



wwPDB EM Validation Summary Report ⓘ

May 4, 2025 – 12:19 PM EDT

PDB ID : 8ETH / pdb_00008eth
EMDB ID : EMD-24409
Title : Ytm1 associated 60S nascent ribosome State 1B
Authors : Zhou, X.; Bilokapic, S.; Deshmukh, A.A.; Halic, M.
Deposited on : 2022-10-17
Resolution : 3.80 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.dev118
MolProbity : 4-5-2 with Phenix2.0rc1
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

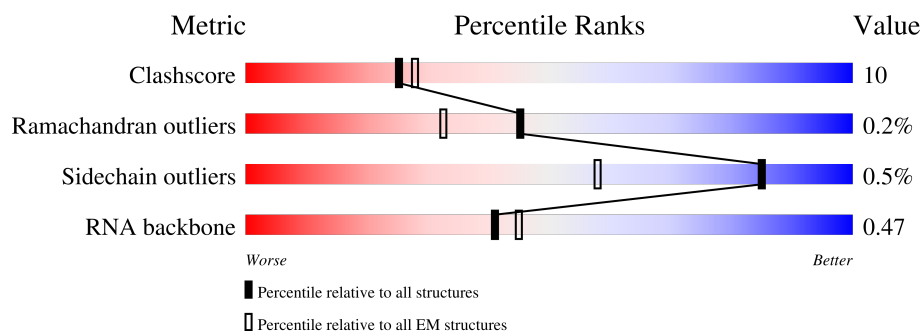
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	1	3497	
2	2	165	
3	3	302	
4	4	217	
5	5	387	
6	6	300	
7	A	295	

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Mol	Chain	Length	Quality of chain
8	B	388	
9	C	363	
10	D	578	
11	E	195	
12	F	250	
13	G	259	
14	H	190	
15	J	333	
16	K	373	
17	L	208	
18	M	134	
19	N	201	
20	O	197	
21	P	187	
22	Q	187	
23	S	176	
24	V	139	
25	Y	126	
26	b	642	
27	e	127	
28	f	108	
29	h	122	
30	i	99	
31	j	91	
32	m	740	

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Mol	Chain	Length	Quality of chain
33	n	607	
34	o	276	
35	r	260	
36	t	249	
37	u	192	
38	v	209	
39	x	306	
40	y	244	
41	T	160	

2 Entry composition

There are 42 unique types of molecules in this entry. The entry contains 77577 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 (1263-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
1	1	1303	Total	C	N	O	P	0	0
			27887	12455	5042	9087	1303		

- Molecule 2 is a RNA chain called RNA (130-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
2	2	130	Total	C	N	O	P	0	0
			2764	1237	489	908	130		

- Molecule 3 is a protein called Protein mak16.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	3	191	Total	C	N	O	S	0	0
			1572	995	301	269	7		

- Molecule 4 is a protein called Ribosomal RNA-processing protein 1 homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	4	209	Total	C	N	O	S	0	0
			1756	1145	301	302	8		

- Molecule 5 is a protein called Ribosome biogenesis protein nsa1.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	336	Total	C	N	O	S	0	0
			2640	1690	463	476	11		

- Molecule 6 is a RNA chain called RNA (75-MER).

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	75	Total	C	N	O	P	0	0
			1587	712	270	530	75		

- Molecule 7 is a protein called Ribosome biogenesis protein brx1.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	246	Total	C	N	O	S	0	0
			1981	1256	360	357	8		

- Molecule 8 is a protein called 60S ribosomal protein L3-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	316	Total	C	N	O	S	0	0
			1557	925	316	316			

- Molecule 9 is a protein called 60S ribosomal protein L4-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	C	328	Total	C	N	O	S	0	0
			2564	1627	486	448	3		

- Molecule 10 is a protein called ATP-dependent RNA helicase has1.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	D	422	Total	C	N	O	S	0	0
			3095	1993	535	557	10		

- Molecule 11 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	170	Total	C	N	O	S	0	0
			1328	854	243	228	3		

- Molecule 12 is a protein called 60S ribosomal protein L7-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	F	239	Total	C	N	O	S	0	0
			1939	1247	355	334	3		

- Molecule 13 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	G	163	Total	C	N	O	S	2	0
			1277	818	224	233	2		

- Molecule 14 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	H	87	Total	C	N	O	S	0	0
			542	328	107	106	1		

- Molecule 15 is a protein called Probable rRNA-processing protein ebp2.

Mol	Chain	Residues	Atoms				AltConf	Trace
15	J	83	Total	C	N	O	0	0
			414	248	83	83		

- Molecule 16 is a protein called Putative ribosome biogenesis protein C8F11.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	K	247	Total	C	N	O	S	0	0
			1845	1181	321	338	5		

- Molecule 17 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	L	116	Total	C	N	O	S	0	0
			942	592	198	151	1		

- Molecule 18 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	M	123	Total	C	N	O	S	0	0
			989	630	189	166	4		

- Molecule 19 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	N	166	Total	C	N	O	S	0	0
			1406	883	291	229	3		

- Molecule 20 is a protein called 60S ribosomal protein L16-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	O	185	Total	C	N	O	S	0	0
			1464	944	276	241	3		

- Molecule 21 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	P	130	Total	C	N	O	S	0	0
			1034	660	187	184	3		

- Molecule 22 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Q	135	Total	C	N	O	S	0	0
			1033	652	198	182	1		

- Molecule 23 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	161	Total	C	N	O	S	0	0
			1172	745	220	202	5		

- Molecule 24 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	V	43	Total	C	N	O	0	0
			210	124	43	43		

- Molecule 25 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	125	Total	C	N	O	S	0	0
			998	622	201	173	2		

- Molecule 26 is a protein called Probable nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
26	b	57	Total	C	N	O	0	0
			282	168	57	57		

- Molecule 27 is a protein called 60S ribosomal protein L32-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	e	124	Total	C	N	O	S	0	0
			993	619	202	167	5		

- Molecule 28 is a protein called 60S ribosomal protein L33-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	f	106	Total	C	N	O	S	0	0
			839	534	162	140	3		

- Molecule 29 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	116	Total	C	N	O		0	0
			960	608	188	164			

- Molecule 30 is a protein called 60S ribosomal protein L36-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	i	98	Total	C	N	O	S	0	0
			767	478	159	129	1		

- Molecule 31 is a protein called 60S ribosomal protein L37-B.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	j	71	Total	C	N	O	S	0	0
			559	343	120	90	6		

- Molecule 32 is a protein called Ribosome biogenesis protein erb1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	m	76	Total	C	N	O		0	0
			622	386	113	123			

- Molecule 33 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	n	208	Total	C	N	O		0	0
			1029	613	208	208			

- Molecule 34 is a protein called Uncharacterized RNA-binding protein C1827.05c.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	o	137	Total	C	N	O	S	0	0
			1043	669	193	176	5		

- Molecule 35 is a protein called Ribosome biogenesis protein nsa2.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	r	51	Total	C	N	O	0	0
			254	152	51	51		

- Molecule 36 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	t	184	Total	C	N	O	S	0	0
			1228	763	244	218	3		

- Molecule 37 is a protein called Ribosome biogenesis protein rlp24.

Mol	Chain	Residues	Atoms				AltConf	Trace
37	u	58	Total	C	N	O	0	0
			287	171	58	58		

- Molecule 38 is a protein called Nucleolar protein 16.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	v	161	Total	C	N	O	S	0	0
			1288	811	243	231	3		

- Molecule 39 is a protein called Brix domain-containing protein C4F8.04.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	x	304	Total	C	N	O	S	0	0
			2497	1568	462	460	7		

- Molecule 40 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	y	171	Total	C	N	O	0	0
			842	500	171	171		

- Molecule 41 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
41	T	18	Total	C	N	O	0	0
			90	54	18	18		

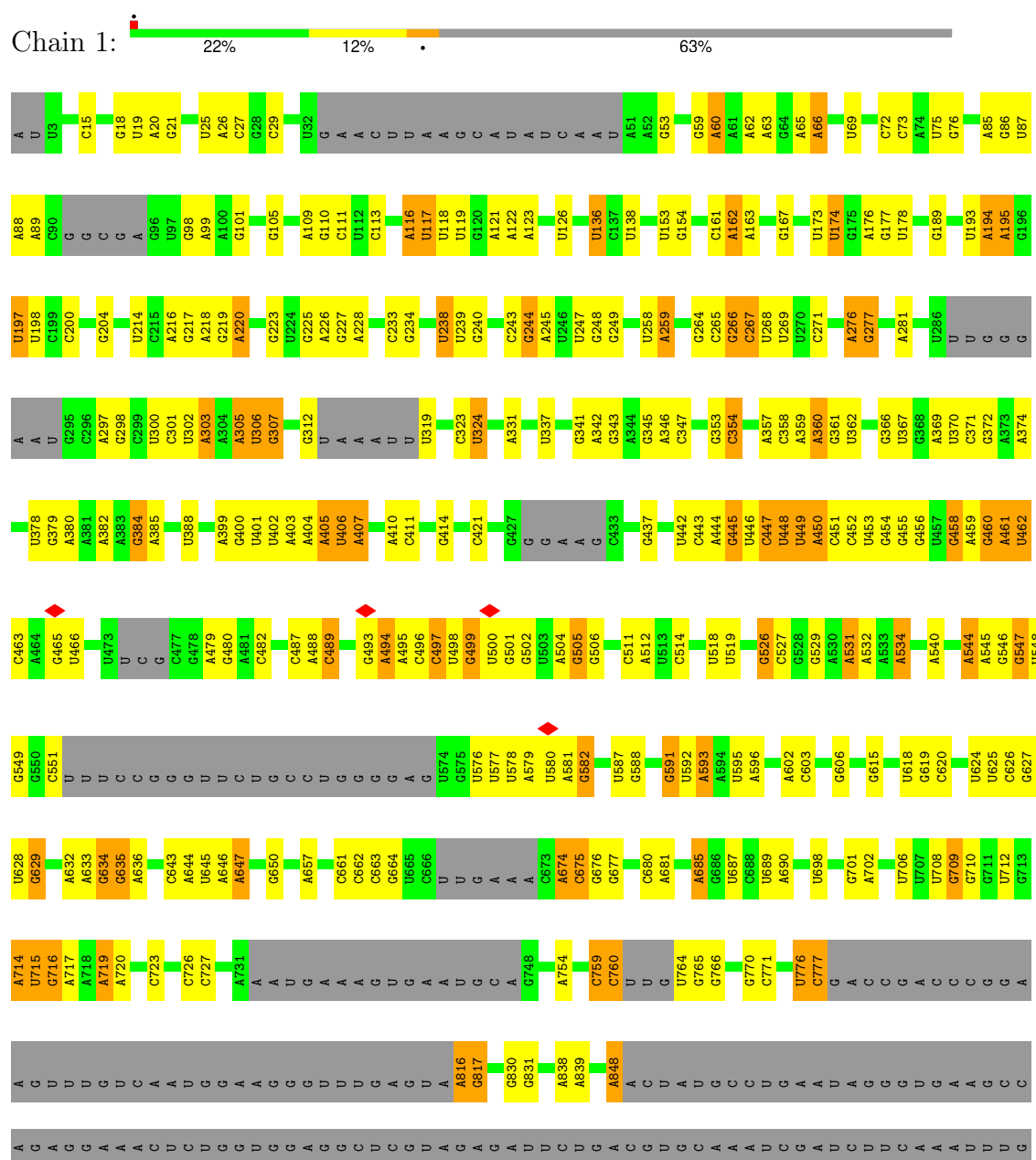
- Molecule 42 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
42	j	1	Total	Zn	0
			1	1	

3 Residue-property plots

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

• Molecule 1: RNA (1263-MER)

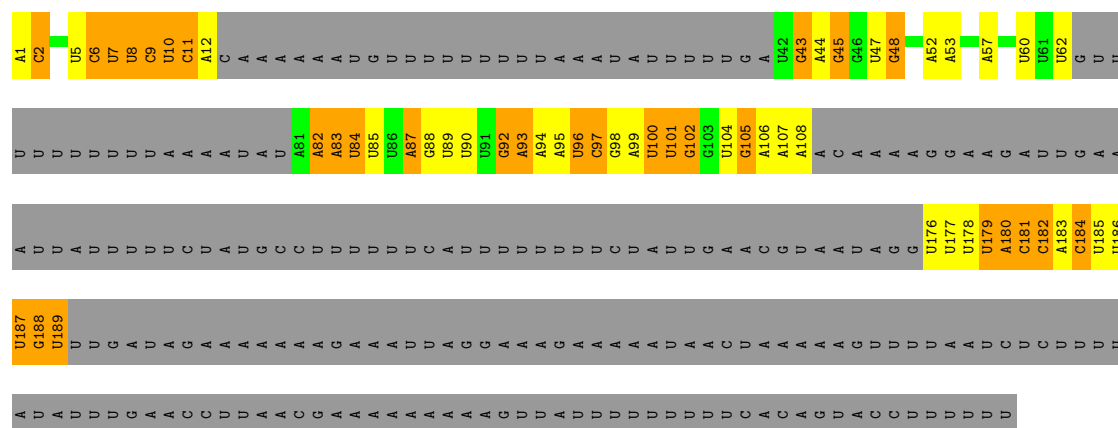






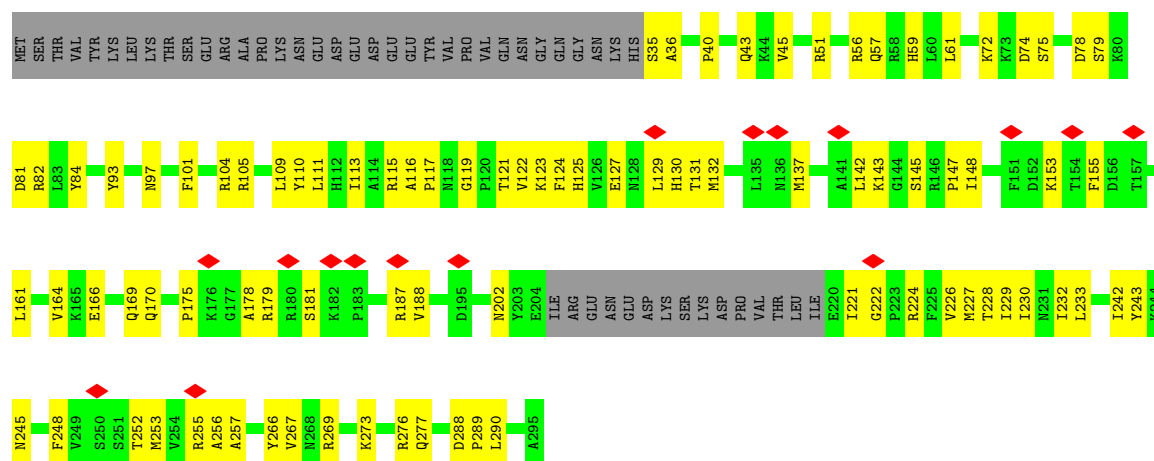
- Molecule 6: RNA (75-MER)

Chain 6:  6% 9% 10% 75%



- Molecule 7: Ribosome biogenesis protein brx1

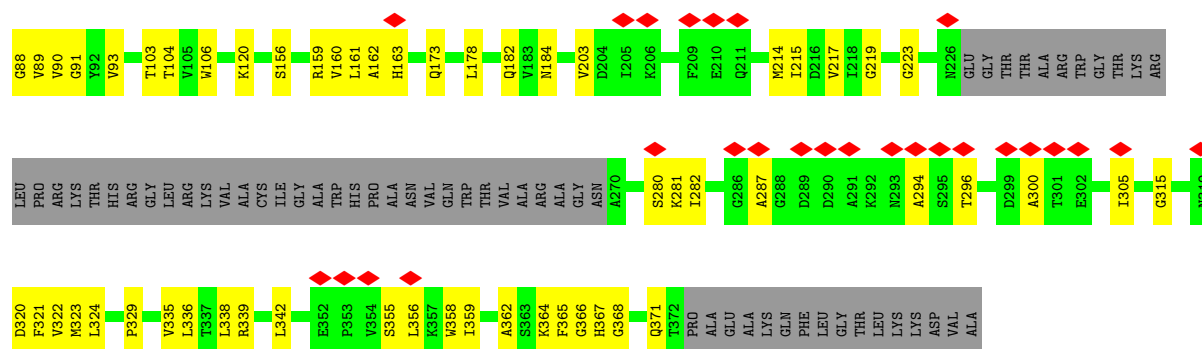
Chain A: 



- Molecule 8: 60S ribosomal protein L3-A

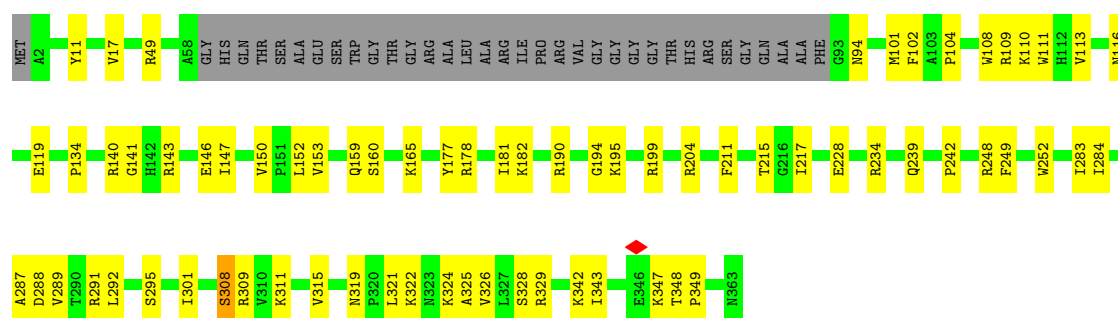
Chain B: 





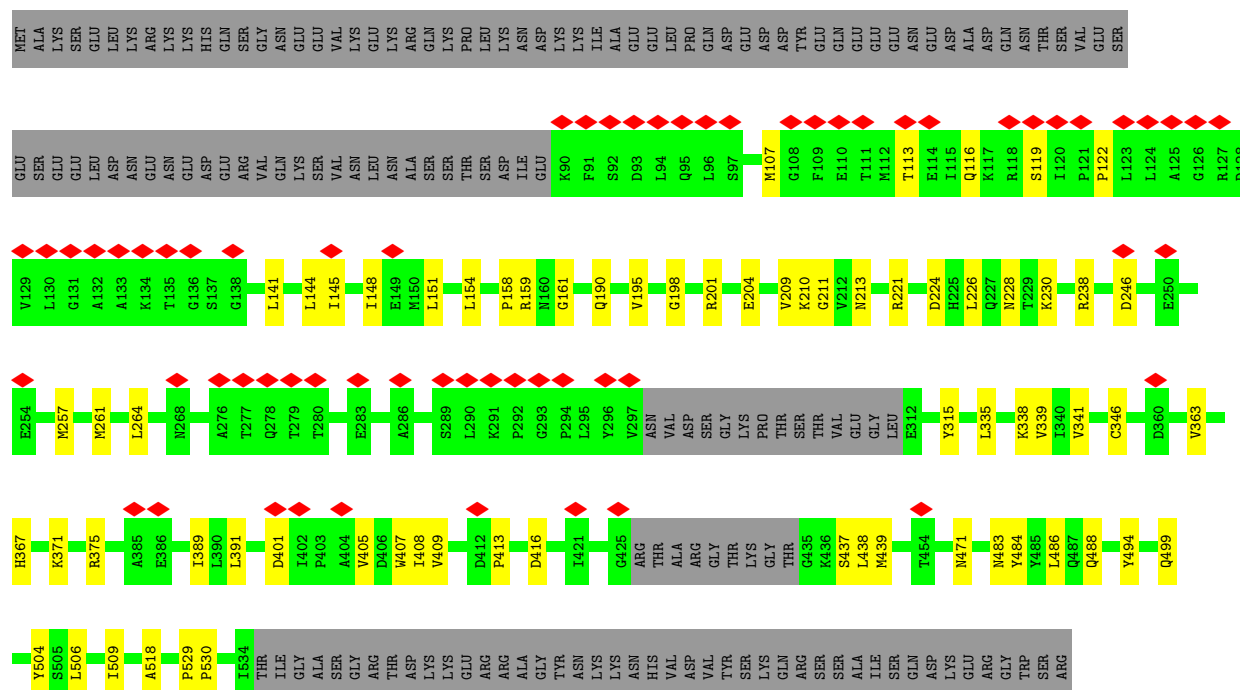
• Molecule 9: 60S ribosomal protein L4-B

Chain C: 71% 19% 10%



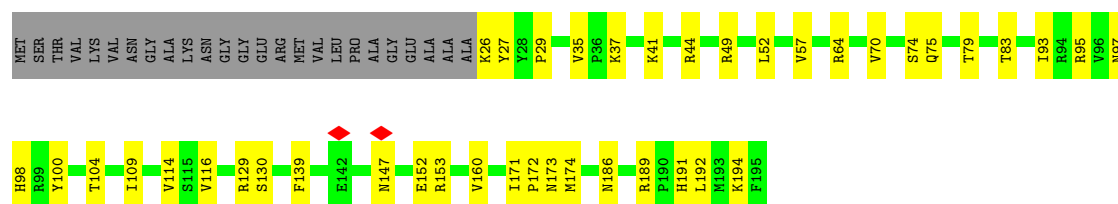
• Molecule 10: ATP-dependent RNA helicase has1

Chain D: 11% 61% 12% 27%



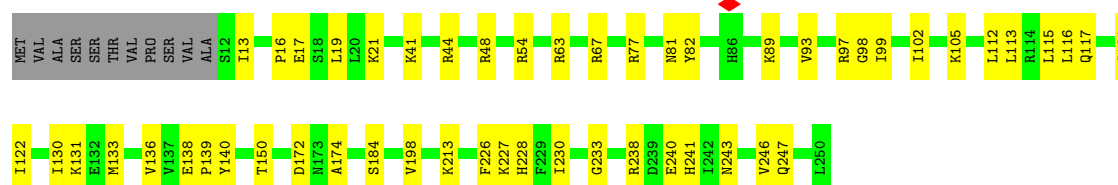
• Molecule 11: 60S ribosomal protein L6

Chain E: 



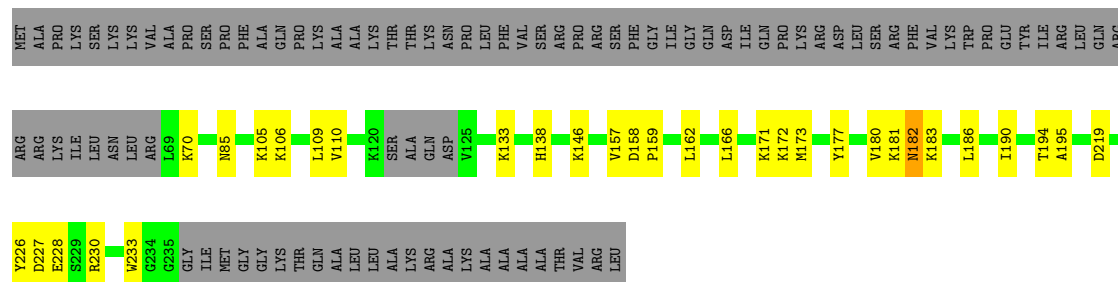
- Molecule 12: 60S ribosomal protein L7-B

Chain F: 




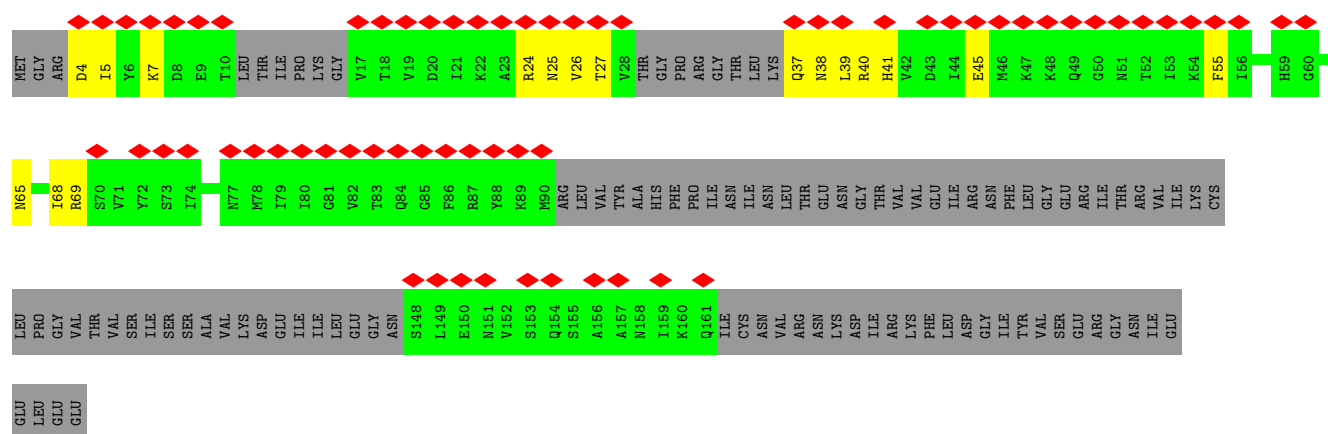
- Molecule 13: 60S ribosomal protein L8

Chain G: 

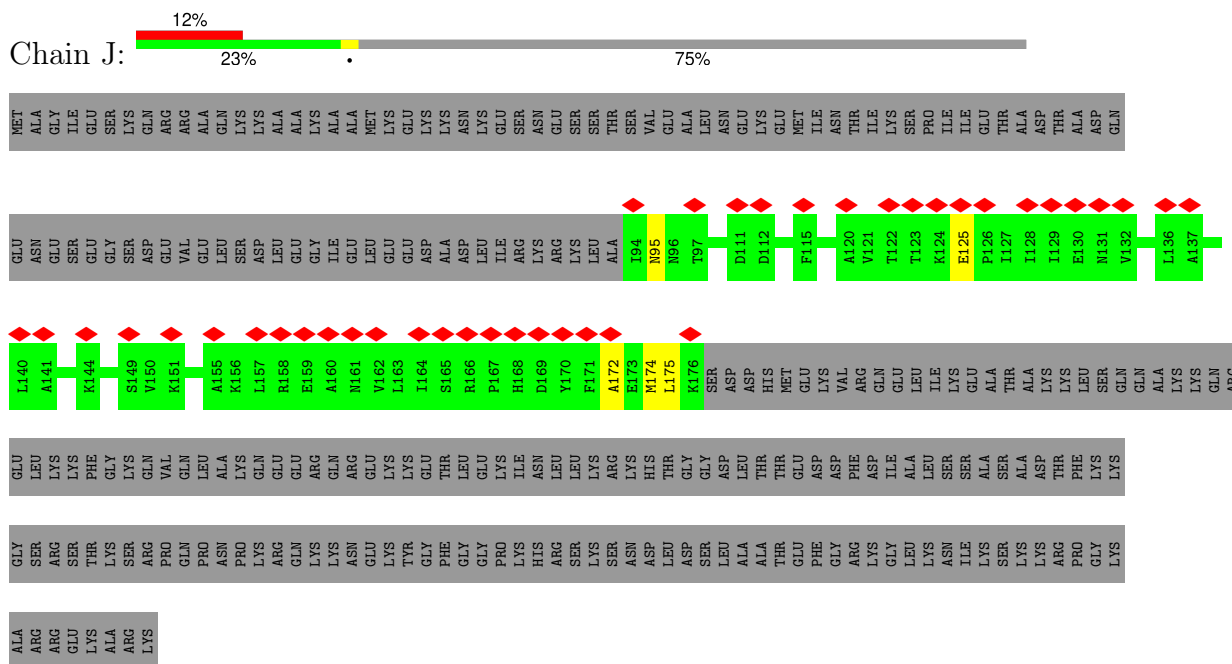


- Molecule 14: 60S ribosomal protein L9-A

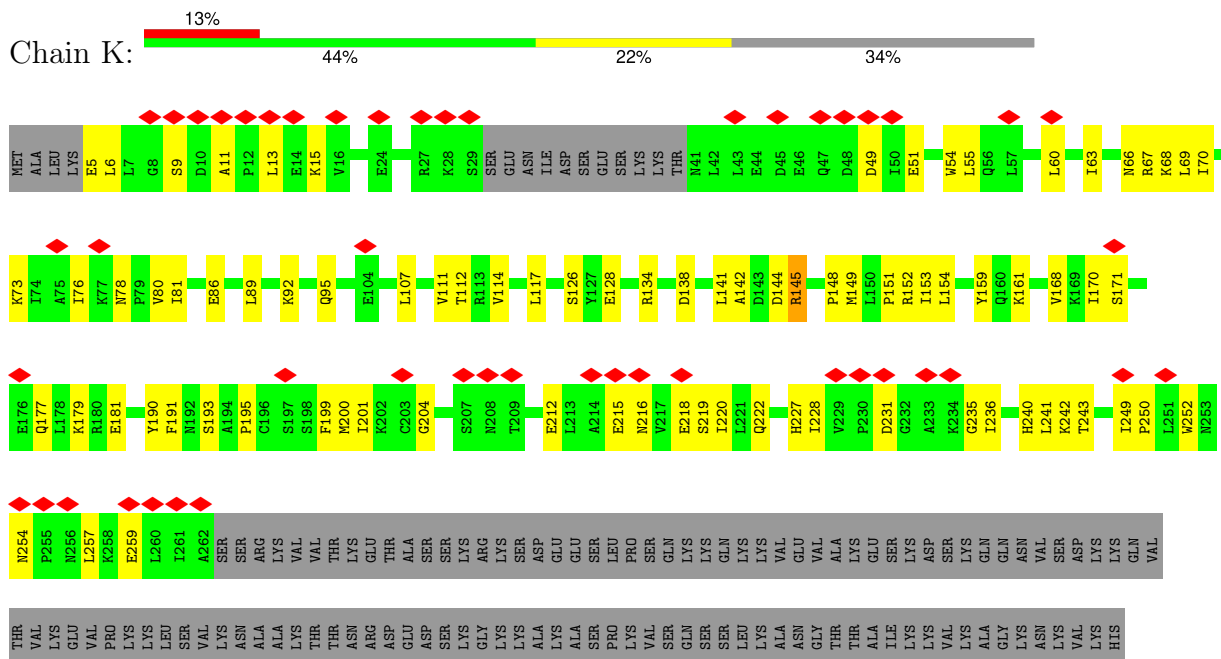
Chain H: 



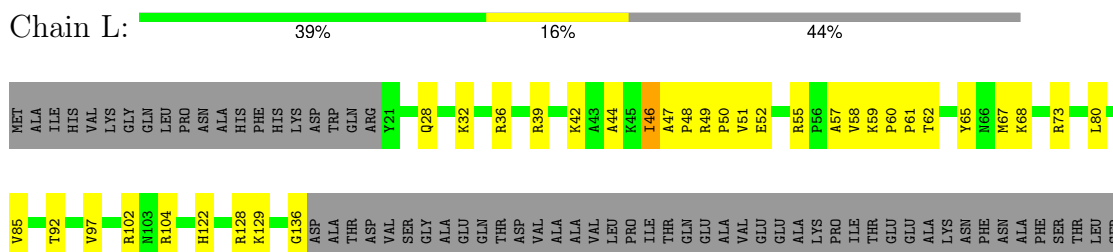
- Molecule 15: Probable rRNA-processing protein ebp2



- Molecule 16: Putative ribosome biogenesis protein C8F11.04



- Molecule 17: 60S ribosomal protein L13



ASN GLU ARG ALA TYR ARG TYR ALA GLY ALA ARG ALA ALA ALA PHE GLN LYS LYS ARG ALA GLU GLU ALA LYS LYS LYS

• Molecule 18: 60S ribosomal protein L14

Chain M:  61% 30% 8%

MET GLU GLY PHE K5 V13 V16 V25 L25 A26 V27 D30 I31 P42 C43 S44 E45 R48 Q49 V50 I51 V56 T59 H60 I61 L65 P66 R70 I73 K76 K77 W78 V83 C84 N85 K86 W87 A88 S89 K94 R102 L105 N106 D109

R110 F111 A112 V113 M114 R115 L116 K117 K118 R119 R120 Q123 A127 VAL ALA LYS ALA LEU LYS ALA

• Molecule 19: 60S ribosomal protein L15-A

Chain N:  60% 22% 17%

MET G2 K5 E8 E9 K12 K13 K14 Q15 S16 N19 V25 E29 Y30 R31 I36 R44 P45 R50 G58 I64 R65 V66 R67 R68 G69 GLY ARG LYS ARG PRO VAL PRO LYS GLY GLN THR THR GLY LYS VAL HIS GLN VAL ASN HIS LEU

LYS TYR GLN R96 S97 A98 E99 C100 E104 R108 W120 V121 N122 Q123 D124 V135 D136 R143 R144 D145 I148 I151 K157 H158 R159 E160 S161 R162 G163 L164 R172 G173 I174 F180 ASN ASN SER PRO GLN THR HIS ALA THR V189 R198 R201

• Molecule 20: 60S ribosomal protein L16-B

Chain O:  73% 20% 6%

MET SER E3 F4 Q5 K6 V7 W8 A12 R38 C39 E40 E41 L42 R50 N51 K52 L53 K54 Y55 L59 R60 LYS ALA CYS ARG TYR ASN PRO SER ARG GLY A71 F72 H73 F74 R79 R88 R89 P111 P112 F113 D114 R118 P122 L125 R126 G133

R134 K135 V136 C137 L142 N151 D152 A155 E159 K162 Q170 K183 P187 V188 N189 Q190 R191 L192 Y197

• Molecule 21: 60S ribosomal protein L17-A

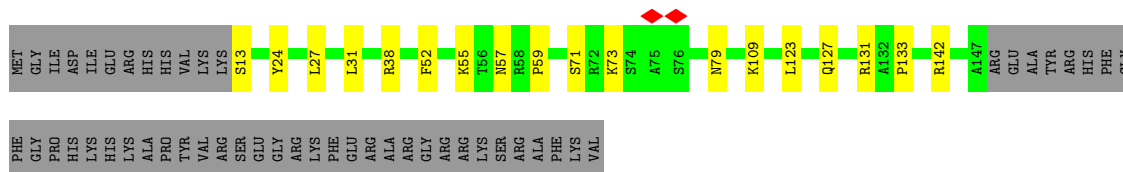
Chain P:  53% 16% 30%

MET VAL R3 E11 K16 R30 K42 N50 K55 Q56 A57 G65 GLY VAL GLY GLY ARG THR ALA GLN GLY LYS GLU PHE GLY VAL Q80 A81 R82 W83 K89 N101 A102 E103 A104 K105 M109 D110 K111 L112 K115 H116 V119 A122 Q125 ARG

ARG ARG THR TYR ARG ALA HIS GLY ARG VAL THR ALA TYR S141 S142 P143 I146 T149 V150 A151 E152 E153 P158 K159 A160 N161 ASP THR VAL SER SER VAL SER LEU LYS GLN GLY ALA LYS ALA ARG ASN LEU ALA ALA ARG LYS ALA ILE THR ALA

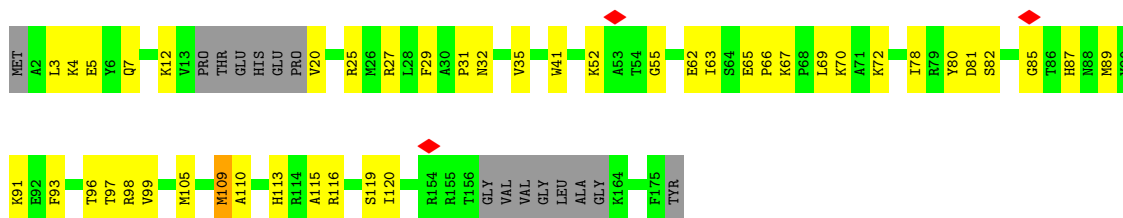
• Molecule 22: 60S ribosomal protein L18-A

Chain Q:  63% 10% 28%



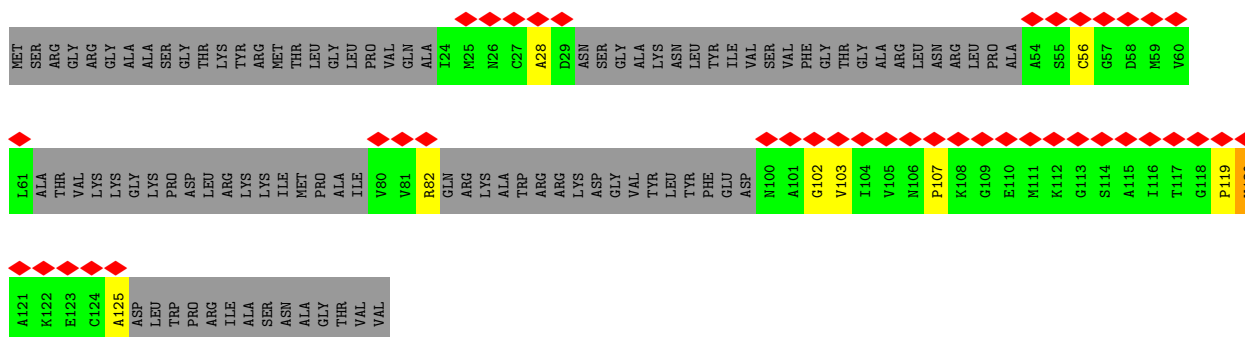
• Molecule 23: 60S ribosomal protein L20-A

Chain S: 66% 24% 9%



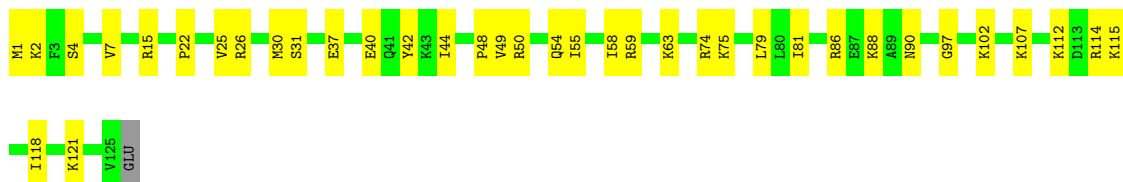
• Molecule 24: 60S ribosomal protein L23-A

Chain V: 30% 24% 6% 69%



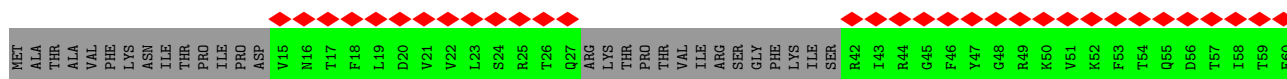
• Molecule 25: 60S ribosomal protein L26

Chain Y: 70% 29% 1%



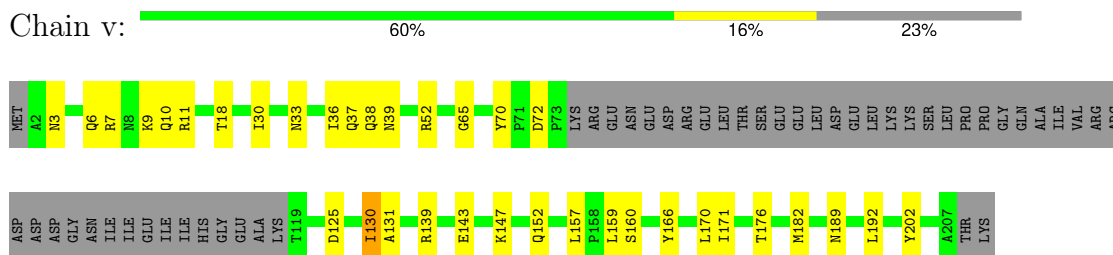
• Molecule 26: Probable nucleolar GTP-binding protein 1

Chain b: 9% 91%



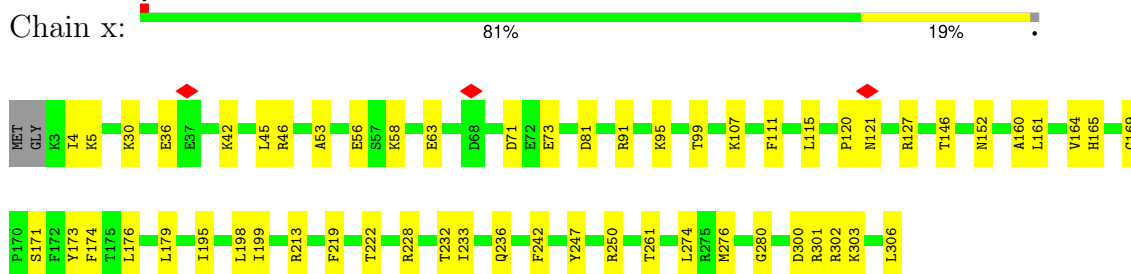
- Molecule 38: Nucleolar protein 16

Chain v:



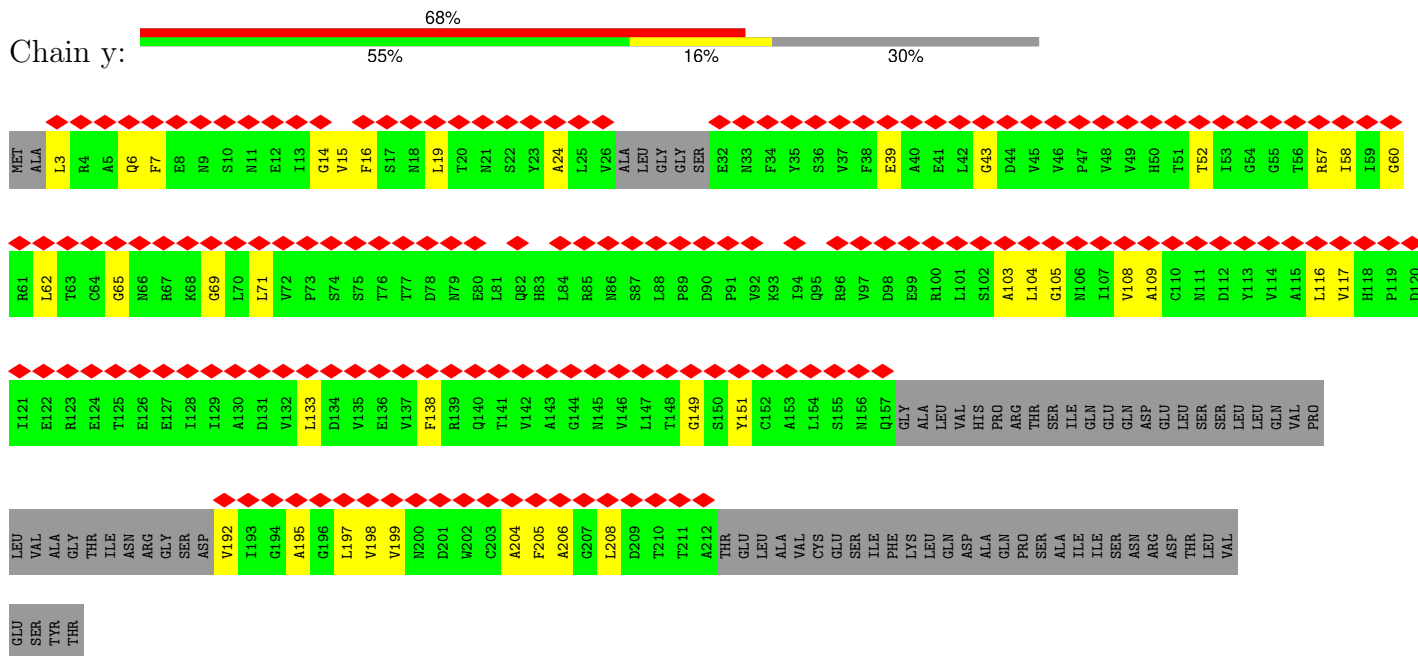
- Molecule 39: Brix domain-containing protein C4F8.04

Chain x:



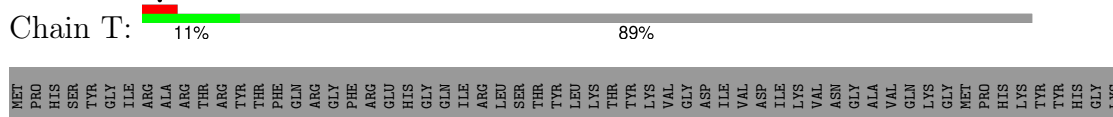
- Molecule 40: Eukaryotic translation initiation factor 6

Chain y:



- Molecule 41: 60S ribosomal protein L21-A

Chain T:





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	14000	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 ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.909	Depositor
Minimum map value	-0.524	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	542.72, 542.72, 542.72	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.06, 1.06, 1.06	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	1	0.30	0/31189	0.32	0/48556
2	2	0.30	0/3087	0.30	0/4799
3	3	0.36	0/1602	0.39	0/2154
4	4	0.26	0/1802	0.33	0/2434
5	5	0.20	0/2693	0.34	0/3642
6	6	0.16	0/1770	0.32	0/2745
7	A	0.16	0/2020	0.33	0/2724
8	B	0.11	0/1555	0.28	0/2160
9	C	0.36	0/2610	0.40	0/3521
10	D	0.15	0/3150	0.28	0/4278
11	E	0.20	0/1356	0.35	0/1829
12	F	0.25	0/1977	0.31	0/2651
13	G	0.31	0/1295	0.37	0/1748
14	H	0.14	0/543	0.43	0/740
15	J	0.06	0/413	0.19	0/576
16	K	0.15	0/1878	0.36	0/2550
17	L	0.36	0/960	0.48	2/1288 (0.2%)
18	M	0.13	0/1005	0.29	0/1349
19	N	0.35	0/1436	0.35	0/1920
20	O	0.16	0/1492	0.29	0/2000
21	P	0.19	0/1054	0.27	0/1414
22	Q	0.33	0/1044	0.37	0/1406
23	S	0.16	0/1191	0.31	0/1607
24	V	0.13	0/206	0.48	0/279
25	Y	0.27	0/1008	0.35	0/1341
26	b	0.05	0/278	0.15	0/381
27	e	0.32	0/1007	0.37	0/1342
28	f	0.26	0/859	0.31	0/1152
29	h	0.28	0/968	0.36	0/1288
30	i	0.26	0/774	0.33	0/1029
31	j	0.22	0/571	0.30	0/757
32	m	0.24	0/635	0.32	0/855

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	n	0.06	0/1024	0.22	0/1419
34	o	0.18	0/1066	0.43	0/1439
35	r	0.04	0/252	0.15	0/349
36	t	0.16	0/1239	0.46	0/1681
37	u	0.12	0/286	0.30	0/397
38	v	0.26	0/1308	0.37	0/1754
39	x	0.23	0/2542	0.33	0/3406
40	y	0.11	0/839	0.40	0/1162
41	T	0.08	0/89	0.25	0/123
All	All	0.26	0/82073	0.33	2/118245 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	L	47	ALA	CA-C-N	-6.48	113.05	120.04
17	L	47	ALA	C-N-CA	-6.48	113.05	120.04

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	1	27887	0	14042	355	0
2	2	2764	0	1399	30	0
3	3	1572	0	1621	47	0
4	4	1756	0	1774	37	0
5	5	2640	0	2698	68	0
6	6	1587	0	800	68	0
7	A	1981	0	1997	71	0
8	B	1557	0	710	54	0
9	C	2564	0	2698	53	0
10	D	3095	0	2963	49	0
11	E	1328	0	1408	32	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	F	1939	0	2030	38	0
13	G	1277	0	1350	22	0
14	H	542	0	388	11	0
15	J	414	0	190	5	0
16	K	1845	0	1828	70	0
17	L	942	0	1012	32	0
18	M	989	0	1054	34	0
19	N	1406	0	1441	34	0
20	O	1464	0	1550	35	0
21	P	1034	0	1050	25	0
22	Q	1033	0	1108	18	0
23	S	1172	0	1059	33	0
24	V	210	0	103	4	0
25	Y	998	0	1090	29	0
26	b	282	0	122	0	0
27	e	993	0	1052	27	0
28	f	839	0	866	10	0
29	h	960	0	1049	28	0
30	i	767	0	832	27	0
31	j	559	0	567	16	0
32	m	622	0	594	18	0
33	n	1029	0	455	5	0
34	o	1043	0	1003	59	0
35	r	254	0	119	0	0
36	t	1228	0	1037	59	0
37	u	287	0	127	5	0
38	v	1288	0	1327	30	0
39	x	2497	0	2500	40	0
40	y	842	0	386	22	0
41	T	90	0	39	0	0
42	j	1	0	0	0	0
All	All	77577	0	59438	1326	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 1326 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)
6:6:82:A:HO2'	6:6:83:A:H8	1.05	0.96
10:D:346:CYS:HG	10:D:367:HIS:HD1	1.11	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
34:o:106:VAL:HA	34:o:152:GLU:HA	1.59	0.83
22:Q:123:LEU:HD11	22:Q:131:ARG:HH21	1.46	0.81
6:6:106:A:H4'	6:6:188:G:H5'	1.63	0.81

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	3	189/302 (63%)	184 (97%)	5 (3%)	0	100	100
4	4	207/217 (95%)	201 (97%)	6 (3%)	0	100	100
5	5	332/387 (86%)	314 (95%)	18 (5%)	0	100	100
7	A	242/295 (82%)	224 (93%)	17 (7%)	1 (0%)	30	63
8	B	312/388 (80%)	277 (89%)	34 (11%)	1 (0%)	37	69
9	C	324/363 (89%)	305 (94%)	18 (6%)	1 (0%)	37	69
10	D	416/578 (72%)	409 (98%)	7 (2%)	0	100	100
11	E	168/195 (86%)	148 (88%)	19 (11%)	1 (1%)	22	55
12	F	237/250 (95%)	228 (96%)	9 (4%)	0	100	100
13	G	161/259 (62%)	154 (96%)	5 (3%)	2 (1%)	11	40
14	H	79/190 (42%)	68 (86%)	11 (14%)	0	100	100
15	J	81/333 (24%)	79 (98%)	2 (2%)	0	100	100
16	K	243/373 (65%)	229 (94%)	12 (5%)	2 (1%)	16	49
17	L	114/208 (55%)	109 (96%)	5 (4%)	0	100	100
18	M	121/134 (90%)	116 (96%)	5 (4%)	0	100	100
19	N	160/201 (80%)	156 (98%)	4 (2%)	0	100	100
20	O	181/197 (92%)	180 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
21	P	124/187 (66%)	116 (94%)	8 (6%)	0	100	100
22	Q	133/187 (71%)	124 (93%)	9 (7%)	0	100	100
23	S	155/176 (88%)	146 (94%)	9 (6%)	0	100	100
24	V	35/139 (25%)	21 (60%)	10 (29%)	4 (11%)	0	5
25	Y	123/126 (98%)	121 (98%)	2 (2%)	0	100	100
26	b	49/642 (8%)	49 (100%)	0	0	100	100
27	e	122/127 (96%)	118 (97%)	4 (3%)	0	100	100
28	f	104/108 (96%)	101 (97%)	3 (3%)	0	100	100
29	h	112/122 (92%)	110 (98%)	2 (2%)	0	100	100
30	i	96/99 (97%)	91 (95%)	5 (5%)	0	100	100
31	j	69/91 (76%)	65 (94%)	4 (6%)	0	100	100
32	m	72/740 (10%)	68 (94%)	4 (6%)	0	100	100
33	n	198/607 (33%)	189 (96%)	9 (4%)	0	100	100
34	o	135/276 (49%)	133 (98%)	2 (2%)	0	100	100
35	r	47/260 (18%)	46 (98%)	1 (2%)	0	100	100
36	t	180/249 (72%)	160 (89%)	19 (11%)	1 (1%)	22	55
37	u	56/192 (29%)	51 (91%)	5 (9%)	0	100	100
38	v	157/209 (75%)	148 (94%)	8 (5%)	1 (1%)	22	55
39	x	302/306 (99%)	294 (97%)	8 (3%)	0	100	100
40	y	165/244 (68%)	141 (86%)	24 (14%)	0	100	100
41	T	16/160 (10%)	15 (94%)	1 (6%)	0	100	100
All	All	6017/10117 (60%)	5688 (94%)	315 (5%)	14 (0%)	45	74

5 of 14 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
7	A	248	PHE
8	B	82	PRO
24	V	107	PRO
24	V	119	PRO
16	K	6	LEU

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	3	165/271 (61%)	165 (100%)	0	100	100
4	4	188/197 (95%)	187 (100%)	1 (0%)	86	90
5	5	293/345 (85%)	292 (100%)	1 (0%)	91	92
7	A	217/266 (82%)	217 (100%)	0	100	100
9	C	274/297 (92%)	273 (100%)	1 (0%)	89	91
10	D	294/505 (58%)	294 (100%)	0	100	100
11	E	139/155 (90%)	139 (100%)	0	100	100
12	F	201/210 (96%)	201 (100%)	0	100	100
13	G	136/212 (64%)	133 (98%)	3 (2%)	47	64
14	H	32/170 (19%)	32 (100%)	0	100	100
16	K	190/333 (57%)	189 (100%)	1 (0%)	86	90
17	L	97/167 (58%)	96 (99%)	1 (1%)	73	80
18	M	106/113 (94%)	104 (98%)	2 (2%)	52	69
19	N	146/176 (83%)	146 (100%)	0	100	100
20	O	150/162 (93%)	148 (99%)	2 (1%)	65	76
21	P	108/149 (72%)	108 (100%)	0	100	100
22	Q	110/159 (69%)	110 (100%)	0	100	100
23	S	96/154 (62%)	95 (99%)	1 (1%)	73	80
25	Y	110/111 (99%)	110 (100%)	0	100	100
27	e	105/107 (98%)	105 (100%)	0	100	100
28	f	89/91 (98%)	88 (99%)	1 (1%)	70	79
29	h	101/107 (94%)	101 (100%)	0	100	100
30	i	78/84 (93%)	77 (99%)	1 (1%)	65	76
31	j	57/71 (80%)	56 (98%)	1 (2%)	54	71
32	m	67/659 (10%)	67 (100%)	0	100	100
34	o	99/246 (40%)	98 (99%)	1 (1%)	73	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
36	t	85/223 (38%)	81 (95%)	4 (5%)	22	46
38	v	134/181 (74%)	134 (100%)	0	100	100
39	x	267/273 (98%)	266 (100%)	1 (0%)	89	91
All	All	4134/6194 (67%)	4112 (100%)	22 (0%)	85	90

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
30	i	57	GLU
36	t	55	GLU
34	o	106	VAL
36	t	109	LEU
16	K	145	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 38 such sidechains are listed below:

Mol	Chain	Res	Type
29	h	21	GLN
38	v	39	ASN
29	h	99	GLN
38	v	21	ASN
39	x	264	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	1	1272/3497 (36%)	273 (21%)	21 (1%)
2	2	126/165 (76%)	22 (17%)	0
6	6	72/300 (24%)	46 (63%)	2 (2%)
All	All	1470/3962 (37%)	341 (23%)	23 (1%)

5 of 341 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	1	15	C
1	1	21	G
1	1	26	A
1	1	60	A
1	1	65	A

5 of 23 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	1	1010	A
1	1	3318	A
1	1	2447	C
1	1	3328	U
1	1	493	G

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](#)

Of 1 ligands modelled in this entry, 1 is 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
1	1	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	1	3247:U	O3'	3269:A	P	35.09

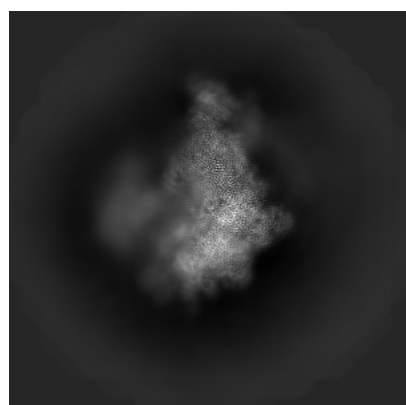
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-24409. These allow visual inspection of the internal detail of the map and identification of artifacts.

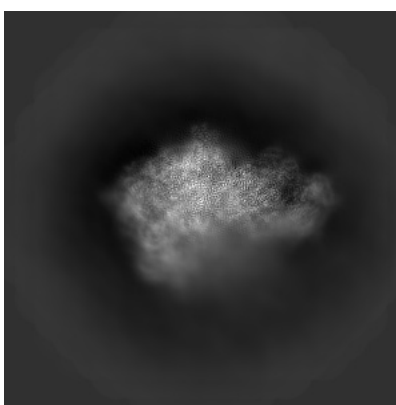
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

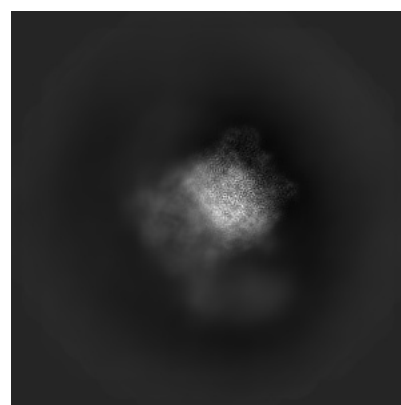
6.1.1 Primary map



X



Y

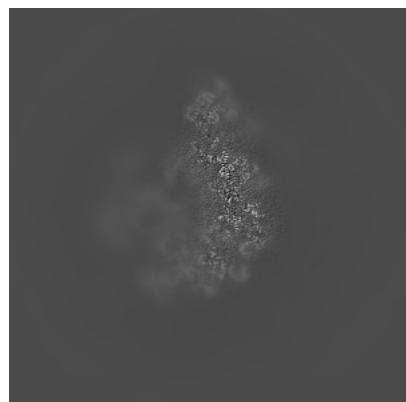


Z

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

6.2 Central slices [i](#)

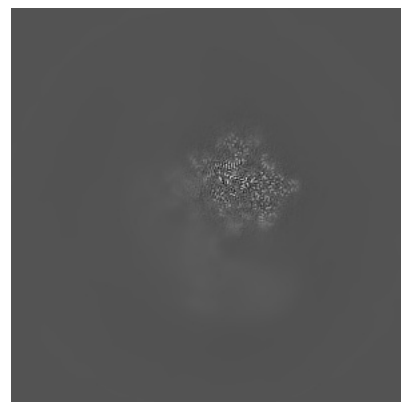
6.2.1 Primary map



X Index: 256



Y Index: 256

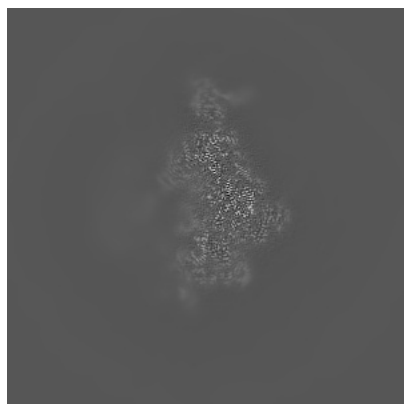


Z Index: 256

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

6.3 Largest variance slices [i](#)

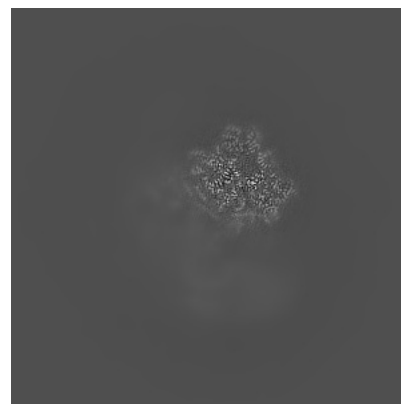
6.3.1 Primary map



X Index: 282



Y Index: 274

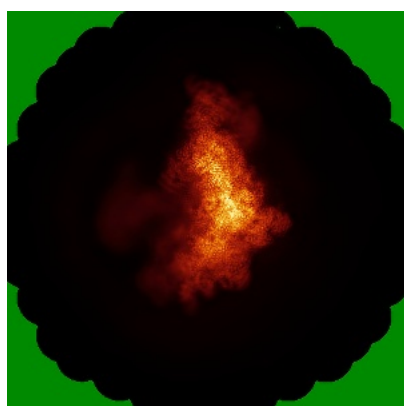


Z Index: 249

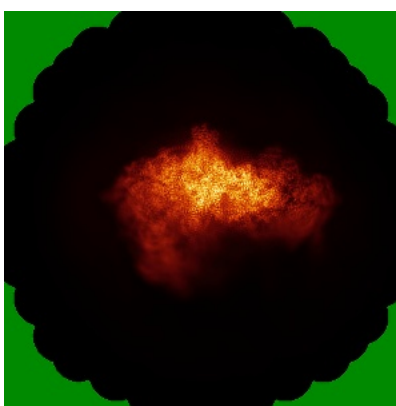
The images above show the largest variance slices of the map in three orthogonal directions.

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

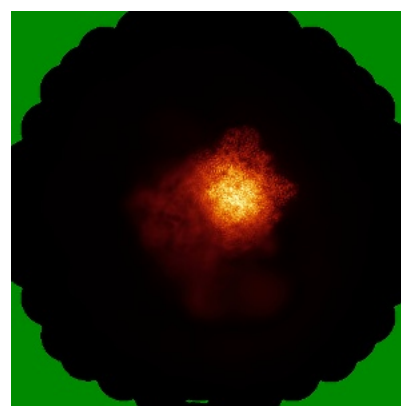
6.4.1 Primary map



X



Y

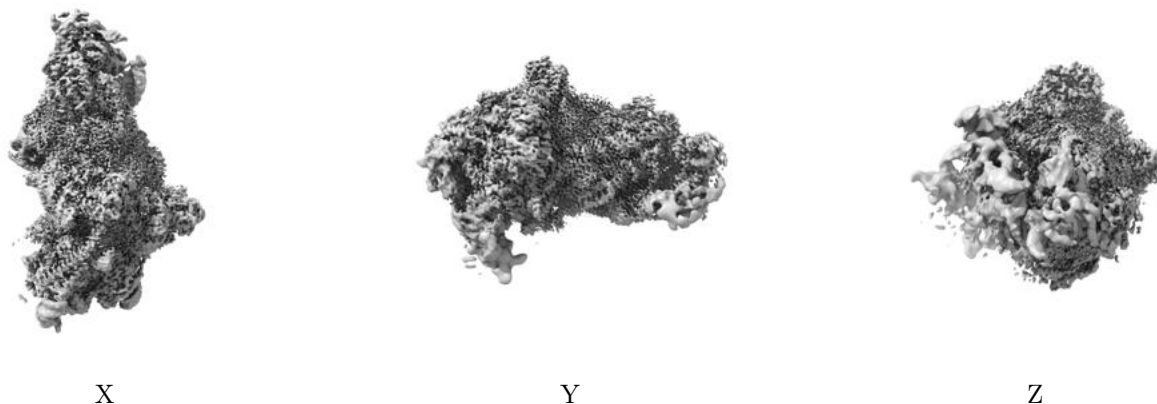


Z

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 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

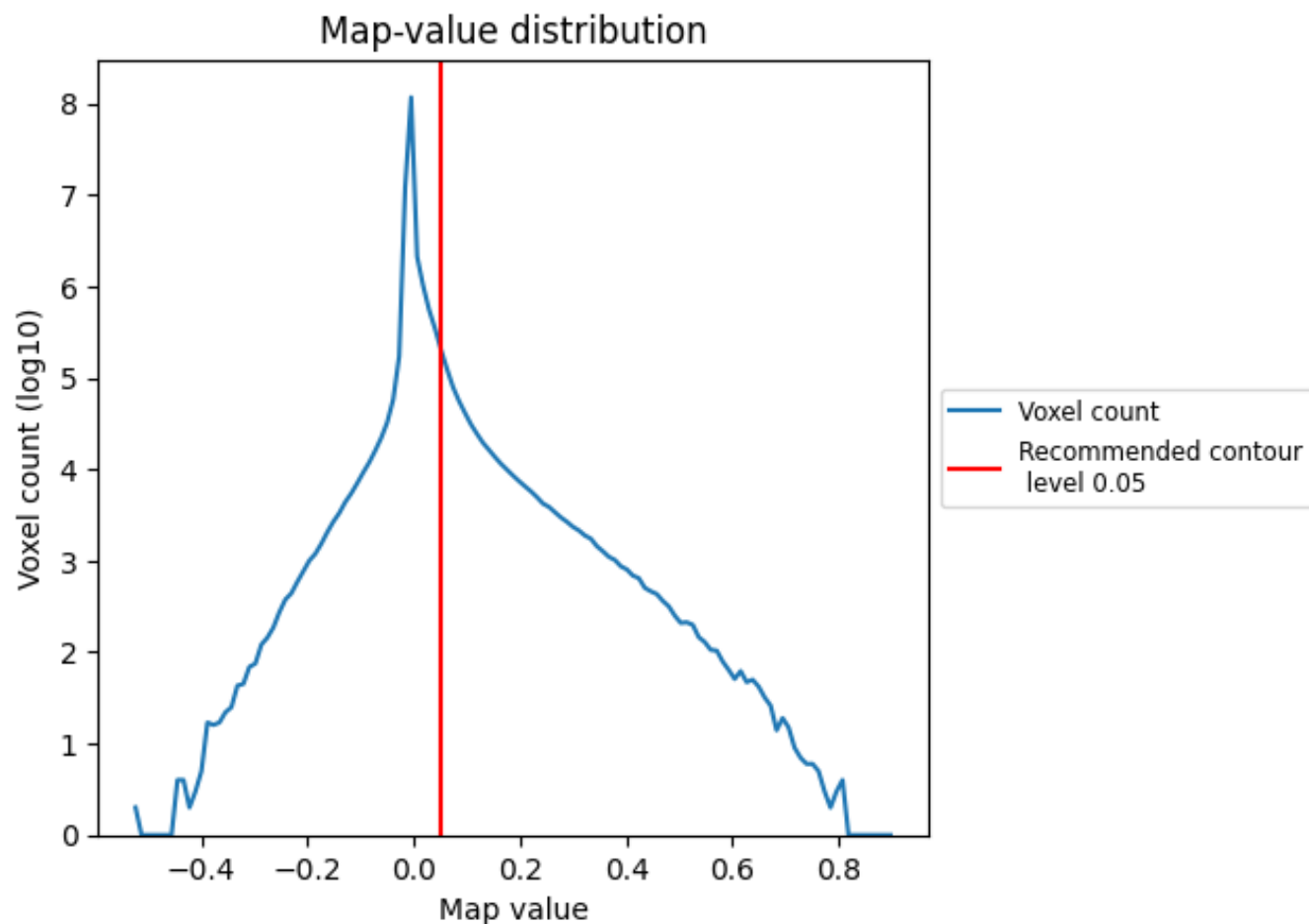
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

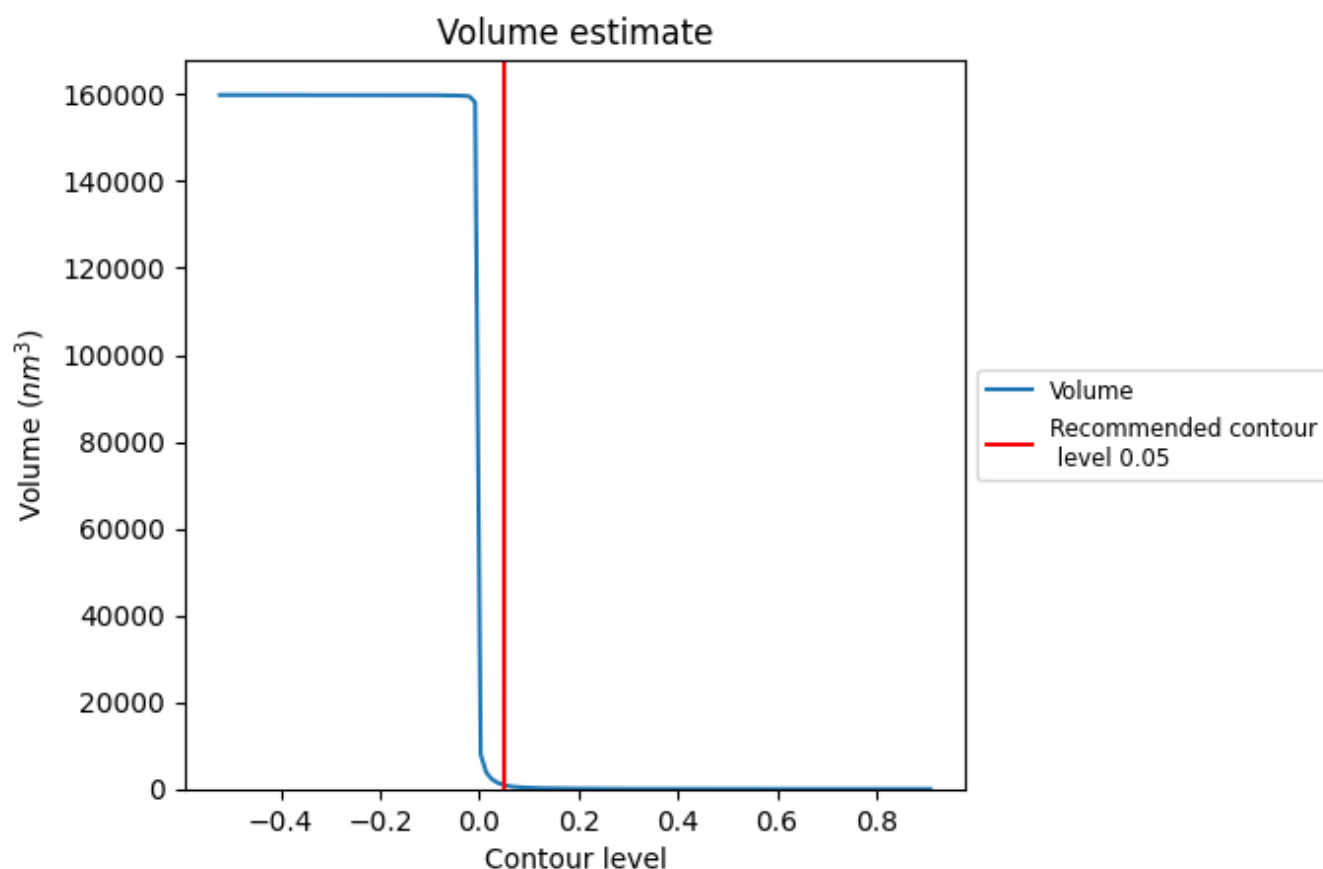
This section contains the results of statistical analysis of the map.

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.

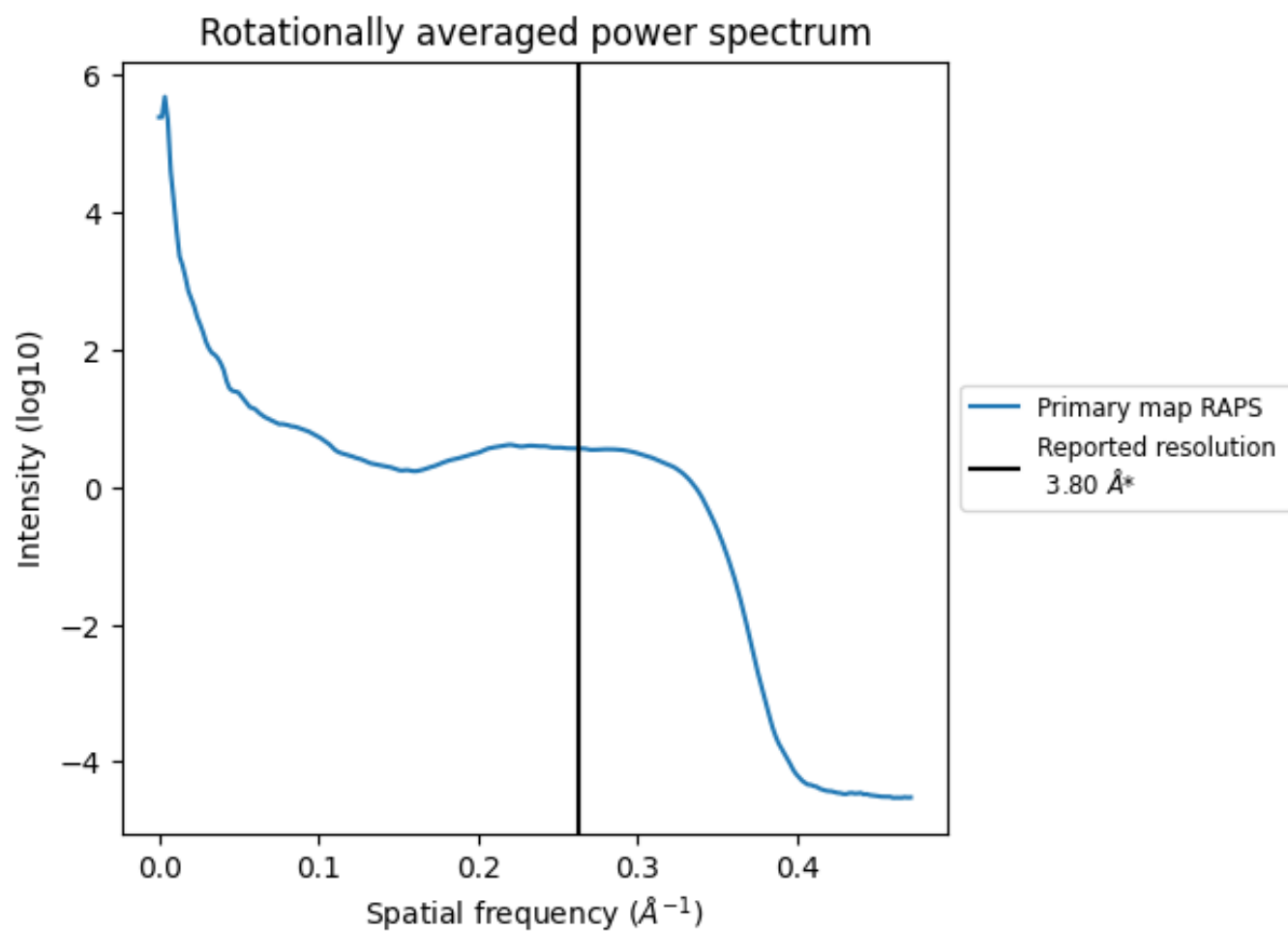
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 896 nm³; this corresponds to an approximate mass of 809 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 0.263 Å⁻¹

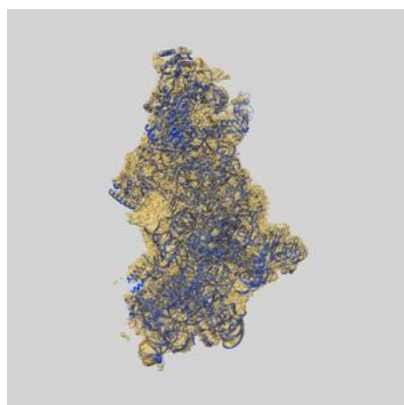
8 Fourier-Shell correlation

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

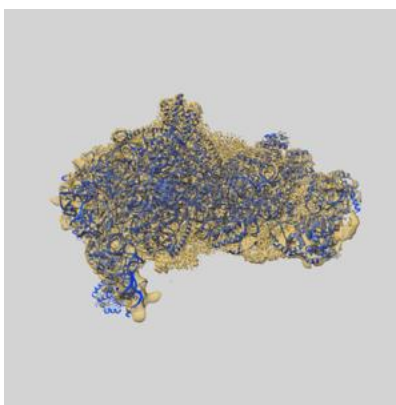
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-24409 and PDB model 8ETH. Per-residue inclusion information can be found in section 3 on page 12.

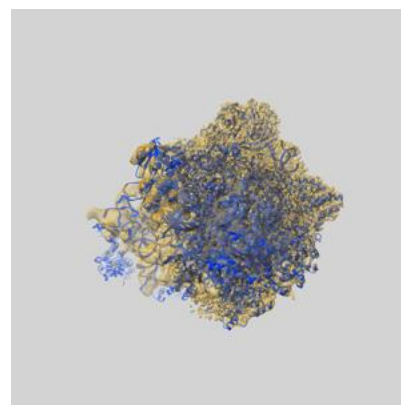
9.1 Map-model overlay [i](#)



X



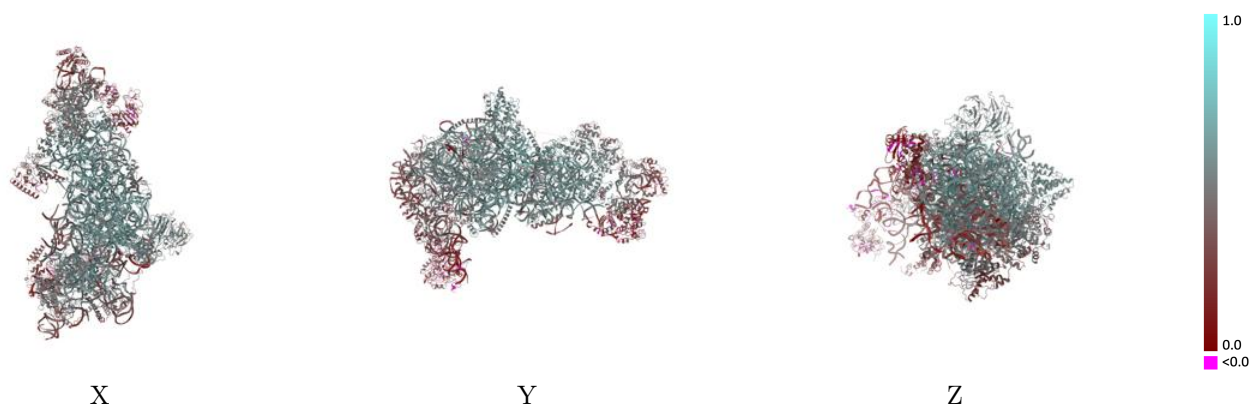
Y



Z

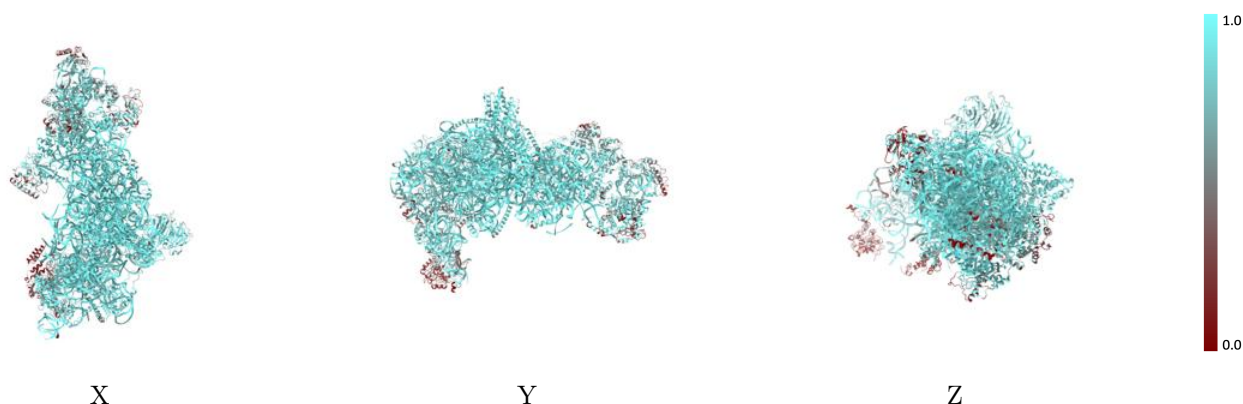
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



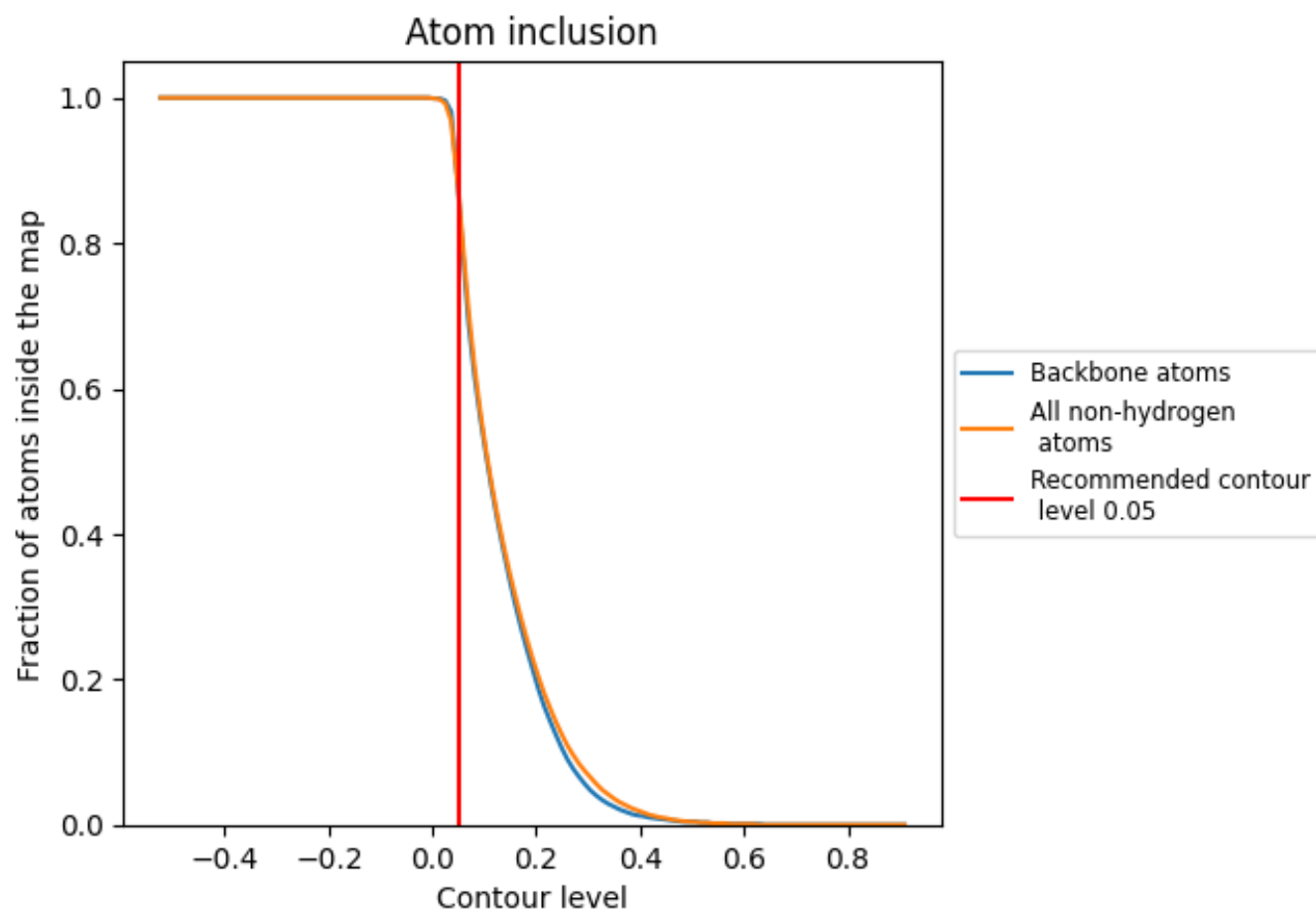
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.05).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% of all backbone atoms, 87% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8720	 0.4800
1	 0.9370	 0.4840
2	 0.9550	 0.5180
3	 0.9470	 0.5910
4	 0.9220	 0.5660
5	 0.8750	 0.5220
6	 0.8350	 0.2840
A	 0.7750	 0.3680
B	 0.8300	 0.2820
C	 0.9690	 0.6090
D	 0.7300	 0.4780
E	 0.8870	 0.4940
F	 0.9240	 0.5410
G	 0.9670	 0.5800
H	 0.2530	 0.2410
J	 0.5020	 0.2830
K	 0.6710	 0.3730
L	 0.9830	 0.6220
M	 0.8860	 0.4510
N	 0.9850	 0.6140
O	 0.8800	 0.4600
P	 0.9570	 0.5580
Q	 0.9710	 0.5900
S	 0.8770	 0.4520
T	 0.4780	 0.3320
V	 0.0430	 0.2120
Y	 0.9620	 0.5860
b	 0.0000	 0.2610
e	 0.9660	 0.5940
f	 0.9600	 0.5770
h	 0.9090	 0.5260
i	 0.9490	 0.5620
j	 0.9760	 0.5810
m	 0.8580	 0.5040
n	 0.5480	 0.1740



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Chain	Atom inclusion	Q-score
o	 0.7130	 0.3980
r	 0.0670	 0.2140
t	 0.7230	 0.2860
u	 0.4600	 0.1470
v	 0.9300	 0.5560
x	 0.9030	 0.5440
y	 0.0440	 0.1850