Full wwPDB EM Validation Report

Apr 18, 2024 – 05:55 pm BST

PDB ID	:	8PFG
EMDB ID	:	EMD-17646
Title	:	autoinhibited RfaH bound to E. coli transcription complex paused at ops site (encounter complex), not fully complementary scaffold
Authors	:	Zuber, P.K.; Said, N.; Hilal, T.; Loll, B.; Wahl, M.C.; Knauer, S.H.
Deposited on	:	2023-06-15
Resolution	:	3.10 Å(reported)

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:

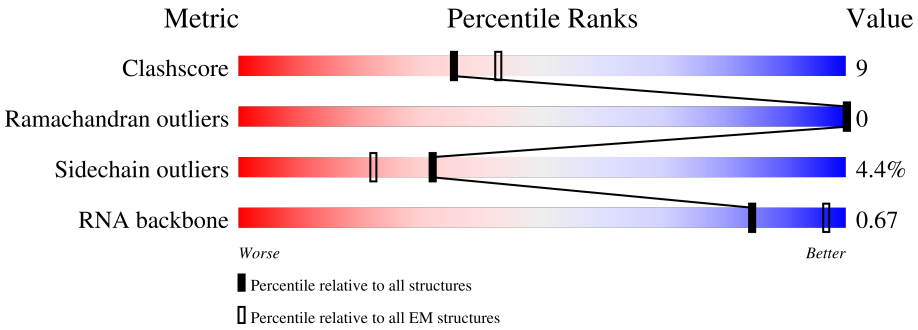
EMDB validation analysis	:	0.0.1.dev92
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 3.10 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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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 <=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	P	164	9% 57% 25% • 17%
2	I	1342	• 77% 20% ••
3	J	1416	• 70% 21% • 7%
4	K	91	12% 54% 35% • 9%
5	G	329	• 54% 16% 29%
5	H	329	48% 17% • 33%
6	R	17	6% 29% 29% 12% 29%

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Mol	Chain	Length	Quality of chain
7	B	40	30% 70%
8	A	40	8% 60% 40%

2 Entry composition

There are 10 unique types of molecules in this entry. The entry contains 27809 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 protein called Transcription antitermination protein RfaH.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	P	136	Total	C	N	O	S	0	0
			1080	693	190	190	7		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	-1	GLY	-	expression tag	UNP P0AFW0
P	0	HIS	-	expression tag	UNP P0AFW0
P	51	CYS	PHE	engineered mutation	UNP P0AFW0
P	139	CYS	SER	engineered mutation	UNP P0AFW0

- Molecule 2 is a protein called DNA-directed RNA polymerase subunit beta.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	I	1321	Total	C	N	O	S	0	0
			10423	6539	1816	2024	44		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	1317	Total	C	N	O	S	0	0
			10240	6434	1824	1936	46		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	1	VAL	-	expression tag	UNP P0A8T7
J	1408	LEU	-	expression tag	UNP P0A8T7
J	1409	GLU	-	expression tag	UNP P0A8T7
J	1410	VAL	-	expression tag	UNP P0A8T7
J	1411	HIS	-	expression tag	UNP P0A8T7
J	1412	HIS	-	expression tag	UNP P0A8T7
J	1413	HIS	-	expression tag	UNP P0A8T7

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Chain	Residue	Modelled	Actual	Comment	Reference
J	1414	HIS	-	expression tag	UNP P0A8T7
J	1415	HIS	-	expression tag	UNP P0A8T7
J	1416	HIS	-	expression tag	UNP P0A8T7

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

Mol	Chain	Residues	Atoms					AltConf	Trace
4	K	83	Total	C	N	O	S	0	0
			655	399	123	132	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
5	G	232	Total	C	N	O	S	1	0
			1807	1125	322	354	6		
5	H	222	Total	C	N	O	S	0	0
			1710	1068	301	335	6		

- Molecule 6 is a RNA chain called RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	R	12	Total	C	N	O	P	0	0
			256	114	44	86	12		

- Molecule 7 is a DNA chain called template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	40	Total	C	N	O	P	0	0
			828	391	167	231	39		

- Molecule 8 is a DNA chain called non-template DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	40	Total	C	N	O	P	0	0
			808	386	139	244	39		

- Molecule 9 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
9	J	1	Total	Zn	0
			1	1	

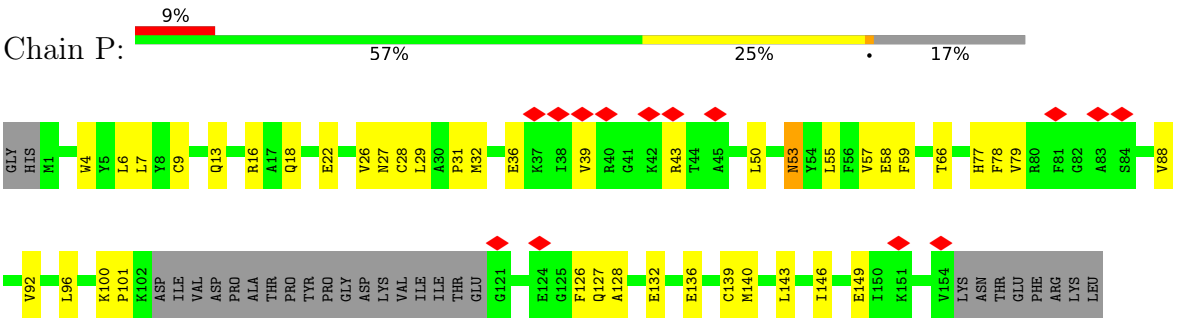
- Molecule 10 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
10	J	1	Total Mg 1 1	0

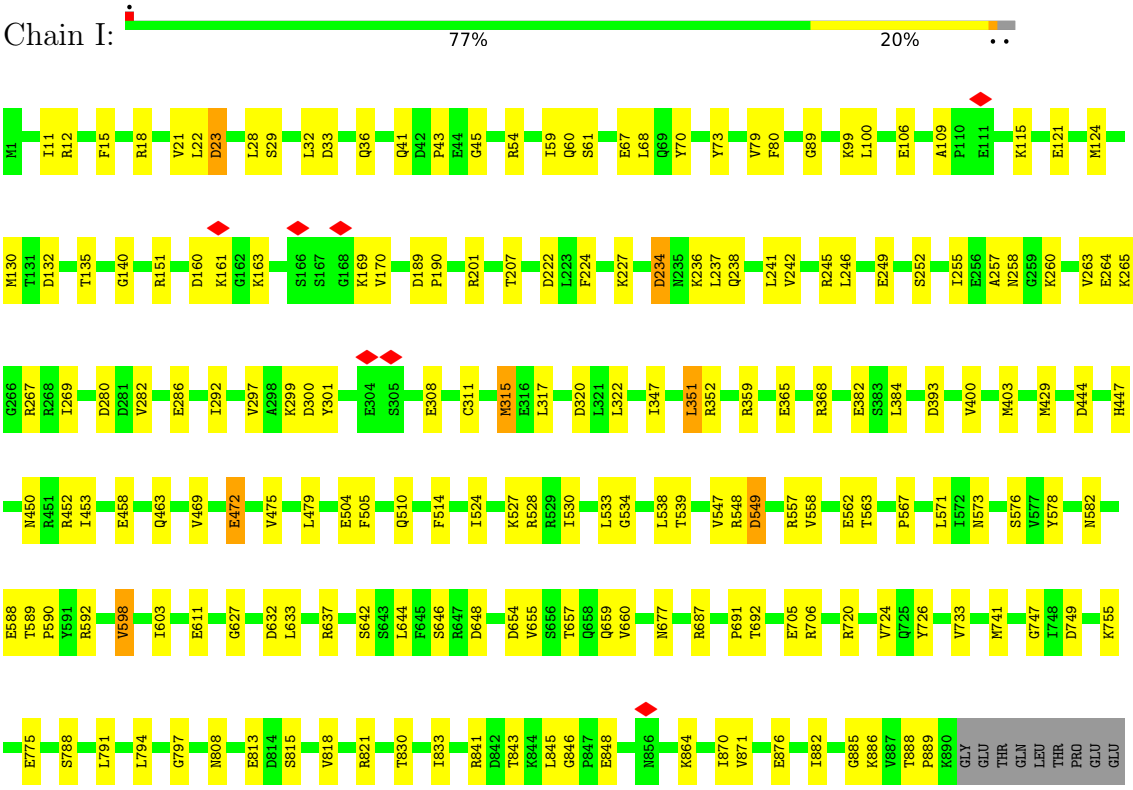
3 Residue-property plots (i)

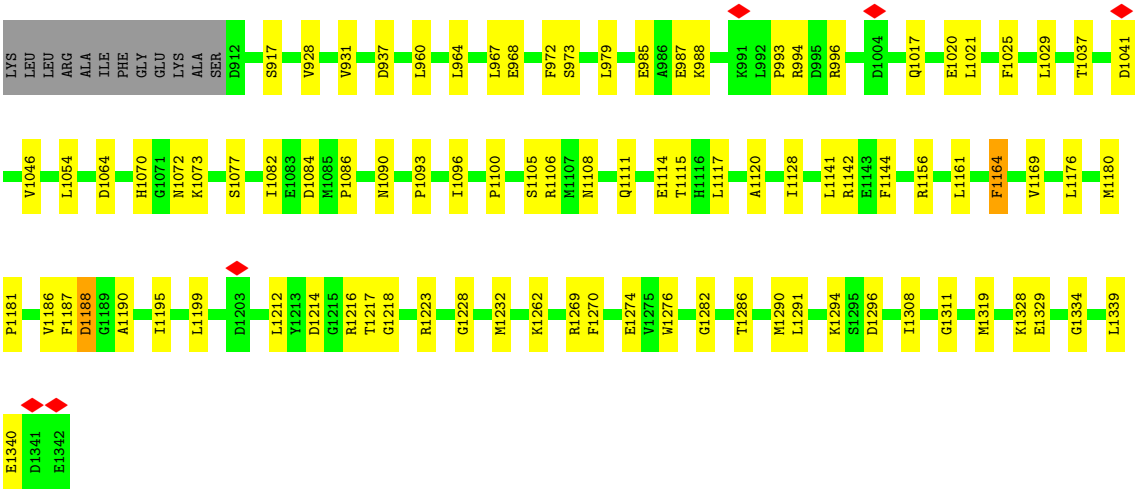
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Transcription antitermination protein RfaH



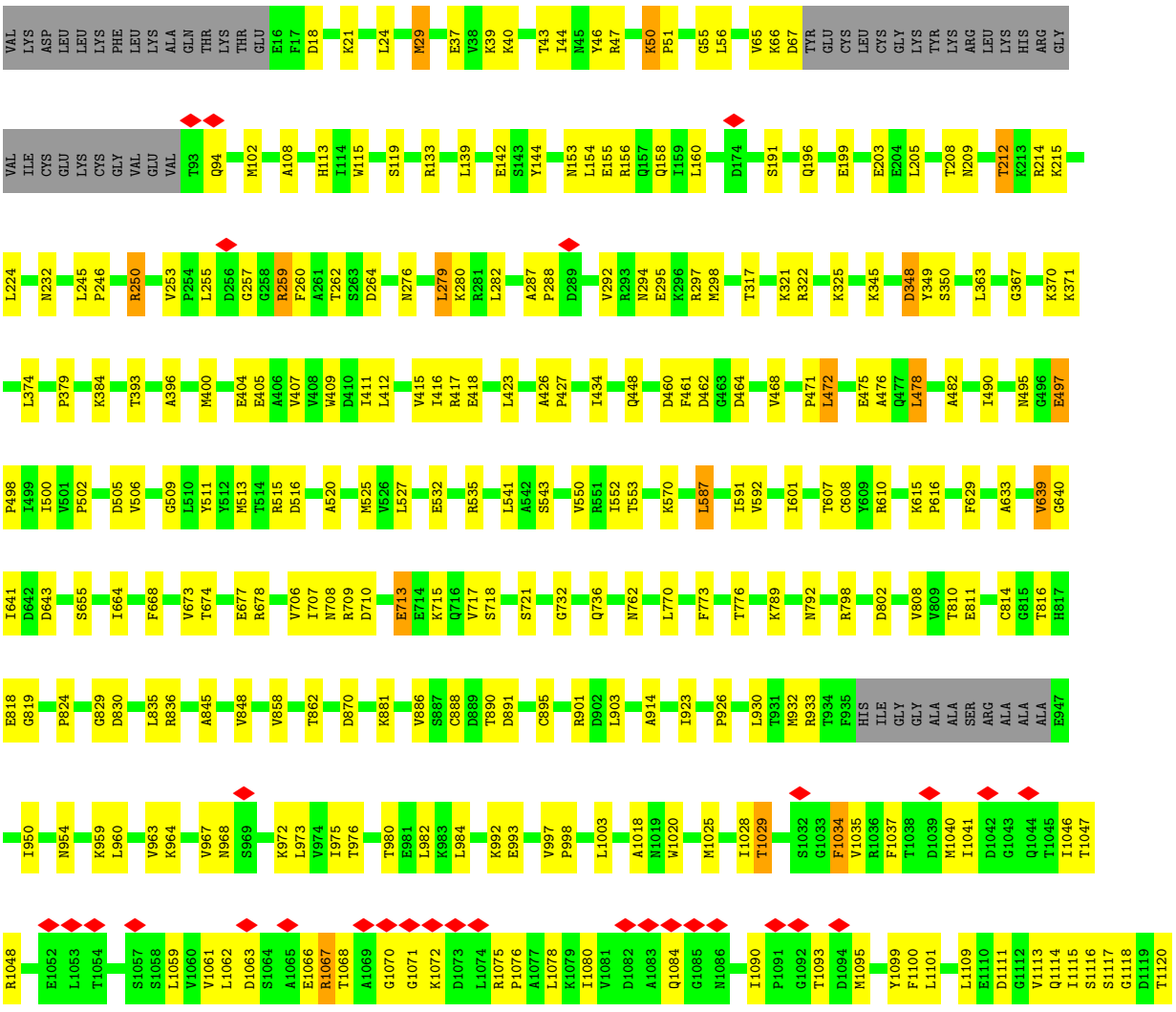
• Molecule 2: DNA-directed RNA polymerase subunit beta

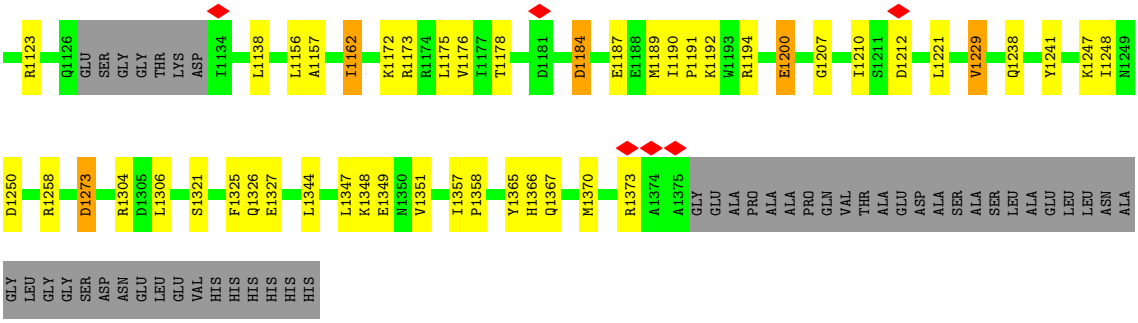




• Molecule 3: DNA-directed RNA polymerase subunit beta'

Chain J:



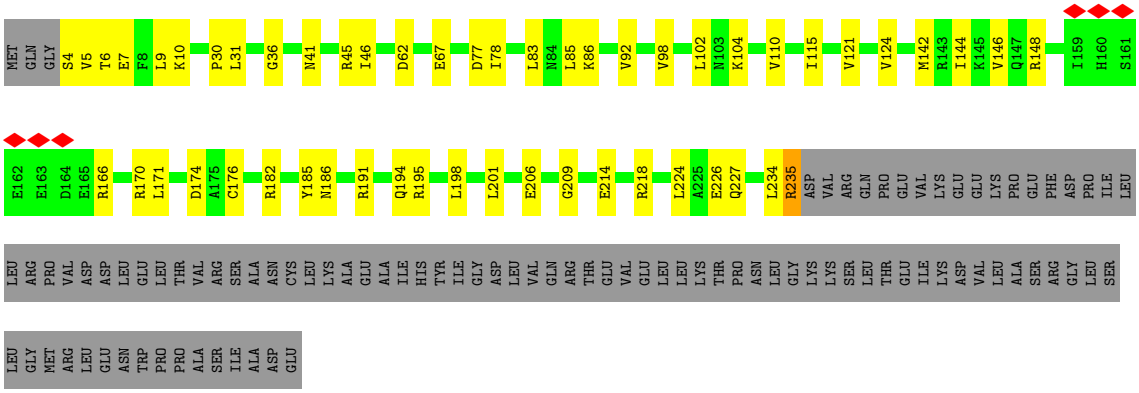


• Molecule 4: DNA-directed RNA polymerase subunit omega

Chain K:

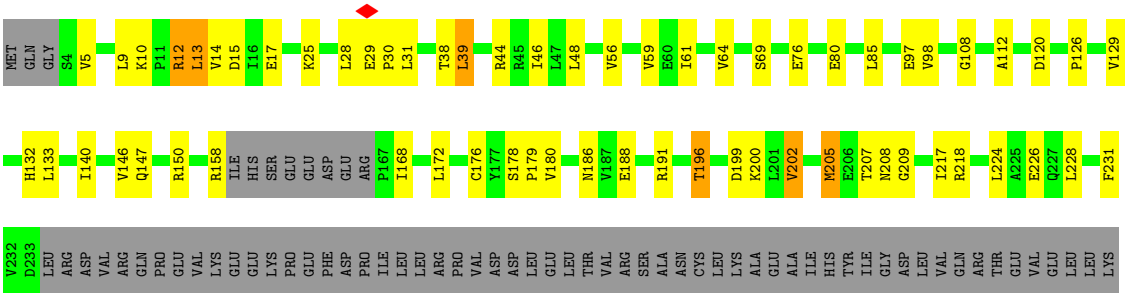
• Molecule 5: DNA-directed RNA polymerase subunit alpha

Chain G:

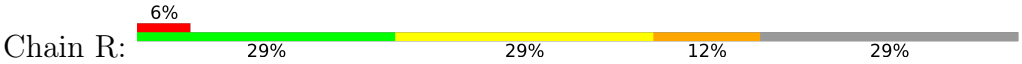


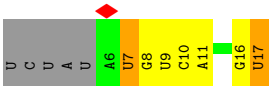
• Molecule 5: DNA-directed RNA polymerase subunit alpha

Chain H:

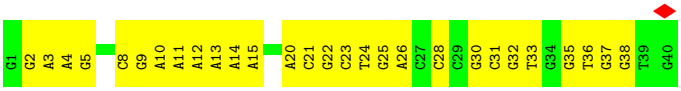


• Molecule 6: RNA

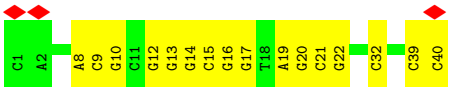




• Molecule 7: template DNA



• Molecule 8: non-template DNA



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	509867	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 ($e^-/Å^2$)	42	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	96000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	2.090	Depositor
Minimum map value	0.000	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.048	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	319.488, 319.488, 319.488	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.832, 0.832, 0.832	Depositor

5 Model quality

5.1 Standard geometry

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	P	0.25	0/1104	0.46	0/1494
2	I	0.26	0/10589	0.48	0/14286
3	J	0.25	0/10394	0.49	0/14037
4	K	0.24	0/657	0.50	0/886
5	G	0.25	0/1832	0.51	0/2482
5	H	0.25	0/1730	0.51	0/2344
6	R	0.28	0/285	0.88	0/442
7	B	0.51	0/933	0.84	0/1440
8	A	0.51	0/902	0.96	0/1389
All	All	0.28	0/28426	0.54	0/38800

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	P	1080	0	1096	24	0
2	I	10423	0	10436	154	0
3	J	10240	0	10453	194	0
4	K	655	0	663	21	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	G	1807	0	1840	41	0
5	H	1710	0	1745	40	0
6	R	256	0	129	7	0
7	B	828	0	447	27	0
8	A	808	0	453	14	0
9	J	1	0	0	0	0
10	J	1	0	0	0	0
All	All	27809	0	27262	474	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 9.

All (474) 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:J:1172:LYS:HB3	3:J:1189:MET:HB3	1.66	0.78
3:J:1172:LYS:HA	3:J:1190:ILE:O	1.86	0.74
5:G:45:ARG:HE	5:H:38:THR:HG22	1.52	0.74
2:I:808:ASN:H	3:J:633:ALA:HB2	1.52	0.73
1:P:27:ASN:HB2	1:P:58:GLU:HB3	1.70	0.73
3:J:322:ARG:NH1	6:R:9:U:O2'	2.25	0.70
3:J:520:ALA:HB1	3:J:543:SER:HB3	1.74	0.70
3:J:245:LEU:O	3:J:250:ARG:NH1	2.25	0.69
2:I:1218:GLY:HA3	5:G:41:ASN:HD21	1.56	0.69
3:J:960:LEU:HB3	3:J:963:VAL:HG11	1.74	0.69
3:J:975:ILE:HD13	3:J:997:VAL:HG11	1.75	0.68
3:J:984:LEU:HB3	3:J:993:GLU:HB2	1.73	0.68
3:J:1326:GLN:HG3	3:J:1327:GLU:HG3	1.76	0.68
5:H:59:VAL:HG21	5:H:85:LEU:HD13	1.75	0.68
2:I:400:VAL:HG21	2:I:452:ARG:HD2	1.76	0.68
5:H:108:GLY:HA3	5:H:133:LEU:H	1.56	0.68
3:J:1035:VAL:HG13	3:J:1078:LEU:HD11	1.76	0.66
2:I:1269:ARG:NH1	7:B:20:DA:OP1	2.25	0.66
3:J:848:VAL:HB	3:J:858:VAL:HG22	1.77	0.66
3:J:209:ASN:HA	3:J:214:ARG:HH21	1.61	0.65
3:J:798:ARG:NH2	3:J:1325:PHE:O	2.29	0.65
2:I:1217:THR:O	5:G:41:ASN:ND2	2.31	0.63
5:H:108:GLY:O	5:H:132:HIS:ND1	2.31	0.63
2:I:68:LEU:HD21	2:I:100:LEU:HD13	1.80	0.63
3:J:1075:ARG:HD3	3:J:1076:PRO:HD2	1.80	0.63
8:A:16:DG:H1'	8:A:19:DA:H61	1.64	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:876:GLU:HG3	5:G:166:ARG:HH12	1.64	0.63
2:I:359:ARG:NH1	2:I:382:GLU:OE2	2.27	0.63
3:J:527:LEU:HB2	3:J:550:VAL:HG12	1.81	0.62
1:P:92:VAL:HB	1:P:149:GLU:HG2	1.81	0.62
3:J:294:ASN:OD1	3:J:297:ARG:NH2	2.32	0.62
5:G:185:TYR:HB2	5:G:201:LEU:HD11	1.82	0.62
3:J:515:ARG:NH2	3:J:718:SER:O	2.33	0.62
1:P:88:VAL:HG13	1:P:146:ILE:HD11	1.81	0.61
3:J:24:LEU:HD11	3:J:232:ASN:HB3	1.81	0.61
3:J:1120:THR:OG1	3:J:1123:ARG:NH1	2.33	0.61
5:H:12:ARG:H	5:H:30:PRO:HD2	1.65	0.61
5:H:191:ARG:HB2	5:H:196:THR:HA	1.83	0.60
2:I:1223:ARG:NH2	3:J:721:SER:OG	2.34	0.60
2:I:241:LEU:HD21	2:I:246:LEU:HD11	1.83	0.60
2:I:61:SER:HB2	2:I:479:LEU:HG	1.82	0.60
2:I:1084:ASP:OD1	5:G:45:ARG:NH1	2.26	0.60
5:G:166:ARG:NH2	5:G:170:ARG:O	2.35	0.60
2:I:720:ARG:NH2	2:I:749:ASP:OD1	2.34	0.60
2:I:234:ASP:OD1	2:I:236:LYS:NZ	2.35	0.60
2:I:549:ASP:OD1	3:J:933:ARG:NH2	2.35	0.60
3:J:46:TYR:HB2	3:J:47:ARG:HH21	1.66	0.60
3:J:1035:VAL:HG12	3:J:1111:ASP:HA	1.82	0.60
3:J:709:ARG:HG2	3:J:710:ASP:H	1.67	0.59
3:J:816:THR:HG22	3:J:818:GLU:H	1.66	0.59
2:I:1311:GLY:O	4:K:31:GLN:NE2	2.35	0.59
2:I:510:GLN:NE2	6:R:11:A:O3'	2.36	0.59
3:J:502:PRO:HB3	3:J:506:VAL:HB	1.85	0.59
2:I:845:LEU:HD23	2:I:889:PRO:HB2	1.83	0.59
3:J:901:ARG:HG2	3:J:903:LEU:H	1.68	0.59
2:I:12:ARG:HG3	2:I:1181:PRO:HB2	1.83	0.59
1:P:28:CYS:HB2	1:P:55:LEU:HD11	1.85	0.59
2:I:252:SER:O	2:I:265:LYS:NZ	2.33	0.59
2:I:299:LYS:NZ	2:I:300:ASP:O	2.36	0.59
3:J:65:VAL:HG13	3:J:66:LYS:HG3	1.84	0.59
2:I:841:ARG:HA	2:I:1046:VAL:HA	1.85	0.58
2:I:993:PRO:HD2	2:I:996:ARG:HD2	1.84	0.58
5:H:188:GLU:OE1	5:H:200:LYS:NZ	2.36	0.58
2:I:967:LEU:HD13	2:I:1021:LEU:HD11	1.85	0.58
3:J:108:ALA:H	3:J:276:ASN:HD21	1.49	0.58
2:I:1117:LEU:HD13	2:I:1195:ILE:HG12	1.84	0.58
3:J:1162:ILE:HG12	3:J:1178:THR:HB	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:241:LEU:HD11	2:I:246:LEU:HD21	1.84	0.58
5:G:104:LYS:HG2	5:G:110:VAL:HG22	1.86	0.58
5:G:31:LEU:HD13	5:G:36:GLY:HA2	1.85	0.58
8:A:13:DG:H2"	8:A:14:DG:H3'	1.83	0.58
1:P:6:LEU:HB3	1:P:79:VAL:HB	1.86	0.58
1:P:143:LEU:HB3	3:J:288:PRO:HG3	1.86	0.58
2:I:28:LEU:HD22	2:I:527:LYS:HD2	1.84	0.58
5:H:158:ARG:HH11	5:H:172:LEU:HD22	1.69	0.58
2:I:1072:ASN:ND2	2:I:1111:GLN:OE1	2.31	0.57
3:J:253:VAL:HG21	6:R:7:U:H1'	1.86	0.57
3:J:706:VAL:HG22	3:J:715:LYS:HG2	1.85	0.57
2:I:201:ARG:NH2	8:A:22:DG:O6	2.37	0.57
3:J:1059:LEU:HD23	3:J:1059:LEU:H	1.70	0.57
2:I:562:GLU:OE2	2:I:687:ARG:NH1	2.36	0.57
2:I:1108:ASN:OD1	2:I:1111:GLN:NE2	2.36	0.57
3:J:1093:THR:HG22	3:J:1095:MET:H	1.68	0.57
2:I:43:PRO:O	2:I:54:ARG:NH2	2.38	0.57
3:J:462:ASP:OD2	6:R:17:U:OP1	2.22	0.57
5:H:205:MET:HE1	5:H:217:ILE:HG13	1.86	0.57
7:B:25:DG:H2"	7:B:26:DA:H5'	1.87	0.57
7:B:24:DT:H2'	7:B:25:DG:C8	2.40	0.56
4:K:52:ARG:HA	4:K:55:GLU:HG3	1.85	0.56
2:I:533:LEU:HD21	2:I:571:LEU:HD13	1.86	0.56
3:J:950:ILE:HD13	3:J:1018:ALA:HB3	1.86	0.56
2:I:255:ILE:HB	2:I:263:VAL:HB	1.87	0.56
3:J:56:LEU:HB3	3:J:250:ARG:HH21	1.70	0.56
5:H:112:ALA:HB3	5:H:126:PRO:HA	1.88	0.56
3:J:674:THR:OG1	3:J:677:GLU:OE1	2.23	0.56
3:J:1080:ILE:HD12	3:J:1115:ILE:HD11	1.87	0.56
2:I:1073:LYS:NZ	6:R:16:G:OP1	2.35	0.56
3:J:418:GLU:OE2	4:K:2:ALA:N	2.38	0.56
3:J:926:PRO:HG2	3:J:1248:ILE:HD11	1.88	0.56
5:G:5:VAL:O	5:H:150:ARG:NH1	2.39	0.56
5:H:186:ASN:HB3	5:H:202:VAL:HG23	1.87	0.56
3:J:482:ALA:O	4:K:16:ARG:NH1	2.39	0.56
5:H:61:ILE:HB	5:H:64:VAL:HB	1.88	0.55
2:I:642:SER:HB3	3:J:770:LEU:HD21	1.86	0.55
2:I:821:ARG:HG3	2:I:1082:ILE:HD13	1.87	0.55
5:G:224:LEU:HD23	5:H:228:LEU:HD11	1.89	0.55
2:I:41:GLN:NE2	2:I:73:TYR:O	2.35	0.55
5:G:92:VAL:O	5:G:148:ARG:NH2	2.40	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:1067:ARG:HD3	3:J:1072:LYS:HA	1.89	0.55
8:A:19:DA:H2"	8:A:20:DG:H5"	1.88	0.55
2:I:1186:VAL:HG13	2:I:1187:PHE:HD2	1.71	0.55
2:I:263:VAL:HA	2:I:267:ARG:HH21	1.71	0.54
4:K:56:GLU:HG3	4:K:58:LEU:HD13	1.88	0.54
2:I:60:GLN:NE2	2:I:67:GLU:OE1	2.40	0.54
3:J:1178:THR:HA	3:J:1184:ASP:HB3	1.88	0.54
7:B:21:DC:H2'	7:B:22:DG:H8	1.71	0.54
1:P:31:PRO:HB2	1:P:50:LEU:HB2	1.90	0.54
2:I:18:ARG:O	2:I:1156:ARG:NH1	2.38	0.54
2:I:315:MET:HA	2:I:352:ARG:HH12	1.71	0.54
5:G:235:ARG:NH2	5:H:14:VAL:O	2.29	0.54
1:P:36:GLU:HB3	1:P:43:ARG:HB3	1.90	0.54
2:I:985:GLU:HA	2:I:988:LYS:HZ3	1.73	0.54
2:I:1218:GLY:HA3	5:G:41:ASN:ND2	2.22	0.54
3:J:1344:LEU:HD12	3:J:1349:GLU:HB3	1.88	0.54
3:J:212:THR:HA	3:J:215:LYS:HD2	1.90	0.54
3:J:1090:ILE:HB	3:J:1093:THR:HB	1.90	0.54
3:J:102:MET:HG2	3:J:246:PRO:HD3	1.90	0.54
3:J:497:GLU:HG3	3:J:498:PRO:HD2	1.90	0.54
3:J:412:LEU:O	3:J:416:ILE:HG13	2.08	0.53
2:I:258:ASN:O	2:I:260:LYS:NZ	2.37	0.53
2:I:1100:PRO:HB3	3:J:639:VAL:HG22	1.90	0.53
3:J:1046:ILE:HB	3:J:1061:VAL:HA	1.89	0.53
5:H:17:GLU:HG3	5:H:25:LYS:HB2	1.90	0.53
2:I:207:THR:HG21	2:I:351:LEU:HG	1.90	0.53
3:J:367:GLY:HA3	3:J:448:GLN:HB2	1.91	0.53
2:I:28:LEU:HD21	2:I:524:ILE:HD13	1.89	0.53
2:I:841:ARG:N	2:I:848:GLU:OE2	2.41	0.53
2:I:886:LYS:H	2:I:917:SER:HB3	1.72	0.53
2:I:1082:ILE:HD11	2:I:1093:PRO:HG2	1.90	0.53
2:I:1176:LEU:HD13	2:I:1180:MET:HE2	1.91	0.53
3:J:50:LYS:HD3	3:J:51:PRO:HD2	1.90	0.53
7:B:37:DG:H2"	7:B:38:DG:C8	2.43	0.53
1:P:32:MET:O	1:P:100:LYS:NZ	2.42	0.53
5:H:13:LEU:HD22	5:H:29:GLU:HB2	1.91	0.52
3:J:276:ASN:OD1	3:J:280:LYS:NZ	2.43	0.52
3:J:1175:LEU:HB2	3:J:1190:ILE:HD13	1.92	0.52
7:B:35:DG:H2'	7:B:36:DT:H71	1.91	0.52
2:I:598:VAL:HG23	2:I:627:GLY:HA3	1.92	0.52
3:J:964:LYS:O	3:J:976:THR:OG1	2.22	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:264:ASP:OD2	3:J:325:LYS:N	2.28	0.52
3:J:348:ASP:N	3:J:348:ASP:OD1	2.41	0.52
2:I:160:ASP:OD1	2:I:160:ASP:N	2.43	0.52
2:I:161:LYS:H	2:I:163:LYS:HZ3	1.58	0.52
2:I:843:THR:OG1	2:I:846:GLY:O	2.24	0.52
2:I:1276:TRP:HH2	3:J:798:ARG:HG3	1.75	0.52
2:I:1308:ILE:HD11	3:J:472:LEU:HB2	1.90	0.52
3:J:1238:GLN:NE2	3:J:1250:ASP:OD1	2.43	0.52
7:B:10:DA:H2"	7:B:11:DA:H8	1.75	0.52
1:P:143:LEU:HA	1:P:146:ILE:HG22	1.92	0.51
7:B:24:DT:H2'	7:B:25:DG:H8	1.76	0.51
3:J:371:LYS:NZ	3:J:404:GLU:OE2	2.41	0.51
3:J:591:ILE:HG13	3:J:592:VAL:HG13	1.91	0.51
3:J:144:TYR:N	3:J:160:LEU:O	2.43	0.51
3:J:1100:PHE:HB2	3:J:1200:GLU:HB3	1.93	0.51
5:G:98:VAL:HG11	5:G:121:VAL:HG21	1.93	0.51
7:B:12:DA:H2"	7:B:13:DA:H8	1.76	0.51
3:J:1035:VAL:HG21	3:J:1109:LEU:HD11	1.93	0.51
5:H:44:ARG:HG2	5:H:48:LEU:HD23	1.92	0.51
3:J:156:ARG:NH1	3:J:191:SER:OG	2.44	0.51
1:P:4:TRP:CE2	1:P:58:GLU:HB2	2.46	0.51
1:P:26:VAL:HG13	1:P:59:PHE:HB3	1.92	0.51
3:J:393:THR:HG23	3:J:396:ALA:H	1.76	0.50
2:I:1286:THR:HG22	3:J:476:ALA:HA	1.94	0.50
5:H:46:ILE:HD11	5:H:224:LEU:HD13	1.94	0.50
2:I:578:TYR:HB3	2:I:590:PRO:HG2	1.92	0.50
3:J:113:HIS:CE1	3:J:115:TRP:HB2	2.47	0.50
3:J:968:ASN:OD1	3:J:972:LYS:N	2.44	0.50
3:J:1191:PRO:HB2	3:J:1194:ARG:HG2	1.94	0.50
5:G:102:LEU:HD12	5:G:115:ILE:HG13	1.92	0.50
3:J:773:PHE:O	3:J:776:THR:OG1	2.29	0.50
2:I:538:LEU:HD11	2:I:547:VAL:HG21	1.94	0.50
2:I:365:GLU:OE1	2:I:368:ARG:NH2	2.44	0.50
2:I:1120:ALA:HB2	2:I:1199:LEU:HG	1.94	0.50
1:P:100:LYS:HB3	1:P:101:PRO:HD3	1.93	0.50
3:J:155:GLU:HG3	3:J:158:GLN:HG3	1.93	0.50
3:J:829:GLY:N	3:J:993:GLU:OE1	2.45	0.50
3:J:208:THR:O	3:J:214:ARG:NH2	2.44	0.49
7:B:23:DC:H2'	7:B:24:DT:C6	2.46	0.49
1:P:128:ALA:O	1:P:132:GLU:HG2	2.11	0.49
2:I:444:ASP:O	2:I:450:ASN:ND2	2.41	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1070:HIS:NE2	2:I:1114:GLU:OE1	2.36	0.49
3:J:1037:PHE:HB3	3:J:1040:MET:HG3	1.94	0.49
3:J:1040:MET:HB3	3:J:1076:PRO:HB3	1.93	0.49
4:K:3:ARG:NH1	4:K:5:THR:O	2.45	0.49
3:J:535:ARG:NH1	5:H:180:VAL:O	2.45	0.49
7:B:10:DA:H2"	7:B:11:DA:C8	2.47	0.49
3:J:640:GLY:N	3:J:643:ASP:OD2	2.35	0.49
3:J:1034:PHE:HA	3:J:1114:GLN:HA	1.95	0.49
2:I:463:GLN:HG3	2:I:505:PHE:HB2	1.94	0.49
2:I:691:PRO:HB3	2:I:788:SER:HB3	1.93	0.49
3:J:417:ARG:NH1	4:K:43:ASN:O	2.46	0.49
3:J:1003:LEU:HD23	3:J:1018:ALA:HB2	1.95	0.49
2:I:23:ASP:OD1	2:I:23:ASP:N	2.45	0.49
2:I:548:ARG:NH1	2:I:567:PRO:O	2.43	0.49
3:J:587:LEU:HD21	3:J:608:CYS:HB2	1.95	0.49
1:P:77:HIS:ND1	1:P:78:PHE:O	2.41	0.49
2:I:1290:MET:HA	2:I:1294:LYS:HD3	1.94	0.49
2:I:589:THR:OG1	2:I:659:GLN:NE2	2.36	0.48
3:J:475:GLU:OE2	4:K:28:ARG:NH1	2.42	0.48
3:J:1067:ARG:NH1	3:J:1071:GLY:O	2.46	0.48
3:J:502:PRO:HG2	3:J:601:ILE:HG21	1.96	0.48
3:J:535:ARG:NH2	5:H:176:CYS:SG	2.87	0.48
2:I:280:ASP:HB3	2:I:282:VAL:HG23	1.94	0.48
3:J:199:GLU:O	3:J:203:GLU:HG2	2.14	0.48
2:I:242:VAL:HB	2:I:245:ARG:HG3	1.95	0.48
2:I:870:ILE:HG21	2:I:931:VAL:HG11	1.95	0.48
3:J:363:LEU:HD21	3:J:500:ILE:HD13	1.95	0.48
3:J:1028:ILE:HG23	3:J:1118:GLY:HA2	1.95	0.48
5:G:4:SER:O	5:G:6:THR:N	2.46	0.48
5:G:67:GLU:HG3	5:G:171:LEU:HD22	1.95	0.48
1:P:18:GLN:HG3	1:P:28:CYS:SG	2.54	0.48
3:J:43:THR:HG22	3:J:56:LEU:HD12	1.95	0.48
3:J:824:PRO:HD3	3:J:835:LEU:HB2	1.96	0.48
3:J:587:LEU:HD11	3:J:608:CYS:HA	1.96	0.47
7:B:3:DA:H2"	7:B:4:DA:C8	2.49	0.47
2:I:646:SER:OG	2:I:648:ASP:OD1	2.21	0.47
3:J:1176:VAL:HG13	3:J:1187:GLU:HG3	1.96	0.47
5:G:62:ASP:OD1	5:G:62:ASP:N	2.46	0.47
3:J:426:ALA:HB3	3:J:427:PRO:HD3	1.96	0.47
3:J:998:PRO:HG2	3:J:1020:TRP:CE2	2.49	0.47
2:I:1291:LEU:HD11	3:J:1351:VAL:HG23	1.95	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:1142:ARG:NH1	2:I:1161:LEU:O	2.48	0.47
3:J:196:GLN:O	3:J:199:GLU:HG3	2.14	0.47
3:J:836:ARG:NH1	3:J:870:ASP:OD1	2.45	0.47
1:P:136:GLU:O	1:P:140:MET:HG2	2.15	0.47
2:I:1296:ASP:OD2	3:J:345:LYS:NZ	2.34	0.47
5:H:208:ASN:OD1	5:H:209:GLY:N	2.48	0.47
6:R:7:U:H2'	6:R:8:G:C8	2.50	0.47
2:I:22:LEU:HD13	2:I:603:ILE:HG13	1.96	0.47
3:J:56:LEU:HB3	3:J:250:ARG:NH2	2.29	0.47
3:J:153:ASN:OD1	3:J:153:ASN:N	2.48	0.47
8:A:16:DG:H1'	8:A:19:DA:N6	2.28	0.47
2:I:1334:GLY:H	3:J:113:HIS:HE2	1.62	0.47
5:G:77:ASP:OD1	5:G:78:ILE:N	2.48	0.47
2:I:320:ASP:OD1	2:I:320:ASP:N	2.48	0.47
3:J:819:GLY:H	3:J:881:LYS:HE2	1.80	0.47
4:K:44:ASP:HB3	4:K:49:ILE:HG13	1.97	0.47
2:I:1086:PRO:HB2	2:I:1212:LEU:HD13	1.97	0.46
2:I:582:ASN:ND2	2:I:588:GLU:OE1	2.48	0.46
3:J:18:ASP:OD1	3:J:1373:ARG:NH2	2.48	0.46
3:J:959:LYS:NZ	3:J:960:LEU:O	2.48	0.46
5:G:174:ASP:OD1	5:G:174:ASP:N	2.48	0.46
2:I:106:GLU:HA	2:I:115:LYS:HG3	1.98	0.46
3:J:490:ILE:HG22	3:J:500:ILE:HD12	1.96	0.46
3:J:1221:LEU:HB2	3:J:1229:VAL:HG21	1.98	0.46
5:G:234:LEU:O	5:H:218:ARG:NH2	2.49	0.46
2:I:99:LYS:HG2	2:I:121:GLU:HG2	1.96	0.46
3:J:789:LYS:HA	3:J:932:MET:SD	2.55	0.46
3:J:886:VAL:HA	3:J:1258:ARG:HB2	1.98	0.46
3:J:1029:THR:HG23	3:J:1099:TYR:HE2	1.79	0.46
2:I:45:GLY:HA3	2:I:54:ARG:HD2	1.98	0.46
2:I:444:ASP:HB3	2:I:447:HIS:HB2	1.97	0.46
4:K:15:ASN:OD1	4:K:18:ASP:N	2.41	0.46
5:G:30:PRO:HB2	5:G:198:LEU:HD13	1.96	0.46
2:I:818:VAL:HG22	2:I:1096:ILE:HD13	1.97	0.46
2:I:1115:THR:HG23	2:I:1228:GLY:HA3	1.98	0.46
7:B:13:DA:H2"	7:B:14:DA:H8	1.80	0.46
2:I:964:LEU:HD13	2:I:1025:PHE:HD2	1.81	0.46
8:A:15:DC:H2"	8:A:16:DG:C8	2.50	0.46
2:I:18:ARG:HD2	2:I:1188:ASP:OD2	2.15	0.46
2:I:224:PHE:CZ	2:I:429:MET:HE2	2.51	0.46
7:B:4:DA:H2"	7:B:5:DG:C8	2.51	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:P:7:LEU:HD23	1:P:78:PHE:HA	1.97	0.45
7:B:30:DG:H2"	7:B:31:DC:C6	2.51	0.45
5:H:29:GLU:HG2	5:H:200:LYS:HD3	1.98	0.45
8:A:8:DA:H1'	8:A:9:DC:H5'	1.98	0.45
2:I:59:ILE:HD13	2:I:475:VAL:HG11	1.99	0.45
2:I:706:ARG:NH1	2:I:791:LEU:O	2.49	0.45
3:J:511:TYR:OH	3:J:515:ARG:NH1	2.50	0.45
4:K:73:GLN:O	4:K:76:GLU:HG3	2.16	0.45
5:G:142:MET:HE2	5:G:144:ILE:HD11	1.99	0.45
2:I:510:GLN:HG2	2:I:534:GLY:HA2	1.98	0.45
3:J:396:ALA:O	3:J:400:MET:HG3	2.16	0.45
4:K:3:ARG:NH1	4:K:55:GLU:OE2	2.49	0.45
5:H:76:GLU:OE1	5:H:132:HIS:N	2.50	0.45
2:I:1262:LYS:N	7:B:22:DG:OP1	2.49	0.45
3:J:255:LEU:HD21	7:B:28:DC:C4	2.51	0.45
8:A:39:DC:H2"	8:A:40:DC:C5	2.51	0.45
3:J:708:ASN:HA	3:J:713:GLU:HA	1.98	0.45
3:J:1273:ASP:OD1	3:J:1273:ASP:N	2.33	0.45
5:H:120:ASP:OD1	5:H:120:ASP:N	2.49	0.45
2:I:106:GLU:OE1	2:I:109:ALA:N	2.45	0.45
2:I:960:LEU:HD12	2:I:1029:LEU:HD23	1.99	0.45
2:I:972:PHE:HD2	2:I:994:ARG:HD3	1.80	0.45
7:B:32:DG:H2"	7:B:33:DT:H71	1.99	0.45
8:A:21:DC:OP2	8:A:22:DG:N1	2.48	0.45
1:P:9:CYS:SG	1:P:53:ASN:HA	2.57	0.45
3:J:552:ILE:HD11	3:J:570:LYS:HG3	1.98	0.45
3:J:1041:ILE:O	3:J:1046:ILE:HG12	2.17	0.45
3:J:1348:LYS:HA	3:J:1351:VAL:HG12	1.98	0.45
2:I:705:GLU:HB3	2:I:794:LEU:H	1.82	0.45
3:J:973:LEU:HD12	3:J:973:LEU:HA	1.87	0.45
2:I:726:TYR:HB3	2:I:733:VAL:HB	1.99	0.44
3:J:37:GLU:OE1	3:J:39:LYS:HG3	2.17	0.44
3:J:460:ASP:OD1	3:J:460:ASP:N	2.50	0.44
3:J:1109:LEU:HD12	3:J:1113:VAL:HB	1.99	0.44
3:J:1367:GLN:O	3:J:1370:MET:HG2	2.17	0.44
6:R:9:U:H2'	6:R:10:C:C6	2.52	0.44
2:I:393:ASP:OD1	2:I:393:ASP:N	2.51	0.44
2:I:11:ILE:HD11	2:I:1164:PHE:HZ	1.82	0.44
2:I:882:ILE:HD11	2:I:885:GLY:HA2	1.99	0.44
3:J:43:THR:OG1	3:J:44:ILE:N	2.51	0.44
3:J:282:LEU:HB3	3:J:292:VAL:HG12	1.99	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:G:4:SER:HB3	5:G:7:GLU:HB2	1.99	0.44
2:I:472:GLU:HA	2:I:475:VAL:HG12	1.99	0.44
2:I:1214:ASP:HB3	2:I:1218:GLY:H	1.82	0.44
3:J:505:ASP:HB2	3:J:629:PHE:HE1	1.81	0.44
5:H:15:ASP:OD1	5:H:15:ASP:N	2.50	0.44
5:H:31:LEU:HB2	5:H:199:ASP:O	2.17	0.44
8:A:12:DG:H2"	8:A:13:DG:C8	2.52	0.44
2:I:21:VAL:HG11	2:I:592:ARG:HD2	2.00	0.44
2:I:632:ASP:OD1	2:I:632:ASP:N	2.45	0.44
5:G:124:VAL:HG11	5:G:209:GLY:HA3	1.99	0.44
2:I:169:LYS:NZ	2:I:190:PRO:O	2.46	0.44
2:I:1164:PHE:HB3	2:I:1169:VAL:HG23	2.00	0.44
3:J:255:LEU:HD12	3:J:255:LEU:HA	1.80	0.44
3:J:808:VAL:HG12	3:J:914:ALA:HA	2.00	0.44
3:J:1114:GLN:NE2	3:J:1115:ILE:O	2.50	0.44
3:J:1347:LEU:HD23	3:J:1358:PRO:HD2	2.00	0.44
2:I:557:ARG:NH2	2:I:611:GLU:OE1	2.36	0.43
3:J:29:MET:H	3:J:29:MET:HG3	1.64	0.43
3:J:1034:PHE:HD1	3:J:1114:GLN:HB2	1.82	0.43
3:J:1063:ASP:HB3	3:J:1066:GLU:HB2	2.00	0.43
2:I:347:ILE:HD13	2:I:347:ILE:HA	1.92	0.43
4:K:21:LEU:HD13	4:K:21:LEU:HA	1.88	0.43
7:B:8:DC:H2"	7:B:9:DG:C8	2.54	0.43
1:P:127:GLN:O	1:P:127:GLN:NE2	2.51	0.43
5:H:179:PRO:O	5:H:207:THR:HG23	2.18	0.43
2:I:1017:GLN:O	2:I:1020:GLU:HG2	2.18	0.43
5:H:191:ARG:HB2	5:H:196:THR:HG23	2.00	0.43
2:I:741:MET:SD	2:I:747:GLY:HA3	2.58	0.43
2:I:815:SER:HB3	2:I:1077:SER:HB3	1.99	0.43
3:J:1029:THR:O	3:J:1118:GLY:N	2.39	0.43
5:H:14:VAL:HG22	5:H:28:LEU:HD22	1.99	0.43
2:I:236:LYS:HB2	2:I:238:GLN:HG3	2.01	0.43
2:I:755:LYS:HE3	2:I:755:LYS:HB3	1.85	0.43
3:J:370:LYS:HB3	3:J:409:TRP:CH2	2.53	0.43
3:J:923:ILE:O	3:J:1241:TYR:OH	2.24	0.43
3:J:1068:THR:O	3:J:1072:LYS:N	2.49	0.43
4:K:3:ARG:HB2	4:K:48:VAL:HG13	2.00	0.43
3:J:349:TYR:HE1	3:J:379:PRO:HG2	1.84	0.43
3:J:607:THR:HG22	3:J:610:ARG:HH21	1.84	0.43
8:A:16:DG:H2"	8:A:17:DG:C8	2.53	0.43
2:I:297:VAL:HB	2:I:317:LEU:HD21	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:I:528:ARG:NH2	2:I:576:SER:O	2.40	0.43
5:G:98:VAL:HB	5:G:146:VAL:HG13	2.00	0.43
2:I:249:GLU:HB3	2:I:269:ILE:HD13	2.00	0.43
2:I:633:LEU:HG	2:I:644:LEU:HB3	2.00	0.43
3:J:891:ASP:OD1	3:J:891:ASP:N	2.45	0.43
4:K:38:LEU:HB3	4:K:58:LEU:HD23	2.00	0.43
5:H:97:GLU:HB3	5:H:147:GLN:HG2	2.01	0.43
3:J:295:GLU:HA	3:J:298:MET:HG2	2.00	0.42
3:J:1156:LEU:HD23	3:J:1207:GLY:HA2	2.01	0.42
2:I:453:ILE:HD13	2:I:530:ILE:HD12	2.01	0.42
2:I:1090:ASN:O	5:G:182:ARG:HD3	2.19	0.42
2:I:1128:ILE:HG13	2:I:1144:PHE:HE2	1.84	0.42
3:J:495:ASN:HD22	3:J:1247:LYS:HB3	1.84	0.42
3:J:930:LEU:HD12	3:J:1138:LEU:HD13	2.01	0.42
3:J:1304:ARG:HE	3:J:1304:ARG:HB3	1.73	0.42
1:P:100:LYS:HA	1:P:100:LYS:HD2	1.82	0.42
2:I:724:VAL:HG23	2:I:775:GLU:O	2.18	0.42
3:J:527:LEU:HD22	3:J:532:GLU:HG2	2.01	0.42
2:I:301:TYR:HB2	2:I:311:CYS:SG	2.60	0.42
4:K:72:GLN:O	4:K:75:GLN:HG3	2.19	0.42
5:H:133:LEU:HD11	5:H:140:ILE:HG22	2.01	0.42
2:I:292:ILE:HG21	2:I:322:LEU:HD13	2.01	0.42
2:I:1072:ASN:OD1	2:I:1072:ASN:N	2.51	0.42
3:J:384:LYS:HD2	3:J:384:LYS:HA	1.89	0.42
3:J:1068:THR:HG22	3:J:1070:GLY:H	1.84	0.42
5:G:86:LYS:NZ	5:G:176:CYS:SG	2.68	0.42
3:J:44:ILE:HG21	3:J:260:PHE:HE2	1.85	0.42
3:J:668:PHE:CG	3:J:678:ARG:HD2	2.55	0.42
4:K:22:VAL:HG12	4:K:54:ILE:HD11	2.02	0.42
4:K:69:ARG:O	4:K:72:GLN:HG3	2.19	0.42
8:A:14:DG:H5'	8:A:14:DG:C8	2.55	0.42
3:J:509:GLY:O	3:J:513:MET:HG3	2.20	0.42
3:J:992:LYS:HD3	3:J:992:LYS:HA	1.90	0.42
3:J:1157:ALA:HB2	3:J:1210:ILE:HD11	2.02	0.42
3:J:1212:ASP:OD1	3:J:1212:ASP:N	2.53	0.42
4:K:62:GLN:HA	4:K:65:ASP:OD1	2.20	0.42
5:G:46:ILE:HD11	5:G:224:LEU:HD13	2.00	0.42
5:G:191:ARG:NH1	5:G:194:GLN:H	2.17	0.42
7:B:9:DG:H2"	7:B:10:DA:C8	2.55	0.42
7:B:23:DC:H2'	7:B:24:DT:H6	1.85	0.42
5:G:182:ARG:HB3	5:G:206:GLU:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
7:B:22:DG:H2'	7:B:23:DC:C6	2.55	0.41
3:J:40:LYS:O	3:J:55:GLY:HA2	2.20	0.41
3:J:411:ILE:O	3:J:415:VAL:HG13	2.19	0.41
3:J:478:LEU:HD13	3:J:478:LEU:HA	1.79	0.41
3:J:732:GLY:HA2	3:J:736:GLN:OE1	2.20	0.41
3:J:1062:LEU:HD12	3:J:1062:LEU:HA	1.88	0.41
5:G:214:GLU:O	5:G:218:ARG:HG3	2.20	0.41
2:I:238:GLN:HG2	2:I:286:GLU:HA	2.02	0.41
3:J:471:PRO:HB3	3:J:476:ALA:HB1	2.02	0.41
3:J:810:THR:O	3:J:810:THR:OG1	2.36	0.41
3:J:845:ALA:HB3	3:J:881:LYS:HG2	2.02	0.41
5:G:4:SER:O	5:G:4:SER:OG	2.36	0.41
5:G:10:LYS:NZ	5:H:226:GLU:HB3	2.35	0.41
2:I:79:VAL:HG22	2:I:80:PHE:CD1	2.56	0.41
3:J:133:ARG:NH2	8:A:32:DC:H5"	2.36	0.41
3:J:287:ALA:HB3	3:J:292:VAL:HG13	2.02	0.41
3:J:405:GLU:HG3	3:J:407:VAL:HG22	2.02	0.41
7:B:2:DG:H2"	7:B:3:DA:N7	2.35	0.41
8:A:9:DC:H2"	8:A:10:DG:N7	2.36	0.41
1:P:96:LEU:HD12	1:P:126:PHE:HE1	1.86	0.41
2:I:33:ASP:O	2:I:36:GLN:HB2	2.21	0.41
2:I:692:THR:HA	2:I:830:THR:HG22	2.02	0.41
2:I:864:LYS:HB3	2:I:871:VAL:HG23	2.02	0.41
3:J:67:ASP:HA	3:J:94:GLN:HA	2.02	0.41
3:J:279:LEU:HD23	3:J:295:GLU:HB3	2.02	0.41
2:I:15:PHE:CG	2:I:1190:ALA:HB2	2.56	0.41
2:I:558:VAL:HG13	2:I:573:ASN:HB3	2.02	0.41
2:I:637:ARG:NH2	2:I:654:ASP:OD1	2.54	0.41
3:J:350:SER:HA	3:J:468:VAL:O	2.21	0.41
3:J:1347:LEU:HD22	3:J:1357:ILE:HB	2.01	0.41
7:B:12:DA:H2"	7:B:13:DA:C8	2.55	0.41
2:I:833:ILE:HA	2:I:1054:LEU:O	2.20	0.41
2:I:1105:SER:HA	3:J:736:GLN:OE1	2.21	0.41
2:I:1270:PHE:CE1	2:I:1274:GLU:HB3	2.56	0.41
3:J:317:THR:HG23	3:J:321:LYS:HA	2.03	0.41
3:J:615:LYS:HB2	3:J:616:PRO:HD3	2.03	0.41
5:H:64:VAL:HG13	5:H:69:SER:HB2	2.03	0.41
7:B:21:DC:H2'	7:B:22:DG:C8	2.54	0.41
2:I:89:GLY:HA2	2:I:140:GLY:HA3	2.03	0.41
2:I:257:ALA:HB1	2:I:282:VAL:HG11	2.02	0.41
2:I:871:VAL:HG11	2:I:928:VAL:HG21	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:J:963:VAL:HB	3:J:980:THR:HG23	2.02	0.41
3:J:1173:ARG:HG3	3:J:1192:LYS:HG2	2.03	0.41
5:G:226:GLU:HG2	5:H:10:LYS:HE3	2.02	0.41
3:J:257:GLY:HA3	3:J:259:ARG:NH1	2.36	0.41
3:J:515:ARG:HH22	3:J:717:VAL:HG12	1.86	0.41
3:J:664:ILE:HD13	3:J:664:ILE:HA	1.80	0.41
5:G:9:LEU:HD23	5:G:9:LEU:HA	1.90	0.41
5:G:85:LEU:HD23	5:G:85:LEU:HA	1.83	0.41
5:H:168:ILE:H	5:H:168:ILE:HG12	1.68	0.41
5:H:178:SER:HA	5:H:179:PRO:HD3	1.92	0.41
7:B:31:DC:H1'	7:B:32:DG:C8	2.56	0.41
2:I:813:GLU:HB2	3:J:461:PHE:HD2	1.86	0.41
2:I:1282:GLY:HA3	4:K:17:PHE:CE1	2.56	0.41
3:J:115:TRP:O	3:J:119:SER:OG	2.21	0.41
3:J:641:ILE:HD12	3:J:641:ILE:HA	1.90	0.41
3:J:811:GLU:OE1	3:J:890:THR:OG1	2.24	0.41
7:B:14:DA:H2"	7:B:15:DA:H8	1.86	0.41
2:I:797:GLY:HA3	2:I:1232:MET:O	2.20	0.40
2:I:1340:GLU:HB3	3:J:21:LYS:HZ3	1.85	0.40
3:J:325:LYS:HE3	3:J:325:LYS:HB3	1.76	0.40
5:G:227:GLN:HG2	5:H:39:LEU:HD21	2.02	0.40
1:P:22:GLU:HG2	1:P:28:CYS:SG	2.61	0.40
2:I:657:THR:HB	2:I:1187:PHE:HB2	2.03	0.40
3:J:516:ASP:OD1	3:J:516:ASP:N	2.50	0.40
3:J:954:ASN:HB2	3:J:984:LEU:HD21	2.03	0.40
1:P:13:GLN:OE1	1:P:16:ARG:NH1	2.42	0.40
2:I:222:ASP:OD1	2:I:227:LYS:NZ	2.34	0.40
2:I:452:ARG:HH22	2:I:458:GLU:CD	2.25	0.40
2:I:1328:LYS:HA	2:I:1328:LYS:HD2	1.83	0.40
2:I:469:VAL:O	2:I:472:GLU:HG3	2.21	0.40
3:J:1047:THR:OG1	3:J:1048:ARG:N	2.54	0.40
4:K:26:ARG:O	4:K:30:MET:HG3	2.22	0.40
5:G:195:ARG:HE	5:G:195:ARG:HB3	1.75	0.40
2:I:32:LEU:HD23	2:I:130:MET:SD	2.62	0.40
2:I:1216:ARG:HA	5:G:45:ARG:NH1	2.37	0.40
3:J:802:ASP:OD2	3:J:1348:LYS:NZ	2.55	0.40
3:J:1221:LEU:HD22	3:J:1306:LEU:HB2	2.04	0.40
5:H:56:VAL:HG22	5:H:146:VAL:HG12	2.02	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	
1	P	132/164 (80%)	129 (98%)	3 (2%)	0	100	100
2	I	1317/1342 (98%)	1283 (97%)	34 (3%)	0	100	100
3	J	1309/1416 (92%)	1266 (97%)	43 (3%)	0	100	100
4	K	81/91 (89%)	80 (99%)	1 (1%)	0	100	100
5	G	231/329 (70%)	225 (97%)	6 (3%)	0	100	100
5	H	218/329 (66%)	208 (95%)	10 (5%)	0	100	100
All	All	3288/3671 (90%)	3191 (97%)	97 (3%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

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	
1	P	118/143 (82%)	112 (95%)	6 (5%)	24	56
2	I	1140/1157 (98%)	1097 (96%)	43 (4%)	33	66
3	J	1103/1177 (94%)	1049 (95%)	54 (5%)	25	57
4	K	70/75 (93%)	64 (91%)	6 (9%)	10	37
5	G	201/286 (70%)	198 (98%)	3 (2%)	65	85
5	H	190/286 (66%)	178 (94%)	12 (6%)	18	48
All	All	2822/3124 (90%)	2698 (96%)	124 (4%)	32	61

All (124) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	P	29	LEU
1	P	39	VAL
1	P	53	ASN
1	P	57	VAL
1	P	66	THR
1	P	139	CYS
2	I	23	ASP
2	I	29	SER
2	I	70	TYR
2	I	124	MET
2	I	132	ASP
2	I	135	THR
2	I	151	ARG
2	I	170	VAL
2	I	189	ASP
2	I	234	ASP
2	I	237	LEU
2	I	264	GLU
2	I	308	GLU
2	I	315	MET
2	I	351	LEU
2	I	384	LEU
2	I	403	MET
2	I	472	GLU
2	I	504	GLU
2	I	514	PHE
2	I	539	THR
2	I	549	ASP
2	I	563	THR
2	I	598	VAL
2	I	655	VAL
2	I	660	VAL
2	I	677	ASN
2	I	888	THR
2	I	937	ASP
2	I	968	GLU
2	I	973	SER
2	I	979	LEU
2	I	987	GLU
2	I	1037	THR
2	I	1041	ASP
2	I	1064	ASP

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Mol	Chain	Res	Type
2	I	1106	ARG
2	I	1141	LEU
2	I	1164	PHE
2	I	1188	ASP
2	I	1319	MET
2	I	1329	GLU
2	I	1339	LEU
3	J	29	MET
3	J	50	LYS
3	J	139	LEU
3	J	142	GLU
3	J	154	LEU
3	J	205	LEU
3	J	212	THR
3	J	224	LEU
3	J	250	ARG
3	J	259	ARG
3	J	262	THR
3	J	279	LEU
3	J	348	ASP
3	J	374	LEU
3	J	423	LEU
3	J	434	ILE
3	J	464	ASP
3	J	472	LEU
3	J	478	LEU
3	J	497	GLU
3	J	525	MET
3	J	541	LEU
3	J	553	THR
3	J	587	LEU
3	J	639	VAL
3	J	655	SER
3	J	673	VAL
3	J	707	ILE
3	J	713	GLU
3	J	762	ASN
3	J	792	ASN
3	J	814	CYS
3	J	830	ASP
3	J	862	THR
3	J	888	CYS

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Mol	Chain	Res	Type
3	J	895	CYS
3	J	967	VAL
3	J	982	LEU
3	J	1025	MET
3	J	1029	THR
3	J	1034	PHE
3	J	1067	ARG
3	J	1084	GLN
3	J	1101	LEU
3	J	1116	SER
3	J	1117	SER
3	J	1162	ILE
3	J	1184	ASP
3	J	1200	GLU
3	J	1229	VAL
3	J	1273	ASP
3	J	1321	SER
3	J	1365	TYR
3	J	1366	HIS
4	K	3	ARG
4	K	4	VAL
4	K	25	ARG
4	K	44	ASP
4	K	47	THR
4	K	67	ARG
5	G	83	LEU
5	G	186	ASN
5	G	235	ARG
5	H	5	VAL
5	H	9	LEU
5	H	12	ARG
5	H	13	LEU
5	H	39	LEU
5	H	80	GLU
5	H	98	VAL
5	H	129	VAL
5	H	196	THR
5	H	202	VAL
5	H	205	MET
5	H	231	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
5	G	41	ASN

5.3.3 RNA (i)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
6	R	11/17 (64%)	2 (18%)	0

All (2) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	R	7	U
6	R	17	U

There are no RNA pucker outliers to report.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 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 (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

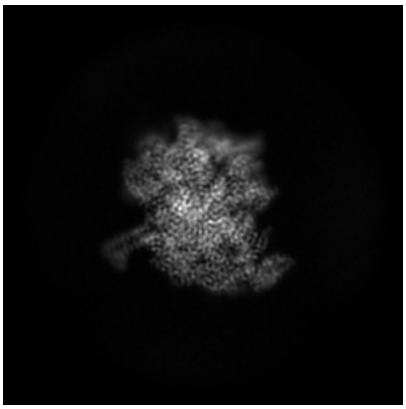
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-17646. These allow visual inspection of the internal detail of the map and identification of artifacts.

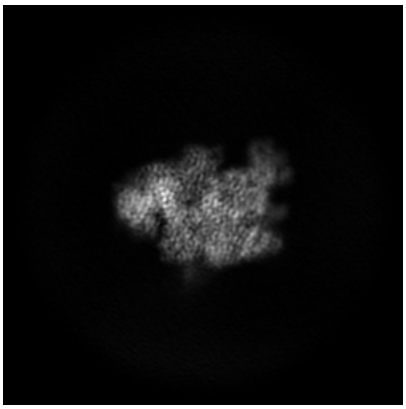
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

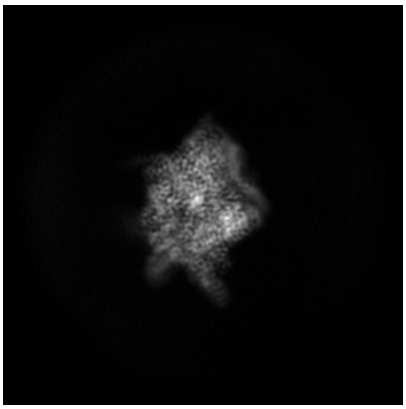
6.1.1 Primary map



X

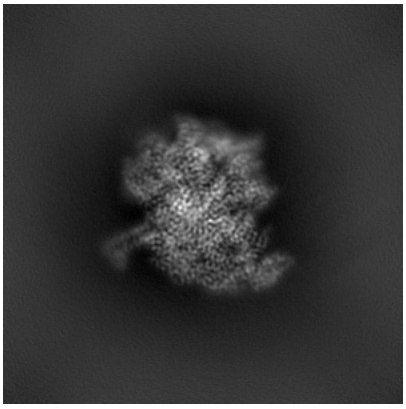


Y

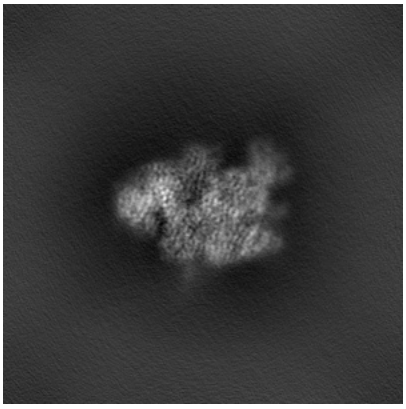


Z

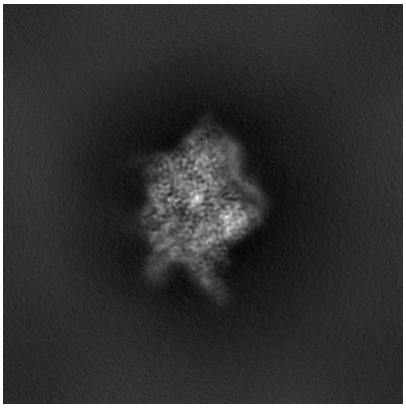
6.1.2 Raw map



X



Y

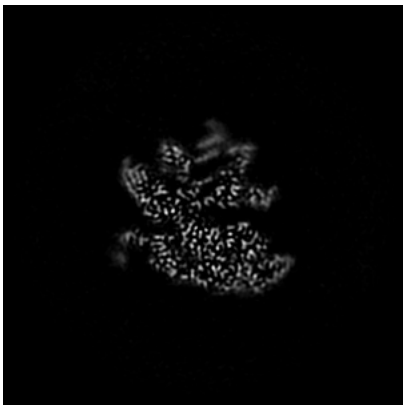


Z

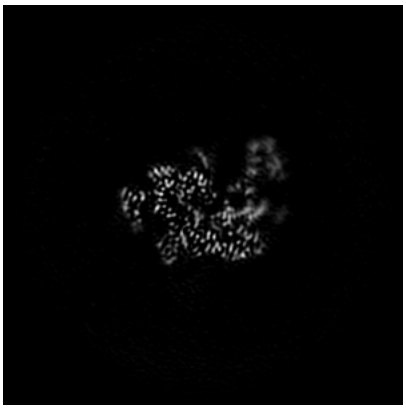
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

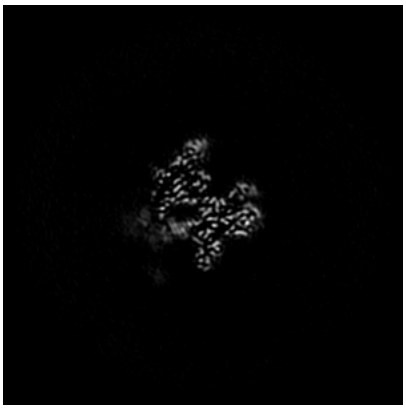
6.2.1 Primary map



X Index: 192

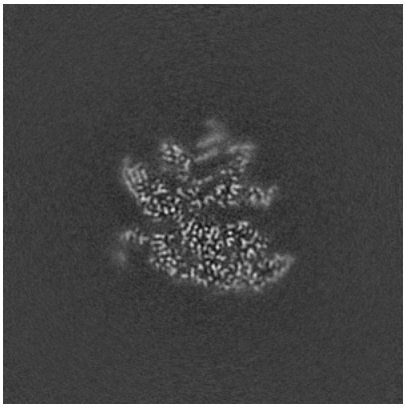


Y Index: 192

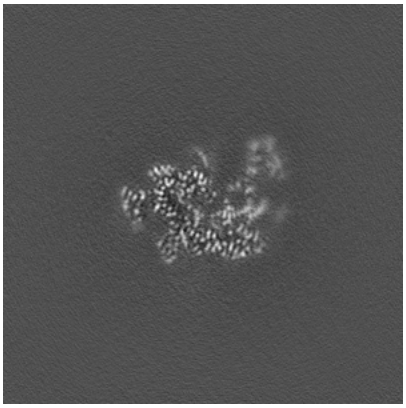


Z Index: 192

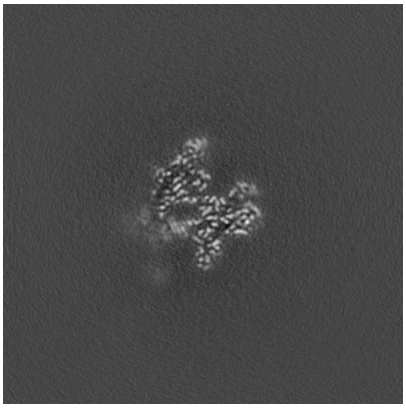
6.2.2 Raw map



X Index: 192



Y Index: 192

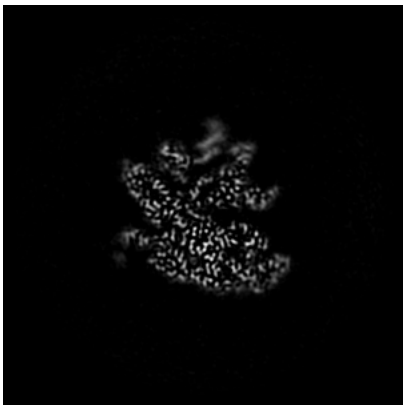


Z Index: 192

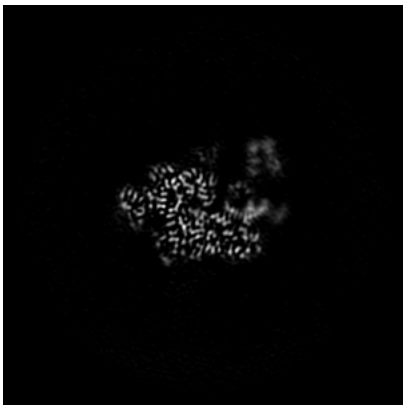
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

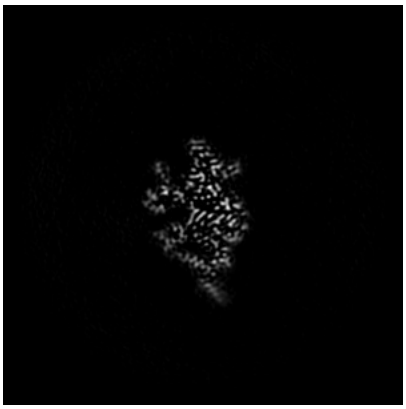
6.3.1 Primary map



X Index: 190

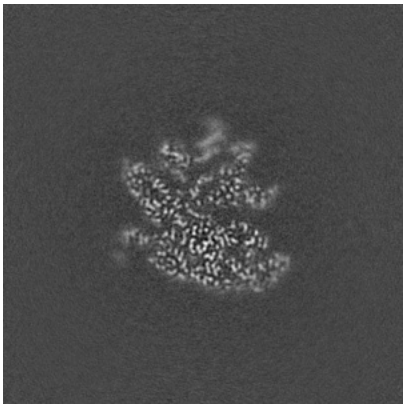


Y Index: 194

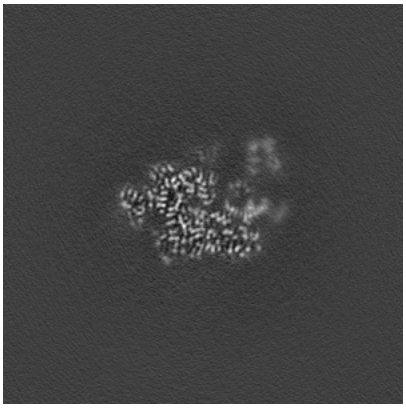


Z Index: 157

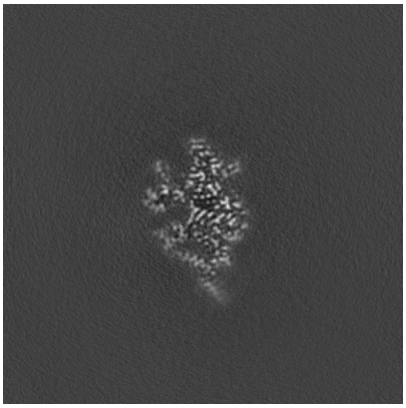
6.3.2 Raw map



X Index: 190



Y Index: 194

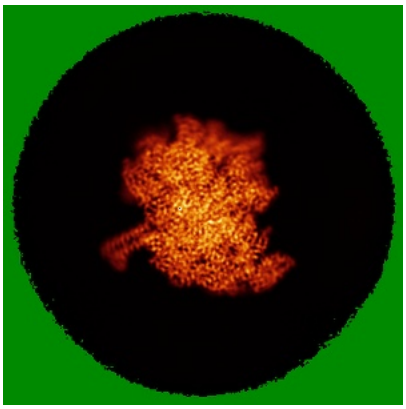


Z Index: 157

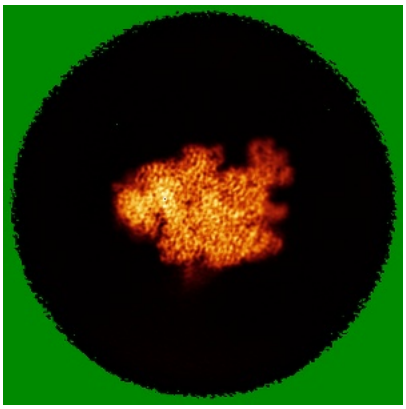
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

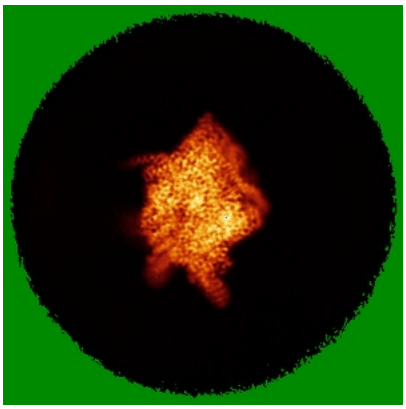
6.4.1 Primary map



X

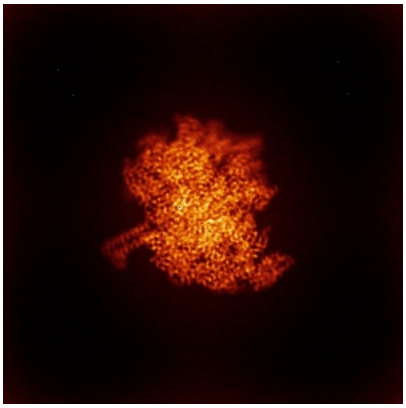


Y

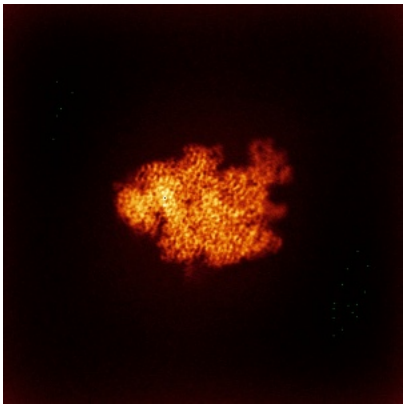


Z

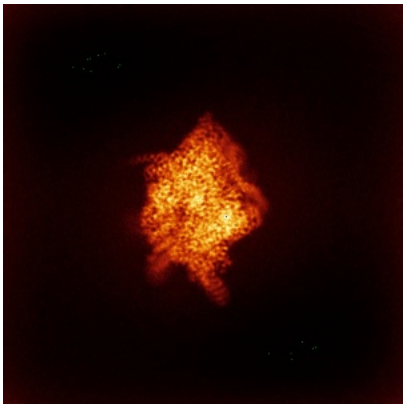
6.4.2 Raw map



X



Y

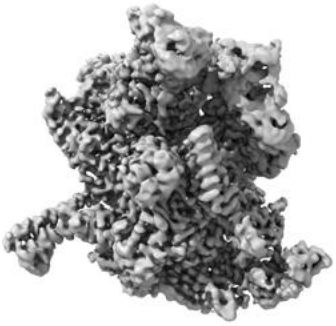


Z

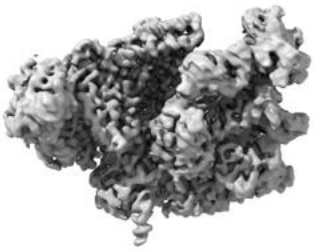
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views (i)

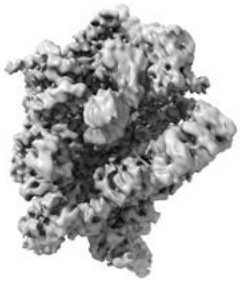
6.5.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map

X

Y

Z

These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

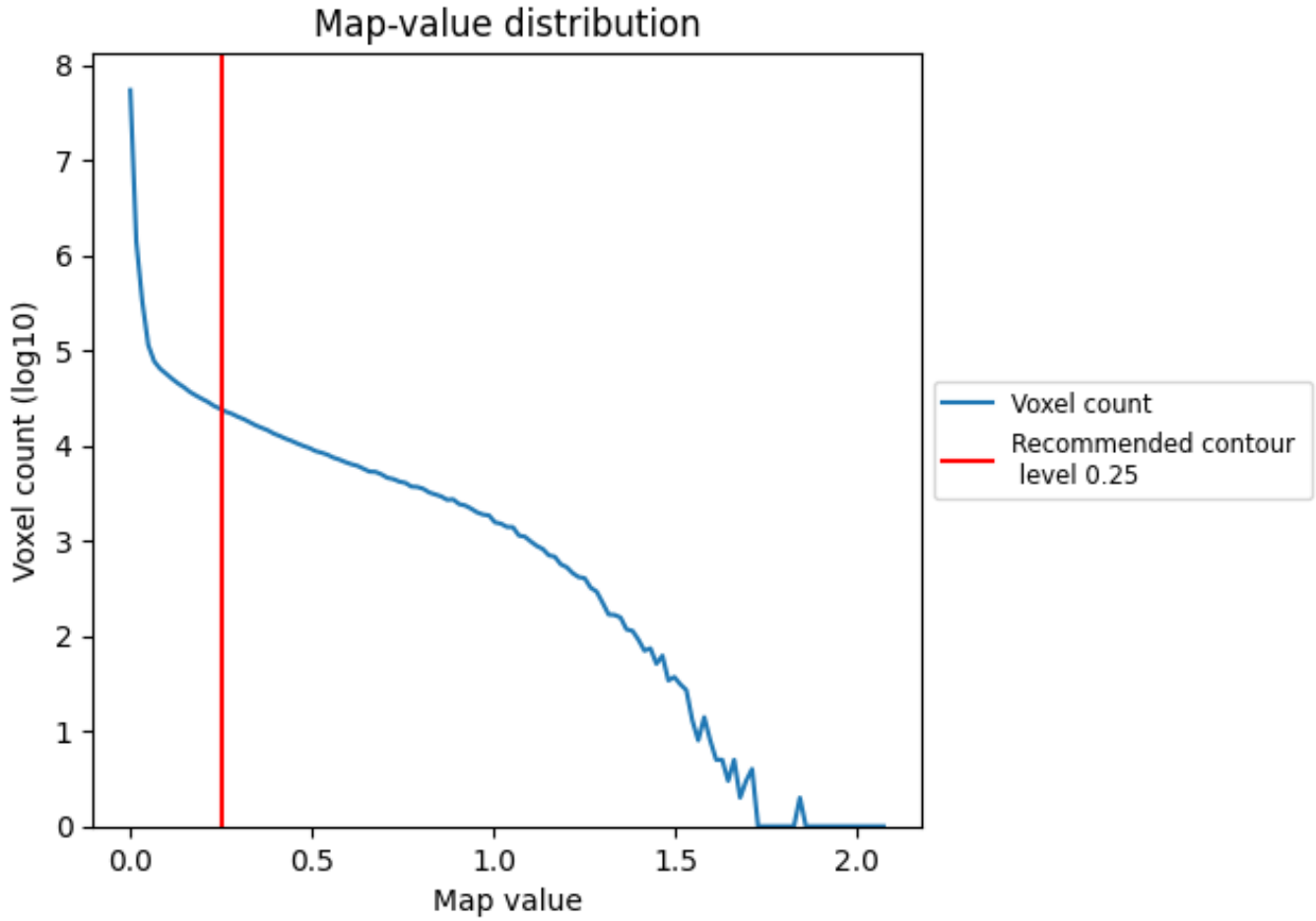
6.6 Mask visualisation (i)

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

7 Map analysis

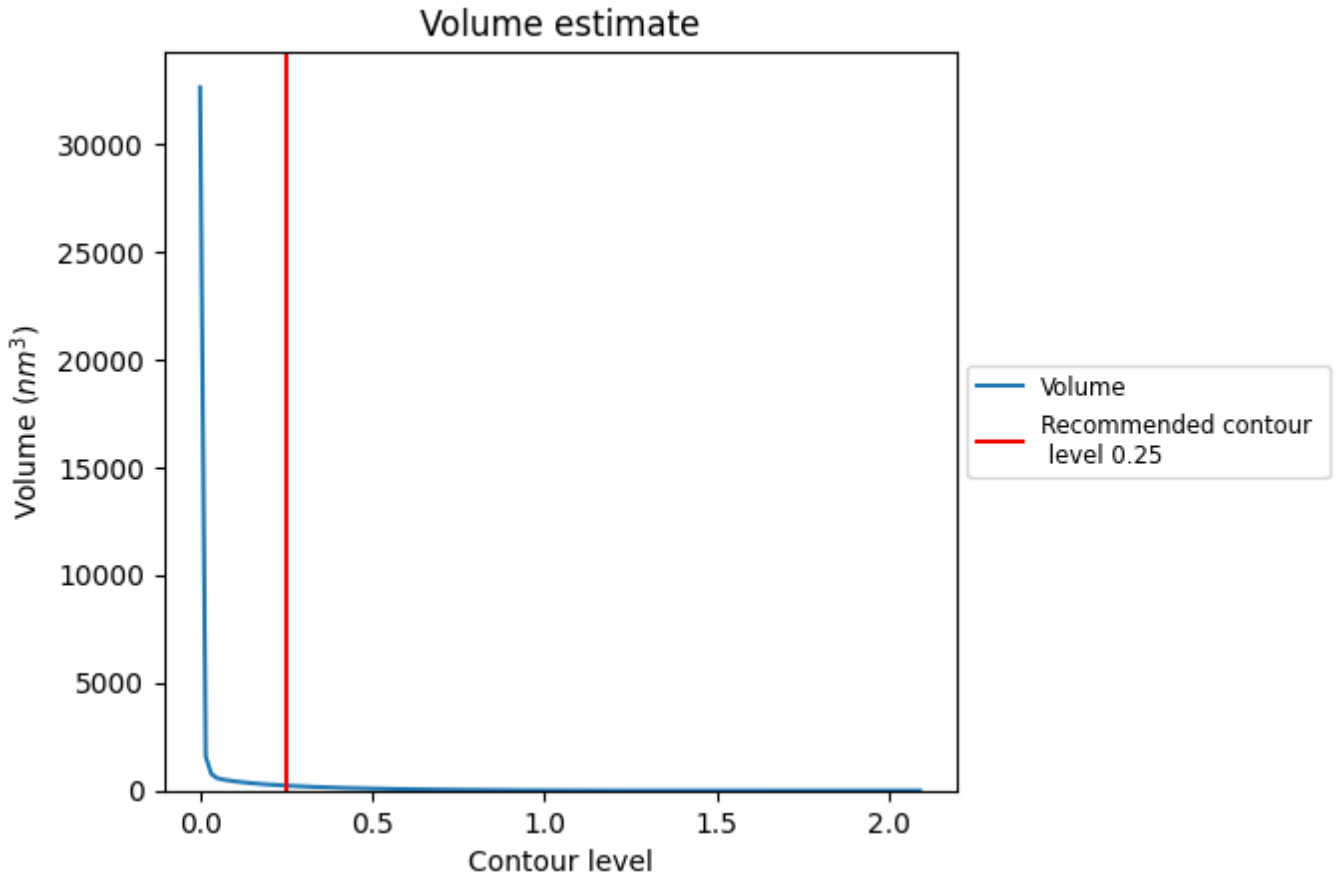
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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.

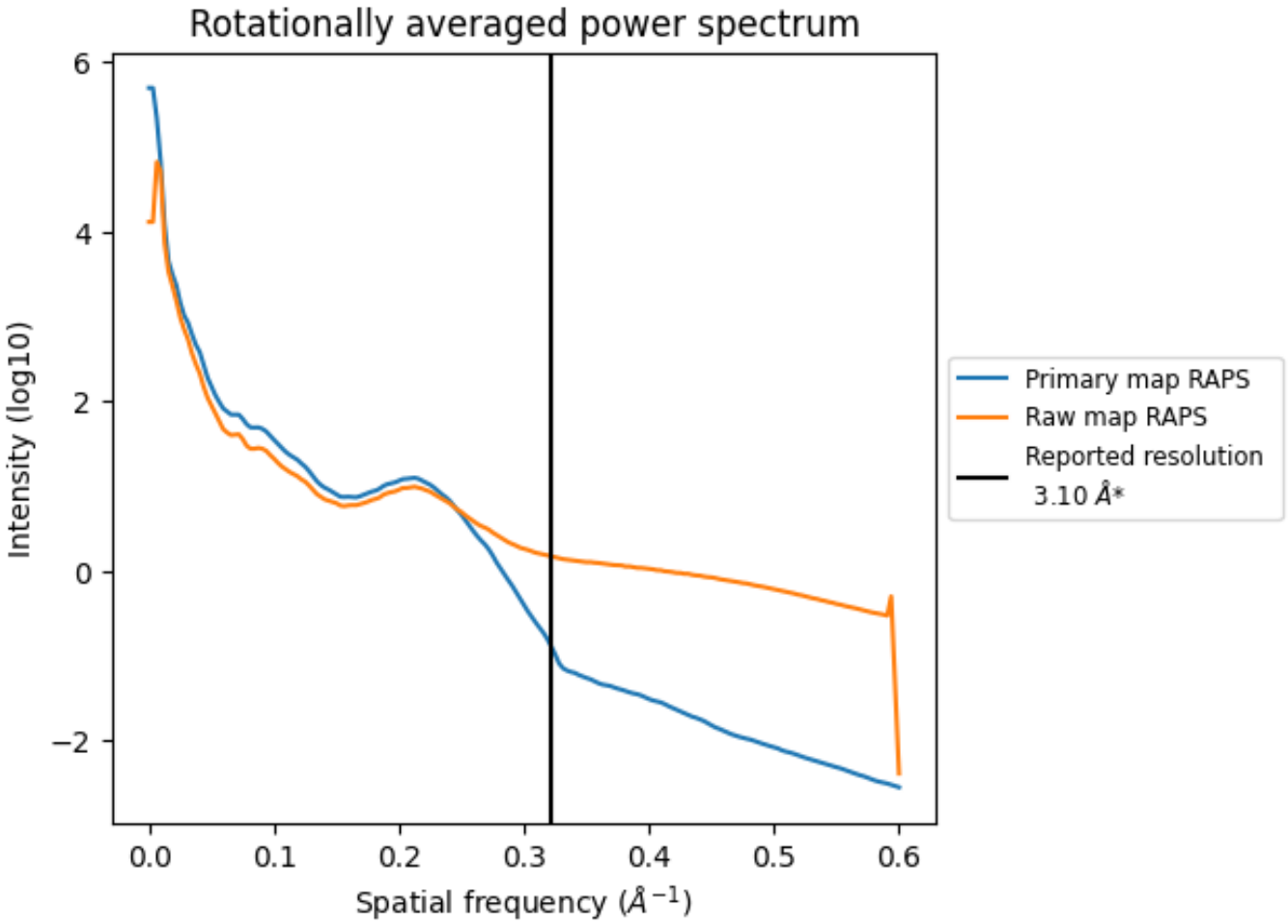
7.2 Volume estimate



The volume at the recommended contour level is 229 nm^3; this corresponds to an approximate mass of 206 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 (i)

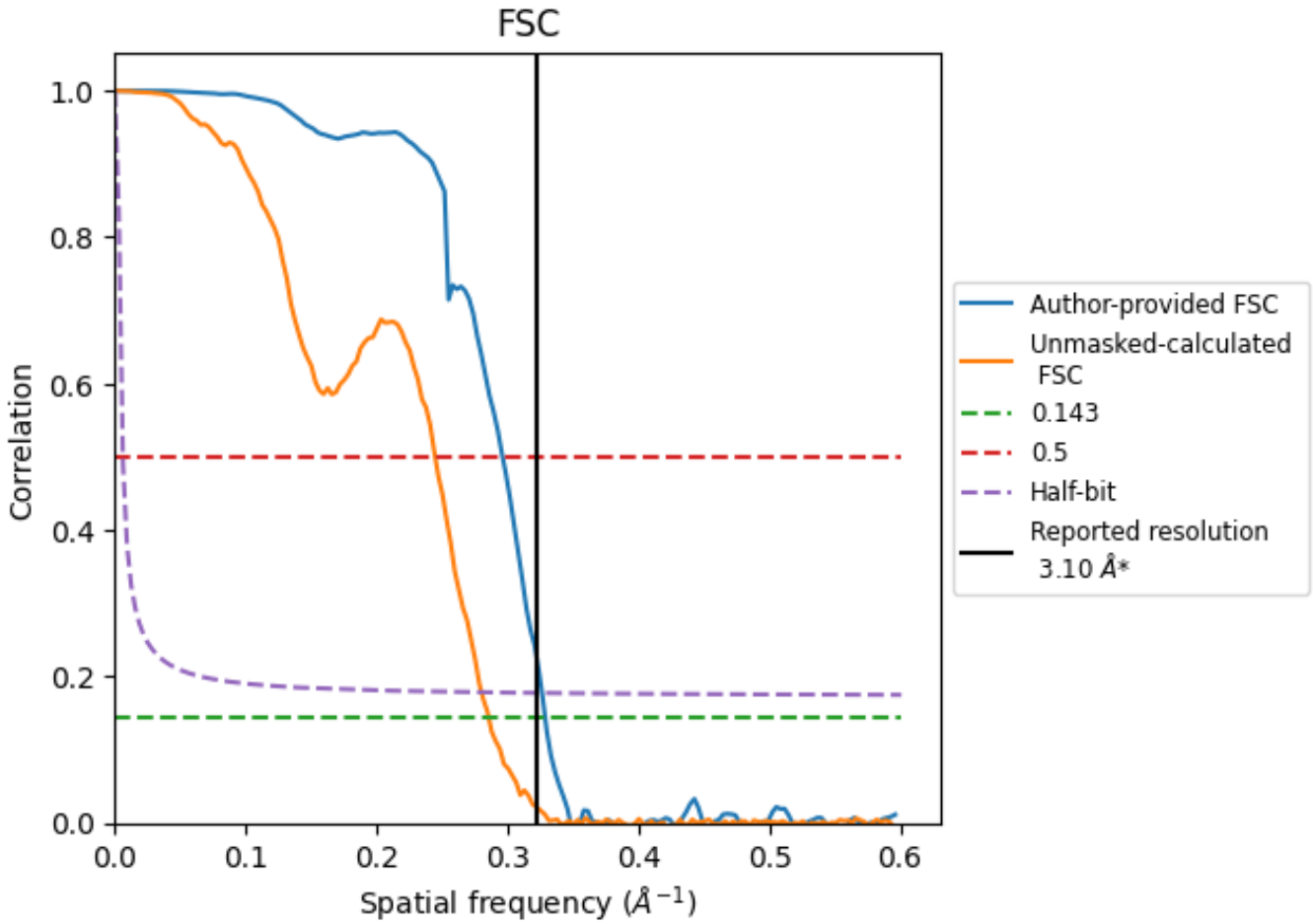


*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.323 Å^{-1}

8.2 Resolution estimates (i)

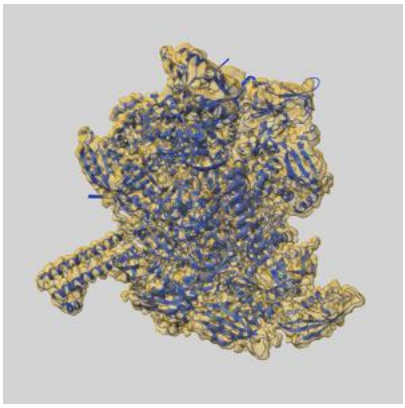
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.04	3.37	3.06
Unmasked-calculated*	3.50	4.08	3.57

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.50 differs from the reported value 3.1 by more than 10 %

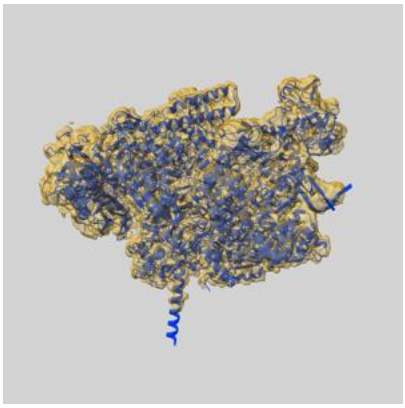
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-17646 and PDB model 8PFG. Per-residue inclusion information can be found in section 3 on page 7.

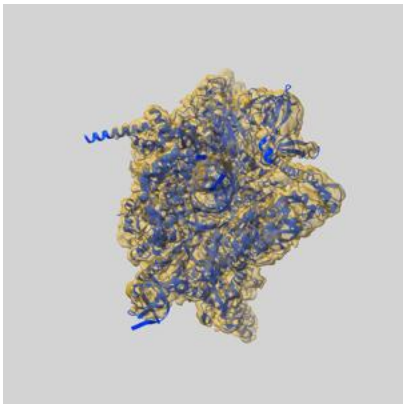
9.1 Map-model overlay



X



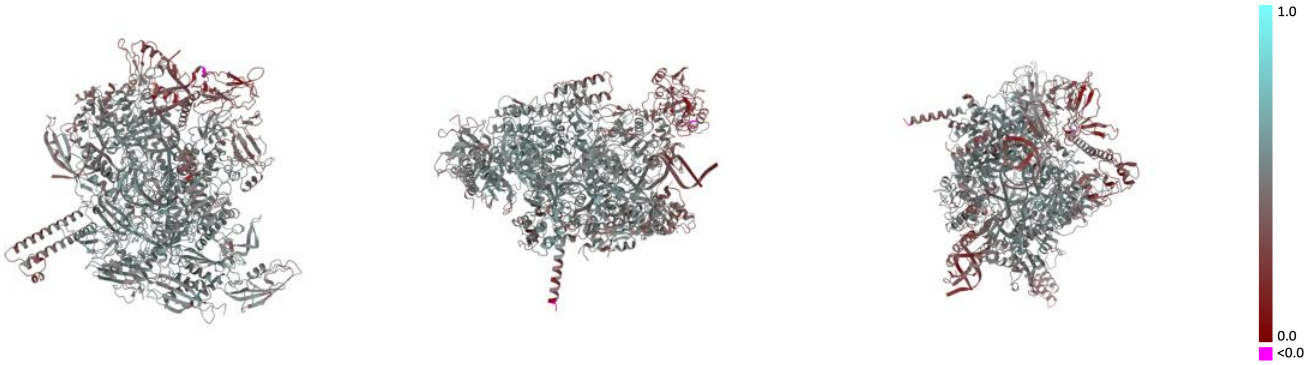
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.25 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.

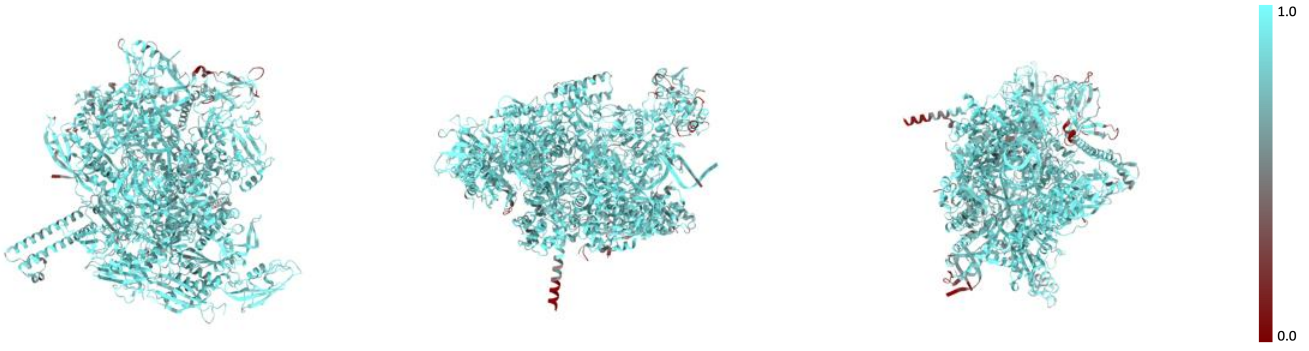
9.2 Q-score mapped to coordinate model (i)



X Y Z

The images above show the model with each residue coloured according 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.

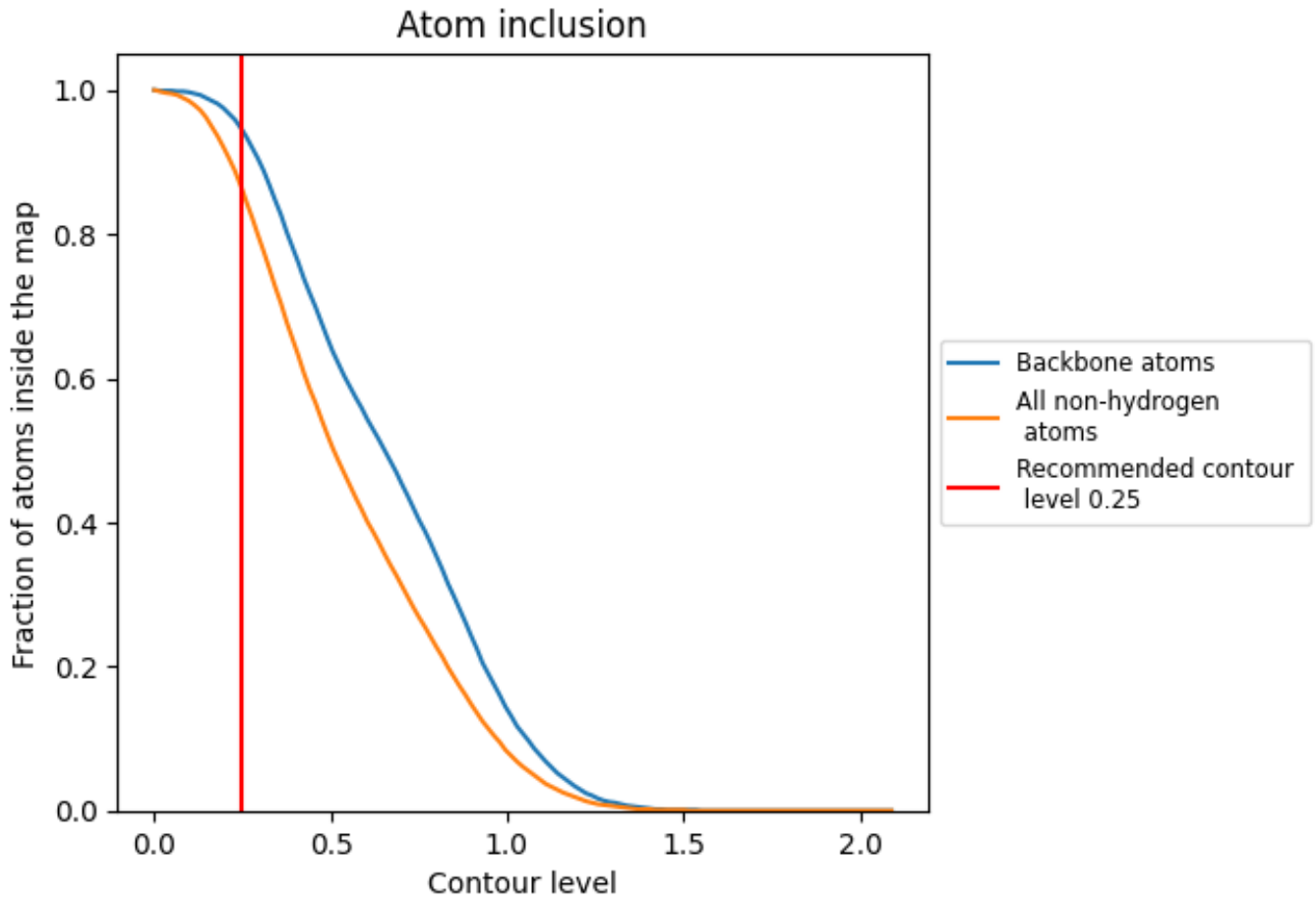
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (0.25).

9.4 Atom inclusion (i)



At the recommended contour level, 94% of all backbone atoms, 86% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8610	0.4710
A	0.8490	0.3770
B	0.8660	0.3600
G	0.8560	0.4990
H	0.8690	0.4790
I	0.8840	0.4910
J	0.8550	0.4700
K	0.7290	0.4560
P	0.7570	0.3910
R	0.8910	0.4570