



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 06:26 AM UTC

PDB ID : 4V19 / pdb_00004v19
EMDB ID : EMD-2787
Title : Structure of the large subunit of the mammalian mitoribosome, part 1 of 2
Authors : Greber, B.J.; Boehringer, D.; Leibundgut, M.; Bieri, P.; Leitner, A.; Schmitz, N.; Aebersold, R.; Ban, N.
Deposited on : 2014-09-25
Resolution : 3.40 Å(reported)

This is a wwPDB EM Validation Summary 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:

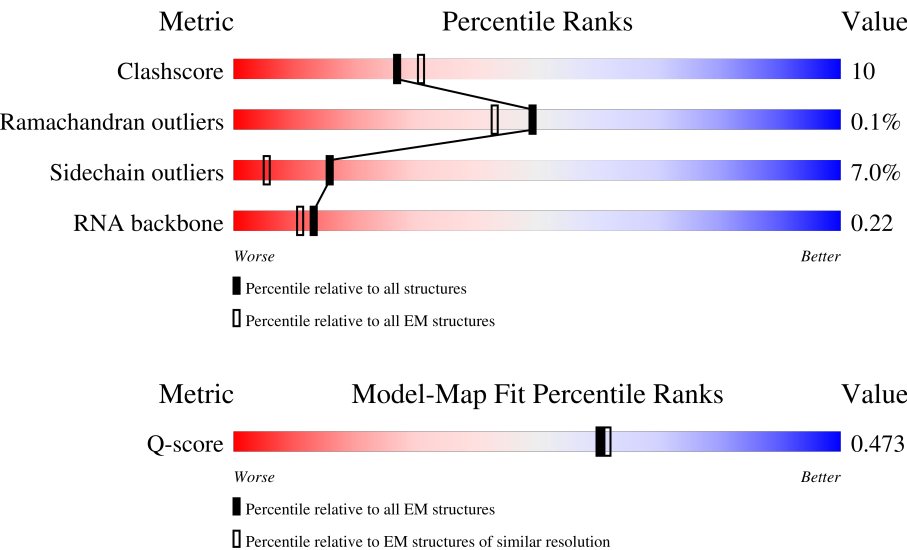
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



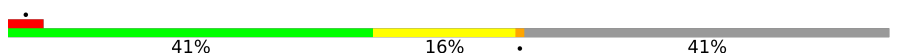
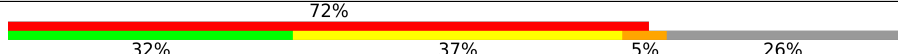
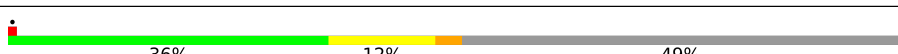
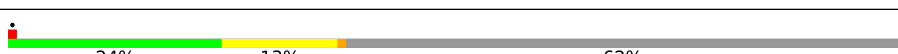
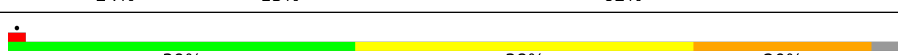
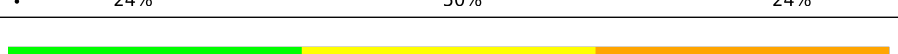
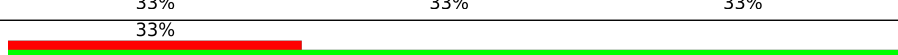
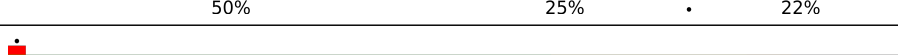
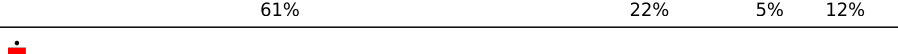
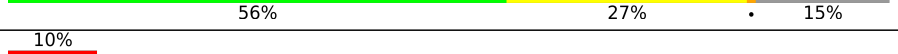
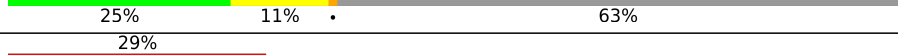
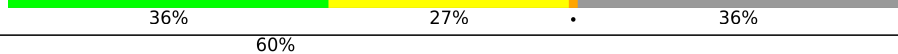
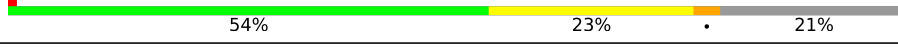
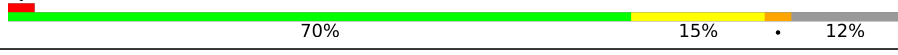
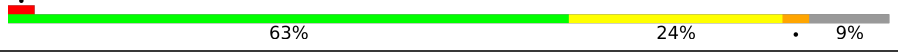
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	0	148	53%21%23%
2	1	256	7% 73%21%5%
3	2	252	56%13%29%

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Mol	Chain	Length	Quality of chain
4	3	161	
5	4	126	
6	5	188	
7	6	65	
8	7	95	
9	8	188	
10	9	100	
11	A	1570	
12	B	62	
13	C	3	
13	Z	3	
14	D	306	
15	E	348	
16	F	294	
17	I	268	
18	J	262	
19	K	192	
20	N	178	
21	O	145	
22	P	296	
23	Q	251	
24	R	169	
25	S	180	
26	T	292	
27	U	149	

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Mol	Chain	Length	Quality of chain
28	V	209	
29	W	210	
30	X	150	
31	Y	216	

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 69409 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 MITORIBOSOMAL PROTEIN BL27M, MRPL27.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	114	Total	C	N	O	S	0	0
			878	564	160	151	3		

- Molecule 2 is a protein called MITORIBOSOMAL PROTEIN BL28M, MRPL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	244	Total	C	N	O	S	0	0
			2036	1315	363	353	5		

- Molecule 3 is a protein called MITORIBOSOMAL PROTEIN UL29M, MRPL47.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	178	Total	C	N	O	S	0	0
			1544	990	289	259	6		

- Molecule 4 is a protein called MITORIBOSOMAL PROTEIN UL30M, MRPL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	118	Total	C	N	O	S	0	0
			968	622	178	165	3		

- Molecule 5 is a protein called MITORIBOSOMAL PROTEIN BL31M, MRPL55.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	45	Total	C	N	O	S	0	0
			381	239	77	62	3		

- Molecule 6 is a protein called MITORIBOSOMAL PROTEIN BL32M, MRPL32.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	5	110	Total	C	N	O	S	0	0
			902	553	181	162	6		

- Molecule 7 is a protein called MITORIBOSOMAL PROTEIN BL33M, MRPL33.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	6	48	Total	C	N	O	S	0	0
			391	253	70	66	2		

- Molecule 8 is a protein called MITORIBOSOMAL PROTEIN BL34M, MRPL34.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	7	46	Total	C	N	O	S	0	0
			387	239	89	58	1		

- Molecule 9 is a protein called MITORIBOSOMAL PROTEIN BL35M, MRPL35.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	8	95	Total	C	N	O	S	0	0
			833	539	163	129	2		

- Molecule 10 is a protein called MITORIBOSOMAL PROTEIN BL36M, MRPL36.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	9	38	Total	C	N	O	S	0	0
			335	214	70	47	4		

- Molecule 11 is a RNA chain called MITORIBOSOMAL 16S RRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	A	1515	Total	C	N	O	P	0	0
			32233	14473	5860	10385	1515		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127A	G	-	insertion	GB 4220565

- Molecule 12 is a RNA chain called MITORIBOSOMAL CP TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	B	62	Total	C	N	O	P	0	0
			1225	594	196	373	62		

- Molecule 13 is a RNA chain called TRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	C	3	Total	C	N	O	P	0	0
			62	28	11	20	3		
13	Z	3	Total	C	N	O	P	0	0
			62	28	11	20	3		

- Molecule 14 is a protein called MITORIBOSOMAL PROTEIN UL2M, MRPL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	D	240	Total	C	N	O	S	0	0
			1860	1160	371	319	10		

- Molecule 15 is a protein called MITORIBOSOMAL PROTEIN UL3M, MRPL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	E	307	Total	C	N	O	S	0	0
			2420	1554	426	430	10		

- Molecule 16 is a protein called MITORIBOSOMAL PROTEIN UL4M, MRPL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	F	250	Total	C	N	O	S	0	0
			2011	1294	367	344	6		

- Molecule 17 is a protein called MITORIBOSOMAL PROTEIN BL9M, MRPL9.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	I	98	Total	C	N	O		0	0
			805	509	155	141			

- Molecule 18 is a protein called MITORIBOSOMAL PROTEIN UL10M, MRPL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	J	168	Total	C	N	O	S	0	0
			1361	879	248	226	8		

- Molecule 19 is a protein called MITORIBOSOMAL PROTEIN UL11M, MRPL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	K	142	Total	C	N	O	S	0	0
			1081	690	197	192	2		

- Molecule 20 is a protein called MITORIBOSOMAL PROTEIN UL13M, MRPL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	N	177	Total	C	N	O	S	0	0
			1444	926	258	253	7		

- Molecule 21 is a protein called MITORIBOSOMAL PROTEIN UL14M, MRPL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	O	115	Total	C	N	O	S	0	0
			896	562	176	154	4		

- Molecule 22 is a protein called MITORIBOSOMAL PROTEIN UL15M, MRPL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	288	Total	C	N	O	S	0	0
			2312	1473	430	403	6		

- Molecule 23 is a protein called MITORIBOSOMAL PROTEIN UL16M, MRPL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	Q	221	Total	C	N	O	S	0	0
			1792	1147	330	305	10		

- Molecule 24 is a protein called MITORIBOSOMAL PROTEIN BL17M, MRPL17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	R	153	Total	C	N	O	S	0	0
			1240	777	236	222	5		

- Molecule 25 is a protein called MITORIBOSOMAL PROTEIN UL18M, MRPL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	S	143	Total	C	N	O	S	0	0
			1168	733	227	204	4		

- Molecule 26 is a protein called MITORIBOSOMAL PROTEIN BL19M, MRPL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	T	224	Total	C	N	O	S	0	0
			1860	1189	324	338	9		

- Molecule 27 is a protein called MITORIBOSOMAL PROTEIN BL20M, MRPL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	U	140	Total	C	N	O	S	0	0
			1159	732	239	185	3		

- Molecule 28 is a protein called MITORIBOSOMAL PROTEIN BL21M, MRPL21.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	V	155	Total	C	N	O	S	0	0
			1231	789	219	219	4		

- Molecule 29 is a protein called MITORIBOSOMAL PROTEIN UL22M, MRPL22.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	166	Total	C	N	O	S	0	0
			1374	876	258	234	6		

- Molecule 30 is a protein called MITORIBOSOMAL PROTEIN UL23M, MRPL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	134	Total	C	N	O	S	0	0
			1120	715	217	186	2		

- Molecule 31 is a protein called MITORIBOSOMAL PROTEIN UL24M, MRPL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Y	204	Total	C	N	O	S	0	0
			1663	1047	305	306	5		

- Molecule 32 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
32	5	1	Total	Zn	0
			1	1	
32	9	1	Total	Zn	0
			1	1	

- Molecule 33 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
33	A	163	Total	Mg	0
			163	163	
33	D	2	Total	Mg	0
			2	2	

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Mol	Chain	Residues	Atoms		AltConf
33	P	2	Total 2	Mg 2	0
33	Q	1	Total 1	Mg 1	0
33	R	1	Total 1	Mg 1	0

- Molecule 34 is water.

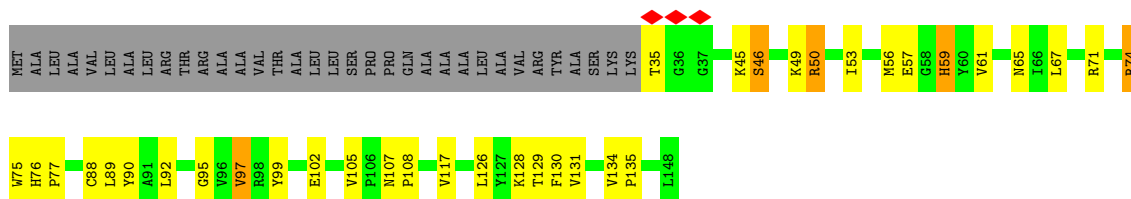
Mol	Chain	Residues	Atoms		AltConf
34	A	192	Total 192	O 192	0
34	D	6	Total 6	O 6	0
34	P	6	Total 6	O 6	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

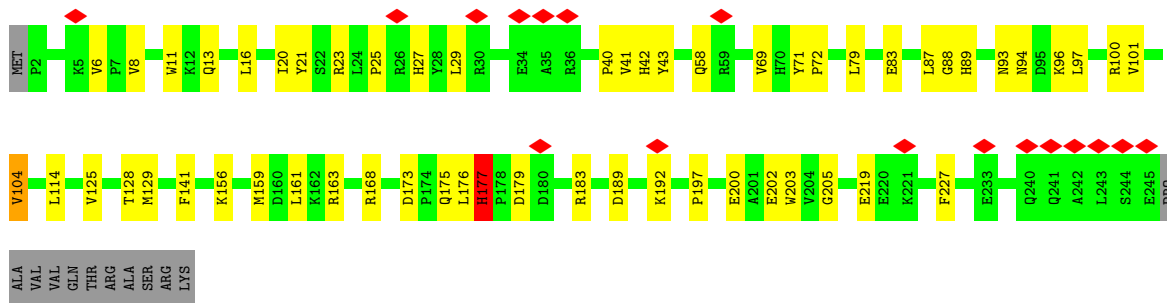
- Molecule 1: MITORIBOSOMAL PROTEIN BL27M, MRPL27

Chain 0: 



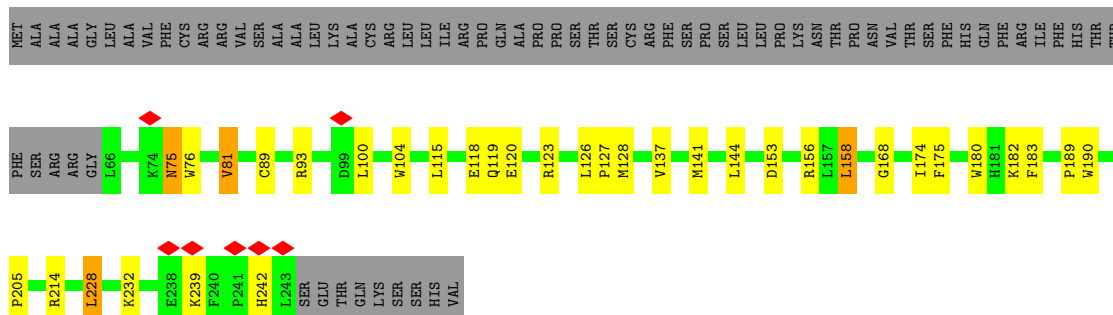
- Molecule 2: MITORIBOSOMAL PROTEIN BL28M, MRPL28

Chain 1: 



- Molecule 3: MITORIBOSOMAL PROTEIN UL29M, MRPL47

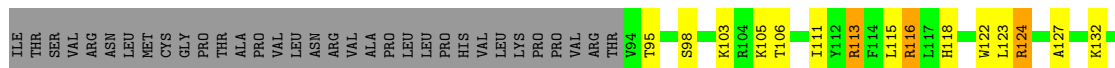
Chain 2: 







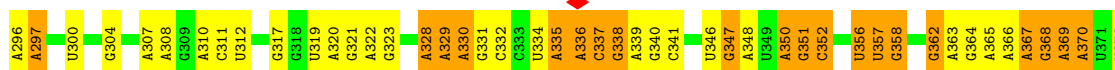
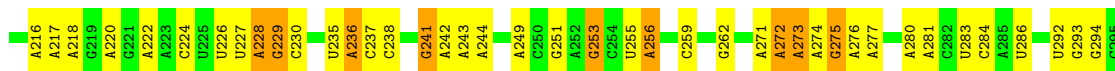
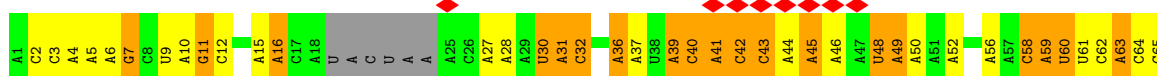
Chain 8: 36% 12% 49%



Chain 9: 24% 13% 62%



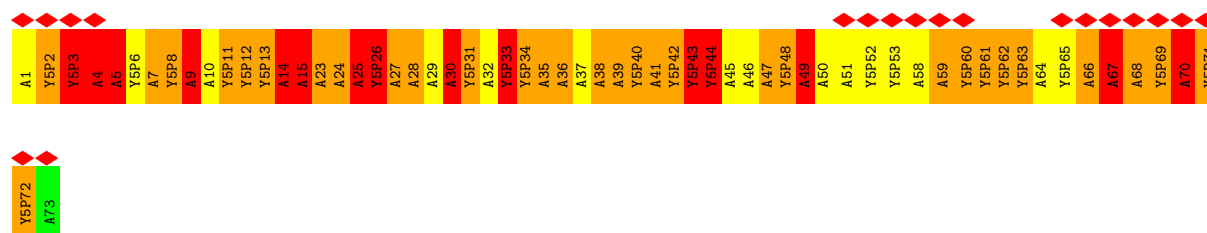
Chain A: 39% 38% 20% .







• Molecule 12: MITORIBOSOMAL CP TRNA



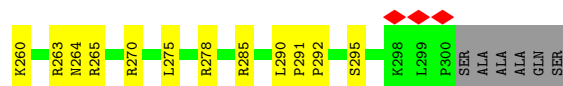
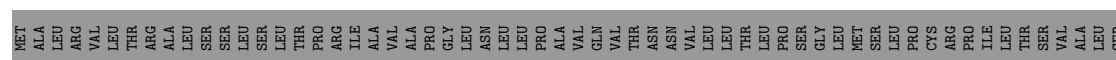
• Molecule 13: TRNA



• Molecule 13: TRNA

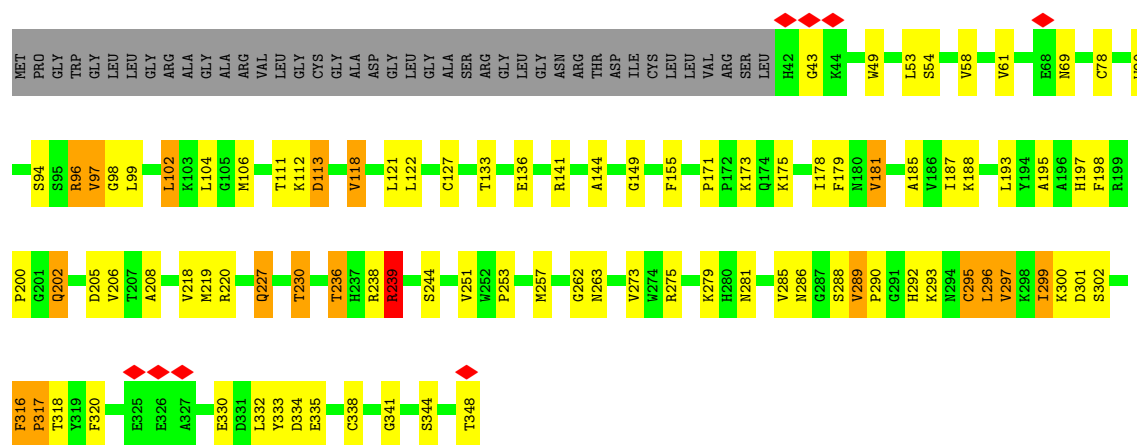


• Molecule 14: MITORIBOSOMAL PROTEIN UL2M, MRPL2

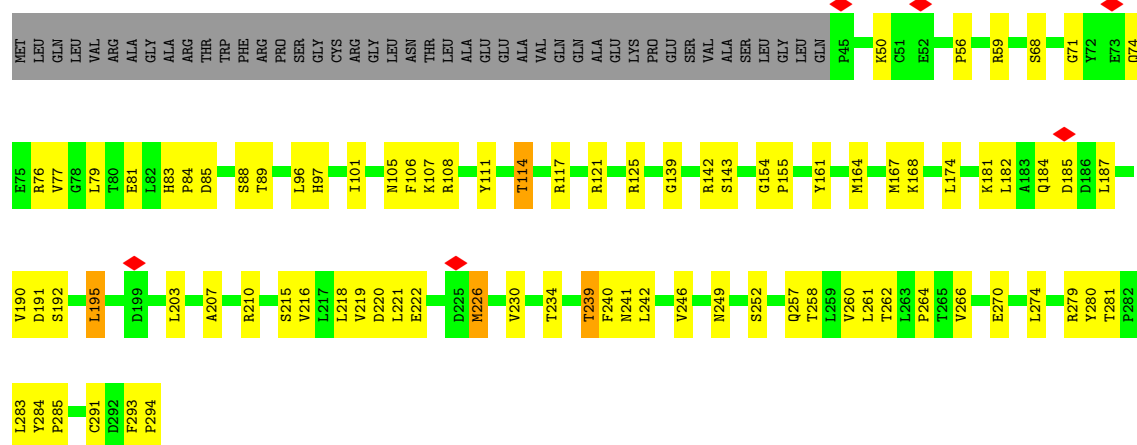


• Molecule 15: MITORIBOSOMAL PROTEIN UL3M, MRPL3

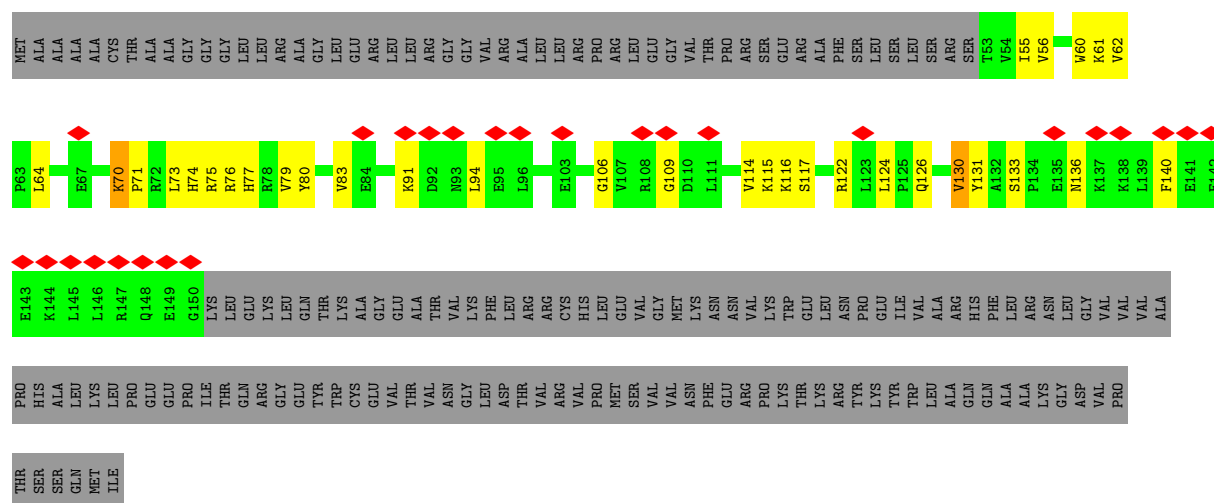




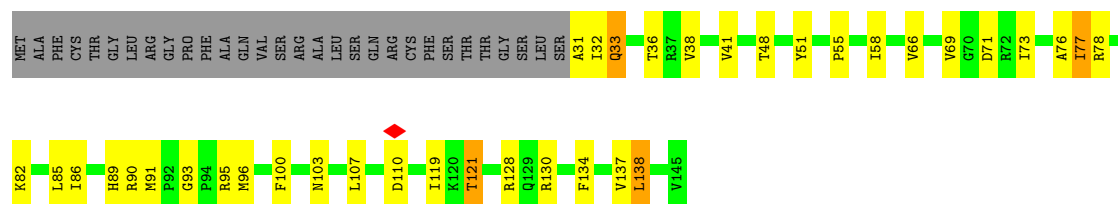
• Molecule 16: MITORIBOSOMAL PROTEIN UL4M, MRPL4



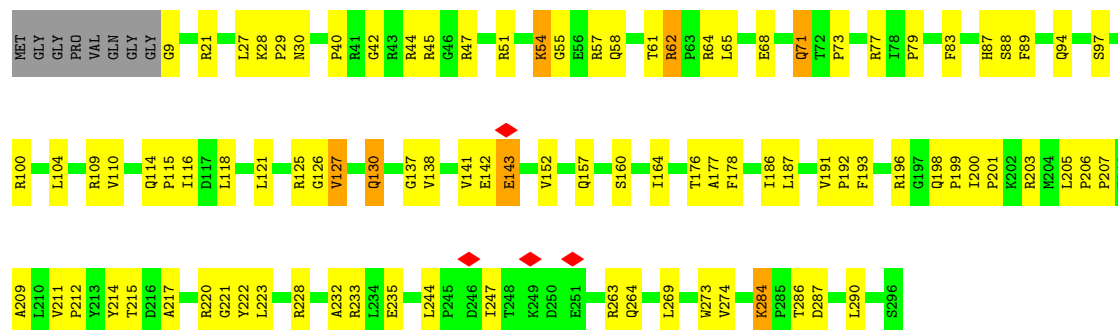
• Molecule 17: MITORIBOSOMAL PROTEIN BL9M, MRPL9



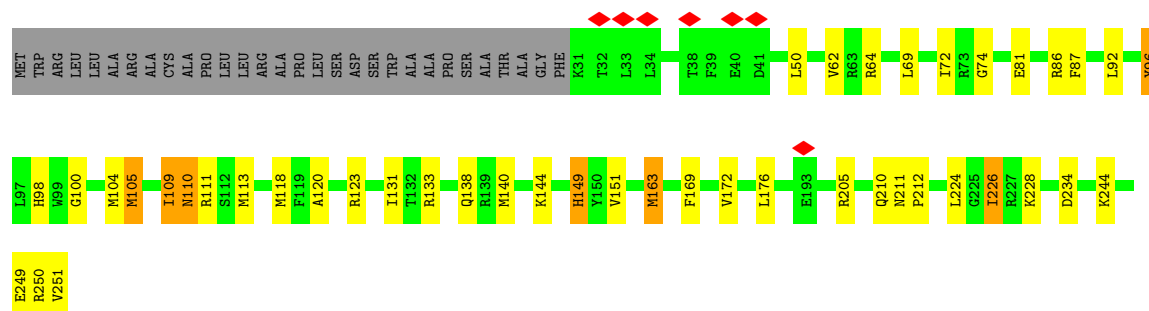




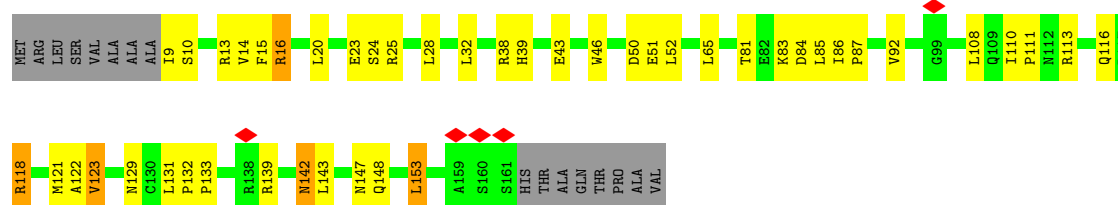
• Molecule 22: MITORIBOSOMAL PROTEIN UL15M, MRPL15



• Molecule 23: MITORIBOSOMAL PROTEIN UL16M, MRPL16

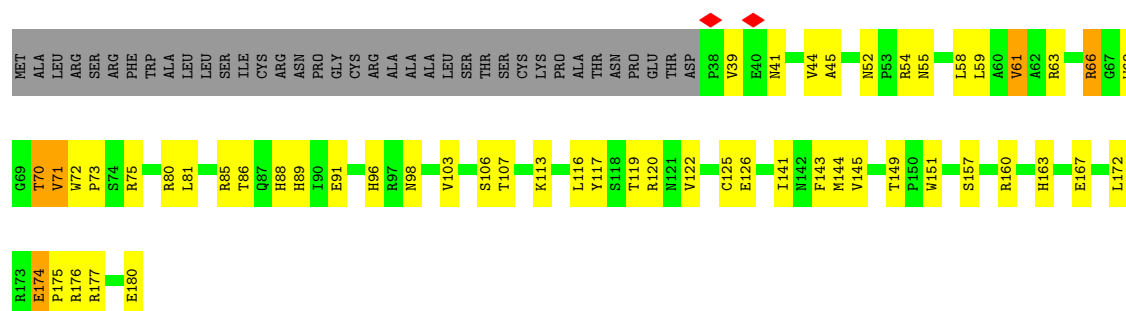


• Molecule 24: MITORIBOSOMAL PROTEIN BL17M, MRPL17

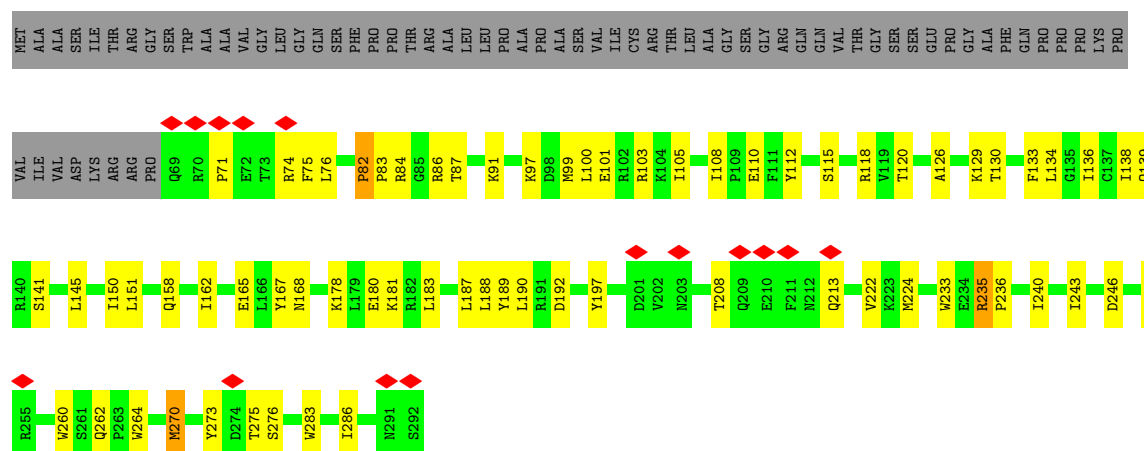


• Molecule 25: MITORIBOSOMAL PROTEIN UL18M, MRPL18

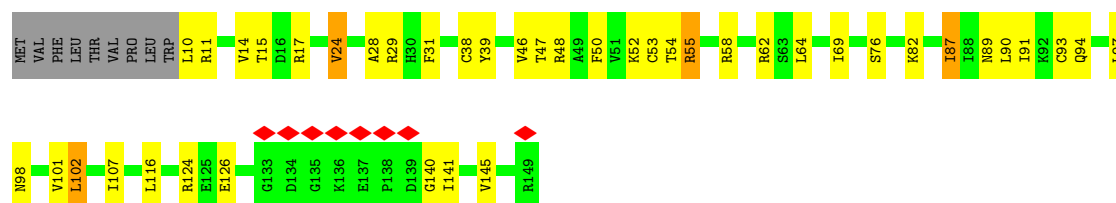




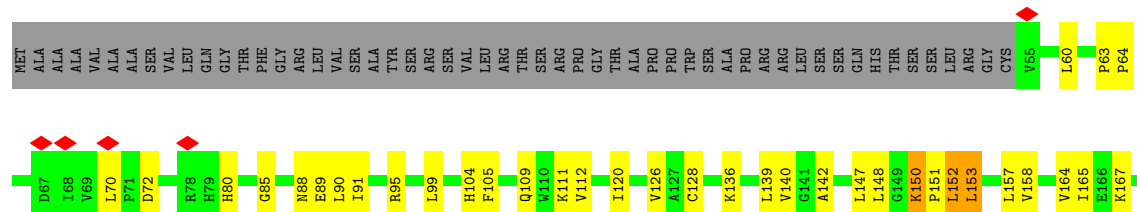
• Molecule 26: MITORIBOSOMAL PROTEIN BL19M, MRPL19

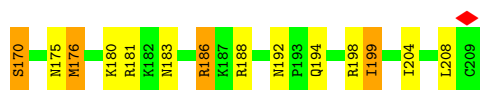


• Molecule 27: MITORIBOSOMAL PROTEIN BL20M, MRPL20

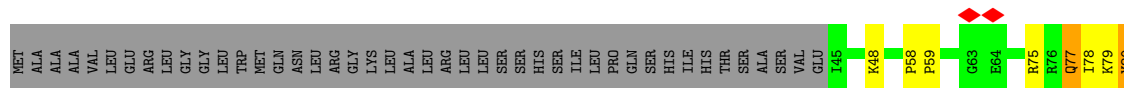


• Molecule 28: MITORIBOSOMAL PROTEIN BL21M, MRPL21

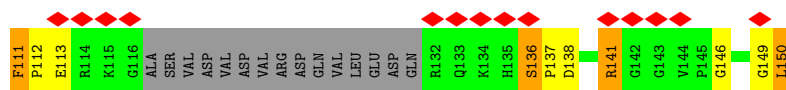




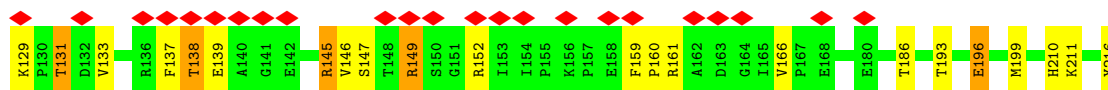
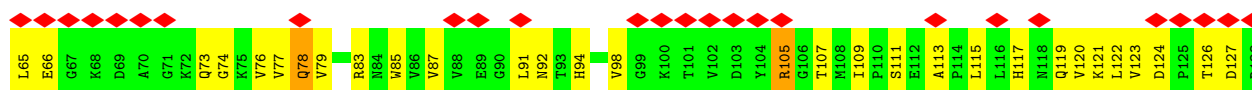
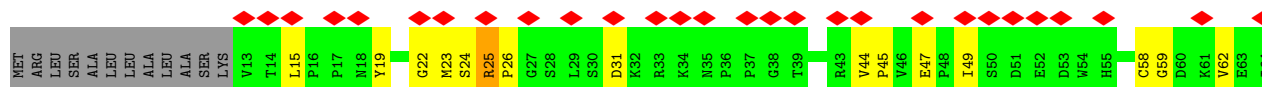
- Molecule 29: MITORIBOSOMAL PROTEIN UL22M, MRPL22



- Molecule 30: MITORIBOSOMAL PROTEIN UL23M, MRPL23



- Molecule 31: MITORIBOSOMAL PROTEIN UL24M, MRPL24



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	141675	Depositor
Resolution determination method	Not provided	
CTF correction method	PER DETECTOR FRAME	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	20	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	100000	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.560	Depositor
Minimum map value	-0.257	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.07	Depositor
Map size ($\text{\AA}$)	302.4, 302.4, 302.4	wwPDB
Map dimensions	216, 216, 216	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.4, 1.4, 1.4	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: Y5P, ZN, P5P, MG

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	0	0.52	0/901	0.99	8/1217 (0.7%)
2	1	0.43	0/2093	0.85	2/2835 (0.1%)
3	2	0.42	0/1582	0.85	1/2118 (0.0%)
4	3	0.52	0/993	1.04	2/1341 (0.1%)
5	4	0.39	0/388	0.94	3/523 (0.6%)
6	5	0.51	0/917	0.88	4/1227 (0.3%)
7	6	0.41	0/396	0.89	2/526 (0.4%)
8	7	0.61	0/395	0.86	0/524
9	8	0.57	0/853	0.92	0/1136
10	9	0.52	0/342	0.78	0/450
11	A	0.32	0/36094	0.52	0/56186
13	C	0.26	0/68	0.46	0/103
13	Z	0.18	0/68	0.26	0/103
14	D	0.50	0/1898	0.97	6/2555 (0.2%)
15	E	0.51	0/2493	1.03	9/3387 (0.3%)
16	F	0.54	0/2069	0.94	4/2816 (0.1%)
17	I	0.42	0/819	0.86	5/1101 (0.5%)
18	J	0.49	0/1392	0.96	6/1881 (0.3%)
19	K	0.49	0/1099	0.92	4/1480 (0.3%)
20	N	0.52	0/1487	0.96	5/2017 (0.2%)
21	O	0.46	0/912	0.92	2/1231 (0.2%)
22	P	0.52	0/2368	0.98	7/3198 (0.2%)
23	Q	0.48	0/1838	0.85	2/2475 (0.1%)
24	R	0.49	0/1262	0.87	0/1700
25	S	0.44	0/1197	0.89	0/1624
26	T	0.43	0/1903	0.94	10/2567 (0.4%)
27	U	0.56	0/1179	0.92	0/1578
28	V	0.50	0/1256	0.97	3/1706 (0.2%)
29	W	0.52	0/1407	0.92	1/1891 (0.1%)
30	X	0.46	0/1149	1.07	8/1554 (0.5%)
31	Y	0.46	0/1704	0.93	6/2310 (0.3%)
All	All	0.41	0/72522	0.74	100/105360 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
15	E	0	2
28	V	0	1
All	All	0	3

There are no bond length outliers.

The worst 5 of 100 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	X	111	PHE	CA-C-N	10.37	130.65	119.87
30	X	111	PHE	C-N-CA	10.37	130.65	119.87
31	Y	15	LEU	CA-C-N	9.23	129.89	120.38
31	Y	15	LEU	C-N-CA	9.23	129.89	120.38
22	P	9	GLY	CA-C-N	8.67	130.67	119.84

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	E	316	PHE	Peptide
15	E	43	GLY	Peptide
28	V	150	LYS	Peptide

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	0	878	0	896	20	0
2	1	2036	0	2058	36	0
3	2	1544	0	1580	30	0
4	3	968	0	1018	23	0
5	4	381	0	400	9	0
6	5	902	0	916	22	0
7	6	391	0	429	19	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	7	387	0	413	11	0
9	8	833	0	883	17	0
10	9	335	0	359	11	0
11	A	32233	0	16310	446	0
12	B	1225	0	675	29	0
13	C	62	0	34	1	0
13	Z	62	0	34	0	0
14	D	1860	0	1923	60	0
15	E	2420	0	2418	68	0
16	F	2011	0	2049	51	0
17	I	805	0	845	21	0
18	J	1361	0	1449	47	0
19	K	1081	0	1146	37	0
20	N	1444	0	1437	23	0
21	O	896	0	946	26	0
22	P	2312	0	2373	64	0
23	Q	1792	0	1832	34	0
24	R	1240	0	1260	40	0
25	S	1168	0	1159	47	0
26	T	1860	0	1875	46	0
27	U	1159	0	1228	37	0
28	V	1231	0	1278	38	0
29	W	1374	0	1405	21	0
30	X	1120	0	1133	29	0
31	Y	1663	0	1665	52	0
32	5	1	0	0	0	0
32	9	1	0	0	0	0
33	A	163	0	0	0	0
33	D	2	0	0	0	0
33	P	2	0	0	0	0
33	Q	1	0	0	0	0
33	R	1	0	0	0	0
34	A	192	0	0	5	0
34	D	6	0	0	0	0
34	P	6	0	0	4	0
All	All	69409	0	53426	1205	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 10.

The worst 5 of 1205 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)
11:A:346:U:H4'	11:A:347:G:H5'	1.53	0.91
27:U:54:THR:HG21	28:V:176:MET:H	1.38	0.88
14:D:111:ARG:HH11	14:D:182:ALA:HB2	1.40	0.86
16:F:262:THR:HG22	16:F:264:PRO:HD2	1.59	0.85
18:J:156:SER:HB3	18:J:159:PRO:HB3	1.59	0.84

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	0	112/148 (76%)	110 (98%)	2 (2%)	0	100	100
2	1	242/256 (94%)	235 (97%)	7 (3%)	0	100	100
3	2	176/252 (70%)	167 (95%)	9 (5%)	0	100	100
4	3	116/161 (72%)	113 (97%)	3 (3%)	0	100	100
5	4	43/126 (34%)	42 (98%)	1 (2%)	0	100	100
6	5	108/188 (57%)	107 (99%)	1 (1%)	0	100	100
7	6	46/65 (71%)	44 (96%)	2 (4%)	0	100	100
8	7	44/95 (46%)	44 (100%)	0	0	100	100
9	8	93/188 (50%)	91 (98%)	2 (2%)	0	100	100
10	9	36/100 (36%)	36 (100%)	0	0	100	100
14	D	238/306 (78%)	230 (97%)	8 (3%)	0	100	100
15	E	305/348 (88%)	279 (92%)	24 (8%)	2 (1%)	18	47
16	F	248/294 (84%)	237 (96%)	10 (4%)	1 (0%)	30	59
17	I	96/268 (36%)	87 (91%)	9 (9%)	0	100	100
18	J	166/262 (63%)	158 (95%)	8 (5%)	0	100	100
19	K	140/192 (73%)	133 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	N	175/178 (98%)	171 (98%)	4 (2%)	0	100	100
21	O	113/145 (78%)	109 (96%)	4 (4%)	0	100	100
22	P	286/296 (97%)	275 (96%)	11 (4%)	0	100	100
23	Q	219/251 (87%)	217 (99%)	2 (1%)	0	100	100
24	R	151/169 (89%)	148 (98%)	3 (2%)	0	100	100
25	S	141/180 (78%)	128 (91%)	12 (8%)	1 (1%)	18	47
26	T	222/292 (76%)	215 (97%)	6 (3%)	1 (0%)	24	54
27	U	138/149 (93%)	136 (99%)	2 (1%)	0	100	100
28	V	153/209 (73%)	148 (97%)	5 (3%)	0	100	100
29	W	164/210 (78%)	159 (97%)	5 (3%)	0	100	100
30	X	130/150 (87%)	125 (96%)	5 (4%)	0	100	100
31	Y	202/216 (94%)	191 (95%)	11 (5%)	0	100	100
All	All	4303/5694 (76%)	4135 (96%)	163 (4%)	5 (0%)	49	78

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
15	E	202	GLN
15	E	317	PRO
26	T	270	MET
16	F	291	CYS
25	S	45	ALA

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	
1	0	92/115 (80%)	79 (86%)	13 (14%)	3	13
2	1	219/229 (96%)	210 (96%)	9 (4%)	27	52
3	2	164/228 (72%)	157 (96%)	7 (4%)	26	51

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	3	110/147 (75%)	104 (94%)	6 (6%)	19	46
5	4	42/114 (37%)	40 (95%)	2 (5%)	23	50
6	5	99/163 (61%)	94 (95%)	5 (5%)	21	48
7	6	45/60 (75%)	41 (91%)	4 (9%)	9	31
8	7	41/78 (53%)	37 (90%)	4 (10%)	7	27
9	8	87/162 (54%)	76 (87%)	11 (13%)	4	18
10	9	36/77 (47%)	33 (92%)	3 (8%)	10	35
14	D	193/248 (78%)	180 (93%)	13 (7%)	15	41
15	E	263/290 (91%)	241 (92%)	22 (8%)	10	34
16	F	217/251 (86%)	199 (92%)	18 (8%)	10	35
17	I	88/228 (39%)	84 (96%)	4 (4%)	24	51
18	J	154/230 (67%)	137 (89%)	17 (11%)	6	22
19	K	115/151 (76%)	106 (92%)	9 (8%)	11	37
20	N	156/157 (99%)	147 (94%)	9 (6%)	18	45
21	O	99/123 (80%)	92 (93%)	7 (7%)	13	39
22	P	245/249 (98%)	230 (94%)	15 (6%)	17	43
23	Q	189/210 (90%)	177 (94%)	12 (6%)	16	42
24	R	132/143 (92%)	123 (93%)	9 (7%)	14	40
25	S	123/153 (80%)	115 (94%)	8 (6%)	15	42
26	T	206/258 (80%)	197 (96%)	9 (4%)	25	51
27	U	118/127 (93%)	107 (91%)	11 (9%)	8	29
28	V	136/178 (76%)	128 (94%)	8 (6%)	18	44
29	W	144/180 (80%)	137 (95%)	7 (5%)	22	49
30	X	119/134 (89%)	110 (92%)	9 (8%)	12	38
31	Y	183/192 (95%)	168 (92%)	15 (8%)	10	35
All	All	3815/4875 (78%)	3549 (93%)	266 (7%)	16	40

5 of 266 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	V	164	VAL
29	W	144	THR
31	Y	149	ARG

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Mol	Chain	Res	Type
15	E	300	LYS
15	E	295	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
22	P	170	ASN
26	T	139	GLN
23	Q	98	HIS
24	R	129	ASN
28	V	80	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
11	A	1508/1570 (96%)	727 (48%)	29 (1%)
12	B	59/62 (95%)	25 (42%)	0
13	C	2/3 (66%)	2 (100%)	0
13	Z	2/3 (66%)	0	0
All	All	1571/1638 (95%)	754 (47%)	29 (1%)

5 of 754 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
11	A	4	A
11	A	5	A
11	A	7	G
11	A	11	G
11	A	12	C

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
11	A	572	A
11	A	1467	C
11	A	617	C
11	A	1139	A
11	A	583	A

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

62 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
12	Y5P	B	11	12	14,19,20	4.57	2 (14%)	18,26,29	1.39	2 (11%)
12	P5P	B	39	12	20,23,24	0.47	0	27,33,36	0.79	1 (3%)
12	P5P	B	67	12	20,23,24	0.46	0	27,33,36	0.83	1 (3%)
12	P5P	B	4	12	20,23,24	0.49	0	27,33,36	0.70	1 (3%)
12	Y5P	B	61	12	14,19,20	4.32	2 (14%)	18,26,29	1.06	1 (5%)
12	Y5P	B	43	12	14,19,20	4.65	2 (14%)	18,26,29	1.33	2 (11%)
12	P5P	B	47	12	20,23,24	0.43	0	27,33,36	0.79	1 (3%)
12	P5P	B	49	12	20,23,24	1.07	3 (15%)	27,33,36	1.93	4 (14%)
12	P5P	B	59	12	20,23,24	1.05	3 (15%)	27,33,36	1.91	4 (14%)
12	P5P	B	73	12	20,23,24	0.56	0	27,33,36	0.65	0
12	P5P	B	5	12	20,23,24	0.51	0	27,33,36	0.78	1 (3%)
12	Y5P	B	31	12	14,19,20	4.48	2 (14%)	18,26,29	1.44	2 (11%)
12	Y5P	B	71	12	14,19,20	4.64	2 (14%)	18,26,29	1.35	2 (11%)
12	Y5P	B	12	12	14,19,20	4.30	2 (14%)	18,26,29	1.00	1 (5%)
12	Y5P	B	62	12	14,19,20	4.32	2 (14%)	18,26,29	1.01	1 (5%)
12	P5P	B	41	12	20,23,24	0.97	2 (10%)	27,33,36	1.83	3 (11%)
12	Y5P	B	40	12	14,19,20	4.23	2 (14%)	18,26,29	1.08	1 (5%)
12	P5P	B	50	12	20,23,24	0.52	0	27,33,36	0.76	1 (3%)
12	P5P	B	9	12	20,23,24	0.47	0	27,33,36	0.75	1 (3%)
12	P5P	B	23	12	20,23,24	0.46	0	27,33,36	0.89	1 (3%)
12	Y5P	B	34	12	14,19,20	4.28	2 (14%)	18,26,29	1.07	1 (5%)
12	Y5P	B	26	12	14,19,20	4.50	2 (14%)	18,26,29	1.41	2 (11%)
12	P5P	B	45	12	20,23,24	0.47	0	27,33,36	0.69	1 (3%)
12	Y5P	B	52	12	14,19,20	4.60	2 (14%)	18,26,29	1.38	2 (11%)
12	Y5P	B	2	12	14,19,20	4.29	2 (14%)	18,26,29	0.97	1 (5%)
12	P5P	B	38	12	20,23,24	0.52	0	27,33,36	0.81	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	Y5P	B	42	12	14,19,20	4.51	2 (14%)	18,26,29	1.42	2 (11%)
12	P5P	B	51	12	20,23,24	1.06	3 (15%)	27,33,36	1.92	4 (14%)
12	P5P	B	14	12	20,23,24	0.48	0	27,33,36	0.75	1 (3%)
12	P5P	B	70	12	20,23,24	0.51	0	27,33,36	0.70	1 (3%)
12	Y5P	B	69	12	14,19,20	4.55	2 (14%)	18,26,29	1.42	2 (11%)
12	Y5P	B	48	12	14,19,20	4.35	2 (14%)	18,26,29	0.97	1 (5%)
12	P5P	B	68	12	20,23,24	0.49	0	27,33,36	0.78	1 (3%)
12	Y5P	B	8	12	14,19,20	4.35	2 (14%)	18,26,29	1.20	1 (5%)
12	P5P	B	30	12	20,23,24	1.01	3 (15%)	27,33,36	1.84	4 (14%)
12	P5P	B	28	12	20,23,24	0.50	0	27,33,36	0.68	1 (3%)
12	Y5P	B	6	12	14,19,20	4.28	2 (14%)	18,26,29	1.01	1 (5%)
12	P5P	B	66	12	20,23,24	0.50	0	27,33,36	0.69	1 (3%)
12	Y5P	B	33	12	14,19,20	4.55	2 (14%)	18,26,29	1.38	2 (11%)
12	Y5P	B	63	12	14,19,20	4.64	2 (14%)	18,26,29	1.34	2 (11%)
12	Y5P	B	65	12	14,19,20	4.26	2 (14%)	18,26,29	1.05	1 (5%)
12	Y5P	B	72	12	14,19,20	4.65	2 (14%)	18,26,29	1.33	2 (11%)
12	P5P	B	64	12	20,23,24	0.50	0	27,33,36	0.74	1 (3%)
12	P5P	B	35	12	20,23,24	1.19	3 (15%)	27,33,36	1.77	3 (11%)
12	P5P	B	25	12	20,23,24	0.95	2 (10%)	27,33,36	2.00	5 (18%)
12	P5P	B	29	12	20,23,24	1.05	3 (15%)	27,33,36	1.97	3 (11%)
12	P5P	B	58	12	20,23,24	0.52	0	27,33,36	0.72	1 (3%)
12	Y5P	B	13	12	14,19,20	4.04	2 (14%)	18,26,29	1.18	1 (5%)
12	P5P	B	27	12	20,23,24	0.45	0	27,33,36	0.86	1 (3%)
12	P5P	B	36	12	20,23,24	0.52	0	27,33,36	0.78	1 (3%)
12	P5P	B	46	12	20,23,24	0.95	2 (10%)	27,33,36	1.91	4 (14%)
12	Y5P	B	3	12	14,19,20	4.22	2 (14%)	18,26,29	1.09	1 (5%)
12	Y5P	B	53	12	14,19,20	4.60	2 (14%)	18,26,29	1.36	2 (11%)
12	Y5P	B	60	12	14,19,20	4.57	2 (14%)	18,26,29	1.42	2 (11%)
12	P5P	B	37	12	20,23,24	0.47	0	27,33,36	0.77	1 (3%)
12	P5P	B	24	12	20,23,24	0.48	0	27,33,36	0.72	1 (3%)
12	P5P	B	7	12	20,23,24	1.02	3 (15%)	27,33,36	2.00	4 (14%)
12	P5P	B	1	12	24,24,24	1.08	3 (12%)	34,36,36	1.75	4 (11%)
12	P5P	B	32	12	20,23,24	0.46	0	27,33,36	0.72	1 (3%)
12	P5P	B	10	12	20,23,24	0.92	2 (10%)	27,33,36	1.91	3 (11%)
12	P5P	B	15	12	20,23,24	0.49	0	27,33,36	0.79	1 (3%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
12	Y5P	B	44	12	14,19,20	4.34	2 (14%)	18,26,29	0.98	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	Y5P	B	11	12	-	1/7/33/34	0/2/2/2
12	P5P	B	39	12	-	1/7/25/26	0/3/3/3
12	P5P	B	67	12	-	3/7/25/26	0/3/3/3
12	P5P	B	4	12	-	0/7/25/26	0/3/3/3
12	Y5P	B	61	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	43	12	-	3/7/33/34	0/2/2/2
12	P5P	B	47	12	-	0/7/25/26	0/3/3/3
12	P5P	B	49	12	-	2/7/25/26	0/3/3/3
12	P5P	B	59	12	-	0/7/25/26	0/3/3/3
12	P5P	B	73	12	-	0/7/25/26	0/3/3/3
12	P5P	B	5	12	-	3/7/25/26	0/3/3/3
12	Y5P	B	31	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	71	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	12	12	-	3/7/33/34	0/2/2/2
12	Y5P	B	62	12	-	1/7/33/34	0/2/2/2
12	P5P	B	41	12	-	1/7/25/26	0/3/3/3
12	Y5P	B	40	12	-	3/7/33/34	0/2/2/2
12	P5P	B	50	12	-	0/7/25/26	0/3/3/3
12	P5P	B	9	12	-	5/7/25/26	0/3/3/3
12	P5P	B	23	12	-	3/7/25/26	0/3/3/3
12	Y5P	B	34	12	-	3/7/33/34	0/2/2/2
12	Y5P	B	26	12	-	3/7/33/34	0/2/2/2
12	P5P	B	45	12	-	0/7/25/26	0/3/3/3
12	Y5P	B	52	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	2	12	-	3/7/33/34	0/2/2/2
12	P5P	B	38	12	-	0/7/25/26	0/3/3/3
12	Y5P	B	42	12	-	1/7/33/34	0/2/2/2
12	P5P	B	51	12	-	0/7/25/26	0/3/3/3
12	P5P	B	14	12	-	1/7/25/26	0/3/3/3
12	P5P	B	70	12	-	2/7/25/26	0/3/3/3
12	Y5P	B	69	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	48	12	-	1/7/33/34	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
12	P5P	B	68	12	-	0/7/25/26	0/3/3/3
12	Y5P	B	8	12	-	2/7/33/34	0/2/2/2
12	P5P	B	30	12	-	3/7/25/26	0/3/3/3
12	P5P	B	28	12	-	2/7/25/26	0/3/3/3
12	Y5P	B	6	12	-	2/7/33/34	0/2/2/2
12	P5P	B	66	12	-	2/7/25/26	0/3/3/3
12	Y5P	B	33	12	-	3/7/33/34	0/2/2/2
12	Y5P	B	63	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	65	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	72	12	-	1/7/33/34	0/2/2/2
12	P5P	B	64	12	-	0/7/25/26	0/3/3/3
12	P5P	B	35	12	-	2/7/25/26	0/3/3/3
12	P5P	B	25	12	-	2/7/25/26	0/3/3/3
12	P5P	B	29	12	-	0/7/25/26	0/3/3/3
12	P5P	B	58	12	-	0/7/25/26	0/3/3/3
12	Y5P	B	13	12	-	1/7/33/34	0/2/2/2
12	P5P	B	27	12	-	1/7/25/26	0/3/3/3
12	P5P	B	36	12	-	1/7/25/26	0/3/3/3
12	P5P	B	46	12	-	3/7/25/26	0/3/3/3
12	Y5P	B	3	12	-	2/7/33/34	0/2/2/2
12	Y5P	B	53	12	-	1/7/33/34	0/2/2/2
12	Y5P	B	60	12	-	1/7/33/34	0/2/2/2
12	P5P	B	37	12	-	0/7/25/26	0/3/3/3
12	P5P	B	24	12	-	0/7/25/26	0/3/3/3
12	P5P	B	7	12	-	1/7/25/26	0/3/3/3
12	P5P	B	1	12	-	3/10/26/26	0/3/3/3
12	P5P	B	32	12	-	2/7/25/26	0/3/3/3
12	P5P	B	10	12	-	0/7/25/26	0/3/3/3
12	P5P	B	15	12	-	3/7/25/26	0/3/3/3
12	Y5P	B	44	12	-	3/7/33/34	0/2/2/2

The worst 5 of 84 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	8	Y5P	C2-N3	14.23	1.38	1.27
12	B	44	Y5P	C2-N3	14.13	1.38	1.27
12	B	48	Y5P	C2-N3	13.98	1.38	1.27
12	B	61	Y5P	C2-N3	13.97	1.38	1.27
12	B	62	Y5P	C2-N3	13.94	1.38	1.27

The worst 5 of 107 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	7	P5P	C6-N1-C2	8.37	125.68	115.80
12	B	29	P5P	C6-N1-C2	8.23	125.51	115.80
12	B	49	P5P	C6-N1-C2	8.10	125.36	115.80
12	B	51	P5P	C6-N1-C2	8.04	125.29	115.80
12	B	59	P5P	C6-N1-C2	8.04	125.29	115.80

There are no chirality outliers.

5 of 91 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	B	1	P5P	C5'-O5'-P-OP1
12	B	1	P5P	C5'-O5'-P-OP2
12	B	1	P5P	C5'-O5'-P-OP3
12	B	5	P5P	O4'-C4'-C5'-O5'
12	B	15	P5P	O4'-C4'-C5'-O5'

There are no ring outliers.

36 monomers are involved in 29 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	B	11	Y5P	1	0
12	B	39	P5P	2	0
12	B	67	P5P	1	0
12	B	4	P5P	2	0
12	B	61	Y5P	2	0
12	B	43	Y5P	1	0
12	B	47	P5P	2	0
12	B	49	P5P	1	0
12	B	59	P5P	1	0
12	B	5	P5P	1	0
12	B	31	Y5P	1	0
12	B	71	Y5P	1	0
12	B	12	Y5P	1	0
12	B	62	Y5P	2	0
12	B	41	P5P	1	0
12	B	9	P5P	2	0
12	B	23	P5P	3	0
12	B	26	Y5P	1	0
12	B	38	P5P	2	0
12	B	42	Y5P	2	0
12	B	14	P5P	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	B	70	P5P	1	0
12	B	69	Y5P	2	0
12	B	48	Y5P	1	0
12	B	68	P5P	1	0
12	B	30	P5P	1	0
12	B	33	Y5P	1	0
12	B	63	Y5P	2	0
12	B	72	Y5P	1	0
12	B	25	P5P	3	0
12	B	13	Y5P	1	0
12	B	3	Y5P	1	0
12	B	60	Y5P	2	0
12	B	24	P5P	1	0
12	B	15	P5P	1	0
12	B	44	Y5P	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 171 ligands modelled in this entry, 171 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
12	B	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	53:Y5P	O3'	58:P5P	P	17.46
1	B	15:P5P	O3'	23:P5P	P	12.62

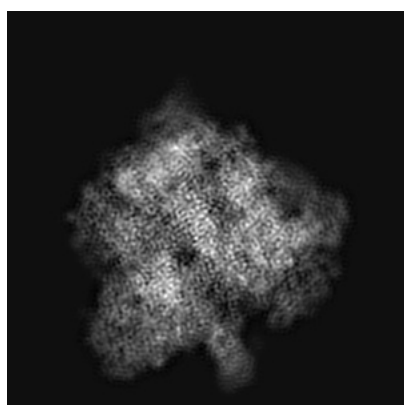
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2787. These allow visual inspection of the internal detail of the map and identification of artifacts.

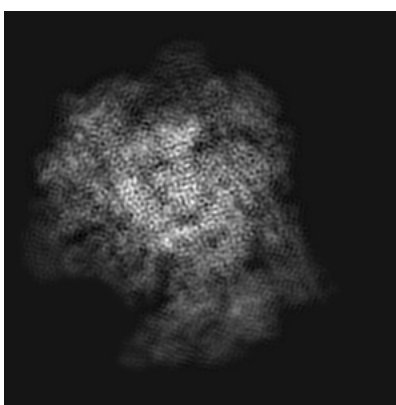
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

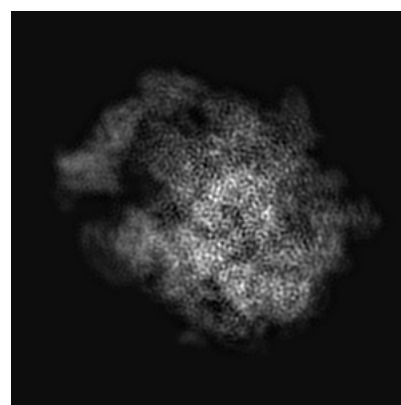
6.1.1 Primary map



X



Y

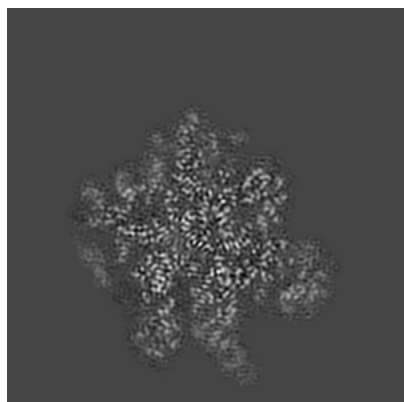


Z

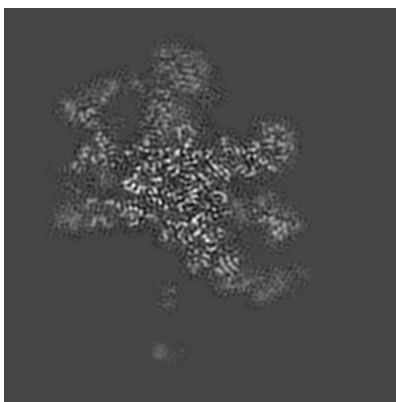
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

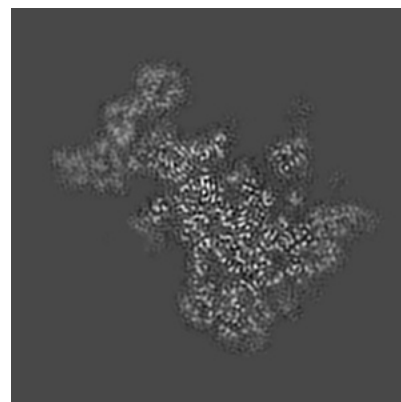
6.2.1 Primary map



X Index: 108



Y Index: 108

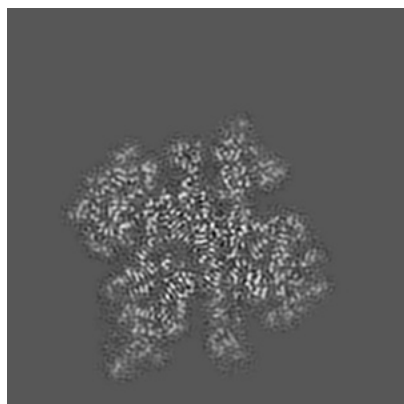


Z Index: 108

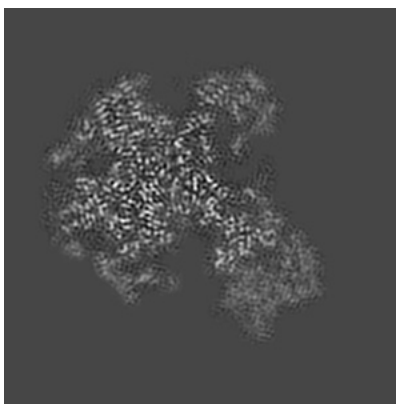
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

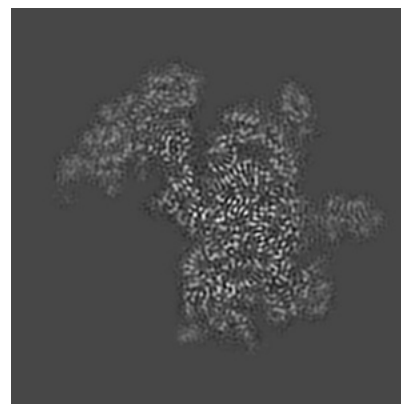
6.3.1 Primary map



X Index: 120



Y Index: 86

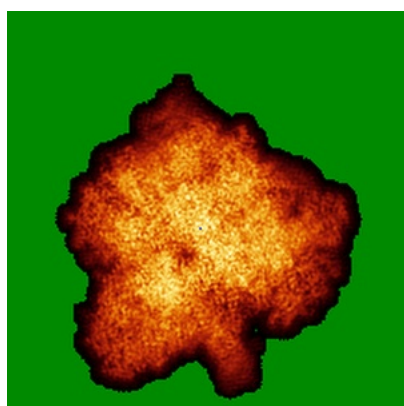


Z Index: 98

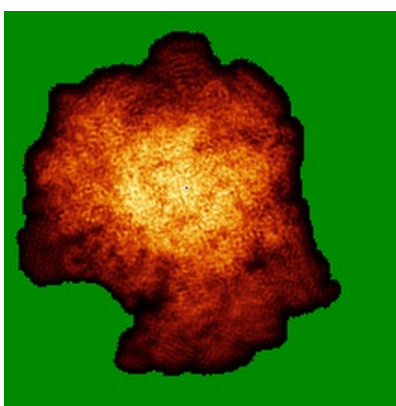
The images above show the largest variance slices of the map in three orthogonal directions.

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

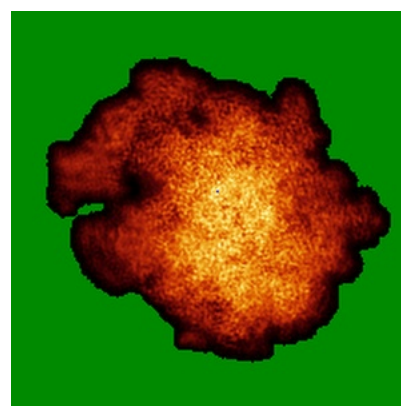
6.4.1 Primary map



X



Y



Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.07. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

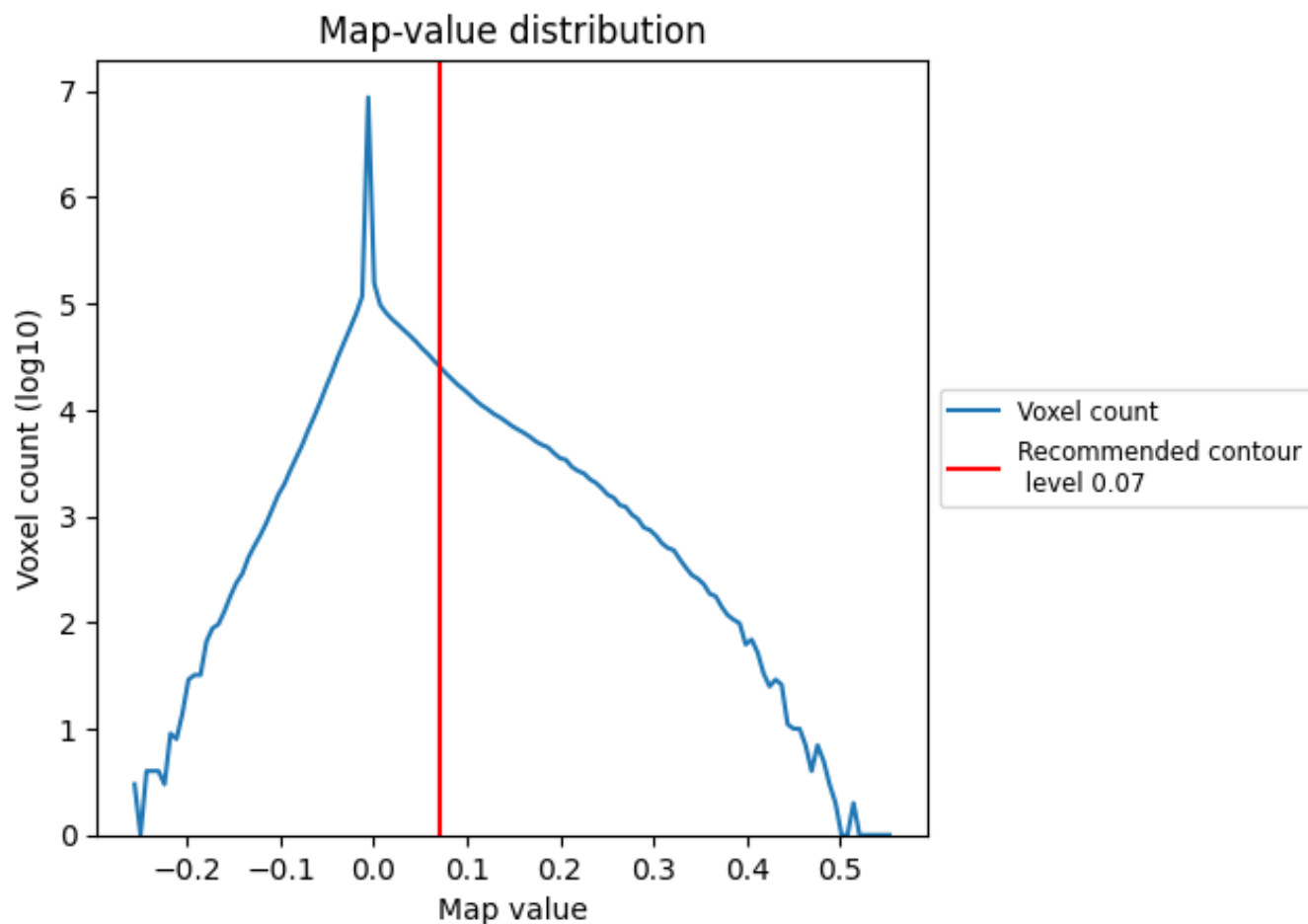
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

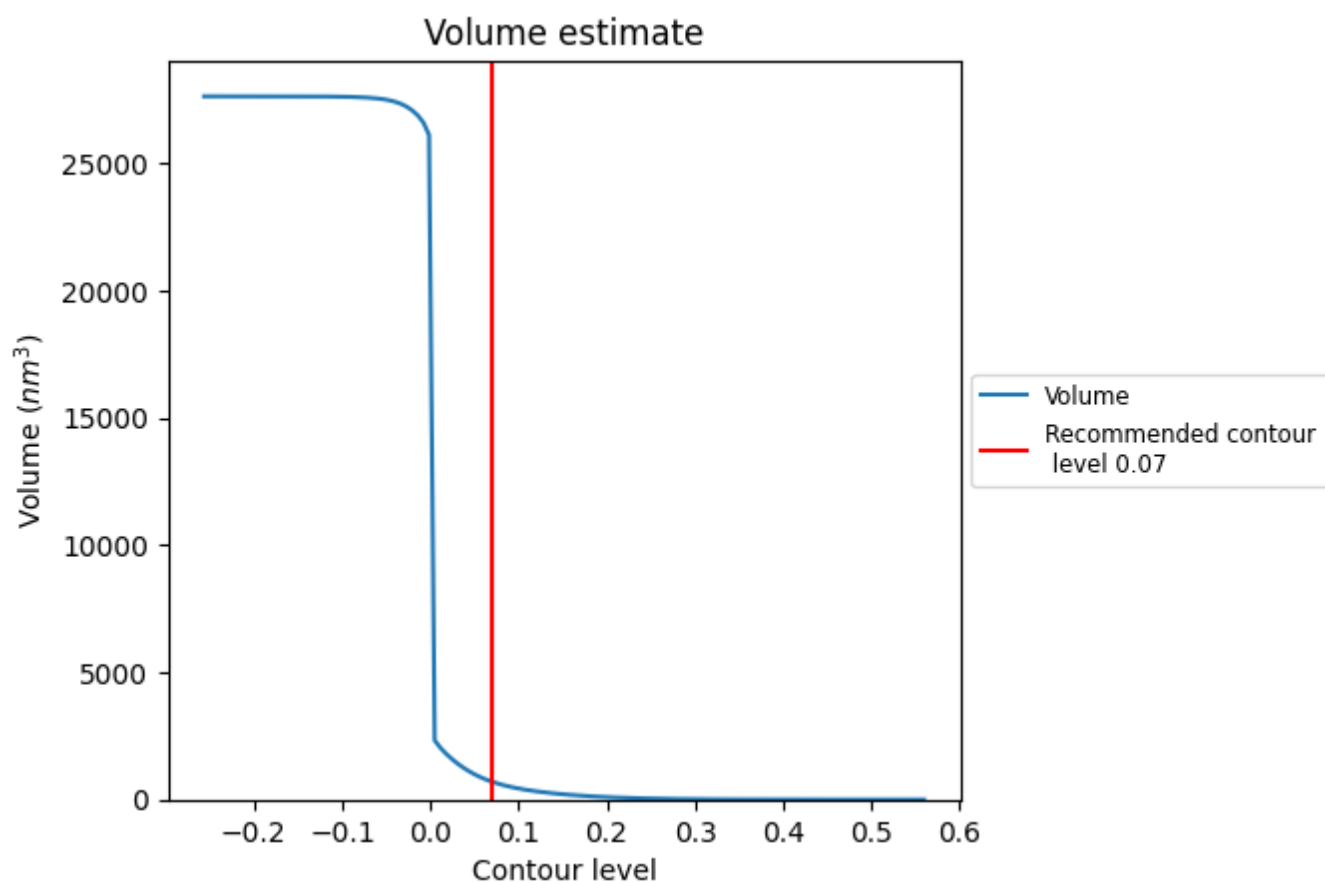
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

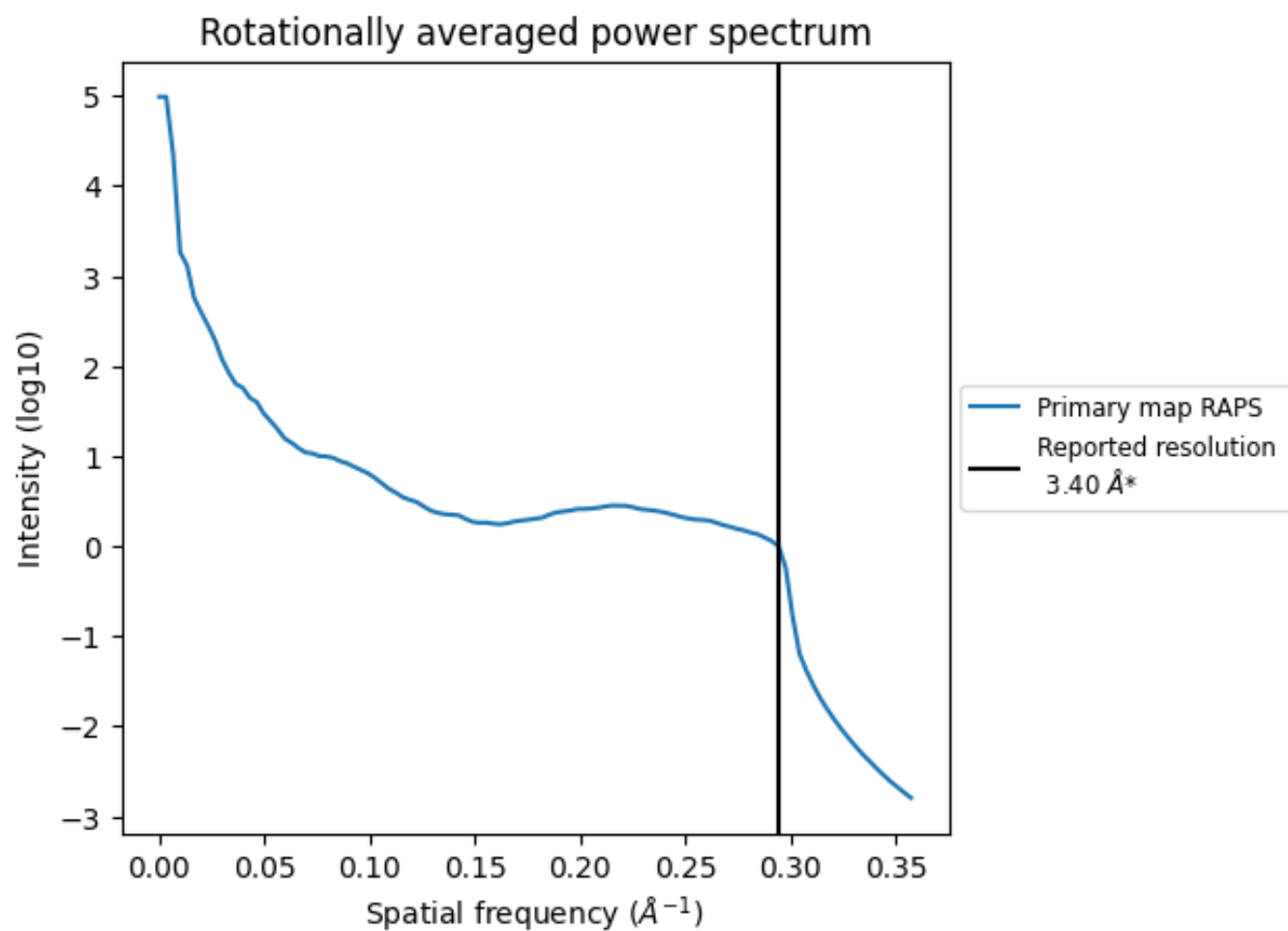
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 700 nm³; this corresponds to an approximate mass of 632 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



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

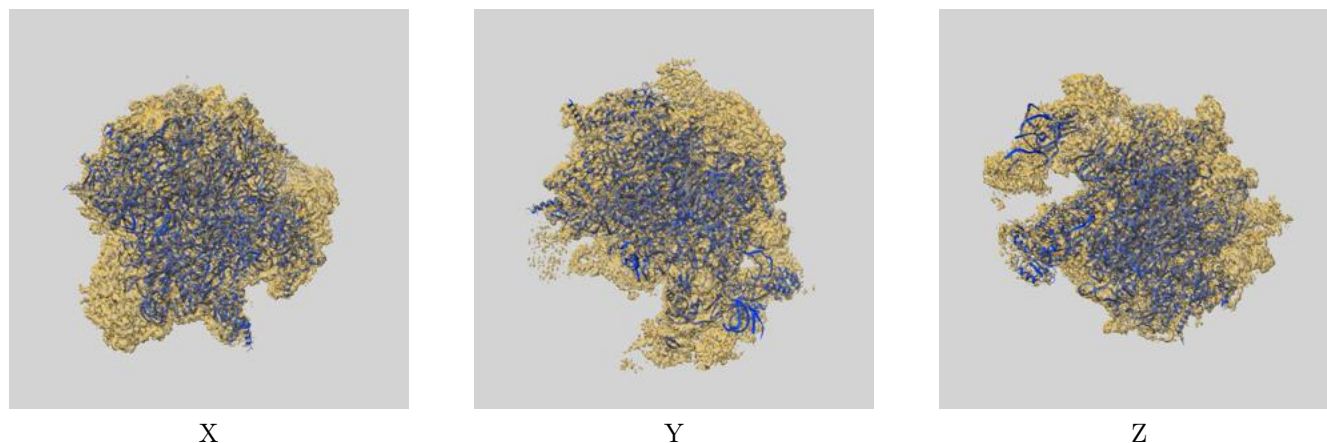
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

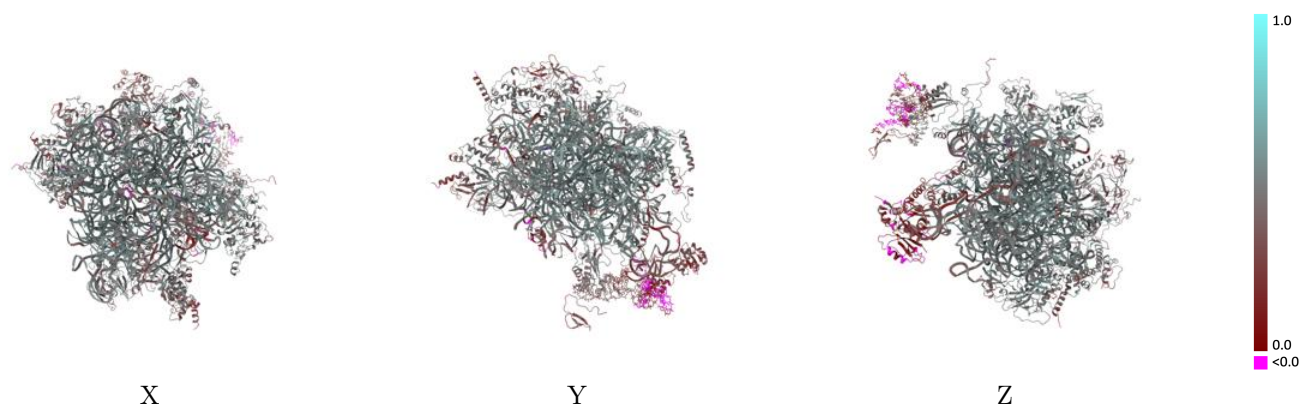
This section contains information regarding the fit between EMDB map EMD-2787 and PDB model 4V19. Per-residue inclusion information can be found in section [3](#) on page [11](#).

9.1 Map-model overlay [i](#)



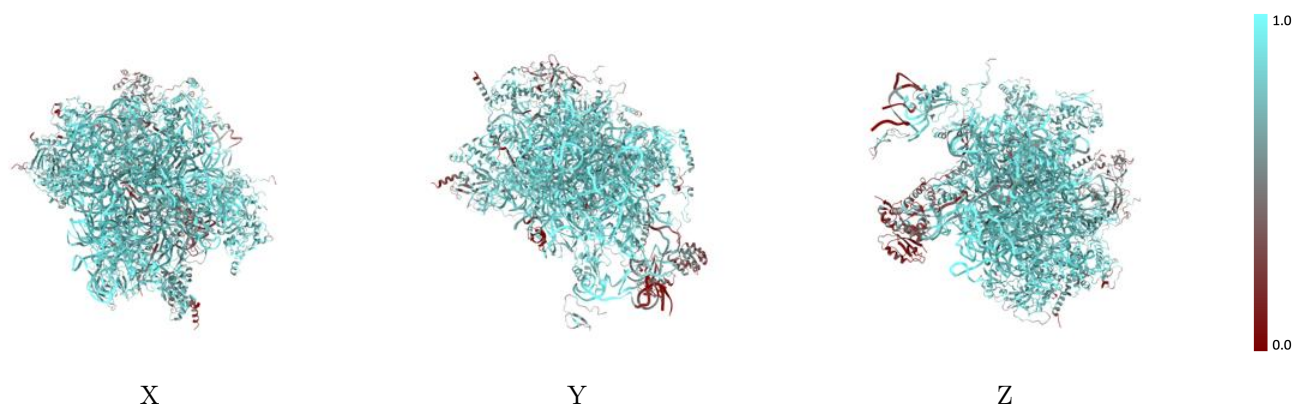
The images above show the 3D surface view of the map at the recommended contour level 0.07 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



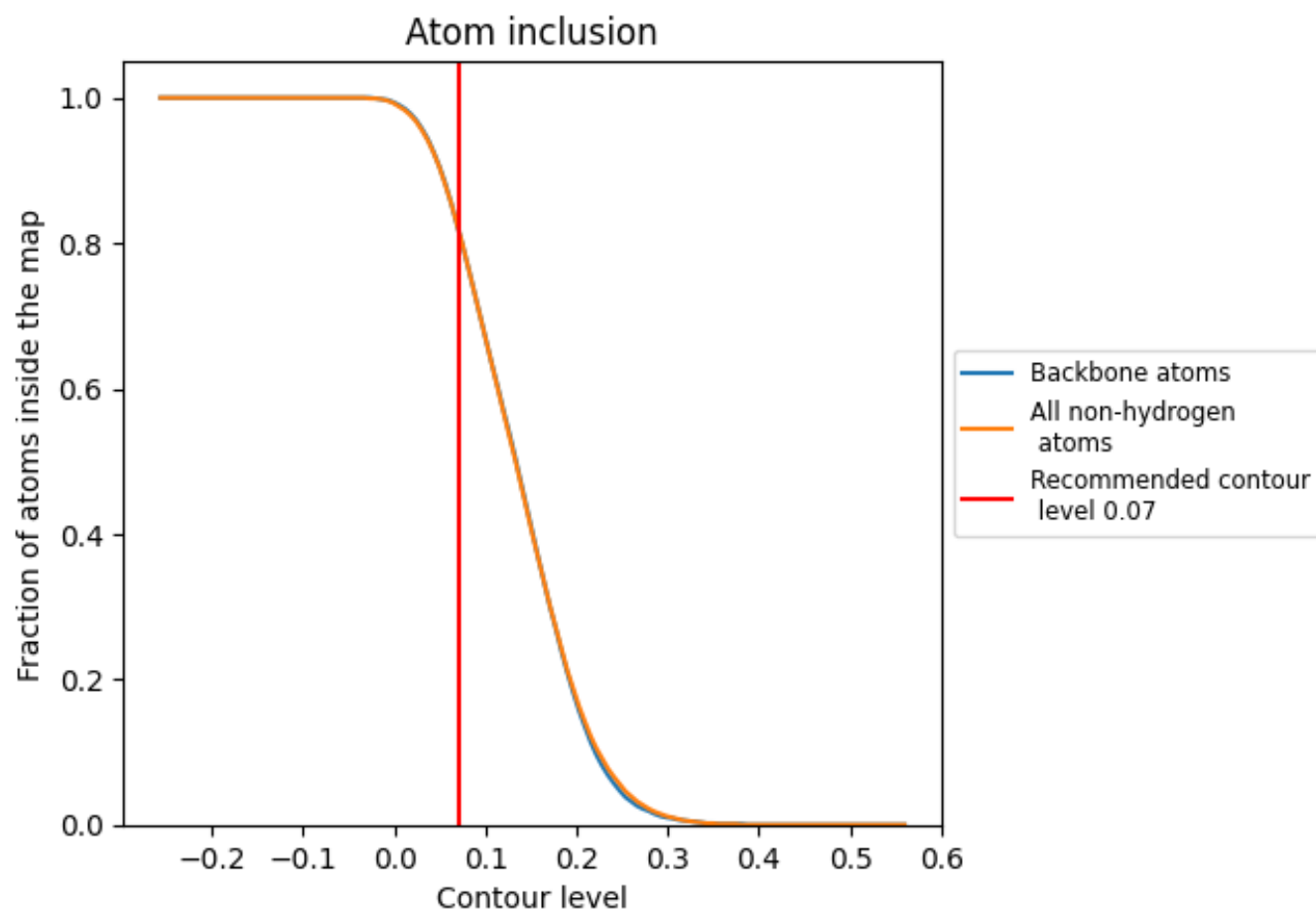
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.07).

9.4 Atom inclusion [i](#)



At the recommended contour level, 82% of all backbone atoms, 82% 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 (0.07) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8200	 0.4730
0	 0.8420	 0.5140
1	 0.7340	 0.4400
2	 0.7980	 0.4680
3	 0.8230	 0.4960
4	 0.5190	 0.2340
5	 0.7710	 0.4430
6	 0.0550	 0.1590
7	 0.8940	 0.5470
8	 0.8730	 0.5350
9	 0.8880	 0.5290
A	 0.9150	 0.5020
B	 0.5990	 0.2180
C	 0.6610	 0.4510
D	 0.8070	 0.4880
E	 0.8260	 0.4920
F	 0.8480	 0.5070
I	 0.5960	 0.3810
J	 0.4680	 0.3080
K	 0.2130	 0.1500
N	 0.8530	 0.5130
O	 0.8150	 0.5010
P	 0.8400	 0.4890
Q	 0.8160	 0.4850
R	 0.8110	 0.4910
S	 0.7810	 0.4340
T	 0.7530	 0.4680
U	 0.8280	 0.5000
V	 0.7970	 0.4890
W	 0.7950	 0.5080
X	 0.7890	 0.4770
Y	 0.4880	 0.3760
Z	 0.3870	 0.4190

