



Full wwPDB EM Validation Report ⓘ

Apr 13, 2026 – 04:18 PM JST

PDB ID : 9UH7 / pdb_00009uh7
EMDB ID : EMD-64157
Title : large lobe of human Ribonuclease MRP
Authors : Zhou, B.; Lan, P.; Wu, J.; Lei, M.
Deposited on : 2025-04-14
Resolution : 2.84 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.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

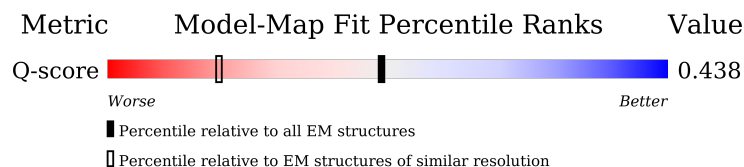
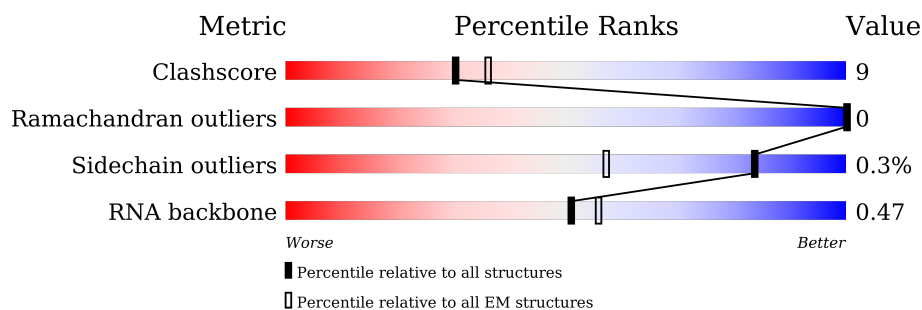
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.84 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.




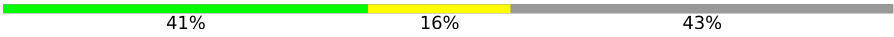







Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	11884 (2.34 - 3.34)

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	A	270	
2	B	1024	
3	D	220	

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Mol	Chain	Length	Quality of chain
4	E	163	 74%18%8%
5	F	199	 41%16%43%
6	G	140	 61%24%14%
7	H	124	 84%15%.
8	I	268	 76%13%12%
8	J	268	 76%16%7%
9	K	220	 10%5%85%
10	L	363	 88%12%
11	M	567	 29%12%59%

2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 24267 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 RNA chain called RNA (270-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	204	Total	C	N	O	P	0	0
			4320	1928	752	1436	204		

- Molecule 2 is a protein called Ribonucleases P/MRP protein subunit POP1.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	718	Total	C	N	O	S	0	0
			5689	3628	1016	1006	39		

- Molecule 3 is a protein called Ribonuclease P protein subunit p29.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	186	Total	C	N	O	S	0	0
			1502	960	268	269	5		

- Molecule 4 is a protein called Ribonuclease P/MRP protein subunit POP5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	150	Total	C	N	O	S	0	0
			1224	778	223	215	8		

- Molecule 5 is a protein called Ribonuclease P protein subunit p25.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	114	Total	C	N	O	S	0	0
			869	547	166	151	5		

- Molecule 6 is a protein called Ribonuclease P protein subunit p20.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	120	Total	C	N	O	S	0	0
			945	587	181	174	3		

- Molecule 7 is a protein called Ribonuclease P protein subunit p14.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	122	Total	C	N	O	S	0	0
			946	614	153	174	5		

- Molecule 8 is a protein called Ribonuclease P protein subunit p30.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	237	Total	C	N	O	S	0	0
			1829	1169	320	333	7		
8	J	248	Total	C	N	O	S	0	0
			1916	1227	336	346	7		

- Molecule 9 is a protein called UPF0711 protein C18orf21.

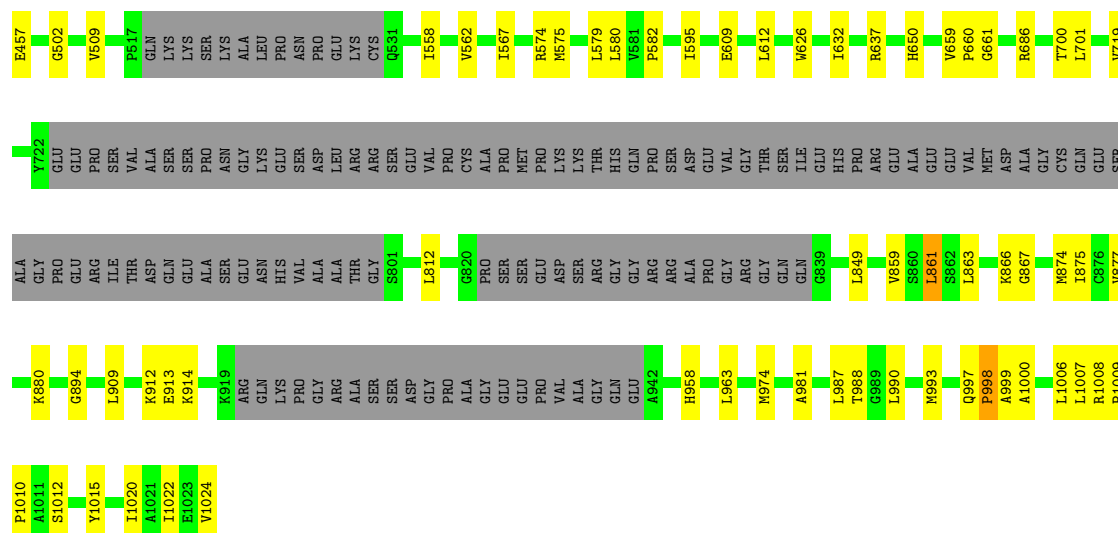
Mol	Chain	Residues	Atoms					AltConf	Trace
9	K	32	Total	C	N	O	S	0	0
			260	163	51	45	1		

- Molecule 10 is a protein called Ribonuclease P protein subunit p40.

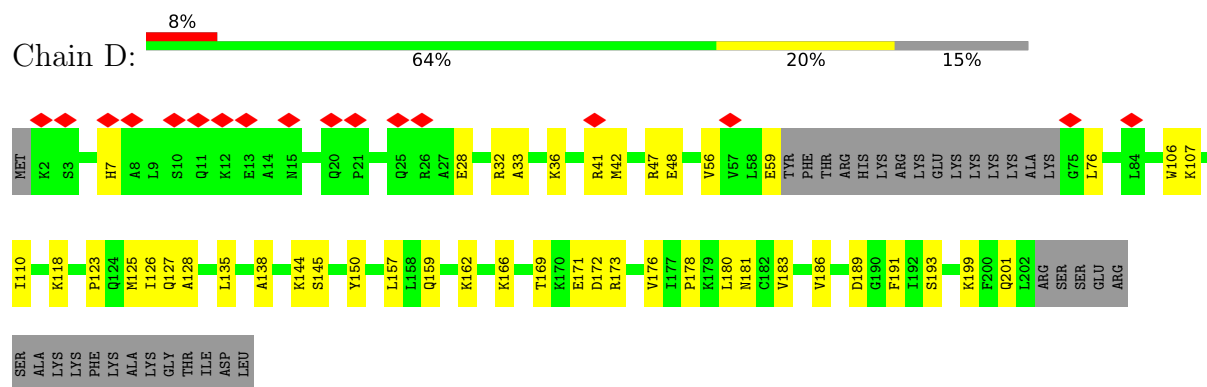
Mol	Chain	Residues	Atoms					AltConf	Trace
10	L	362	Total	C	N	O	S	0	0
			2939	1893	489	540	17		

- Molecule 11 is a protein called Nucleolus and neural progenitor protein.

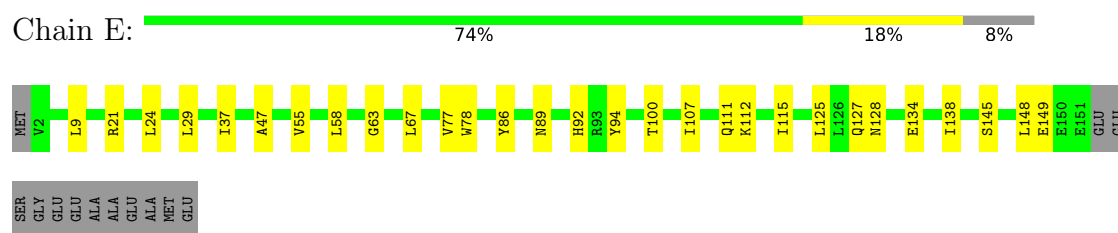
Mol	Chain	Residues	Atoms					AltConf	Trace
11	M	230	Total	C	N	O	S	0	0
			1828	1190	309	315	14		



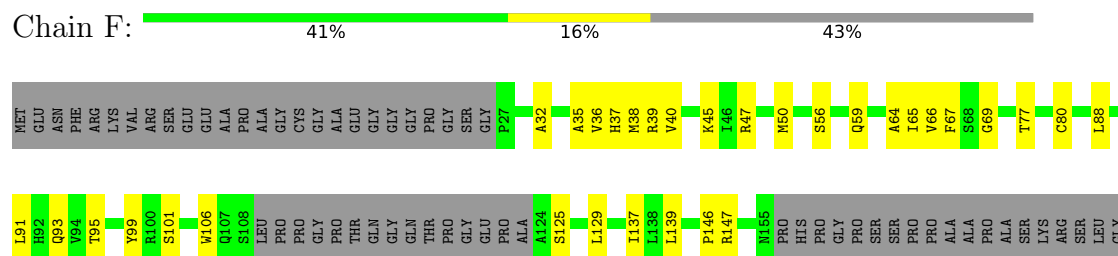
• Molecule 3: Ribonuclease P protein subunit p29

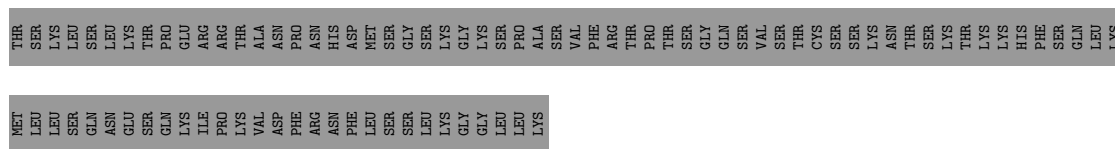


• Molecule 4: Ribonuclease P/MRP protein subunit POP5

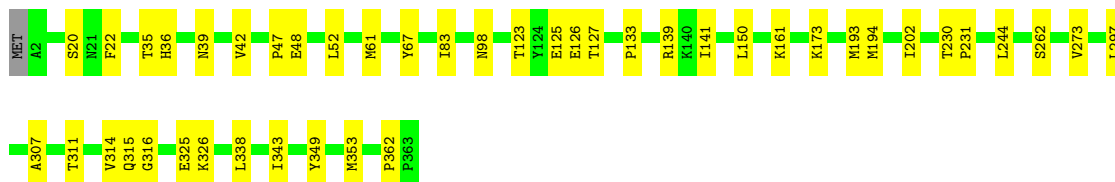
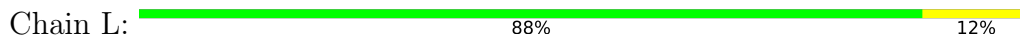


• Molecule 5: Ribonuclease P protein subunit p25

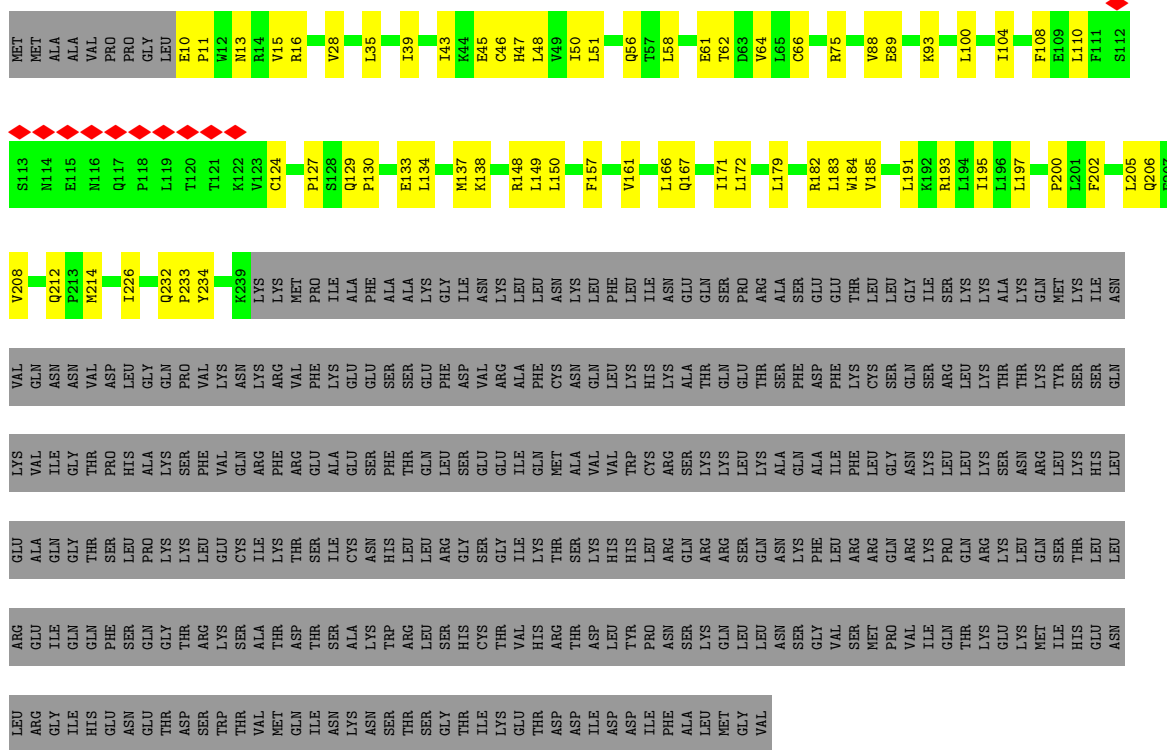




- Molecule 10: Ribonuclease P protein subunit p40



- Molecule 11: Nucleolus and neural progenitor protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	777423	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2200	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.055	Depositor
Minimum map value	-0.020	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size (\AA)	281.6, 281.6, 281.6	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.08	0/4818	0.23	0/7500
2	B	0.17	1/5828 (0.0%)	0.58	9/7885 (0.1%)
3	D	0.17	0/1529	0.49	0/2056
4	E	0.15	0/1247	0.40	0/1683
5	F	0.14	0/884	0.42	0/1194
6	G	0.16	0/957	0.43	0/1293
7	H	0.14	0/963	0.40	0/1303
8	I	0.12	0/1860	0.32	0/2522
8	J	0.13	0/1949	0.32	0/2641
9	K	0.16	0/268	0.50	0/362
10	L	0.09	0/3021	0.28	0/4099
11	M	0.18	0/1864	0.47	0/2526
All	All	0.14	1/25188 (0.0%)	0.41	9/35064 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
7	H	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	PRO	N-CD	9.70	1.61	1.47

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	ALA	N-CA-C	26.45	145.69	112.89
2	B	998	PRO	N-CA-C	-16.91	83.17	110.40
2	B	299	LYS	CB-CA-C	-14.51	88.70	110.62

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	999	ALA	N-CA-CB	-13.87	87.80	110.40
2	B	1000	ALA	N-CA-C	-11.38	99.21	113.55
2	B	299	LYS	N-CA-C	9.22	124.43	108.02
2	B	300	TYR	N-CA-C	8.73	129.10	109.81
2	B	300	TYR	N-CA-CB	-7.30	97.38	110.37
2	B	999	ALA	CB-CA-C	-6.10	97.25	109.99

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
7	H	76	ARG	Sidechain

5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4320	0	2202	72	0
2	B	5689	0	5775	101	0
3	D	1502	0	1561	45	0
4	E	1224	0	1238	23	0
5	F	869	0	912	27	0
6	G	945	0	971	29	0
7	H	946	0	977	13	0
8	I	1829	0	1914	24	0
8	J	1916	0	2015	36	0
9	K	260	0	244	9	0
10	L	2939	0	2884	33	0
11	M	1828	0	1926	57	0
All	All	24267	0	22619	424	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 (424) 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)
4:E:58:LEU:HD13	4:E:145:SER:HB2	1.35	1.04
8:I:212:LEU:HD13	8:I:217:ALA:HA	1.44	0.99
8:J:10:ARG:HE	8:J:36:ASN:ND2	1.70	0.88
8:J:122:VAL:HG23	8:J:150:LEU:HD21	1.59	0.85
8:I:212:LEU:CD1	8:I:217:ALA:HA	2.06	0.85
4:E:58:LEU:HD13	4:E:145:SER:CB	2.11	0.79
3:D:127:GLN:HE21	8:J:244:THR:HG22	1.47	0.79
10:L:230:THR:CG2	10:L:231:PRO:HD2	2.12	0.79
6:G:78:ILE:HD12	6:G:79:ASN:H	1.49	0.78
5:F:38:MET:HB2	5:F:66:VAL:O	1.83	0.77
1:A:247:G:O4'	2:B:227:THR:HG23	1.85	0.77
10:L:230:THR:HG23	10:L:231:PRO:HD2	1.67	0.77
2:B:562:VAL:HG13	2:B:595:ILE:HG22	1.69	0.73
3:D:125:MET:HE3	3:D:125:MET:H	1.52	0.73
11:M:11:PRO:HB2	11:M:137:MET:HE1	1.72	0.71
8:J:246:LYS:HG3	8:J:248:PRO:HD3	1.72	0.71
4:E:111:GLN:OE1	4:E:148:LEU:HB2	1.92	0.70
6:G:98:VAL:HG12	6:G:134:VAL:HG22	1.72	0.70
5:F:93:GLN:HG2	5:F:137:ILE:HD11	1.75	0.69
1:A:237:C:H5''	1:A:238:A:H5'	1.74	0.68
2:B:863:LEU:HD22	2:B:867:GLY:HA3	1.75	0.68
2:B:558:ILE:O	2:B:562:VAL:HG23	1.93	0.68
11:M:171:ILE:HD12	11:M:172:LEU:H	1.59	0.67
2:B:861:LEU:CD2	2:B:1020:ILE:HG22	2.25	0.66
2:B:87:TRP:CD1	11:M:66:CYS:HG	2.13	0.66
6:G:41:MET:HE3	6:G:41:MET:HA	1.77	0.66
2:B:997:GLN:C	2:B:998:PRO:O	2.24	0.66
5:F:106:TRP:O	5:F:125:SER:HA	1.96	0.66
7:H:29:GLN:HE21	7:H:98:LYS:HB3	1.61	0.66
10:L:83:ILE:HD11	10:L:150:LEU:HB3	1.78	0.66
5:F:38:MET:HG2	5:F:65:ILE:HD11	1.78	0.65
1:A:82:G:H2'	1:A:83:A:H8	1.61	0.65
11:M:130:PRO:O	11:M:134:LEU:HD12	1.97	0.65
4:E:78:TRP:HE1	4:E:100:THR:HG21	1.62	0.65
2:B:87:TRP:NE1	11:M:66:CYS:SG	2.70	0.65
3:D:159:GLN:HB2	3:D:166:LYS:HB2	1.80	0.64
1:A:232:C:H2'	1:A:233:G:H8	1.61	0.64
10:L:315:GLN:HG3	10:L:338:LEU:HB3	1.80	0.64
8:J:76:ARG:HB2	8:J:102:VAL:HB	1.80	0.64
2:B:316:ARG:HD3	2:B:317:THR:H	1.63	0.64
11:M:100:LEU:O	11:M:104:ILE:HD12	1.97	0.64
2:B:87:TRP:CD1	11:M:66:CYS:SG	2.91	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:146:PRO:HB2	5:F:147:ARG:HH12	1.63	0.63
6:G:41:MET:SD	6:G:76:LEU:HB2	2.39	0.63
3:D:199:LYS:NZ	8:J:241:ILE:HA	2.14	0.62
8:J:124:LEU:HD11	8:J:186:ILE:HD11	1.81	0.62
1:A:111:C:H2'	1:A:112:G:C8	2.35	0.61
4:E:24:LEU:HD21	4:E:29:LEU:HG	1.82	0.61
6:G:78:ILE:HD12	6:G:79:ASN:N	2.15	0.61
8:J:67:LYS:H	8:J:67:LYS:HD2	1.64	0.61
2:B:140:ARG:HE	11:M:166:LEU:HD11	1.64	0.61
5:F:38:MET:HE3	5:F:38:MET:HA	1.83	0.61
11:M:39:ILE:O	11:M:43:ILE:HG12	2.00	0.61
3:D:162:LYS:HG3	3:D:201:GLN:HB3	1.82	0.60
3:D:199:LYS:HZ3	8:J:241:ILE:HD12	1.65	0.60
2:B:574:ARG:HE	2:B:575:MET:HE3	1.65	0.60
11:M:43:ILE:HG22	11:M:47:HIS:CE1	2.37	0.60
1:A:112:G:H2'	1:A:113:C:H6	1.67	0.60
2:B:449:ALA:HA	2:B:509:VAL:HG12	1.83	0.60
6:G:115:THR:HG22	6:G:117:THR:H	1.66	0.60
8:I:212:LEU:HD13	8:I:217:ALA:CA	2.26	0.60
10:L:230:THR:HG22	10:L:231:PRO:HD2	1.84	0.60
2:B:301:PRO:HG2	2:B:302:ARG:HD2	1.84	0.59
2:B:1006:LEU:HD22	2:B:1015:TYR:HB3	1.83	0.59
1:A:8:U:H2'	1:A:9:G:H8	1.67	0.59
2:B:146:HIS:C	2:B:146:HIS:CD2	2.80	0.59
2:B:288:ARG:HB3	2:B:502:GLY:HA3	1.83	0.58
1:A:98:U:H2'	1:A:99:G:H8	1.67	0.58
11:M:214:MET:HE3	11:M:214:MET:O	2.04	0.58
2:B:442:ILE:HG23	2:B:637:ARG:HG2	1.84	0.58
1:A:8:U:H2'	1:A:9:G:C8	2.39	0.58
3:D:41:ARG:HB2	11:M:167:GLN:HE21	1.68	0.58
2:B:812:LEU:HB3	2:B:1024:VAL:HG21	1.84	0.58
6:G:74:LEU:H	6:G:77:ALA:HB3	1.68	0.58
9:K:7:LEU:HD11	9:K:29:TYR:HD2	1.68	0.58
5:F:91:LEU:HD11	5:F:139:LEU:HB3	1.85	0.57
11:M:129:GLN:HG3	11:M:208:VAL:HG12	1.86	0.57
2:B:238:MET:HE1	2:B:650:HIS:HB2	1.86	0.57
10:L:230:THR:CG2	10:L:231:PRO:CD	2.82	0.57
1:A:263:C:H2'	1:A:264:G:H8	1.69	0.57
4:E:89:ASN:HD22	4:E:94:TYR:HE1	1.52	0.57
8:J:116:ALA:HA	8:J:120:LEU:HD12	1.84	0.57
6:G:80:ARG:O	6:G:84:ILE:HG12	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
10:L:67:TYR:HB3	10:L:202:ILE:HD11	1.86	0.57
1:A:62:C:H2'	8:I:67:LYS:HG2	1.86	0.56
2:B:114:GLU:HG2	11:M:182:ARG:HA	1.86	0.56
5:F:95:THR:HB	5:F:137:ILE:HD13	1.87	0.56
11:M:16:ARG:HA	11:M:16:ARG:NH1	2.20	0.56
1:A:56:C:H2'	1:A:57:C:H6	1.71	0.56
3:D:199:LYS:NZ	8:J:241:ILE:HD12	2.20	0.56
1:A:3:G:H22	1:A:267:U:H3	1.53	0.56
6:G:23:ARG:HB3	6:G:110:GLU:HB2	1.87	0.56
2:B:280:ALA:HB3	2:B:283:CYS:HB2	1.87	0.56
3:D:144:LYS:HB3	3:D:183:VAL:HB	1.87	0.56
3:D:199:LYS:HZ1	8:J:241:ILE:HA	1.71	0.56
3:D:41:ARG:HB2	11:M:167:GLN:NE2	2.21	0.56
2:B:335:LEU:O	2:B:335:LEU:HD12	2.06	0.56
6:G:113:PRO:HD3	6:G:120:PRO:HB3	1.89	0.55
8:J:41:PHE:HB3	8:J:86:HIS:HD2	1.71	0.55
11:M:171:ILE:HD12	11:M:172:LEU:N	2.21	0.55
1:A:222:U:H2'	1:A:223:G:H8	1.70	0.55
3:D:180:LEU:O	3:D:181:ASN:OD1	2.25	0.55
2:B:349:CYS:HB2	2:B:415:SER:HB2	1.89	0.55
2:B:849:LEU:HD11	2:B:988:THR:HA	1.89	0.55
2:B:87:TRP:NE1	11:M:66:CYS:HG	2.05	0.54
4:E:127:GLN:HG3	4:E:128:ASN:ND2	2.22	0.54
2:B:861:LEU:HD23	2:B:1020:ILE:HG22	1.89	0.54
3:D:125:MET:HE3	3:D:125:MET:N	2.23	0.54
8:J:96:ARG:H	8:J:96:ARG:HE	1.55	0.54
9:K:24:TYR:HD1	9:K:24:TYR:O	1.90	0.54
1:A:98:U:H2'	1:A:99:G:C8	2.42	0.54
3:D:138:ALA:H	3:D:157:LEU:HD23	1.71	0.54
1:A:82:G:H2'	1:A:83:A:C8	2.42	0.54
1:A:40:A:H2'	1:A:41:G:H8	1.72	0.54
1:A:91:C:H2'	1:A:92:A:H8	1.72	0.54
10:L:61:MET:HE2	10:L:61:MET:HA	1.89	0.54
5:F:35:ALA:HA	5:F:64:ALA:O	2.08	0.54
11:M:46:CYS:O	11:M:50:ILE:HG13	2.08	0.54
6:G:74:LEU:HA	6:G:78:ILE:HG23	1.89	0.53
2:B:861:LEU:HD22	2:B:1020:ILE:HG22	1.88	0.53
8:J:124:LEU:HD11	8:J:186:ILE:CD1	2.38	0.53
2:B:331:LEU:HD12	2:B:332:HIS:O	2.09	0.53
5:F:45:LYS:HD2	5:F:47:ARG:HH12	1.73	0.53
2:B:308:VAL:HG12	2:B:331:LEU:HB3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:245:C:H2'	1:A:246:G:H8	1.72	0.53
11:M:191:LEU:O	11:M:195:ILE:HG13	2.08	0.53
11:M:47:HIS:O	11:M:51:LEU:HG	2.08	0.53
11:M:157:PHE:O	11:M:161:VAL:HG12	2.08	0.53
1:A:80:C:H2'	1:A:81:G:H8	1.73	0.53
11:M:89:GLU:O	11:M:93:LYS:HG3	2.09	0.53
1:A:247:G:H2'	1:A:248:G:H8	1.73	0.52
2:B:562:VAL:CG1	2:B:595:ILE:HG22	2.36	0.52
10:L:42:VAL:HG22	10:L:314:VAL:HG22	1.91	0.52
7:H:59:LEU:HD13	7:H:60:PRO:HD2	1.92	0.52
8:J:6:ASP:HB2	8:J:30:TYR:CD1	2.44	0.52
10:L:325:GLU:HB3	10:L:326:LYS:HD3	1.90	0.52
3:D:42:MET:HB2	3:D:47:ARG:HE	1.73	0.52
2:B:252:CYS:HA	2:B:329:ILE:O	2.10	0.52
4:E:92:HIS:CE1	4:E:94:TYR:CE2	2.97	0.52
2:B:659:VAL:HG23	2:B:661:GLY:H	1.74	0.52
2:B:719:VAL:HG21	2:B:988:THR:HG22	1.91	0.52
2:B:659:VAL:HB	2:B:660:PRO:HD2	1.92	0.52
4:E:107:ILE:O	4:E:111:GLN:HG2	2.10	0.52
7:H:90:THR:HG23	8:J:198:ARG:HG2	1.91	0.52
3:D:144:LYS:HD2	10:L:125:GLU:OE1	2.10	0.52
6:G:78:ILE:HG22	6:G:130:ILE:HG22	1.91	0.52
2:B:580:LEU:HD13	11:M:15:VAL:HG22	1.91	0.52
7:H:62:ASP:HB2	10:L:262:SER:HA	1.91	0.52
2:B:701:LEU:HD11	2:B:958:HIS:CG	2.45	0.51
7:H:29:GLN:NE2	7:H:98:LYS:HB3	2.25	0.51
7:H:117:ASN:HD21	7:H:119:ARG:HG3	1.76	0.51
11:M:167:GLN:OE1	11:M:167:GLN:HA	2.11	0.51
1:A:11:U:H2'	1:A:12:G:H8	1.74	0.51
4:E:112:LYS:O	4:E:115:ILE:HG13	2.10	0.51
3:D:125:MET:HA	3:D:128:ALA:HB3	1.93	0.51
2:B:987:LEU:HA	2:B:990:LEU:HB3	1.93	0.51
2:B:198:LYS:H	2:B:198:LYS:HD2	1.76	0.51
1:A:247:G:O4'	2:B:227:THR:CG2	2.55	0.50
5:F:99:TYR:CE1	6:G:86:LEU:HB3	2.46	0.50
11:M:133:GLU:HG3	11:M:205:LEU:HD21	1.92	0.50
11:M:58:LEU:O	11:M:62:THR:HG23	2.11	0.50
4:E:37:ILE:HD11	4:E:77:VAL:HG23	1.92	0.50
4:E:92:HIS:HE1	4:E:94:TYR:CE2	2.30	0.50
8:J:162:ASP:HB3	8:J:165:MET:HG3	1.94	0.50
3:D:106:TRP:HE1	3:D:135:LEU:HA	1.77	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:47:ARG:HA	5:F:50:MET:SD	2.52	0.49
1:A:64:C:H2'	1:A:65:C:C6	2.47	0.49
2:B:874:MET:HE1	2:B:1008:ARG:HH21	1.76	0.49
4:E:127:GLN:HE22	6:G:93:PHE:HB3	1.77	0.49
5:F:37:HIS:CE1	5:F:39:ARG:HB3	2.47	0.49
3:D:150:TYR:HE2	3:D:178:PRO:HD2	1.76	0.49
2:B:993:MET:O	2:B:997:GLN:HG2	2.13	0.49
2:B:150:ARG:HH11	2:B:151:LEU:HD23	1.77	0.49
10:L:244:LEU:HD11	10:L:311:THR:HG21	1.94	0.49
2:B:252:CYS:SG	2:B:425:LEU:HB2	2.52	0.49
2:B:320:ASP:N	2:B:321:PRO:HD3	2.27	0.49
1:A:41:G:H2'	1:A:42:G:H8	1.77	0.49
11:M:48:LEU:HD21	11:M:193:ARG:HE	1.76	0.49
11:M:61:GLU:HB3	11:M:183:LEU:HD11	1.94	0.49
5:F:39:ARG:H	5:F:39:ARG:HD3	1.78	0.49
3:D:41:ARG:HA	3:D:41:ARG:HD3	1.69	0.48
3:D:199:LYS:HD2	3:D:199:LYS:C	2.37	0.48
1:A:245:C:H2'	1:A:246:G:C8	2.49	0.48
3:D:42:MET:HE1	11:M:167:GLN:OE1	2.13	0.48
3:D:125:MET:H	3:D:125:MET:CE	2.24	0.48
6:G:37:ILE:HD11	6:G:55:LEU:HD23	1.95	0.48
2:B:148:VAL:HG21	2:B:151:LEU:HD12	1.95	0.48
2:B:457:GLU:HG2	2:B:457:GLU:O	2.14	0.48
4:E:149:GLU:OE1	4:E:149:GLU:N	2.47	0.48
10:L:20:SER:HB3	10:L:349:TYR:CZ	2.48	0.48
7:H:55:VAL:HG23	8:I:170:ILE:HD13	1.95	0.48
8:J:124:LEU:HD21	8:J:186:ILE:HD11	1.95	0.48
1:A:22:A:H5'	1:A:23:U:OP2	2.14	0.48
1:A:247:G:C1'	2:B:227:THR:HG23	2.43	0.48
5:F:88:LEU:HD11	5:F:91:LEU:HD23	1.95	0.48
8:I:130:THR:HG23	8:I:165:MET:HE1	1.95	0.48
2:B:111:ARG:O	2:B:115:ILE:HG13	2.14	0.48
11:M:28:VAL:HB	11:M:124:CYS:SG	2.54	0.47
11:M:43:ILE:HG23	11:M:108:PHE:HE1	1.79	0.47
8:I:61:LEU:HB2	8:I:70:PRO:HB3	1.95	0.47
11:M:179:LEU:O	11:M:183:LEU:HD22	2.13	0.47
2:B:274:THR:HG21	2:B:293:VAL:HG22	1.96	0.47
3:D:7:HIS:CG	3:D:7:HIS:O	2.67	0.47
9:K:26:LEU:O	9:K:30:THR:HG23	2.14	0.47
1:A:6:C:H2'	1:A:7:G:C8	2.49	0.47
1:A:217:G:H2'	1:A:218:G:H8	1.80	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:C:H2'	1:A:233:G:C8	2.48	0.47
2:B:909:LEU:HA	2:B:912:LYS:HG2	1.96	0.47
8:I:44:LYS:HG3	8:I:46:GLN:OE1	2.14	0.47
9:K:4:LYS:O	9:K:8:GLU:HG3	2.15	0.47
1:A:224:C:H2'	1:A:225:G:C8	2.49	0.47
1:A:263:C:H2'	1:A:264:G:C8	2.48	0.47
2:B:119:LEU:HD23	2:B:119:LEU:HA	1.76	0.47
3:D:123:PRO:HA	3:D:126:ILE:HB	1.97	0.47
3:D:145:SER:H	10:L:125:GLU:CD	2.23	0.47
4:E:9:LEU:CD2	4:E:67:LEU:HB2	2.45	0.47
6:G:30:LEU:HD13	6:G:31:PRO:HD2	1.97	0.47
7:H:112:LEU:HD11	10:L:244:LEU:HD23	1.95	0.47
10:L:126:GLU:HB3	10:L:173:LYS:HD2	1.96	0.47
2:B:331:LEU:CD1	2:B:332:HIS:O	2.63	0.47
2:B:562:VAL:HG12	2:B:626:TRP:HE1	1.79	0.47
8:I:7:LEU:HA	8:I:34:ALA:HB3	1.97	0.47
8:J:93:THR:HA	8:J:98:ARG:HH21	1.79	0.47
6:G:113:PRO:HB3	6:G:118:ARG:HB3	1.96	0.47
2:B:575:MET:HA	2:B:575:MET:HE2	1.97	0.47
2:B:863:LEU:HD21	2:B:1007:LEU:HD11	1.97	0.47
3:D:107:LYS:O	3:D:110:ILE:HG13	2.15	0.47
4:E:134:GLU:O	4:E:138:ILE:HG13	2.15	0.47
1:A:112:G:H2'	1:A:113:C:C6	2.47	0.46
1:A:202:C:H2'	1:A:202:C:O2	2.15	0.46
2:B:232:ARG:HG2	2:B:974:MET:HE1	1.97	0.46
2:B:305:LEU:HD11	2:B:342:GLU:HG2	1.96	0.46
2:B:335:LEU:HD12	2:B:335:LEU:C	2.41	0.46
1:A:40:A:H2'	1:A:41:G:C8	2.50	0.46
5:F:146:PRO:HB2	5:F:147:ARG:NH1	2.30	0.46
9:K:7:LEU:HD11	9:K:29:TYR:CD2	2.48	0.46
2:B:331:LEU:HD12	2:B:331:LEU:C	2.39	0.46
1:A:57:C:H2'	1:A:58:U:H6	1.81	0.46
8:I:170:ILE:O	8:I:174:LEU:HG	2.15	0.46
11:M:45:GLU:HG2	11:M:197:LEU:HD13	1.97	0.46
10:L:161:LYS:HB2	10:L:161:LYS:HE2	1.68	0.46
1:A:65:C:H2'	1:A:66:U:C6	2.50	0.46
1:A:193:C:N4	2:B:146:HIS:CE1	2.84	0.46
9:K:7:LEU:HA	9:K:25:LEU:HD21	1.98	0.46
4:E:9:LEU:HD23	4:E:67:LEU:HB2	1.98	0.46
5:F:69:GLY:HA3	5:F:77:THR:HG21	1.98	0.46
2:B:582:PRO:HD2	11:M:148:ARG:HG2	1.98	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:J:156:TYR:CZ	8:J:189:SER:HB3	2.51	0.46
11:M:56:GLN:OE1	11:M:56:GLN:N	2.47	0.46
11:M:191:LEU:HD13	11:M:195:ILE:HD11	1.98	0.46
2:B:700:THR:HG21	2:B:1010:PRO:HB3	1.98	0.45
5:F:56:SER:HA	5:F:59:GLN:NE2	2.31	0.45
11:M:88:VAL:HG13	11:M:149:LEU:HD11	1.97	0.45
1:A:56:C:H2'	1:A:57:C:C6	2.49	0.45
8:I:10:ARG:NH1	8:I:36:ASN:HD22	2.14	0.45
8:J:230:LEU:O	8:J:233:GLU:HG3	2.16	0.45
10:L:230:THR:HG22	10:L:231:PRO:CD	2.44	0.45
1:A:23:U:H4'	1:A:24:C:H3'	1.98	0.45
2:B:574:ARG:NE	2:B:575:MET:HE3	2.31	0.45
2:B:859:VAL:HG12	2:B:1022:ILE:HG12	1.98	0.45
8:I:10:ARG:HH11	8:I:36:ASN:HD22	1.63	0.45
8:I:156:TYR:CZ	8:I:189:SER:HB3	2.52	0.45
8:J:67:LYS:HA	10:L:98:ASN:HB3	1.99	0.45
1:A:6:C:H2'	1:A:7:G:H8	1.81	0.45
1:A:13:A:H4'	2:B:686:ARG:HH21	1.82	0.45
3:D:169:THR:HG22	3:D:173:ARG:O	2.17	0.45
3:D:171:GLU:OE2	3:D:172:ASP:N	2.49	0.45
8:J:10:ARG:HE	8:J:36:ASN:HD22	1.55	0.45
8:J:42:LYS:HE2	8:J:82:SER:HB3	1.99	0.45
2:B:305:LEU:HD13	2:B:339:ILE:HD13	1.98	0.45
10:L:47:PRO:HG2	10:L:307:ALA:HB1	1.98	0.45
1:A:8:U:H4'	3:D:180:LEU:HD23	1.98	0.45
4:E:55:VAL:HG22	4:E:67:LEU:HD23	1.98	0.45
11:M:100:LEU:HG	11:M:104:ILE:HD11	1.99	0.45
2:B:287:LYS:HB3	2:B:288:ARG:HD2	1.98	0.45
2:B:335:LEU:HD13	2:B:339:ILE:HG12	1.99	0.45
10:L:39:ASN:HA	10:L:316:GLY:HA2	1.99	0.45
11:M:150:LEU:HD22	11:M:184:TRP:CD1	2.52	0.45
2:B:249:TYR:O	2:B:333:PRO:HG3	2.17	0.44
8:J:65:GLN:OE1	8:J:65:GLN:HA	2.17	0.44
1:A:28:G:H2'	1:A:29:G:C8	2.51	0.44
1:A:38:U:H4'	1:A:39:G:H5''	1.99	0.44
1:A:58:U:H2'	1:A:59:U:H6	1.83	0.44
1:A:80:C:H2'	1:A:81:G:C8	2.52	0.44
1:A:222:U:H2'	1:A:223:G:C8	2.51	0.44
2:B:242:CYS:HA	2:B:435:ILE:O	2.18	0.44
2:B:861:LEU:HD12	2:B:981:ALA:HB3	1.99	0.44
2:B:914:LYS:HB3	2:B:914:LYS:HE3	1.82	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
5:F:40:VAL:HB	5:F:77:THR:HG22	2.00	0.44
11:M:226:ILE:HD13	11:M:226:ILE:HA	1.84	0.44
1:A:12:G:H2'	1:A:13:A:C8	2.53	0.44
1:A:115:C:H2'	1:A:116:G:H8	1.82	0.44
3:D:42:MET:HG2	3:D:47:ARG:HD3	2.00	0.44
6:G:57:ASP:OD1	6:G:57:ASP:C	2.61	0.44
10:L:48:GLU:HG2	10:L:273:VAL:HG13	2.00	0.44
8:I:10:ARG:HH22	8:I:190:ALA:HB1	1.82	0.44
11:M:47:HIS:O	11:M:50:ILE:HD12	2.17	0.44
11:M:197:LEU:O	11:M:200:PRO:HD2	2.18	0.44
1:A:223:G:H2'	1:A:224:C:C6	2.53	0.44
3:D:150:TYR:CE2	3:D:178:PRO:HD2	2.52	0.44
6:G:97:GLN:OE1	6:G:97:GLN:HA	2.17	0.44
8:I:183:LYS:HE3	8:I:183:LYS:HA	1.99	0.44
8:J:3:VAL:H	8:J:226:ARG:HH22	1.66	0.44
9:K:4:LYS:N	9:K:4:LYS:HD3	2.33	0.44
1:A:250:C:H2'	1:A:251:U:C6	2.53	0.44
2:B:259:GLU:HB3	2:B:325:ARG:HG3	2.00	0.44
3:D:33:ALA:HA	3:D:36:LYS:HE3	1.98	0.44
6:G:45:PHE:N	6:G:80:ARG:HH21	2.15	0.44
7:H:98:LYS:HD3	7:H:98:LYS:N	2.33	0.44
11:M:232:GLN:N	11:M:233:PRO:HD2	2.32	0.44
2:B:144:MET:O	11:M:75:ARG:HD2	2.18	0.44
8:J:206:LEU:HD12	8:J:206:LEU:HA	1.84	0.44
11:M:134:LEU:O	11:M:138:LYS:HG3	2.18	0.44
2:B:199:ASN:HD22	2:B:216:LYS:HD3	1.83	0.43
10:L:194:MET:HE2	10:L:194:MET:HA	2.00	0.43
1:A:11:U:H2'	1:A:12:G:C8	2.52	0.43
6:G:30:LEU:HD13	6:G:31:PRO:CD	2.48	0.43
7:H:50:ASP:OD2	7:H:50:ASP:C	2.60	0.43
2:B:912:LYS:HG3	2:B:913:GLU:N	2.34	0.43
1:A:115:C:H2'	1:A:116:G:C8	2.54	0.43
4:E:125:LEU:HD12	4:E:125:LEU:HA	1.85	0.43
5:F:32:ALA:HB1	5:F:35:ALA:HB2	2.00	0.43
8:I:138:LYS:HA	8:I:138:LYS:HD3	1.72	0.43
10:L:52:LEU:HD12	10:L:52:LEU:HA	1.86	0.43
6:G:56:LEU:HD23	6:G:56:LEU:HA	1.88	0.43
1:A:247:G:H2'	1:A:248:G:C8	2.52	0.43
3:D:28:GLU:O	3:D:32:ARG:HG2	2.19	0.43
3:D:199:LYS:HD2	3:D:199:LYS:O	2.18	0.43
1:A:72:A:C8	1:A:253:A:N6	2.87	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:99:G:H2'	1:A:100:C:C6	2.53	0.43
1:A:199:G:H2'	1:A:199:G:N3	2.33	0.43
5:F:77:THR:HA	5:F:80:CYS:SG	2.58	0.43
10:L:353:MET:SD	10:L:362:PRO:HB2	2.59	0.43
2:B:861:LEU:HD21	2:B:875:ILE:HD13	2.01	0.43
4:E:29:LEU:HD23	4:E:29:LEU:HA	1.87	0.43
5:F:101:SER:HB3	5:F:129:LEU:HD12	2.01	0.43
9:K:2:ARG:HH12	9:K:6:TYR:HB2	1.84	0.43
11:M:16:ARG:HA	11:M:16:ARG:HH11	1.84	0.43
8:J:42:LYS:HG2	8:J:82:SER:HB3	2.01	0.43
1:A:194:C:H2'	2:B:155:LEU:HD23	2.00	0.42
6:G:124:ILE:HD12	6:G:124:ILE:HA	1.92	0.42
8:I:193:ARG:HB3	8:I:196:GLU:OE1	2.19	0.42
1:A:12:G:H2'	1:A:13:A:H8	1.84	0.42
8:J:51:PRO:HG3	8:J:100:TYR:CZ	2.54	0.42
1:A:65:C:H5''	2:B:866:LYS:H	1.84	0.42
2:B:137:ARG:HA	2:B:140:ARG:HG3	2.00	0.42
3:D:48:GLU:OE2	3:D:48:GLU:HA	2.18	0.42
3:D:186:VAL:HG22	3:D:193:SER:OG	2.19	0.42
5:F:65:ILE:HG23	5:F:139:LEU:HB2	2.02	0.42
8:I:139:ARG:HB3	8:I:140:PRO:HD3	2.01	0.42
8:J:94:SER:O	8:J:98:ARG:HG2	2.20	0.42
10:L:123:THR:O	10:L:127:THR:HG22	2.19	0.42
2:B:335:LEU:HD13	2:B:339:ILE:CG1	2.49	0.42
8:I:233:GLU:O	8:I:237:THR:HG23	2.19	0.42
8:J:130:THR:HG23	8:J:165:MET:SD	2.60	0.42
11:M:202:PHE:O	11:M:206:GLN:HG3	2.20	0.42
2:B:338:ASP:O	2:B:341:GLU:HG3	2.19	0.42
2:B:880:LYS:HA	2:B:880:LYS:HD3	1.90	0.42
8:J:125:VAL:HG23	8:J:150:LEU:HD22	2.01	0.42
8:J:216:ASP:HA	10:L:139:ARG:HH21	1.85	0.42
10:L:297:LEU:HD23	10:L:297:LEU:HA	1.88	0.42
2:B:272:ILE:HD12	2:B:272:ILE:HA	1.90	0.42
2:B:316:ARG:HD3	2:B:317:THR:N	2.33	0.42
4:E:86:TYR:CG	4:E:86:TYR:O	2.73	0.42
8:I:127:ILE:HD11	8:I:152:PHE:HD2	1.84	0.42
8:I:187:ILE:HD12	8:I:187:ILE:N	2.34	0.42
1:A:253:A:H2'	1:A:254:U:C6	2.55	0.42
6:G:54:LYS:NZ	6:G:59:GLY:H	2.17	0.42
2:B:579:LEU:HA	11:M:13:ASN:O	2.20	0.42
11:M:129:GLN:H	11:M:129:GLN:CD	2.27	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:963:LEU:C	2:B:963:LEU:HD12	2.44	0.42
11:M:129:GLN:NE2	11:M:212:GLN:HB3	2.34	0.42
2:B:257:GLY:O	2:B:325:ARG:HB2	2.20	0.41
3:D:123:PRO:HB3	3:D:191:PHE:HE2	1.85	0.41
4:E:47:ALA:HB2	8:J:167:ARG:HG3	2.02	0.41
7:H:111:LEU:HD12	7:H:114:LEU:HD12	2.02	0.41
1:A:5:U:H2'	1:A:6:C:C6	2.55	0.41
5:F:36:VAL:O	5:F:65:ILE:HD12	2.19	0.41
10:L:193:MET:HE3	10:L:193:MET:HB3	1.91	0.41
3:D:118:LYS:HE2	3:D:118:LYS:HB2	1.86	0.41
8:I:218:LYS:HA	8:I:218:LYS:HD3	1.91	0.41
11:M:61:GLU:HA	11:M:64:VAL:HG12	2.03	0.41
6:G:78:ILE:O	6:G:82:ILE:HG13	2.20	0.41
1:A:34:A:N1	6:G:76:LEU:HD21	2.35	0.41
1:A:51:C:H2'	1:A:52:C:C6	2.55	0.41
2:B:429:MET:HE2	2:B:429:MET:HB3	1.90	0.41
2:B:609:GLU:HA	2:B:612:LEU:HD11	2.01	0.41
8:J:241:ILE:O	8:J:242:ILE:HD13	2.20	0.41
11:M:35:LEU:HD12	11:M:35:LEU:HA	1.82	0.41
1:A:41:G:C2	1:A:42:G:N7	2.88	0.41
3:D:189:ASP:OD2	3:D:189:ASP:C	2.64	0.41
4:E:21:ARG:HH11	4:E:63:GLY:HA3	1.85	0.41
7:H:36:ASN:HD22	7:H:38:ALA:H	1.69	0.41
2:B:114:GLU:HG3	11:M:185:VAL:HG21	2.01	0.41
5:F:38:MET:HG3	5:F:67:PHE:CE2	2.56	0.41
10:L:133:PRO:HB3	10:L:141:ILE:HG21	2.02	0.41
2:B:418:THR:HG22	2:B:420:ILE:HG13	2.03	0.41
1:A:194:C:H2'	1:A:194:C:H6	1.71	0.41
1:A:264:G:H4'	3:D:176:VAL:HG11	2.02	0.41
2:B:567:ILE:HD12	2:B:567:ILE:O	2.20	0.41
7:H:44:LEU:O	7:H:48:VAL:HG12	2.21	0.41
1:A:34:A:C2	6:G:76:LEU:HD21	2.56	0.41
1:A:38:U:C2	5:F:50:MET:HE1	2.56	0.41
2:B:101:TYR:HD1	3:D:56:VAL:HG22	1.86	0.41
2:B:1009:PRO:HD2	2:B:1012:SER:HB3	2.03	0.41
2:B:111:ARG:H	2:B:111:ARG:HG2	1.75	0.40
10:L:35:THR:HG23	10:L:325:GLU:HG3	2.02	0.40
11:M:10:GLU:HA	11:M:11:PRO:HD3	1.97	0.40
2:B:146:HIS:HE1	3:D:59:GLU:O	2.05	0.40
6:G:54:LYS:NZ	6:G:60:ALA:H	2.19	0.40
6:G:54:LYS:HD2	6:G:54:LYS:O	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:I:133:LEU:HD23	8:I:133:LEU:HA	1.83	0.40
9:K:7:LEU:HD11	9:K:29:TYR:HB2	2.03	0.40
3:D:76:LEU:HD12	3:D:76:LEU:HA	1.89	0.40
3:D:123:PRO:HB3	3:D:191:PHE:CE2	2.56	0.40
8:I:102:VAL:HG13	8:I:123:ASP:OD1	2.22	0.40
10:L:22:PHE:HE2	10:L:343:ILE:HD12	1.87	0.40
1:A:229:C:H3'	1:A:230:C:H6	1.85	0.40
2:B:632:ILE:HD13	2:B:632:ILE:HA	1.92	0.40
11:M:50:ILE:HD12	11:M:51:LEU:N	2.36	0.40
2:B:877:VAL:HG13	2:B:993:MET:HG3	2.04	0.40
2:B:894:GLY:HA3	2:B:1015:TYR:O	2.22	0.40
5:F:93:GLN:CG	5:F:137:ILE:HD11	2.49	0.40
11:M:110:LEU:HD21	11:M:127:PRO:HB3	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	
2	B	704/1024 (69%)	667 (95%)	37 (5%)	0	100	100
3	D	182/220 (83%)	176 (97%)	6 (3%)	0	100	100
4	E	148/163 (91%)	143 (97%)	5 (3%)	0	100	100
5	F	110/199 (55%)	109 (99%)	1 (1%)	0	100	100
6	G	118/140 (84%)	114 (97%)	4 (3%)	0	100	100
7	H	120/124 (97%)	112 (93%)	8 (7%)	0	100	100
8	I	235/268 (88%)	229 (97%)	6 (3%)	0	100	100
8	J	246/268 (92%)	238 (97%)	8 (3%)	0	100	100
9	K	30/220 (14%)	29 (97%)	1 (3%)	0	100	100
10	L	360/363 (99%)	345 (96%)	15 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	M	228/567 (40%)	223 (98%)	5 (2%)	0	100	100
All	All	2481/3556 (70%)	2385 (96%)	96 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	
2	B	624/883 (71%)	623 (100%)	1 (0%)	87	95
3	D	166/196 (85%)	166 (100%)	0	100	100
4	E	134/143 (94%)	134 (100%)	0	100	100
5	F	92/150 (61%)	92 (100%)	0	100	100
6	G	102/118 (86%)	101 (99%)	1 (1%)	68	83
7	H	104/106 (98%)	104 (100%)	0	100	100
8	I	202/228 (89%)	201 (100%)	1 (0%)	81	90
8	J	212/228 (93%)	211 (100%)	1 (0%)	81	90
9	K	25/201 (12%)	25 (100%)	0	100	100
10	L	331/332 (100%)	330 (100%)	1 (0%)	86	94
11	M	208/513 (40%)	207 (100%)	1 (0%)	81	90
All	All	2200/3098 (71%)	2194 (100%)	6 (0%)	84	94

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	861	LEU
6	G	48	GLN
8	I	58	PHE
8	J	58	PHE
10	L	36	HIS
11	M	234	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (22) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	146	HIS
2	B	156	GLN
2	B	332	HIS
2	B	430	ASN
2	B	658	ASN
2	B	713	GLN
2	B	891	HIS
3	D	127	GLN
4	E	41	HIS
4	E	92	HIS
4	E	128	ASN
5	F	148	GLN
6	G	40	ASN
7	H	29	GLN
7	H	36	ASN
7	H	39	GLN
8	I	36	ASN
8	I	114	HIS
8	J	86	HIS
10	L	255	ASN
10	L	327	ASN
10	L	358	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	202/270 (74%)	47 (23%)	1 (0%)

All (47) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	16	G
1	A	22	A
1	A	23	U
1	A	34	A
1	A	35	C
1	A	36	A
1	A	37	C
1	A	38	U
1	A	39	G

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Mol	Chain	Res	Type
1	A	50	U
1	A	55	C
1	A	56	C
1	A	61	C
1	A	62	C
1	A	69	G
1	A	70	G
1	A	72	A
1	A	74	A
1	A	76	U
1	A	82	G
1	A	89	G
1	A	109	U
1	A	110	A
1	A	111	C
1	A	112	G
1	A	118	A
1	A	119	G
1	A	120	A
1	A	191	A
1	A	192	U
1	A	193	C
1	A	194	C
1	A	199	G
1	A	203	C
1	A	205	U
1	A	206	C
1	A	207	U
1	A	208	A
1	A	209	G
1	A	212	A
1	A	227	G
1	A	228	U
1	A	233	G
1	A	243	C
1	A	244	A
1	A	245	C
1	A	269	U

All (1) RNA pucker outliers are listed below:

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Mol	Chain	Res	Type
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Mol	Chain	Res	Type
1	A	117	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

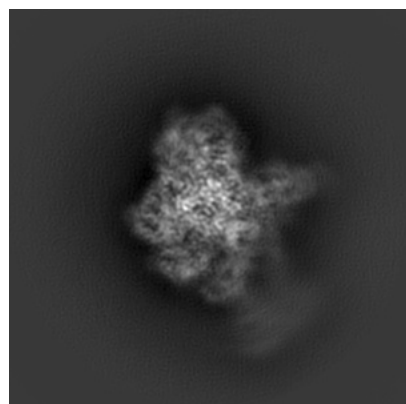
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-64157. These allow visual inspection of the internal detail of the map and identification of artifacts.

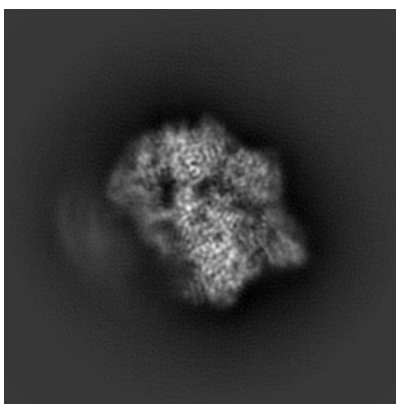
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

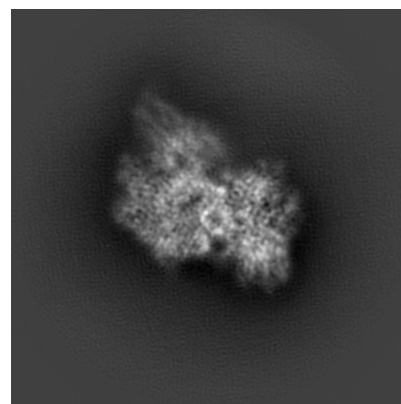
6.1.1 Primary map



X

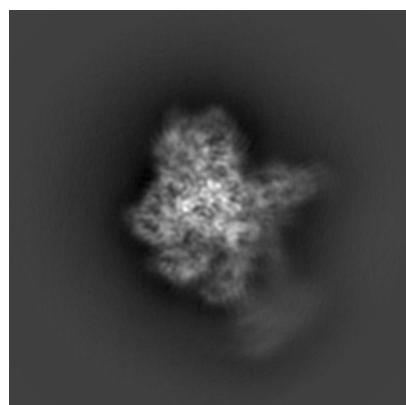


Y

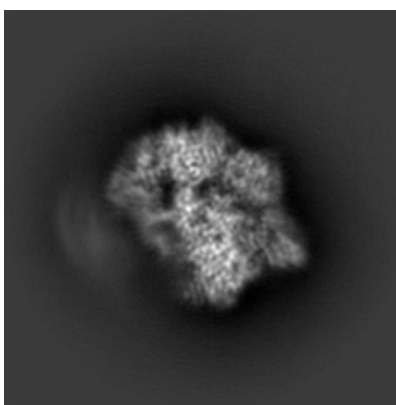


Z

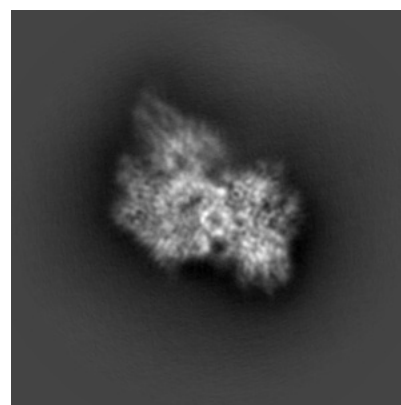
6.1.2 Raw map



X



Y

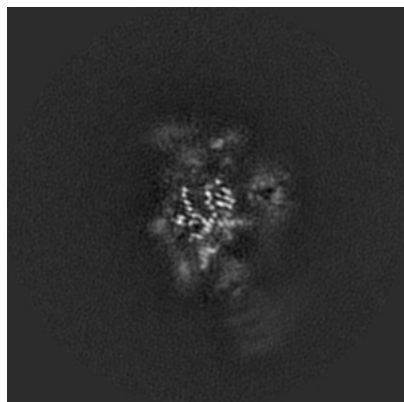


Z

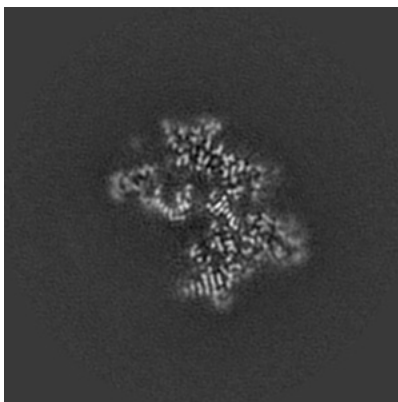
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

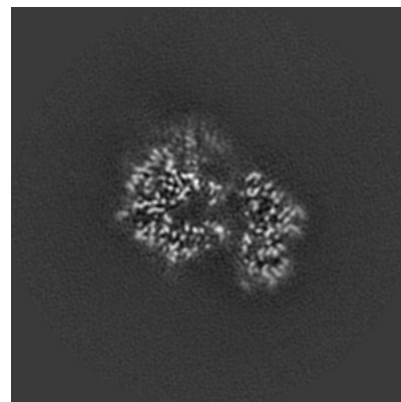
6.2.1 Primary map



X Index: 128

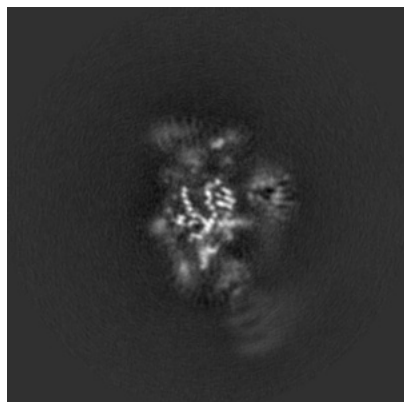


Y Index: 128

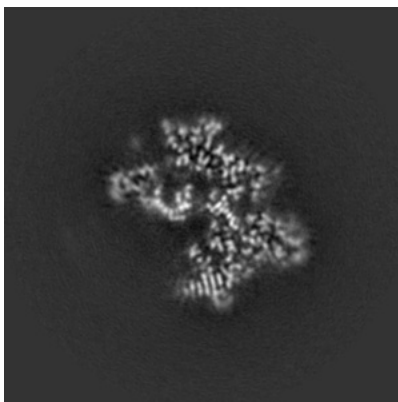


Z Index: 128

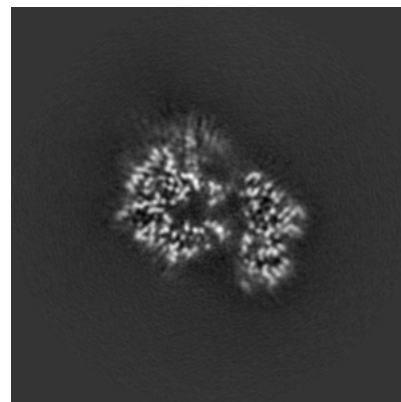
6.2.2 Raw map



X Index: 128



Y Index: 128

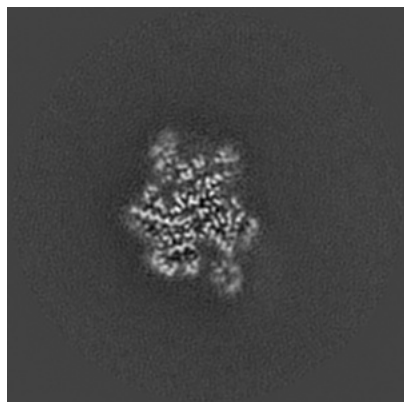


Z Index: 128

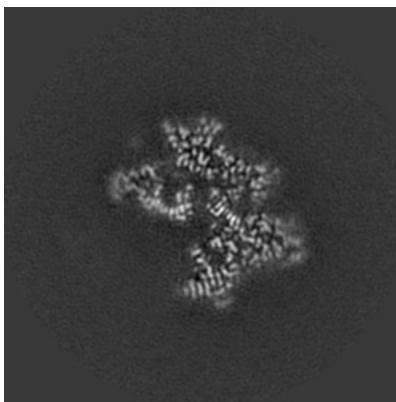
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

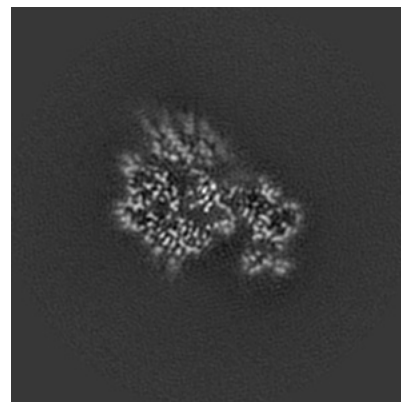
6.3.1 Primary map



X Index: 159

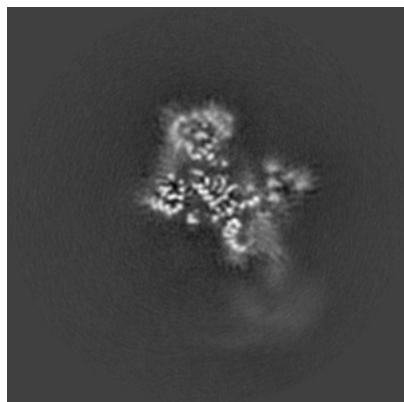


Y Index: 127

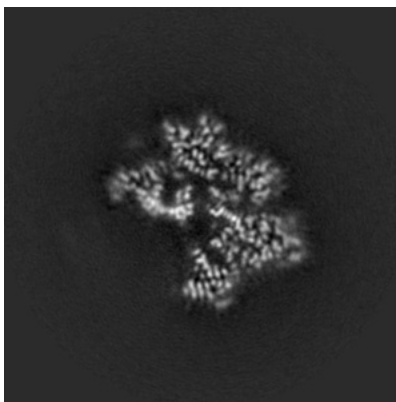


Z Index: 133

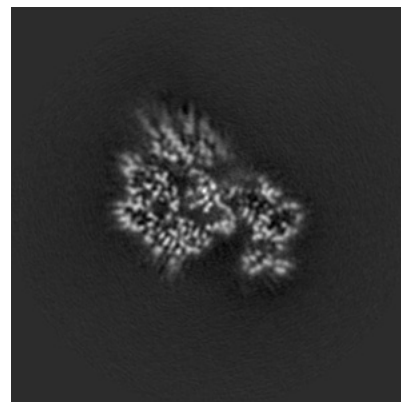
6.3.2 Raw map



X Index: 104



Y Index: 126

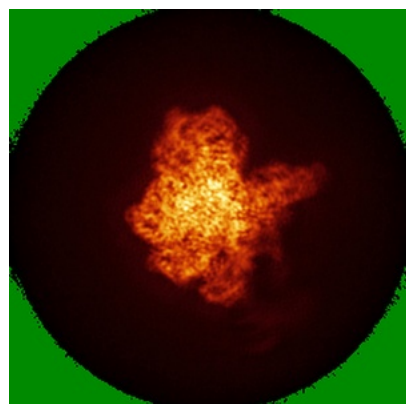


Z Index: 133

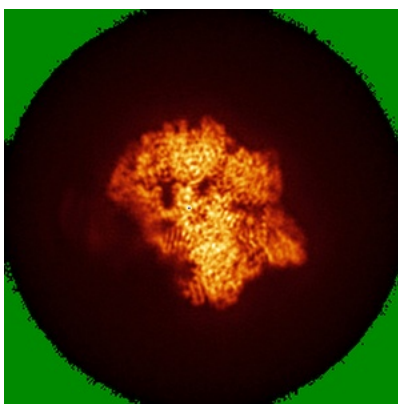
The images above show the largest variance slices of the map in three orthogonal directions.

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

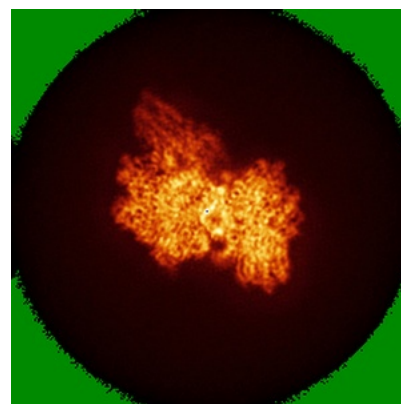
6.4.1 Primary map



X

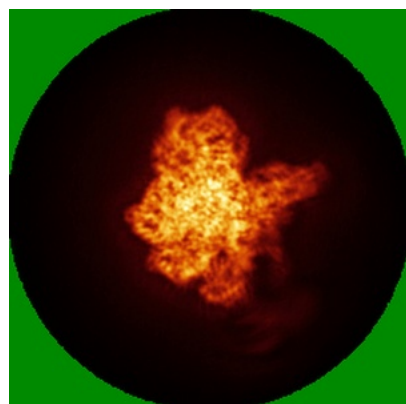


Y

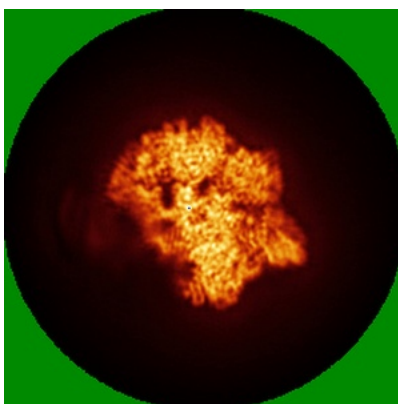


Z

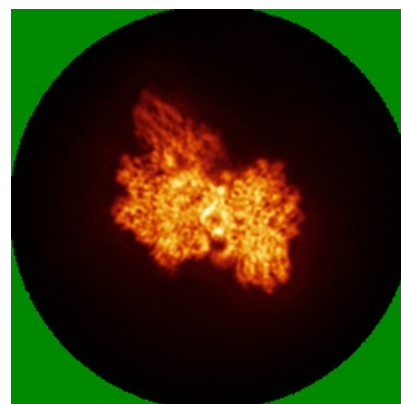
6.4.2 Raw map



X



Y



Z

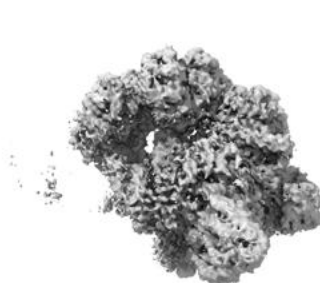
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



Y



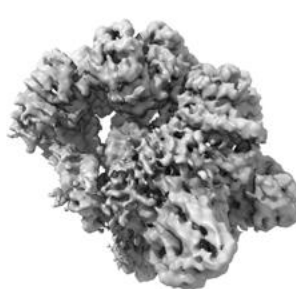
Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. 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.

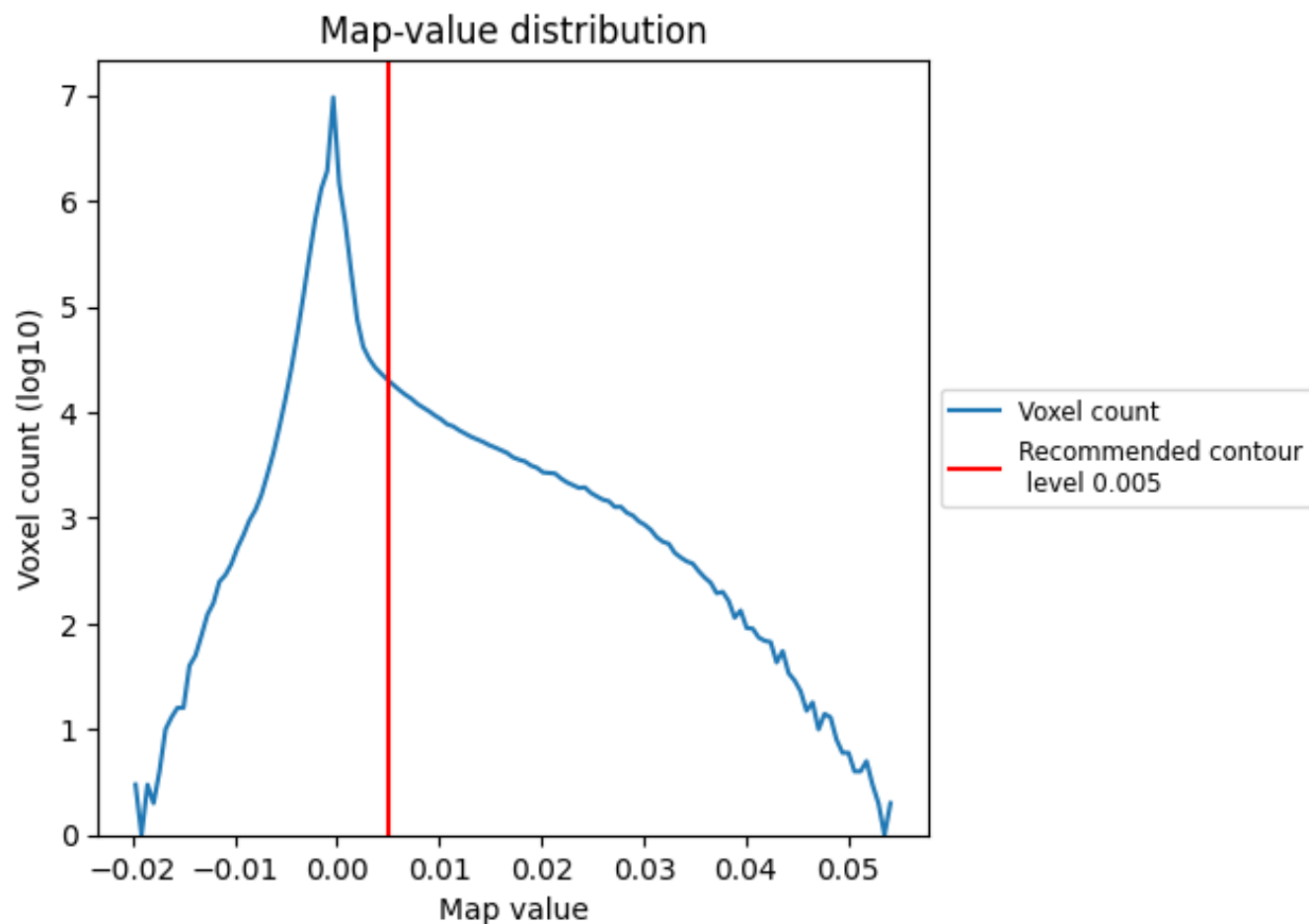
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

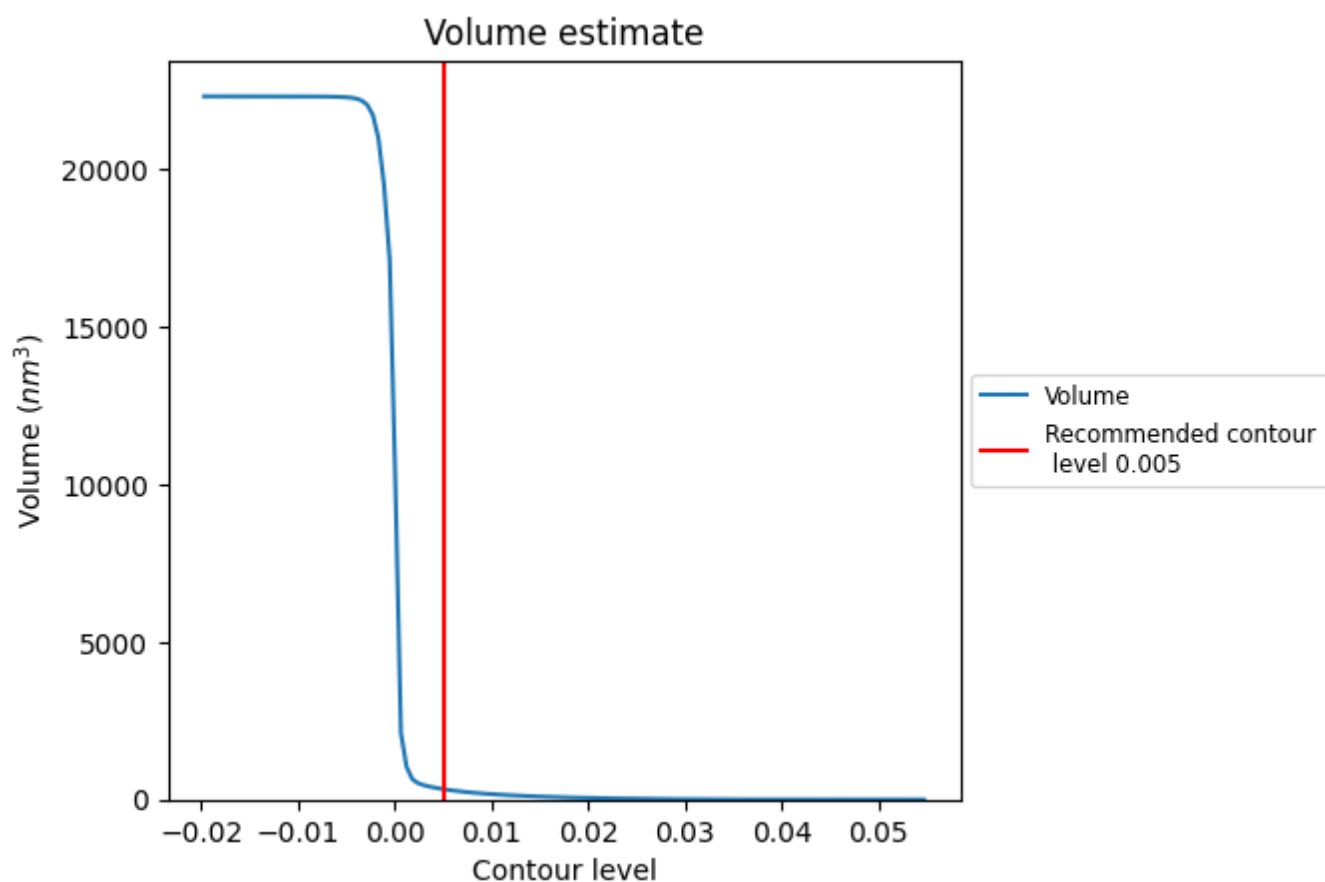
This section contains the results of statistical analysis of the map.

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.

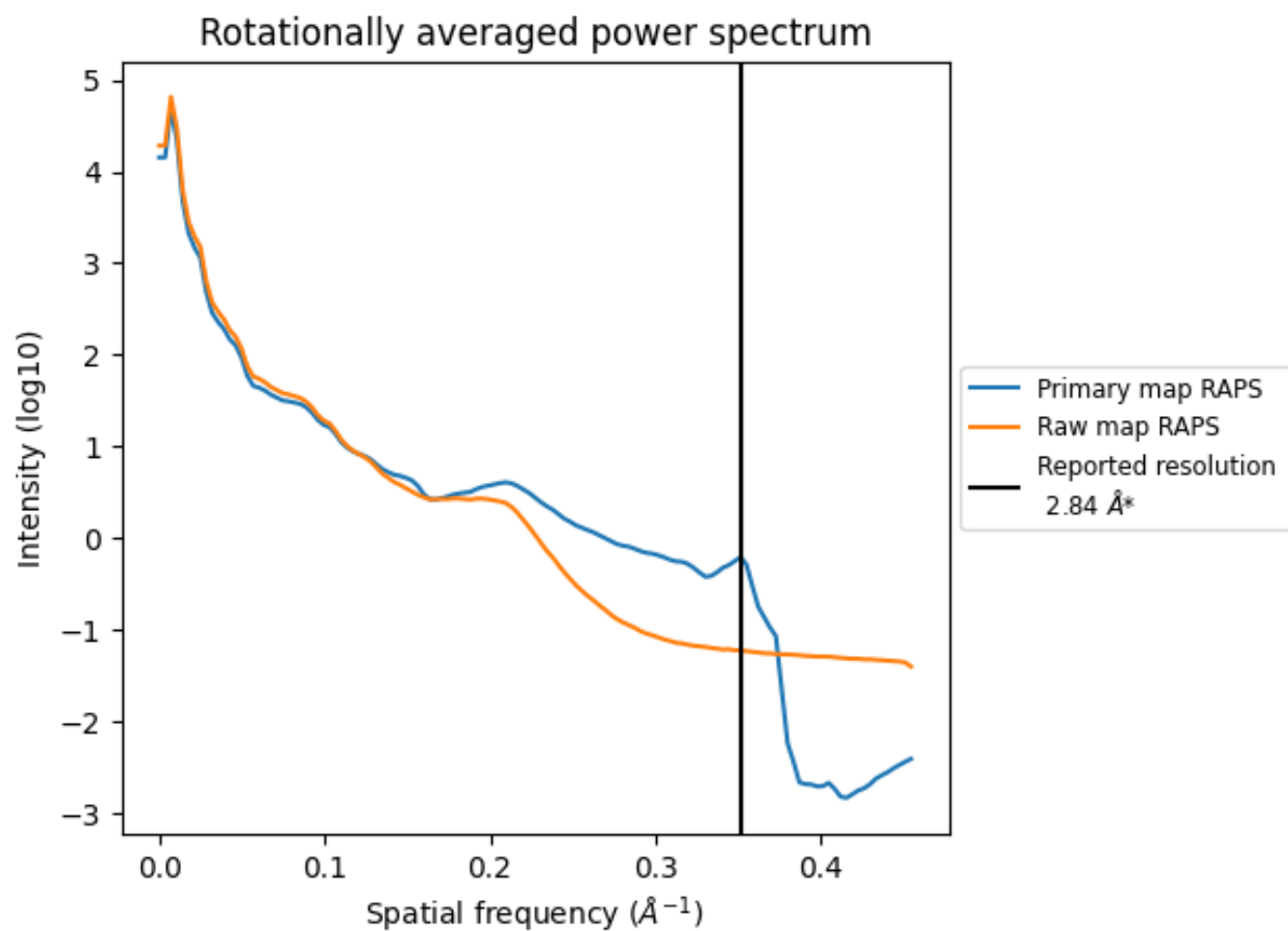
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 332 nm^3 ; this corresponds to an approximate mass of 300 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 ⓘ

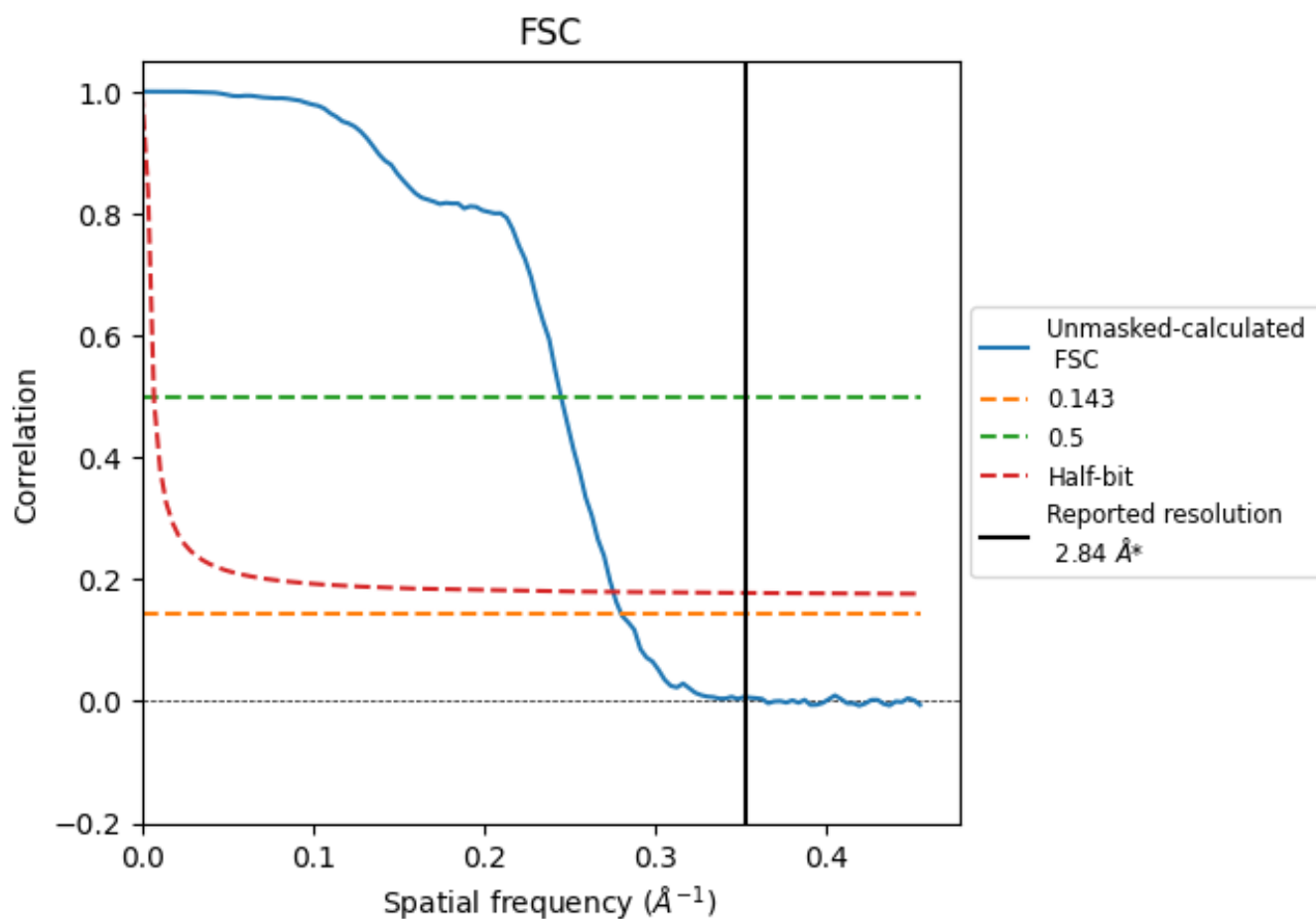


*Reported resolution corresponds to spatial frequency of 0.352 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.352 \AA^{-1}

8.2 Resolution estimates [i](#)

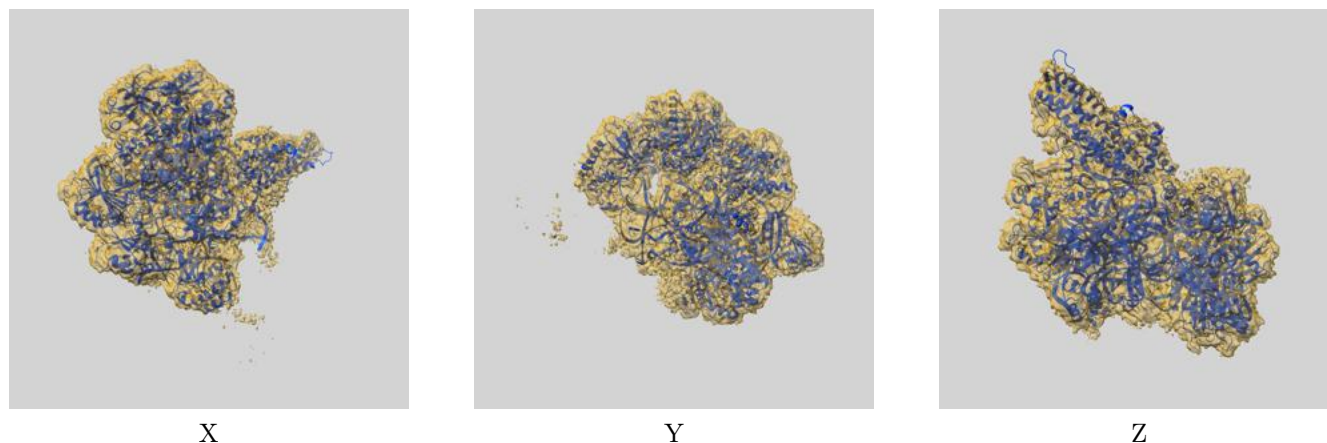
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.84	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.57	4.08	3.63

*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 3.57 differs from the reported value 2.84 by more than 10 %

9 Map-model fit [i](#)

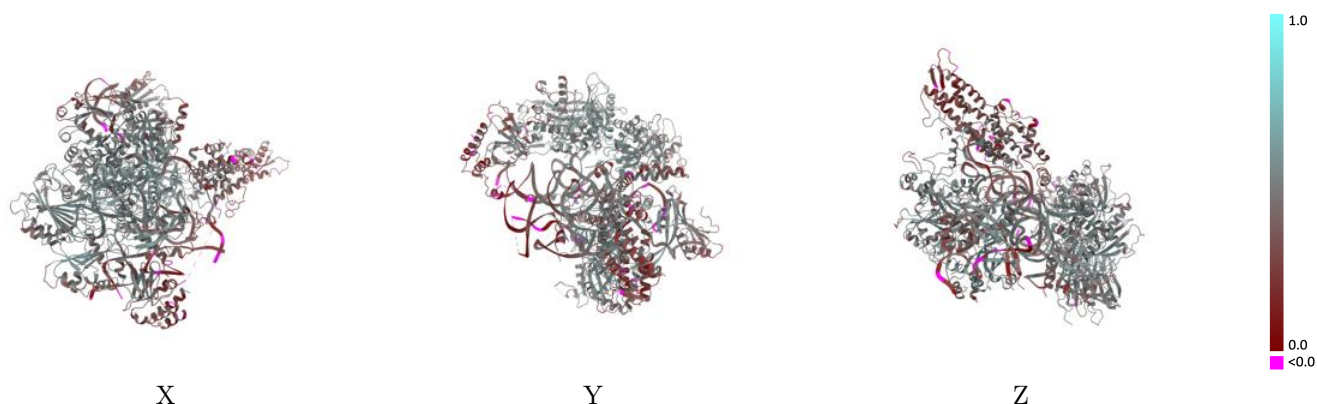
This section contains information regarding the fit between EMDB map EMD-64157 and PDB model 9UH7. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

9.1 Map-model overlay [i](#)



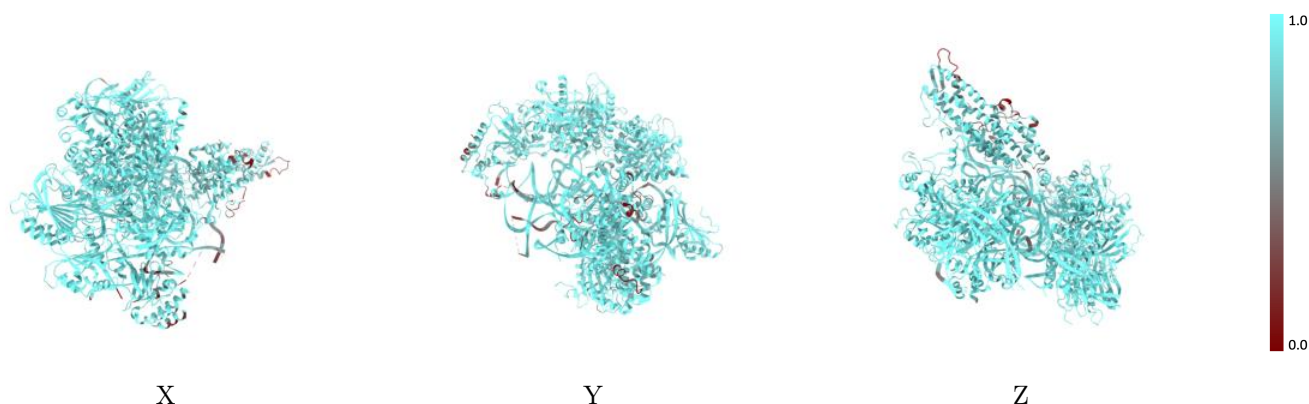
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



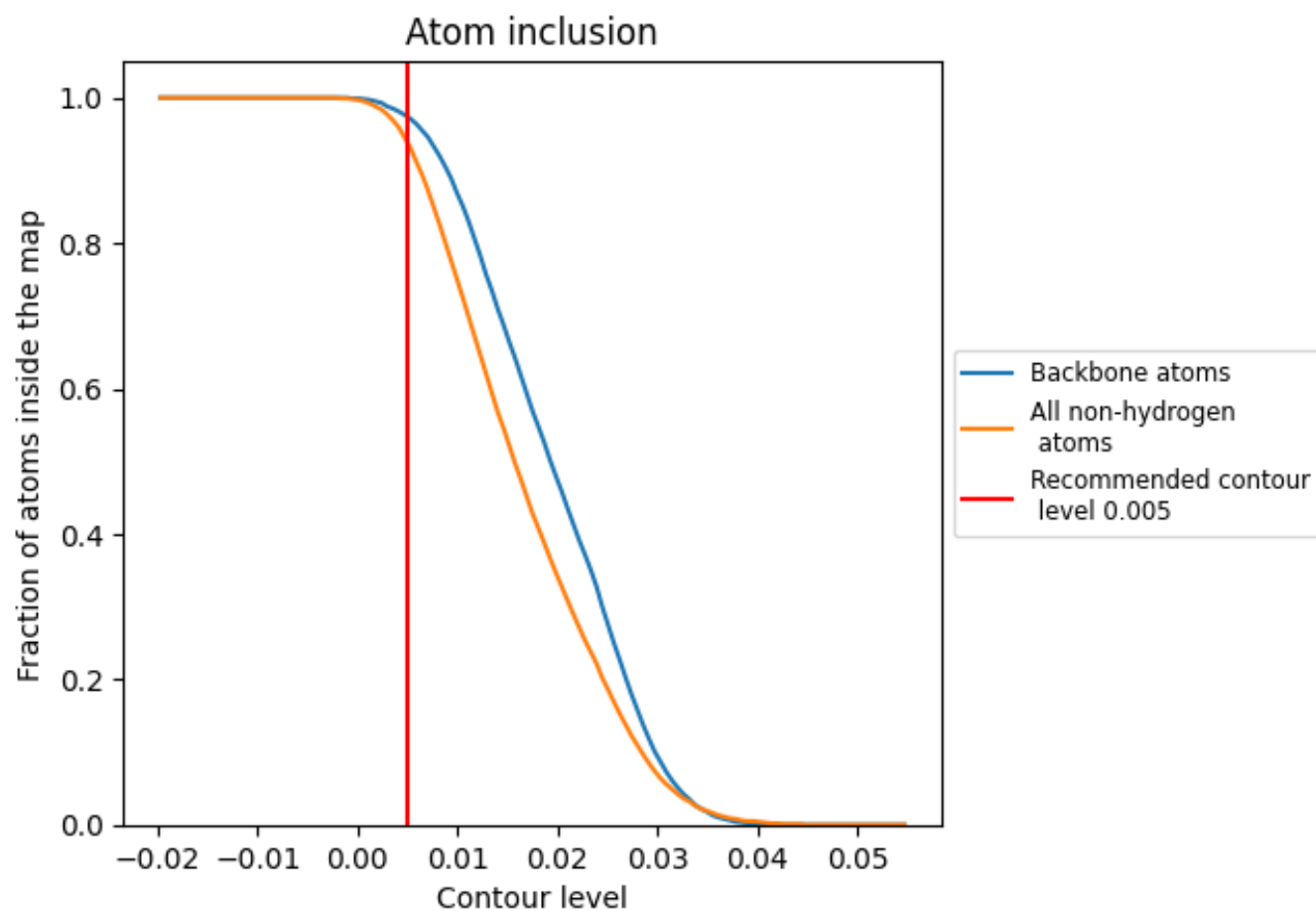
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).



























9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9380	 0.4380
A	 0.9200	 0.3580
B	 0.9580	 0.4910
D	 0.8190	 0.3460
E	 0.9690	 0.4850
F	 0.9810	 0.3800
G	 0.9690	 0.4890
H	 0.9860	 0.5180
I	 0.9690	 0.4590
J	 0.9590	 0.4720
K	 0.7600	 0.2340
L	 0.9700	 0.4980
M	 0.8600	 0.3450

