	4:C:1006:GLU:OE1	2.17	0.45
5:D:416:ILE:HG13	5:D:441:LEU:HD11	1.98	0.45
5:D:986:ASP:OD2	5:D:990:ARG:HB3	2.17	0.45
5:D:1195:GLN:C	5:D:1196:LEU:HD12	2.42	0.45
5:D:1344:LEU:HD23	5:D:1344:LEU:HA	1.54	0.45
3:B:51:MET:HB3	3:B:51:MET:HE3	1.72	0.45
4:C:519:ASN:OD1	4:C:520:PRO:HD2	2.17	0.45
4:C:1246:ARG:HH21	4:C:1249:GLY:N	2.15	0.45
5:D:373:ALA:O	5:D:376:LEU:N	2.49	0.45
5:D:741:ALA:O	5:D:762:ASN:ND2	2.27	0.45
5:D:814:CYS:SG	5:D:883:ARG:NH2	2.89	0.45
5:D:1162:ILE:HG13	5:D:1163:VAL:H	1.80	0.45
3:A:135:ASP:HB3	3:A:138:ALA:HB3	1.99	0.45
3:B:19:VAL:O	3:B:21:SER:N	2.50	0.45
3:B:100:LEU:HB2	3:B:144:ILE:CG1	2.46	0.45
5:D:37:GLU:O	5:D:61:ILE:HD11	2.17	0.45
5:D:103:GLY:C	5:D:244:VAL:HG22	2.42	0.45
5:D:113:HIS:HD2	5:D:239:LEU:HD11	1.81	0.45
5:D:490:ILE:HD11	5:D:609:TYR:CE1	2.52	0.45
5:D:573:THR:O	5:D:574:VAL:C	2.60	0.45
4:C:110:PRO:O	4:C:112:GLY:N	2.48	0.45
4:C:152:SER:O	4:C:153:PRO:C	2.59	0.45
4:C:511:LEU:HD23	4:C:511:LEU:HA	1.77	0.45
4:C:1233:LEU:N	4:C:1233:LEU:HD12	2.32	0.45
5:D:526:VAL:C	5:D:527:LEU:HD12	2.42	0.45
3:A:171:LEU:HD12	3:A:171:LEU:N	2.32	0.44
4:C:803:ALA:HB2	4:C:1227:VAL:HG12	1.99	0.44
5:D:127:LEU:HD21	5:D:234:PRO:HB3	1.98	0.44
5:D:268:LEU:HD21	5:D:324:LEU:HD11	1.99	0.44
5:D:279:LEU:HD12	5:D:295:GLU:HG3	1.99	0.44
5:D:343:LEU:HD23	5:D:343:LEU:HA	1.75	0.44
5:D:1356:LEU:HD23	5:D:1356:LEU:HA	1.79	0.44
2:T:17:DA:H2'	2:T:18:DT:O4'	2.17	0.44
3:A:177:TYR:O	3:A:178:SER:C	2.60	0.44
4:C:1246:ARG:NH1	4:C:1258:PRO:HB3	2.31	0.44
5:D:380:PHE:CD1	5:D:380:PHE:N	2.84	0.44
5:D:534:GLU:HA	5:D:578:ILE:HD11	1.98	0.44
5:D:921:GLN:O	5:D:922:SER:C	2.60	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1031:VAL:HG21	5:D:1088:VAL:HG11	1.99	0.44
5:D:1034:PHE:HB3	5:D:1036:ARG:HG3	1.98	0.44
5:D:1061:VAL:O	5:D:1104:LYS:N	2.50	0.44
5:D:1357:ILE:O	5:D:1362:GLY:HA3	2.17	0.44
4:C:727:VAL:HG12	4:C:728:ASP:N	2.33	0.44
5:D:308:ASP:OD2	5:D:311:ARG:NE	2.22	0.44
5:D:495:ASN:ND2	5:D:1247:LYS:HB2	2.30	0.44
5:D:780:ARG:O	5:D:781:LYS:C	2.60	0.44
1:N:25:DG:O3'	4:C:542:ARG:HD3	2.17	0.44
4:C:153:PRO:O	4:C:401:GLY:HA2	2.16	0.44
4:C:367:TYR:CZ	4:C:371:ARG:HD2	2.52	0.44
4:C:985:GLU:O	4:C:989:LEU:HB2	2.14	0.44
4:C:1296:ASP:OD1	4:C:1321:GLU:HB3	2.18	0.44
4:C:1336:ASN:HB2	5:D:25:ALA:HB2	1.99	0.44
5:D:139:LEU:HD23	5:D:139:LEU:HA	1.75	0.44
5:D:598:LYS:O	5:D:601:ILE:HG22	2.17	0.44
4:C:1314:GLN:HG3	6:E:28:ARG:NH2	2.33	0.44
5:D:40:LYS:HB3	5:D:42:GLU:OE1	2.17	0.44
3:B:44:ARG:HG3	3:B:183:ILE:HD11	1.99	0.44
3:B:166:ARG:HH11	3:B:170:ARG:HH22	1.64	0.44
4:C:615:VAL:HG21	4:C:645:PHE:HD2	1.83	0.44
5:D:117:LEU:HD13	5:D:118:LYS:HG3	2.00	0.44
5:D:514:THR:HG23	5:D:514:THR:O	2.18	0.44
5:D:1216:ALA:O	5:D:1220:ILE:HG12	2.17	0.44
4:C:631:GLU:N	4:C:631:GLU:OE1	2.51	0.44
5:D:224:LEU:HA	5:D:224:LEU:HD23	1.61	0.44
5:D:709:ARG:NH1	5:D:713:GLU:H	2.13	0.44
5:D:1250:ASP:O	5:D:1251:LYS:C	2.60	0.44
6:E:3:ARG:NH1	6:E:55:GLU:OE2	2.51	0.44
7:R:7:G:C4	7:R:8:A:C8	3.06	0.44
1:N:11:DC:N3	1:N:12:DA:N6	2.65	0.44
4:C:998:LEU:HA	4:C:1015:ALA:CB	2.47	0.44
5:D:885:VAL:HG12	5:D:1258:ARG:HD2	1.99	0.44
6:E:15:ASN:C	6:E:17:PHE:H	2.25	0.44
2:T:16:DC:H4'	4:C:1273:MET:HE2	1.99	0.44
4:C:138:ILE:CG1	4:C:143:ARG:HD3	2.48	0.44
4:C:468:LEU:HA	4:C:468:LEU:HD23	1.71	0.44
4:C:628:HIS:HB3	4:C:647:ARG:HH21	1.83	0.44
4:C:699:LEU:HA	4:C:699:LEU:HD23	1.79	0.44
5:D:55:GLY:C	5:D:57:PHE:H	2.26	0.44
5:D:380:PHE:HE2	5:D:419:HIS:CE1	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:102:LEU:O	4:C:116:ASP:HA	2.18	0.43
4:C:320:ASP:O	4:C:324:LYS:HG3	2.18	0.43
4:C:433:ILE:HG22	4:C:437:ASN:HD21	1.83	0.43
3:A:48:LEU:HA	3:A:48:LEU:HD23	1.57	0.43
4:C:369:MET:HG3	4:C:370:MET:N	2.33	0.43
5:D:810:THR:HG23	5:D:811:GLU:H	1.82	0.43
5:D:1041:ILE:CG2	5:D:1044:GLN:HB2	2.48	0.43
7:R:8:A:C6	7:R:9:U:C4	3.06	0.43
3:B:93:GLN:CG	3:B:94:GLY:H	2.22	0.43
4:C:165:HIS:C	4:C:167:SER:H	2.26	0.43
4:C:1151:LEU:C	4:C:1151:LEU:HD12	2.43	0.43
5:D:495:ASN:OD1	5:D:495:ASN:N	2.49	0.43
5:D:959:LYS:O	5:D:982:LEU:HD12	2.19	0.43
1:N:13:DT:C2'	1:N:14:DT:H71	2.48	0.43
3:A:14:VAL:HG12	3:A:27:THR:O	2.18	0.43
3:B:16:ILE:HG12	3:B:16:ILE:O	2.18	0.43
3:B:57:THR:HG23	3:B:158:ARG:CZ	2.49	0.43
4:C:12:ARG:HH21	4:C:793:GLU:CD	2.23	0.43
4:C:498:ILE:HD12	4:C:498:ILE:H	1.83	0.43
4:C:1010:GLN:O	4:C:1014:LEU:HB2	2.18	0.43
5:D:646:ILE:HD11	5:D:762:ASN:HD21	1.82	0.43
6:E:21:LEU:HA	6:E:21:LEU:HD23	1.79	0.43
3:B:100:LEU:HB2	3:B:144:ILE:HD11	1.98	0.43
4:C:620:ASN:HD21	5:D:768:ASN:CB	2.31	0.43
4:C:836:LEU:N	4:C:836:LEU:HD12	2.33	0.43
5:D:416:ILE:O	5:D:417:ARG:C	2.61	0.43
5:D:802:ASP:OD1	5:D:1348:LYS:NZ	2.31	0.43
5:D:986:ASP:HB3	5:D:992:LYS:HD2	2.00	0.43
5:D:1031:VAL:C	5:D:1117:SER:HA	2.44	0.43
5:D:1081:VAL:HA	5:D:1088:VAL:H	1.84	0.43
7:R:5:G:H2'	7:R:6:C:C6	2.53	0.43
3:B:117:HIS:CD2	3:B:119:GLY:H	2.36	0.43
4:C:699:LEU:HG	4:C:799:ASN:HD22	1.83	0.43
4:C:705:GLU:OE1	4:C:705:GLU:N	2.39	0.43
4:C:1251:TYR:OH	4:C:1301:ARG:HD2	2.18	0.43
5:D:364:HIS:O	5:D:364:HIS:CG	2.70	0.43
5:D:541:LEU:HA	5:D:541:LEU:HD23	1.79	0.43
5:D:1009:GLU:O	5:D:1011:VAL:HG13	2.18	0.43
3:B:28:LEU:HA	3:B:28:LEU:HD23	1.81	0.43
4:C:53:PHE:HE1	4:C:468:LEU:HD11	1.82	0.43
4:C:551:HIS:H	4:C:554:HIS:CE1	2.36	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:722:GLY:HA2	4:C:737:ASN:CG	2.44	0.43
4:C:976:ARG:O	4:C:980:VAL:HG23	2.17	0.43
5:D:363:LEU:HD12	5:D:363:LEU:O	2.17	0.43
5:D:548:VAL:HG12	5:D:573:THR:HA	2.01	0.43
5:D:788:LEU:H	5:D:788:LEU:HG	1.53	0.43
5:D:1138:LEU:HD12	5:D:1138:LEU:HA	1.81	0.43
5:D:1157:ALA:HB2	5:D:1210:ILE:HD11	2.01	0.43
3:B:30:PRO:C	3:B:31:LEU:HD12	2.44	0.43
4:C:724:VAL:HA	4:C:734:ILE:HD13	2.01	0.43
5:D:316:ILE:O	5:D:316:ILE:HG13	2.18	0.43
5:D:596:LEU:HD23	5:D:596:LEU:HA	1.74	0.43
5:D:825:VAL:HG22	5:D:833:GLU:HB2	2.01	0.43
5:D:1006:GLY:H	5:D:1009:GLU:CD	2.27	0.43
5:D:1173:ARG:HB3	5:D:1192:LYS:HD2	2.00	0.43
5:D:1344:LEU:O	5:D:1345:ARG:C	2.62	0.43
3:A:43:LEU:HA	3:A:43:LEU:HD23	1.86	0.43
3:B:85:LEU:HD23	3:B:85:LEU:HA	1.71	0.43
3:B:171:LEU:HD23	3:B:171:LEU:HA	1.83	0.43
3:B:181:GLU:HG2	5:D:535:ARG:HH12	1.84	0.43
3:B:192:VAL:CG1	3:B:193:GLU:H	2.26	0.43
4:C:211:ARG:NH2	4:C:217:THR:OG1	2.46	0.43
4:C:632:ASP:HA	4:C:647:ARG:HD2	2.01	0.43
4:C:1080:ASN:HD22	4:C:1085:MET:HE1	1.84	0.43
4:C:1313:HIS:HD2	6:E:31:GLN:HE22	1.66	0.43
4:C:1329:GLU:O	4:C:1332:SER:OG	2.28	0.43
5:D:117:LEU:CD1	5:D:118:LYS:HG3	2.49	0.43
5:D:720:ASN:O	5:D:723:TYR:N	2.51	0.43
3:A:149:GLY:HA3	3:A:177:TYR:CE1	2.53	0.43
3:B:56:VAL:HG22	3:B:146:VAL:HG12	2.01	0.43
4:C:211:ARG:HH21	4:C:351:LEU:HD11	1.83	0.43
4:C:1328:LYS:HD3	4:C:1328:LYS:HA	1.88	0.43
5:D:1284:ARG:O	5:D:1287:ILE:HG13	2.18	0.43
5:D:1360:GLY:O	5:D:1361:THR:C	2.60	0.43
6:E:58:LEU:HD12	6:E:59:ILE:HG12	2.01	0.43
3:B:104:LYS:C	3:B:139:SER:HG	2.24	0.42
4:C:747:GLY:HA2	4:C:974:ARG:HE	1.84	0.42
5:D:97:VAL:HG12	5:D:101:ARG:HG3	2.01	0.42
5:D:1051:ASP:OD1	5:D:1052:GLU:N	2.52	0.42
1:N:12:DA:H2'	1:N:13:DT:C7	2.48	0.42
3:A:211:ILE:HA	3:A:211:ILE:HD13	1.80	0.42
4:C:1078:LYS:HG2	4:C:1079:ILE:H	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:1235:LEU:HD23	4:C:1235:LEU:HA	1.66	0.42
5:D:850:LYS:HB3	5:D:855:ASP:HB2	2.00	0.42
3:A:107:ILE:HG13	3:A:135:ASP:O	2.19	0.42
4:C:69:GLN:NE2	4:C:101:ARG:HD2	2.21	0.42
4:C:221:LEU:HA	4:C:221:LEU:HD23	1.84	0.42
4:C:580:GLN:NE2	4:C:605:TYR:OH	2.51	0.42
4:C:1113:LEU:HD11	5:D:641:ILE:HD13	2.01	0.42
5:D:1145:PHE:O	5:D:1309:ILE:HG12	2.20	0.42
1:N:13:DT:H2''	1:N:14:DT:H71	2.01	0.42
3:A:57:THR:HG23	3:A:158:ARG:HH12	1.84	0.42
4:C:360:LEU:O	4:C:364:VAL:HG23	2.19	0.42
4:C:817:LEU:HD11	4:C:1080:ASN:HD21	1.84	0.42
4:C:847:PRO:O	4:C:889:PRO:HD3	2.19	0.42
5:D:211:GLU:HA	5:D:214:ARG:HD2	2.02	0.42
5:D:1163:VAL:HG22	5:D:1164:SER:N	2.34	0.42
5:D:735:ALA:O	5:D:738:ARG:HB3	2.20	0.42
5:D:1223:LEU:HA	5:D:1223:LEU:HD23	1.74	0.42
4:C:1000:LEU:HD12	4:C:1011:LEU:HD22	2.02	0.42
4:C:1053:TYR:C	4:C:1054:LEU:HD12	2.44	0.42
4:C:1211:ARG:CZ	4:C:1220:GLN:HE22	2.33	0.42
5:D:496:GLY:N	5:D:903:LEU:HD23	2.34	0.42
5:D:858:VAL:HG12	5:D:868:TRP:CZ3	2.54	0.42
5:D:1098:GLN:O	5:D:1098:GLN:HG2	2.19	0.42
5:D:268:LEU:HD23	5:D:268:LEU:HA	1.82	0.42
5:D:288:PRO:HG2	5:D:291:ILE:HD12	2.00	0.42
5:D:424:ASN:OD1	5:D:424:ASN:C	2.63	0.42
3:B:35:PHE:CA	3:B:38:THR:HG22	2.47	0.42
3:B:73:GLY:O	3:B:133:LEU:HA	2.20	0.42
4:C:28:LEU:HD23	4:C:28:LEU:HA	1.85	0.42
4:C:146:VAL:HG13	4:C:529:ARG:HB3	2.02	0.42
4:C:494:ASN:O	4:C:497:PRO:HD2	2.19	0.42
4:C:658:GLN:O	4:C:660:VAL:N	2.53	0.42
4:C:1096:ILE:HD13	4:C:1096:ILE:HG21	1.73	0.42
4:C:1145:ILE:HD12	4:C:1145:ILE:HG23	1.77	0.42
5:D:24:LEU:HA	5:D:24:LEU:HD23	1.88	0.42
5:D:147:ILE:HG13	5:D:147:ILE:O	2.19	0.42
5:D:1089:LEU:HD23	5:D:1096:PRO:HG3	2.00	0.42
3:B:66:HIS:NE2	3:B:68:TYR:HD2	2.17	0.42
4:C:88:ARG:HG3	4:C:934:PHE:CE1	2.55	0.42
4:C:529:ARG:HH11	4:C:572:ILE:HG22	1.84	0.42
4:C:1276:TRP:CZ2	5:D:801:VAL:HG21	2.55	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:131:PRO:HG2	5:D:134:ASP:OD2	2.20	0.42
2:T:30:DG:H2"	2:T:31:DG:N7	2.35	0.42
3:B:228:LEU:HD23	3:B:228:LEU:HA	1.62	0.42
4:C:945:ALA:O	4:C:949:GLU:HB2	2.19	0.42
4:C:1204:LEU:HD23	4:C:1204:LEU:HA	1.84	0.42
4:C:1287:LEU:HD22	5:D:1357:ILE:HD11	2.02	0.42
4:C:1293:VAL:HG11	4:C:1304:MET:HG2	2.01	0.42
4:C:1333:LEU:HD22	5:D:307:LEU:HD22	2.01	0.42
5:D:442:ILE:HD13	5:D:442:ILE:HA	1.85	0.42
5:D:579:LEU:HA	5:D:579:LEU:HD12	1.83	0.42
5:D:968:ASN:ND2	5:D:972:LYS:HB2	2.34	0.42
6:E:64:LEU:HD23	6:E:64:LEU:HA	1.84	0.42
4:C:188:PHE:CE1	4:C:194:LEU:HD13	2.54	0.41
4:C:205:PRO:O	4:C:208:ILE:HG22	2.21	0.41
4:C:228:VAL:HB	4:C:335:THR:OG1	2.20	0.41
4:C:519:ASN:ND2	4:C:689:ALA:HB3	2.36	0.41
5:D:450:HIS:CE1	5:D:452:LEU:H	2.38	0.41
5:D:538:ARG:NH1	5:D:634:ARG:HH12	2.18	0.41
4:C:1088:ASP:O	4:C:1090:ASN:N	2.53	0.41
4:C:1292:THR:HG21	4:C:1317:PRO:HA	2.02	0.41
5:D:80:HIS:O	5:D:83:VAL:HG12	2.20	0.41
5:D:146:VAL:HG22	5:D:178:ALA:HB2	2.01	0.41
5:D:509:GLY:O	5:D:510:LEU:C	2.61	0.41
2:T:5:DC:H2"	2:T:6:DT:C6	2.55	0.41
2:T:6:DT:H2"	2:T:7:DA:H8	1.85	0.41
3:A:70:THR:CG2	4:C:755:LYS:HE2	2.50	0.41
3:B:33:ARG:HH11	4:C:1081:PRO:HG3	1.86	0.41
4:C:138:ILE:HD13	4:C:138:ILE:HA	1.88	0.41
4:C:184:LEU:HD12	4:C:184:LEU:HA	1.76	0.41
4:C:252:SER:C	4:C:265:LYS:HG3	2.45	0.41
4:C:569:ILE:HG22	4:C:570:GLY:N	2.35	0.41
4:C:865:LEU:HD22	4:C:869:GLY:O	2.20	0.41
5:D:385:LEU:HD23	5:D:385:LEU:HA	1.78	0.41
4:C:184:LEU:HD13	4:C:389:PHE:HZ	1.84	0.41
4:C:800:MET:HB2	4:C:800:MET:HE3	1.80	0.41
4:C:1247:SER:O	4:C:1248:THR:OG1	2.30	0.41
5:D:120:LEU:HA	5:D:121:PRO:HA	1.84	0.41
5:D:615:LYS:HB2	5:D:616:PRO:HD3	2.02	0.41
5:D:1162:ILE:HG22	5:D:1178:THR:HB	2.01	0.41
5:D:1326:GLN:C	5:D:1327:GLU:OE1	2.63	0.41
3:A:85:LEU:HD23	3:A:85:LEU:HA	1.85	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:A:234:LEU:HD12	3:A:234:LEU:HA	1.89	0.41
4:C:184:LEU:HD22	4:C:389:PHE:CE2	2.56	0.41
4:C:533:LEU:HA	4:C:533:LEU:HD23	1.83	0.41
5:D:818:GLU:OE1	5:D:818:GLU:N	2.52	0.41
4:C:944:ARG:NE	4:C:948:ILE:HD11	2.36	0.41
4:C:1100:PRO:C	4:C:1102:GLY:N	2.78	0.41
5:D:482:ALA:O	5:D:483:LEU:HD23	2.21	0.41
5:D:848:VAL:HB	5:D:858:VAL:HG22	2.02	0.41
5:D:870:ASP:O	5:D:874:GLU:HG2	2.20	0.41
5:D:1230:THR:O	5:D:1234:VAL:HG22	2.21	0.41
6:E:8:ASP:HB2	6:E:55:GLU:HG2	2.03	0.41
4:C:139:ASN:O	4:C:141:THR:N	2.53	0.41
4:C:561:ILE:O	4:C:563:THR:HG22	2.20	0.41
4:C:685:MET:CE	4:C:1071:GLY:HA2	2.51	0.41
5:D:205:LEU:HD23	5:D:205:LEU:HA	1.89	0.41
5:D:355:ILE:HD13	5:D:355:ILE:HG21	1.83	0.41
5:D:397:ALA:O	5:D:400:MET:HB2	2.20	0.41
4:C:202:ARG:HH21	4:C:369:MET:CB	2.33	0.41
4:C:624:ASP:C	4:C:626:GLU:N	2.79	0.41
4:C:684:ASN:O	4:C:687:ARG:N	2.54	0.41
4:C:883:LEU:HA	4:C:883:LEU:HD23	1.76	0.41
4:C:1278:LEU:HA	4:C:1278:LEU:HD23	1.75	0.41
5:D:55:GLY:O	5:D:58:CYS:N	2.38	0.41
5:D:306:LEU:HD23	5:D:306:LEU:C	2.46	0.41
5:D:926:PRO:O	5:D:927:GLY:C	2.63	0.41
5:D:1167:LYS:HB3	5:D:1174:ARG:NH1	2.35	0.41
3:B:15:ASP:OD1	3:B:15:ASP:C	2.62	0.41
4:C:61:SER:O	4:C:63:SER:N	2.52	0.41
4:C:91:THR:OG1	4:C:93:SER:HB3	2.21	0.41
4:C:100:LEU:HD12	4:C:122:VAL:HG11	2.02	0.41
4:C:331:LYS:O	4:C:332:ARG:NH2	2.46	0.41
4:C:404:LYS:HA	4:C:404:LYS:HD2	1.90	0.41
4:C:629:PHE:N	4:C:629:PHE:CD1	2.89	0.41
5:D:55:GLY:C	5:D:57:PHE:N	2.78	0.41
5:D:581:MET:HE2	5:D:581:MET:HB3	1.88	0.41
5:D:605:LEU:HA	5:D:605:LEU:HD12	1.74	0.41
5:D:810:THR:HG22	5:D:893:GLY:HA3	2.02	0.41
5:D:930:LEU:HD23	5:D:930:LEU:HA	1.86	0.41
5:D:950:ILE:H	5:D:1018:ALA:HB3	1.86	0.41
5:D:978:ARG:HH21	5:D:1025:MET:HE1	1.86	0.41
5:D:1030:GLU:HG2	5:D:1031:VAL:HG13	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:D:1061:VAL:O	5:D:1104:LYS:CA	2.69	0.41
5:D:1261:LEU:HD12	5:D:1261:LEU:O	2.21	0.41
5:D:1314:LEU:HA	5:D:1314:LEU:HD23	1.87	0.41
3:B:85:LEU:O	3:B:86:LYS:C	2.64	0.41
3:B:92:VAL:HG12	3:B:93:GLN:O	2.21	0.41
4:C:572:ILE:HD12	4:C:572:ILE:HG23	1.64	0.41
4:C:605:TYR:O	4:C:606:LEU:HD12	2.21	0.41
4:C:687:ARG:HH11	4:C:687:ARG:HD3	1.73	0.41
4:C:862:LEU:HD23	4:C:862:LEU:HA	1.83	0.41
4:C:1308:ILE:HA	4:C:1308:ILE:HD13	1.85	0.41
5:D:356:THR:HG23	5:D:448:GLN:HG2	2.03	0.41
5:D:527:LEU:HB2	5:D:550:VAL:HG12	2.03	0.41
5:D:555:TYR:CE1	5:D:565:ALA:HB2	2.56	0.41
5:D:795:TYR:OH	5:D:1326:GLN:NE2	2.53	0.41
5:D:978:ARG:NH2	5:D:1198:VAL:HA	2.36	0.41
5:D:1035:VAL:HG12	5:D:1040:MET:SD	2.61	0.41
5:D:1172:LYS:HB2	5:D:1190:ILE:N	2.36	0.41
5:D:1263:LYS:NZ	5:D:1315:ALA:HB1	2.35	0.41
2:T:23:DT:H2''	2:T:24:DG:O4'	2.21	0.40
3:A:100:LEU:HD23	3:A:115:ILE:HG21	2.02	0.40
3:A:158:ARG:O	3:A:160:HIS:N	2.54	0.40
3:B:132:HIS:C	3:B:133:LEU:HD12	2.45	0.40
3:B:203:ILE:HG23	3:B:203:ILE:HD12	1.78	0.40
4:C:411:ARG:NH2	4:C:427:ASP:OD2	2.54	0.40
4:C:1079:ILE:HD12	4:C:1079:ILE:HG23	1.80	0.40
5:D:327:LEU:HD23	5:D:327:LEU:HA	1.88	0.40
5:D:426:ALA:HB3	5:D:427:PRO:HD3	2.03	0.40
5:D:548:VAL:HG22	5:D:549:LYS:N	2.36	0.40
5:D:555:TYR:CD2	5:D:585:LYS:HD2	2.56	0.40
5:D:876:SER:HB2	5:D:990:ARG:HH21	1.86	0.40
5:D:967:VAL:HG12	5:D:968:ASN:O	2.22	0.40
5:D:1039:ASP:O	5:D:1041:ILE:HD12	2.21	0.40
2:T:3:DA:H2''	2:T:4:DG:C8	2.56	0.40
3:B:208:ASN:OD1	3:B:208:ASN:C	2.64	0.40
4:C:761:GLN:O	4:C:762:ASN:HB2	2.22	0.40
3:B:83:LEU:O	3:B:86:LYS:N	2.55	0.40
4:C:130:MET:SD	4:C:134:GLY:HA2	2.62	0.40
4:C:569:ILE:HD13	4:C:569:ILE:HG21	1.81	0.40
5:D:1325:PHE:CZ	5:D:1326:GLN:HG3	2.56	0.40
2:T:26:DA:H2''	2:T:27:DA:C8	2.57	0.40
3:A:78:ILE:HD13	3:A:78:ILE:HA	1.89	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:7:GLU:C	4:C:9:LYS:N	2.80	0.40
4:C:150:HIS:CE1	4:C:454:ARG:HE	2.38	0.40
4:C:530:ILE:HG23	4:C:530:ILE:HD12	1.83	0.40
4:C:563:THR:OG1	4:C:564:PRO:HD2	2.22	0.40
4:C:633:LEU:CD1	4:C:644:LEU:HD23	2.51	0.40
5:D:222:LYS:HA	5:D:222:LYS:HD2	1.83	0.40
5:D:960:LEU:HD23	5:D:963:VAL:HG21	2.02	0.40
5:D:1216:ALA:HA	5:D:1217:PRO:HD3	1.93	0.40
1:N:38:DG:H2'	1:N:39:DC:C6	2.57	0.40
3:A:30:PRO:O	3:A:31:LEU:HD22	2.21	0.40
3:A:208:ASN:OD1	3:A:208:ASN:C	2.64	0.40
3:B:29:GLU:HB3	3:B:200:LYS:CG	2.51	0.40
3:B:72:GLU:O	3:B:74:VAL:HG23	2.21	0.40
3:B:224:LEU:HD23	3:B:224:LEU:HA	1.73	0.40
4:C:23:ASP:OD1	4:C:23:ASP:N	2.54	0.40
4:C:365:GLU:OE1	4:C:368:ARG:NH2	2.54	0.40
4:C:618:GLN:HE21	5:D:770:LEU:H	1.66	0.40
4:C:1255:THR:O	4:C:1255:THR:OG1	2.37	0.40
5:D:123:ARG:HA	5:D:123:ARG:HD3	1.91	0.40
5:D:242:LEU:HA	5:D:243:PRO:HD3	1.81	0.40
5:D:624:ILE:HD13	5:D:624:ILE:HA	1.82	0.40
5:D:703:THR:O	5:D:704:GLU:C	2.64	0.40
5:D:1173:ARG:CG	5:D:1174:ARG:H	2.28	0.40
7:R:9:U:C4	7:R:10:G:C6	3.10	0.40

There are no symmetry-related clashes.

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 PDB entries followed by that with respect to all EM entries.

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
3	A	226/329 (69%)	189 (84%)	37 (16%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	B	227/329 (69%)	187 (82%)	40 (18%)	0	100	100
4	C	1315/1342 (98%)	1076 (82%)	238 (18%)	1 (0%)	48	78
5	D	1330/1407 (94%)	1114 (84%)	215 (16%)	1 (0%)	48	78
6	E	71/91 (78%)	58 (82%)	13 (18%)	0	100	100
All	All	3169/3498 (91%)	2624 (83%)	543 (17%)	2 (0%)	49	78

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	D	56	LEU
4	C	1062	PRO

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 PDB entries followed by that with respect to all EM entries.

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	
3	A	196/286 (68%)	196 (100%)	0	100	100
3	B	197/286 (69%)	197 (100%)	0	100	100
4	C	1138/1157 (98%)	1137 (100%)	1 (0%)	88	89
5	D	1121/1168 (96%)	1117 (100%)	4 (0%)	84	83
6	E	63/75 (84%)	63 (100%)	0	100	100
All	All	2715/2972 (91%)	2710 (100%)	5 (0%)	85	85

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	C	817	LEU
5	D	128	LEU
5	D	1233	ILE
5	D	1255	VAL
5	D	1261	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
3	A	37	HIS
3	A	117	HIS
3	B	66	HIS
3	B	117	HIS
3	B	132	HIS
4	C	31	GLN
4	C	69	GLN
4	C	150	HIS
4	C	165	HIS
4	C	273	HIS
4	C	330	HIS
4	C	437	ASN
4	C	580	GLN
4	C	604	HIS
4	C	618	GLN
4	C	628	HIS
4	C	762	ASN
4	C	832	HIS
4	C	1080	ASN
4	C	1116	HIS
4	C	1146	GLN
4	C	1256	GLN
4	C	1313	HIS
5	D	164	GLN
5	D	196	GLN
5	D	232	ASN
5	D	266	ASN
5	D	276	ASN
5	D	419	HIS
5	D	469	HIS
5	D	477	GLN
5	D	817	HIS
5	D	1010	GLN
5	D	1049	GLN
5	D	1238	GLN
5	D	1268	ASN
5	D	1326	GLN
5	D	1366	HIS
5	D	1367	GLN
6	E	31	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
7	R	12/14 (85%)	4 (33%)	0

All (4) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	R	3	A
7	R	4	G
7	R	12	U
7	R	13	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

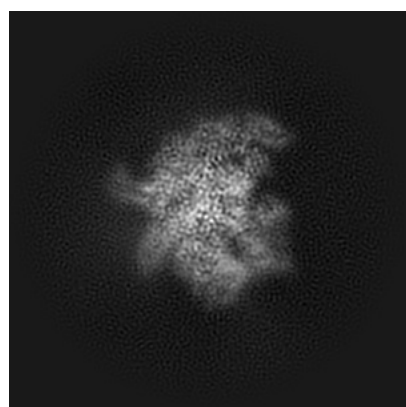
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-4893. These allow visual inspection of the internal detail of the map and identification of artifacts.

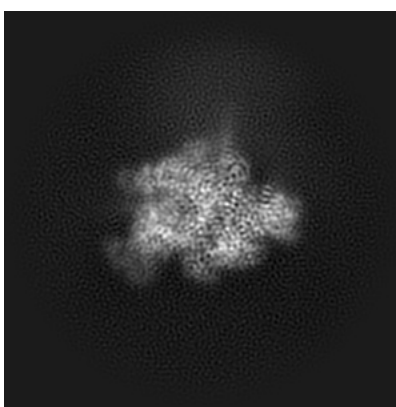
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

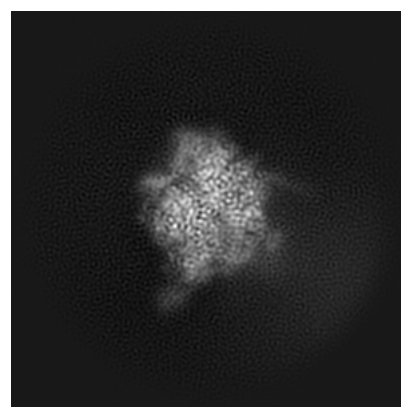
6.1.1 Primary map



X



Y

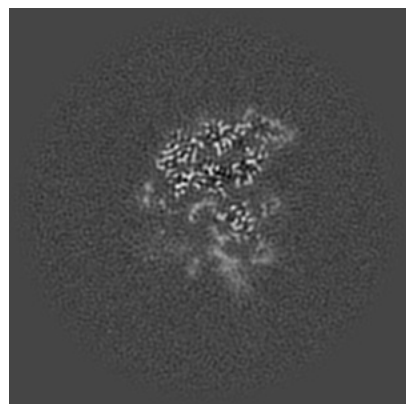


Z

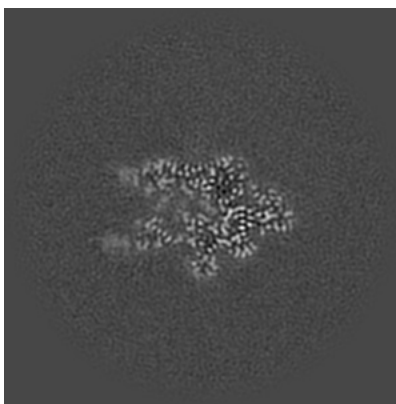
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

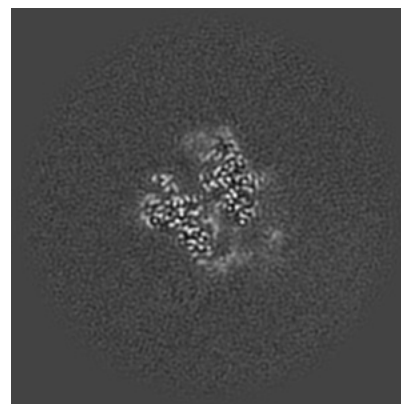
6.2.1 Primary map



X Index: 144



Y Index: 144

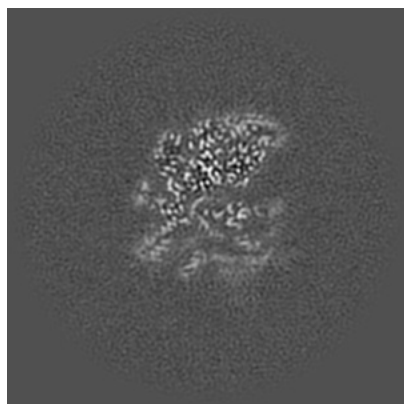


Z Index: 144

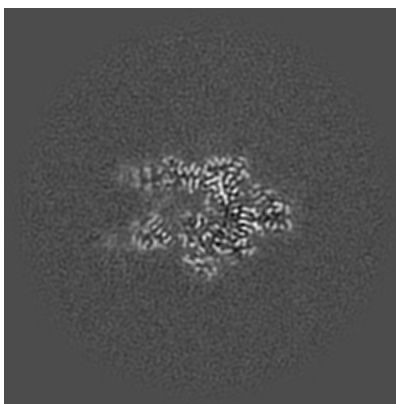
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

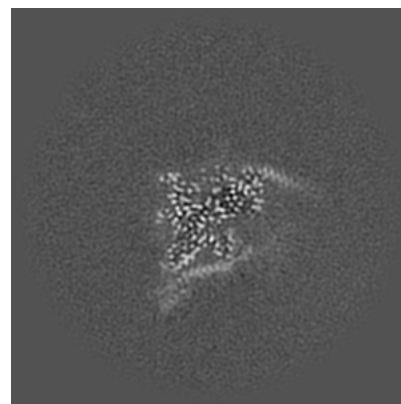
6.3.1 Primary map



X Index: 139



Y Index: 142

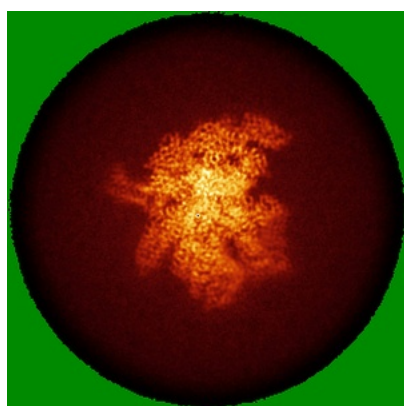


Z Index: 159

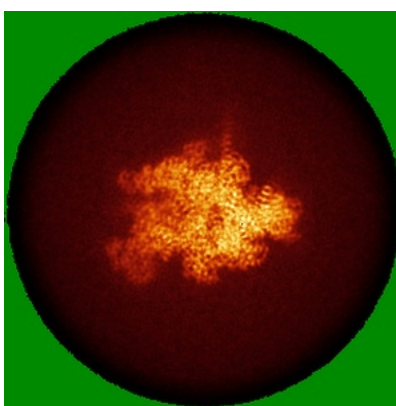
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) [i](#)

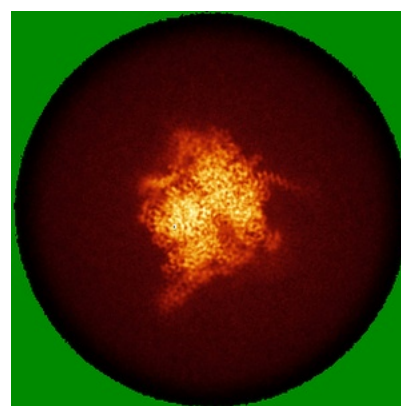
6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.6. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

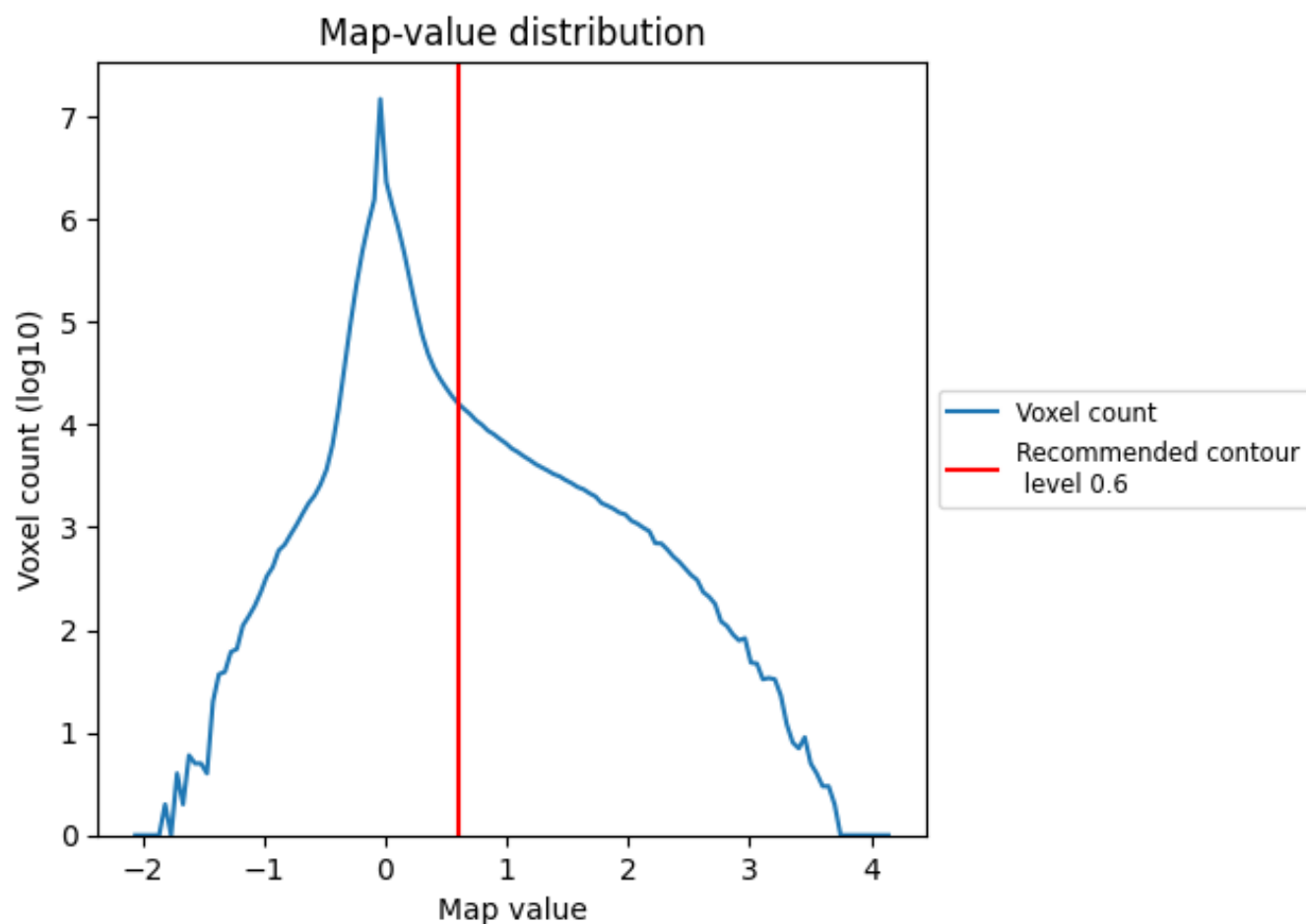
6.6 Mask visualisation [i](#)

This section was not generated. No masks/segmentation were deposited.

7 Map analysis [i](#)

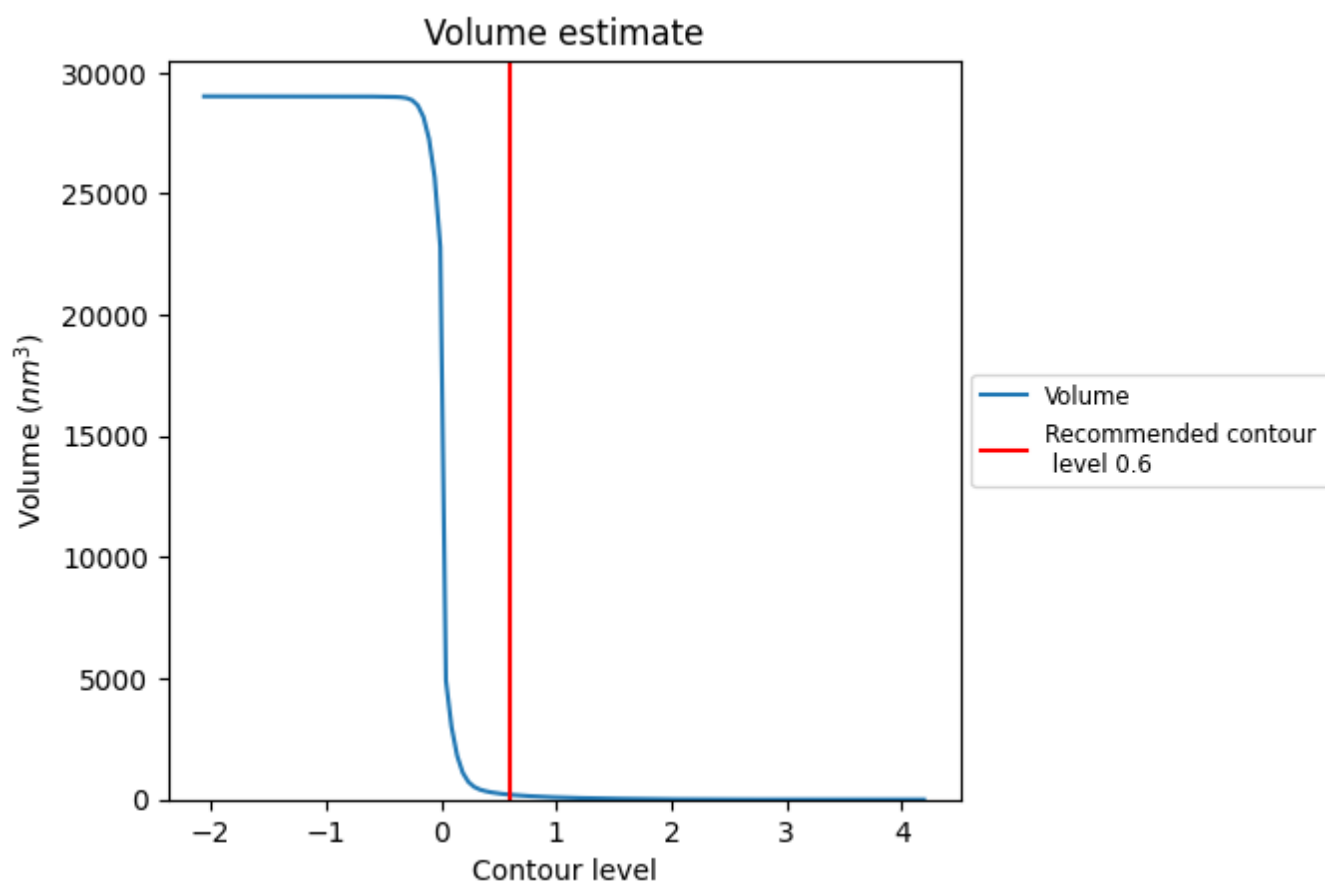
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

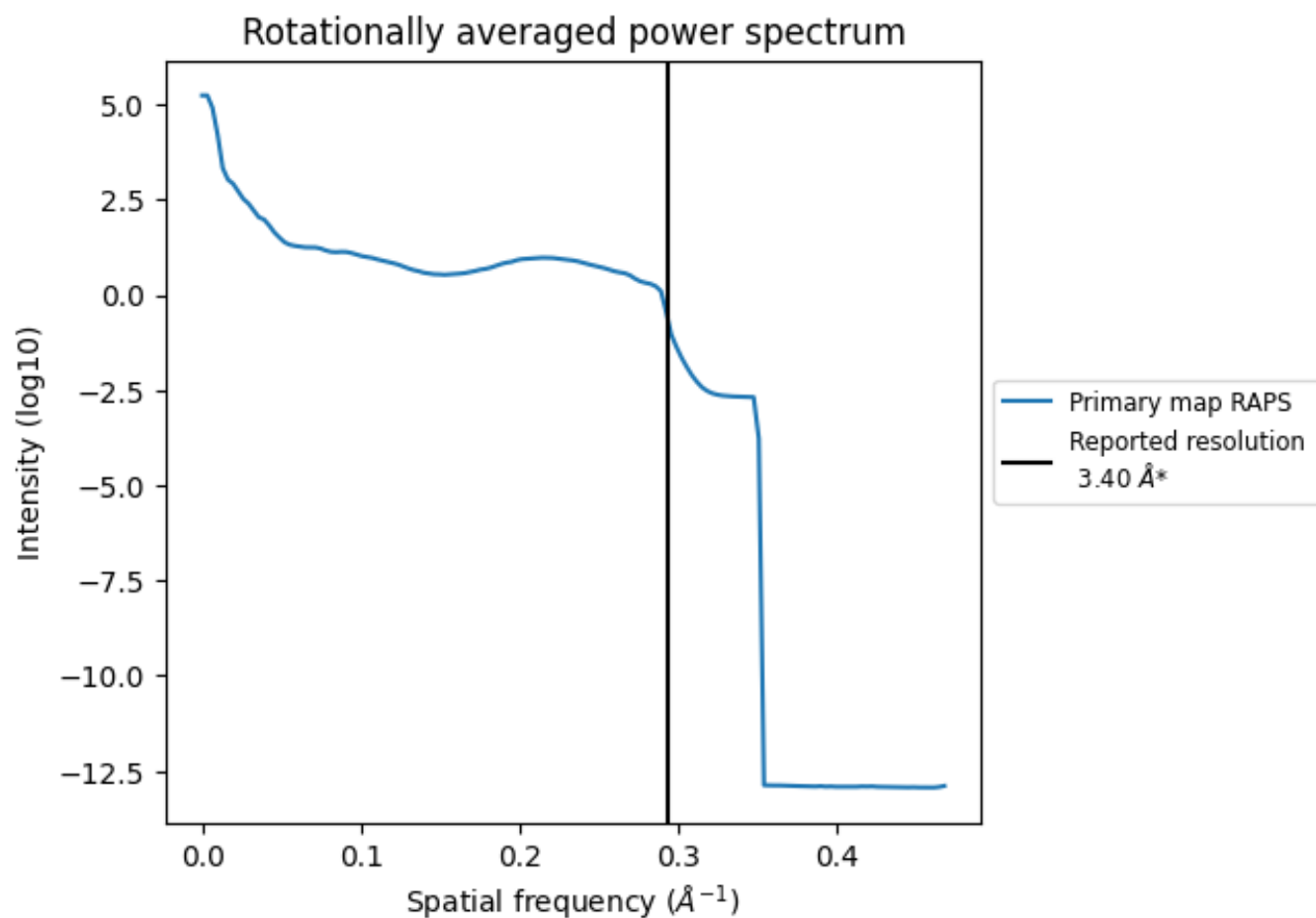
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 200 nm³; this corresponds to an approximate mass of 181 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.294 Å⁻¹

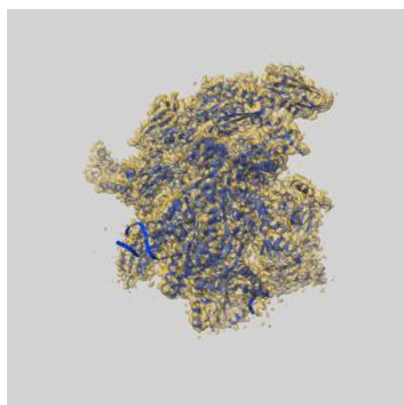
8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

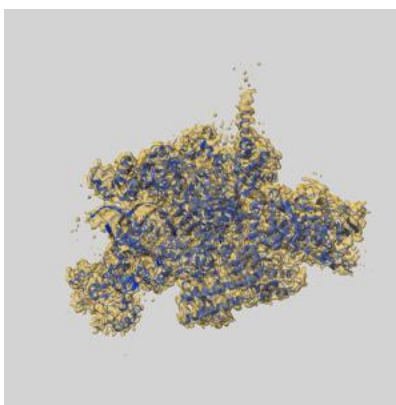
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-4893 and PDB model 6RIP. Per-residue inclusion information can be found in section [3](#) on page [6](#).

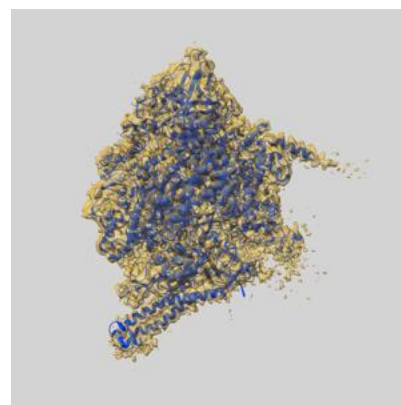
9.1 Map-model overlay [i](#)



X



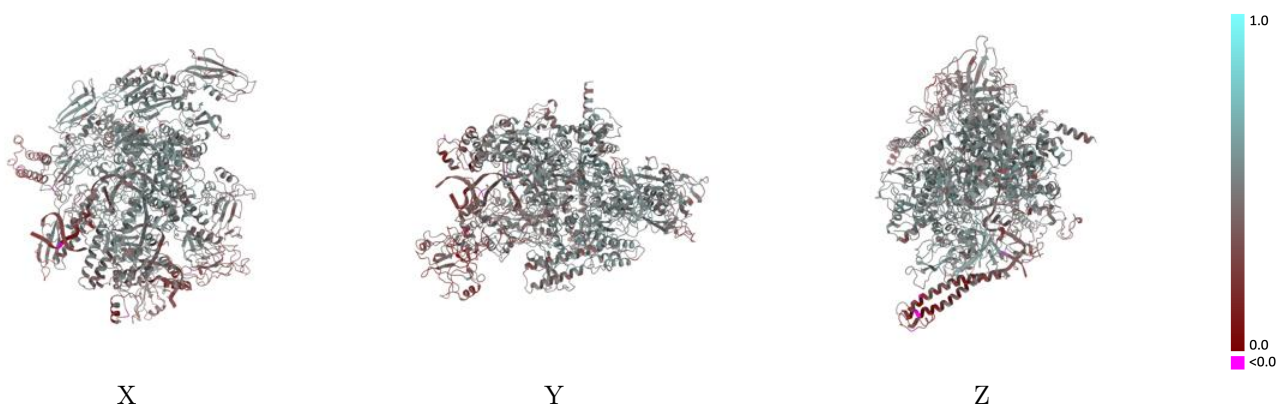
Y



Z

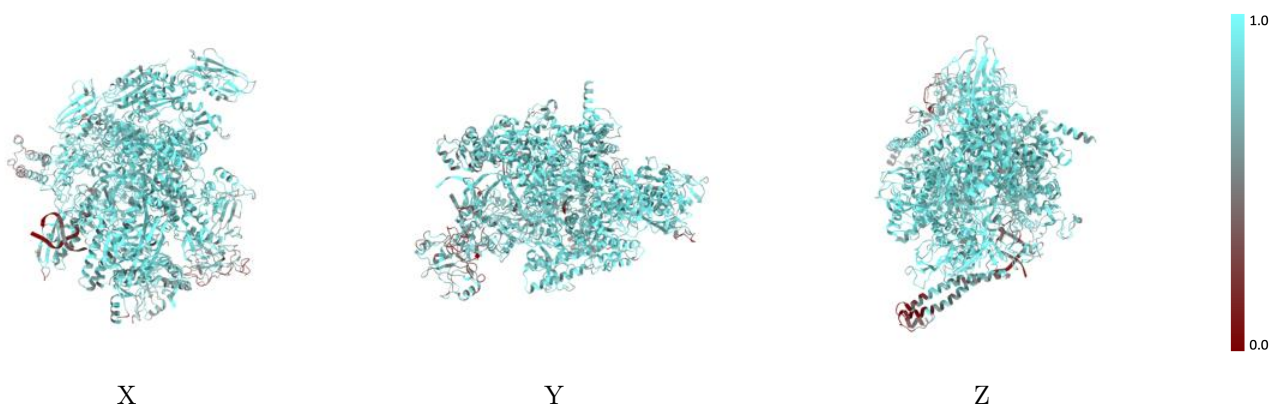
The images above show the 3D surface view of the map at the recommended contour level 0.6 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model [i](#)



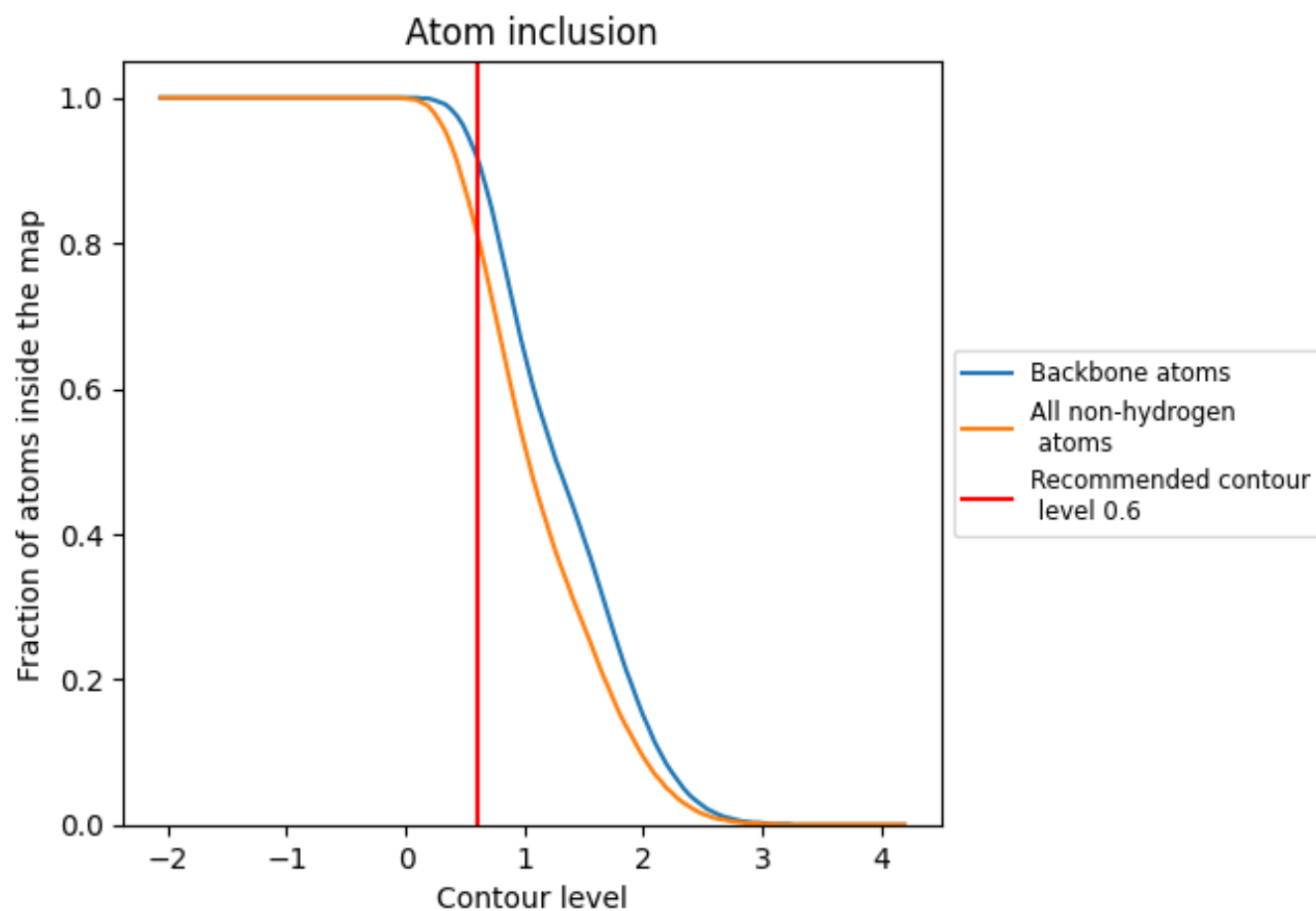
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.6).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 81% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.6) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8140	0.4560
A	0.8530	0.4940
B	0.8170	0.4640
C	0.8280	0.4650
D	0.8090	0.4550
E	0.8220	0.4750
N	0.5990	0.2930
R	0.7950	0.4000
T	0.7310	0.3310

1.0

0.0

<0.0