



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 07:36 PM UTC

PDB ID : 6YLY / pdb_00006yly
EMDB ID : EMD-10842
Title : pre-60S State NE2 (TAP-Flag-Nop53)
Authors : Kater, L.; Beckmann, R.
Deposited on : 2020-04-07
Resolution : 3.80 Å(reported)
Based on initial models : 6N8J, 3JCT

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:

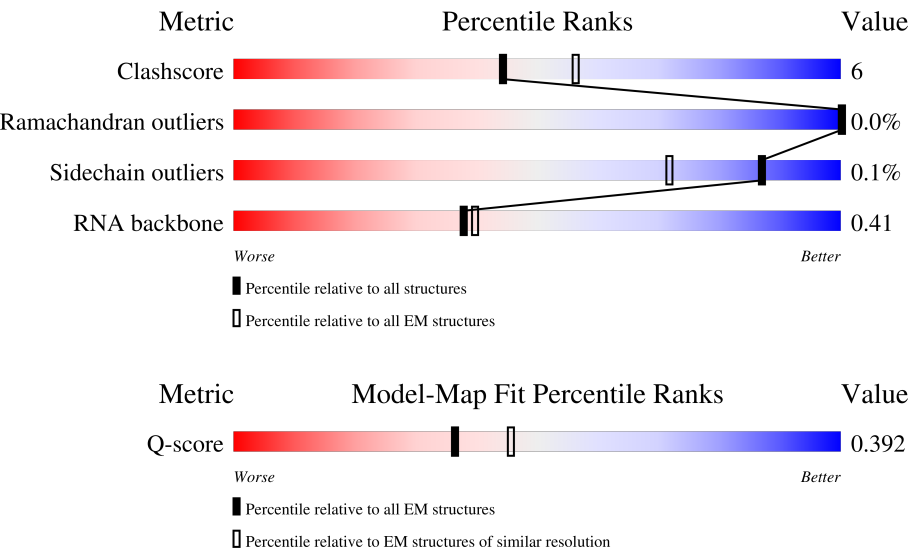
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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	A	254	
2	a	149	
3	B	387	

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Mol	Chain	Length	Quality of chain
4	b	647	
5	C	362	
6	c	105	
7	d	113	
8	E	176	
9	e	130	
10	F	244	
11	f	107	
12	G	256	
13	g	121	
14	I	166	
15	H	191	
16	h	120	
17	i	100	
18	j	88	
19	k	78	
20	L	199	
21	l	51	
22	M	138	
23	p	92	
24	N	204	
25	u	199	
26	O	199	
27	P	184	
28	Q	186	

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Mol	Chain	Length	Quality of chain
29	R	189	
30	r	261	
31	S	172	
32	T	160	
33	U	121	
34	V	137	
35	W	236	
36	X	142	
37	Y	127	
38	y	245	
39	Z	136	
40	z	106	
41	1	3396	
42	3	158	
43	K	376	
44	n	605	
45	o	220	
46	q	455	
47	t	322	
48	6	232	
49	s	520	

2 Entry composition

There are 50 unique types of molecules in this entry. The entry contains 120663 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called 60S ribosomal protein L2-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	A	180	Total	C	N	O	0	0
			1391	877	271	243		

- Molecule 2 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	a	84	Total	C	N	O	0	0
			652	426	113	113		

- Molecule 3 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	B	360	Total	C	N	O	S	0	0
			2866	1821	536	502	7		

- Molecule 4 is a protein called Nucleolar GTP-binding protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	b	451	Total	C	N	O	S	0	0
			3651	2324	628	681	18		

- Molecule 5 is a protein called 60S ribosomal protein L4-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	C	361	Total	C	N	O	S	0	0
			2749	1730	522	494	3		

- Molecule 6 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	c	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 7 is a protein called 60S ribosomal protein L31-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	d	107	Total	C	N	O	S	0	0
			873	553	165	154	1		

- Molecule 8 is a protein called 60S ribosomal protein L6-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	156	Total	C	N	O	S	0	0
			1239	800	222	216	1		

- Molecule 9 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 10 is a protein called 60S ribosomal protein L7-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	222	Total	C	N	O	S	0	0
			1784	1151	324	308	1		

- Molecule 11 is a protein called 60S ribosomal protein L33-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	f	106	Total	C	N	O	S	0	0
			850	540	165	144	1		

- Molecule 12 is a protein called 60S ribosomal protein L8-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	G	230	Total	C	N	O	S	0	0
			1798	1149	323	323	3		

- Molecule 13 is a protein called 60S ribosomal protein L34-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	g	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 14 is a protein called Bud site selection protein 20.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	I	96	Total	C	N	O	S	0	0
			776	487	146	140	3		

- Molecule 15 is a protein called 60S ribosomal protein L9-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	H	188	Total	C	N	O	S	0	0
			1493	948	271	270	4		

- Molecule 16 is a protein called 60S ribosomal protein L35-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	h	118	Total	C	N	O	S	0	0
			964	612	185	166	1		

- Molecule 17 is a protein called 60S ribosomal protein L36-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	i	96	Total	C	N	O	S	0	0
			743	465	148	128	2		

- Molecule 18 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	j	81	Total	C	N	O	S	0	0
			646	394	141	106	5		

- Molecule 19 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
19	k	77	Total	C	N	O	0	0
			612	391	115	106		

- Molecule 20 is a protein called 60S ribosomal protein L13-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
20	L	182	Total	C	N	O	0	0
			1451	902	299	250		

- Molecule 21 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	l	50	Total	C	N	O	S	0	0
			436	272	97	65	2		

- Molecule 22 is a protein called 60S ribosomal protein L14-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	M	137	Total	C	N	O	S	0	0
			1059	678	200	179	2		

- Molecule 23 is a protein called 60S ribosomal protein L43-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	p	91	Total	C	N	O	S	0	0
			694	429	138	121	6		

- Molecule 24 is a protein called 60S ribosomal protein L15-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	N	187	Total	C	N	O	S	0	0
			1607	1005	341	260	1		

- Molecule 25 is a protein called Ribosome biogenesis protein RLP24.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	u	137	Total	C	N	O	S	0	0
			1158	727	234	188	9		

- Molecule 26 is a protein called 60S ribosomal protein L16-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	O	197	Total	C	N	O	S	0	0
			1555	1003	289	262	1		

- Molecule 27 is a protein called 60S ribosomal protein L17-A.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	P	176	Total	C	N	O	0	0
			1393	865	278	250		

- Molecule 28 is a protein called 60S ribosomal protein L18-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	Q	134	Total	C	N	O	S	0	0
			1035	659	196	179	1		

- Molecule 29 is a protein called 60S ribosomal protein L19-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	R	154	Total	C	N	O		0	0
			1241	772	262	207			

- Molecule 30 is a protein called Ribosome biogenesis protein NSA2.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	r	67	Total	C	N	O	S	0	0
			579	358	124	96	1		

- Molecule 31 is a protein called 60S ribosomal protein L20-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	S	170	Total	C	N	O	S	0	0
			1425	916	265	241	3		

- Molecule 32 is a protein called 60S ribosomal protein L21-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	T	56	Total	C	N	O	S	0	0
			434	268	86	79	1		

- Molecule 33 is a protein called 60S ribosomal protein L22-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	U	104	Total	C	N	O		0	0
			826	535	136	155			

- Molecule 34 is a protein called 60S ribosomal protein L23-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	V	136	Total	C	N	O	S	0	0
			1003	628	189	179	7		

- Molecule 35 is a protein called Ribosome assembly factor MRT4.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	W	227	Total	C	N	O	S	0	0
			1814	1149	310	350	5		

- Molecule 36 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	X	141	Total	C	N	O	S	0	0
			1100	705	196	197	2		

- Molecule 37 is a protein called 60S ribosomal protein L26-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Y	126	Total	C	N	O		0	0
			993	625	192	176			

- Molecule 38 is a protein called Eukaryotic translation initiation factor 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	y	227	Total	C	N	O	S	0	0
			1712	1062	298	346	6		

- Molecule 39 is a protein called 60S ribosomal protein L27-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Z	135	Total	C	N	O		0	0
			1092	710	202	180			

- Molecule 40 is a protein called UPF0642 protein YBL028C.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	z	53	Total	C	N	O		0	0
			430	264	85	81			

- Molecule 41 is a RNA chain called 25S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	1	2676	Total	C	N	O	P	0	0
			57244	25566	10318	18684	2676		

- Molecule 42 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	3	158	Total	C	N	O	P	0	0
			3353	1500	586	1109	158		

- Molecule 43 is a protein called Proteasome-interacting protein CIC1.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	K	256	Total	C	N	O	S	0	0
			2064	1332	342	387	3		

- Molecule 44 is a protein called Pescadillo homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	371	Total	C	N	O	S	0	0
			3030	1963	523	534	10		

- Molecule 45 is a protein called Ribosome biogenesis protein 15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	125	Total	C	N	O	S	0	0
			1046	676	188	178	4		

- Molecule 46 is a protein called Ribosome biogenesis protein NOP53.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	141	Total	C	N	O	S	0	0
			1178	743	208	226	1		

- Molecule 47 is a protein called Ribosome biogenesis protein RLP7.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	t	287	Total	C	N	O	S	0	0
			2306	1459	427	417	3		

- Molecule 48 is a RNA chain called ITS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	6	65	Total	C	N	O	P	0	0
			1370	614	228	463	65		

- Molecule 49 is a protein called Nuclear GTP-binding protein NUG1.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	s	36	Total	C	N	O	S	0	0
			301	184	69	46	2		

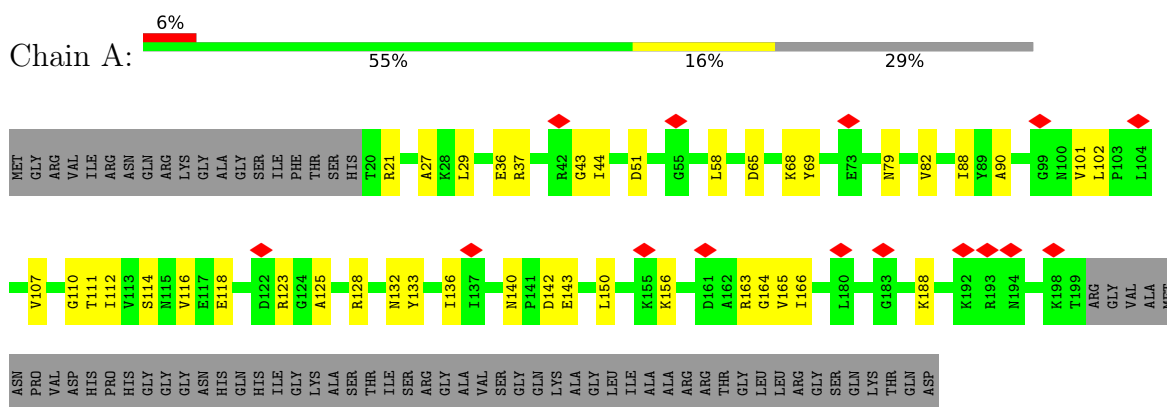
- Molecule 50 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
50	j	1	Total	Zn	0
			1	1	
50	p	1	Total	Zn	0
			1	1	
50	u	1	Total	Zn	0
			1	1	

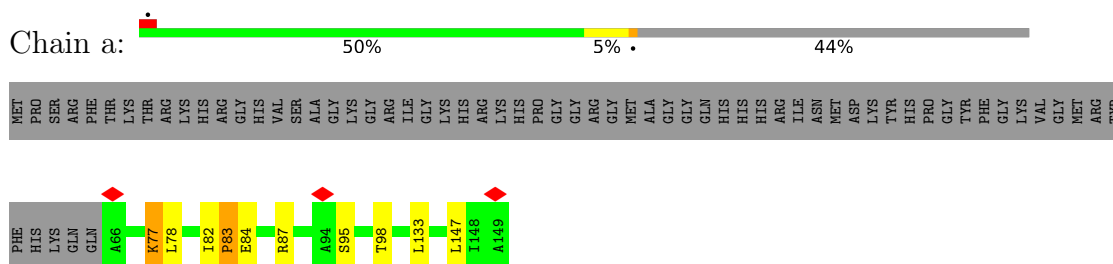
3 Residue-property plots

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.

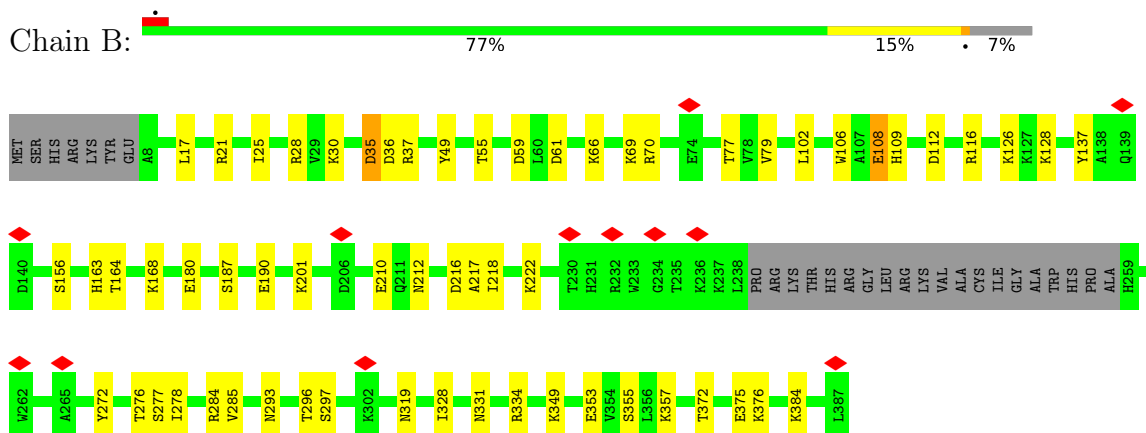
• Molecule 1: 60S ribosomal protein L2-A



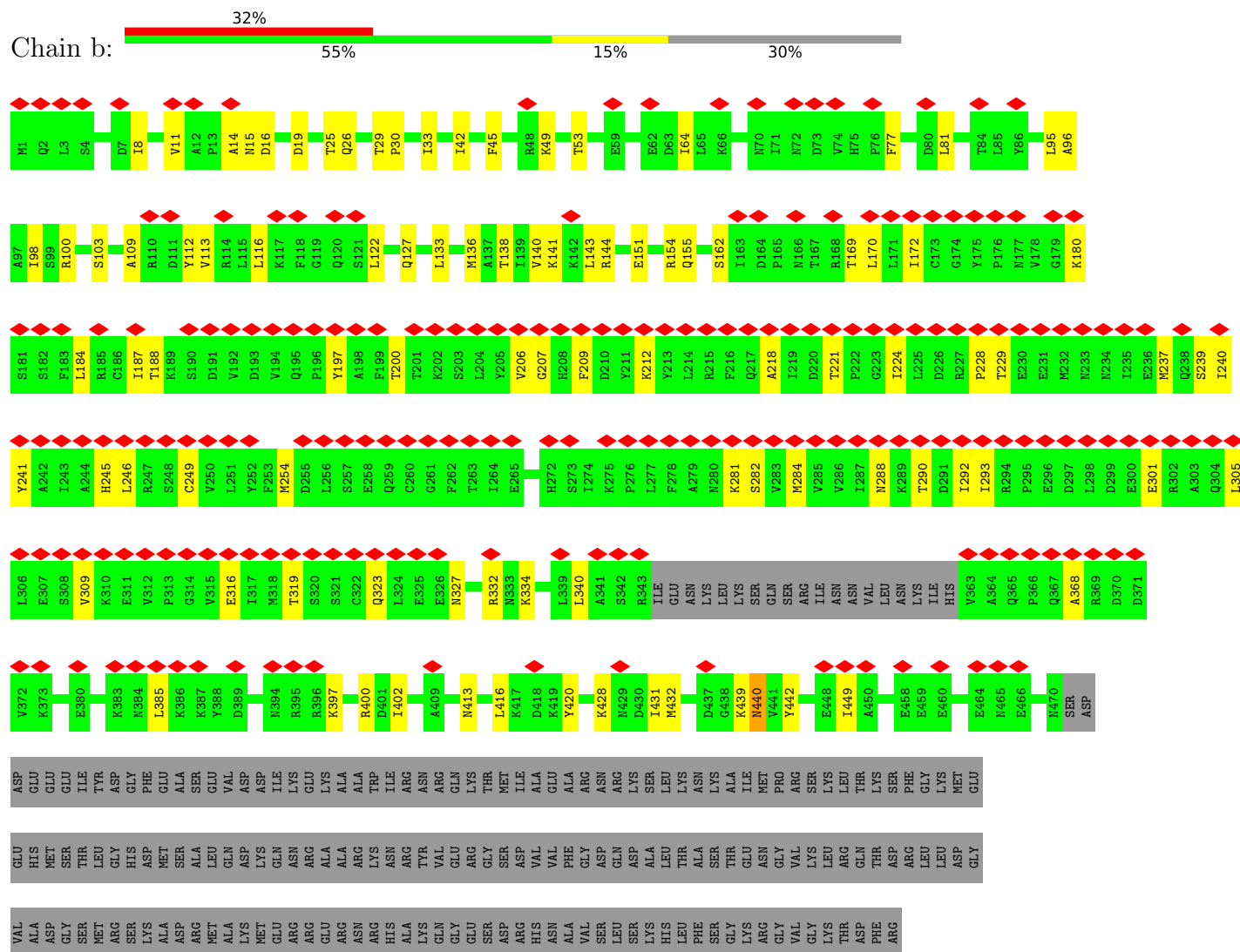
• Molecule 2: 60S ribosomal protein L28



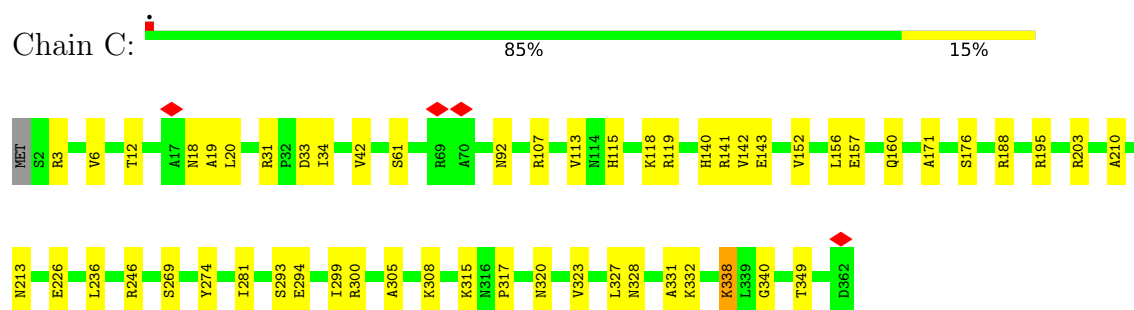
• Molecule 3: 60S ribosomal protein L3



- Molecule 4: Nucleolar GTP-binding protein 1

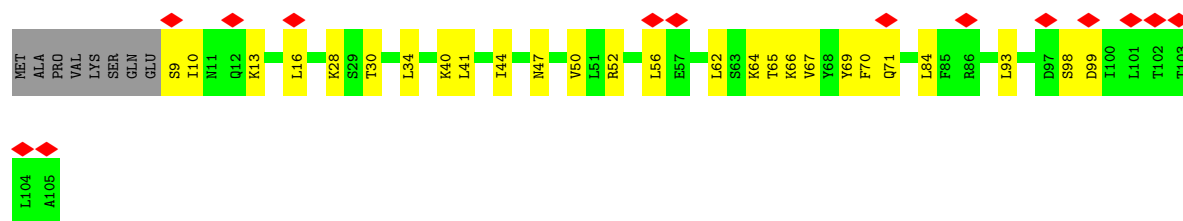


- Molecule 5: 60S ribosomal protein L4-A

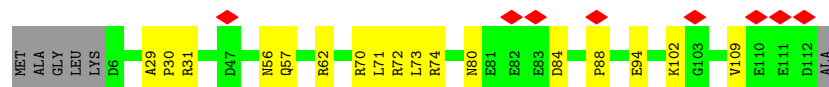
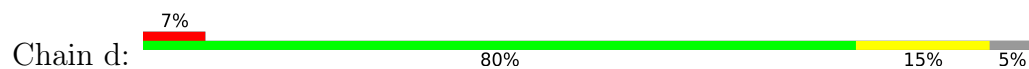


- Molecule 6: 60S ribosomal protein L30

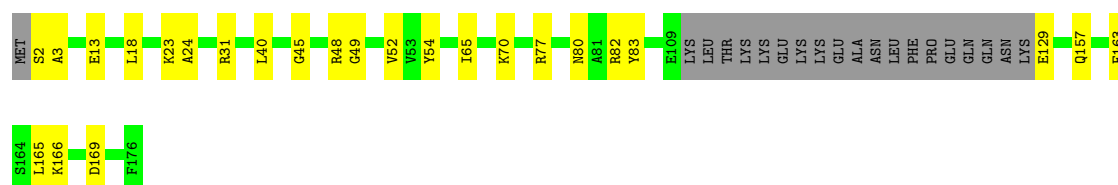




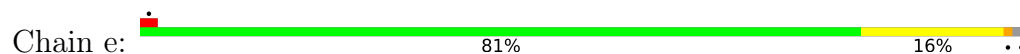
• Molecule 7: 60S ribosomal protein L31-A



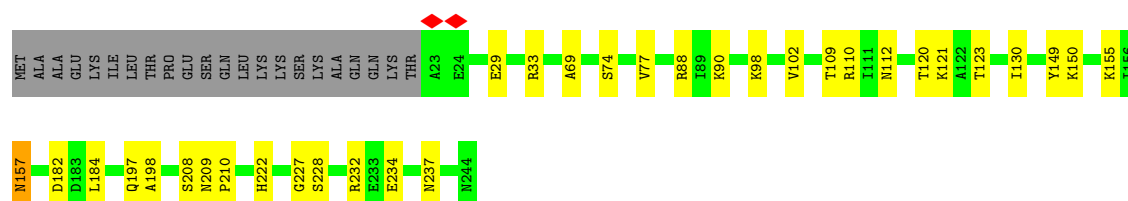
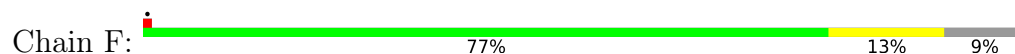
• Molecule 8: 60S ribosomal protein L6-A



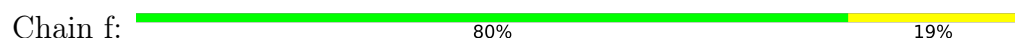
• Molecule 9: 60S ribosomal protein L32



• Molecule 10: 60S ribosomal protein L7-A

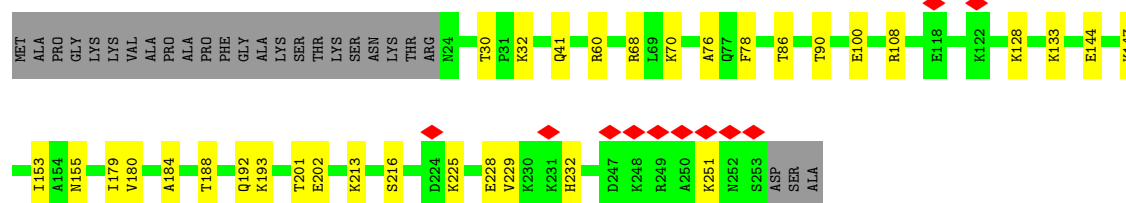


• Molecule 11: 60S ribosomal protein L33-A



- Molecule 12: 60S ribosomal protein L8-A

Chain G: 

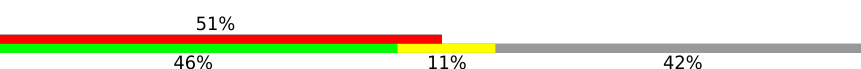


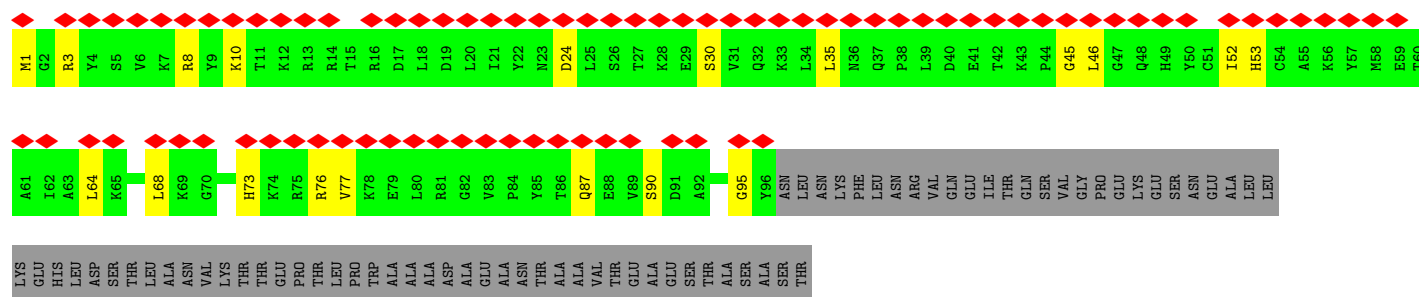
- Molecule 13: 60S ribosomal protein L34-A

Chain g: 



- Molecule 14: Bud site selection protein 20

Chain I: 



- Molecule 15: 60S ribosomal protein L9-A

Chain H: 

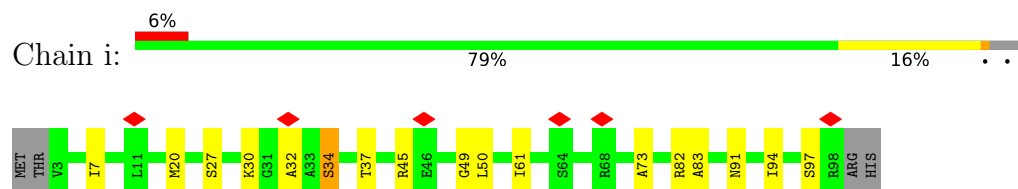


- Molecule 16: 60S ribosomal protein L35-A

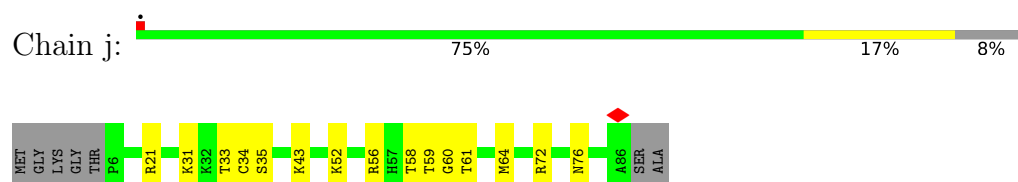
Chain h: 



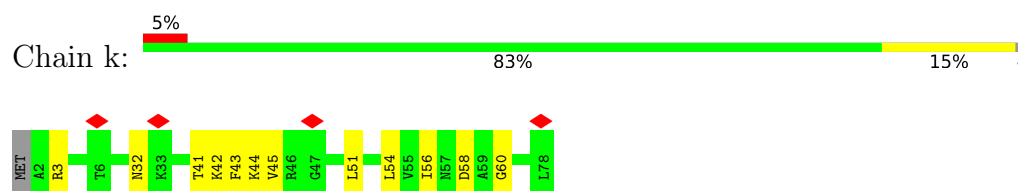
- Molecule 17: 60S ribosomal protein L36-A



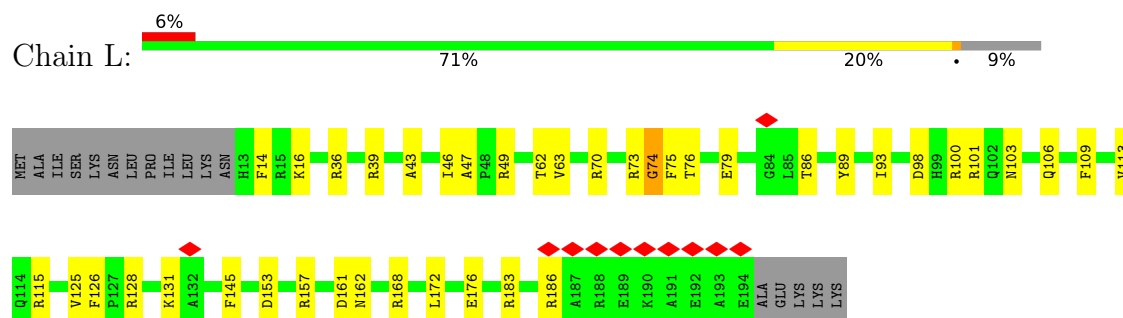
- Molecule 18: 60S ribosomal protein L37-A



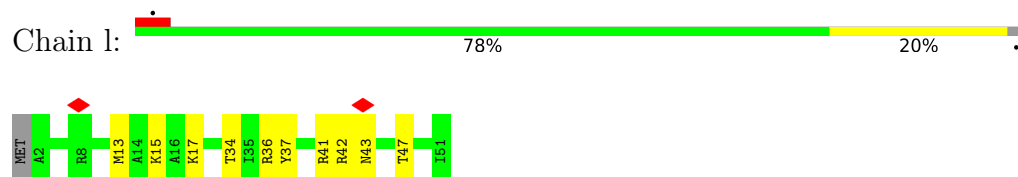
- Molecule 19: 60S ribosomal protein L38



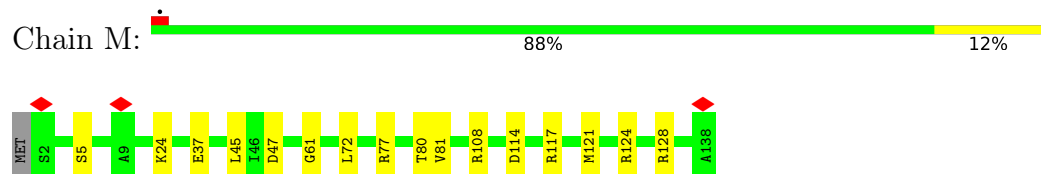
- Molecule 20: 60S ribosomal protein L13-A



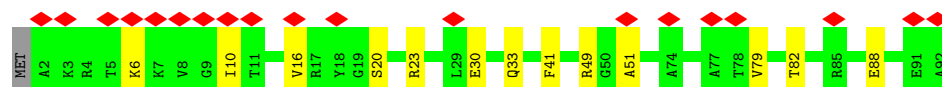
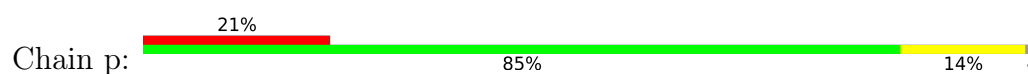
- Molecule 21: 60S ribosomal protein L39



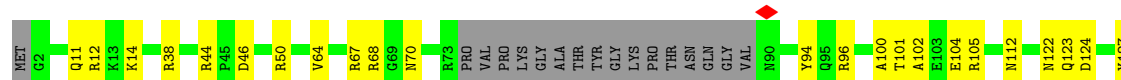
- Molecule 22: 60S ribosomal protein L14-A



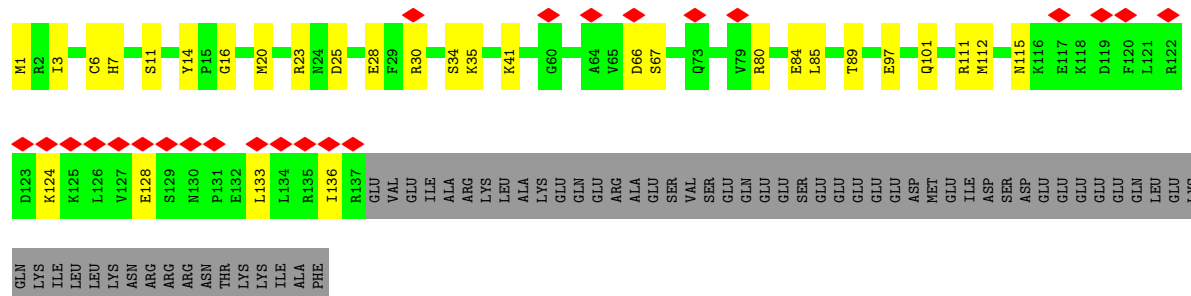
- Molecule 23: 60S ribosomal protein L43-A



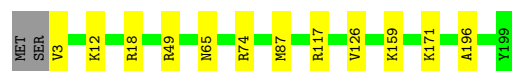
• Molecule 24: 60S ribosomal protein L15-A



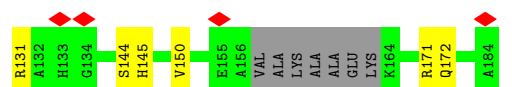
• Molecule 25: Ribosome biogenesis protein RLP24



• Molecule 26: 60S ribosomal protein L16-A

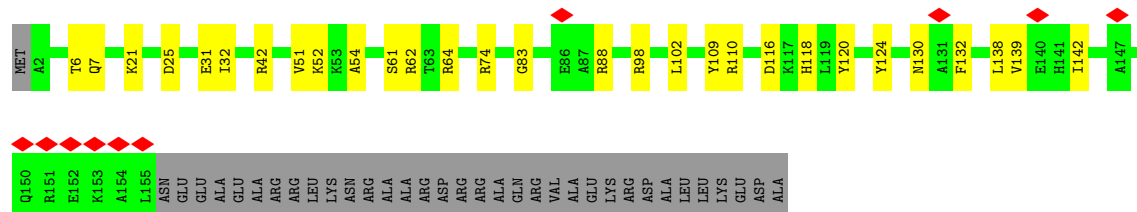


• Molecule 27: 60S ribosomal protein L17-A

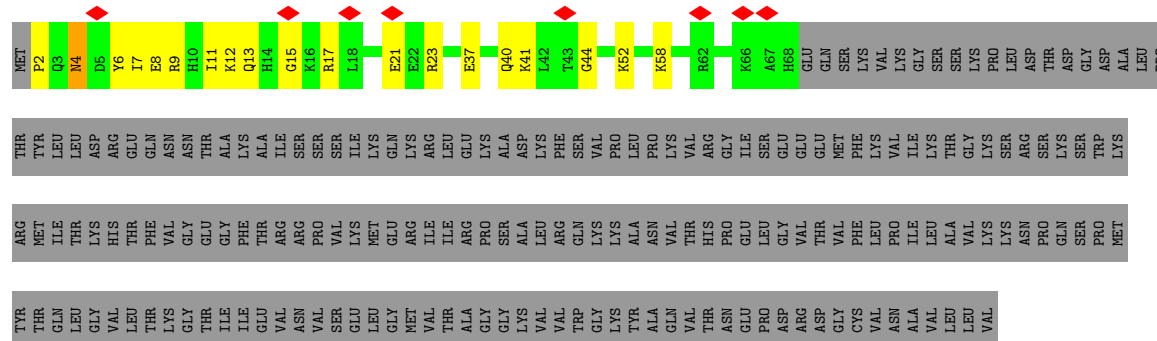


• Molecule 28: 60S ribosomal protein L18-A

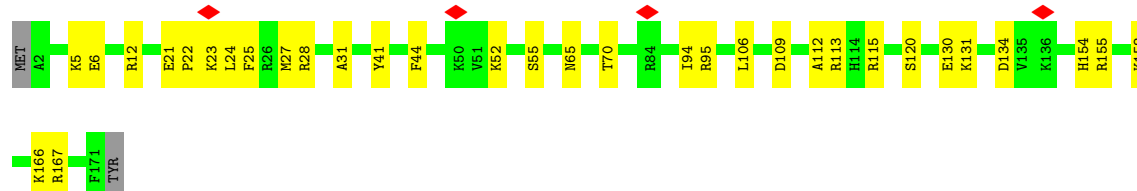
- Molecule 29: 60S ribosomal protein L19-A



- Molecule 30: Ribosome biogenesis protein NSA2

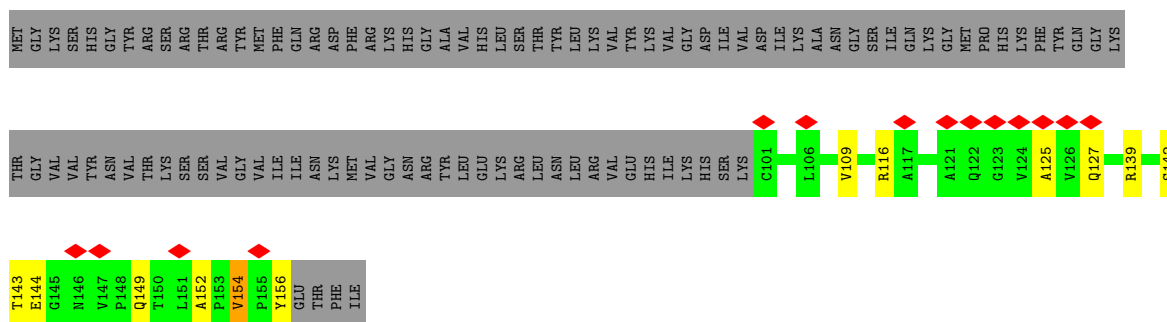


- Molecule 31: 60S ribosomal protein L20-A

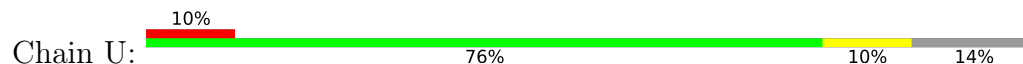


- Molecule 32: 60S ribosomal protein L21-A

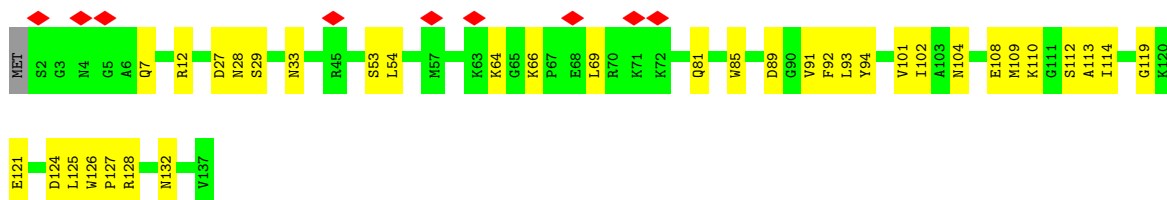




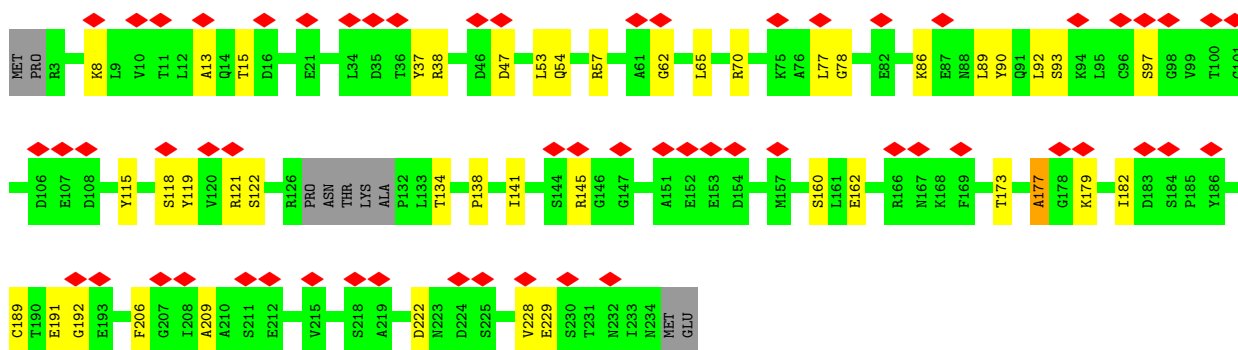
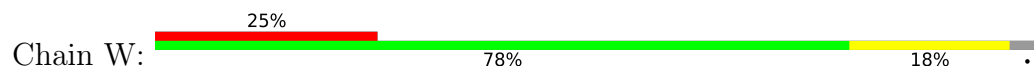
• Molecule 33: 60S ribosomal protein L22-A



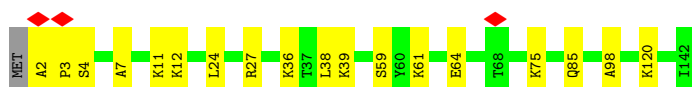
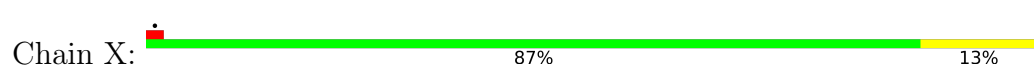
• Molecule 34: 60S ribosomal protein L23-A



• Molecule 35: Ribosome assembly factor MRT4

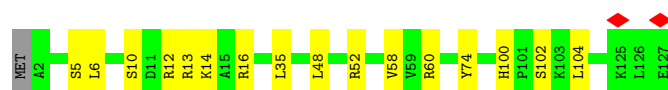


• Molecule 36: 60S ribosomal protein L25



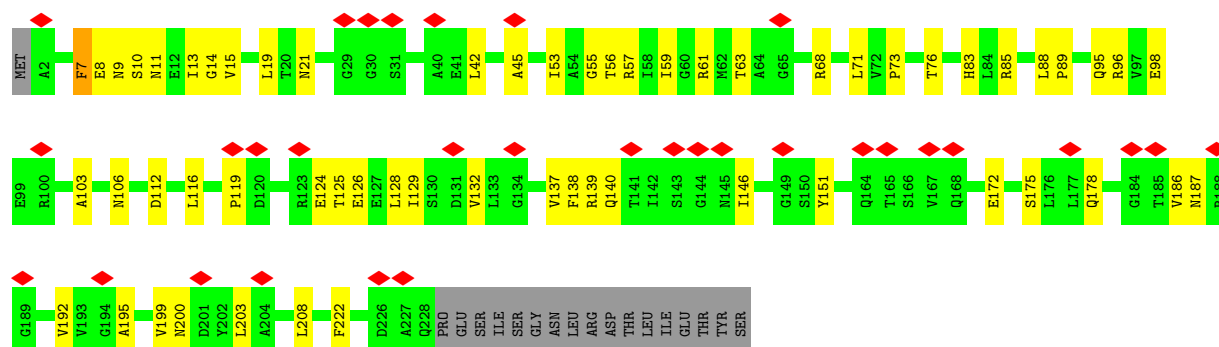
- Molecule 37: 60S ribosomal protein L26-A

Chain Y: 



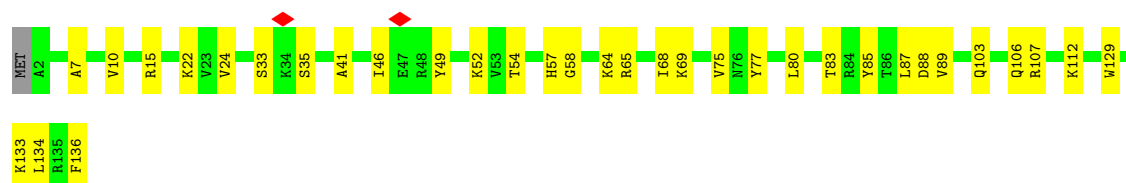
- Molecule 38: Eukaryotic translation initiation factor 6

Chain y: 

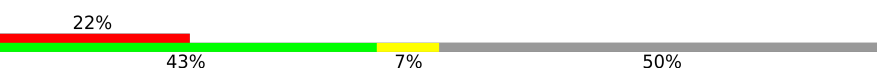


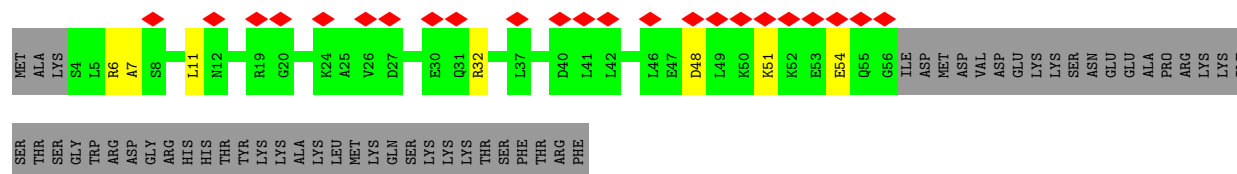
- Molecule 39: 60S ribosomal protein L27-A

Chain Z: 



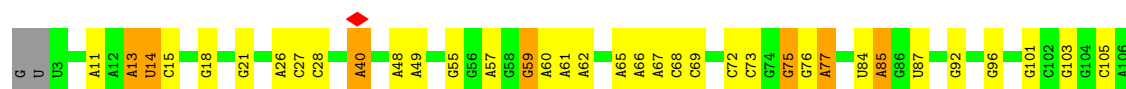
- Molecule 40: UPF0642 protein YBL028C

Chain z: 



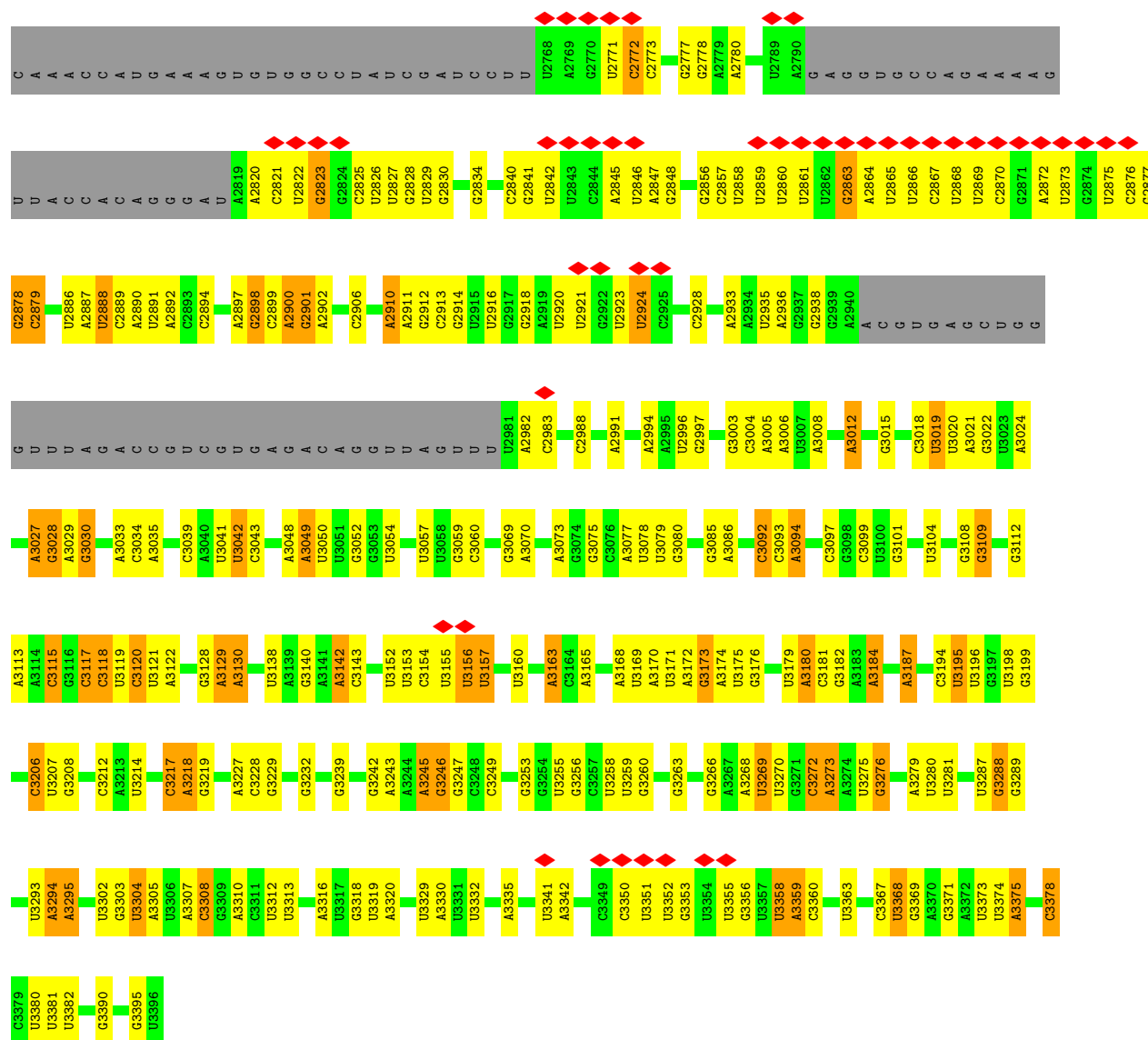
- Molecule 41: 25S rRNA

Chain 1: 

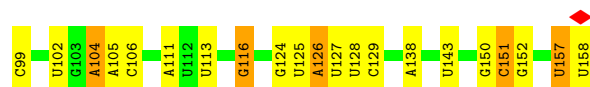
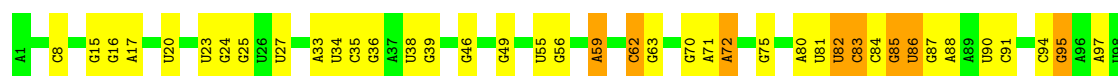






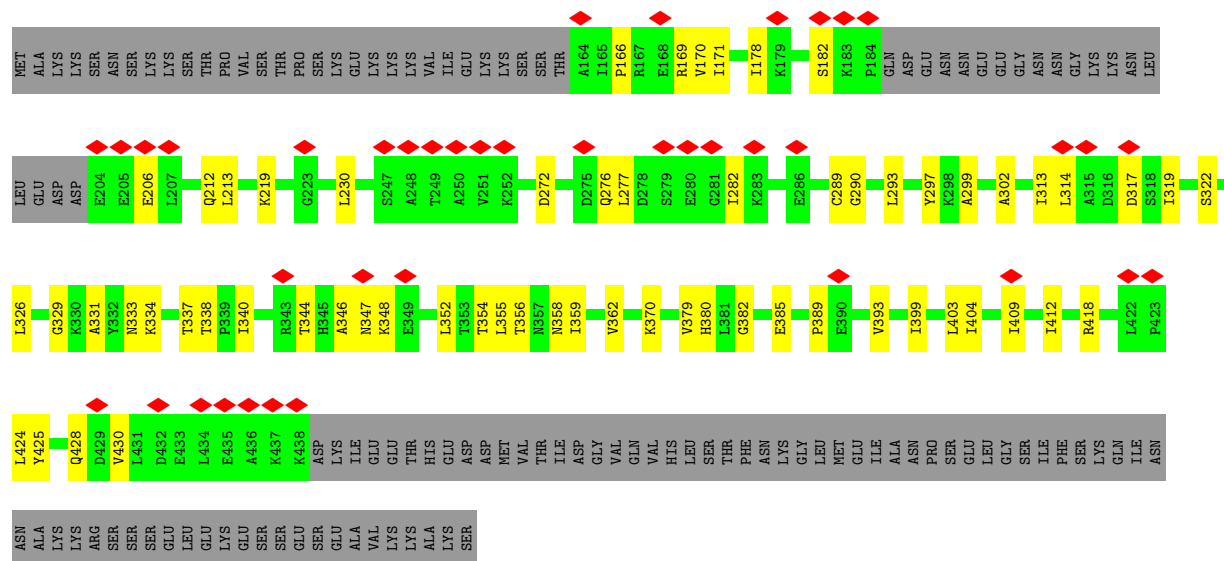


- Molecule 42: 5.8S rRNA

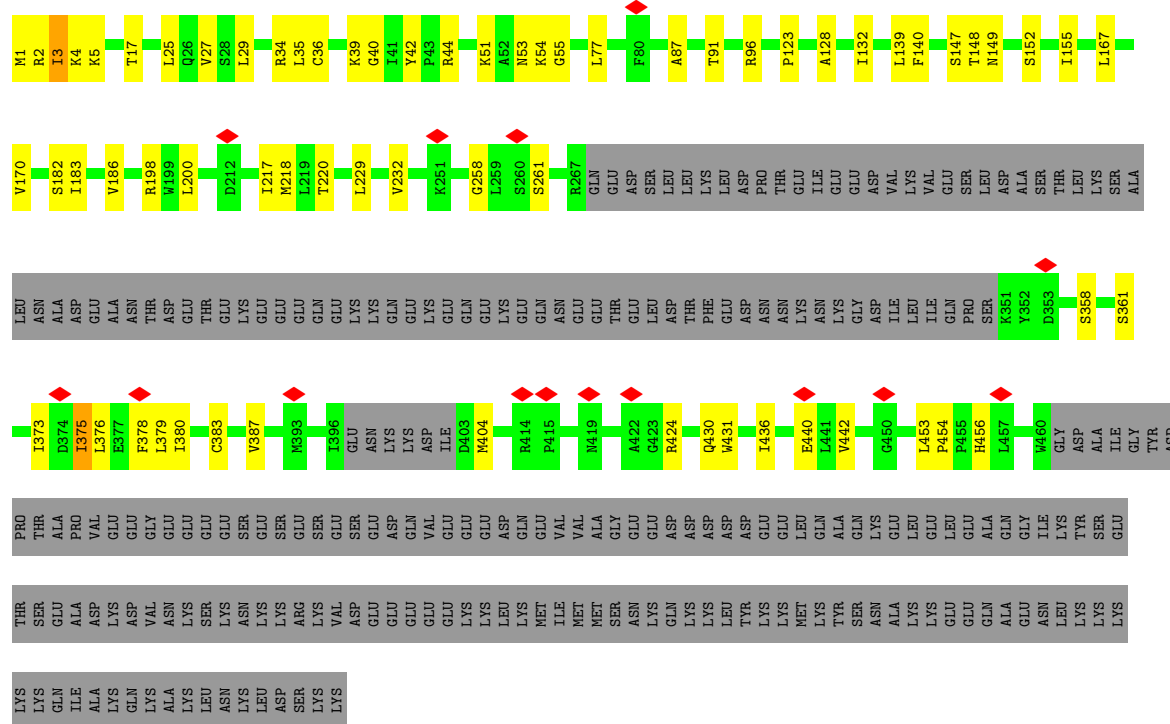


- Molecule 43: Proteasome-interacting protein CIC1

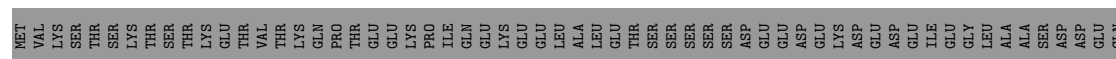




• Molecule 44: Pescadillo homolog

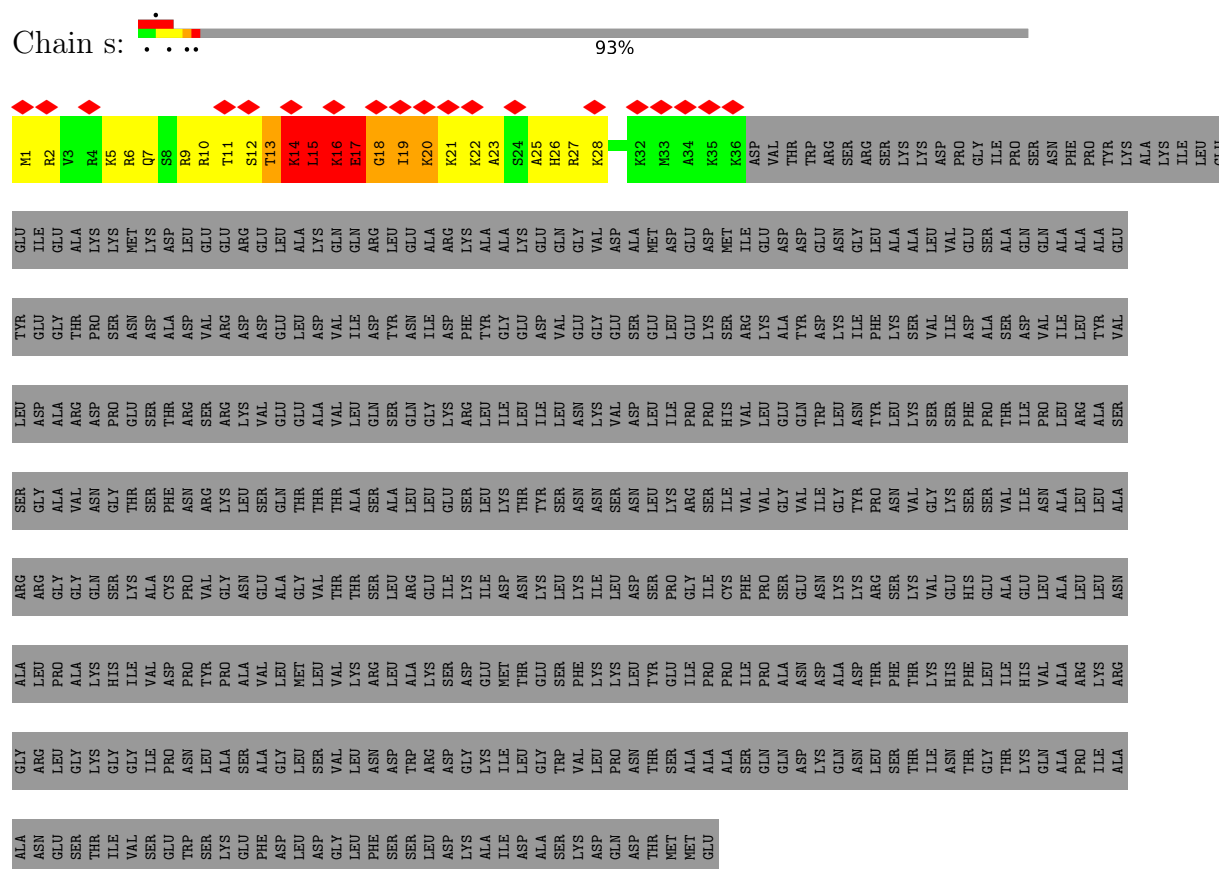


• Molecule 45: Ribosome biogenesis protein 15





- Molecule 49: Nuclear GTP-binding protein NUG1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	30364	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	24	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	0.575	Depositor
Minimum map value	-0.352	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.04	Depositor
Map size ($\text{\AA}$)	416.25598, 416.25598, 416.25598	wwPDB
Map dimensions	384, 384, 384	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.084, 1.084, 1.084	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	A	0.35	0/1417	0.60	0/1907
2	a	0.50	0/665	0.68	2/900 (0.2%)
3	B	0.52	0/2928	0.70	2/3936 (0.1%)
4	b	0.28	0/3720	0.58	0/5021
5	C	0.72	0/2801	0.72	0/3792
6	c	0.29	0/751	0.55	0/1008
7	d	0.53	0/887	0.62	0/1191
8	E	0.48	0/1260	0.60	0/1694
9	e	0.75	0/1041	0.65	0/1394
10	F	0.64	0/1821	0.75	2/2451 (0.1%)
11	f	0.88	0/868	0.75	0/1168
12	G	0.57	0/1830	0.69	0/2469
13	g	0.53	0/891	0.65	0/1191
14	I	0.31	0/789	0.61	0/1058
15	H	0.37	0/1514	0.65	0/2039
16	h	0.66	1/973 (0.1%)	0.68	0/1294
17	i	0.42	0/749	0.63	0/995
18	j	0.79	0/661	0.81	0/876
19	k	0.35	0/618	0.63	0/826
20	L	0.62	0/1475	0.78	2/1982 (0.1%)
21	l	0.52	0/443	0.68	0/588
22	M	0.49	0/1074	0.63	0/1446
23	p	0.32	0/701	0.62	0/934
24	N	0.83	0/1639	0.73	0/2190
25	u	0.35	0/1180	0.72	0/1569
26	O	0.74	0/1585	0.66	0/2128
27	P	0.69	0/1415	0.71	0/1900
28	Q	0.63	0/1050	0.63	0/1419
29	R	0.42	0/1258	0.63	0/1679
30	r	0.34	0/589	0.77	0/773
31	S	0.46	0/1460	0.58	0/1962
32	T	0.33	0/440	0.73	0/594

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	U	0.30	0/843	0.55	0/1143
34	V	0.35	0/1018	0.61	0/1369
35	W	0.24	0/1843	0.52	0/2483
36	X	0.65	0/1115	0.73	0/1500
37	Y	0.62	0/1004	0.65	0/1341
38	y	0.26	0/1733	0.52	0/2359
39	Z	0.34	0/1118	0.58	0/1497
40	z	0.30	0/431	0.60	0/567
41	1	0.75	23/64064 (0.0%)	0.57	33/99858 (0.0%)
42	3	0.65	0/3746	0.61	0/5832
43	K	0.29	0/2098	0.64	2/2830 (0.1%)
44	n	0.46	0/3101	0.75	0/4187
45	o	0.34	0/1067	0.73	2/1417 (0.1%)
46	q	0.32	0/1197	0.68	0/1601
47	t	0.36	0/2333	0.77	2/3128 (0.1%)
48	6	0.26	0/1527	0.47	0/2371
49	s	4.45	15/301 (5.0%)	3.87	24/386 (6.2%)
All	All	0.68	39/129032 (0.0%)	0.64	71/188243 (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	a	0	4
3	B	1	1
4	b	0	2
5	C	0	4
7	d	0	1
9	e	0	3
10	F	0	1
12	G	0	4
15	H	0	3
16	h	0	2
17	i	0	3
19	k	0	1
20	L	0	2
22	M	0	1
23	p	0	1
27	P	0	2
28	Q	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
29	R	0	2
30	r	0	2
31	S	0	3
32	T	0	1
34	V	0	1
35	W	0	1
38	y	0	1
41	1	0	1
43	K	0	1
44	n	0	11
45	o	0	4
46	q	0	3
47	t	0	7
49	s	0	8
All	All	1	82

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
41	1	1200	A	C2-N3	70.97	2.75	1.33
41	1	1200	A	N3-C4	64.17	2.63	1.34
49	s	14	LYS	N-CA	52.31	2.09	1.46
41	1	1200	A	N1-C2	50.44	2.35	1.34
41	1	1200	A	C6-N1	48.22	2.31	1.35

The worst 5 of 71 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
49	s	13	THR	CA-C-N	28.03	158.38	120.54
49	s	13	THR	C-N-CA	28.03	158.38	120.54
49	s	16	LYS	CA-C-N	24.37	155.38	120.28
49	s	16	LYS	C-N-CA	24.37	155.38	120.28
41	1	1199	C	P-O5'-C5'	22.78	155.07	120.90

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	B	17	LEU	CA

5 of 82 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	B	35	ASP	Peptide
2	a	77	LYS	Peptide
2	a	82	ILE	Peptide
2	a	83	PRO	Peptide
2	a	84	GLU	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	A	1391	0	1446	34	0
2	a	652	0	697	4	0
3	B	2866	0	2944	42	0
4	b	3651	0	3692	70	0
5	C	2749	0	2863	40	0
6	c	743	0	797	19	0
7	d	873	0	914	13	0
8	E	1239	0	1326	22	0
9	e	1020	0	1090	15	0
10	F	1784	0	1862	23	0
11	f	850	0	880	17	0
12	G	1798	0	1894	23	0
13	g	881	0	945	10	0
14	I	776	0	803	13	0
15	H	1493	0	1566	23	0
16	h	964	0	1073	7	0
17	i	743	0	822	13	0
18	j	646	0	649	10	0
19	k	612	0	682	7	0
20	L	1451	0	1494	31	0
21	l	436	0	475	10	0
22	M	1059	0	1154	15	0
23	p	694	0	734	10	0
24	N	1607	0	1662	30	0
25	u	1158	0	1202	23	0
26	O	1555	0	1659	13	0
27	P	1393	0	1428	27	0
28	Q	1035	0	1115	23	0
29	R	1241	0	1330	23	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
30	r	579	0	606	16	0
31	S	1425	0	1466	23	0
32	T	434	0	450	10	0
33	U	826	0	843	9	0
34	V	1003	0	1048	24	0
35	W	1814	0	1833	26	0
36	X	1100	0	1186	16	0
37	Y	993	0	1081	12	0
38	y	1712	0	1700	41	0
39	Z	1092	0	1155	24	0
40	z	430	0	460	5	0
41	1	57244	0	28777	602	0
42	3	3353	0	1695	38	0
43	K	2064	0	2156	38	0
44	n	3030	0	3107	43	0
45	o	1046	0	1086	29	0
46	q	1178	0	1200	11	0
47	t	2306	0	2454	41	0
48	6	1370	0	692	27	0
49	s	301	0	358	120	0
50	j	1	0	0	0	0
50	p	1	0	0	0	0
50	u	1	0	0	0	0
All	All	120663	0	92551	1308	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 6.

The worst 5 of 1308 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)
49:s:15:LEU:CB	49:s:15:LEU:HG	1.19	1.65
41:1:1200:A:N9	41:1:1200:A:C4	1.72	1.56
41:1:1199:C:C4'	41:1:1199:C:C5'	1.83	1.54
41:1:1200:A:C5'	41:1:1200:A:C4'	1.80	1.52
41:1:1199:C:C4'	41:1:1199:C:C3'	1.81	1.49

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	
1	A	178/254 (70%)	178 (100%)	0	0	100	100
2	a	82/149 (55%)	78 (95%)	3 (4%)	1 (1%)	10	40
3	B	356/387 (92%)	344 (97%)	12 (3%)	0	100	100
4	b	447/647 (69%)	434 (97%)	13 (3%)	0	100	100
5	C	359/362 (99%)	347 (97%)	12 (3%)	0	100	100
6	c	95/105 (90%)	95 (100%)	0	0	100	100
7	d	105/113 (93%)	105 (100%)	0	0	100	100
8	E	152/176 (86%)	150 (99%)	2 (1%)	0	100	100
9	e	125/130 (96%)	124 (99%)	1 (1%)	0	100	100
10	F	220/244 (90%)	210 (96%)	10 (4%)	0	100	100
11	f	104/107 (97%)	104 (100%)	0	0	100	100
12	G	228/256 (89%)	228 (100%)	0	0	100	100
13	g	110/121 (91%)	110 (100%)	0	0	100	100
14	I	94/166 (57%)	92 (98%)	2 (2%)	0	100	100
15	H	186/191 (97%)	182 (98%)	4 (2%)	0	100	100
16	h	116/120 (97%)	116 (100%)	0	0	100	100
17	i	94/100 (94%)	90 (96%)	4 (4%)	0	100	100
18	j	79/88 (90%)	78 (99%)	1 (1%)	0	100	100
19	k	75/78 (96%)	75 (100%)	0	0	100	100
20	L	180/199 (90%)	172 (96%)	7 (4%)	1 (1%)	21	54
21	l	48/51 (94%)	48 (100%)	0	0	100	100
22	M	135/138 (98%)	134 (99%)	1 (1%)	0	100	100
23	p	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
24	N	183/204 (90%)	179 (98%)	4 (2%)	0	100	100
25	u	135/199 (68%)	133 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
26	O	195/199 (98%)	195 (100%)	0	0	100	100
27	P	172/184 (94%)	171 (99%)	1 (1%)	0	100	100
28	Q	132/186 (71%)	132 (100%)	0	0	100	100
29	R	152/189 (80%)	149 (98%)	3 (2%)	0	100	100
30	r	65/261 (25%)	57 (88%)	8 (12%)	0	100	100
31	S	168/172 (98%)	163 (97%)	5 (3%)	0	100	100
32	T	54/160 (34%)	50 (93%)	4 (7%)	0	100	100
33	U	102/121 (84%)	101 (99%)	1 (1%)	0	100	100
34	V	134/137 (98%)	133 (99%)	1 (1%)	0	100	100
35	W	223/236 (94%)	221 (99%)	2 (1%)	0	100	100
36	X	137/142 (96%)	136 (99%)	1 (1%)	0	100	100
37	Y	124/127 (98%)	124 (100%)	0	0	100	100
38	y	225/245 (92%)	223 (99%)	2 (1%)	0	100	100
39	Z	133/136 (98%)	131 (98%)	2 (2%)	0	100	100
40	z	51/106 (48%)	51 (100%)	0	0	100	100
43	K	252/376 (67%)	245 (97%)	7 (3%)	0	100	100
44	n	365/605 (60%)	342 (94%)	23 (6%)	0	100	100
45	o	121/220 (55%)	117 (97%)	4 (3%)	0	100	100
46	q	137/455 (30%)	128 (93%)	9 (7%)	0	100	100
47	t	283/322 (88%)	264 (93%)	19 (7%)	0	100	100
49	s	34/520 (6%)	30 (88%)	4 (12%)	0	100	100
All	All	7234/9776 (74%)	7056 (98%)	176 (2%)	2 (0%)	100	100

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	a	78	LEU
20	L	63	VAL

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	142/196 (72%)	142 (100%)	0	100	100
2	a	68/119 (57%)	68 (100%)	0	100	100
3	B	301/323 (93%)	301 (100%)	0	100	100
4	b	404/573 (70%)	404 (100%)	0	100	100
5	C	288/289 (100%)	287 (100%)	1 (0%)	86	84
6	c	81/88 (92%)	81 (100%)	0	100	100
7	d	94/97 (97%)	94 (100%)	0	100	100
8	E	134/153 (88%)	134 (100%)	0	100	100
9	e	109/111 (98%)	109 (100%)	0	100	100
10	F	186/205 (91%)	186 (100%)	0	100	100
11	f	90/91 (99%)	90 (100%)	0	100	100
12	G	189/208 (91%)	189 (100%)	0	100	100
13	g	95/103 (92%)	94 (99%)	1 (1%)	65	73
14	I	83/141 (59%)	83 (100%)	0	100	100
15	H	168/171 (98%)	168 (100%)	0	100	100
16	h	104/105 (99%)	104 (100%)	0	100	100
17	i	78/82 (95%)	78 (100%)	0	100	100
18	j	67/71 (94%)	67 (100%)	0	100	100
19	k	68/69 (99%)	68 (100%)	0	100	100
20	L	142/159 (89%)	141 (99%)	1 (1%)	76	77
21	l	45/46 (98%)	45 (100%)	0	100	100
22	M	108/109 (99%)	108 (100%)	0	100	100
23	p	71/72 (99%)	71 (100%)	0	100	100
24	N	163/176 (93%)	162 (99%)	1 (1%)	78	79
25	u	122/180 (68%)	122 (100%)	0	100	100
26	O	160/162 (99%)	160 (100%)	0	100	100
27	P	141/146 (97%)	139 (99%)	2 (1%)	59	70
28	Q	110/151 (73%)	110 (100%)	0	100	100
29	R	127/154 (82%)	127 (100%)	0	100	100
30	r	59/229 (26%)	59 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	S	154/156 (99%)	154 (100%)	0	100	100
32	T	45/137 (33%)	45 (100%)	0	100	100
33	U	91/107 (85%)	91 (100%)	0	100	100
34	V	104/105 (99%)	104 (100%)	0	100	100
35	W	201/213 (94%)	201 (100%)	0	100	100
36	X	117/118 (99%)	117 (100%)	0	100	100
37	Y	109/110 (99%)	109 (100%)	0	100	100
38	y	193/211 (92%)	193 (100%)	0	100	100
39	Z	115/116 (99%)	115 (100%)	0	100	100
40	z	47/95 (50%)	47 (100%)	0	100	100
43	K	236/346 (68%)	236 (100%)	0	100	100
44	n	334/548 (61%)	334 (100%)	0	100	100
45	o	111/199 (56%)	111 (100%)	0	100	100
46	q	131/420 (31%)	131 (100%)	0	100	100
47	t	256/287 (89%)	256 (100%)	0	100	100
49	s	32/445 (7%)	31 (97%)	1 (3%)	35	57
All	All	6273/8392 (75%)	6266 (100%)	7 (0%)	87	89

5 of 7 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	N	153	ASP
27	P	119	VAL
49	s	15	LEU
27	P	120	ASN
20	L	172	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 40 such sidechains are listed below:

Mol	Chain	Res	Type
27	P	145	HIS
39	Z	36	HIS
29	R	141	HIS
31	S	65	ASN
45	o	154	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
41	1	2663/3396 (78%)	695 (26%)	43 (1%)
42	3	157/158 (99%)	36 (22%)	3 (1%)
48	6	63/232 (27%)	38 (60%)	0
All	All	2883/3786 (76%)	769 (26%)	46 (1%)

5 of 769 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
41	1	11	A
41	1	14	U
41	1	15	C
41	1	18	G
41	1	26	A

5 of 46 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
41	1	2541	U
41	1	3078	U
41	1	2593	A
41	1	2886	U
41	1	3218	A

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 oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 3 ligands modelled in this entry, 3 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
36	X	1
41	1	1
49	s	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	X	23:ALA	C	24:LEU	N	5.12
1	1	1199:C	O3'	1200:A	P	1.89
1	s	13:THR	C	14:LYS	N	1.75

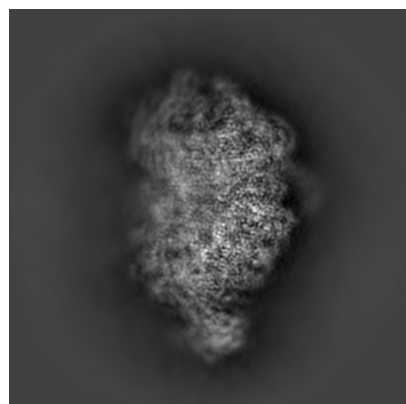
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10842. These allow visual inspection of the internal detail of the map and identification of artifacts.

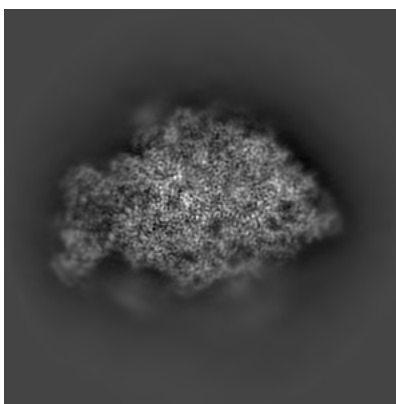
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

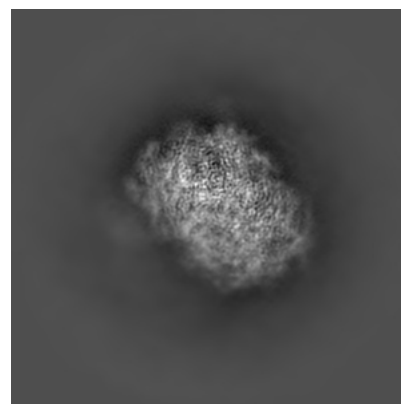
6.1.1 Primary map



X

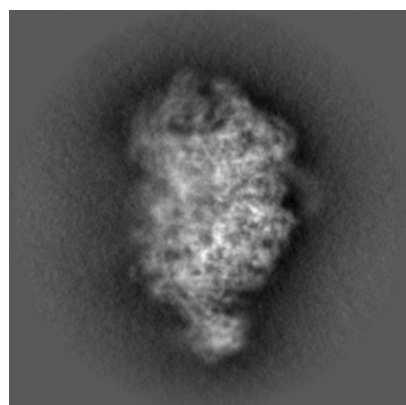


Y

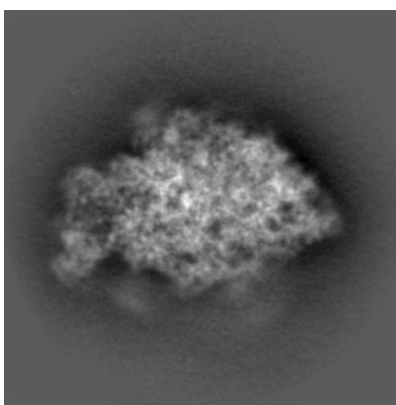


Z

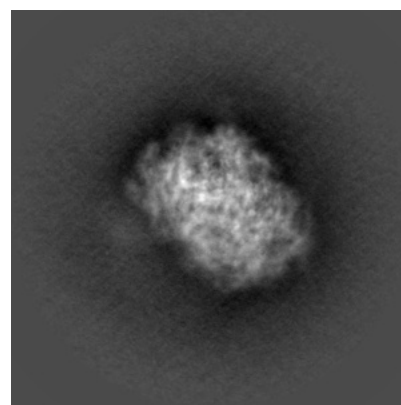
6.1.2 Raw map



X



Y

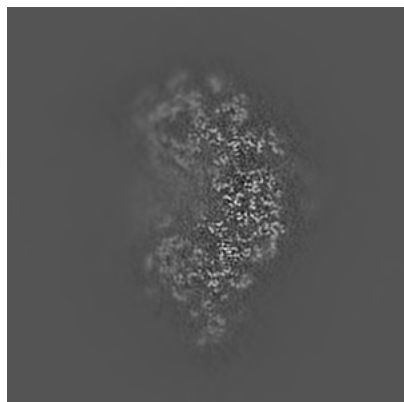


Z

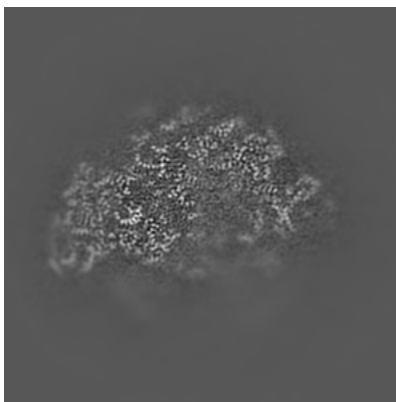
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

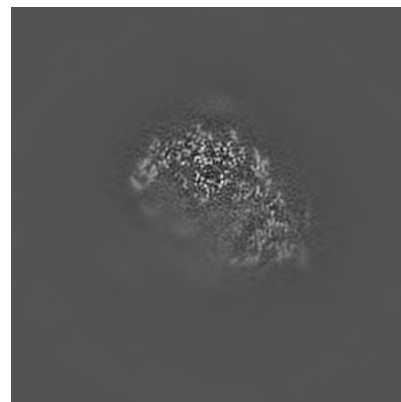
6.2.1 Primary map



X Index: 192

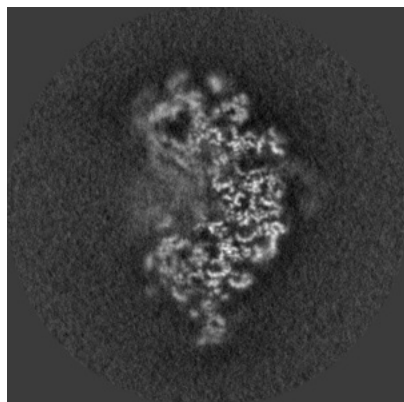


Y Index: 192

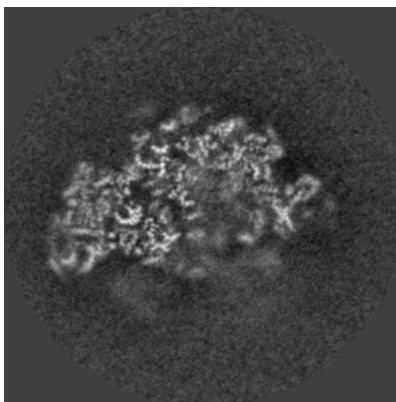


Z Index: 192

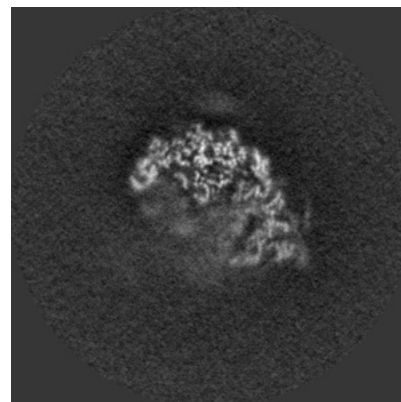
6.2.2 Raw map



X Index: 192



Y Index: 192

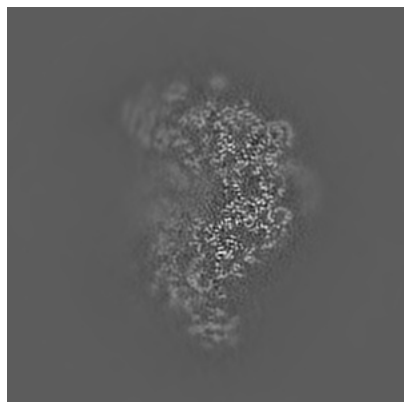


Z Index: 192

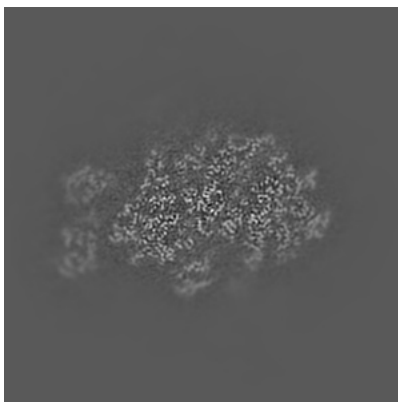
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

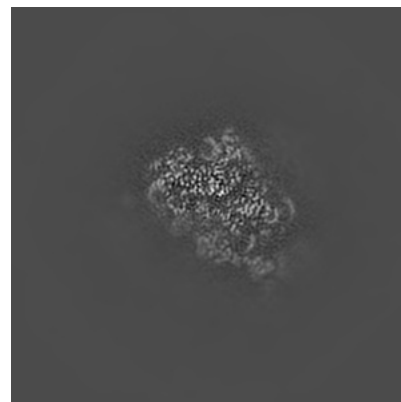
6.3.1 Primary map



X Index: 201

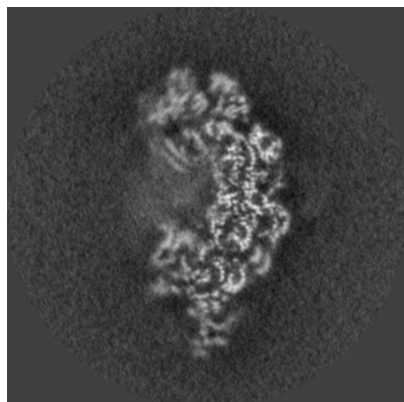


Y Index: 216

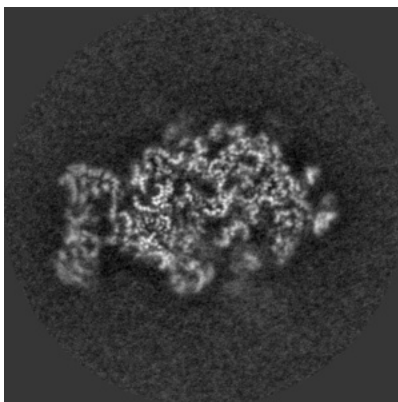


Z Index: 152

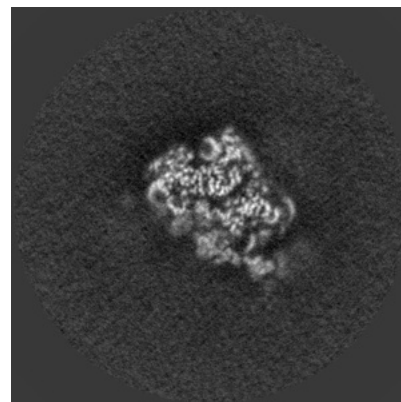
6.3.2 Raw map



X Index: 185



Y Index: 209

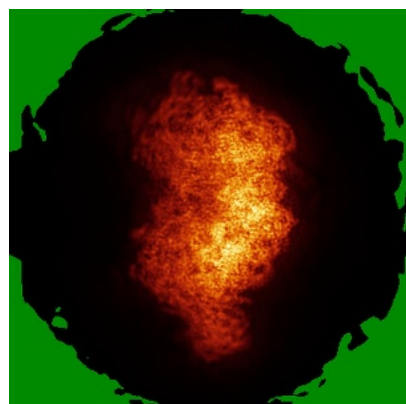


Z Index: 152

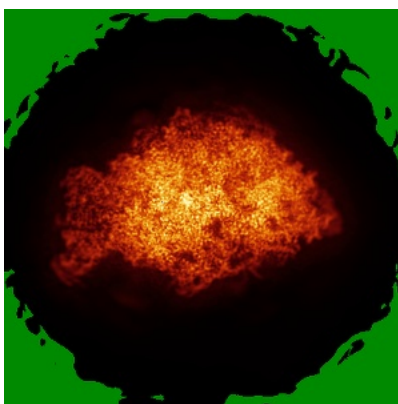
The images above show the largest variance slices of the map in three orthogonal directions.

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

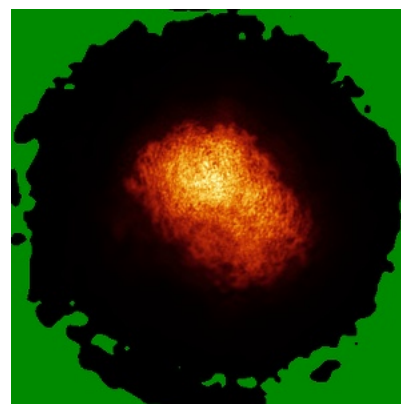
6.4.1 Primary map



X

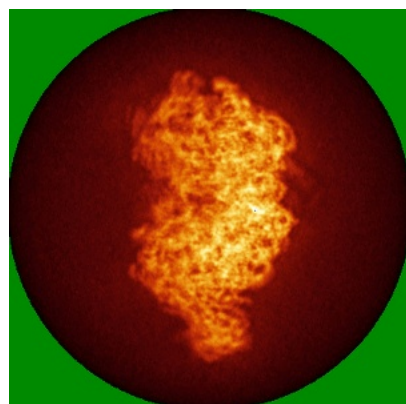


Y

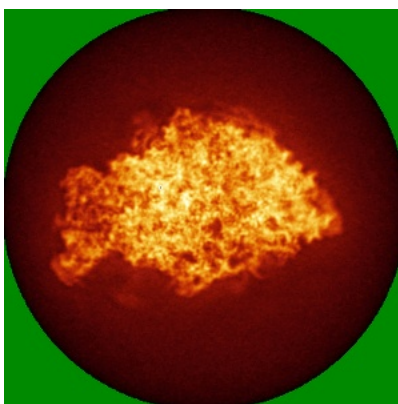


Z

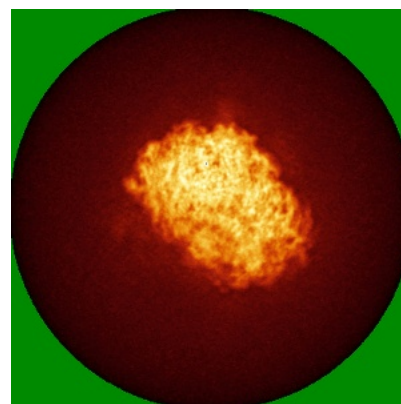
6.4.2 Raw map



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 0.04. 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.

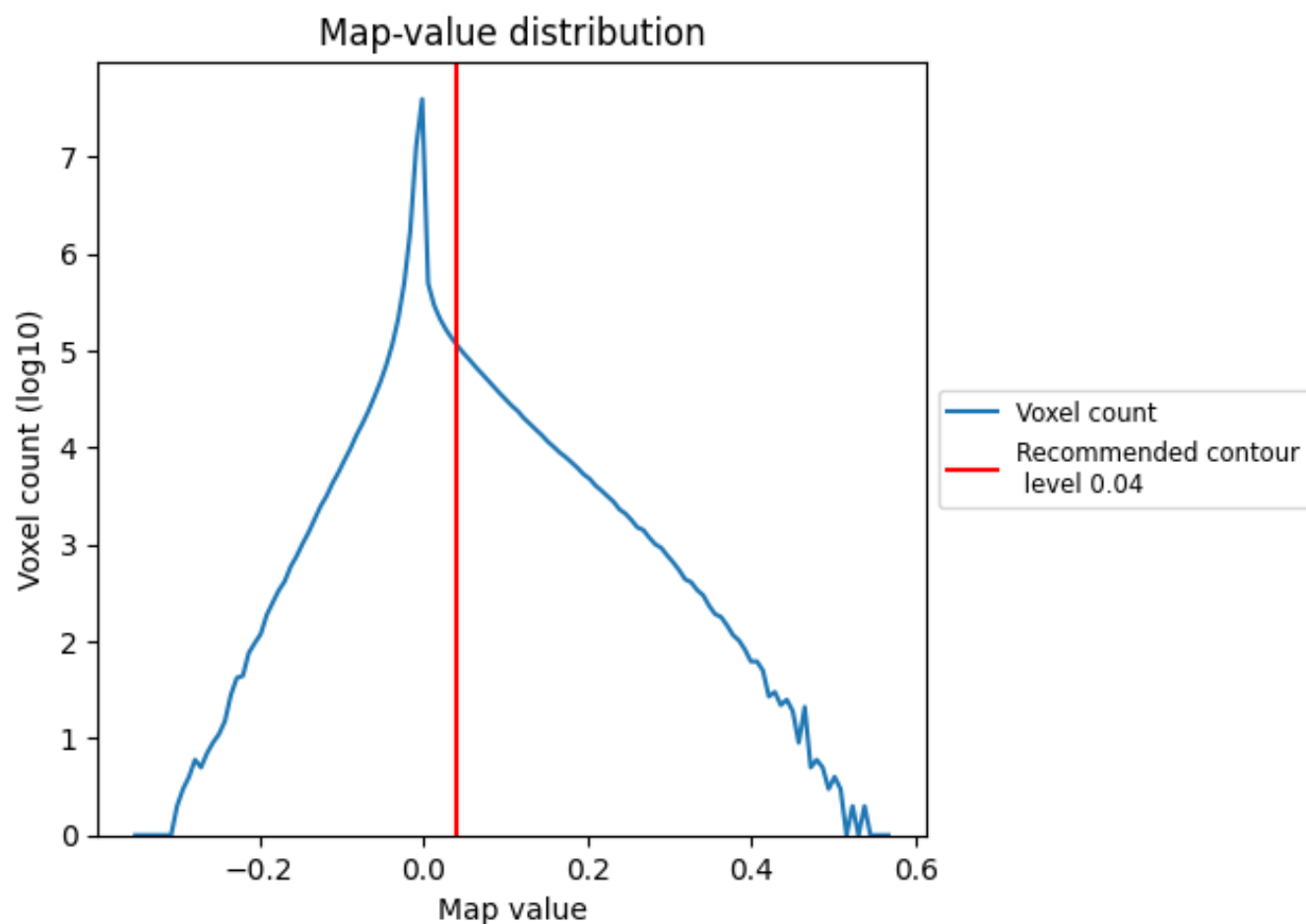
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

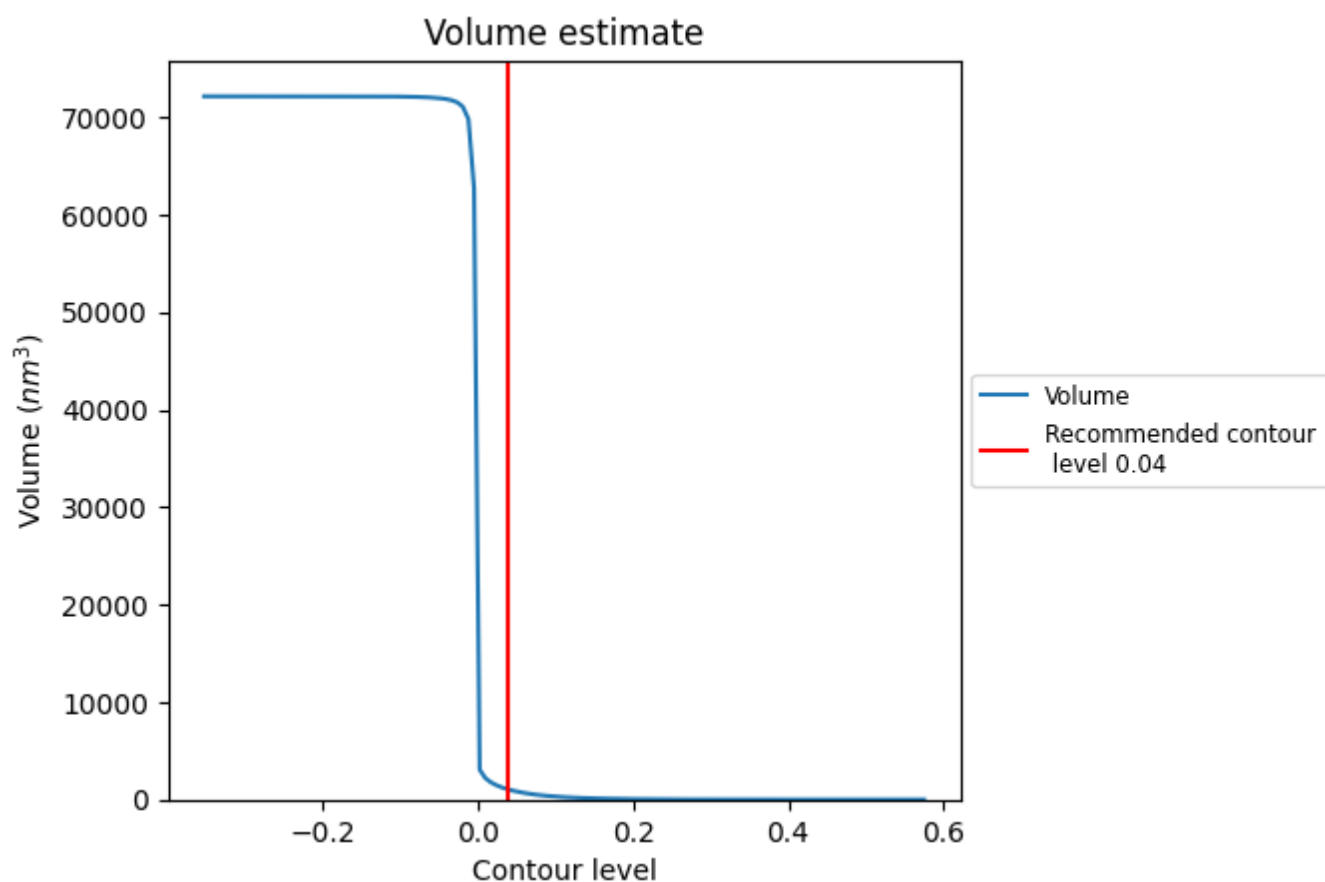
This section contains the results of statistical analysis of the map.

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.

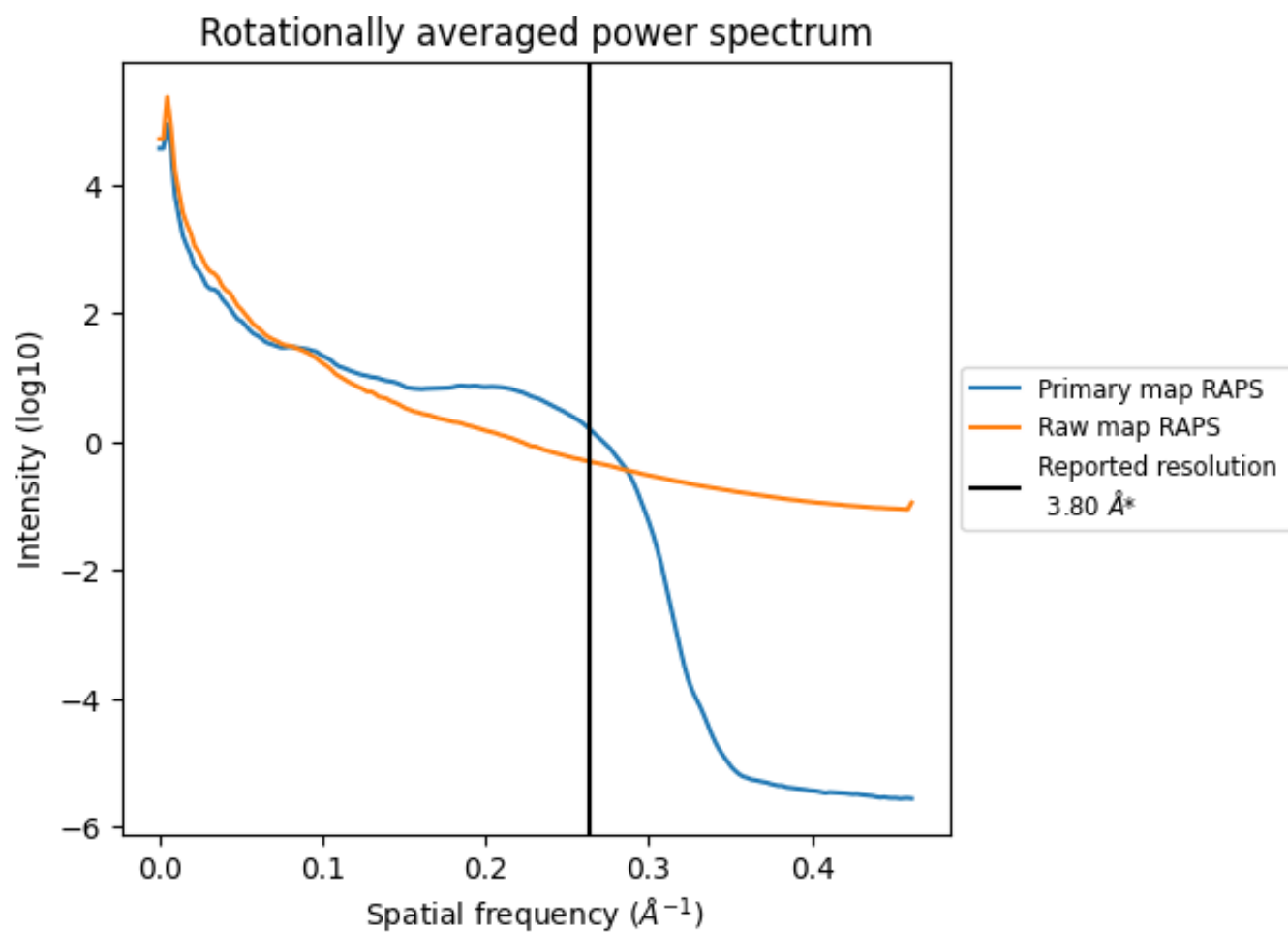
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1033 nm³; this corresponds to an approximate mass of 934 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 ⓘ

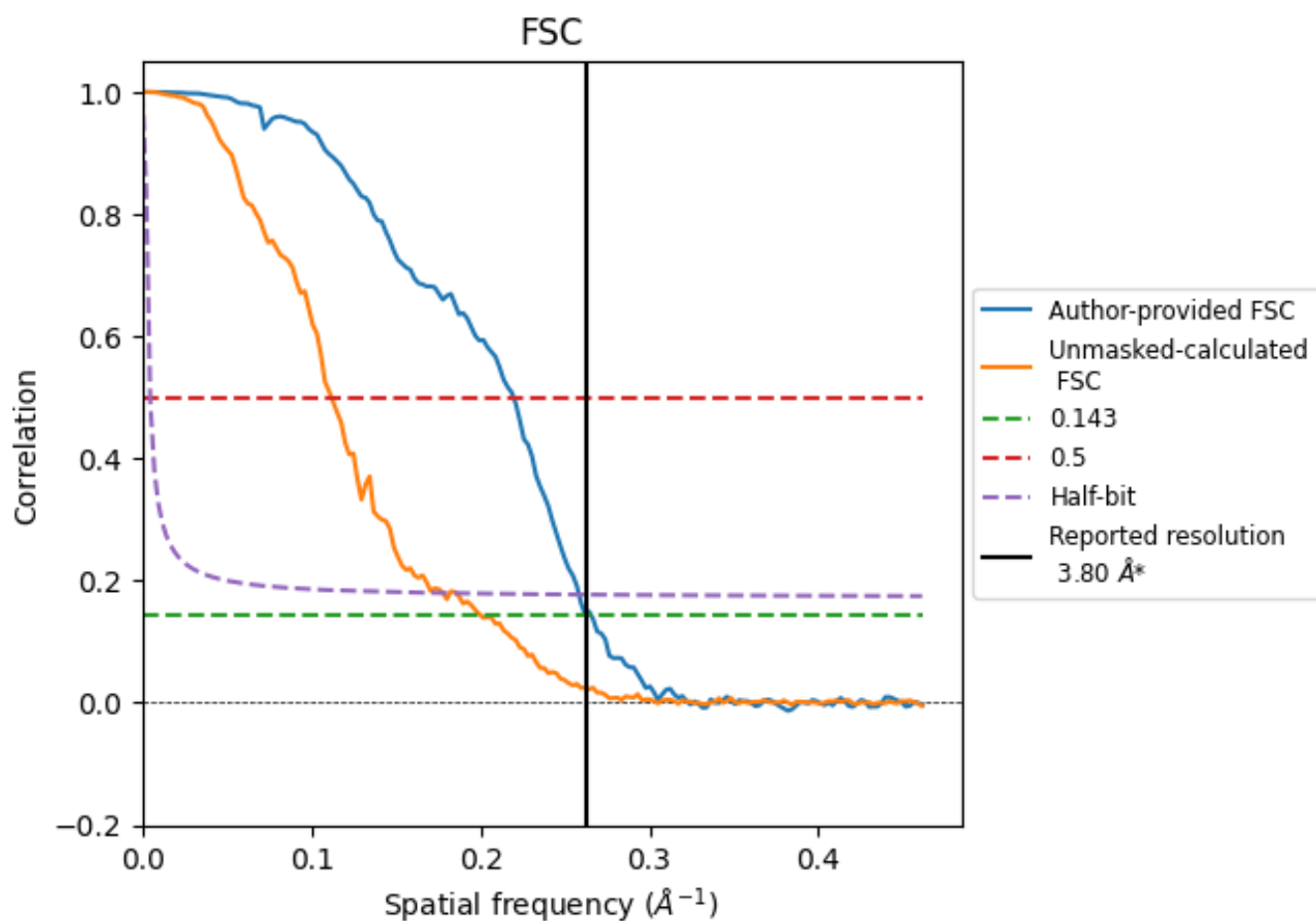


*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

8 Fourier-Shell correlation [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 Å⁻¹

8.2 Resolution estimates [i](#)

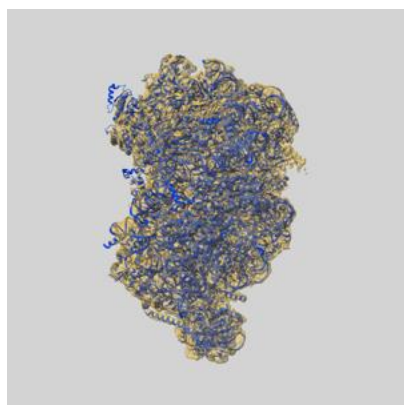
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.77	4.55	3.87
Unmasked-calculated*	5.00	8.94	5.62

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

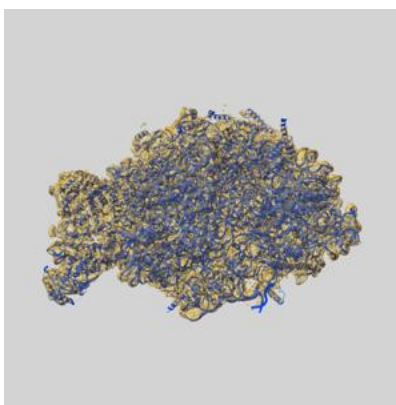
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-10842 and PDB model 6YLY. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

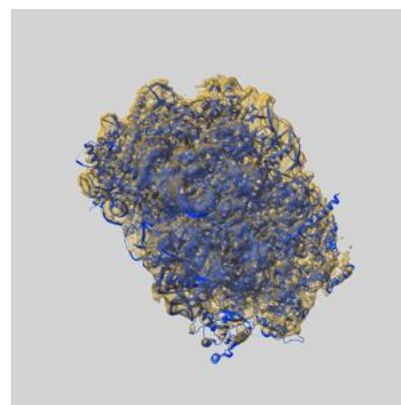
9.1 Map-model overlay [i](#)



X



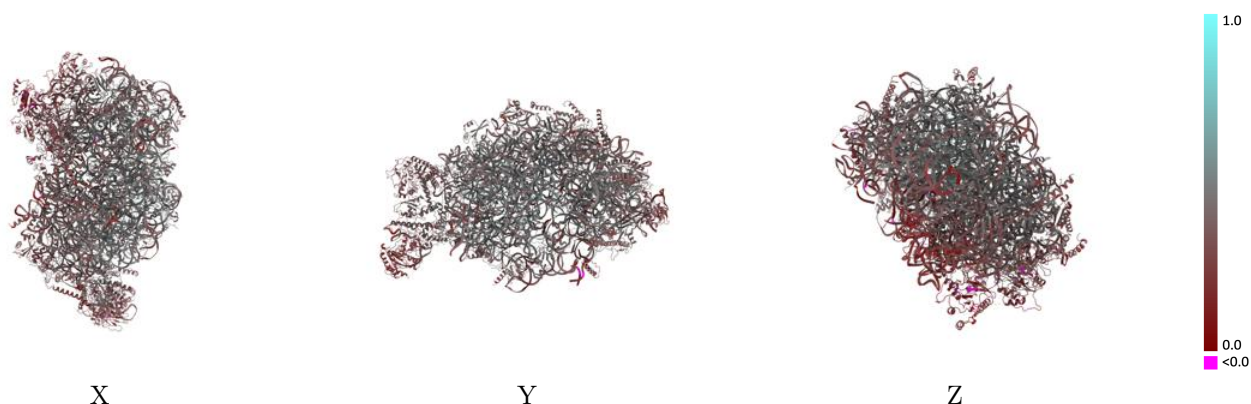
Y



Z

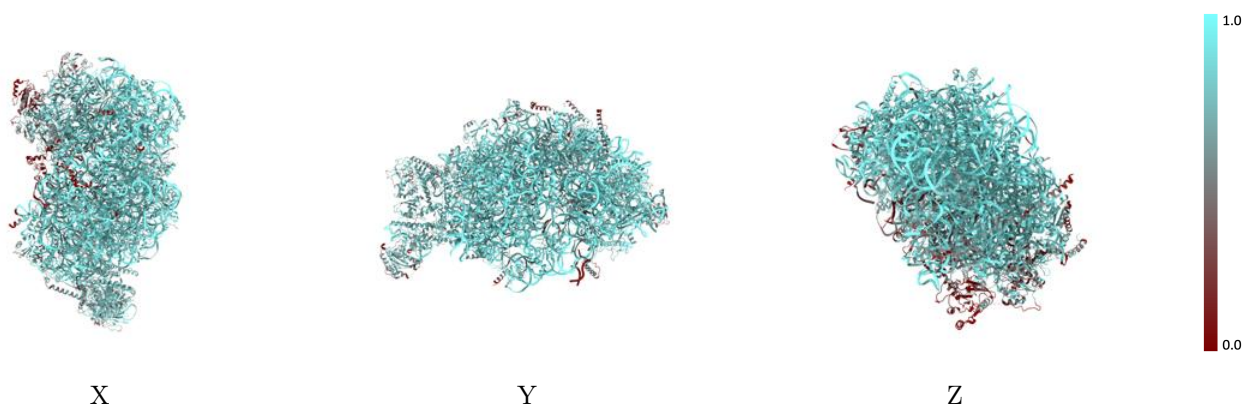
The images above show the 3D surface view of the map at the recommended contour level 0.04 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



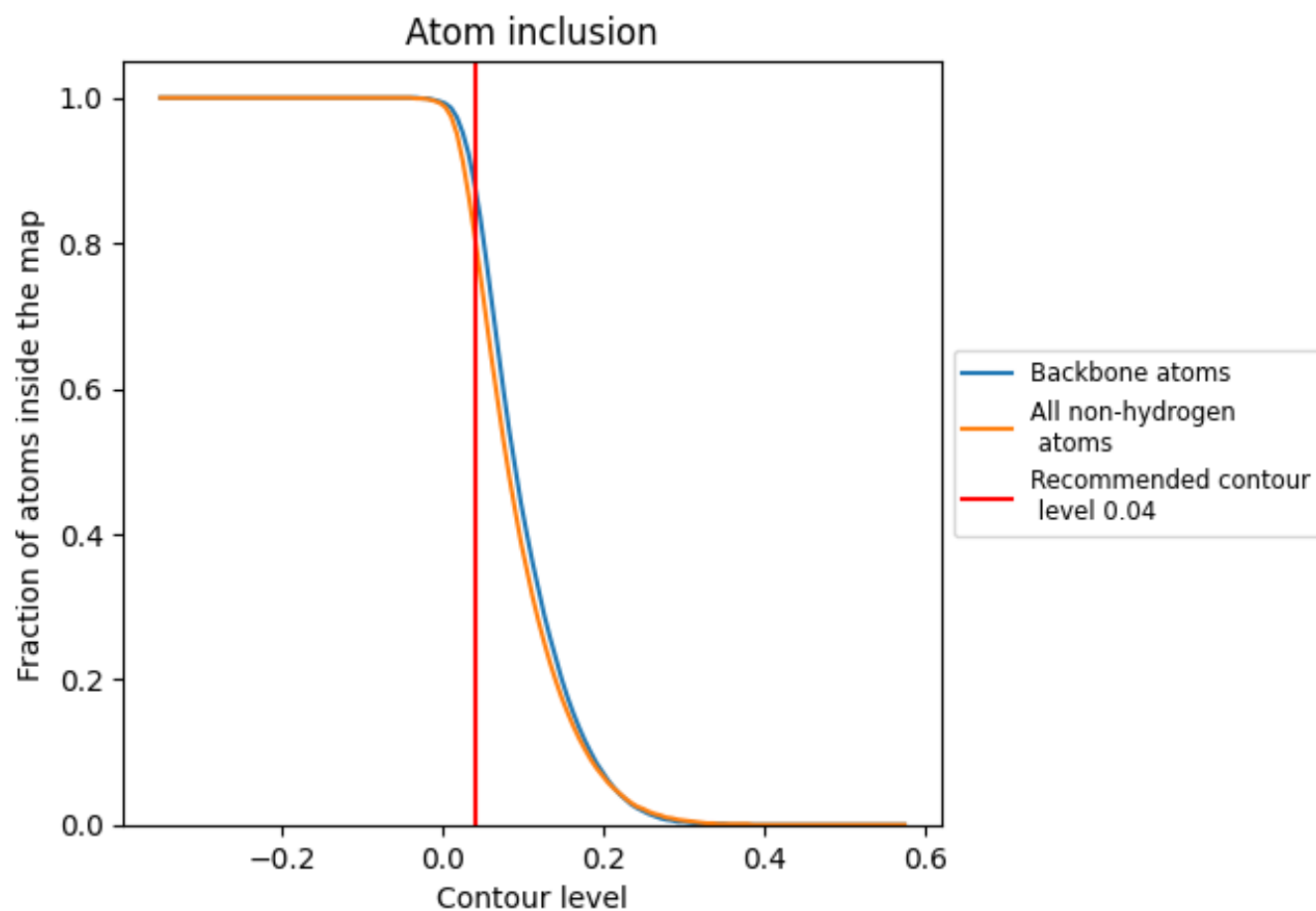
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.04).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 81% 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 (0.04) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8060	 0.3920
1	 0.8710	 0.3950
3	 0.9430	 0.4660
6	 0.8750	 0.3270
A	 0.7190	 0.3890
B	 0.8170	 0.4290
C	 0.8520	 0.4680
E	 0.8300	 0.4200
F	 0.8540	 0.4290
G	 0.7940	 0.4100
H	 0.7670	 0.3790
I	 0.1280	 0.3230
K	 0.6080	 0.2480
L	 0.8090	 0.4350
M	 0.8410	 0.4230
N	 0.8550	 0.4960
O	 0.8690	 0.4670
P	 0.8430	 0.4560
Q	 0.8560	 0.4510
R	 0.7580	 0.3970
S	 0.8310	 0.4330
T	 0.5630	 0.3010
U	 0.7220	 0.3520
V	 0.7140	 0.4080
W	 0.5470	 0.2400
X	 0.8570	 0.4680
Y	 0.8690	 0.4720
Z	 0.7740	 0.3700
a	 0.8410	 0.4200
b	 0.3950	 0.2420
c	 0.6570	 0.3000
d	 0.7990	 0.4370
e	 0.8450	 0.5010
f	 0.8880	 0.5020
g	 0.7690	 0.4370



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Chain	Atom inclusion	Q-score
h	 0.8690	 0.4650
i	 0.7950	 0.3940
j	 0.8550	 0.5000
k	 0.7300	 0.3980
l	 0.7180	 0.4520
n	 0.7580	 0.3690
o	 0.7000	 0.3010
p	 0.6050	 0.3380
q	 0.5960	 0.3320
r	 0.6810	 0.3290
s	 0.4120	 0.2620
t	 0.7130	 0.3390
u	 0.6440	 0.3560
y	 0.6680	 0.2980
z	 0.4810	 0.3480