



wwPDB EM Validation Summary Report ⓘ

Mar 7, 2026 – 02:07 AM UTC

PDB ID : 6Y7C / pdb_00006y7c
EMDB ID : EMD-10713
Title : Early cytoplasmic yeast pre-40S particle (purified with Tsr1 as bait)
Authors : Shayan, R.; Plassart, L.; Plisson-Chastang, C.
Deposited on : 2020-02-28
Resolution : 3.80 Å (reported)
Based on initial model : 6FAI

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:

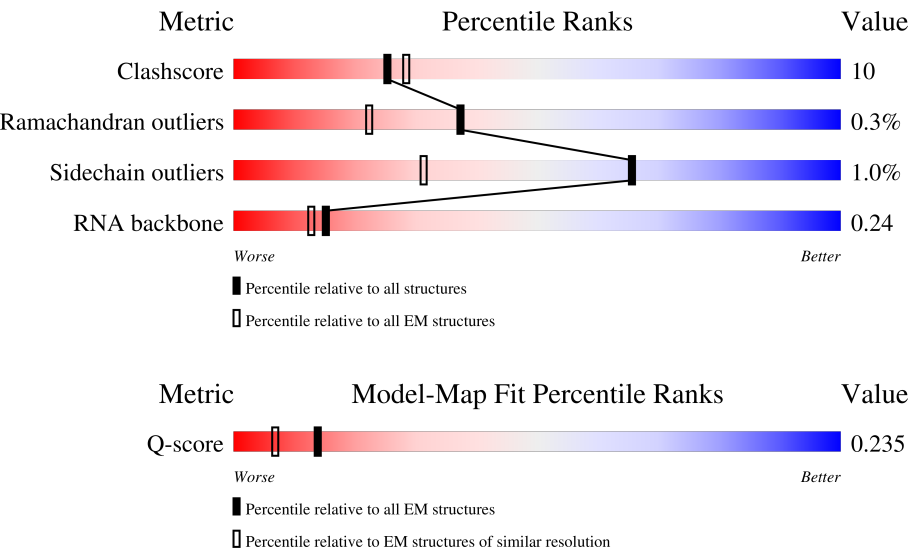
EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
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 3.80 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)	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	10198 (3.30 - 4.30)

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	2	1735	
2	A	252	
3	B	255	

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Mol	Chain	Length	Quality of chain
4	C	254	
5	E	261	
6	F	225	
7	G	236	
8	H	190	
9	I	200	
10	J	197	
11	L	156	
12	M	143	
13	N	151	
14	O	137	
15	P	142	
16	Q	143	
17	R	136	
18	S	146	
19	T	144	
20	U	121	
21	V	87	
22	W	130	
23	X	145	
24	Y	135	
25	Z	108	
26	b	82	
27	c	67	
28	d	56	

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Mol	Chain	Length	Quality of chain
29	e	63	
30	h	274	
31	i	483	
32	j	463	
33	l	425	
34	t	788	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	A2M	2	420	-	-	X	-
1	A2M	2	436	-	-	X	-
1	A2M	2	796	-	-	X	-

2 Entry composition

There are 34 unique types of molecules in this entry. The entry contains 79690 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 20S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2	1735	Total	C	N	O	P	0	0
			36965	16530	6537	12163	1735		

- Molecule 2 is a protein called 40S ribosomal protein S0-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	206	Total	C	N	O	S	0	0
			1614	1039	284	289	2		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	206	PHE	ASP	conflict	UNP P32905

- Molecule 3 is a protein called 40S ribosomal protein S1-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 4 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	220	Total	C	N	O	S	0	0
			1662	1065	295	300	2		

- Molecule 5 is a protein called 40S ribosomal protein S4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	260	Total	C	N	O	S	0	0
			2068	1316	389	360	3		

- Molecule 6 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	206	Total	C	N	O	S	0	0
			1609	1007	300	299	3		

- Molecule 7 is a protein called 40S ribosomal protein S6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	226	Total	C	N	O	S	0	0
			1799	1129	346	321	3		

- Molecule 8 is a protein called 40S ribosomal protein S7-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
8	H	168	Total	C	N	O	0	0
			1362	880	239	243		

- Molecule 9 is a protein called 40S ribosomal protein S8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	188	Total	C	N	O	S	0	0
			1489	925	298	264	2		

- Molecule 10 is a protein called 40S ribosomal protein S9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 11 is a protein called 40S ribosomal protein S11-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L	155	Total	C	N	O	S	0	0
			1213	774	230	206	3		

- Molecule 12 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	125	Total	C	N	O	S	0	0
			941	591	166	182	2		

- Molecule 13 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	N	150	Total	C	N	O	S	0	0
			1193	759	224	208	2		

- Molecule 14 is a protein called 40S ribosomal protein S14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	O	128	Total	C	N	O	S	0	0
			950	582	188	177	3		

- Molecule 15 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	P	127	Total	C	N	O	S	0	0
			1001	637	186	171	7		

- Molecule 16 is a protein called 40S ribosomal protein S16-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
16	Q	127	Total	C	N	O		
			993	640	177	176	0	0

- Molecule 17 is a protein called 40S ribosomal protein S17-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	R	115	Total	C	N	O	S	0	0
			924	575	173	174	2		

- Molecule 18 is a protein called 40S ribosomal protein S18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	S	135	Total	C	N	O	S	0	0
			1110	696	215	197	2		

- Molecule 19 is a protein called 40S ribosomal protein S19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	T	143	Total	C	N	O	S	0	0
			1112	694	208	208	2		

- Molecule 20 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	U	67	Total	C	N	O	0	0
			541	344	102	95		

- Molecule 21 is a protein called 40S ribosomal protein S21-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	V	87	Total	C	N	O	S	0
			685	420	125	138	2	0

- Molecule 22 is a protein called 40S ribosomal protein S22-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	W	129	Total	C	N	O	S	0
			1019	650	188	178	3	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	51	VAL	GLU	conflict	UNP P0C0W1

- Molecule 23 is a protein called 40S ribosomal protein S23-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	X	144	Total	C	N	O	S	0
			1121	708	220	191	2	0

- Molecule 24 is a protein called 40S ribosomal protein S24-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Y	134	Total	C	N	O	0	0
			1073	676	208	189		

- Molecule 25 is a protein called 40S ribosomal protein S25-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Z	63	Total	C	N	O	0	0
			512	328	94	90		

- Molecule 26 is a protein called 40S ribosomal protein S27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	81	Total	C	N	O	S	0	0
			611	382	110	114	5		

- Molecule 27 is a protein called 40S ribosomal protein S28-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	63	Total	C	N	O	S	0	0
			497	306	99	91	1		

- Molecule 28 is a protein called 40S ribosomal protein S29-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	27	Total	C	N	O	S	0	0
			219	133	46	36	4		

- Molecule 29 is a protein called 40S ribosomal protein S30-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 30 is a protein called Pre-rRNA-processing protein PNO1.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	h	179	Total	C	N	O	S	0	0
			1416	906	256	250	4		

- Molecule 31 is a protein called Essential nuclear protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	i	261	Total	C	N	O	S	0	0
			2125	1384	363	375	3		

- Molecule 32 is a protein called Protein LTV1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	j	55	Total	C	N	O	S	0	0
			465	283	66	113	3		

- Molecule 33 is a protein called Serine/threonine-protein kinase RIO2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	l	286	Total	C	N	O	S	0	0
			2322	1464	410	430	18		

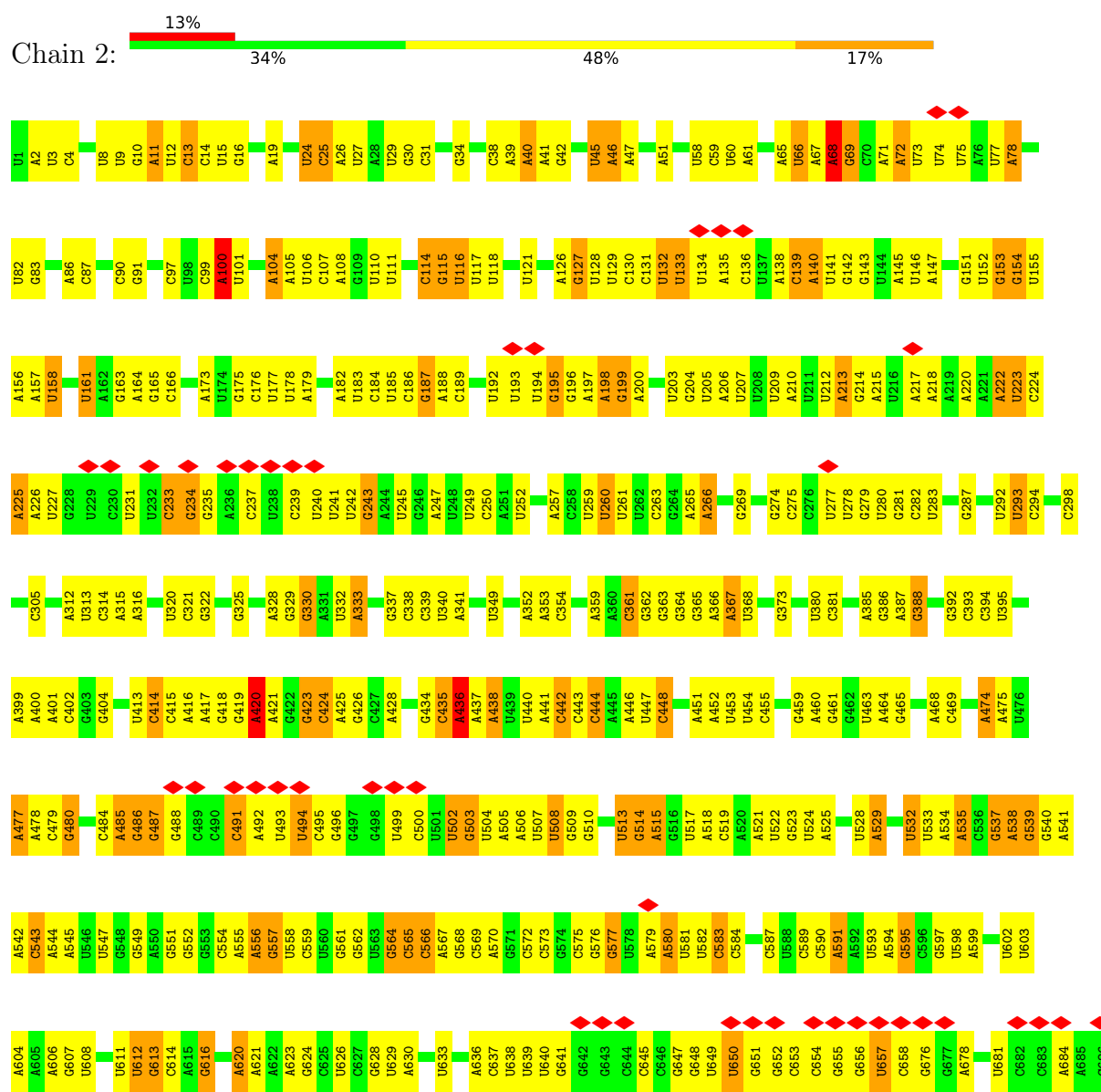
- Molecule 34 is a protein called Ribosome biogenesis protein TSR1.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	t	667	Total	C	N	O	S	0	0
			5401	3447	932	1008	14		

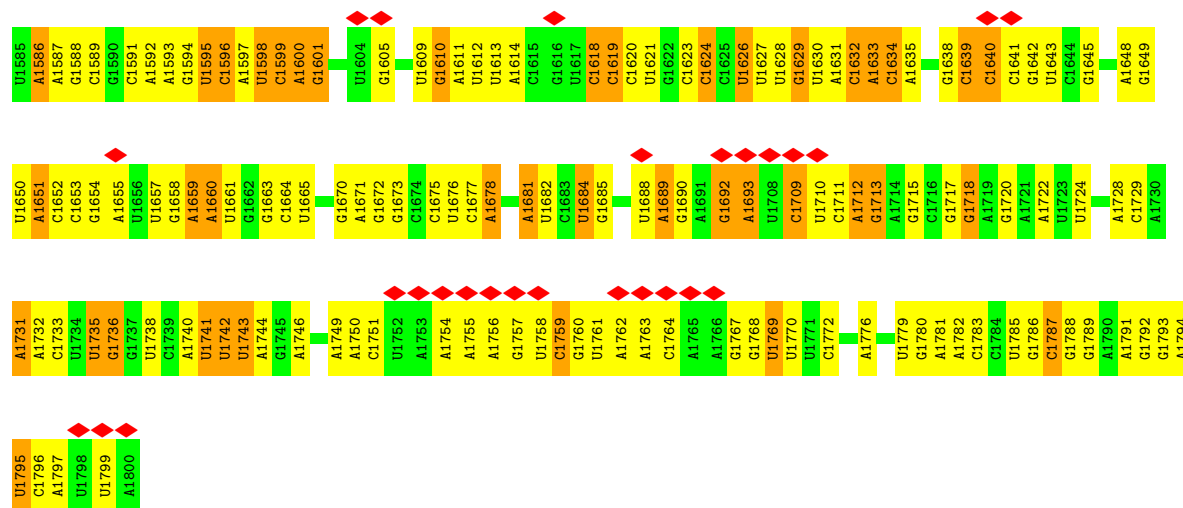
3 Residue-property plots

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: 20S ribosomal RNA

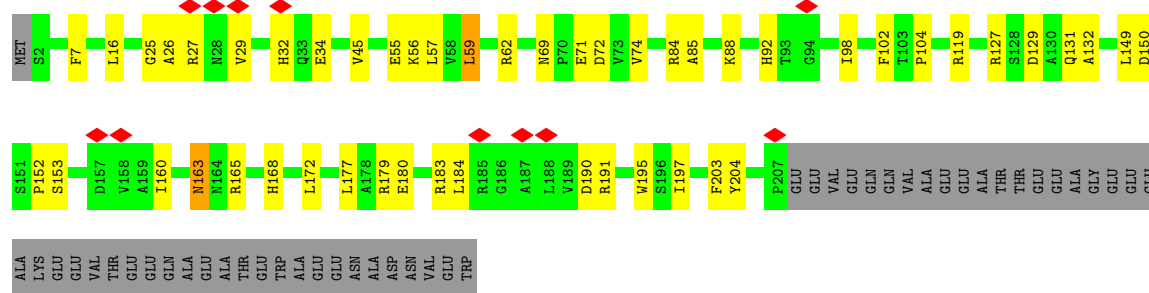






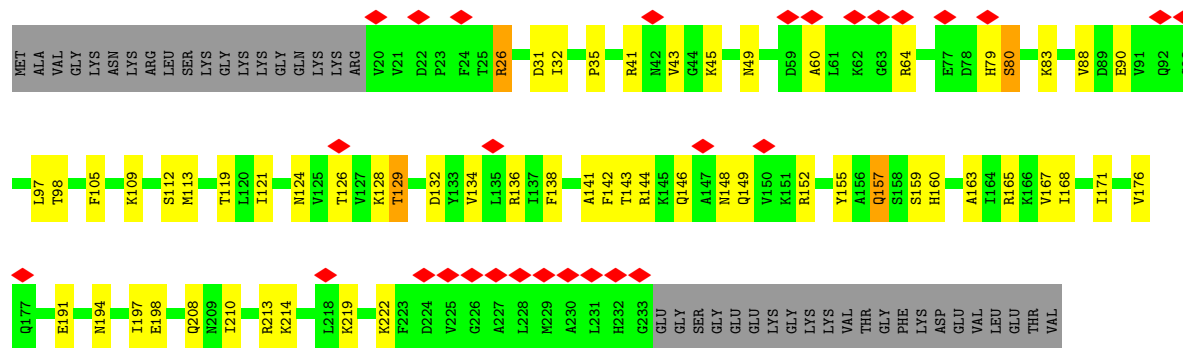
• Molecule 2: 40S ribosomal protein S0-A

Chain A: 62% 19% 18%



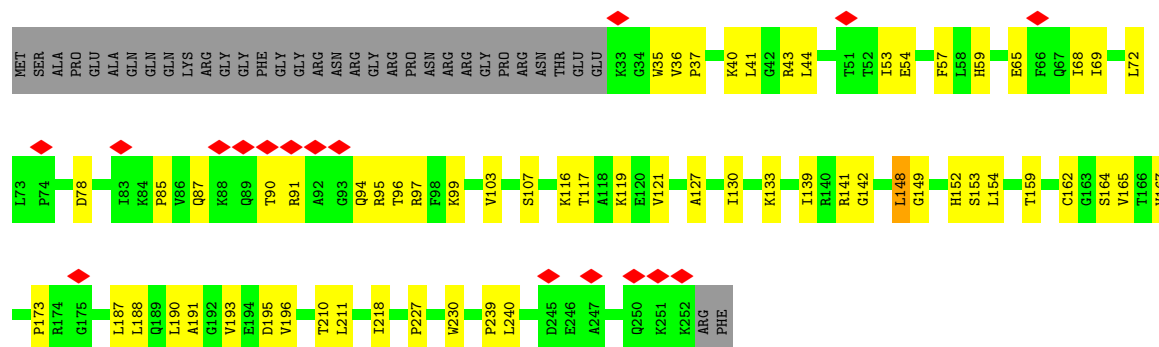
• Molecule 3: 40S ribosomal protein S1-A

Chain B: 61% 22% 16%



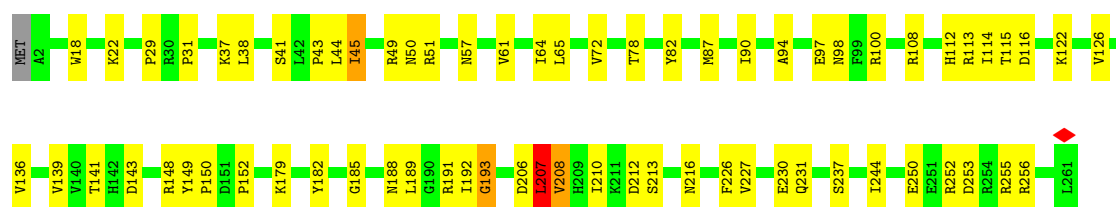
• Molecule 4: 40S ribosomal protein S2

Chain C: 62% 24% 13%



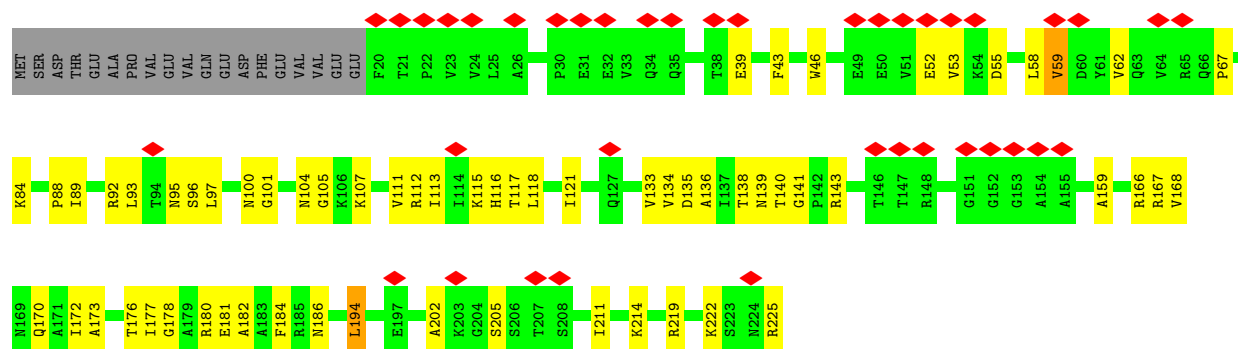
• Molecule 5: 40S ribosomal protein S4-A

Chain E: 74% 25%



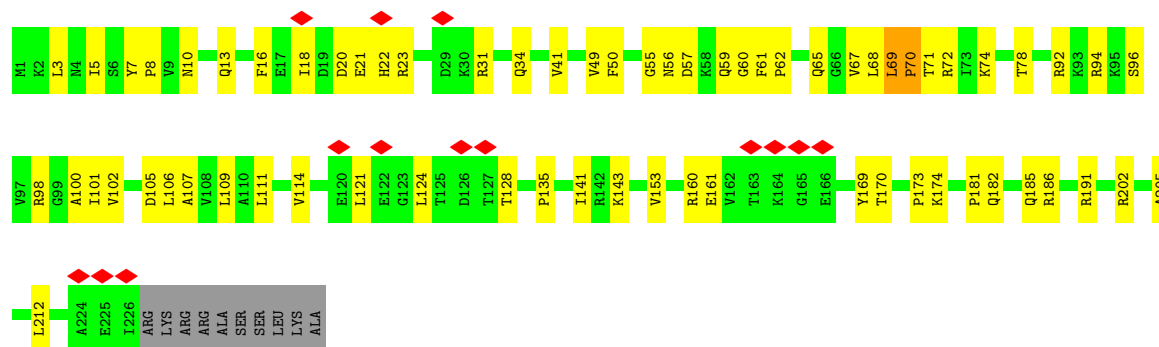
• Molecule 6: 40S ribosomal protein S5

Chain F: 17% 64% 27% 8%

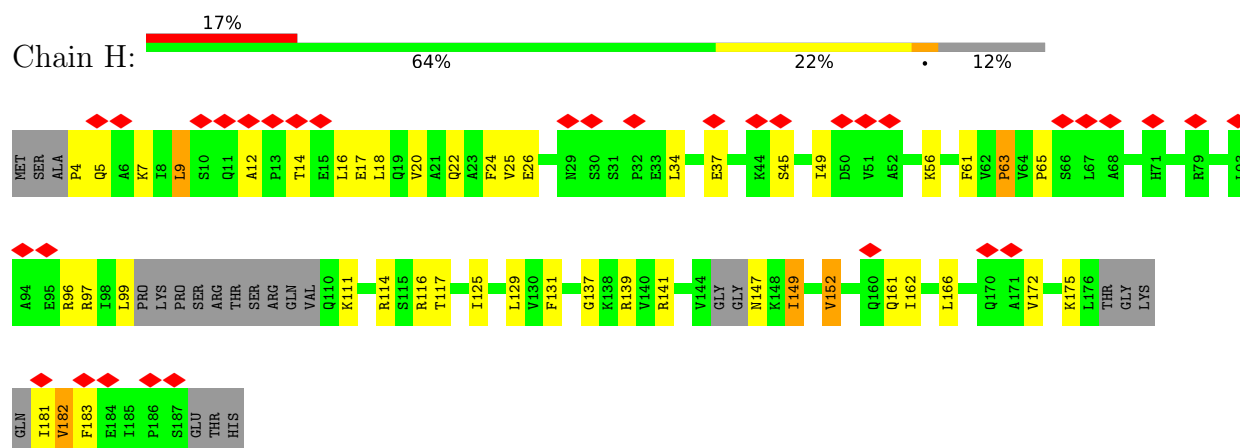


• Molecule 7: 40S ribosomal protein S6-A

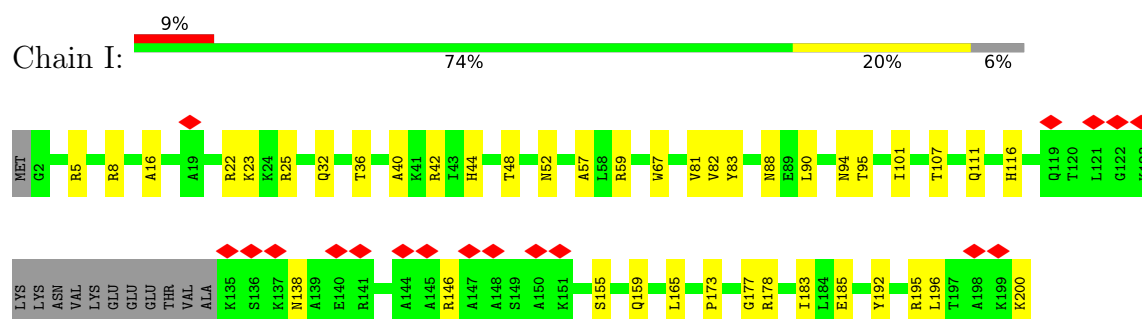
Chain G: 6% 67% 28%



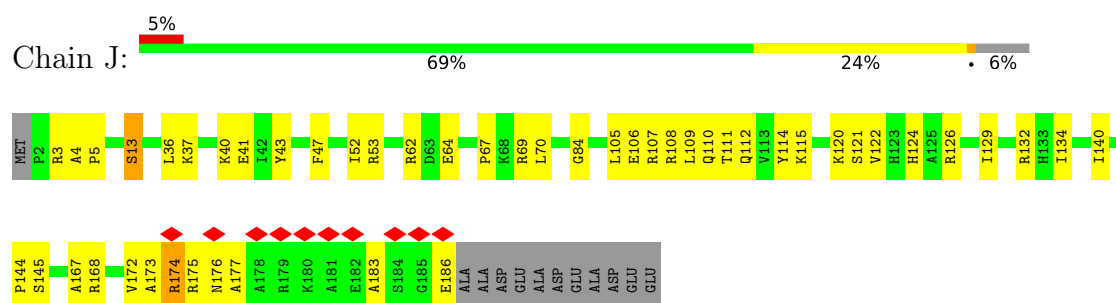
- Molecule 8: 40S ribosomal protein S7-A



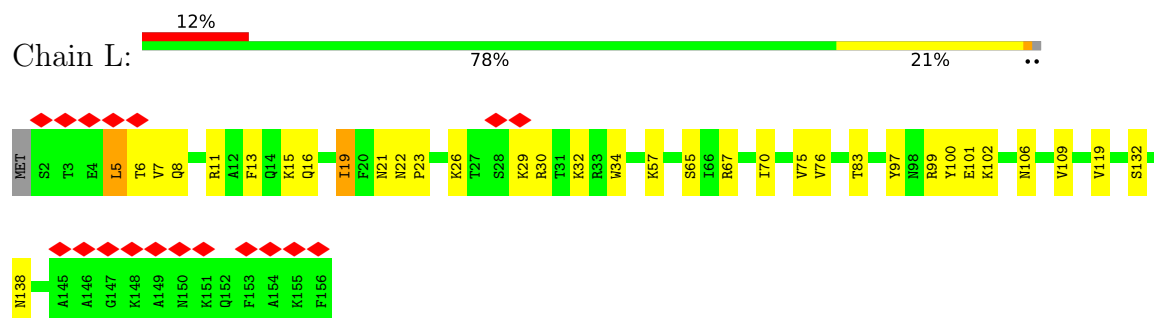
- Molecule 9: 40S ribosomal protein S8-A



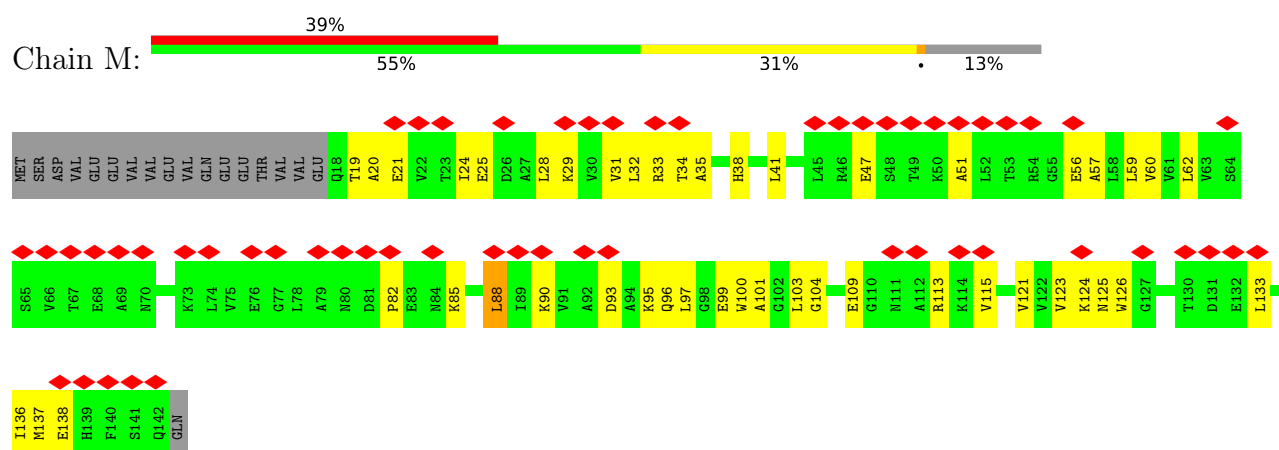
- Molecule 10: 40S ribosomal protein S9-A



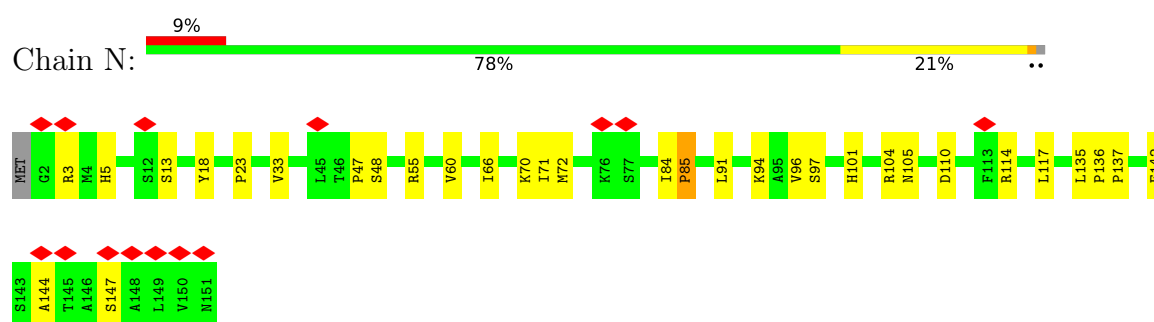
- Molecule 11: 40S ribosomal protein S11-A



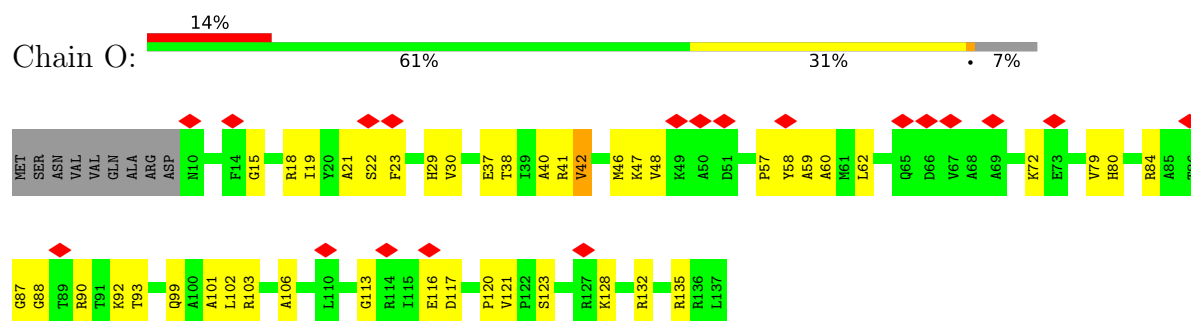
- Molecule 12: 40S ribosomal protein S12



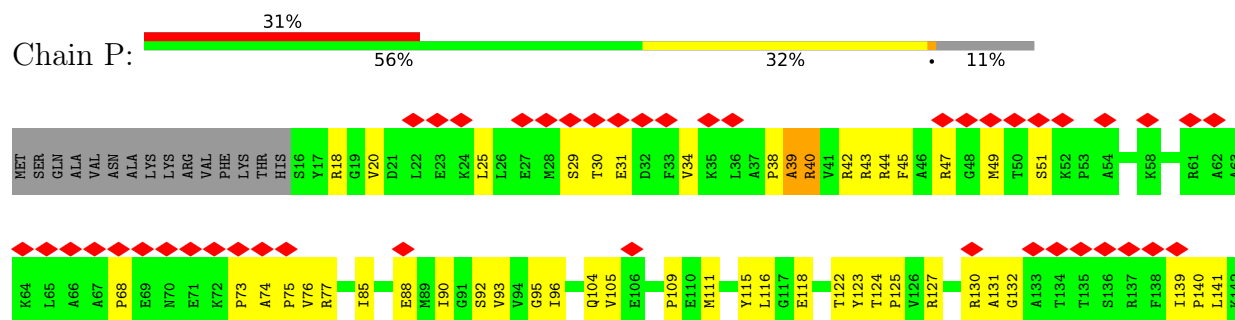
- Molecule 13: 40S ribosomal protein S13



- Molecule 14: 40S ribosomal protein S14-A

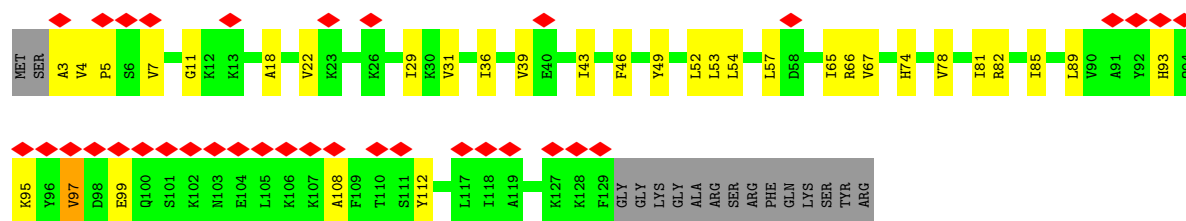


- Molecule 15: 40S ribosomal protein S15

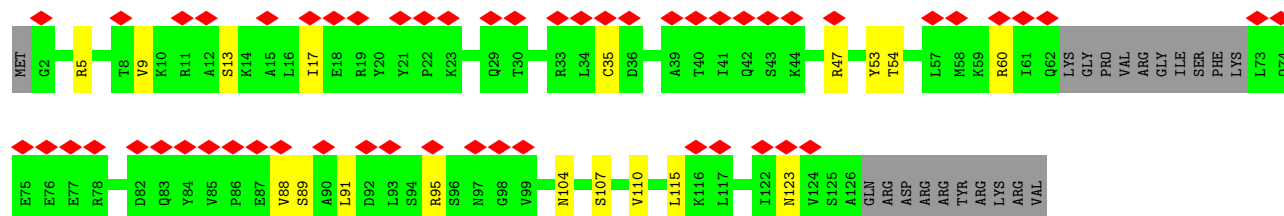
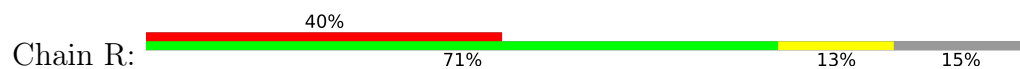


- Molecule 16: 40S ribosomal protein S16-A

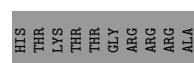
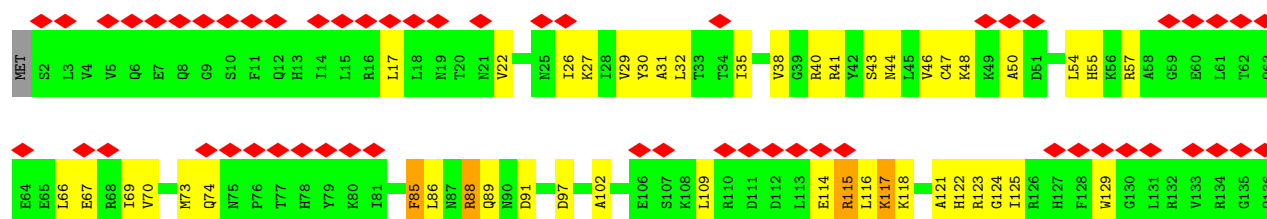
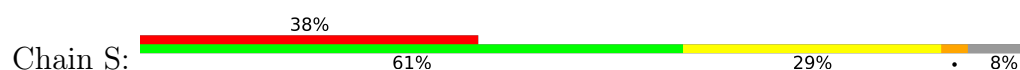




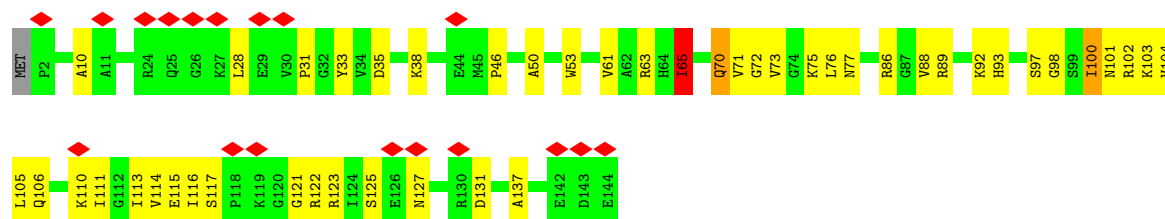
• Molecule 17: 40S ribosomal protein S17-A



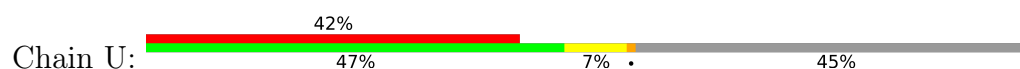
• Molecule 18: 40S ribosomal protein S18-A

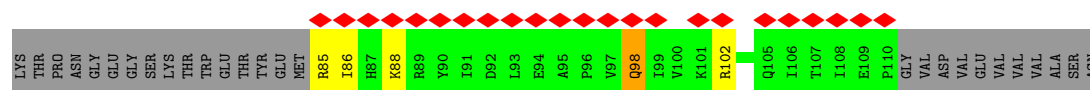


• Molecule 19: 40S ribosomal protein S19-A

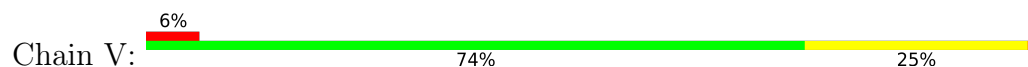


• Molecule 20: 40S ribosomal protein S20

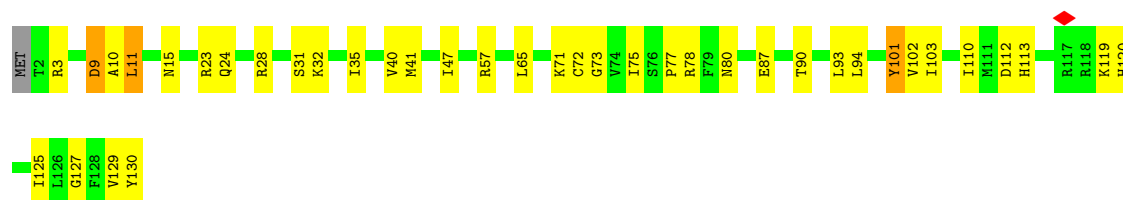




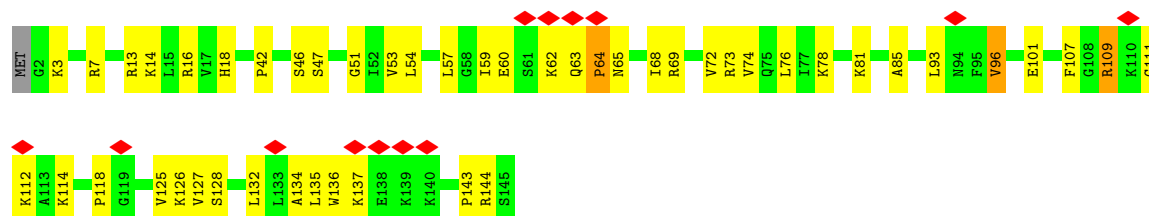
• Molecule 21: 40S ribosomal protein S21-A



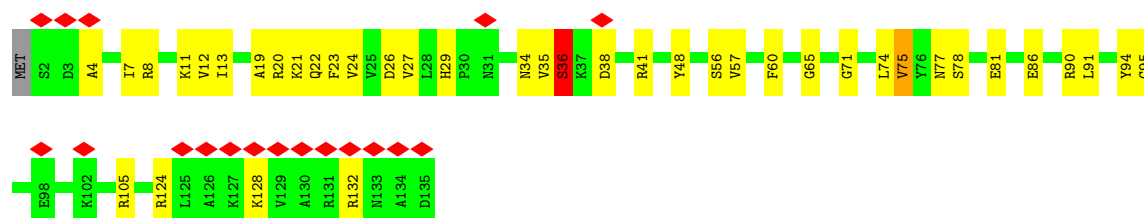
• Molecule 22: 40S ribosomal protein S22-A



• Molecule 23: 40S ribosomal protein S23-A



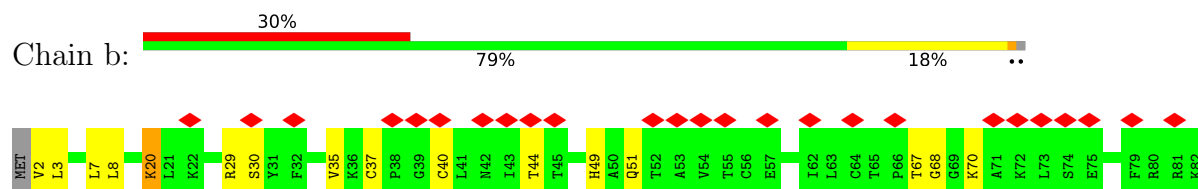
• Molecule 24: 40S ribosomal protein S24-A



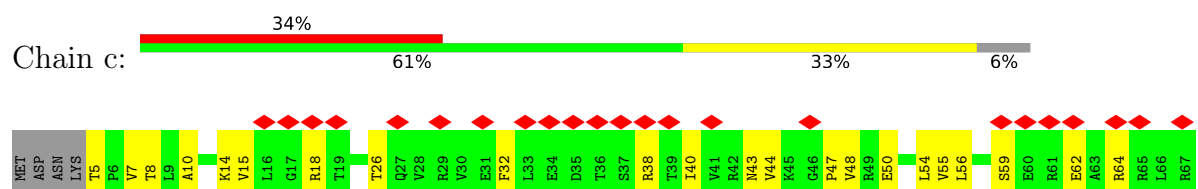
• Molecule 25: 40S ribosomal protein S25-A



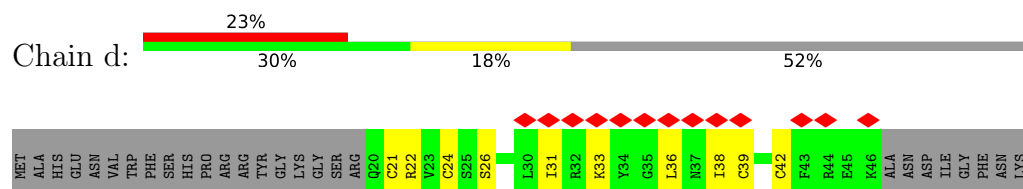
- Molecule 26: 40S ribosomal protein S27-A



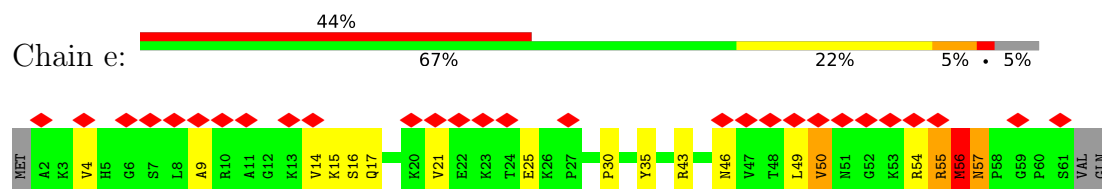
- Molecule 27: 40S ribosomal protein S28-A



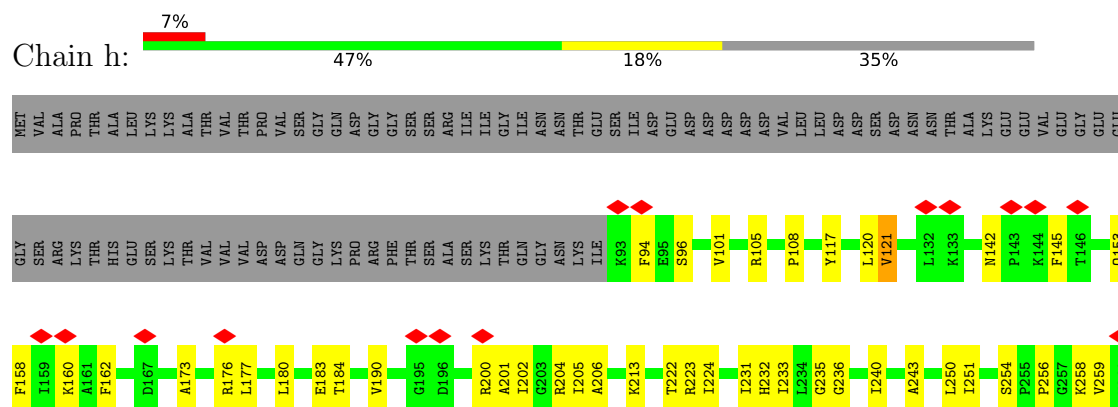
- Molecule 28: 40S ribosomal protein S29-A



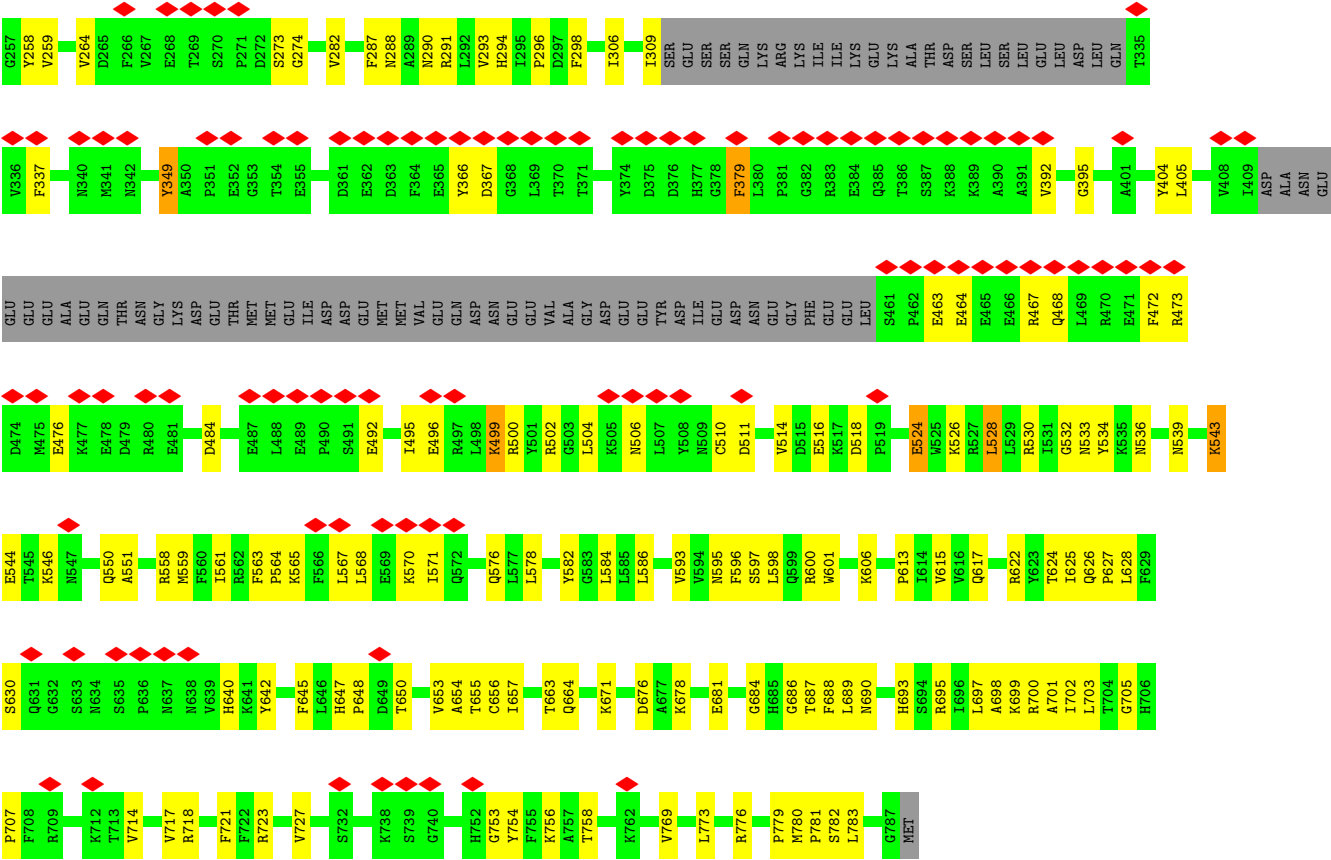
- Molecule 29: 40S ribosomal protein S30-A



- Molecule 30: Pre-rRNA-processing protein PNO1







4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	19564	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	29.4	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.410	Depositor
Minimum map value	-0.139	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.020	Depositor
Recommended contour level	0.085	Depositor
Map size ($\text{\AA}$)	384.12003, 384.12003, 384.12003	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.067, 1.067, 1.067	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: A2M

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	2	0.65	4/41219 (0.0%)	0.69	21/64175 (0.0%)
2	A	0.29	0/1656	0.71	2/2264 (0.1%)
3	B	0.28	0/1733	0.75	1/2329 (0.0%)
4	C	0.27	0/1692	0.67	0/2296
5	E	0.34	0/2109	0.78	4/2839 (0.1%)
6	F	0.27	0/1629	0.76	0/2202
7	G	0.29	0/1823	0.70	1/2439 (0.0%)
8	H	0.30	0/1382	0.85	2/1857 (0.1%)
9	I	0.34	0/1514	0.71	0/2021
10	J	0.31	0/1519	0.84	2/2035 (0.1%)
11	L	0.35	0/1239	0.67	0/1673
12	M	0.31	0/942	0.80	0/1263
13	N	0.27	0/1216	0.71	0/1638
14	O	0.28	0/961	0.71	0/1290
15	P	0.34	0/1020	0.82	1/1367 (0.1%)
16	Q	0.38	0/1011	0.96	3/1362 (0.2%)
17	R	0.25	0/931	0.71	0/1249
18	S	0.30	0/1128	0.84	0/1518
19	T	0.28	0/1129	0.76	2/1514 (0.1%)
20	U	0.23	0/545	0.62	0/733
21	V	0.28	0/693	0.75	2/932 (0.2%)
22	W	0.32	0/1036	0.76	0/1393
23	X	0.36	0/1139	0.87	1/1518 (0.1%)
24	Y	0.36	0/1087	0.84	1/1449 (0.1%)
25	Z	0.23	0/519	0.71	0/696
26	b	0.25	0/621	0.69	0/838
27	c	0.25	0/499	0.69	0/670
28	d	0.25	0/221	0.87	2/291 (0.7%)
29	e	0.38	0/483	1.00	3/643 (0.5%)
30	h	0.31	0/1441	0.74	0/1940
31	i	0.40	0/2179	1.00	12/2956 (0.4%)
32	j	0.24	0/470	0.78	1/632 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	l	0.27	0/2364	0.72	0/3169
34	t	1.58	7/5520 (0.1%)	0.70	5/7456 (0.1%)
All	All	0.64	11/84670 (0.0%)	0.73	66/122647 (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
2	A	0	1
3	B	0	4
4	C	0	2
5	E	0	3
6	F	0	3
7	G	0	2
8	H	0	3
10	J	0	4
11	L	0	2
12	M	0	2
13	N	0	1
14	O	0	2
15	P	0	6
16	Q	0	1
17	R	0	1
18	S	0	6
19	T	0	5
20	U	0	1
21	V	0	1
22	W	0	2
23	X	0	2
24	Y	0	4
26	b	0	1
29	e	0	6
30	h	0	4
31	i	0	13
33	l	0	4
34	t	0	5
All	All	0	91

The worst 5 of 11 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	t	524	GLU	CB-CG	99.44	4.50	1.52
1	2	436	A2M	O3'-P	-95.42	0.60	1.56
1	2	420	A2M	O3'-P	-60.90	0.88	1.61
1	2	796	A2M	O3'-P	-29.45	1.25	1.61
34	t	349	TYR	CD1-CE1	29.40	2.26	1.38

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	420	A2M	P-O3'-C3'	-62.56	44.63	119.70
1	2	796	A2M	OP2-P-O3'	-35.31	27.51	105.20
1	2	436	A2M	O3'-P-O5'	-31.29	44.55	104.00
1	2	420	A2M	OP1-P-O3'	-29.92	39.37	105.20
1	2	436	A2M	P-O3'-C3'	-29.56	84.23	119.70

There are no chirality outliers.

5 of 91 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	A	34	GLU	Peptide
3	B	129	THR	Peptide
3	B	157	GLN	Peptide
3	B	79	HIS	Peptide
3	B	80	SER	Peptide

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	2	36965	0	18612	552	0
2	A	1614	0	1627	34	0
3	B	1709	0	1782	35	0
4	C	1662	0	1762	42	0
5	E	2068	0	2154	42	0
6	F	1609	0	1675	47	0
7	G	1799	0	1879	44	0
8	H	1362	0	1438	32	0
9	I	1489	0	1525	33	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	1494	0	1573	26	0
11	L	1213	0	1257	25	0
12	M	941	0	975	32	0
13	N	1193	0	1255	20	0
14	O	950	0	985	32	0
15	P	1001	0	1040	33	0
16	Q	993	0	1051	19	0
17	R	924	0	976	12	0
18	S	1110	0	1134	35	0
19	T	1112	0	1123	31	0
20	U	541	0	597	5	0
21	V	685	0	671	15	0
22	W	1019	0	1063	25	0
23	X	1121	0	1196	31	0
24	Y	1073	0	1132	28	0
25	Z	512	0	551	3	0
26	b	611	0	633	14	0
27	c	497	0	535	14	0
28	d	219	0	222	5	0
29	e	475	0	525	10	0
30	h	1416	0	1495	34	0
31	i	2125	0	2167	59	0
32	j	465	0	384	8	0
33	l	2322	0	2301	52	0
34	t	5401	0	5266	151	0
All	All	79690	0	62561	1395	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 1395 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)
34:t:349:TYR:CD2	34:t:349:TYR:CG	1.80	1.68
34:t:349:TYR:CG	34:t:349:TYR:CD1	1.81	1.64
34:t:349:TYR:CZ	34:t:349:TYR:CE1	1.90	1.59
34:t:349:TYR:CZ	34:t:349:TYR:CE2	1.90	1.57
1:2:434:G:N1	1:2:436:A2M:H3'	1.22	1.42

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	A	204/252 (81%)	184 (90%)	20 (10%)	0	100	100
3	B	208/255 (82%)	174 (84%)	33 (16%)	1 (0%)	24	57
4	C	218/254 (86%)	191 (88%)	27 (12%)	0	100	100
5	E	258/261 (99%)	218 (84%)	38 (15%)	2 (1%)	16	48
6	F	204/225 (91%)	168 (82%)	36 (18%)	0	100	100
7	G	224/236 (95%)	200 (89%)	22 (10%)	2 (1%)	14	45
8	H	160/190 (84%)	130 (81%)	30 (19%)	0	100	100
9	I	184/200 (92%)	167 (91%)	17 (9%)	0	100	100
10	J	183/197 (93%)	149 (81%)	33 (18%)	1 (0%)	24	57
11	L	153/156 (98%)	126 (82%)	27 (18%)	0	100	100
12	M	111/143 (78%)	83 (75%)	28 (25%)	0	100	100
13	N	148/151 (98%)	133 (90%)	13 (9%)	2 (1%)	9	37
14	O	126/137 (92%)	108 (86%)	18 (14%)	0	100	100
15	P	121/142 (85%)	96 (79%)	25 (21%)	0	100	100
16	Q	125/143 (87%)	93 (74%)	32 (26%)	0	100	100
17	R	111/136 (82%)	98 (88%)	13 (12%)	0	100	100
18	S	133/146 (91%)	112 (84%)	21 (16%)	0	100	100
19	T	139/144 (96%)	126 (91%)	13 (9%)	0	100	100
20	U	61/121 (50%)	56 (92%)	5 (8%)	0	100	100
21	V	83/87 (95%)	66 (80%)	16 (19%)	1 (1%)	10	40
22	W	127/130 (98%)	112 (88%)	13 (10%)	2 (2%)	7	35
23	X	142/145 (98%)	123 (87%)	18 (13%)	1 (1%)	18	51
24	Y	132/135 (98%)	107 (81%)	24 (18%)	1 (1%)	16	48
25	Z	61/108 (56%)	55 (90%)	6 (10%)	0	100	100
26	b	79/82 (96%)	70 (89%)	8 (10%)	1 (1%)	9	38

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
27	c	61/67 (91%)	52 (85%)	9 (15%)	0	100	100
28	d	25/56 (45%)	23 (92%)	1 (4%)	1 (4%)	2	20
29	e	58/63 (92%)	41 (71%)	17 (29%)	0	100	100
30	h	176/274 (64%)	157 (89%)	19 (11%)	0	100	100
31	i	257/483 (53%)	200 (78%)	55 (21%)	2 (1%)	16	48
32	j	51/463 (11%)	42 (82%)	9 (18%)	0	100	100
33	l	274/425 (64%)	241 (88%)	33 (12%)	0	100	100
34	t	649/788 (82%)	577 (89%)	72 (11%)	0	100	100
All	All	5246/6795 (77%)	4478 (85%)	751 (14%)	17 (0%)	37	67

5 of 17 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
5	E	207	LEU
5	E	208	VAL
22	W	11	LEU
31	i	279	ILE
3	B	80	SER

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	A	172/210 (82%)	170 (99%)	2 (1%)	63	72
3	B	191/224 (85%)	190 (100%)	1 (0%)	81	81
4	C	179/205 (87%)	177 (99%)	2 (1%)	65	73
5	E	221/222 (100%)	217 (98%)	4 (2%)	51	67
6	F	173/191 (91%)	171 (99%)	2 (1%)	63	72
7	G	188/201 (94%)	187 (100%)	1 (0%)	81	81
8	H	151/170 (89%)	147 (97%)	4 (3%)	40	60
9	I	150/161 (93%)	150 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	J	158/166 (95%)	155 (98%)	3 (2%)	50	66
11	L	129/137 (94%)	125 (97%)	4 (3%)	35	57
12	M	101/119 (85%)	99 (98%)	2 (2%)	48	65
13	N	127/128 (99%)	127 (100%)	0	100	100
14	O	97/105 (92%)	96 (99%)	1 (1%)	68	74
15	P	105/118 (89%)	105 (100%)	0	100	100
16	Q	107/119 (90%)	105 (98%)	2 (2%)	50	66
17	R	105/124 (85%)	105 (100%)	0	100	100
18	S	120/129 (93%)	120 (100%)	0	100	100
19	T	115/116 (99%)	113 (98%)	2 (2%)	53	67
20	U	64/114 (56%)	64 (100%)	0	100	100
21	V	74/74 (100%)	73 (99%)	1 (1%)	59	70
22	W	110/111 (99%)	109 (99%)	1 (1%)	70	74
23	X	119/120 (99%)	116 (98%)	3 (2%)	42	61
24	Y	112/113 (99%)	110 (98%)	2 (2%)	51	67
25	Z	56/89 (63%)	56 (100%)	0	100	100
26	b	70/71 (99%)	70 (100%)	0	100	100
27	c	56/60 (93%)	56 (100%)	0	100	100
28	d	25/49 (51%)	25 (100%)	0	100	100
29	e	51/54 (94%)	50 (98%)	1 (2%)	48	65
30	h	156/238 (66%)	156 (100%)	0	100	100
31	i	233/424 (55%)	227 (97%)	6 (3%)	40	60
32	j	53/419 (13%)	52 (98%)	1 (2%)	50	66
33	l	260/384 (68%)	260 (100%)	0	100	100
34	t	582/703 (83%)	581 (100%)	1 (0%)	87	87
All	All	4610/5868 (79%)	4564 (99%)	46 (1%)	65	74

5 of 46 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	T	65	ILE
24	Y	7	ILE
19	T	114	VAL

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Mol	Chain	Res	Type
23	X	57	LEU
29	e	54	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 91 such sidechains are listed below:

Mol	Chain	Res	Type
24	Y	63	GLN
33	l	160	ASN
26	b	51	GLN
31	i	426	GLN
34	t	56	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1714/1735 (98%)	822 (47%)	28 (1%)

5 of 822 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	U
1	2	4	C
1	2	8	U
1	2	11	A

5 of 28 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2	819	G
1	2	1652	C
1	2	1086	A
1	2	1573	A
1	2	1041	G

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

4 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
1	A2M	2	796	1	22,25,26	2.04	5 (22%)	30,36,39	2.39	10 (33%)
1	A2M	2	436	1	22,25,26	1.96	4 (18%)	30,36,39	2.12	10 (33%)
1	A2M	2	100	1	22,25,26	2.00	6 (27%)	30,36,39	2.47	12 (40%)
1	A2M	2	420	1	22,25,26	1.42	2 (9%)	30,36,39	2.90	11 (36%)

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
1	A2M	2	796	1	-	2/9/27/28	0/3/3/3
1	A2M	2	436	1	-	0/9/27/28	0/3/3/3
1	A2M	2	100	1	-	2/9/27/28	0/3/3/3
1	A2M	2	420	1	-	0/9/27/28	0/3/3/3

The worst 5 of 17 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	2	796	A2M	C5-C4	6.30	1.50	1.39
1	2	436	A2M	C5-C4	6.29	1.50	1.39
1	2	100	A2M	C5-C4	5.97	1.49	1.39
1	2	420	A2M	C5-C4	4.34	1.46	1.39
1	2	436	A2M	C5-C6	3.65	1.51	1.41

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	420	A2M	N3-C4-N9	6.77	138.68	127.17
1	2	796	A2M	C5-C4-N3	-6.70	117.49	126.72
1	2	100	A2M	C5-C4-N3	-6.54	117.71	126.72
1	2	420	A2M	C2'-C1'-N9	-6.34	103.33	113.75
1	2	796	A2M	N3-C4-N9	6.20	137.71	127.17

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	2	100	A2M	O4'-C4'-C5'-O5'
1	2	796	A2M	O4'-C4'-C5'-O5'
1	2	100	A2M	C3'-C4'-C5'-O5'
1	2	796	A2M	C3'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 56 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	2	796	A2M	16	0
1	2	436	A2M	16	0
1	2	100	A2M	7	0
1	2	420	A2M	17	0

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	2	28
12	M	7
34	t	6
33	l	4
32	j	2

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Mol	Chain	Number of breaks
15	P	2
3	B	2
30	h	1
19	T	1
20	U	1
21	V	1

The worst 5 of 55 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	2	1293:U	O3'	1301:U	P	19.14
1	2	658:C	O3'	676:G	P	16.52
1	2	1693:A	O3'	1708:U	P	10.88
1	2	705:U	O3'	733:A	P	9.46
1	2	1508:U	O3'	1509:C	P	9.19

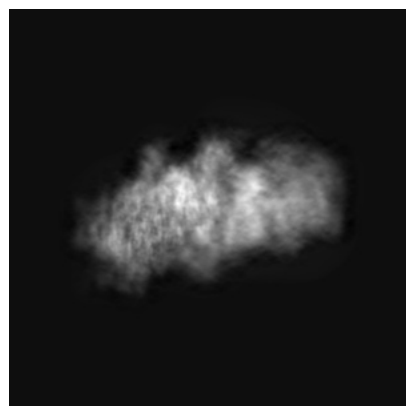
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10713. These allow visual inspection of the internal detail of the map and identification of artifacts.

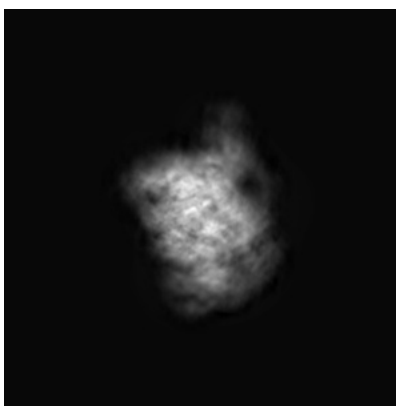
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

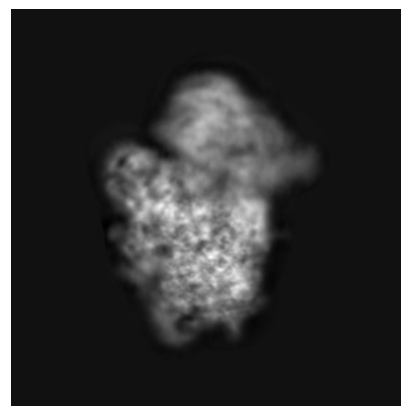
6.1.1 Primary map



X

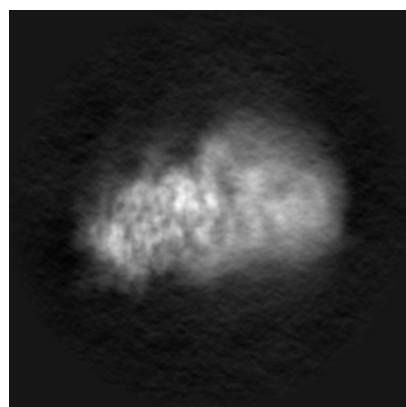


Y

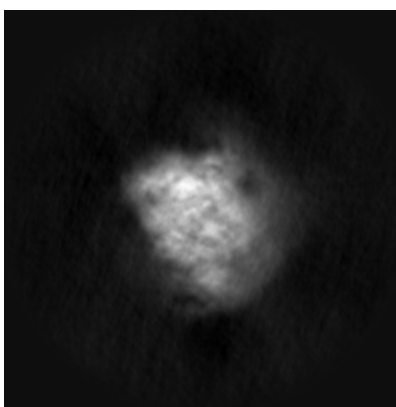


Z

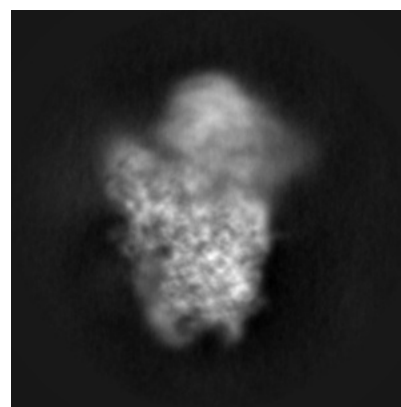
6.1.2 Raw map



X



Y

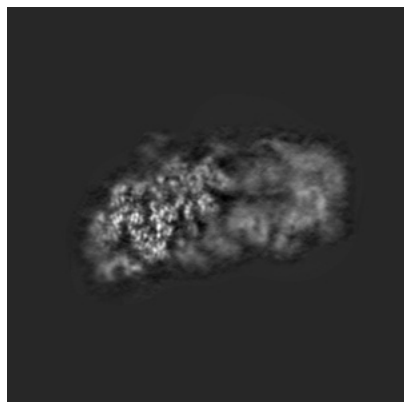


Z

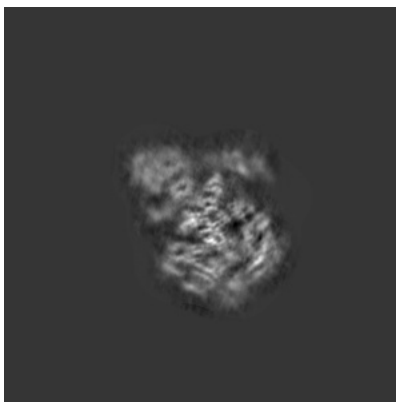
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

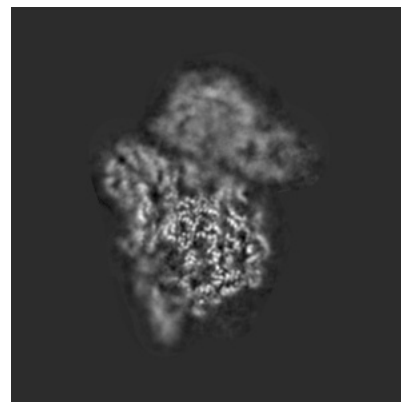
6.2.1 Primary map



X Index: 180

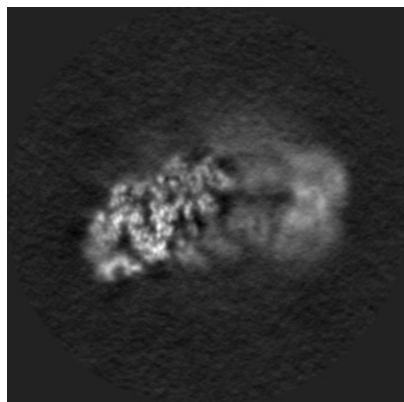


Y Index: 180

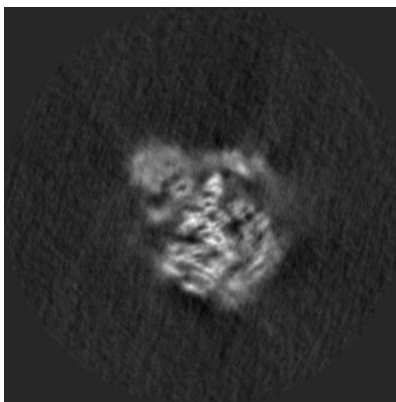


Z Index: 180

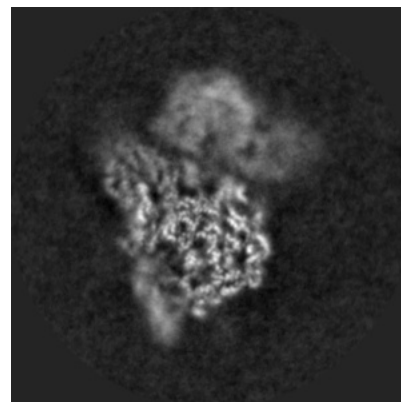
6.2.2 Raw map



X Index: 180



Y Index: 180

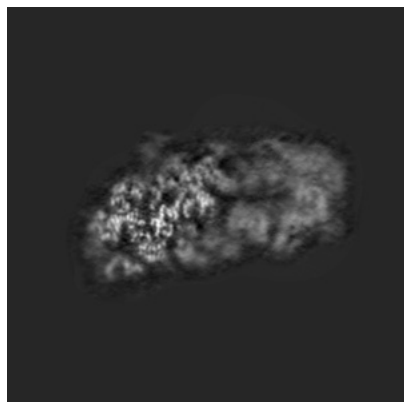


Z Index: 180

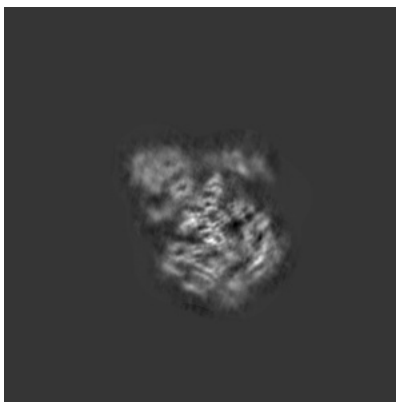
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

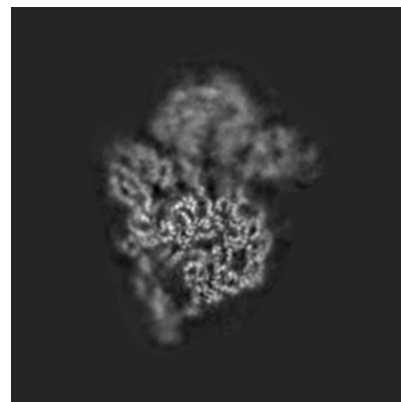
6.3.1 Primary map



X Index: 178

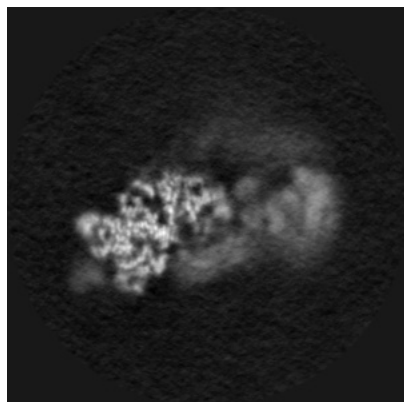


Y Index: 180

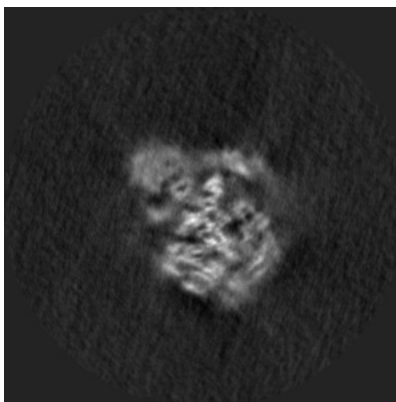


Z Index: 185

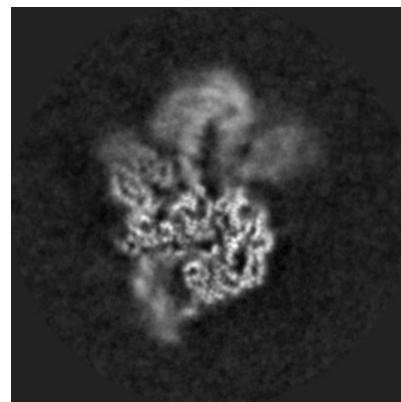
6.3.2 Raw map



X Index: 202



Y Index: 179

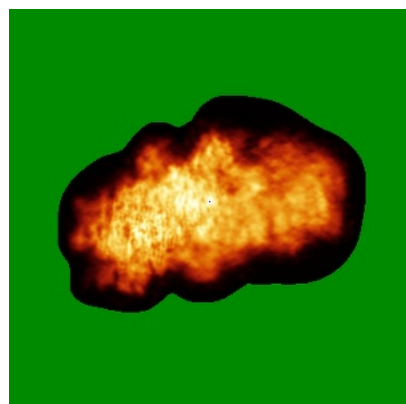


Z Index: 187

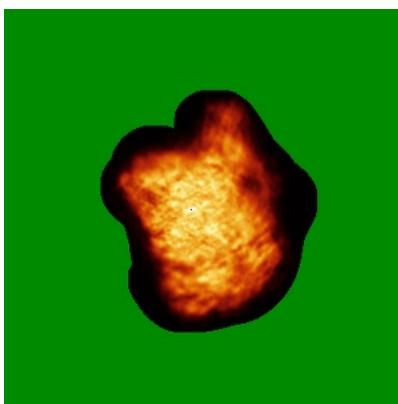
The images above show the largest variance slices of the map in three orthogonal directions.

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

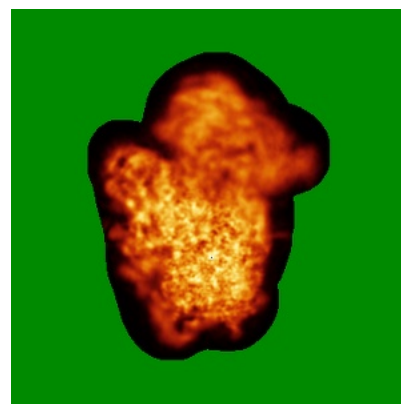
6.4.1 Primary map



X

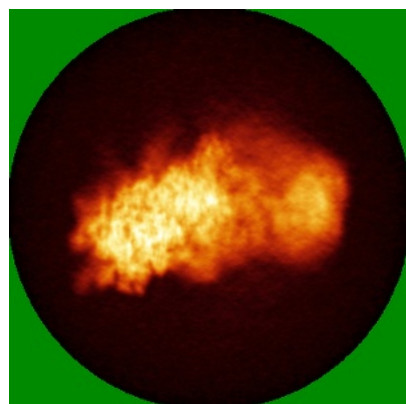


Y

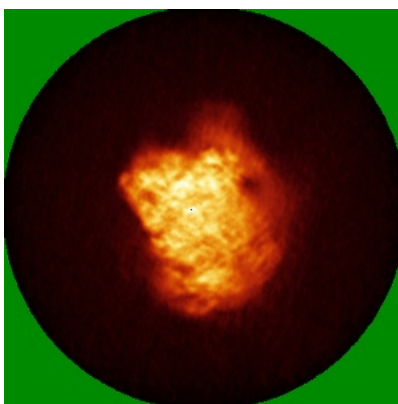


Z

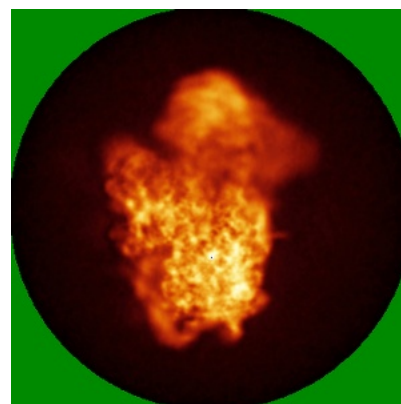
6.4.2 Raw map



X



Y

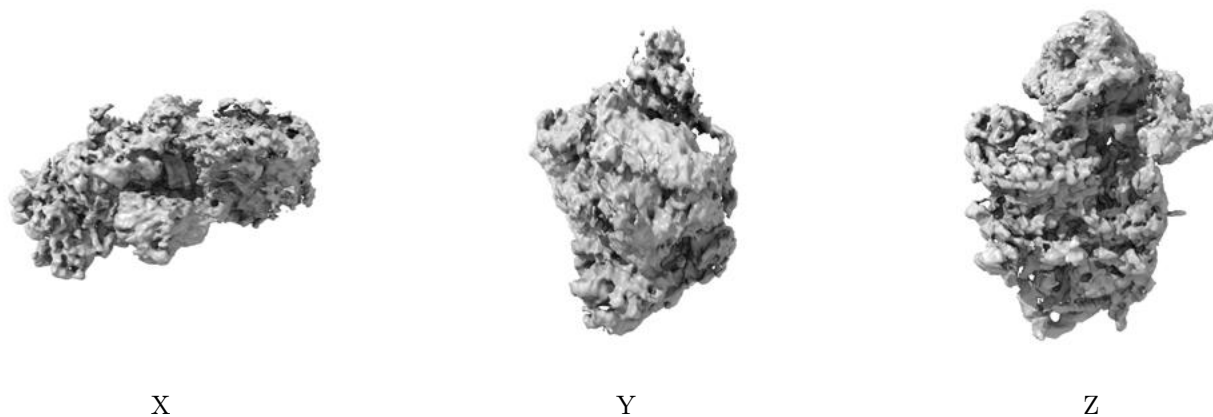


Z

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.

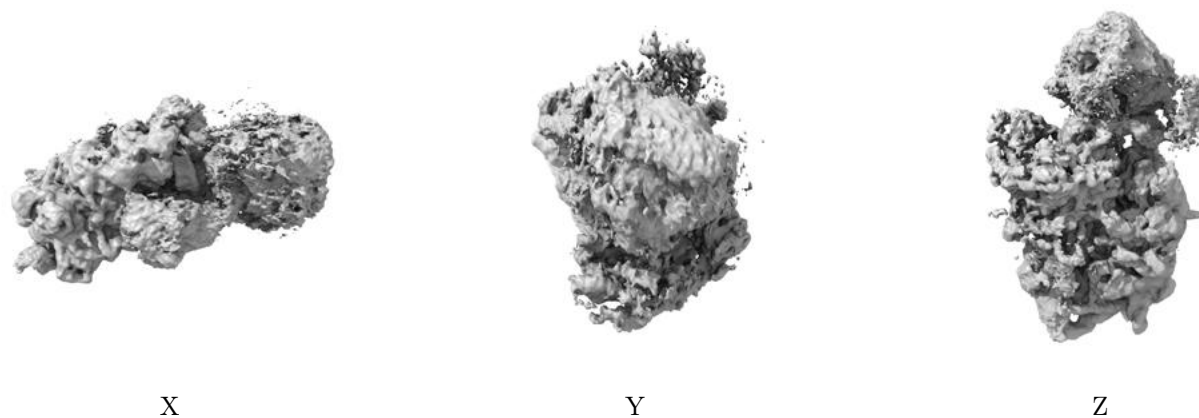
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.085. 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



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.

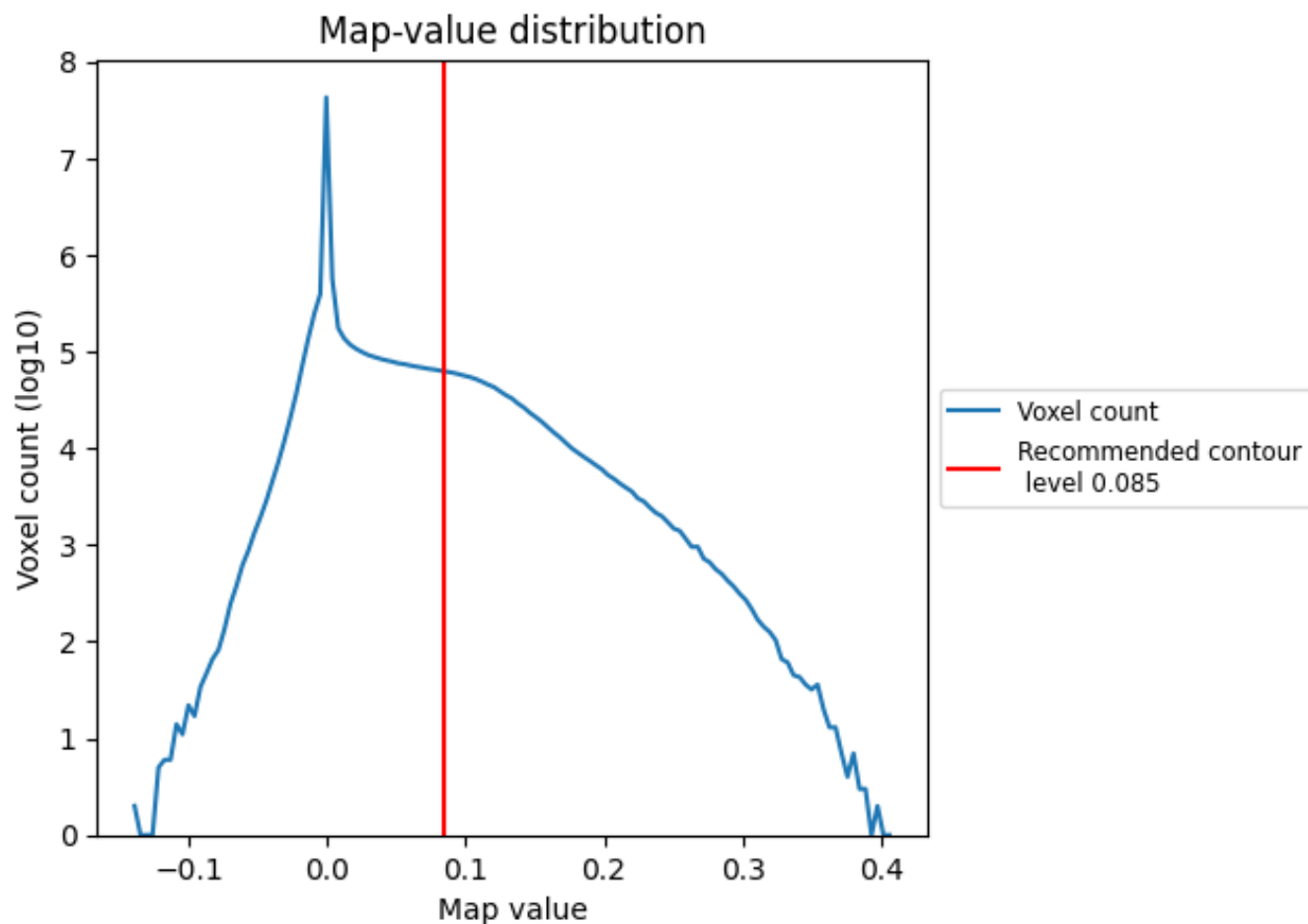
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

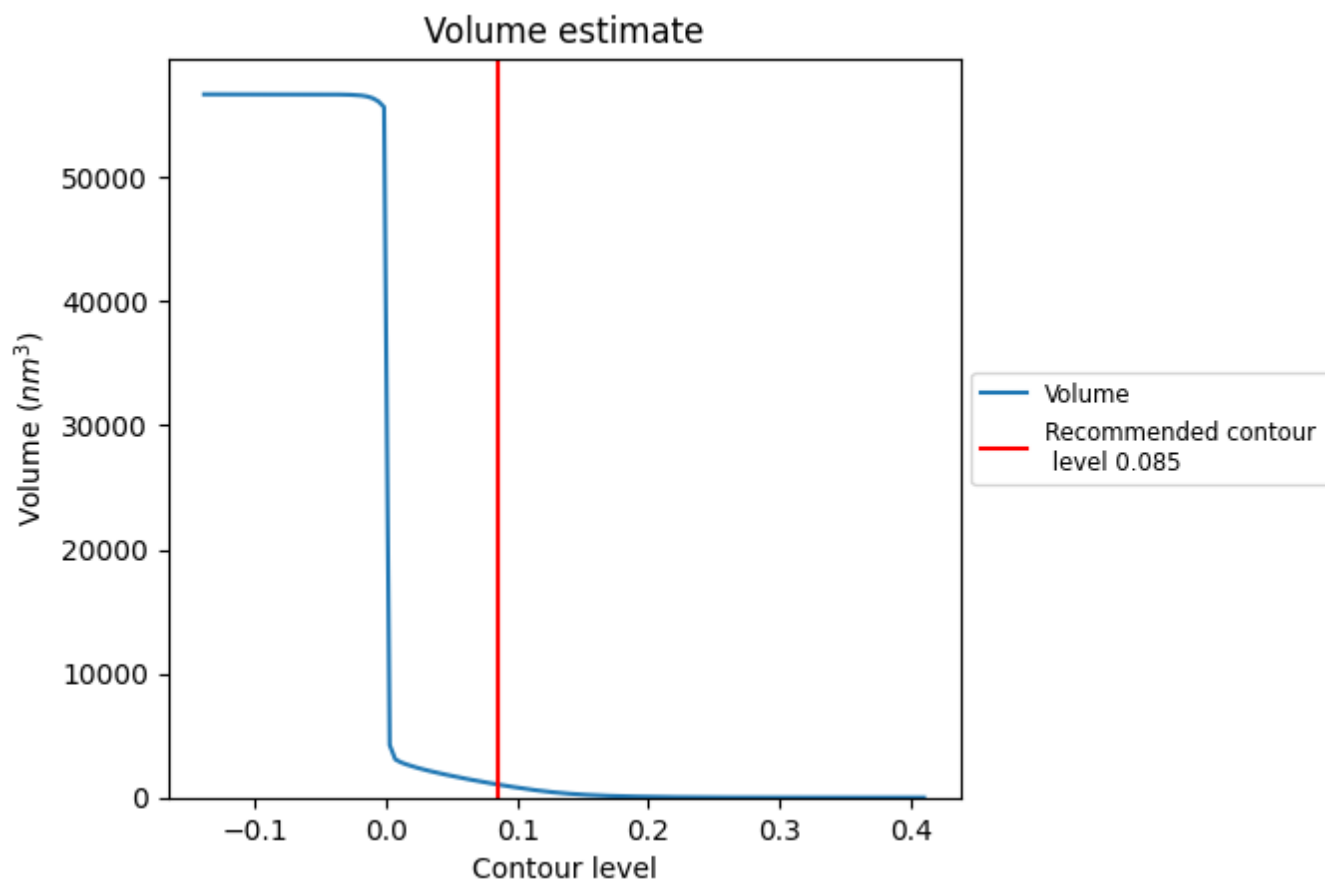
This section contains the results of statistical analysis of the map.

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.

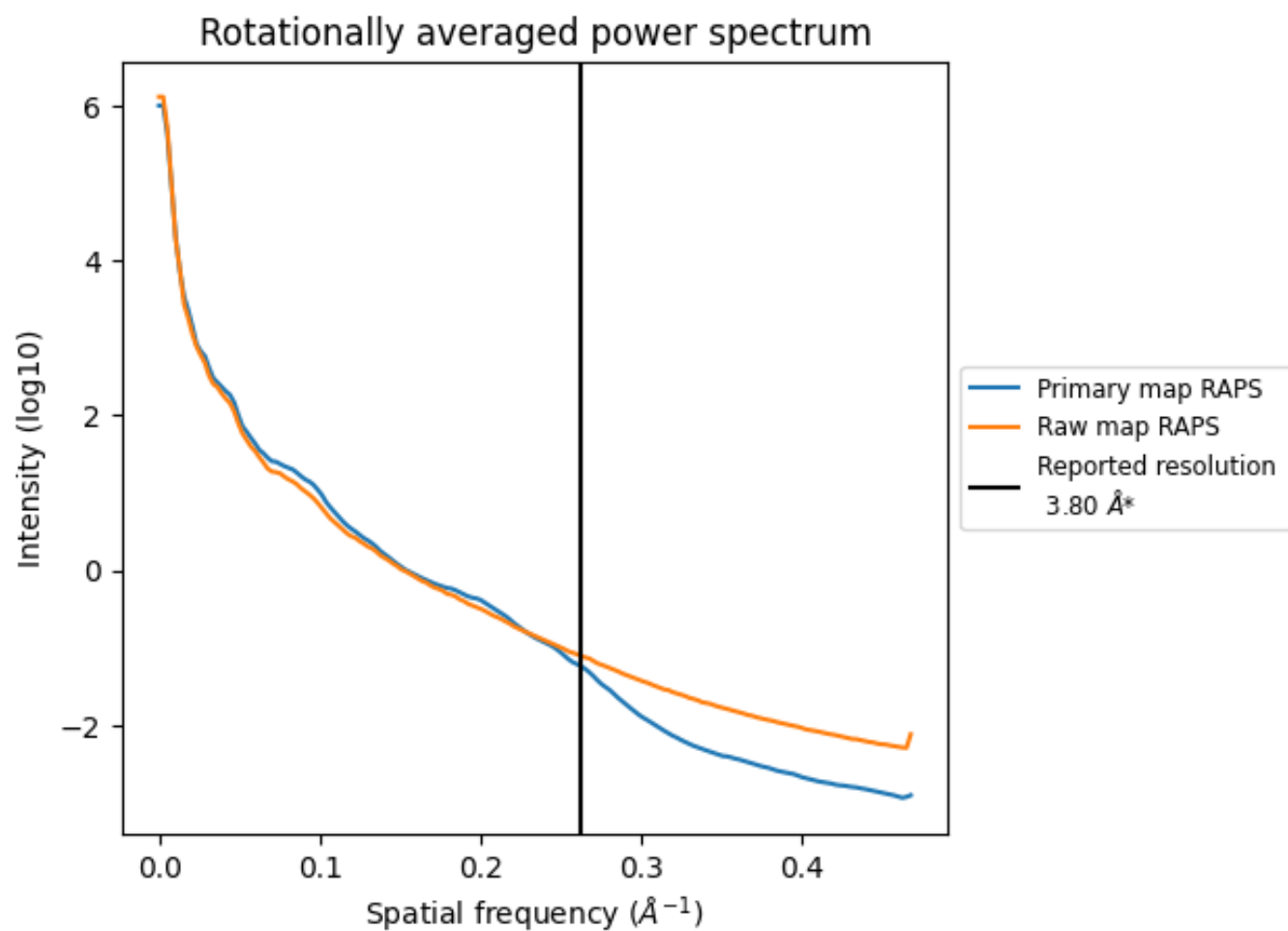
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1058 nm³; this corresponds to an approximate mass of 955 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 ⓘ

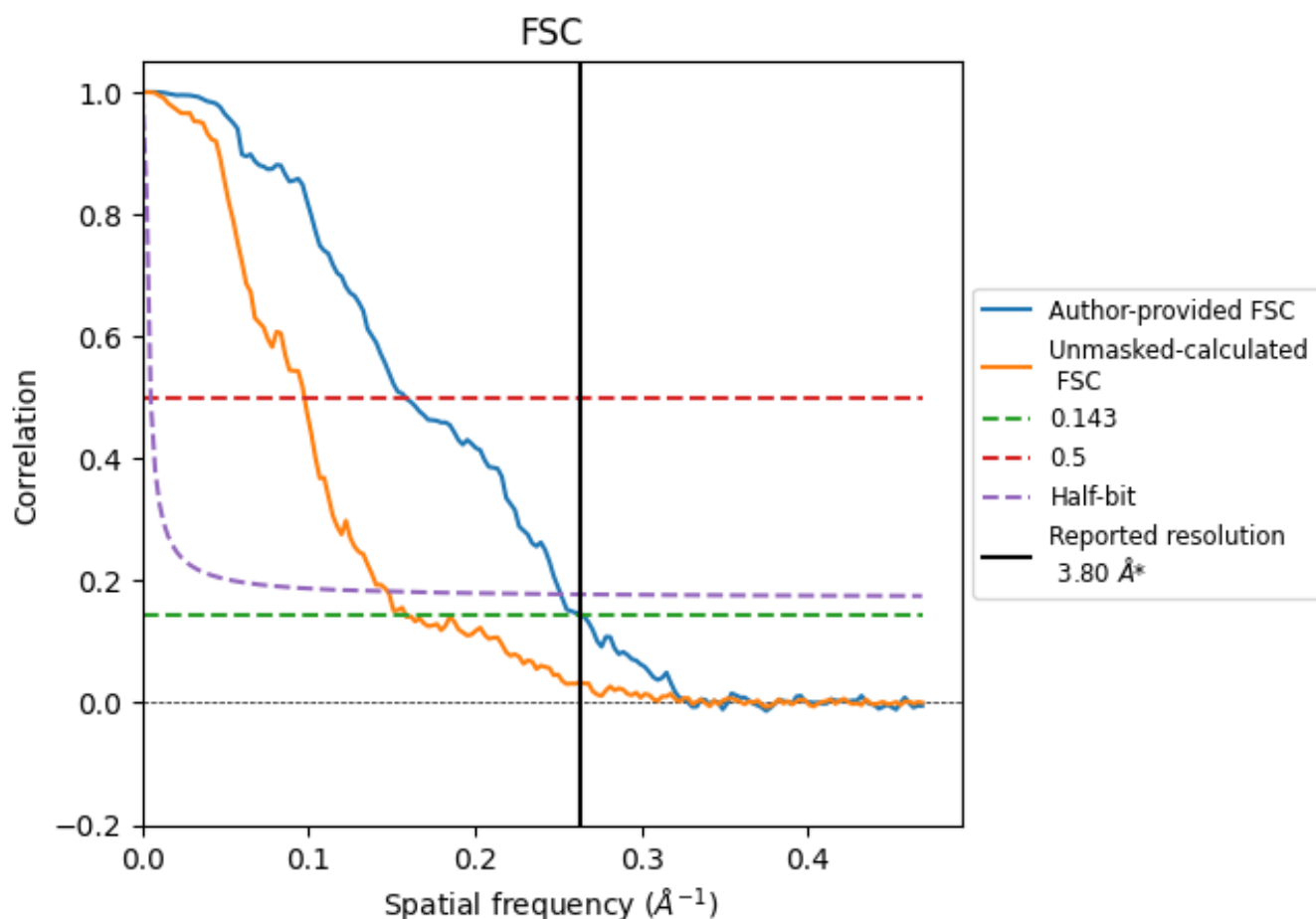


*Reported resolution corresponds to spatial frequency of 0.263 $\text{\AA}^{-1}$

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 0.263 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

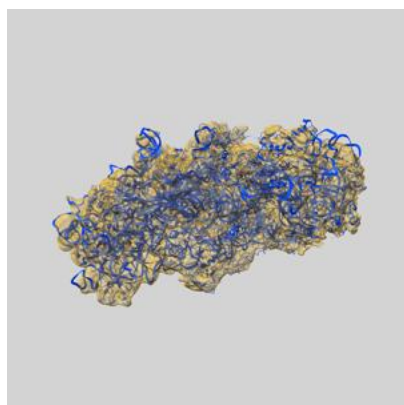
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.78	6.33	3.97
Unmasked-calculated*	6.31	10.27	6.78

*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 6.31 differs from the reported value 3.8 by more than 10 %

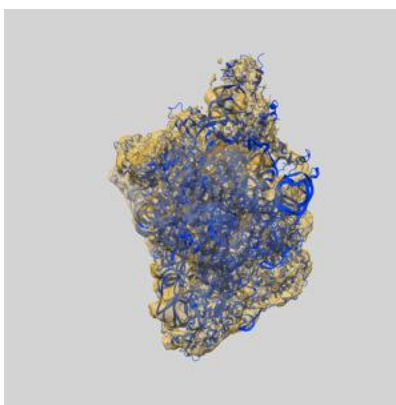
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10713 and PDB model 6Y7C. Per-residue inclusion information can be found in [section 3](#) on [page 11](#).

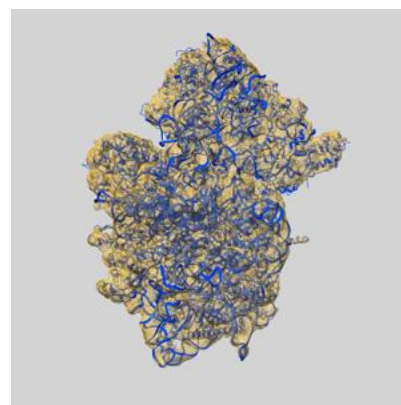
9.1 Map-model overlay [i](#)



X



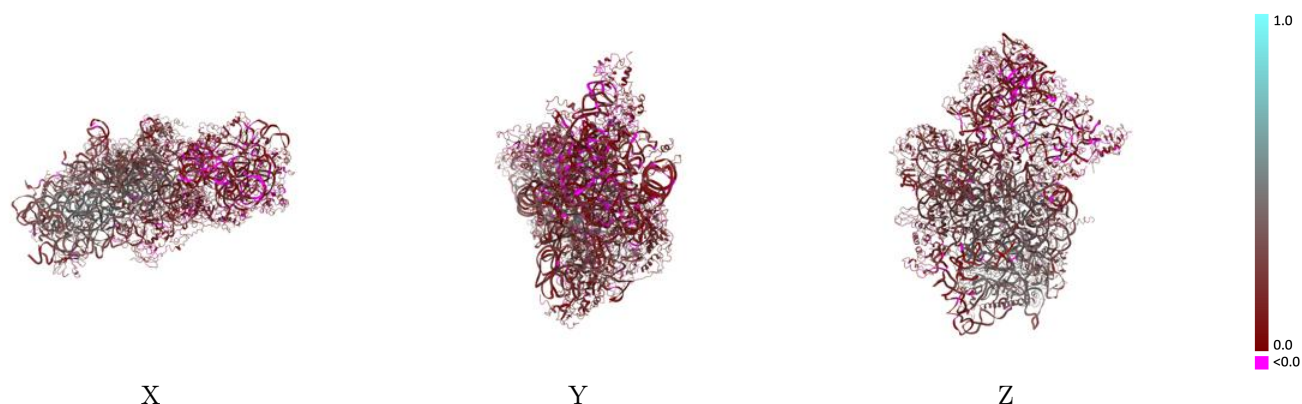
Y



Z

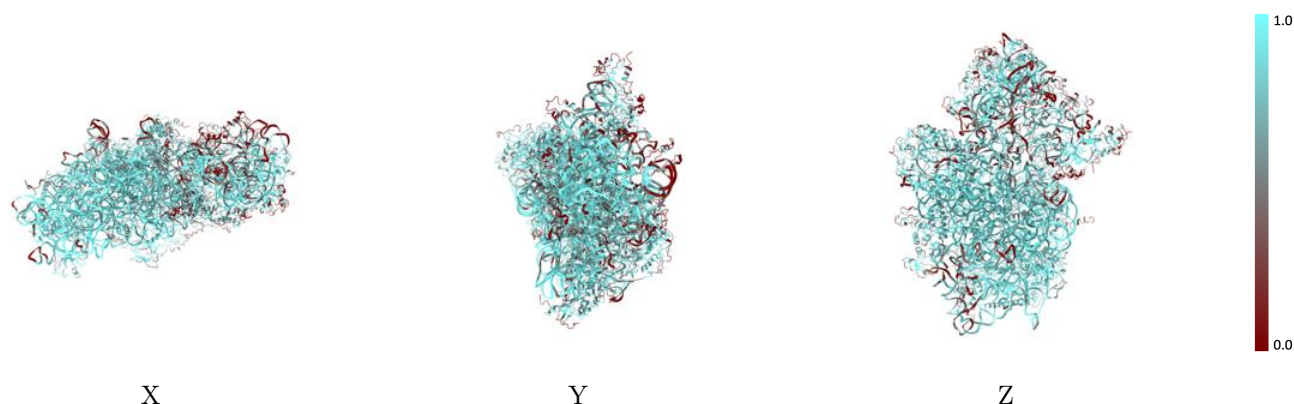
The images above show the 3D surface view of the map at the recommended contour level 0.085 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



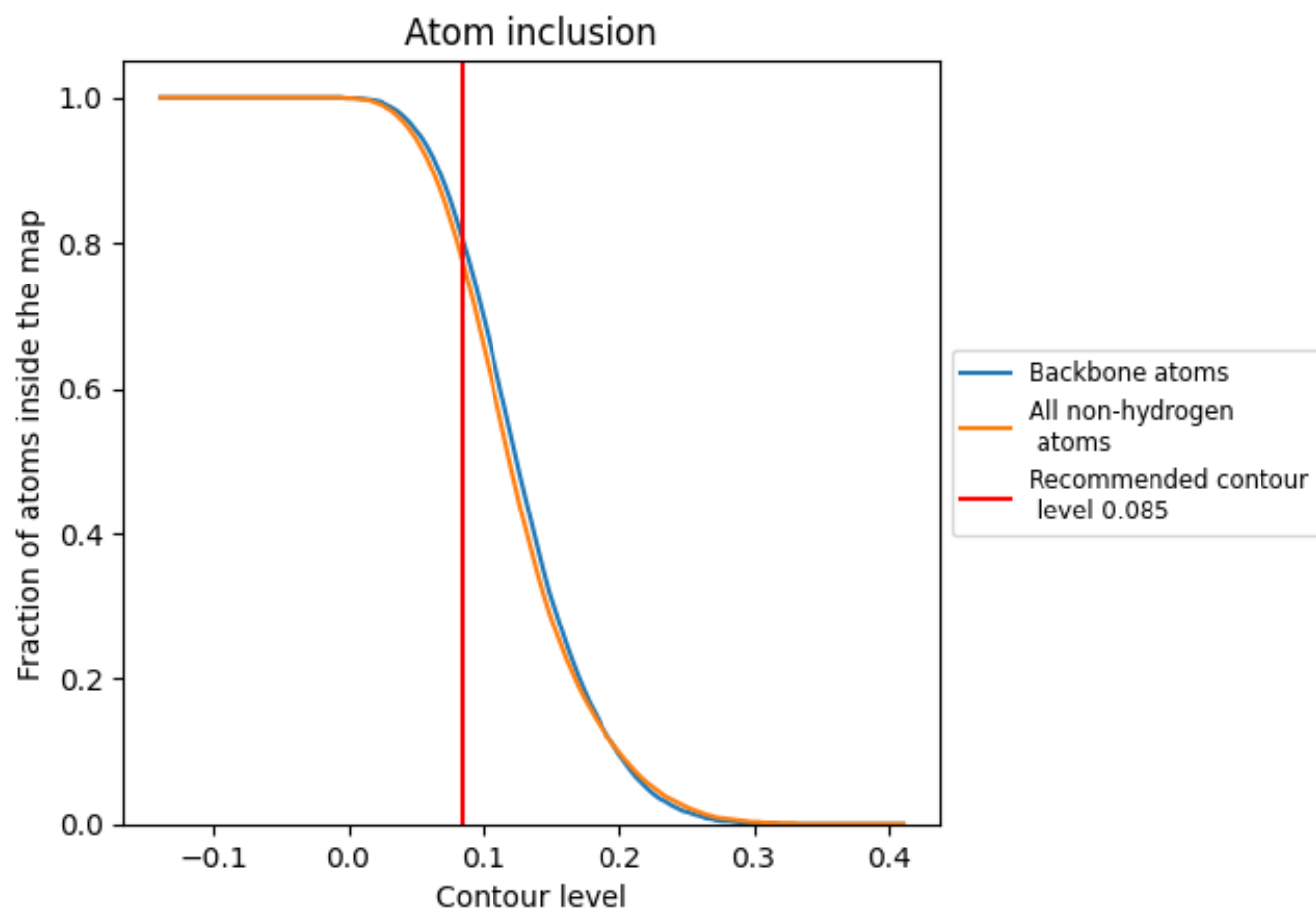
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.085).

9.4 Atom inclusion ⓘ



At the recommended contour level, 80% of all backbone atoms, 77% 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 (0.085) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7710	 0.2350
2	 0.8230	 0.2550
A	 0.8480	 0.2370
B	 0.7460	 0.2040
C	 0.8230	 0.2960
E	 0.9110	 0.3860
F	 0.7490	 0.1460
G	 0.8130	 0.2940
H	 0.7180	 0.1730
I	 0.8250	 0.3600
J	 0.8540	 0.3110
L	 0.8390	 0.4070
M	 0.4970	 0.1130
N	 0.7820	 0.2340
O	 0.7520	 0.1890
P	 0.6140	 0.1420
Q	 0.6620	 0.1260
R	 0.4560	 0.1930
S	 0.5680	 0.1420
T	 0.8080	 0.1350
U	 0.2230	 0.1450
V	 0.8680	 0.2430
W	 0.9220	 0.3060
X	 0.8170	 0.2890
Y	 0.7650	 0.3030
Z	 0.5240	 0.1520
b	 0.5960	 0.2240
c	 0.5700	 0.1390
d	 0.3290	 0.1210
e	 0.4640	 0.2070
h	 0.7640	 0.2230
i	 0.6180	 0.1120
j	 0.3290	 0.1540
l	 0.6650	 0.1440
t	 0.7200	 0.1630

