wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 01:19 am GMT

PDB ID	:	6G4S
EMDB ID	:	EMD-4348
Title	:	Cryo-EM structure of a late human pre-40S ribosomal subunit - State B
Authors	:	Ameismeier, M.; Cheng, J.; Berninghausen, O.; Beckmann, R.
Deposited on	:	2018-03-28
Resolution	:	4.00 Å(reported)

The following versions of software and data (see references ⓘ) were used in the production of this report:

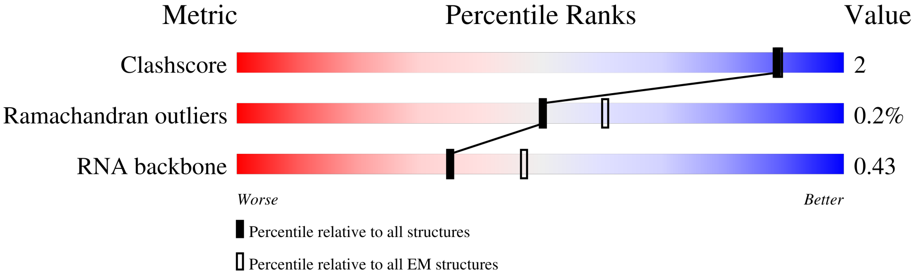
EMDB validation analysis	:	0.0.1.dev43
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.31.2

1 Overall quality at a glance ⓘ

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

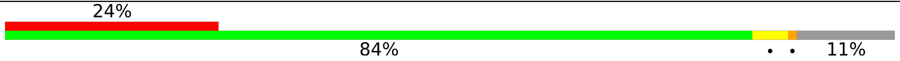
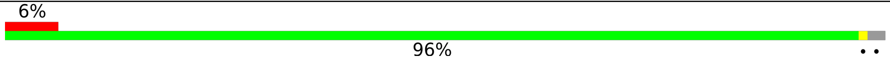
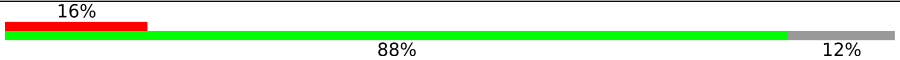
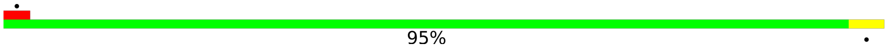
The reported resolution of this entry is 4.00 Å.

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



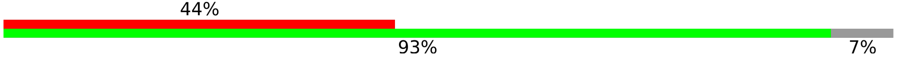
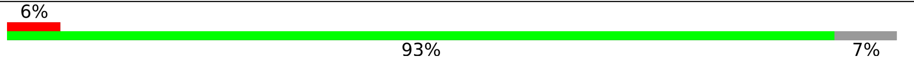
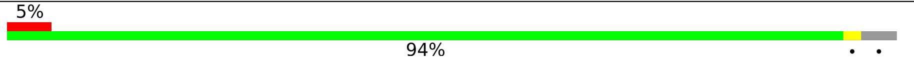
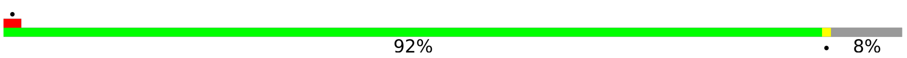
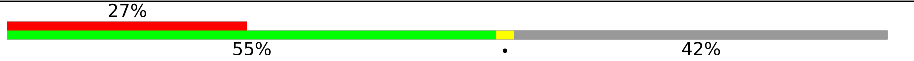
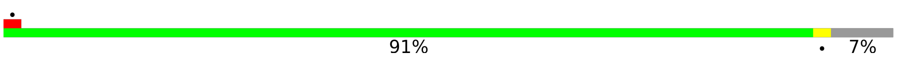
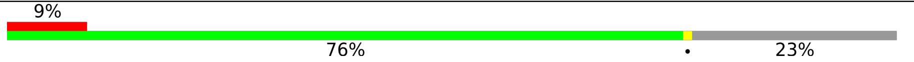
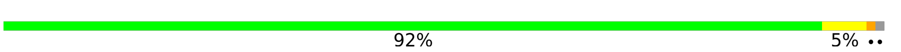
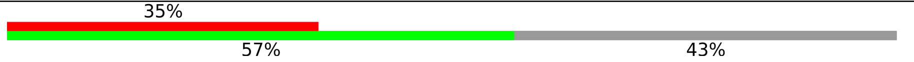
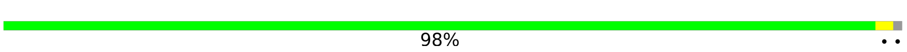
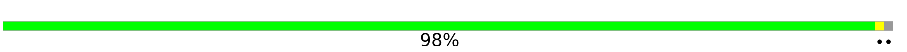
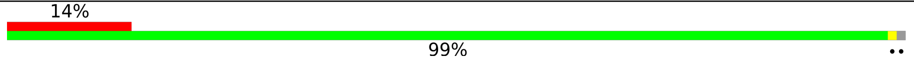
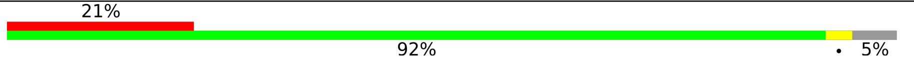
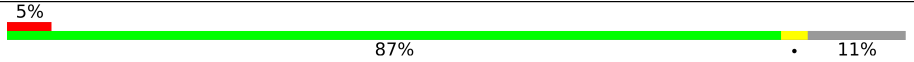
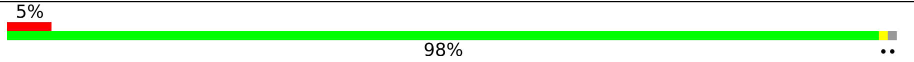
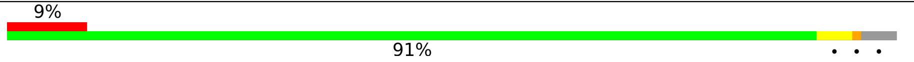
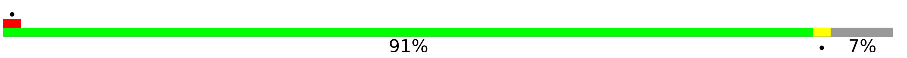
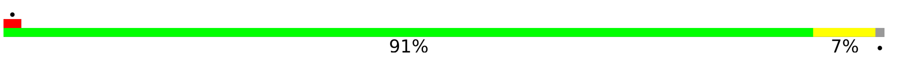
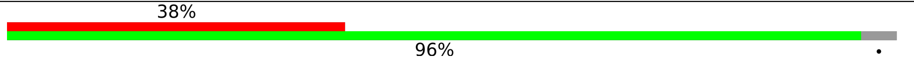
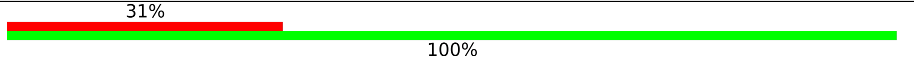
Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
RNA backbone	4643	859

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

Mol	Chain	Length	Quality of chain
1	2	1882	 8% 57% 27% • 14%
2	R	135	 24% 84% • • 11%
3	A	295	 • 72% • 27%
4	b	84	 6% 96% • •
5	B	264	 • 79% • 19%
6	C	293	 • 72% • 26%
7	c	69	 16% 88% 12%
8	E	263	 • 95% •

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
9	e	59	
10	F	204	
11	H	194	
12	G	249	
13	Z	125	
14	Y	133	
15	y	412	
16	x	252	
17	X	143	
18	w	437	
19	W	130	
20	V	83	
21	u	804	
22	t	475	
23	T	145	
24	S	152	
25	Q	146	
26	P	145	
27	O	151	
28	N	151	
29	L	158	
30	J	194	
31	I	208	
32	s	800	
33	k	39	

2 Entry composition ⓘ

There are 33 unique types of molecules in this entry. The entry contains 48967 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 pre-18S ribosomal RNA.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	O	P		
1	2	1613	19353	8065	9676	1612	0	0

- Molecule 2 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	R	120	595	355	120	120	0	0

- Molecule 3 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
3	A	216	1068	636	216	216	0	0

- Molecule 4 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
4	b	82	405	241	82	82	0	0

- Molecule 5 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
5	B	213	1054	628	213	213	0	0

- Molecule 6 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	C	218	1072	636	218	218	0	0

- Molecule 7 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
7	c	61	300	178	61	61	0	0

- Molecule 8 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
8	E	262	1287	763	262	262	0	0

- Molecule 9 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
9	e	55	270	160	55	55	0	0

- Molecule 10 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
10	F	189	935	557	189	189	0	0

- Molecule 11 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
11	H	186	920	548	186	186	0	0

- Molecule 12 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
12	G	230	1135	675	230	230	0	0

- Molecule 13 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
13	Z	72	358	214	72	72	0	0

- Molecule 14 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
14	Y	124	610	362	124	124	0	0

- Molecule 15 is a protein called RNA-binding protein NOB1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
15	y	317	1566	932	317	317	0	0

- Molecule 16 is a protein called RNA-binding protein PNO1.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
16	x	175	865	515	175	175	0	0

- Molecule 17 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
17	X	141	690	408	141	141	0	0

- Molecule 18 is a protein called Bystin.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
18	w	248	1232	736	248	248	0	0

- Molecule 19 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
19	W	129	634	376	129	129	0	0

- Molecule 20 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
20	V	82	403	239	82	82	0	0

- Molecule 21 is a protein called Pre-rRNA-processing protein TSR1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
21	u	628	3106	1850	628	628	0	0

- Molecule 22 is a protein called Protein LTV1 homolog.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
22	t	71	355	213	71	71	0	0

- Molecule 23 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
23	T	144	705	417	144	144	0	0

- Molecule 24 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
24	S	143	704	418	143	143	0	0

- Molecule 25 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
25	Q	139	683	405	139	139	0	0

- Molecule 26 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
26	P	120	590	350	120	120	0	0

- Molecule 27 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
27	O	135	659	389	135	135	0	0

- Molecule 28 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
28	N	149	737	439	149	149	0	0

- Molecule 29 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
29	L	151	744	442	151	151	0	0

- Molecule 30 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
30	J	180	888	528	180	180	0	0

- Molecule 31 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
31	I	205	1009	599	205	205	0	0

- Molecule 32 is a protein called RRP12.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
32	s	768	3840	2304	768	768	0	0

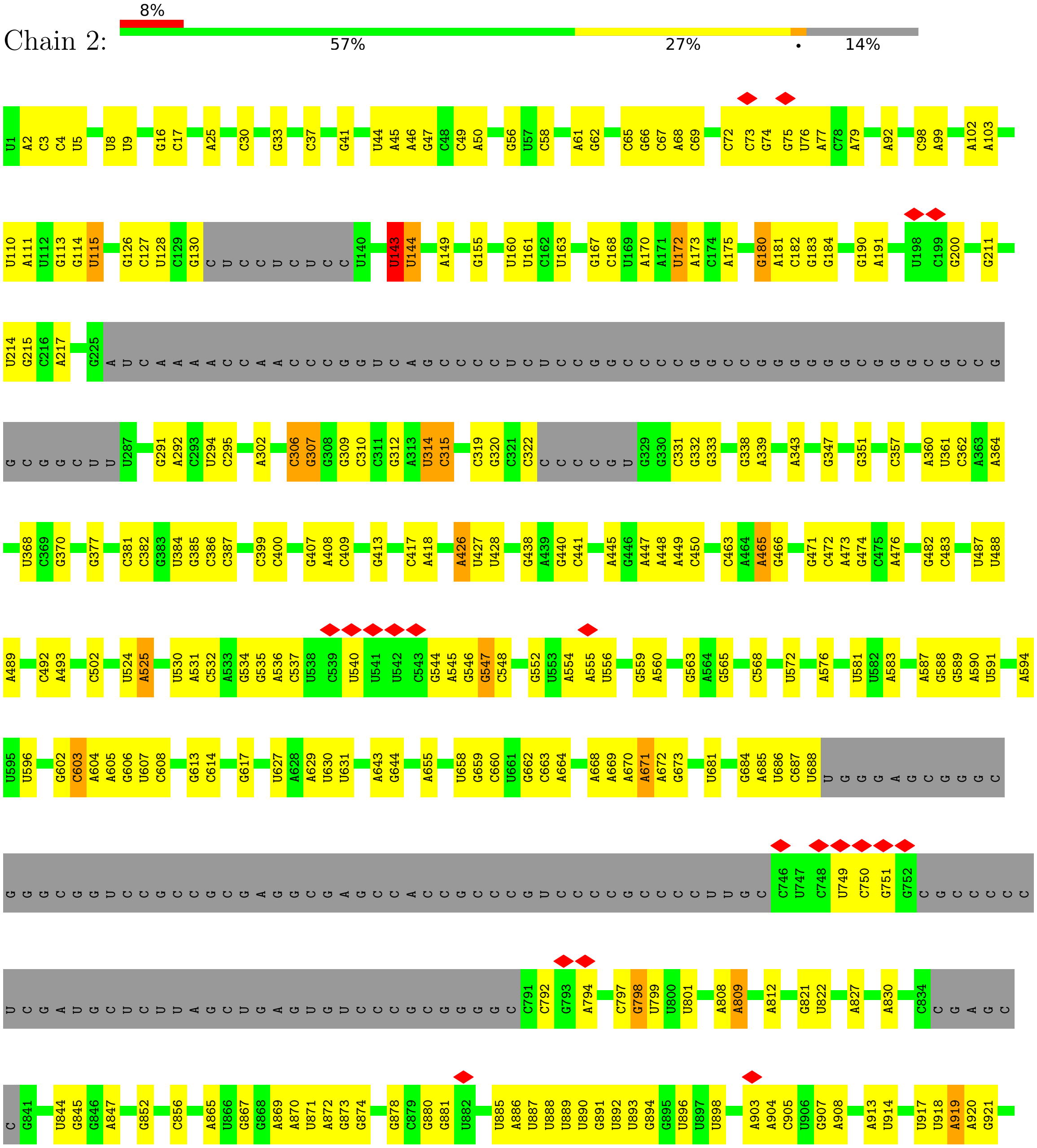
- Molecule 33 is a protein called Unknown.

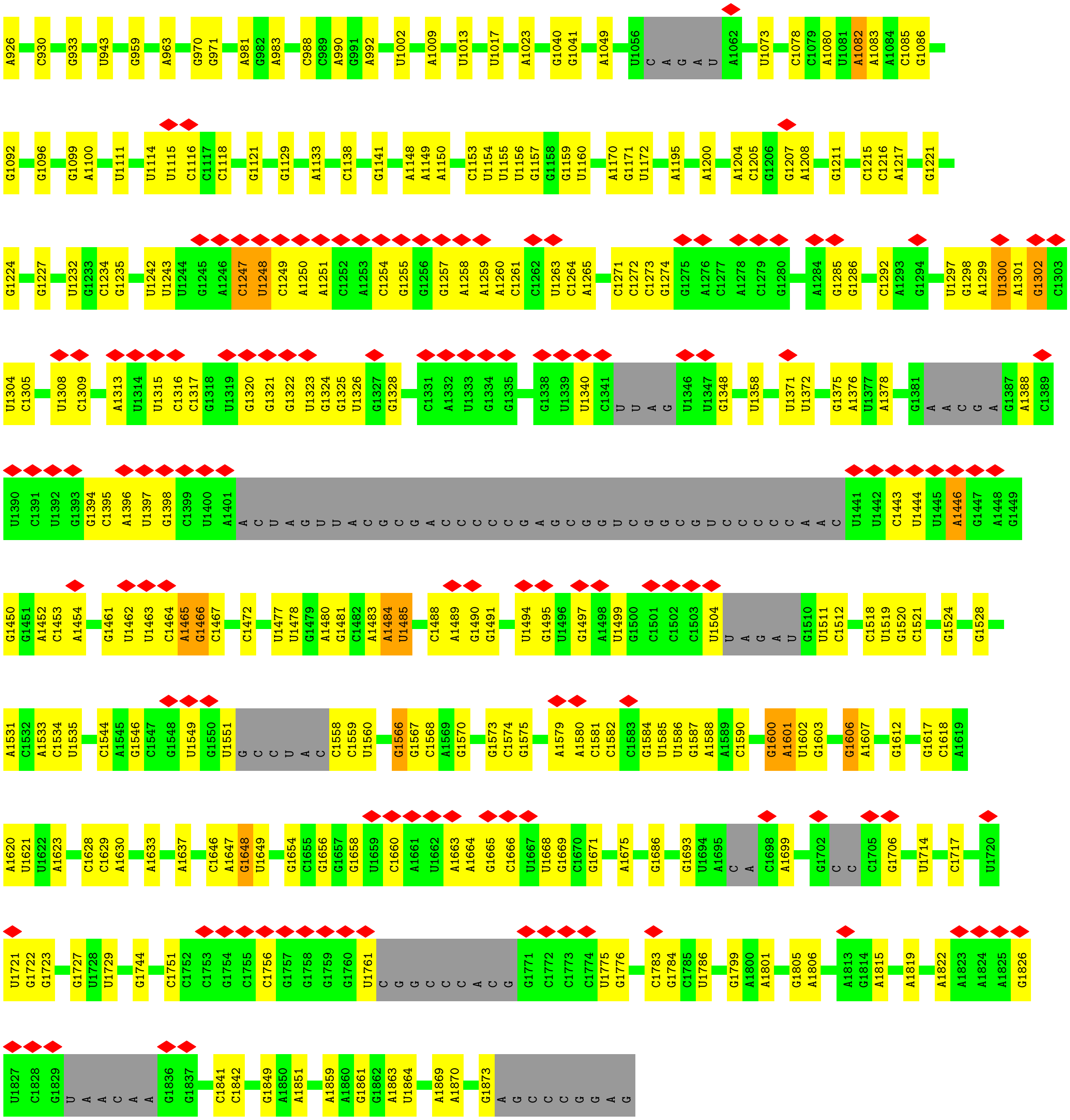
Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
33	k	39	195	117	39	39	0	0

3 Residue-property plots ⓘ

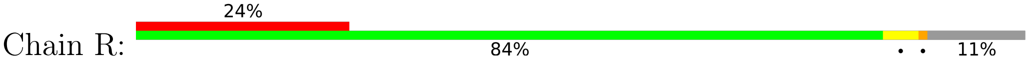
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

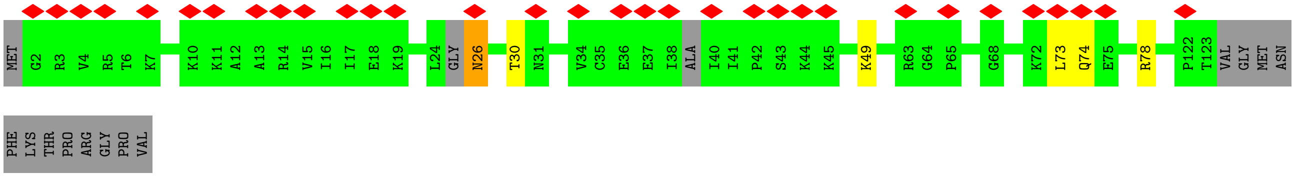
- Molecule 1: pre-18S ribosomal RNA



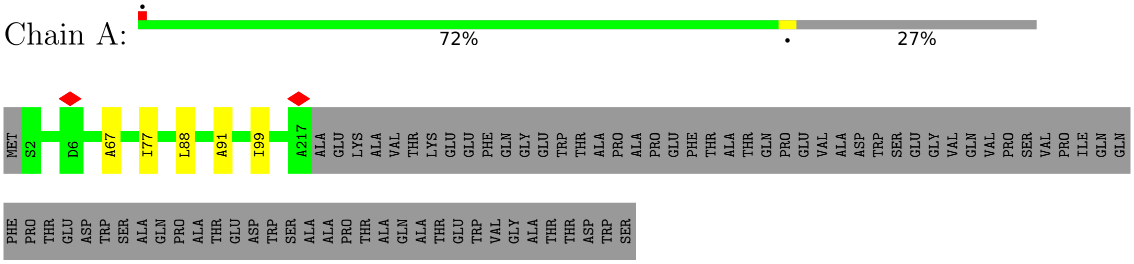


- Molecule 2: 40S ribosomal protein S17

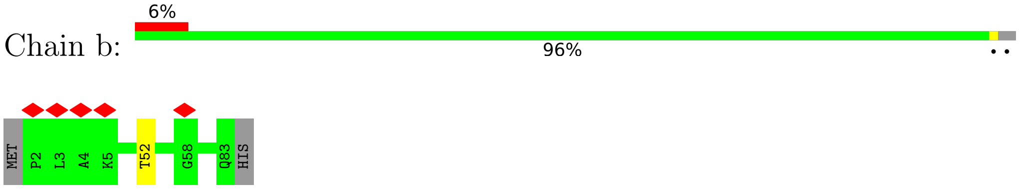




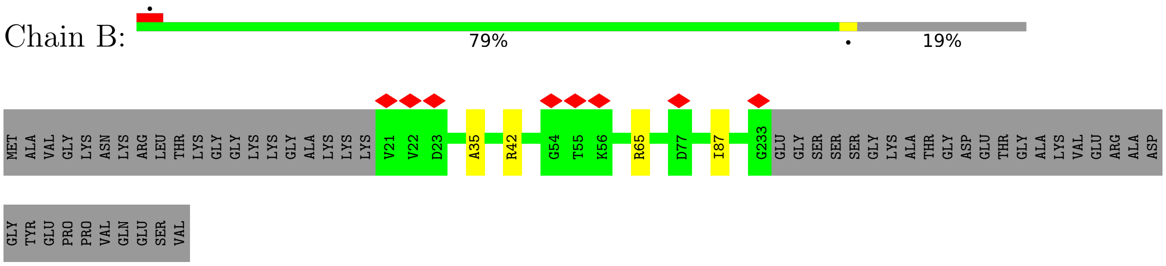
- Molecule 3: 40S ribosomal protein SA



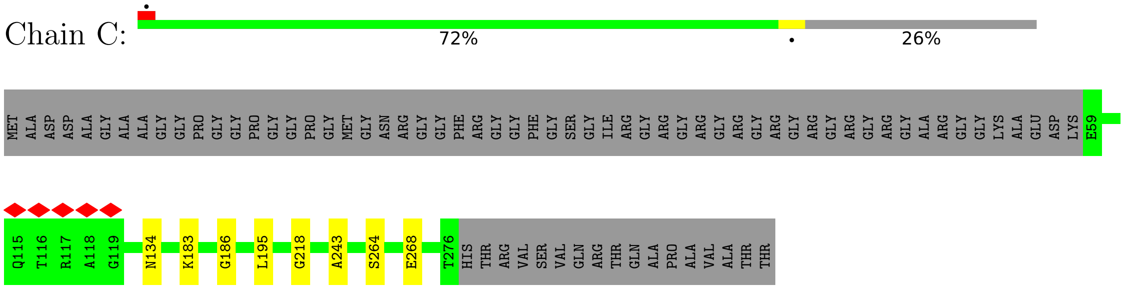
- Molecule 4: 40S ribosomal protein S27



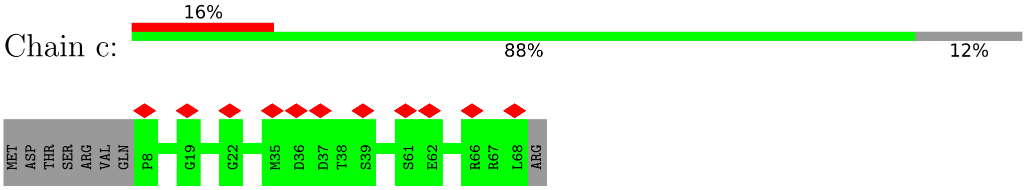
- Molecule 5: 40S ribosomal protein S3a



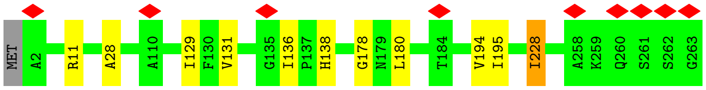
- Molecule 6: 40S ribosomal protein S2



- Molecule 7: 40S ribosomal protein S28

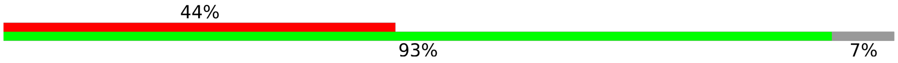


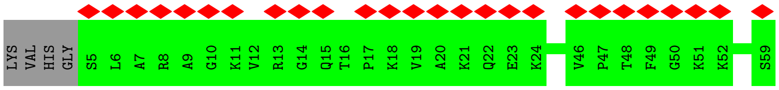
- Molecule 8: 40S ribosomal protein S4, X isoform



- Molecule 9: 40S ribosomal protein S30

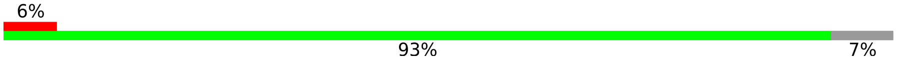
Chain e:

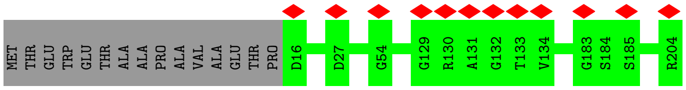




- Molecule 10: 40S ribosomal protein S5

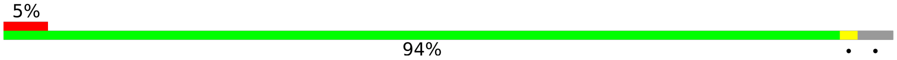
Chain F:

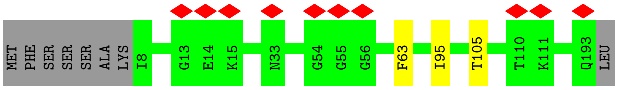




- Molecule 11: 40S ribosomal protein S7

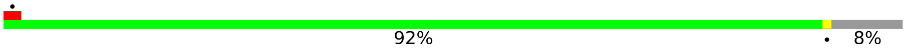
Chain H:

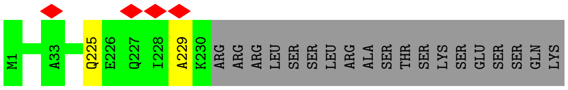




- Molecule 12: 40S ribosomal protein S6

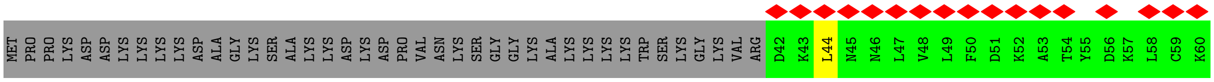
Chain G:

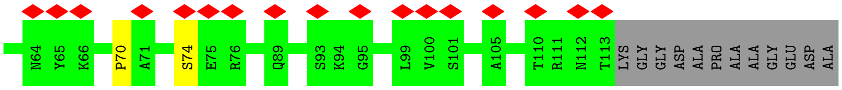




- Molecule 13: 40S ribosomal protein S25

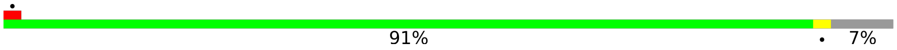
Chain Z:

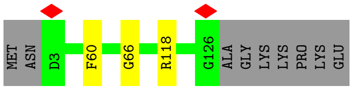




- Molecule 14: 40S ribosomal protein S24

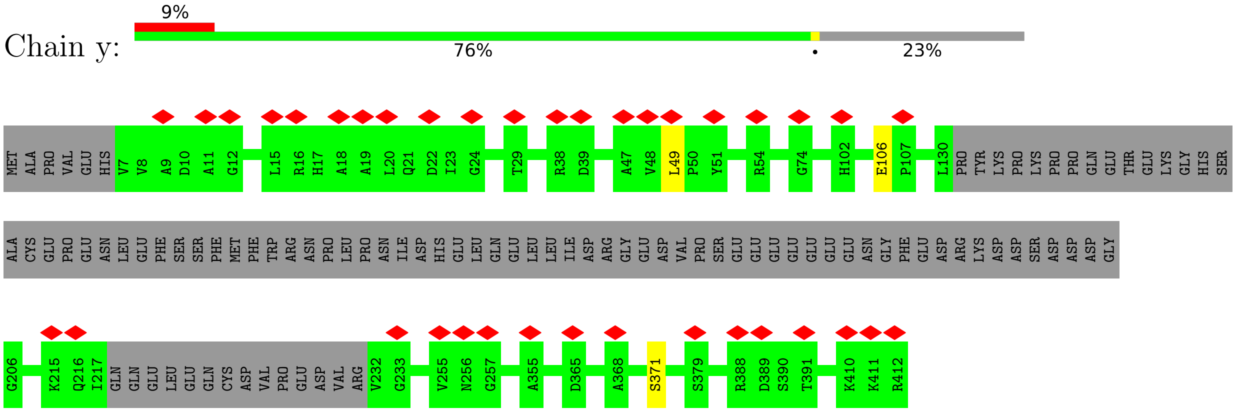
Chain Y:





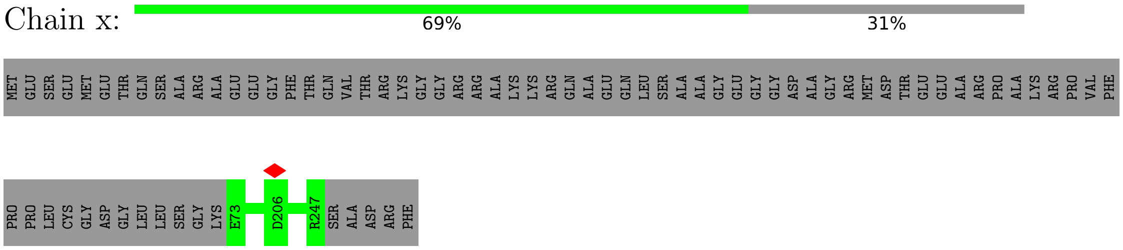
- Molecule 15: RNA-binding protein NOB1

Chain y:



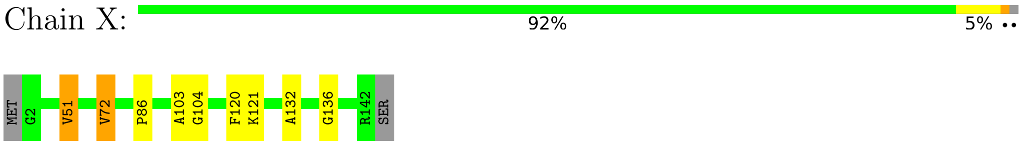
- Molecule 16: RNA-binding protein PNO1

Chain x:



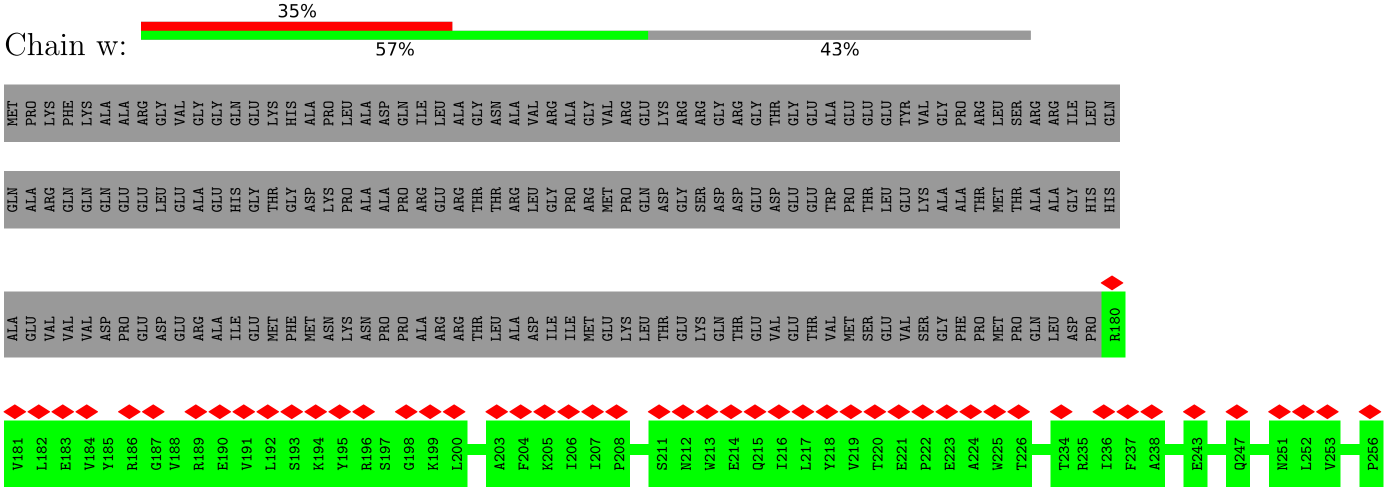
- Molecule 17: 40S ribosomal protein S23

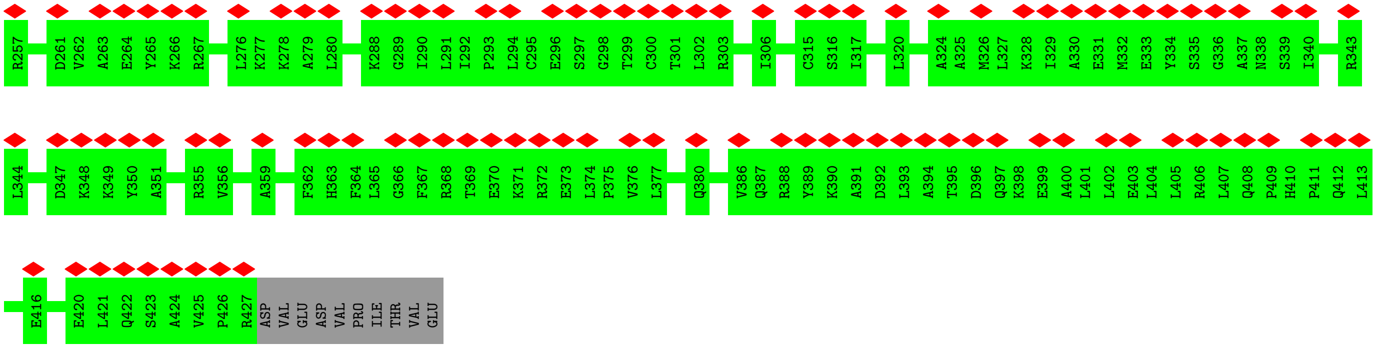
Chain X:



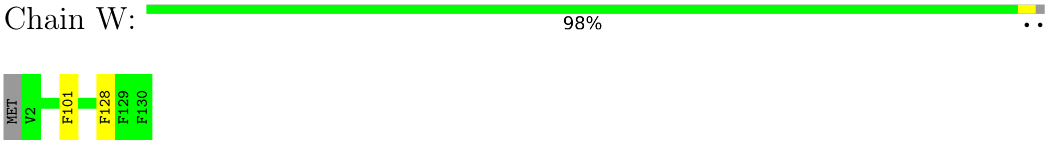
- Molecule 18: Bystin

Chain w:

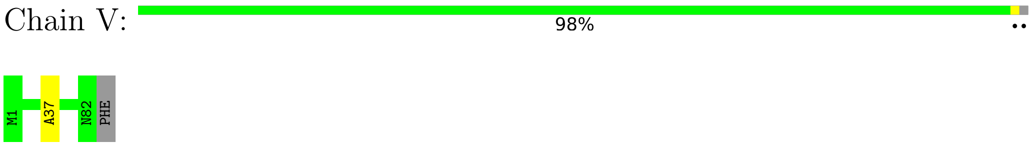




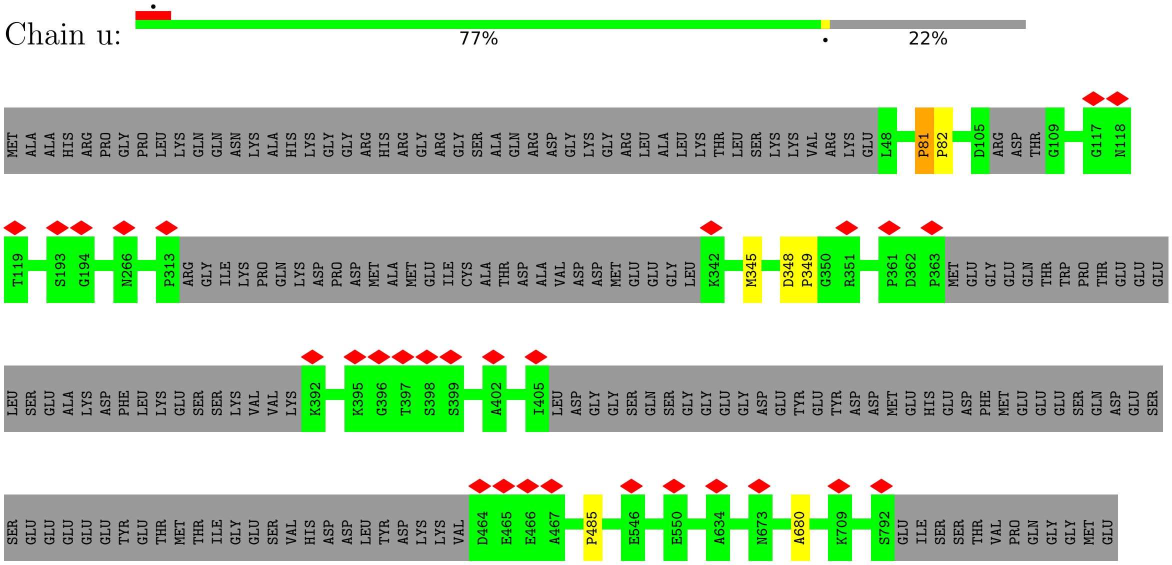
- Molecule 19: 40S ribosomal protein S15a



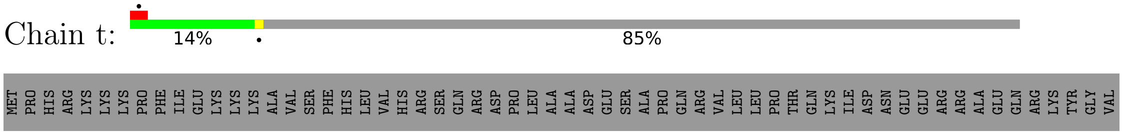
- Molecule 20: 40S ribosomal protein S21

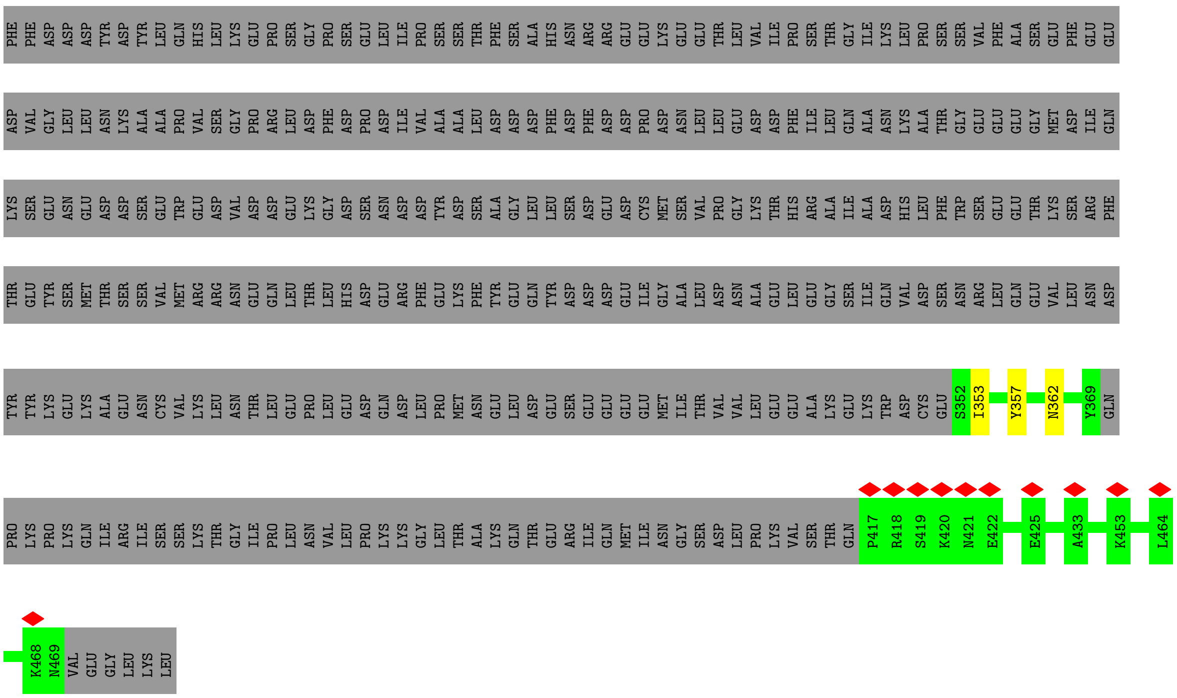


- Molecule 21: Pre-rRNA-processing protein TSR1 homolog



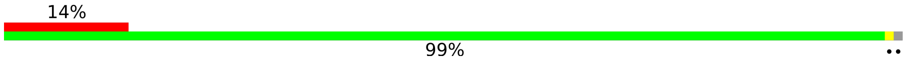
- Molecule 22: Protein LTV1 homolog

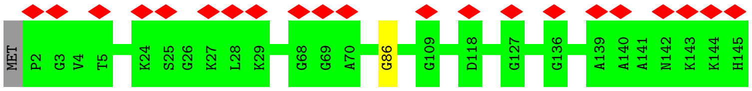




- Molecule 23: 40S ribosomal protein S19

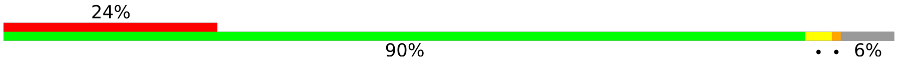
Chain T:

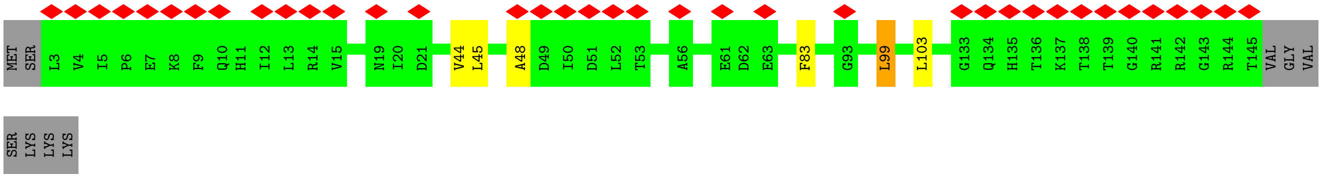




- Molecule 24: 40S ribosomal protein S18

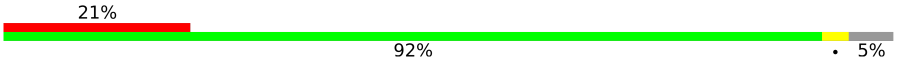
Chain S:

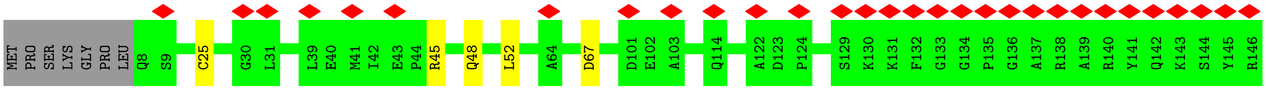




- Molecule 25: 40S ribosomal protein S16

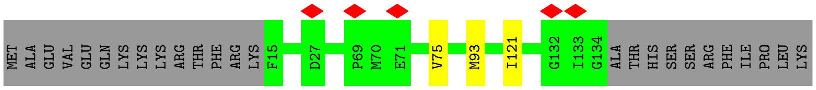
Chain Q:





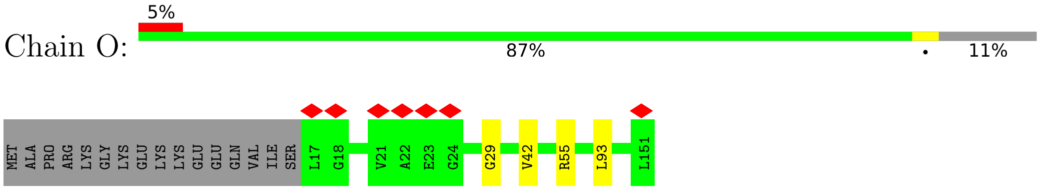
- Molecule 26: 40S ribosomal protein S15

Chain P:



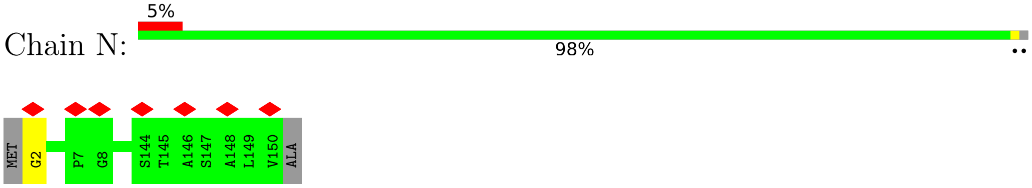
- Molecule 27: 40S ribosomal protein S14

Chain O:



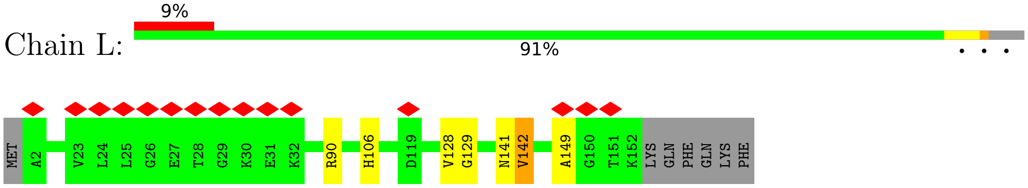
- Molecule 28: 40S ribosomal protein S13

Chain N:



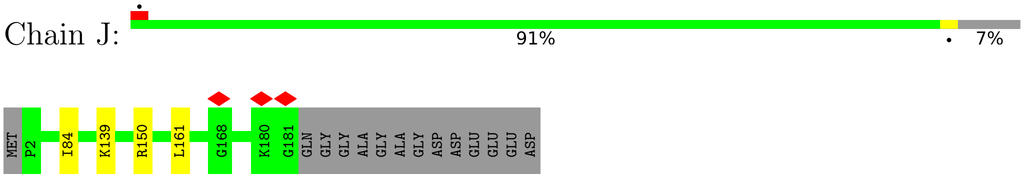
- Molecule 29: 40S ribosomal protein S11

Chain L:



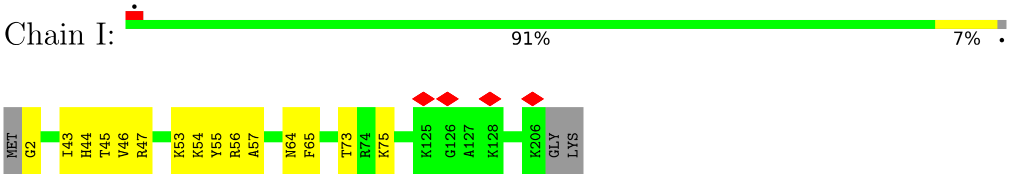
- Molecule 30: 40S ribosomal protein S9

Chain J:



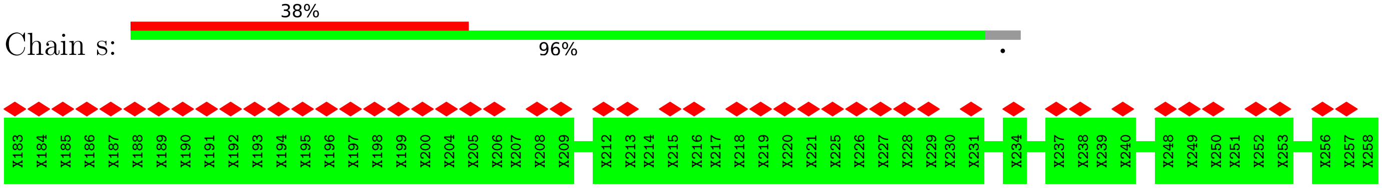
- Molecule 31: 40S ribosomal protein S8

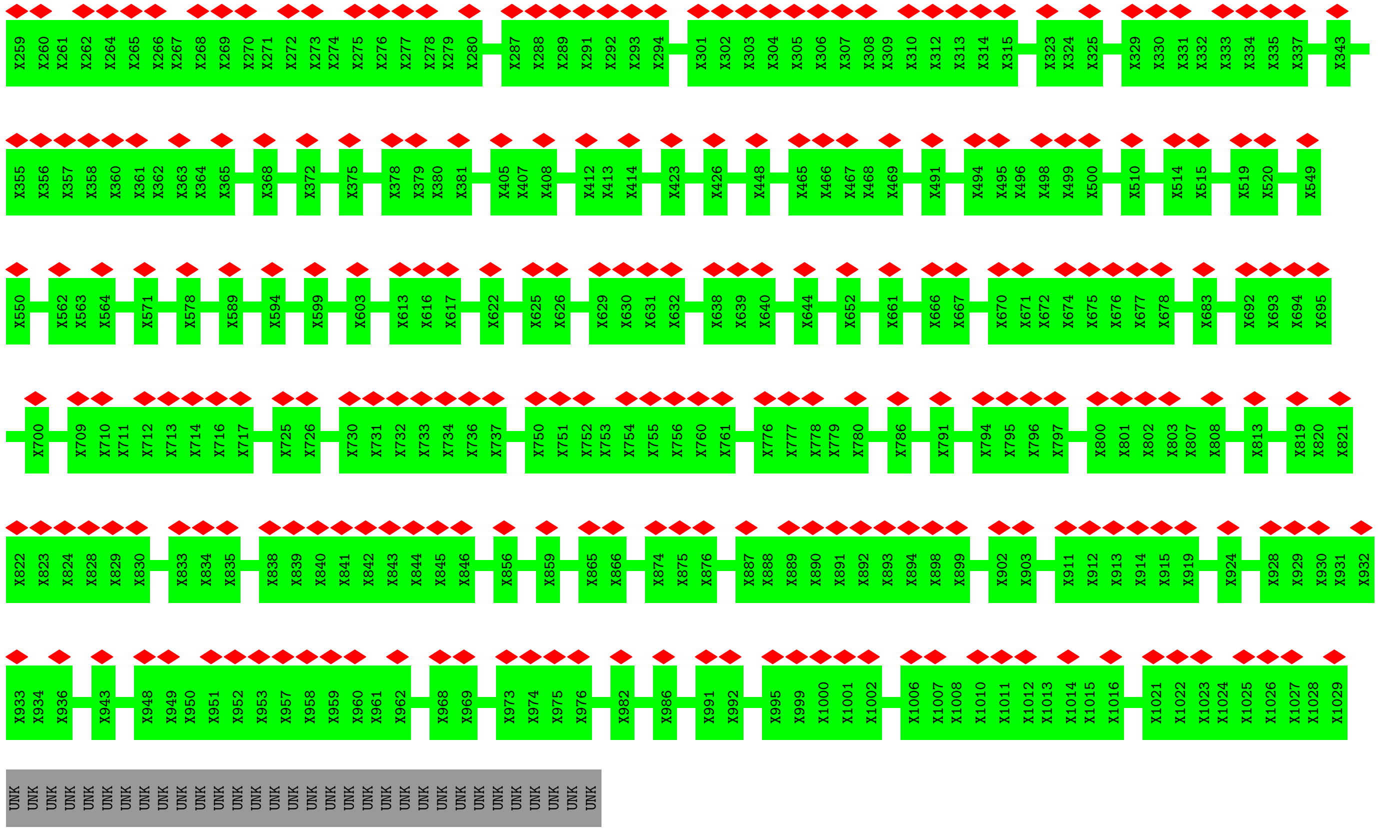
Chain I:



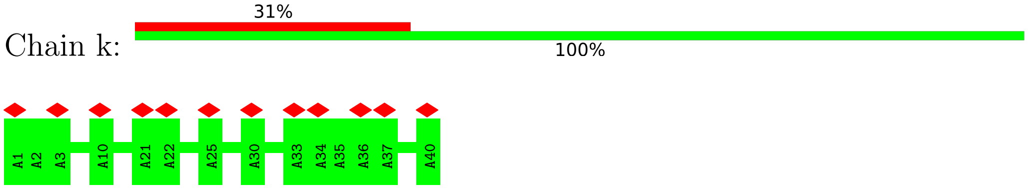
- Molecule 32: RRP12

Chain s:





- Molecule 33: Unknown



4 Experimental information ⓘ

Property	**Value**	**Source**
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	73661	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 ($e^-/\text{Å}^2$)	2.5	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.203	Depositor
Minimum map value	-0.075	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	390.24, 390.24, 390.24	wwPDB
Map dimensions	360, 360, 360	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.084, 1.084, 1.084	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\| > 5$	RMSZ	$\#\|Z\| > 5$
1	2	0.42	0/20941	0.87	22/32156 (0.1%)
2	R	0.29	0/592	0.61	0/821
3	A	0.38	0/1067	0.56	0/1485
4	b	0.37	0/404	0.64	0/561
5	B	0.33	0/1053	0.60	0/1466
6	C	0.37	0/1071	0.58	0/1487
7	c	0.31	0/299	0.67	0/414
8	E	0.36	0/1286	0.61	0/1785
9	e	0.31	0/269	0.60	0/372
10	F	0.28	0/934	0.51	0/1300
11	H	0.31	0/919	0.55	0/1279
12	G	0.34	0/1134	0.55	0/1577
13	Z	0.31	0/357	0.58	0/497
14	Y	0.35	0/609	0.61	0/845
15	y	0.33	0/1563	0.61	0/2172
16	x	0.33	0/864	0.59	0/1202
17	X	0.36	0/689	0.68	0/954
18	w	0.28	0/1231	0.53	0/1717
19	W	0.44	0/633	0.61	0/878
20	V	0.44	0/402	0.55	0/557
21	u	0.34	0/3101	0.60	0/4313
22	t	0.29	0/353	0.52	0/491
23	T	0.30	0/704	0.50	0/975
24	S	0.30	0/703	0.53	0/976
25	Q	0.29	0/682	0.58	0/946
26	P	0.35	0/589	0.52	0/817
27	O	0.34	0/658	0.58	0/910
28	N	0.37	0/736	0.50	0/1024
29	L	0.37	0/743	0.61	0/1032
30	J	0.34	0/887	0.57	0/1233
31	I	0.33	0/1008	0.57	0/1400
33	k	0.65	0/193	0.87	0/267
All	All	0.38	0/46674	0.74	22/67909 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	R	0	2
4	b	0	1
8	E	0	2
14	Y	0	1
15	y	0	3
17	X	0	1
21	u	0	4
24	S	0	1
26	P	0	1
30	J	0	1
All	All	0	17

There are no bond length outliers.

The worst 5 of 22 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	2	1316	C	P-O3'-C3'	7.25	128.40	119.70
1	2	547	G	P-O3'-C3'	7.10	128.22	119.70
1	2	1494	U	P-O3'-C3'	6.62	127.64	119.70
1	2	1534	C	P-O3'-C3'	6.59	127.61	119.70
1	2	1566	G	O5'-P-OP1	6.57	118.58	110.70

There are no chirality outliers.

5 of 17 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
8	E	228	ILE	Mainchain,Peptide
2	R	26	ASN	Peptide
2	R	73	LEU	Peptide
14	Y	118	ARG	Peptide
4	b	52	THR	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	2	19353	0	9704	34	0
2	R	595	0	249	3	0
3	A	1068	0	503	3	0
4	b	405	0	172	0	0
5	B	1054	0	455	2	0
6	C	1072	0	489	4	0
7	c	300	0	131	0	0
8	E	1287	0	577	6	0
9	e	270	0	126	0	0
10	F	935	0	442	0	0
11	H	920	0	399	2	0
12	G	1135	0	512	2	0
13	Z	358	0	161	2	0
14	Y	610	0	271	2	0
15	y	1566	0	693	0	0
16	x	865	0	394	0	0
17	X	690	0	330	5	0
18	w	1232	0	562	0	0
19	W	634	0	283	2	0
20	V	403	0	199	1	0
21	u	3106	0	1357	0	0
22	t	355	0	151	0	0
23	T	705	0	343	1	0
24	S	704	0	317	4	0
25	Q	683	0	320	3	0
26	P	590	0	251	1	0
27	O	659	0	321	2	0
28	N	737	0	330	1	0
29	L	744	0	321	5	0
30	J	888	0	389	1	0
31	I	1009	0	451	8	0
32	s	3840	0	848	0	0
33	k	195	0	196	0	0
All	All	48967	0	22247	83	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 2.

The worst 5 of 83 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)
8:E:131:VAL:HA	8:E:136:ILE:O	1.28	1.26
19:W:101:PHE:O	19:W:128:PHE:HA	1.49	1.09
8:E:129:ILE:HA	8:E:138:HIS:O	1.59	1.02
8:E:131:VAL:CA	8:E:136:ILE:O	2.22	0.80
5:B:65:ARG:O	5:B:87:ILE:HA	1.92	0.69

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	
2	R	114/135 (84%)	98 (86%)	16 (14%)	0	100	100
3	A	214/295 (72%)	197 (92%)	17 (8%)	0	100	100
4	b	80/84 (95%)	72 (90%)	8 (10%)	0	100	100
5	B	211/264 (80%)	196 (93%)	15 (7%)	0	100	100
6	C	216/293 (74%)	203 (94%)	13 (6%)	0	100	100
7	c	59/69 (86%)	53 (90%)	6 (10%)	0	100	100
8	E	260/263 (99%)	235 (90%)	24 (9%)	1 (0%)	34	71
9	e	53/59 (90%)	41 (77%)	12 (23%)	0	100	100
10	F	187/204 (92%)	173 (92%)	14 (8%)	0	100	100
11	H	184/194 (95%)	172 (94%)	12 (6%)	0	100	100
12	G	228/249 (92%)	210 (92%)	18 (8%)	0	100	100
13	Z	70/125 (56%)	63 (90%)	7 (10%)	0	100	100
14	Y	122/133 (92%)	111 (91%)	11 (9%)	0	100	100
15	y	311/412 (76%)	271 (87%)	40 (13%)	0	100	100
16	x	173/252 (69%)	165 (95%)	8 (5%)	0	100	100
17	X	139/143 (97%)	129 (93%)	8 (6%)	2 (1%)	11	46

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
18	w	246/437 (56%)	226 (92%)	20 (8%)	0	100	100
19	W	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
20	V	80/83 (96%)	73 (91%)	7 (9%)	0	100	100
21	u	618/804 (77%)	550 (89%)	64 (10%)	4 (1%)	25	63
22	t	67/475 (14%)	58 (87%)	6 (9%)	3 (4%)	2	24
23	T	142/145 (98%)	136 (96%)	6 (4%)	0	100	100
24	S	141/152 (93%)	131 (93%)	10 (7%)	0	100	100
25	Q	137/146 (94%)	119 (87%)	18 (13%)	0	100	100
26	P	118/145 (81%)	111 (94%)	7 (6%)	0	100	100
27	O	133/151 (88%)	120 (90%)	13 (10%)	0	100	100
28	N	147/151 (97%)	138 (94%)	9 (6%)	0	100	100
29	L	149/158 (94%)	138 (93%)	10 (7%)	1 (1%)	22	61
30	J	178/194 (92%)	163 (92%)	14 (8%)	1 (1%)	25	63
31	I	203/208 (98%)	184 (91%)	19 (9%)	0	100	100
33	k	35/39 (90%)	35 (100%)	0	0	100	100
All	All	5142/6592 (78%)	4688 (91%)	442 (9%)	12 (0%)	50	79

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
21	u	81	PRO
22	t	353	ILE
30	J	161	LEU
21	u	82	PRO
21	u	485	PRO

5.3.2 Protein sidechains ⓘ

There are no protein residues with a non-rotameric sidechain to report in this entry.

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2	1588/1882 (84%)	503 (31%)	0

5 of 503 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2	2	A
1	2	3	C
1	2	4	C
1	2	5	U
1	2	8	U

There are no RNA pucker outliers to report.

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

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

There are no ligands in this entry.

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
32	s	39
1	2	8
33	k	1

The worst 5 of 48 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	s	915:UNK	C	919:UNK	N	17.96
1	s	688:UNK	C	692:UNK	N	17.29

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	s	358:UNK	C	360:UNK	N	16.52
1	s	803:UNK	C	807:UNK	N	16.48
1	s	381:UNK	C	383:UNK	N	15.07

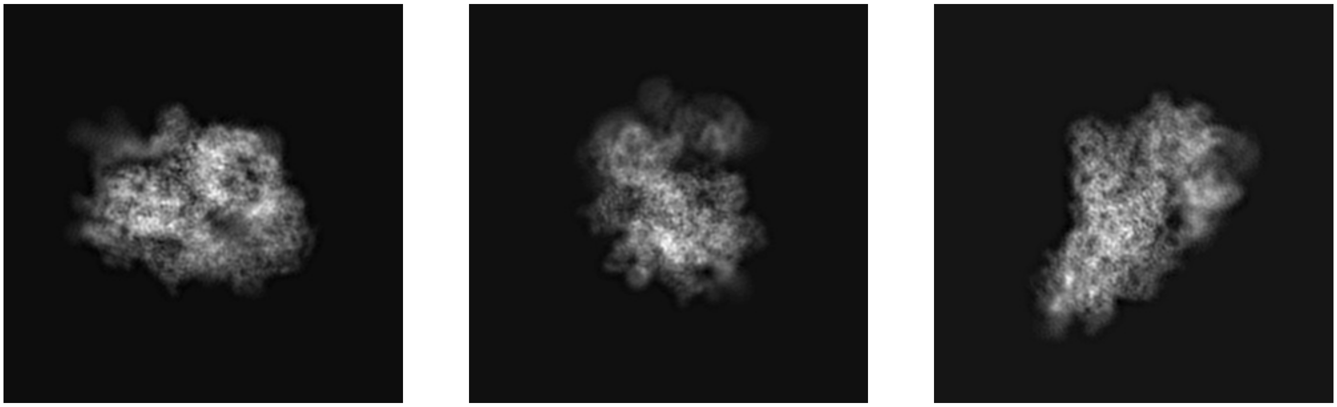
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-4348. 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

6.1.1 Primary map

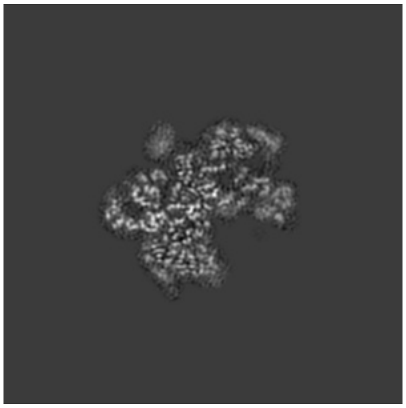


X Y Z

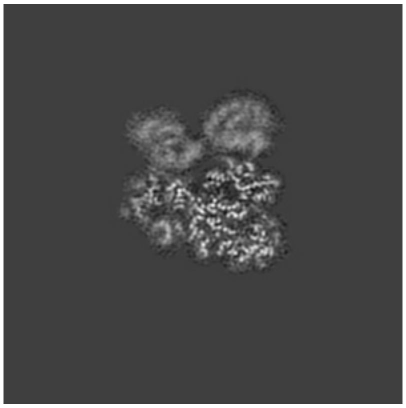
The images above show the map projected in three orthogonal directions.

6.2 Central slices

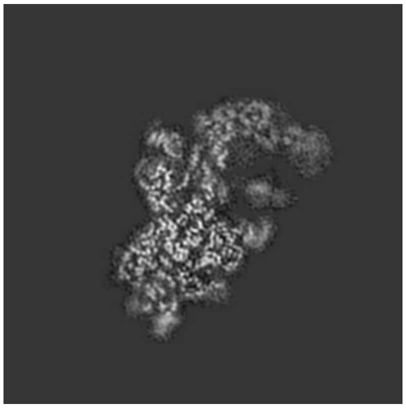
6.2.1 Primary map



X Index: 180



Y Index: 180

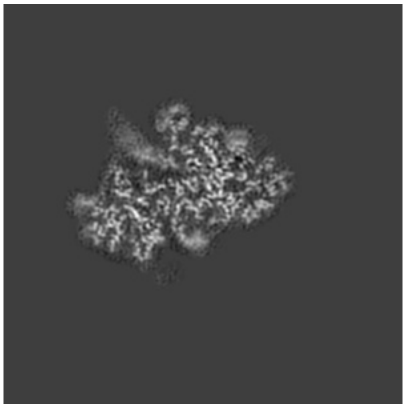


Z Index: 180

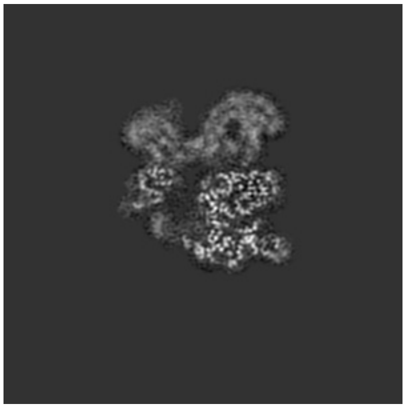
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices ⓘ

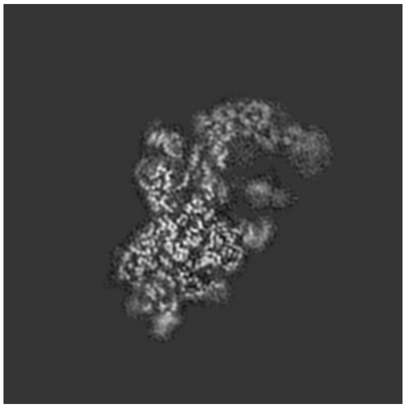
6.3.1 Primary map



X Index: 146



Y Index: 189

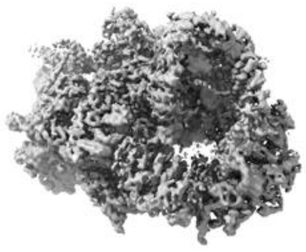


Z Index: 180

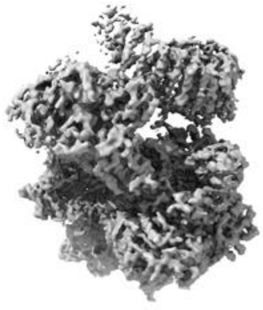
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal surface views ⓘ

6.4.1 Primary map



X



Y

Z

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.

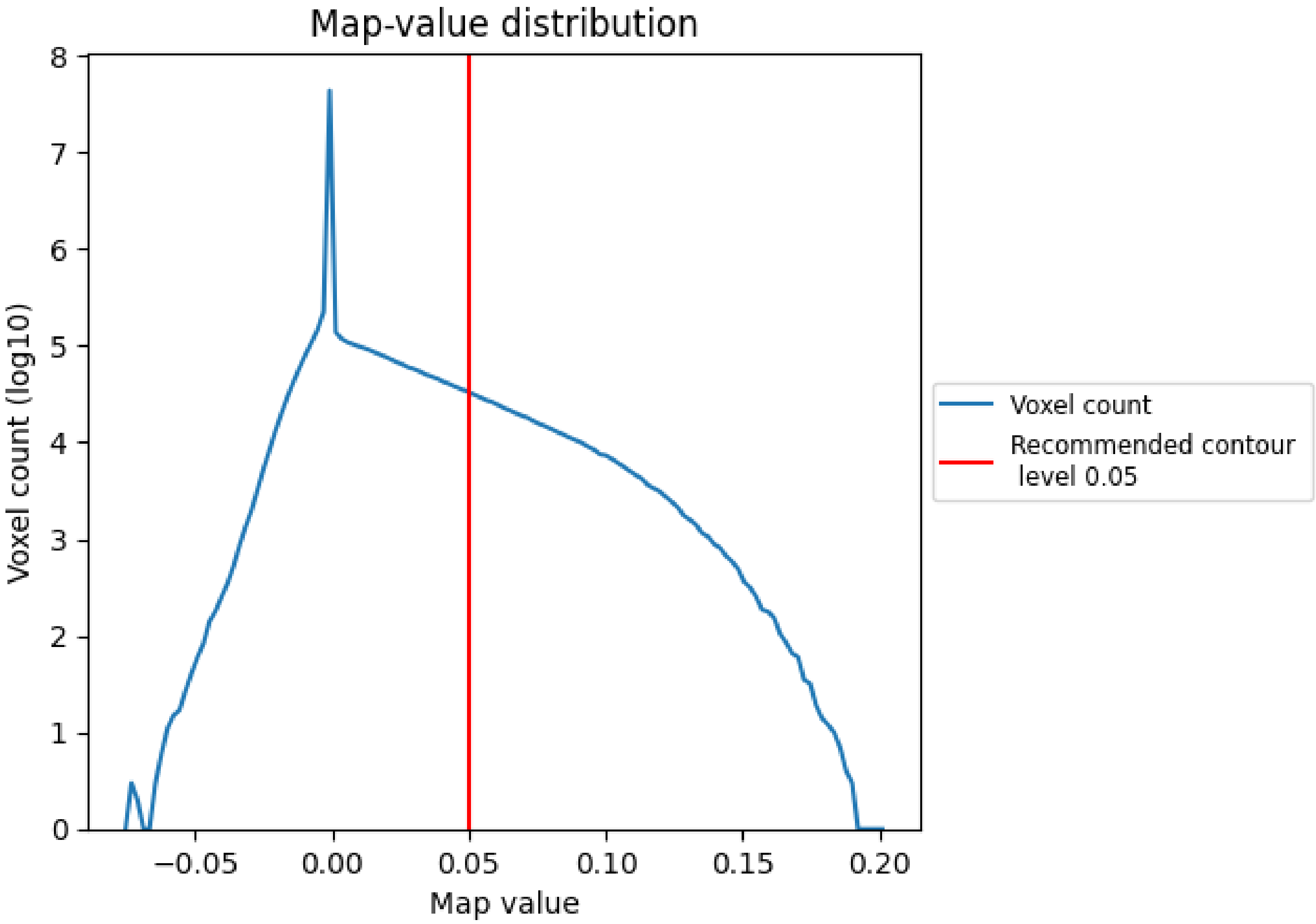
6.5 Mask visualisation ⓘ

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

7 Map analysis ⓘ

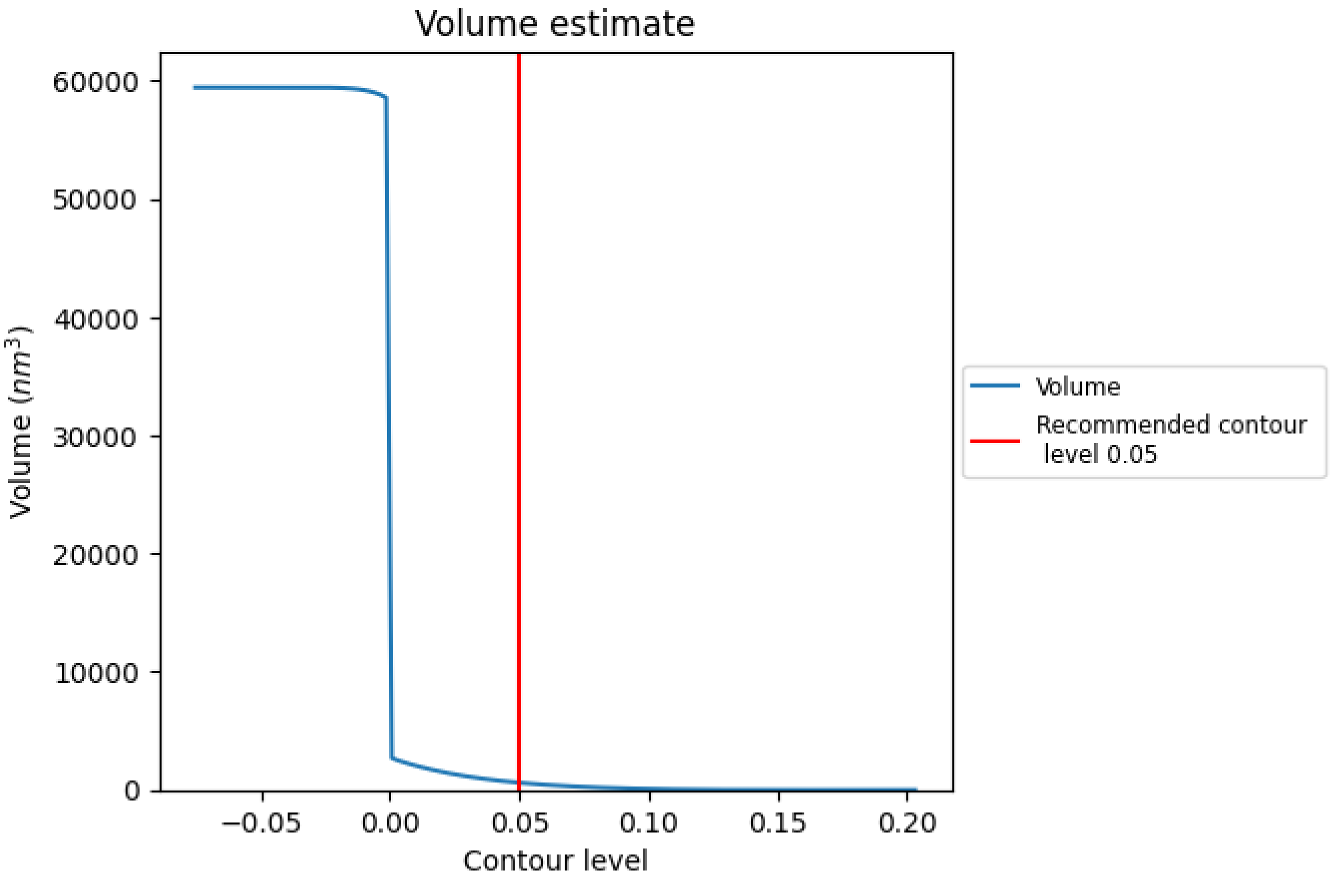
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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

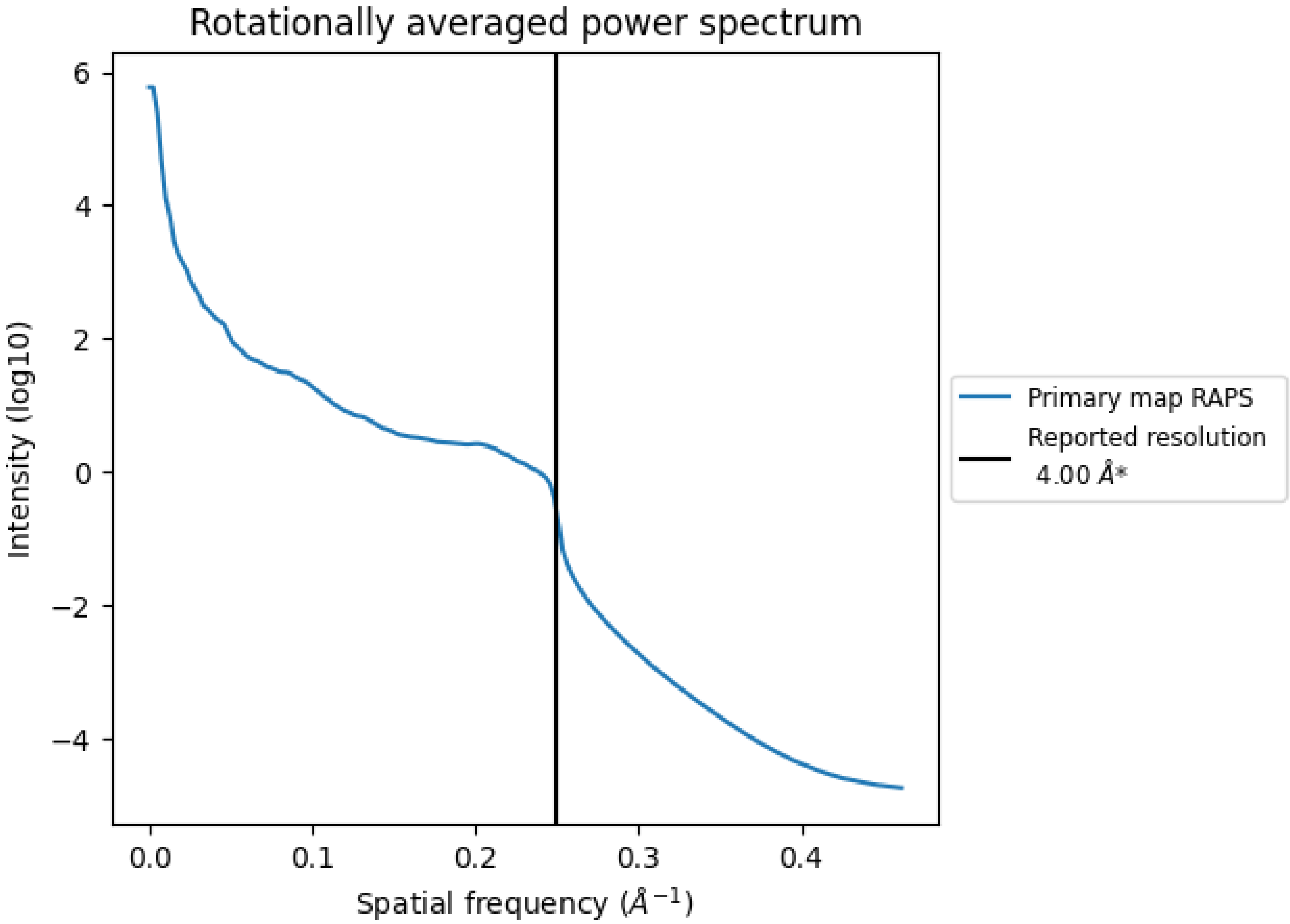
7.2 Volume estimate ⓘ



The volume at the recommended contour level is 611 nm^3; this corresponds to an approximate mass of 552 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 ⓘ

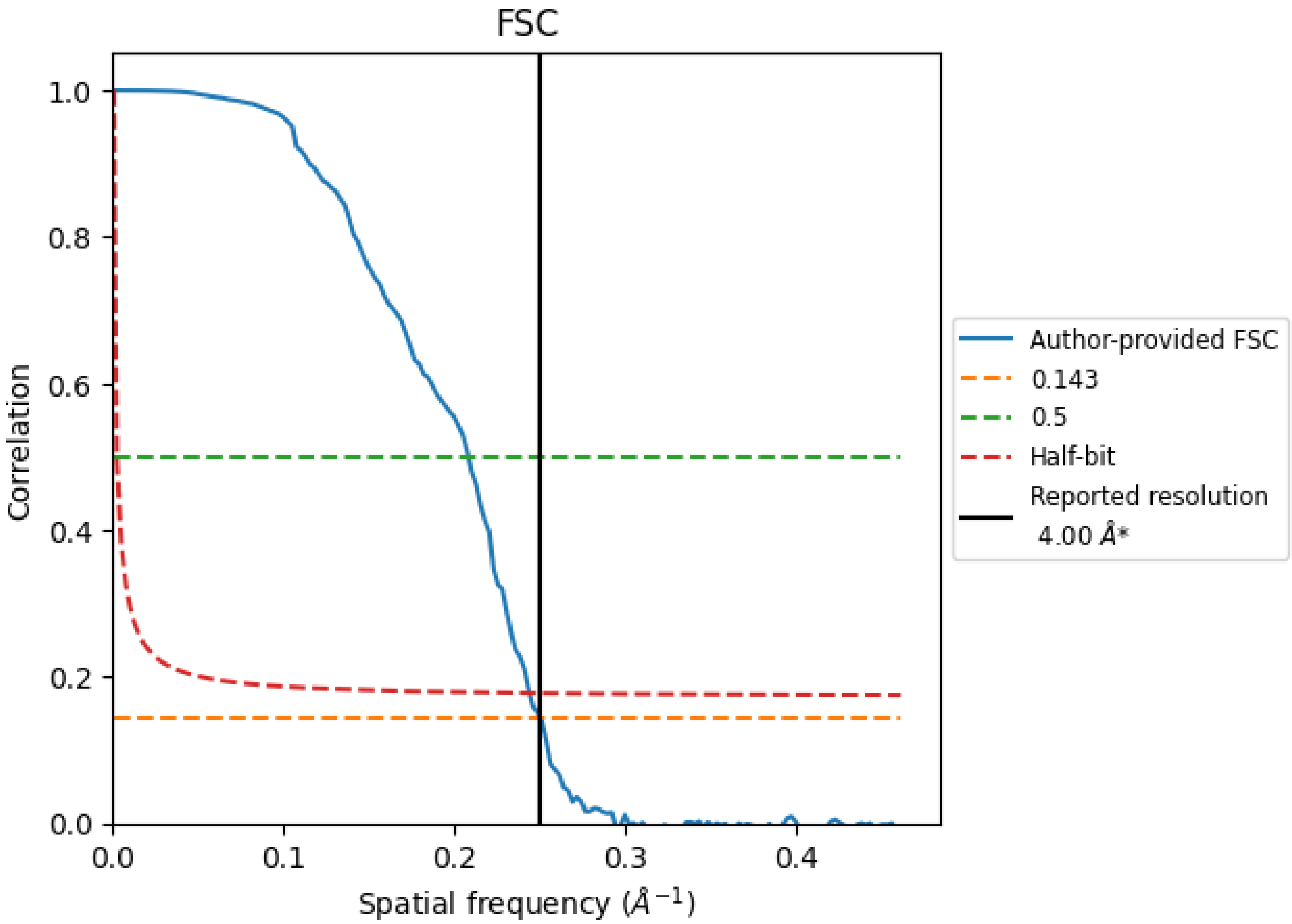


*Reported resolution corresponds to spatial frequency of 0.250 $\AA^{-1}$

8 Fourier-Shell correlation ⓘ

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

8.1 FSC ⓘ



*Reported resolution corresponds to spatial frequency of 0.250 Å^{-1}

8.2 Resolution estimates ⓘ

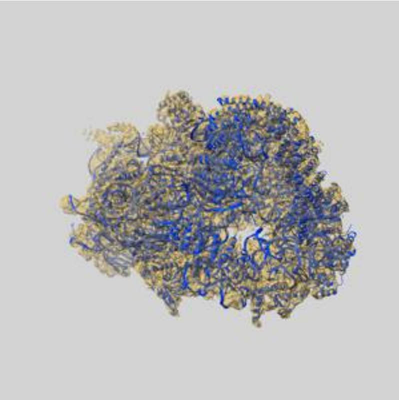
Resolution estimate (Å)	**Estimation criterion (FSC cut-off)**		
	0.143	0.5	Half-bit
Reported by author	4.00	-	-
Author-provided FSC curve	4.00	4.80	4.10
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

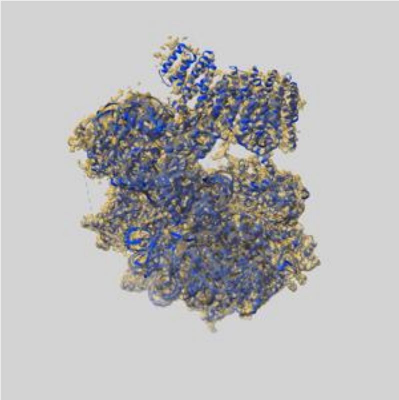
9 Map-model fit ⓘ

This section contains information regarding the fit between EMDB map EMD-4348 and PDB model 6G4S. Per-residue inclusion information can be found in section 3 on page 9.

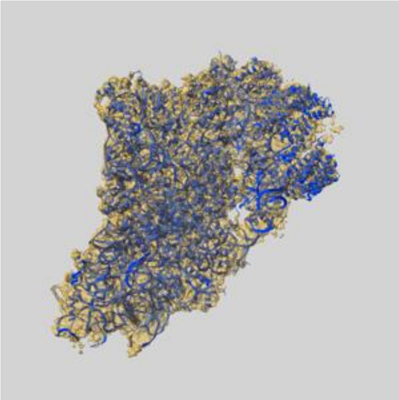
9.1 Map-model overlay ⓘ



X



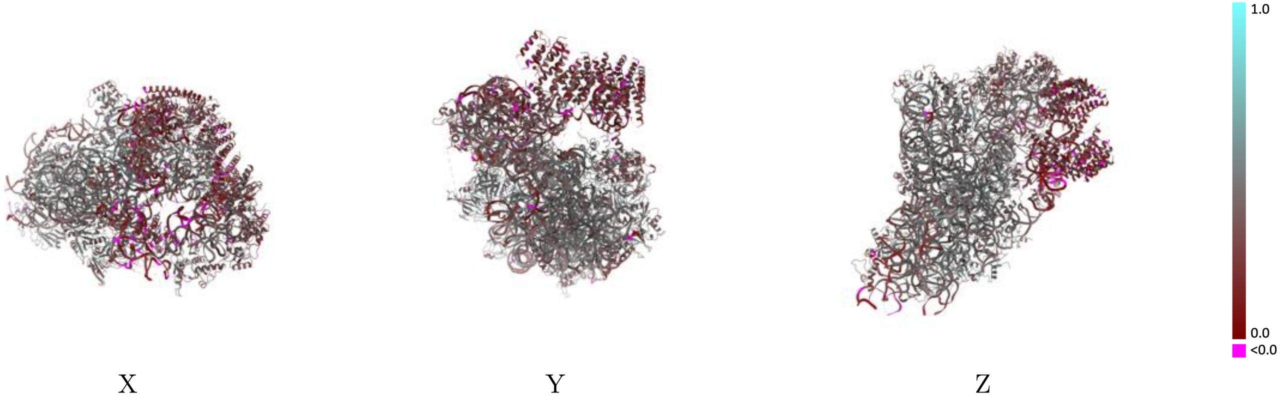
Y



Z

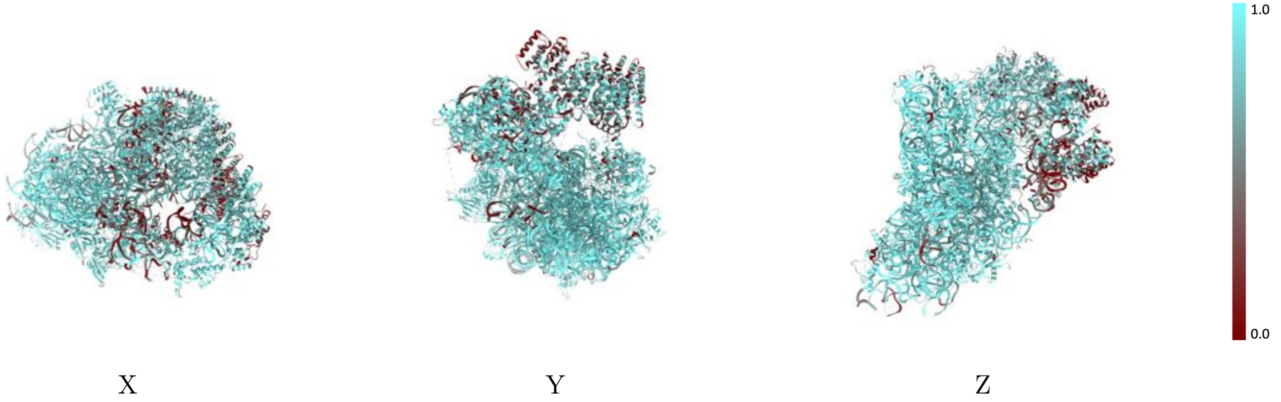
The images above show the 3D surface view of the map at the recommended contour level 0.05 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model



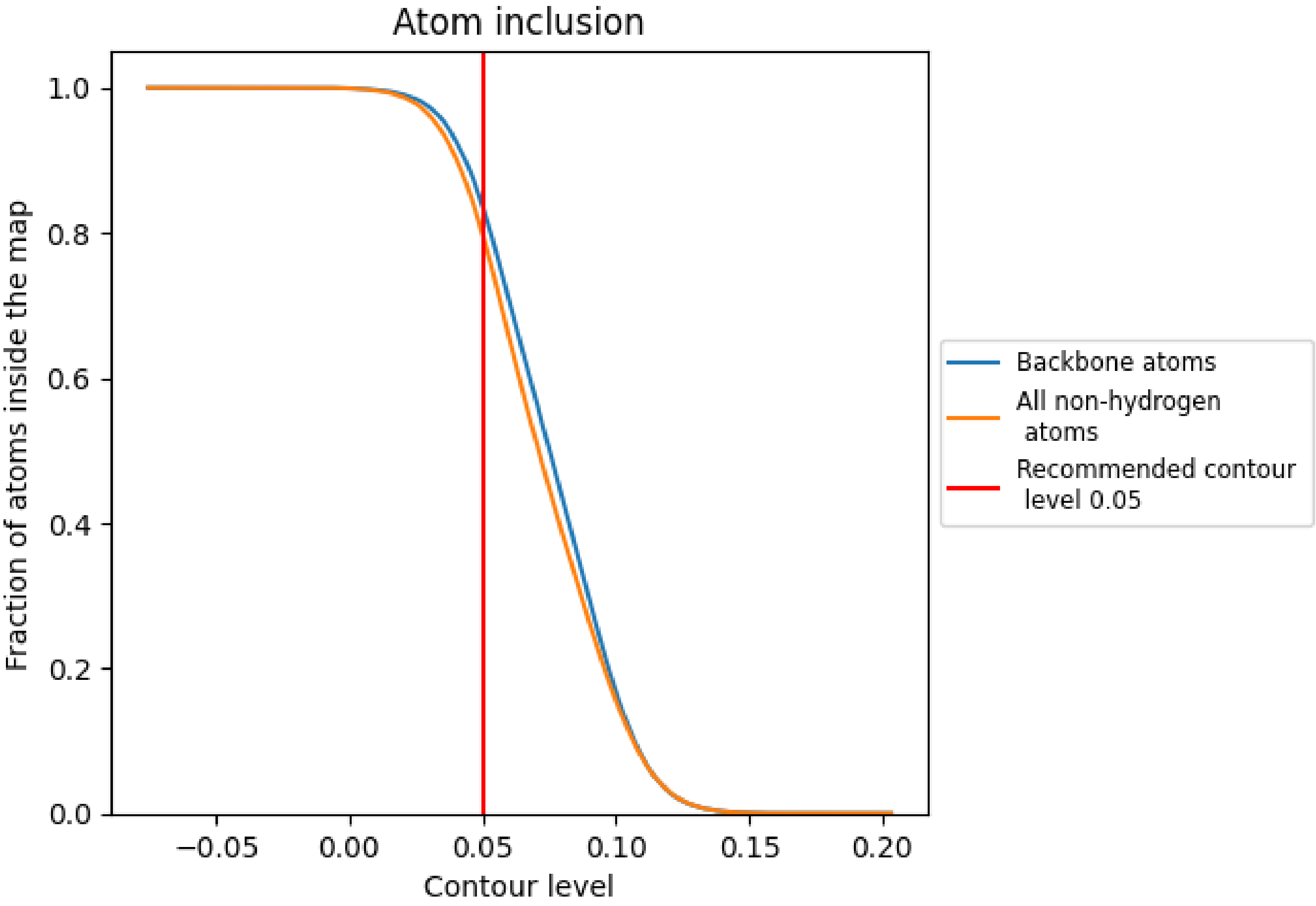
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

9.3 Atom inclusion mapped to coordinate model



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 ⓘ



At the recommended contour level, 84% of all backbone atoms, 80% 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	0.7981	0.3850
2	0.8173	0.3770
A	0.8764	0.4510
B	0.9032	0.4470
C	0.8741	0.4710
E	0.8866	0.4670
F	0.8160	0.3810
G	0.9119	0.4200
H	0.8848	0.4230
I	0.9158	0.4230
J	0.9043	0.4460
L	0.8333	0.4630
N	0.8969	0.4280
O	0.8361	0.4360
P	0.8847	0.4160
Q	0.6837	0.3290
R	0.6756	0.3130
S	0.6861	0.3170
T	0.7617	0.3500
V	0.8834	0.4660
W	0.8975	0.4710
X	0.9043	0.4770
Y	0.9164	0.4510
Z	0.4944	0.2940
b	0.8617	0.4580
c	0.7800	0.4240
e	0.4963	0.3780
k	0.5897	0.2590
s	0.5544	0.2410
t	0.7437	0.3890
u	0.8777	0.4400
w	0.4034	0.2070
x	0.9006	0.4470
y	0.7682	0.4040