



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 09:22 PM UTC

PDB ID : 8Y0W / pdb_00008y0w
EMDB ID : EMD-37991
Title : dormant ribosome with eIF5A, eEF2 and SERBP1
Authors : Du, M.; Zeng, F.
Deposited on : 2024-01-23
Resolution : 3.40 Å(reported)

This is a wwPDB EM Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

EMDB validation analysis : 0.0.1.dev132
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

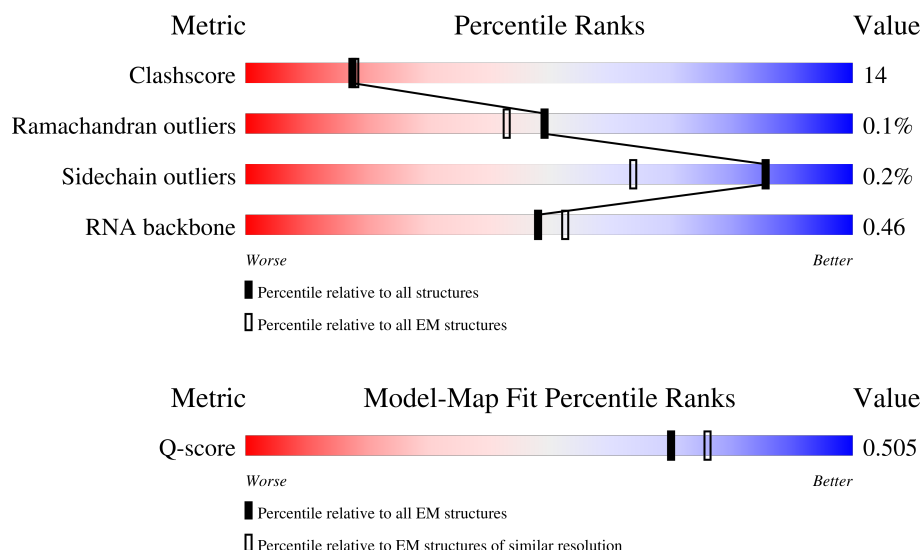
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 Å.

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



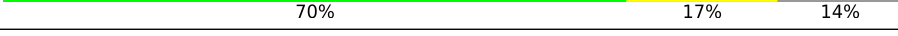
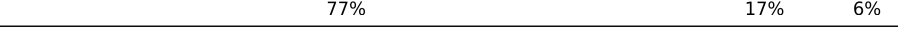
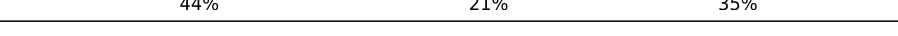
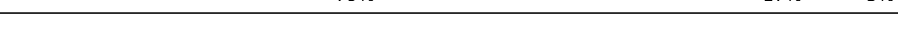
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14717 (2.90 - 3.90)

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

Mol	Chain	Length	Quality of chain
1	5	154	
2	CB	858	
3	L5	5070	

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Mol	Chain	Length	Quality of chain
4	L7	121	
5	L8	157	
6	LA	257	
7	LB	403	
8	LC	427	
9	LD	297	
10	LE	288	
11	LF	248	
12	LG	266	
13	LH	192	
14	LI	214	
15	LJ	178	
16	LL	211	
17	LM	215	
18	LN	204	
19	LO	203	
20	LP	184	
21	LQ	188	
22	LR	196	
23	LS	176	
24	LT	160	
25	LU	128	
26	LV	140	
27	LW	157	
28	LX	156	

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Mol	Chain	Length	Quality of chain
29	LY	145	
30	LZ	136	
31	La	148	
32	Lb	159	
33	Lc	115	
34	Ld	125	
35	Le	135	
36	Lf	110	
37	Lg	117	
38	Lh	123	
39	Li	105	
40	Lj	97	
41	Lk	70	
42	Ll	51	
43	Lm	128	
44	Ln	25	
45	Lo	106	
46	Lp	92	
47	Lr	137	
48	LZ	217	
49	S	402	
50	S2	1869	
51	SA	295	
52	SB	264	
53	SC	293	

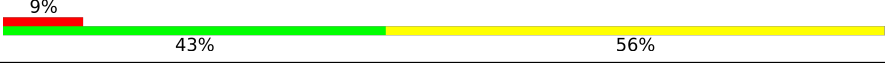
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Mol	Chain	Length	Quality of chain
54	SD	243	
55	SE	263	
56	SF	204	
57	SG	249	
58	SH	194	
59	SI	208	
60	SJ	194	
61	SK	165	
62	SL	158	
63	SN	151	
64	SO	151	
65	SP	145	
66	SQ	146	
67	SR	135	
68	SS	152	
69	ST	145	
70	SU	119	
71	SV	83	
72	SW	130	
73	SX	143	
74	SY	133	
75	SZ	125	
76	Sa	115	
77	Sb	84	
78	Sc	69	

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Mol	Chain	Length	Quality of chain
79	Sd	56	
80	Se	59	
81	Sg	317	

2 Entry composition

There are 83 unique types of molecules in this entry. The entry contains 220486 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 Eukaryotic translation initiation factor 5A-1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	131	Total	C	N	O	S	0	0
			992	620	168	196	8		

- Molecule 2 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	CB	768	Total	C	N	O	S	0	0
			6014	3818	1036	1121	39		

- Molecule 3 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	L5	3666	Total	C	N	O	P	0	0
			78591	34997	14383	25546	3665		

- Molecule 4 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L7	120	Total	C	N	O	P	0	0
			2561	1141	456	844	120		

- Molecule 5 is a RNA chain called 5.8S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 6 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LA	248	Total	C	N	O	S	0	0
			1898	1189	389	314	6		

- Molecule 7 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	LB	402	Total	C	N	O	S	0	0
			3238	2060	608	556	14		

- Molecule 8 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LC	366	Total	C	N	O	S	0	0
			2914	1832	581	487	14		

- Molecule 9 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LD	293	Total	C	N	O	S	0	0
			2382	1507	434	427	14		

- Molecule 10 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LE	232	Total	C	N	O	S	0	0
			1873	1203	353	313	4		

- Molecule 11 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LF	225	Total	C	N	O	S	0	0
			1870	1202	358	301	9		

- Molecule 12 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	LG	230	Total	C	N	O	S	0	0
			1858	1185	357	312	4		

- Molecule 13 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LH	190	Total	C	N	O	S	0	0
			1518	956	284	272	6		

- Molecule 14 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	LI	202	Total	C	N	O	S	0	0
			1634	1037	314	269	14		

- Molecule 15 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	LJ	174	Total	C	N	O	S	0	0
			1398	880	261	251	6		

- Molecule 16 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LL	210	Total	C	N	O	S	0	0
			1701	1064	352	281	4		

- Molecule 17 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	LM	139	Total	C	N	O	S	0	0
			1138	730	218	183	7		

- Molecule 18 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	LN	203	Total	C	N	O	S	0	0
			1701	1072	359	266	4		

- Molecule 19 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LO	201	Total	C	N	O	S	0	0
			1650	1063	321	261	5		

- Molecule 20 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LP	153	Total	C	N	O	S	0	0
			1242	776	241	216	9		

- Molecule 21 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LQ	185	Total	C	N	O	S	0	0
			1496	933	310	248	5		

- Molecule 22 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	LR	187	Total	C	N	O	S	0	0
			1566	971	336	250	9		

- Molecule 23 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	LS	173	Total	C	N	O	S	0	0
			1437	914	280	233	10		

- Molecule 24 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	LT	159	Total	C	N	O	S	0	0
			1298	823	252	217	6		

- Molecule 25 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	LU	101	Total	C	N	O	S	0	0
			825	529	144	150	2		

- Molecule 26 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LV	131	Total	C	N	O	S	0	0
			979	618	184	172	5		

- Molecule 27 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	LW	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 28 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LX	115	Total	C	N	O	S	0	0
			939	600	174	164	1		

- Molecule 29 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LY	134	Total	C	N	O	S	0	0
			1115	700	226	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	LZ	135	Total	C	N	O	S	0	0
			1107	714	208	182	3		

- Molecule 31 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	La	145	Total	C	N	O	S	0	0
			1149	728	234	184	3		

- Molecule 32 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Lb	109	Total	C	N	O	S	0	0
			876	546	189	137	4		

- Molecule 33 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	Lc	98	Total	C	N	O	S	0	0
			764	485	135	138	6		

- Molecule 34 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Ld	107	Total	C	N	O	S	0	0
			888	560	171	155	2		

- Molecule 35 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Le	128	Total	C	N	O	S	0	0
			1053	667	216	165	5		

- Molecule 36 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	Lf	109	Total	C	N	O	S	0	0
			876	555	174	144	3		

- Molecule 37 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	Lg	114	Total	C	N	O	S	0	0
			906	566	187	147	6		

- Molecule 38 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Lh	122	Total	C	N	O	S	0	0
			1015	641	205	168	1		

- Molecule 39 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Li	102	Total	C	N	O	S	0	0
			832	521	177	129	5		

- Molecule 40 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Lj	86	Total	C	N	O	S	0	0
			705	434	155	111	5		

- Molecule 41 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	Lk	69	Total	C	N	O	S	0	0
			569	366	103	99	1		

- Molecule 42 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	Ll	50	Total	C	N	O	S	0	0
			444	281	98	64	1		

- Molecule 43 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lm	52	Total	C	N	O	S	0	0
			429	266	90	67	6		

- Molecule 44 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	Ln	24	Total	C	N	O	S	0	0
			230	139	62	26	3		

- Molecule 45 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Lo	102	Total	C	N	O	S	0	0
			834	522	171	135	6		

- Molecule 46 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lp	91	Total	C	N	O	S	0	0
			708	445	136	120	7		

- Molecule 47 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 48 is a protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Lz	205	Total	C	N	O	S	0	0
			1643	1054	291	290	8		

- Molecule 49 is a protein called Isoform 2 of SERPINE1 mRNA-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	S	55	Total	C	N	O	0	0
			440	263	87	90		

- Molecule 50 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S2	1735	Total	C	N	O	P	0	0
			36789	16410	6578	12067	1734		

- Molecule 51 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SA	217	Total	C	N	O	S	0	0
			1718	1092	301	317	8		

- Molecule 52 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SB	214	Total	C	N	O	S	0	0
			1738	1103	310	311	14		

- Molecule 53 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	SC	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 54 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SD	227	Total	C	N	O	S	0	0
			1765	1125	317	315	8		

- Molecule 55 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SE	262	Total	C	N	O	S	0	0
			2076	1324	386	358	8		

- Molecule 56 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SF	189	Total	C	N	O	S	0	0
			1495	934	284	270	7		

- Molecule 57 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SG	237	Total	C	N	O	S	0	0
			1923	1200	387	329	7		

- Molecule 58 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	SH	186	Total	C	N	O	S	0	0
			1497	956	274	266	1		

- Molecule 59 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SI	206	Total	C	N	O	S	0	0
			1686	1058	332	291	5		

- Molecule 60 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	SJ	185	Total	C	N	O	S	0	0
			1525	969	306	248	2		

- Molecule 61 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SK	98	Total	C	N	O	S	0	0
			827	539	148	134	6		

- Molecule 62 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SL	145	Total	C	N	O	S	0	0
			1188	757	224	201	6		

- Molecule 63 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SN	150	Total	C	N	O	S	0	0
			1208	773	229	205	1		

- Molecule 64 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO	134	Total	C	N	O	S	0	0
			1002	612	197	187	6		

- Molecule 65 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SP	121	Total	C	N	O	S	0	0
			985	623	185	170	7		

- Molecule 66 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	SQ	144	Total	C	N	O	S	0	0
			1142	726	216	197	3		

- Molecule 67 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SR	132	Total	C	N	O	S	0	0
			1067	671	196	195	5		

- Molecule 68 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	145	Total	C	N	O	S	0	0
			1198	751	242	203	2		

- Molecule 69 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	ST	140	Total	C	N	O	S	0	0
			1094	685	211	195	3		

- Molecule 70 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SU	103	Total	C	N	O	S	0	0
			817	511	155	147	4		

- Molecule 71 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SV	83	Total	C	N	O	S	0	0
			636	393	117	121	5		

- Molecule 72 is a protein called 40S ribosomal protein S15a.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SW	129	Total	C	N	O	S	0	0
			1034	659	193	176	6		

- Molecule 73 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SX	141	Total	C	N	O	S	0	0
			1098	693	219	183	3		

- Molecule 74 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY	131	Total	C	N	O	S	0	0
			1059	667	209	178	5		

- Molecule 75 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	SZ	69	Total	C	N	O	S	0	0
			546	352	99	94	1		

- Molecule 76 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sa	102	Total	C	N	O	S	0	0
			821	512	171	133	5		

- Molecule 77 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Sb	83	Total	C	N	O	S	0	0
			651	408	121	115	7		

- Molecule 78 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Sc	64	Total	C	N	O	S	0	0
			506	308	102	94	2		

- Molecule 79 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 80 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Se	58	Total	C	N	O	S	0	0
			459	284	100	74	1		

- Molecule 81 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Sg	313	Total	C	N	O	S	0	0
			2430	1532	421	465	12		

- Molecule 82 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	L5	211	Total	Mg	0
			211	211	
82	L7	3	Total	Mg	0
			3	3	
82	L8	5	Total	Mg	0
			5	5	
82	LA	1	Total	Mg	0
			1	1	
82	LB	1	Total	Mg	0
			1	1	
82	LI	1	Total	Mg	0
			1	1	

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Continued from previous page...

Mol	Chain	Residues	Atoms		AltConf
82	LP	1	Total 1	Mg 1	0
82	LV	1	Total 1	Mg 1	0
82	Le	1	Total 1	Mg 1	0
82	Lg	1	Total 1	Mg 1	0

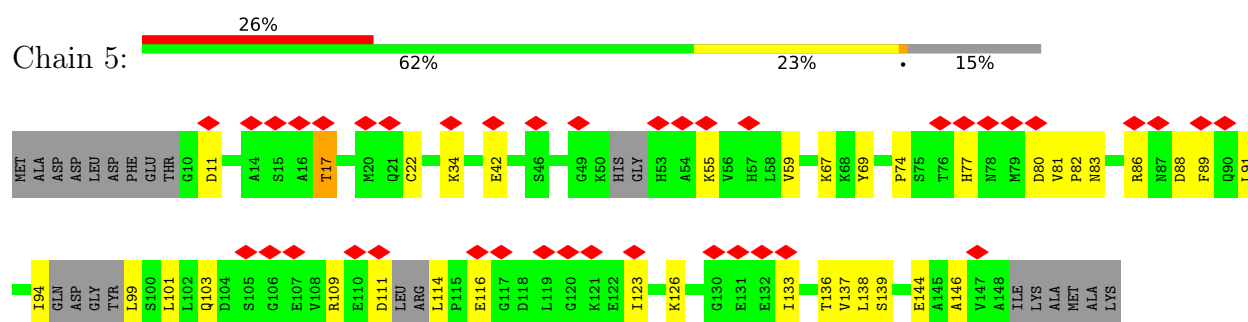
- Molecule 83 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
83	Lg	1	Total 1	Zn 1	0
83	Lj	1	Total 1	Zn 1	0
83	Lm	1	Total 1	Zn 1	0
83	Lo	1	Total 1	Zn 1	0
83	Lp	1	Total 1	Zn 1	0

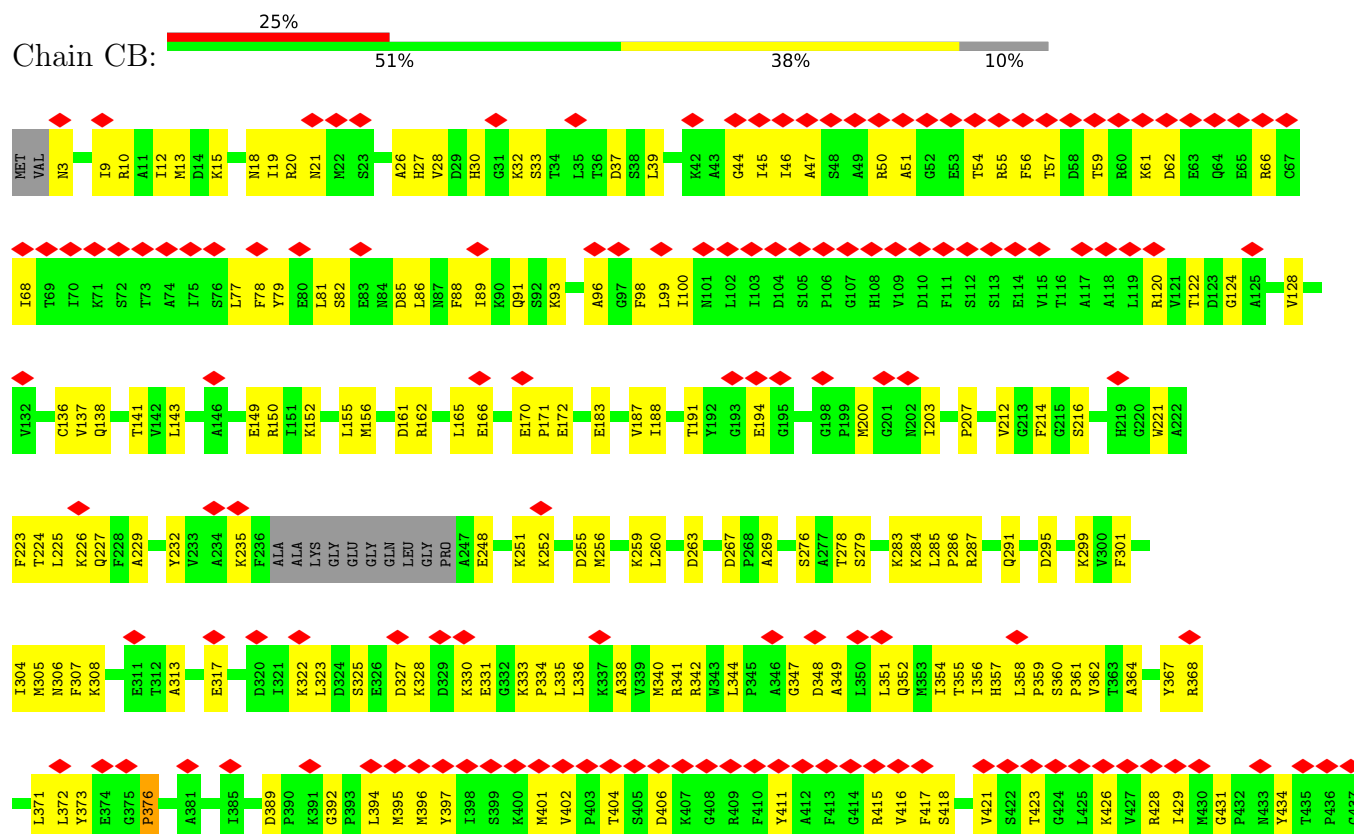
3 Residue-property plots

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: Eukaryotic translation initiation factor 5A-1



- Molecule 2: Elongation factor 2

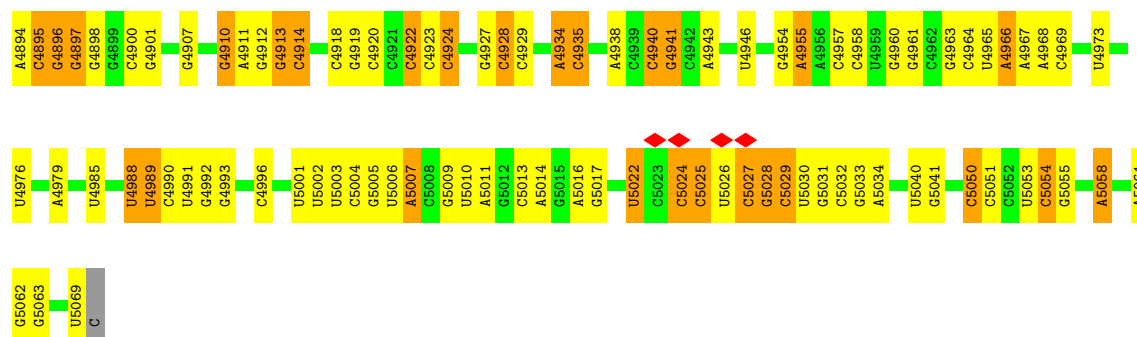






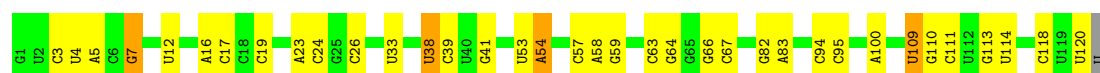






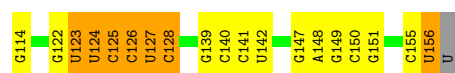
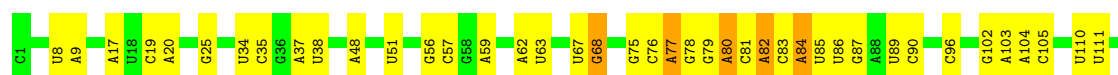
• Molecule 4: 5S rRNA

Chain L7: 69% 26% . .



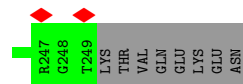
• Molecule 5: 5.8S rRNA

Chain L8: 61% 31% 8% .



• Molecule 6: 60S ribosomal protein L8

Chain LA: 84% 13% .



• Molecule 7: 60S ribosomal protein L3

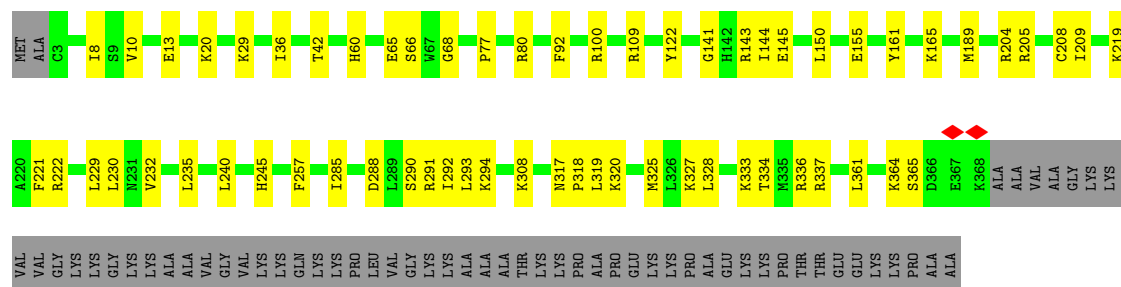
Chain LB: 76% 23%





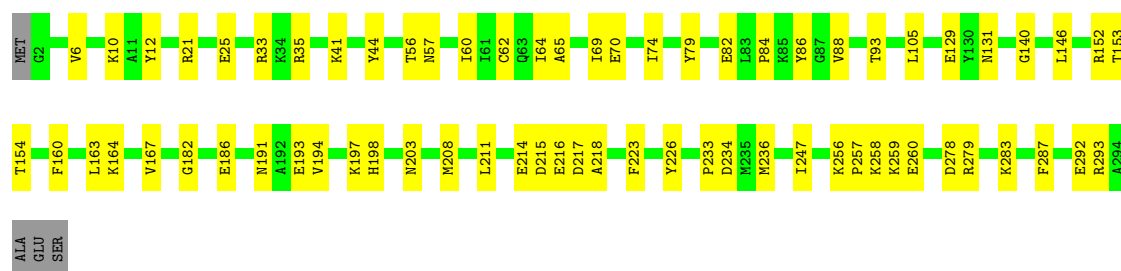
• Molecule 8: 60S ribosomal protein L4

Chain LC: 71% 15% 14%



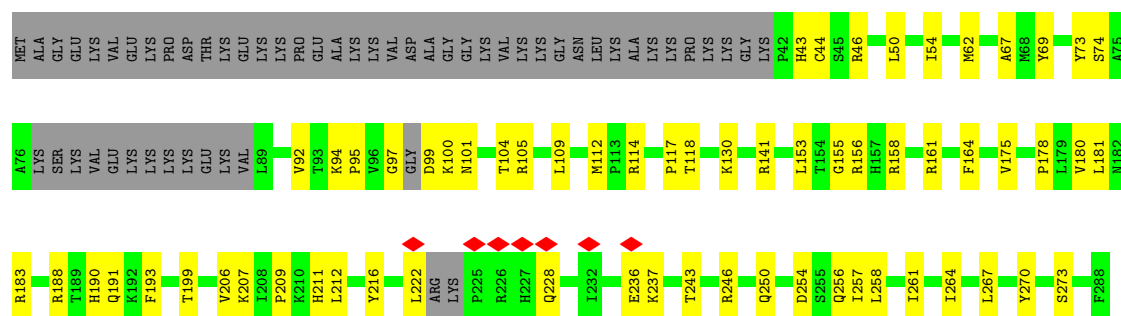
• Molecule 9: 60S ribosomal protein L5

Chain LD: 76% 23%



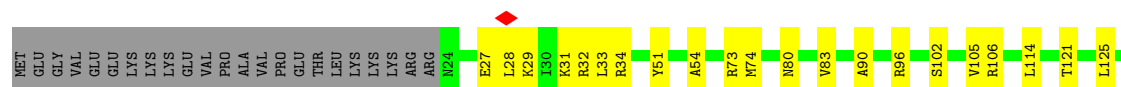
• Molecule 10: 60S ribosomal protein L6

Chain LE: 58% 22% 19%



• Molecule 11: 60S ribosomal protein L7

Chain LF: 71% 20% 9%

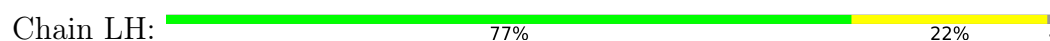




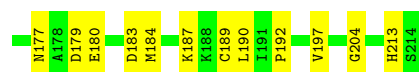
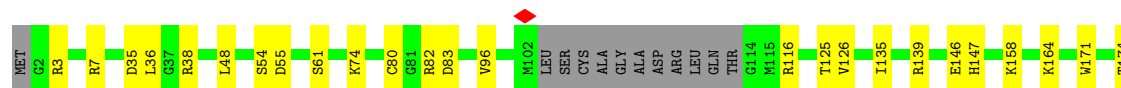
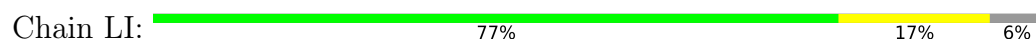
- Molecule 12: 60S ribosomal protein L7a



- Molecule 13: 60S ribosomal protein L9



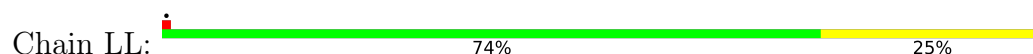
- Molecule 14: 60S ribosomal protein L10-like

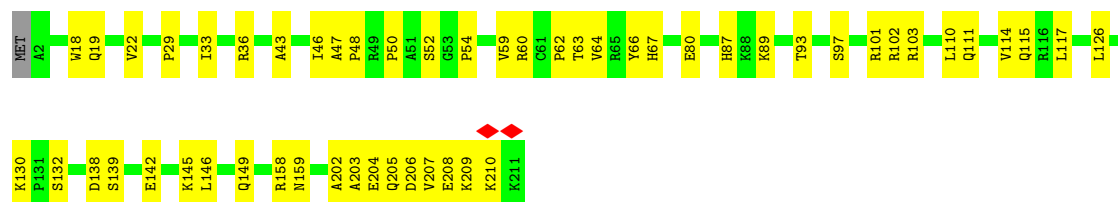


- Molecule 15: 60S ribosomal protein L11

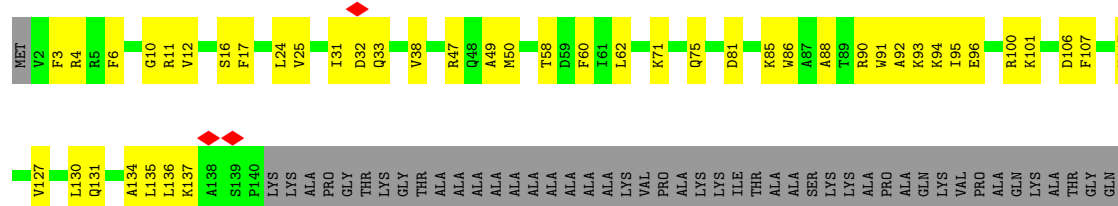


- Molecule 16: 60S ribosomal protein L13

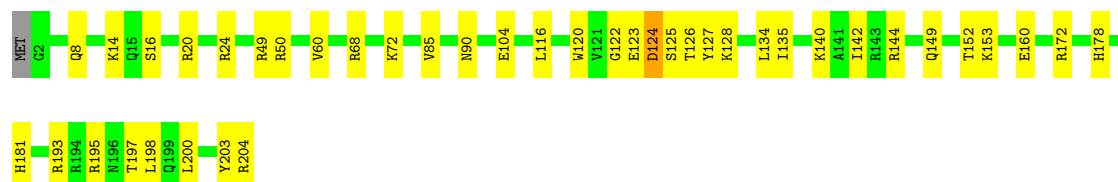
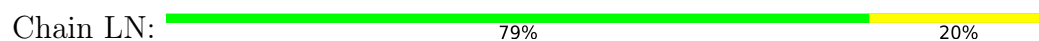




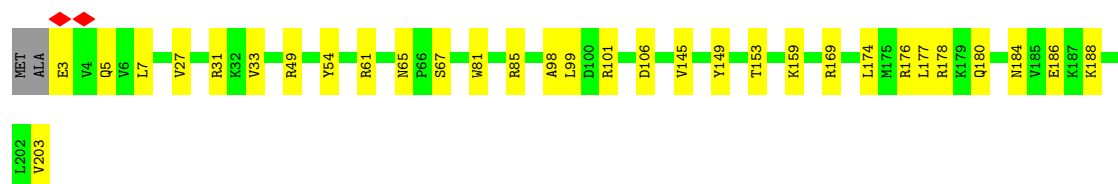
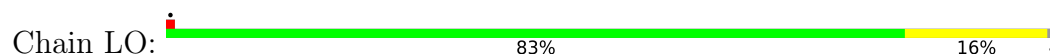
• Molecule 17: 60S ribosomal protein L14



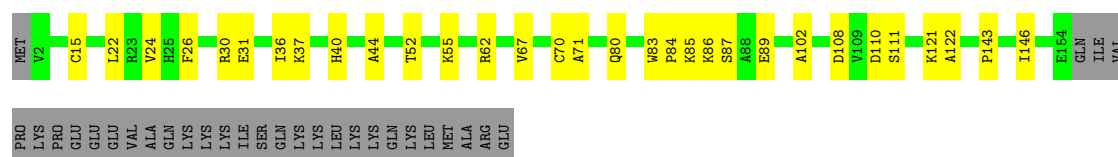
• Molecule 18: 60S ribosomal protein L15



• Molecule 19: 60S ribosomal protein L13a

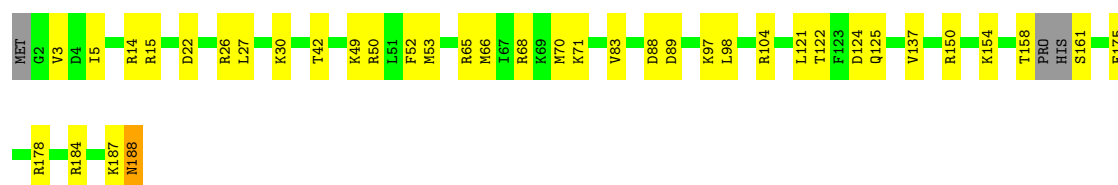


• Molecule 20: 60S ribosomal protein L17



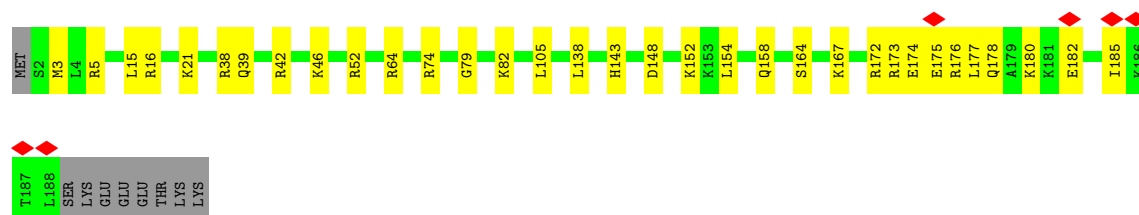
- Molecule 21: 60S ribosomal protein L18

Chain LQ:  78% 20% ..



- Molecule 22: 60S ribosomal protein L19

Chain LR:  79% 17% 5%



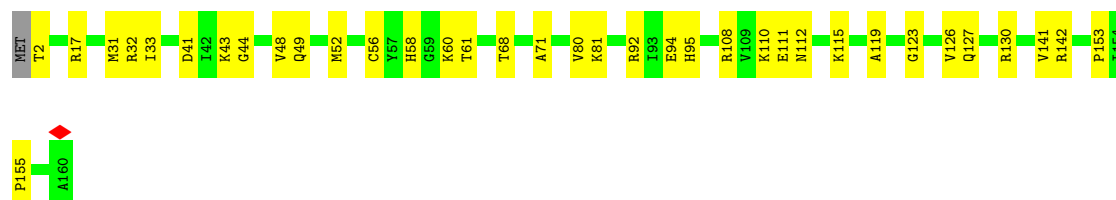
- Molecule 23: 60S ribosomal protein L18a

Chain LS:  83% 15% .



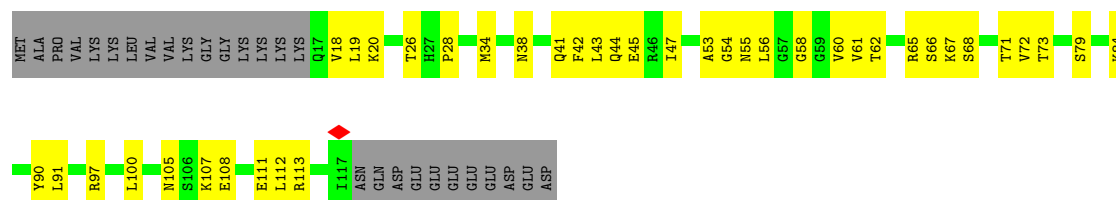
- Molecule 24: 60S ribosomal protein L21

Chain LT:  77% 22% .



- Molecule 25: 60S ribosomal protein L22

Chain LU:  48% 31% 21%



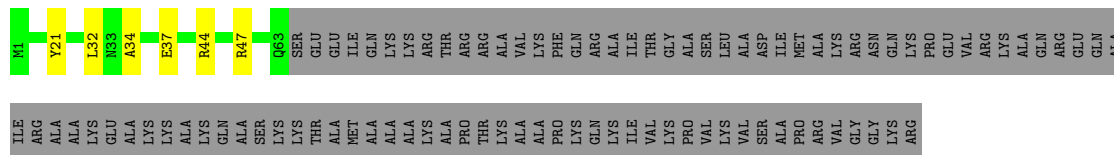
- Molecule 26: 60S ribosomal protein L23

Chain LV:  83% 11% 6%



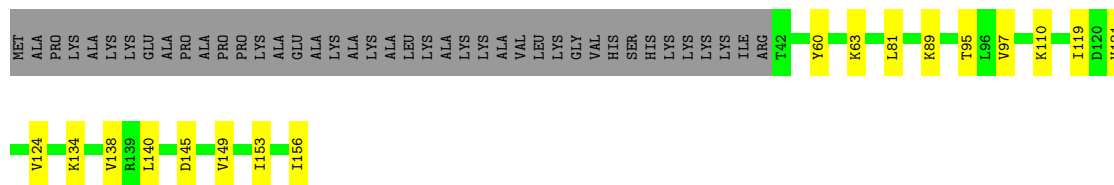
- Molecule 27: 60S ribosomal protein L24

Chain LW:  36% . 60%



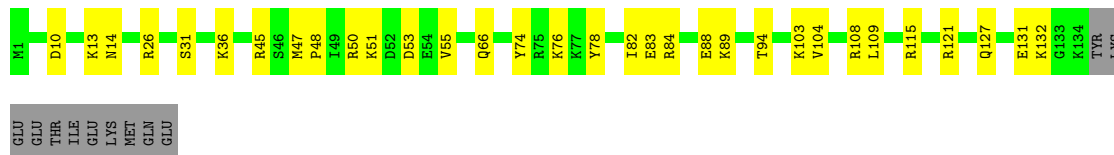
- Molecule 28: 60S ribosomal protein L23a

Chain LX:  63% 11% 26%



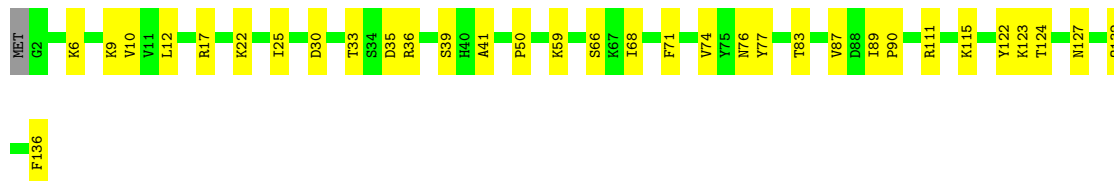
- Molecule 29: 60S ribosomal protein L26

Chain LY:  70% 22% 8%



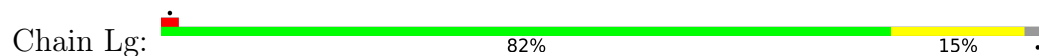
- Molecule 30: 60S ribosomal protein L27

Chain LZ:  75% 24% .



- Molecule 31: 60S ribosomal protein L27a

Chain La:  83% 15% .



- Molecule 44: 60S ribosomal protein L41

Chain Ln:  88% 8%



- Molecule 45: 60S ribosomal protein L36a

Chain Lo:  75% 21%



- Molecule 46: 60S ribosomal protein L37a

Chain Lp:  82% 17%



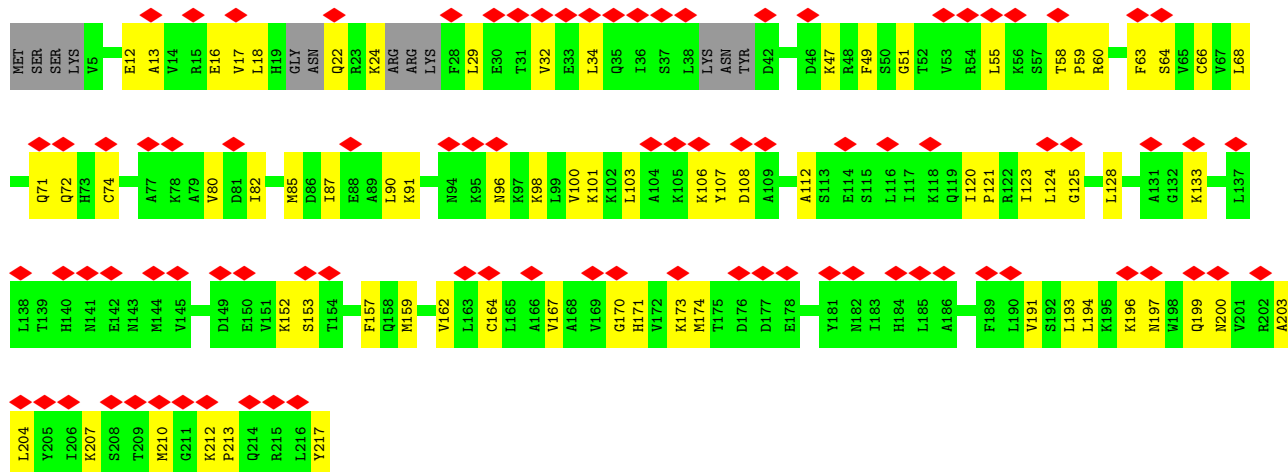
- Molecule 47: 60S ribosomal protein L28

Chain Lr:  76% 15% 9%

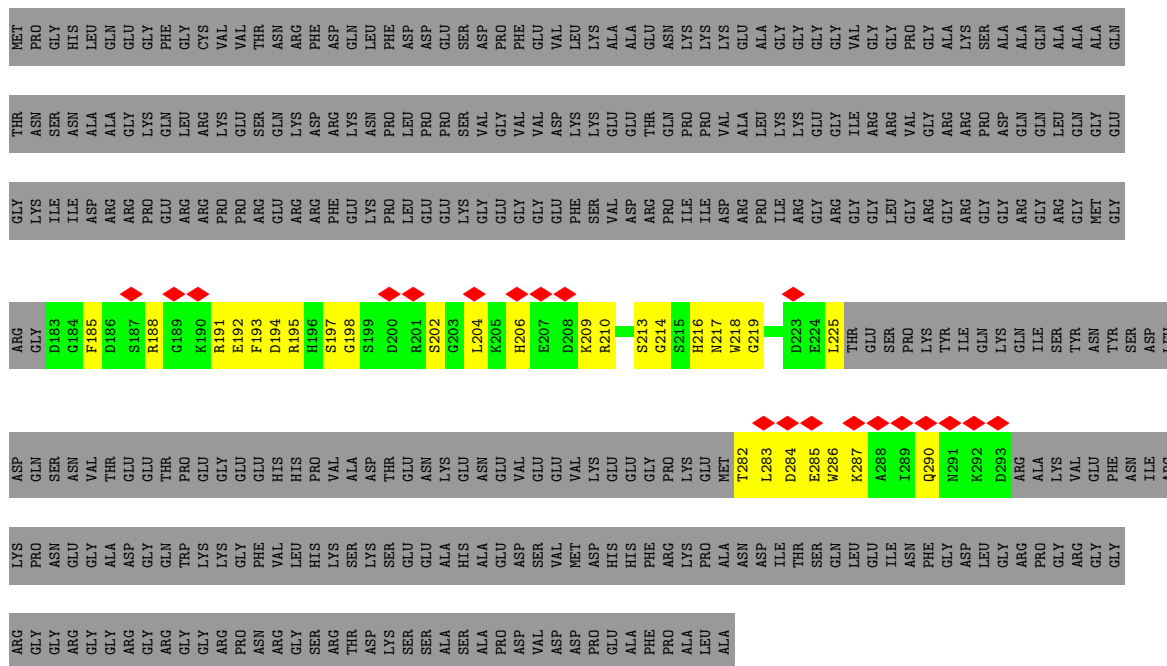


- Molecule 48: 60S ribosomal protein L10a

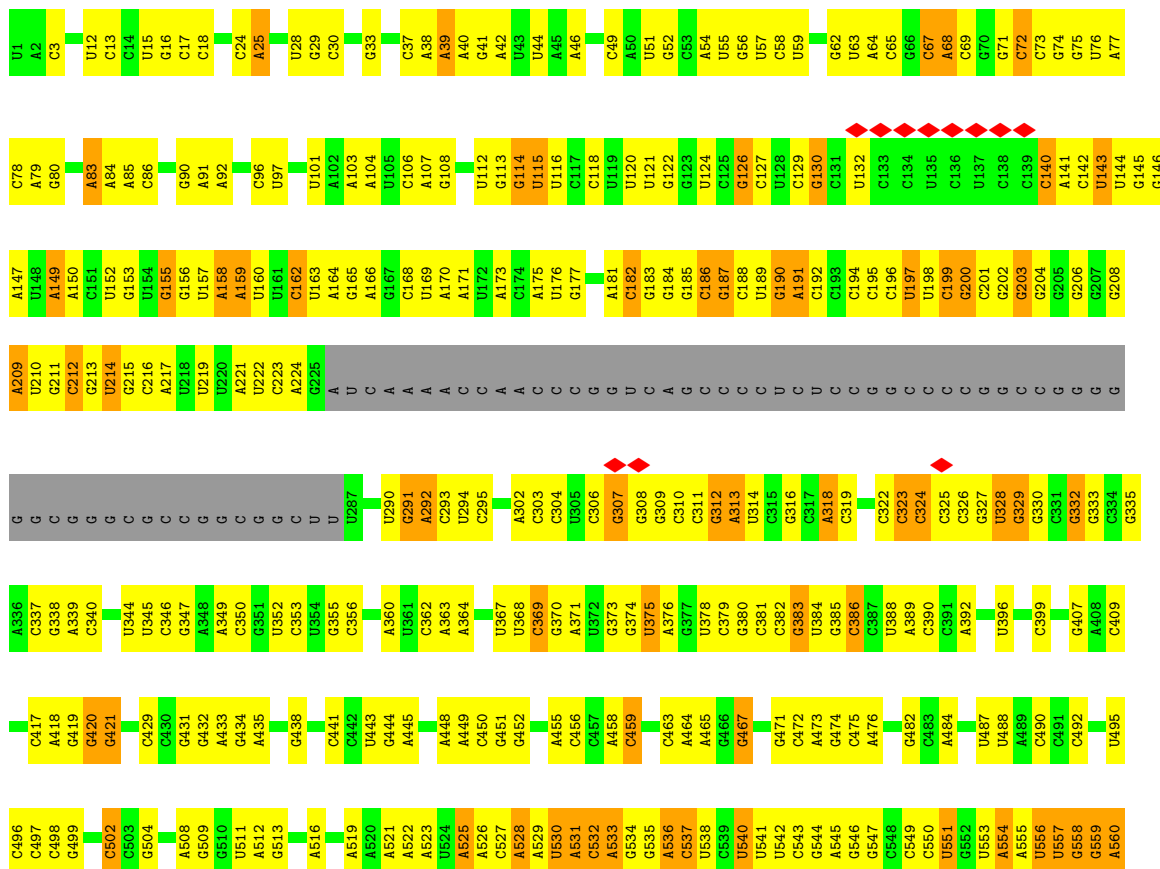
Chain Lz:  41% 62% 33% 6%



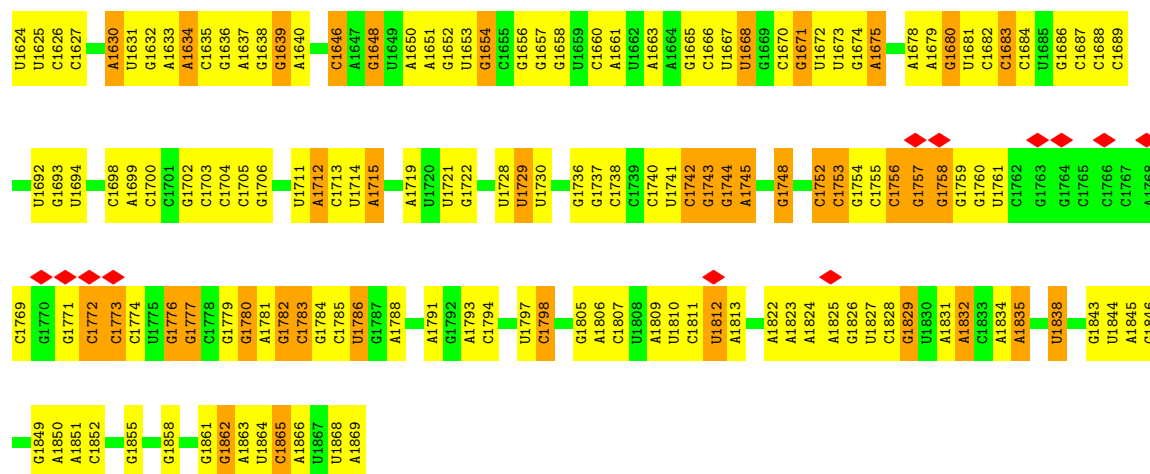
- Molecule 49: Isoform 2 of SERPINE1 mRNA-binding protein 1



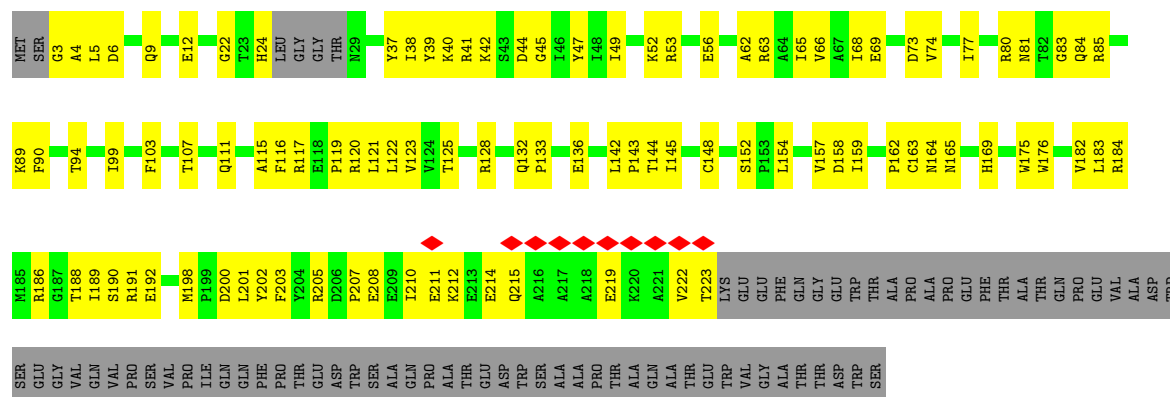
Chain S2:



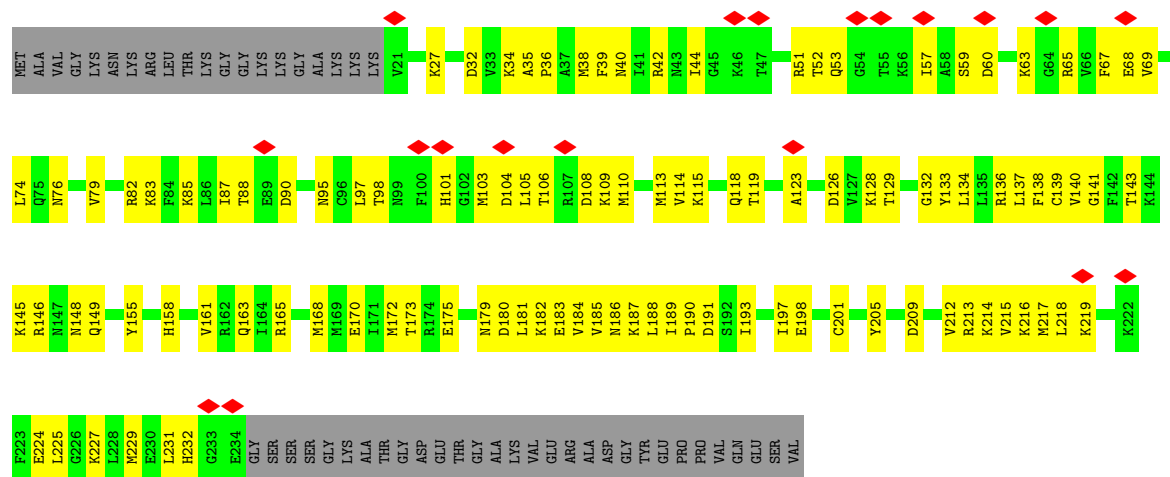
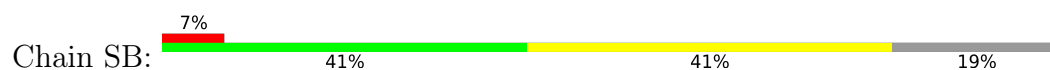




• Molecule 51: 40S ribosomal protein SA



• Molecule 52: 40S ribosomal protein S3a

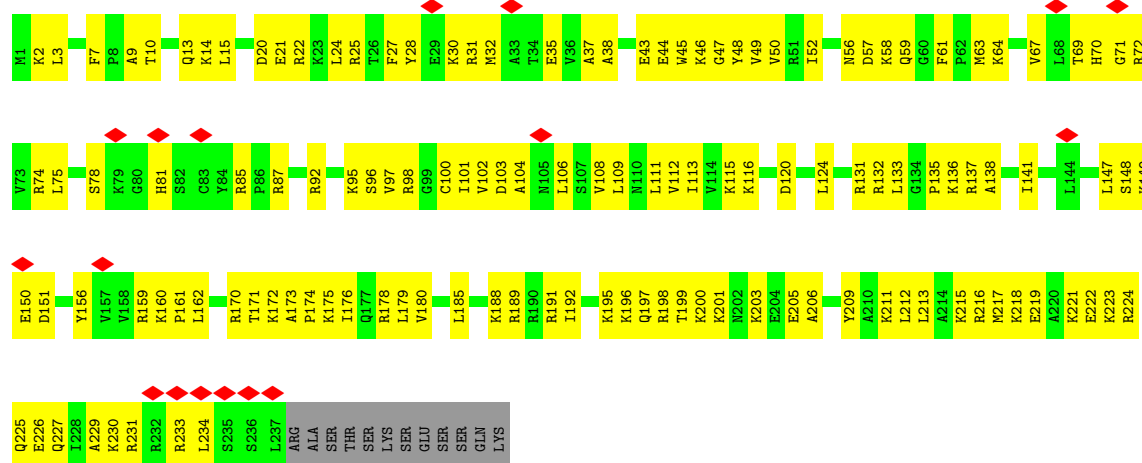


• Molecule 53: 40S ribosomal protein S2

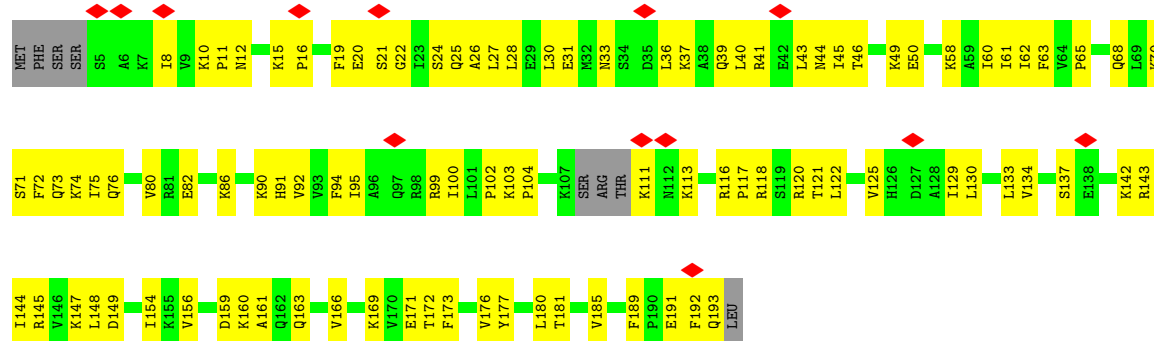




• Molecule 57: 40S ribosomal protein S6

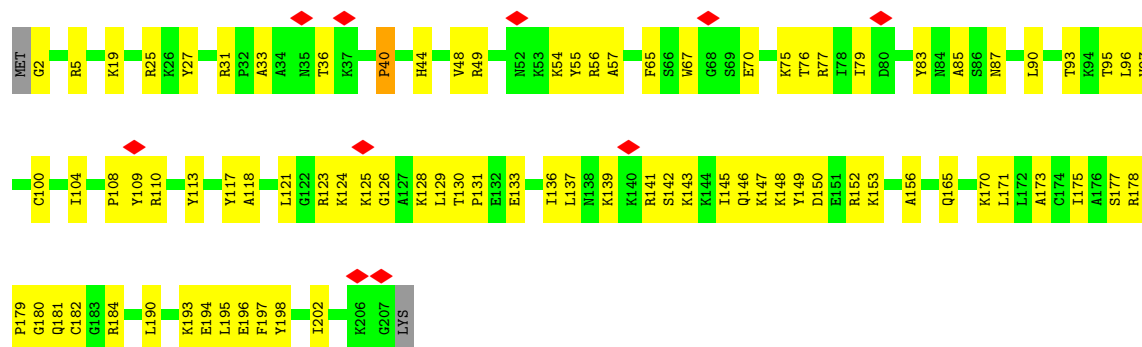


• Molecule 58: 40S ribosomal protein S7

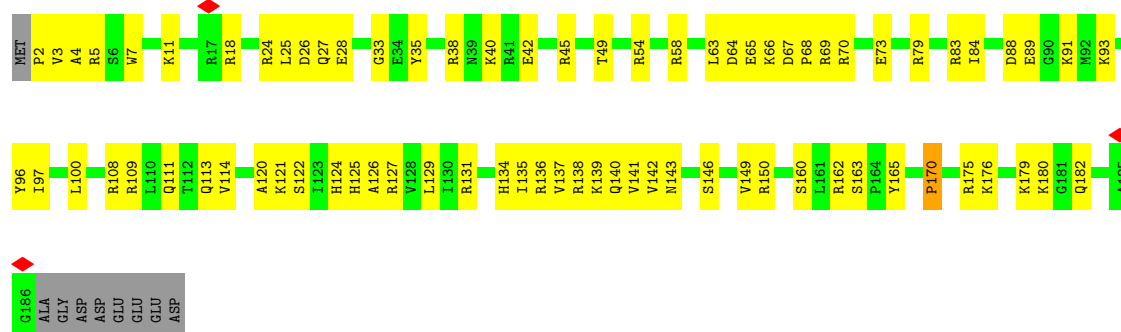


• Molecule 59: 40S ribosomal protein S8

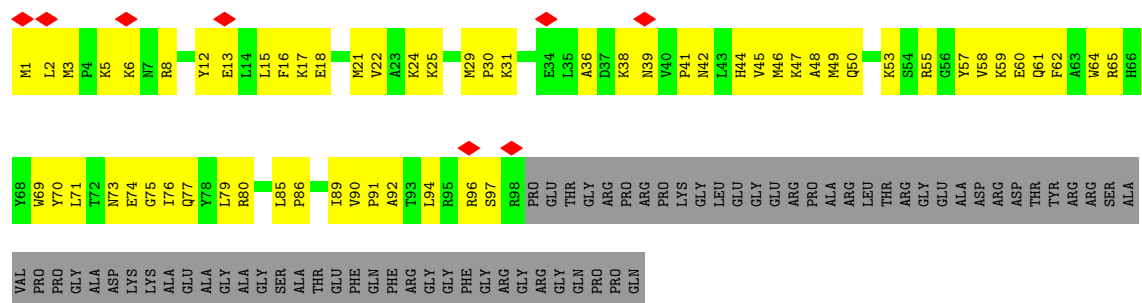
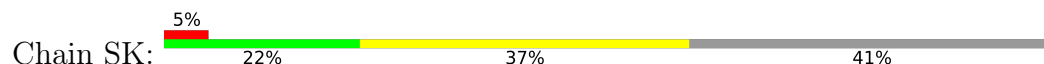




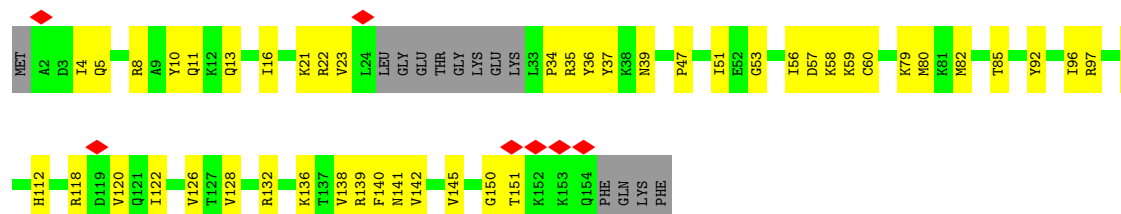
- Molecule 60: 40S ribosomal protein S9



- Molecule 61: 40S ribosomal protein S10

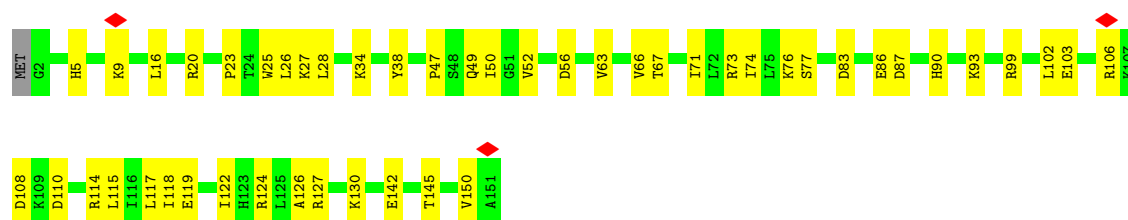


- Molecule 62: 40S ribosomal protein S11



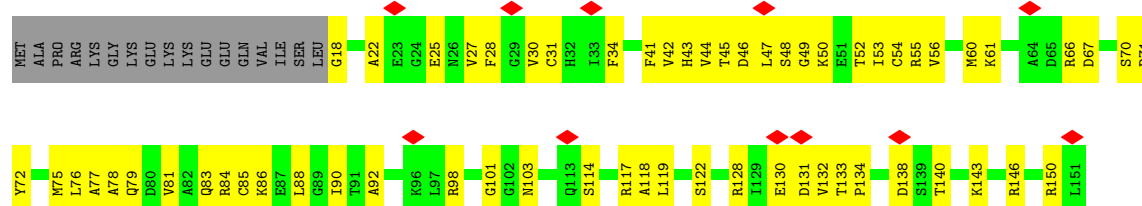
- Molecule 63: 40S ribosomal protein S13

Chain SN: 



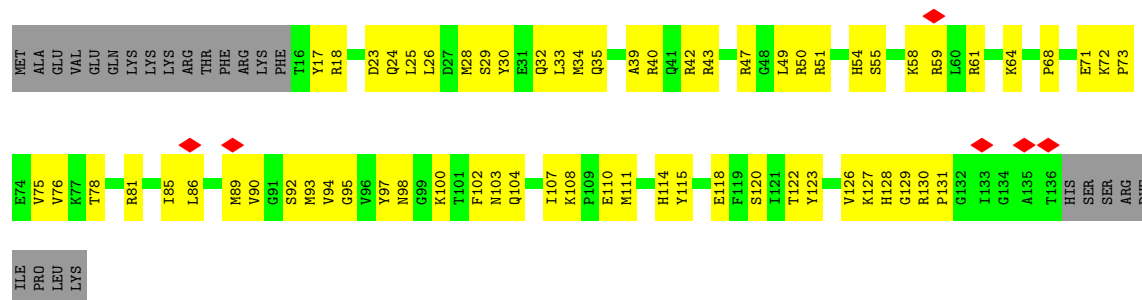
- Molecule 64: 40S ribosomal protein S14

Chain SO: 



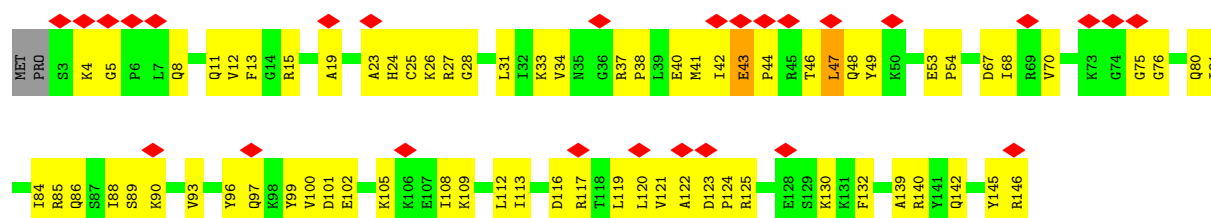
- Molecule 65: 40S ribosomal protein S15

Chain SP: 



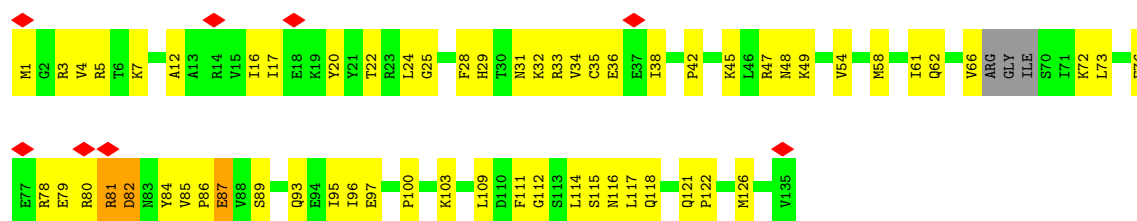
- Molecule 66: 40S ribosomal protein S16

Chain SQ: 

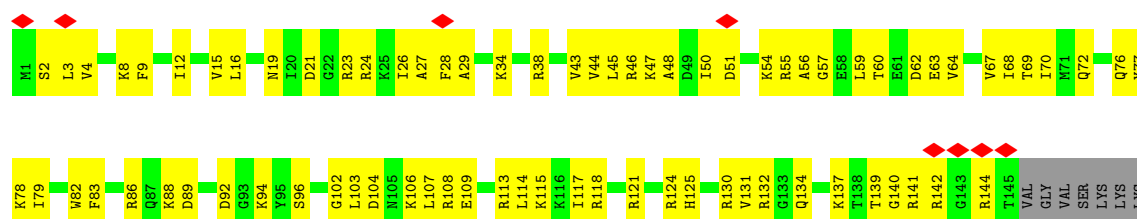


- Molecule 67: 40S ribosomal protein S17

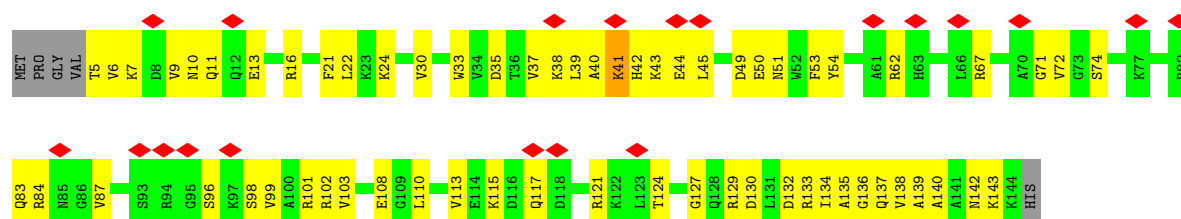
Chain SR: 



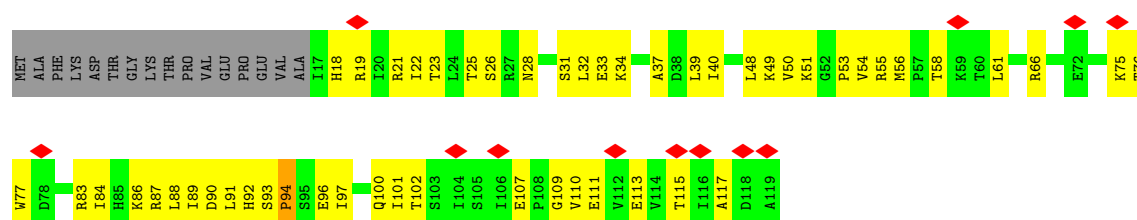
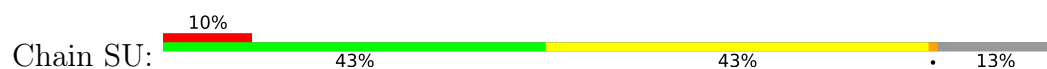
- Molecule 68: 40S ribosomal protein S18



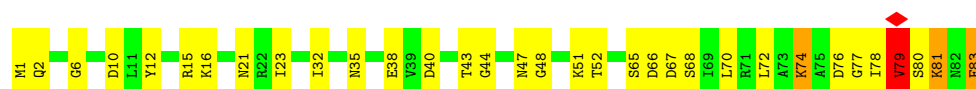
- Molecule 69: 40S ribosomal protein S19



- Molecule 70: 40S ribosomal protein S20

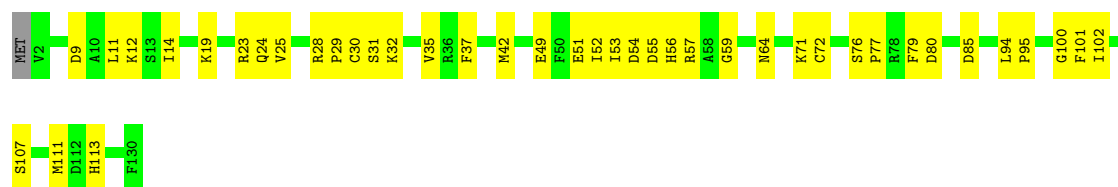


- Molecule 71: 40S ribosomal protein S21



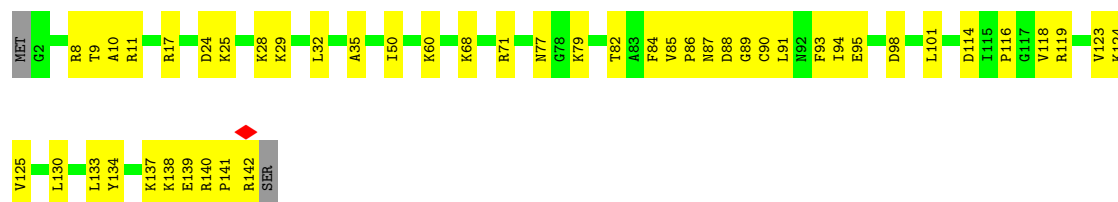
- Molecule 72: 40S ribosomal protein S15a

Chain SW:  68% 32%



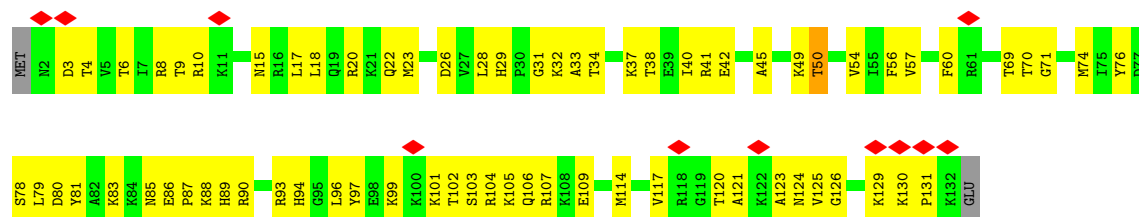
- Molecule 73: 40S ribosomal protein S23

Chain SX:  66% 33%



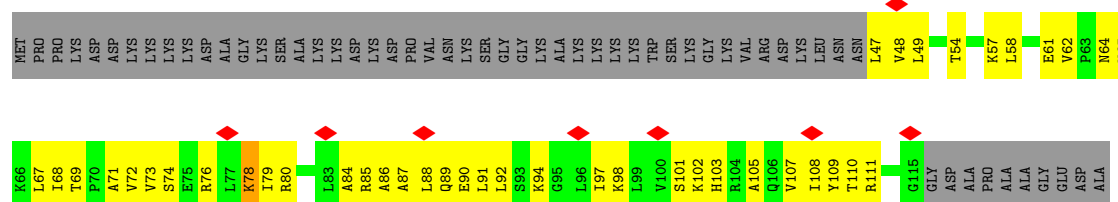
- Molecule 74: 40S ribosomal protein S24

Chain SY:  8% 45% 53%



- Molecule 75: 40S ribosomal protein S25

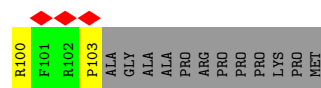
Chain SZ:  6% 22% 33% 45%



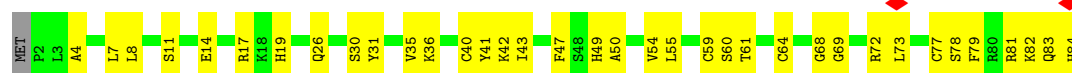
- Molecule 76: 40S ribosomal protein S26

Chain Sa:  5% 56% 32% 11%

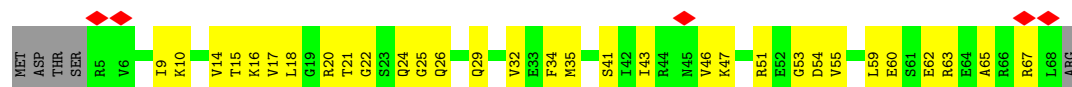




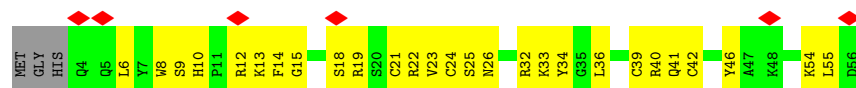
- Molecule 77: 40S ribosomal protein S27



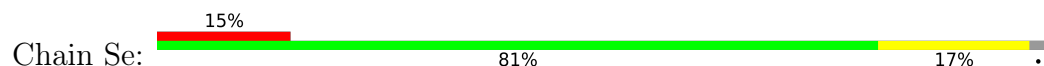
- Molecule 78: 40S ribosomal protein S28



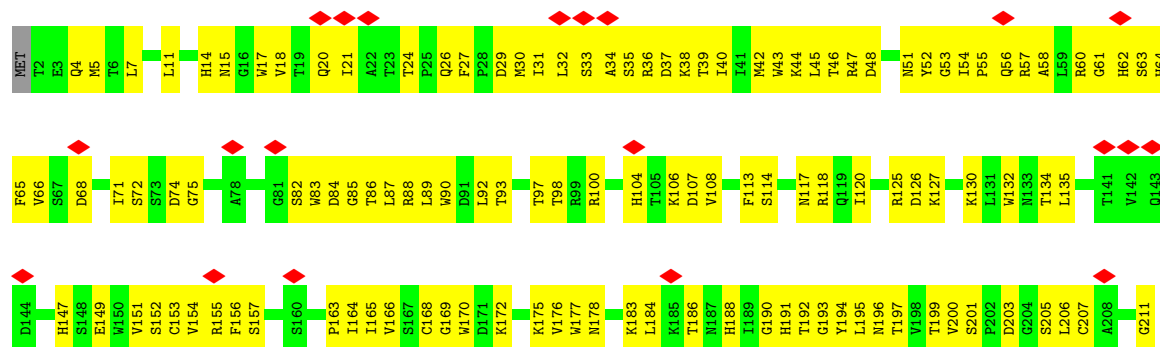
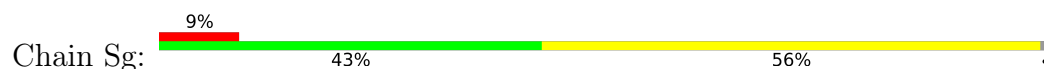
- Molecule 79: 40S ribosomal protein S29

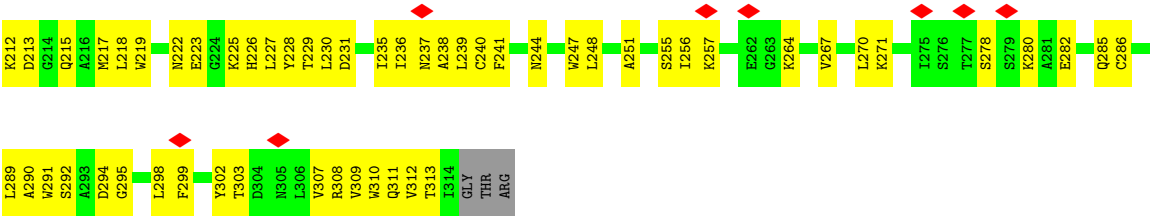


- Molecule 80: 40S ribosomal protein S30



- Molecule 81: Receptor of activated protein C kinase 1





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	74020	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.064	Depositor
Minimum map value	-0.034	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.005	Depositor
Map size ($\text{\AA}$)	483.84003, 483.84003, 483.84003	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.08, 1.08, 1.08	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, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	5	0.23	0/1002	0.58	0/1343
2	CB	0.21	0/6133	0.47	1/8281 (0.0%)
3	L5	0.47	0/87914	0.36	0/137143
4	L7	0.49	0/2861	0.31	0/4459
5	L8	0.48	0/3701	0.33	0/5766
6	LA	0.53	0/1936	0.58	0/2596
7	LB	0.47	0/3306	0.56	1/4424 (0.0%)
8	LC	0.49	0/2968	0.52	0/3985
9	LD	0.43	0/2428	0.50	0/3252
10	LE	0.41	0/1909	0.57	0/2559
11	LF	0.50	0/1905	0.51	0/2539
12	LG	0.42	0/1889	0.49	0/2541
13	LH	0.45	0/1537	0.53	0/2066
14	LI	0.44	0/1673	0.52	0/2233
15	LJ	0.38	0/1420	0.59	0/1896
16	LL	0.46	0/1732	0.53	0/2315
17	LM	0.45	0/1161	0.53	0/1554
18	LN	0.52	0/1746	0.55	0/2338
19	LO	0.49	0/1682	0.48	0/2250
20	LP	0.49	0/1268	0.51	0/1701
21	LQ	0.52	0/1517	0.57	0/2022
22	LR	0.42	0/1582	0.50	0/2091
23	LS	0.49	0/1475	0.47	0/1977
24	LT	0.46	0/1326	0.51	0/1770
25	LU	0.37	0/839	0.63	0/1126
26	LV	0.48	0/993	0.48	0/1332
27	LW	0.44	0/541	0.49	0/720
28	LX	0.48	0/956	0.46	0/1287
29	LY	0.48	0/1132	0.48	0/1504
30	LZ	0.42	0/1130	0.51	0/1507
31	La	0.50	0/1177	0.47	0/1572
32	Lb	0.41	0/889	0.56	0/1175

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lc	0.42	0/774	0.46	0/1038
34	Ld	0.49	0/903	0.50	0/1216
35	Le	0.51	0/1071	0.53	0/1429
36	Lf	0.50	0/895	0.59	0/1198
37	Lg	0.45	0/916	0.47	0/1220
38	Lh	0.44	0/1023	0.50	0/1351
39	Li	0.40	0/843	0.48	0/1115
40	Lj	0.49	0/720	0.61	0/952
41	Lk	0.39	0/575	0.49	0/761
42	Ll	0.47	0/454	0.56	0/599
43	Lm	0.42	0/435	0.48	0/575
44	Ln	0.35	0/231	0.47	0/294
45	Lo	0.45	0/847	0.48	0/1117
46	Lp	0.46	0/718	0.47	0/953
47	Lr	0.49	0/1017	0.53	0/1364
48	Lz	0.20	0/1667	0.43	0/2234
49	S	0.21	0/447	0.41	0/592
50	S2	0.29	0/41120	0.35	0/64066
51	SA	0.29	0/1754	0.51	0/2382
52	SB	0.28	0/1765	0.55	0/2362
53	SC	0.33	0/1726	0.53	0/2332
54	SD	0.27	0/1793	0.52	0/2414
55	SE	0.27	0/2118	0.50	0/2849
56	SF	0.23	0/1516	0.57	0/2037
57	SG	0.24	0/1946	0.55	0/2590
58	SH	0.26	0/1519	0.55	0/2033
59	SI	0.27	0/1715	0.54	2/2287 (0.1%)
60	SJ	0.30	0/1550	0.53	1/2069 (0.0%)
61	SK	0.25	0/851	0.56	0/1147
62	SL	0.30	0/1208	0.50	0/1616
63	SN	0.26	0/1232	0.42	0/1656
64	SO	0.23	0/1015	0.51	0/1361
65	SP	0.26	0/1003	0.54	0/1342
66	SQ	0.25	0/1160	0.61	0/1553
67	SR	0.25	0/1081	0.58	0/1451
68	SS	0.24	0/1216	0.53	0/1628
69	ST	0.22	0/1112	0.49	0/1489
70	SU	0.25	0/827	0.58	1/1110 (0.1%)
71	SV	0.33	0/643	0.57	0/860
72	SW	0.37	0/1051	0.48	0/1406
73	SX	0.36	0/1116	0.54	0/1490
74	SY	0.25	0/1076	0.57	0/1429
75	SZ	0.22	0/552	0.61	1/741 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sa	0.32	0/836	0.57	0/1121
77	Sb	0.25	0/665	0.57	0/891
78	Sc	0.22	0/508	0.63	0/680
79	Sd	0.29	0/455	0.55	0/603
80	Se	0.23	0/465	0.55	0/612
81	Sg	0.24	0/2487	0.57	0/3387
All	All	0.41	0/236345	0.43	7/346326 (0.0%)

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SI	40	PRO	CA-N-CD	-7.48	101.53	112.00
60	SJ	170	PRO	CA-N-CD	-6.25	103.25	112.00
59	SI	40	PRO	N-CD-CG	-5.68	94.69	103.20
2	CB	376	PRO	CA-N-CD	-5.67	104.06	112.00
7	LB	299	ILE	N-CA-C	-5.60	107.81	113.47

There are no chirality outliers.

There are no planarity outliers.

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	5	992	0	995	35	0
2	CB	6014	0	6059	272	0
3	L5	78591	0	39715	1108	0
4	L7	2561	0	1295	21	0
5	L8	3314	0	1683	33	0
6	LA	1898	0	1993	25	0
7	LB	3238	0	3376	77	0
8	LC	2914	0	3087	52	0
9	LD	2382	0	2410	57	0
10	LE	1873	0	2016	61	0
11	LF	1870	0	1996	39	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
12	LG	1858	0	2000	30	0
13	LH	1518	0	1601	34	0
14	LI	1634	0	1671	28	0
15	LJ	1398	0	1426	47	0
16	LL	1701	0	1818	39	0
17	LM	1138	0	1204	46	0
18	LN	1701	0	1749	40	0
19	LO	1650	0	1794	27	0
20	LP	1242	0	1269	18	0
21	LQ	1496	0	1613	34	0
22	LR	1566	0	1729	31	0
23	LS	1437	0	1469	26	0
24	LT	1298	0	1366	29	0
25	LU	825	0	850	34	0
26	LV	979	0	1039	11	0
27	LW	528	0	541	7	0
28	LX	939	0	1003	14	0
29	LY	1115	0	1205	26	0
30	LZ	1107	0	1182	23	0
31	La	1149	0	1196	18	0
32	Lb	876	0	948	31	0
33	Lc	764	0	804	15	0
34	Ld	888	0	930	14	0
35	Le	1053	0	1147	31	0
36	Lf	876	0	912	12	0
37	Lg	906	0	999	14	0
38	Lh	1015	0	1148	22	0
39	Li	832	0	917	8	0
40	Lj	705	0	737	8	0
41	Lk	569	0	637	16	0
42	Ll	444	0	483	16	0
43	Lm	429	0	465	7	0
44	Ln	230	0	276	2	0
45	Lo	834	0	903	18	0
46	Lp	708	0	756	13	0
47	Lr	1002	0	1068	20	0
48	Lz	1643	0	1745	61	0
49	S	440	0	402	30	0
50	S2	36789	0	18548	1060	0
51	SA	1718	0	1721	110	0
52	SB	1738	0	1809	109	0
53	SC	1690	0	1777	55	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
54	SD	1765	0	1865	89	0
55	SE	2076	0	2177	98	0
56	SF	1495	0	1549	115	0
57	SG	1923	0	2089	139	0
58	SH	1497	0	1590	79	0
59	SI	1686	0	1772	81	0
60	SJ	1525	0	1640	74	0
61	SK	827	0	854	64	0
62	SL	1188	0	1260	47	0
63	SN	1208	0	1294	42	0
64	SO	1002	0	1023	48	0
65	SP	985	0	1031	79	0
66	SQ	1142	0	1213	90	0
67	SR	1067	0	1121	82	0
68	SS	1198	0	1261	80	0
69	ST	1094	0	1126	68	0
70	SU	817	0	882	47	0
71	SV	636	0	637	37	0
72	SW	1034	0	1080	44	0
73	SX	1098	0	1167	35	0
74	SY	1059	0	1135	86	0
75	SZ	546	0	603	42	0
76	Sa	821	0	874	44	0
77	Sb	651	0	672	36	0
78	Sc	506	0	536	27	0
79	Sd	445	0	442	29	0
80	Se	459	0	503	12	0
81	Sg	2430	0	2382	171	0
82	L5	211	0	0	0	0
82	L7	3	0	0	0	0
82	L8	5	0	0	0	0
82	LA	1	0	0	0	0
82	LB	1	0	0	0	0
82	LI	1	0	0	0	0
82	LP	1	0	0	0	0
82	LV	1	0	0	0	0
82	Le	1	0	0	0	0
82	Lg	1	0	0	0	0
83	Lg	1	0	0	0	0
83	Lj	1	0	0	0	0
83	Lm	1	0	0	0	0
83	Lo	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	Lp	1	0	0	0	0
All	All	220486	0	165260	5129	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 14.

The worst 5 of 5129 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)
66:SQ:43:GLU:HB3	66:SQ:44:PRO:CD	1.42	1.35
51:SA:89:LYS:HD3	67:SR:81:ARG:NH1	1.49	1.26
3:L5:1443:A:H61	3:L5:2104:G:N2	1.36	1.24
66:SQ:43:GLU:CB	66:SQ:44:PRO:CD	2.18	1.18
74:SY:54:VAL:HG13	74:SY:76:TYR:HB2	1.24	1.17

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	5	123/154 (80%)	113 (92%)	10 (8%)	0	100	100
2	CB	762/858 (89%)	711 (93%)	51 (7%)	0	100	100
6	LA	246/257 (96%)	225 (92%)	21 (8%)	0	100	100
7	LB	400/403 (99%)	370 (92%)	29 (7%)	1 (0%)	36	65
8	LC	364/427 (85%)	335 (92%)	28 (8%)	1 (0%)	36	65
9	LD	291/297 (98%)	266 (91%)	25 (9%)	0	100	100
10	LE	224/288 (78%)	201 (90%)	23 (10%)	0	100	100
11	LF	223/248 (90%)	212 (95%)	11 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
12	LG	226/266 (85%)	217 (96%)	9 (4%)	0	100	100
13	LH	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
14	LI	198/214 (92%)	181 (91%)	17 (9%)	0	100	100
15	LJ	170/178 (96%)	155 (91%)	15 (9%)	0	100	100
16	LL	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
17	LM	137/215 (64%)	127 (93%)	10 (7%)	0	100	100
18	LN	201/204 (98%)	188 (94%)	12 (6%)	1 (0%)	24	54
19	LO	199/203 (98%)	190 (96%)	9 (4%)	0	100	100
20	LP	151/184 (82%)	141 (93%)	10 (7%)	0	100	100
21	LQ	181/188 (96%)	170 (94%)	11 (6%)	0	100	100
22	LR	185/196 (94%)	178 (96%)	7 (4%)	0	100	100
23	LS	169/176 (96%)	158 (94%)	11 (6%)	0	100	100
24	LT	157/160 (98%)	149 (95%)	8 (5%)	0	100	100
25	LU	99/128 (77%)	76 (77%)	23 (23%)	0	100	100
26	LV	129/140 (92%)	123 (95%)	6 (5%)	0	100	100
27	LW	61/157 (39%)	59 (97%)	2 (3%)	0	100	100
28	LX	113/156 (72%)	111 (98%)	2 (2%)	0	100	100
29	LY	132/145 (91%)	124 (94%)	8 (6%)	0	100	100
30	LZ	133/136 (98%)	117 (88%)	16 (12%)	0	100	100
31	La	141/148 (95%)	136 (96%)	5 (4%)	0	100	100
32	Lb	105/159 (66%)	96 (91%)	9 (9%)	0	100	100
33	Lc	96/115 (84%)	87 (91%)	9 (9%)	0	100	100
34	Ld	105/125 (84%)	100 (95%)	5 (5%)	0	100	100
35	Le	126/135 (93%)	123 (98%)	3 (2%)	0	100	100
36	Lf	107/110 (97%)	97 (91%)	10 (9%)	0	100	100
37	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100
38	Lh	120/123 (98%)	116 (97%)	3 (2%)	1 (1%)	16	44
39	Li	100/105 (95%)	94 (94%)	6 (6%)	0	100	100
40	Lj	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
41	Lk	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
42	Ll	48/51 (94%)	47 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	Lm	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
44	Ln	22/25 (88%)	22 (100%)	0	0	100	100
45	Lo	100/106 (94%)	93 (93%)	7 (7%)	0	100	100
46	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
47	Lr	123/137 (90%)	113 (92%)	10 (8%)	0	100	100
48	Lz	197/217 (91%)	187 (95%)	10 (5%)	0	100	100
49	S	51/402 (13%)	43 (84%)	8 (16%)	0	100	100
51	SA	213/295 (72%)	187 (88%)	26 (12%)	0	100	100
52	SB	212/264 (80%)	197 (93%)	15 (7%)	0	100	100
53	SC	216/293 (74%)	200 (93%)	16 (7%)	0	100	100
54	SD	225/243 (93%)	201 (89%)	24 (11%)	0	100	100
55	SE	260/263 (99%)	244 (94%)	16 (6%)	0	100	100
56	SF	187/204 (92%)	162 (87%)	25 (13%)	0	100	100
57	SG	235/249 (94%)	221 (94%)	14 (6%)	0	100	100
58	SH	182/194 (94%)	160 (88%)	22 (12%)	0	100	100
59	SI	204/208 (98%)	189 (93%)	15 (7%)	0	100	100
60	SJ	183/194 (94%)	168 (92%)	15 (8%)	0	100	100
61	SK	96/165 (58%)	79 (82%)	17 (18%)	0	100	100
62	SL	141/158 (89%)	124 (88%)	17 (12%)	0	100	100
63	SN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
64	SO	132/151 (87%)	116 (88%)	16 (12%)	0	100	100
65	SP	119/145 (82%)	108 (91%)	11 (9%)	0	100	100
66	SQ	142/146 (97%)	122 (86%)	19 (13%)	1 (1%)	18	47
67	SR	128/135 (95%)	114 (89%)	14 (11%)	0	100	100
68	SS	143/152 (94%)	127 (89%)	16 (11%)	0	100	100
69	ST	138/145 (95%)	124 (90%)	13 (9%)	1 (1%)	18	47
70	SU	101/119 (85%)	94 (93%)	7 (7%)	0	100	100
71	SV	81/83 (98%)	69 (85%)	9 (11%)	3 (4%)	2	16
72	SW	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
73	SX	139/143 (97%)	125 (90%)	12 (9%)	2 (1%)	9	31
74	SY	129/133 (97%)	122 (95%)	7 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	SZ	67/125 (54%)	57 (85%)	10 (15%)	0	100	100
76	Sa	100/115 (87%)	87 (87%)	12 (12%)	1 (1%)	12	40
77	Sb	81/84 (96%)	70 (86%)	11 (14%)	0	100	100
78	Sc	62/69 (90%)	45 (73%)	17 (27%)	0	100	100
79	Sd	51/56 (91%)	48 (94%)	3 (6%)	0	100	100
80	Se	56/59 (95%)	49 (88%)	7 (12%)	0	100	100
81	Sg	311/317 (98%)	268 (86%)	43 (14%)	0	100	100
All	All	12122/14031 (86%)	11137 (92%)	973 (8%)	12 (0%)	49	78

5 of 12 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	LN	124	ASP
66	SQ	43	GLU
71	SV	79	VAL
73	SX	89	GLY
7	LB	10	ARG

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	5	110/128 (86%)	109 (99%)	1 (1%)	70	76
2	CB	655/730 (90%)	655 (100%)	0	100	100
6	LA	190/199 (96%)	190 (100%)	0	100	100
7	LB	348/349 (100%)	348 (100%)	0	100	100
8	LC	305/348 (88%)	305 (100%)	0	100	100
9	LD	246/250 (98%)	246 (100%)	0	100	100
10	LE	206/252 (82%)	206 (100%)	0	100	100
11	LF	194/215 (90%)	194 (100%)	0	100	100
12	LG	198/223 (89%)	198 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
13	LH	169/171 (99%)	169 (100%)	0	100	100
14	LI	172/181 (95%)	172 (100%)	0	100	100
15	LJ	147/149 (99%)	147 (100%)	0	100	100
16	LL	176/177 (99%)	176 (100%)	0	100	100
17	LM	118/161 (73%)	118 (100%)	0	100	100
18	LN	171/172 (99%)	171 (100%)	0	100	100
19	LO	173/174 (99%)	173 (100%)	0	100	100
20	LP	134/163 (82%)	134 (100%)	0	100	100
21	LQ	162/165 (98%)	161 (99%)	1 (1%)	78	80
22	LR	166/175 (95%)	166 (100%)	0	100	100
23	LS	154/157 (98%)	154 (100%)	0	100	100
24	LT	139/140 (99%)	139 (100%)	0	100	100
25	LU	91/115 (79%)	91 (100%)	0	100	100
26	LV	101/107 (94%)	101 (100%)	0	100	100
27	LW	55/126 (44%)	55 (100%)	0	100	100
28	LX	103/133 (77%)	103 (100%)	0	100	100
29	LY	124/135 (92%)	124 (100%)	0	100	100
30	LZ	117/118 (99%)	117 (100%)	0	100	100
31	La	119/121 (98%)	119 (100%)	0	100	100
32	Lb	88/126 (70%)	88 (100%)	0	100	100
33	Lc	83/97 (86%)	83 (100%)	0	100	100
34	Ld	98/110 (89%)	98 (100%)	0	100	100
35	Le	114/121 (94%)	113 (99%)	1 (1%)	70	76
36	Lf	88/89 (99%)	88 (100%)	0	100	100
37	Lg	98/100 (98%)	98 (100%)	0	100	100
38	Lh	109/110 (99%)	109 (100%)	0	100	100
39	Li	86/89 (97%)	86 (100%)	0	100	100
40	Lj	73/80 (91%)	73 (100%)	0	100	100
41	Lk	64/65 (98%)	64 (100%)	0	100	100
42	Ll	47/48 (98%)	47 (100%)	0	100	100
43	Lm	48/116 (41%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
44	Ln	23/24 (96%)	23 (100%)	0	100	100
45	Lo	90/94 (96%)	90 (100%)	0	100	100
46	Lp	74/75 (99%)	74 (100%)	0	100	100
47	Lr	109/121 (90%)	109 (100%)	0	100	100
48	Lz	185/196 (94%)	185 (100%)	0	100	100
49	S	46/322 (14%)	46 (100%)	0	100	100
51	SA	181/243 (74%)	181 (100%)	0	100	100
52	SB	195/231 (84%)	195 (100%)	0	100	100
53	SC	184/225 (82%)	184 (100%)	0	100	100
54	SD	190/202 (94%)	190 (100%)	0	100	100
55	SE	224/225 (100%)	224 (100%)	0	100	100
56	SF	159/170 (94%)	159 (100%)	0	100	100
57	SG	207/218 (95%)	207 (100%)	0	100	100
58	SH	166/174 (95%)	166 (100%)	0	100	100
59	SI	178/180 (99%)	178 (100%)	0	100	100
60	SJ	161/168 (96%)	161 (100%)	0	100	100
61	SK	89/136 (65%)	89 (100%)	0	100	100
62	SL	131/142 (92%)	131 (100%)	0	100	100
63	SN	130/131 (99%)	130 (100%)	0	100	100
64	SO	104/119 (87%)	104 (100%)	0	100	100
65	SP	107/130 (82%)	107 (100%)	0	100	100
66	SQ	119/121 (98%)	117 (98%)	2 (2%)	53	67
67	SR	120/122 (98%)	116 (97%)	4 (3%)	33	57
68	SS	126/132 (96%)	126 (100%)	0	100	100
69	ST	111/115 (96%)	111 (100%)	0	100	100
70	SU	94/107 (88%)	94 (100%)	0	100	100
71	SV	67/67 (100%)	63 (94%)	4 (6%)	17	43
72	SW	112/113 (99%)	112 (100%)	0	100	100
73	SX	113/115 (98%)	112 (99%)	1 (1%)	70	76
74	SY	112/115 (97%)	110 (98%)	2 (2%)	51	67
75	SZ	60/103 (58%)	60 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
76	Sa	89/98 (91%)	89 (100%)	0	100	100
77	Sb	75/76 (99%)	75 (100%)	0	100	100
78	Sc	57/62 (92%)	57 (100%)	0	100	100
79	Sd	47/49 (96%)	47 (100%)	0	100	100
80	Se	47/48 (98%)	47 (100%)	0	100	100
81	Sg	271/275 (98%)	271 (100%)	0	100	100
All	All	10592/11929 (89%)	10576 (100%)	16 (0%)	85	85

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
74	SY	49	LYS
73	SX	85	VAL
67	SR	87	GLU
71	SV	83	PHE
67	SR	85	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 97 such sidechains are listed below:

Mol	Chain	Res	Type
42	L1	43	HIS
56	SF	118	ASN
45	Lo	102	GLN
52	SB	149	GLN
58	SH	165	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	L5	3654/5070 (72%)	841 (23%)	24 (0%)
4	L7	119/121 (98%)	12 (10%)	0
5	L8	155/157 (98%)	30 (19%)	0
50	S2	1709/1869 (91%)	465 (27%)	7 (0%)
All	All	5637/7217 (78%)	1348 (23%)	31 (0%)

5 of 1348 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	L5	2	G
3	L5	17	A
3	L5	25	A
3	L5	26	C
3	L5	30	C

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	L5	2485	U
50	S2	420	G
3	L5	2786	C
50	S2	688	U
50	S2	75	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 231 ligands modelled in this entry, 231 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 ⓘ

There are no chain breaks in this entry.

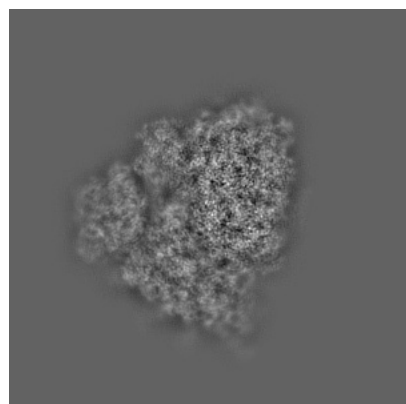
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37991. These allow visual inspection of the internal detail of the map and identification of artifacts.

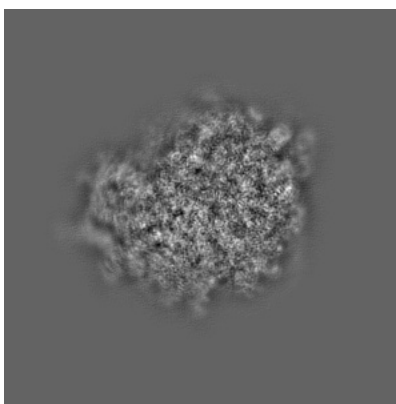
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

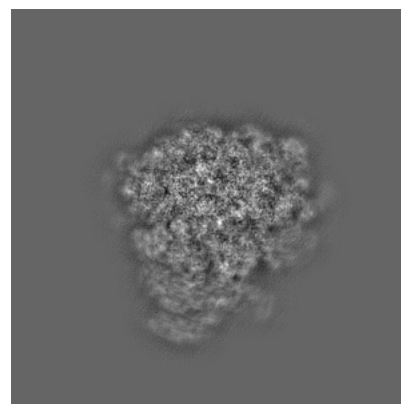
6.1.1 Primary map



X

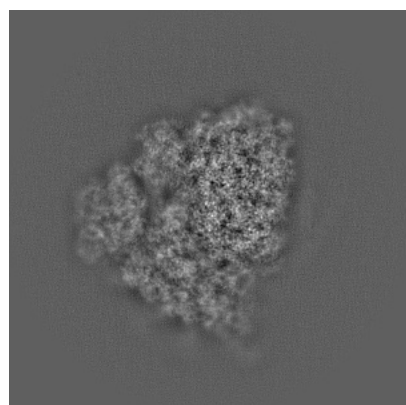


Y

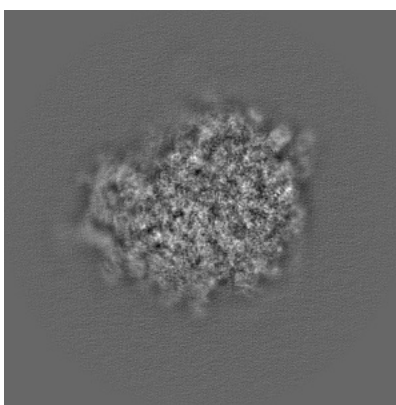


Z

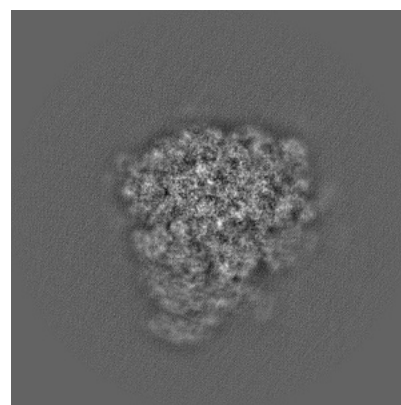
6.1.2 Raw map



X



Y

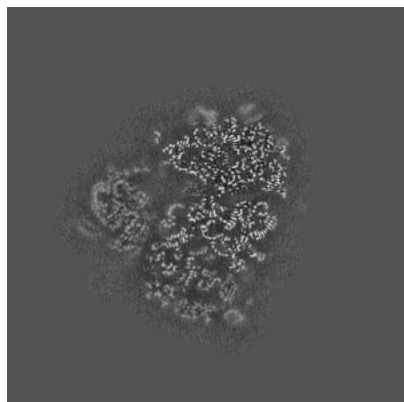


Z

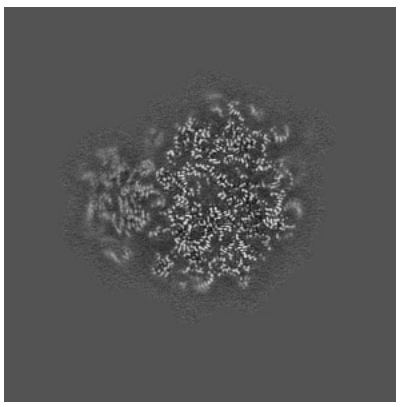
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

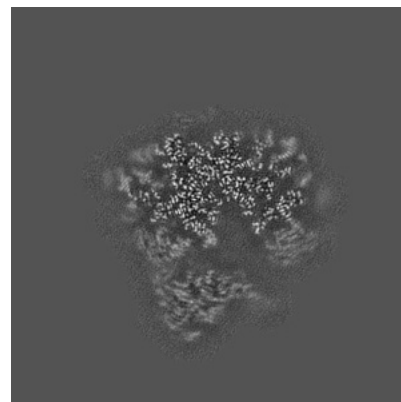
6.2.1 Primary map



X Index: 224

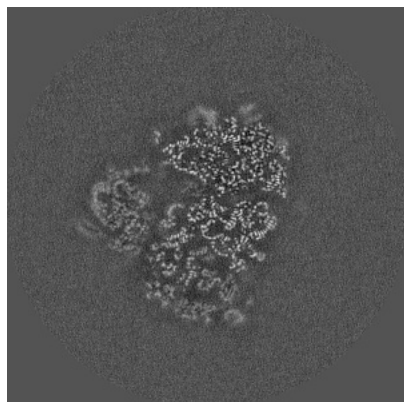


Y Index: 224

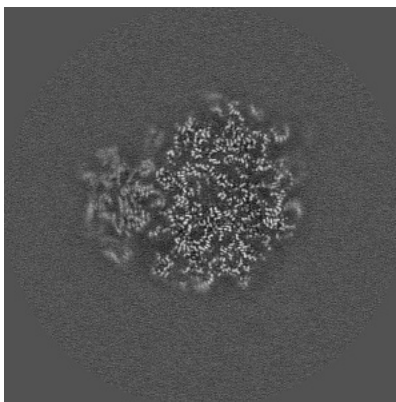


Z Index: 224

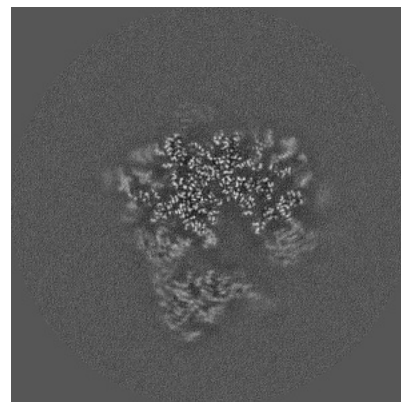
6.2.2 Raw map



X Index: 224



Y Index: 224

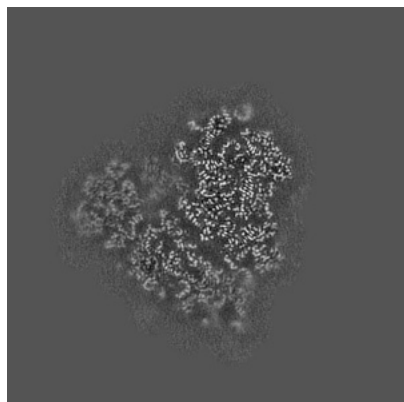


Z Index: 224

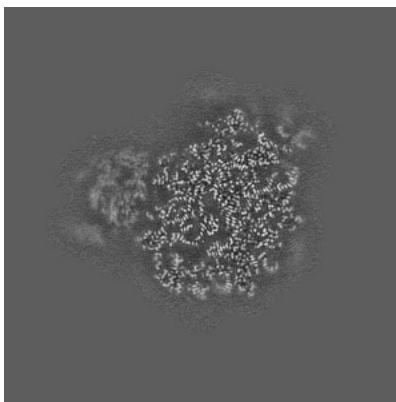
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

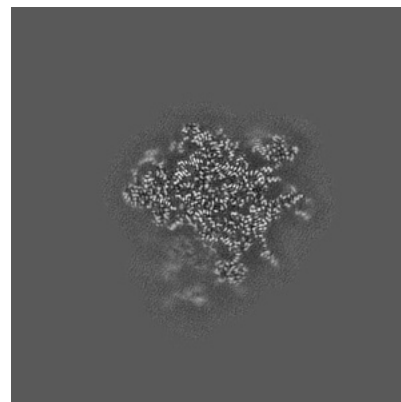
6.3.1 Primary map



X Index: 210

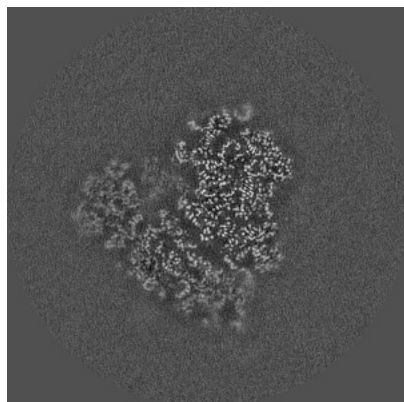


Y Index: 243

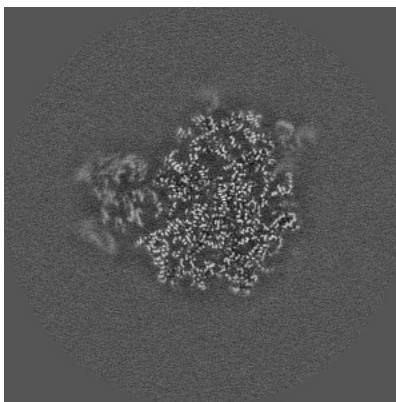


Z Index: 272

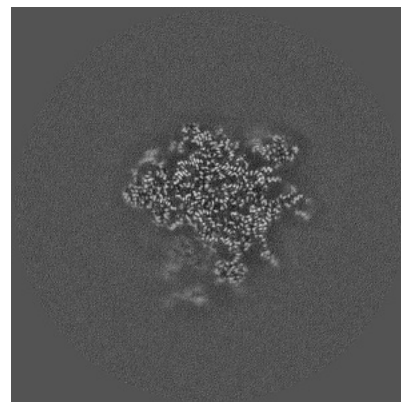
6.3.2 Raw map



X Index: 210



Y Index: 236

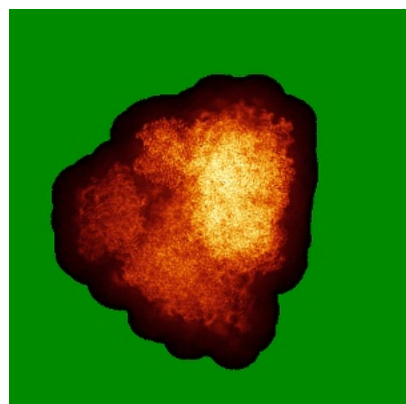


Z Index: 272

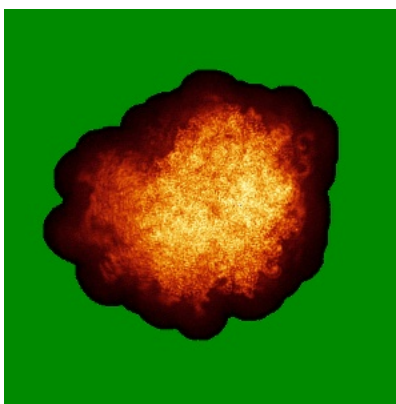
The images above show the largest variance slices of the map in three orthogonal directions.

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

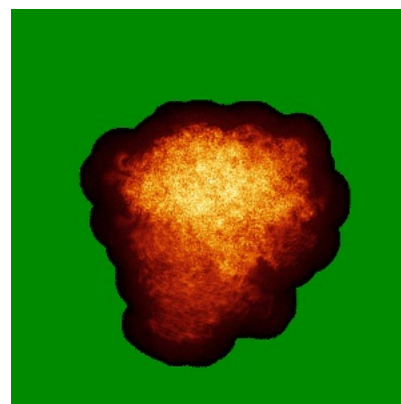
6.4.1 Primary map



X

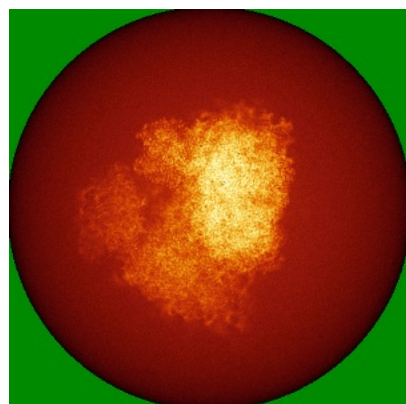


Y

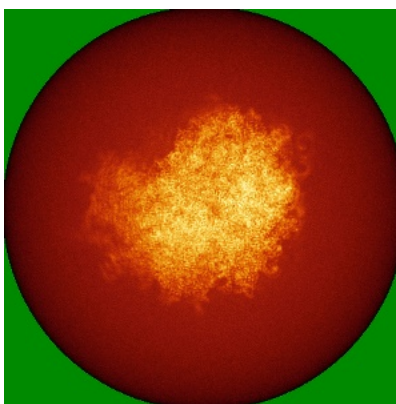


Z

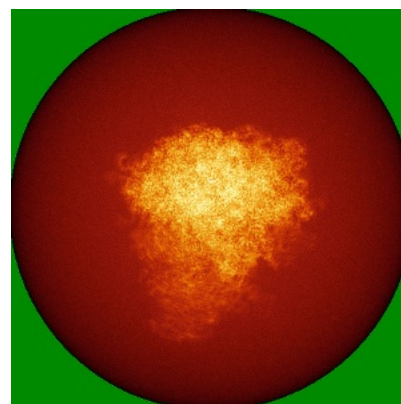
6.4.2 Raw map



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



X



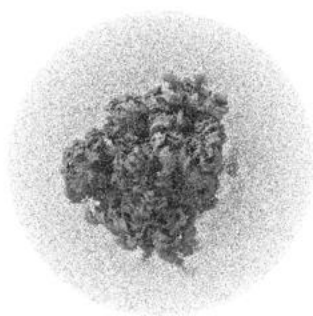
Y



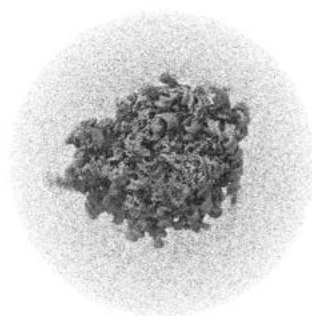
Z

The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

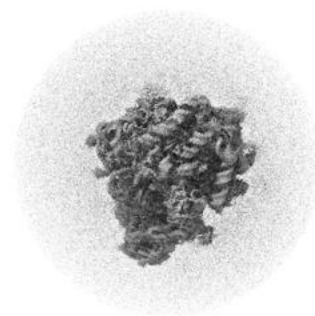
6.5.2 Raw map



X



Y



Z

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.

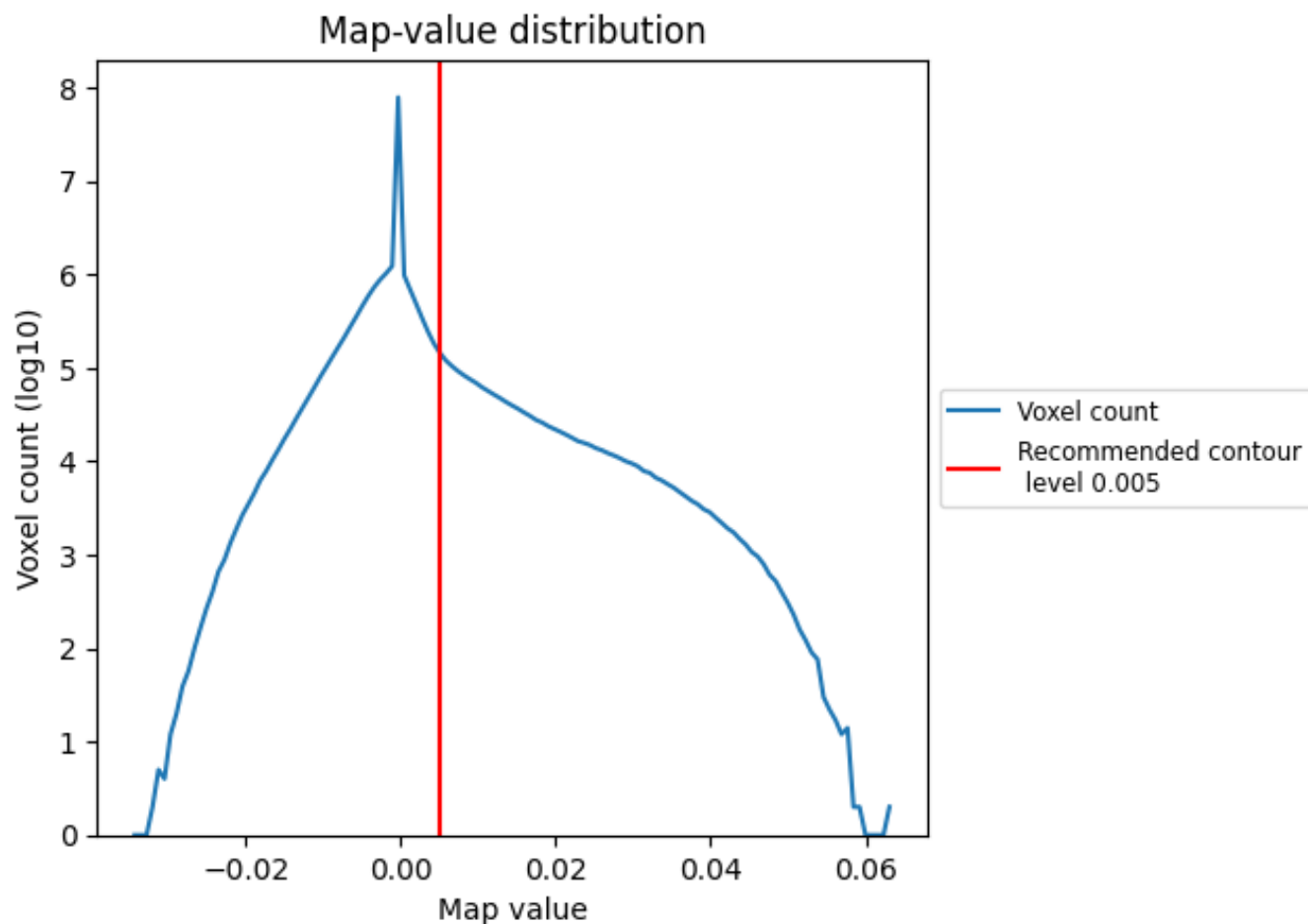
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

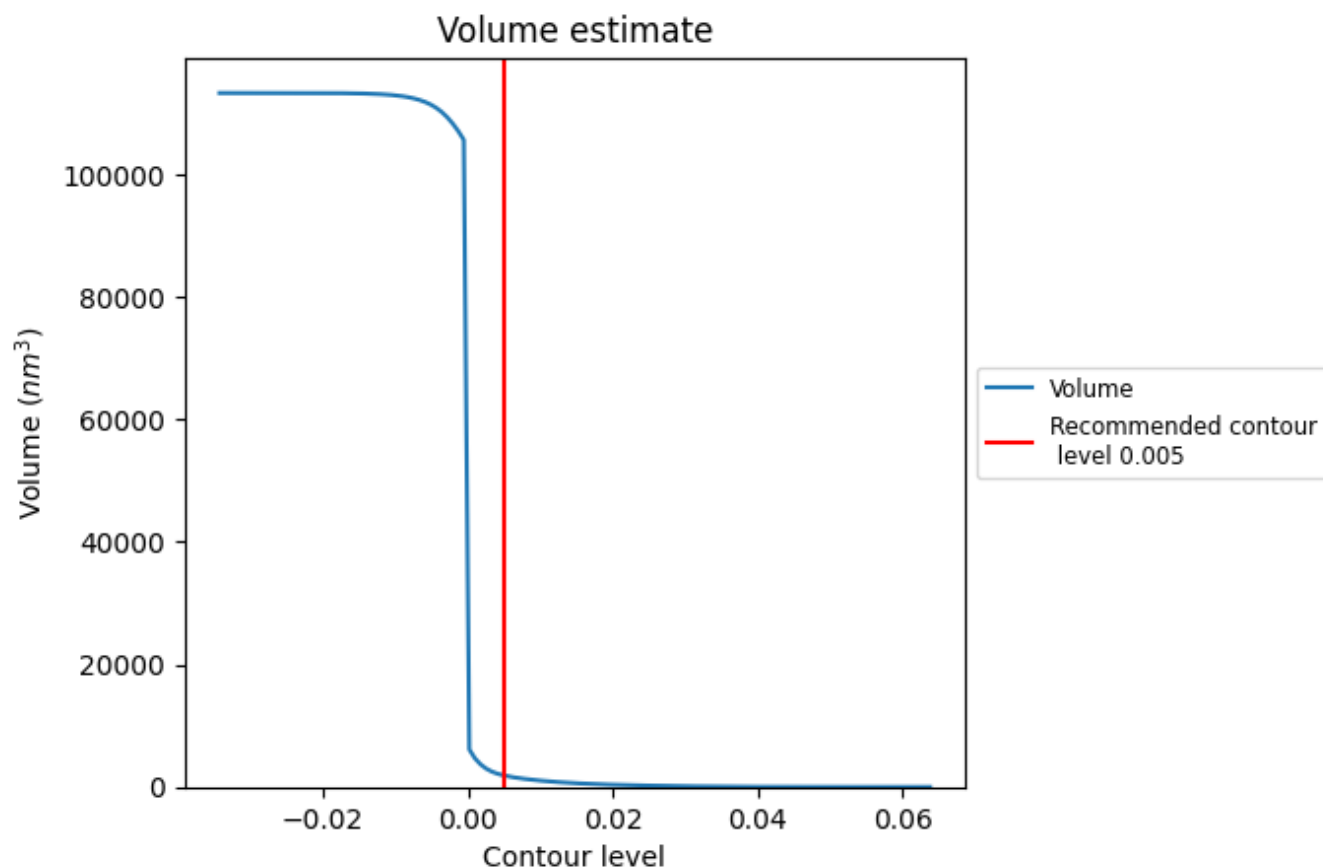
This section contains the results of statistical analysis of the map.

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.

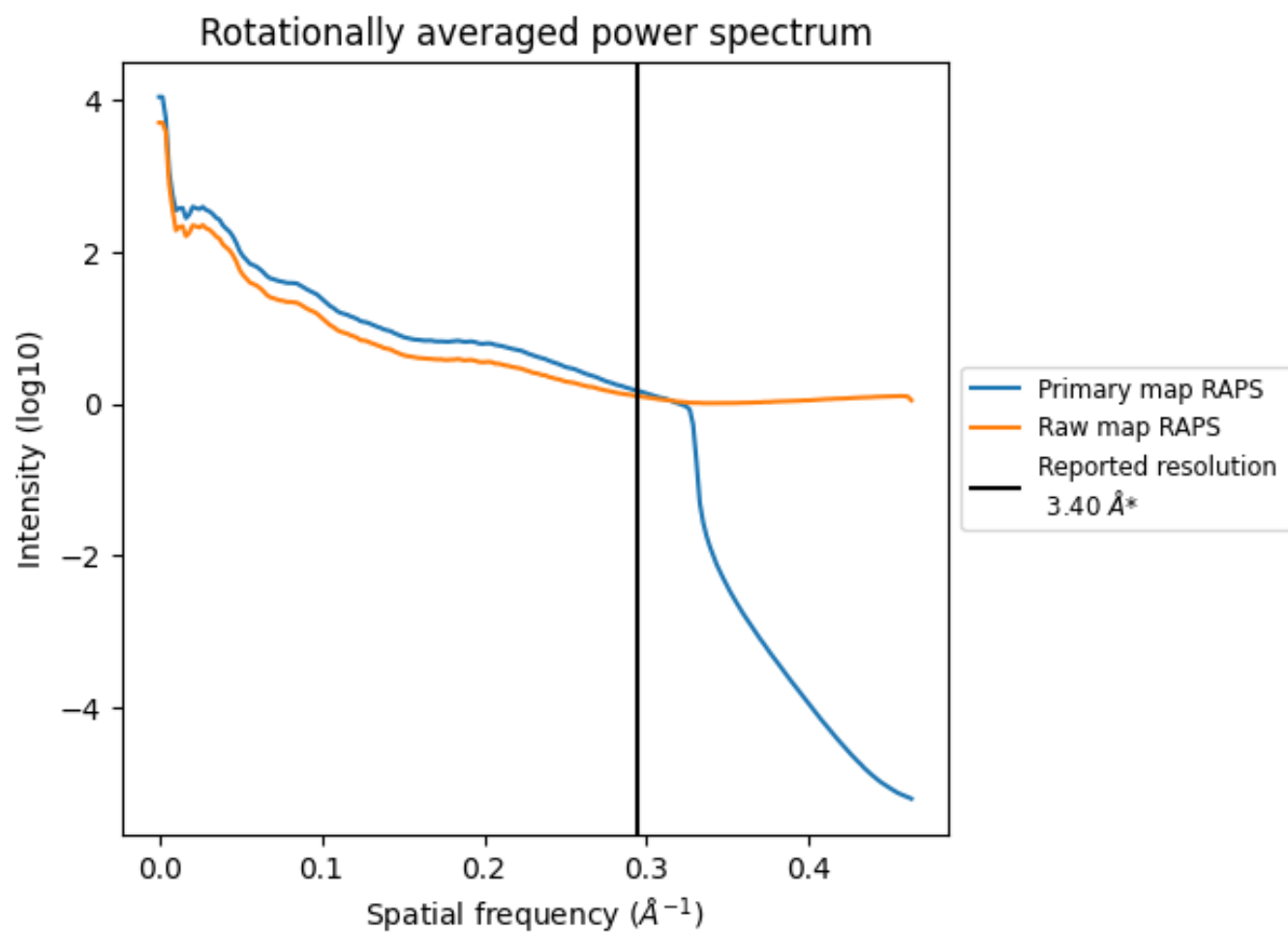
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1877 nm^3 ; this corresponds to an approximate mass of 1696 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

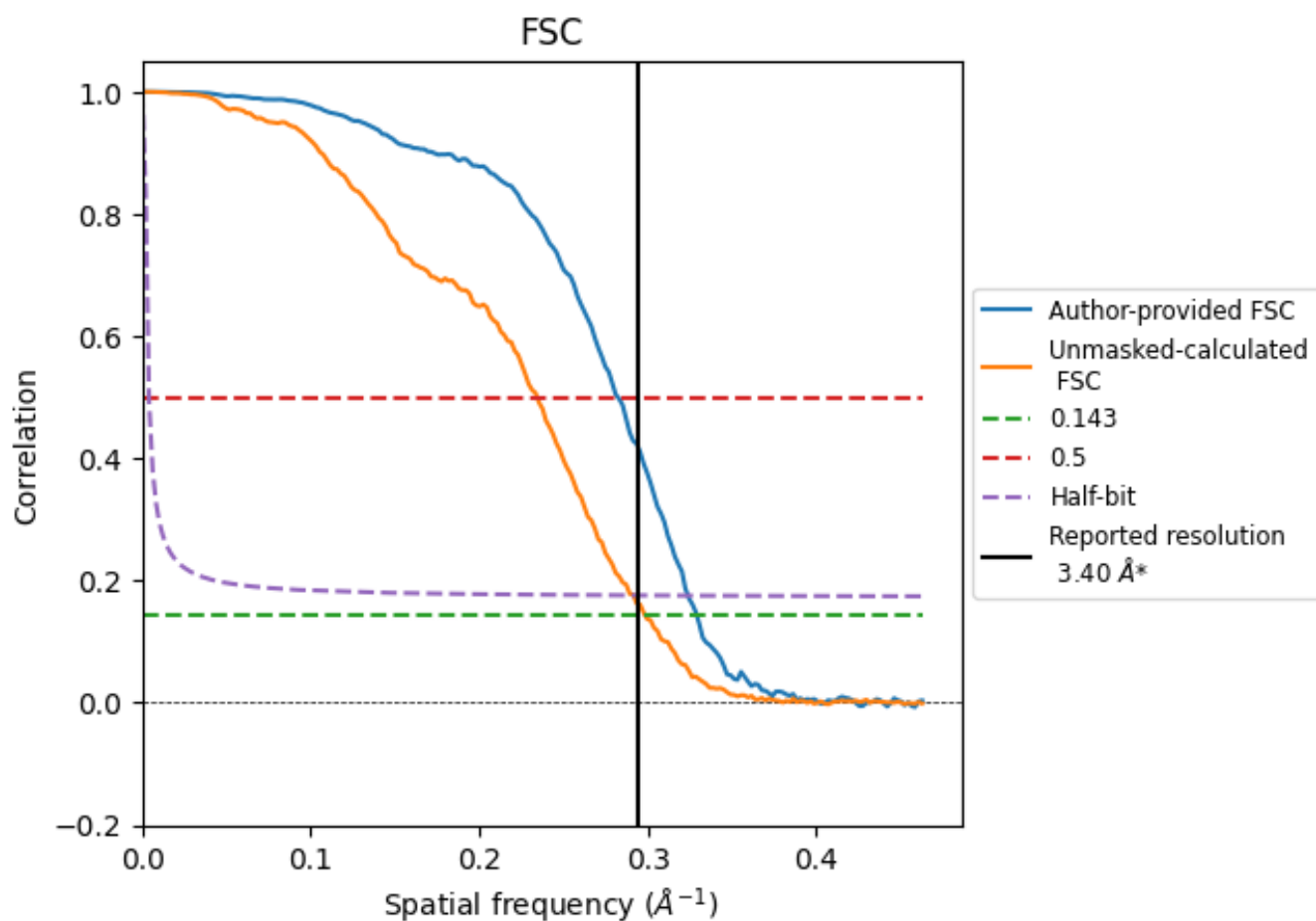


*Reported resolution corresponds to spatial frequency of 0.294 $\text{\AA}^{-1}$

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 0.294 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

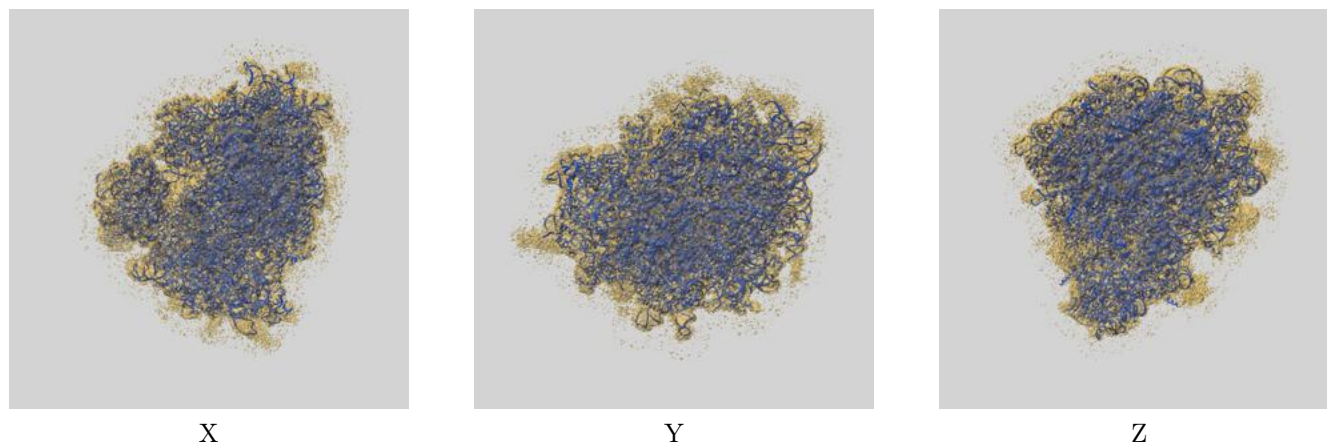
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.40	-	-
Author-provided FSC curve	3.04	3.54	3.09
Unmasked-calculated*	3.35	4.26	3.43

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 3.04 differs from the reported value 3.4 by more than 10 %

9 Map-model fit [i](#)

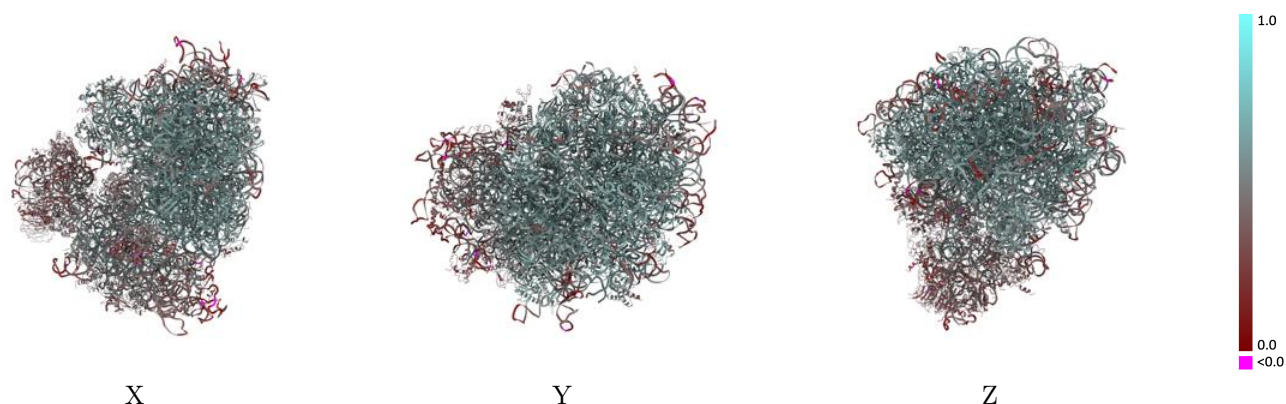
This section contains information regarding the fit between EMDB map EMD-37991 and PDB model 8Y0W. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



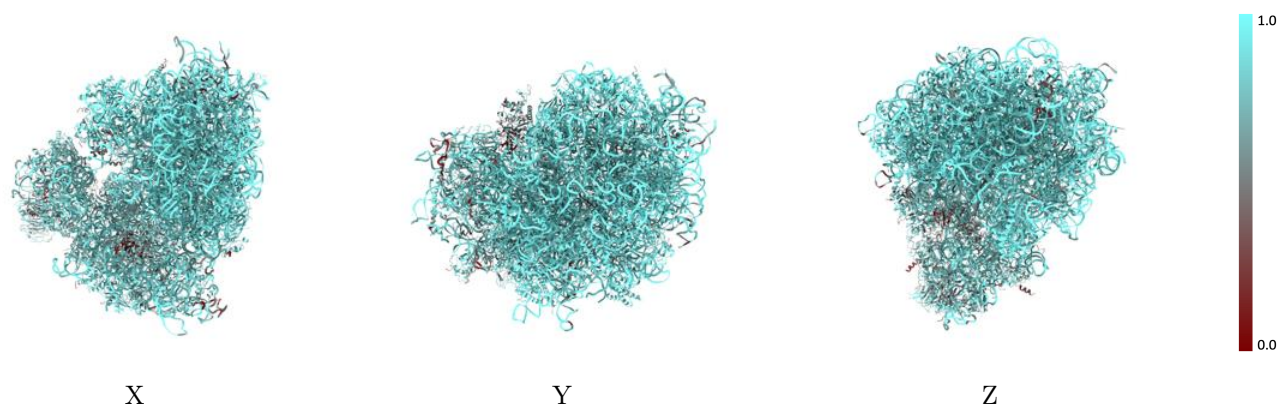
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



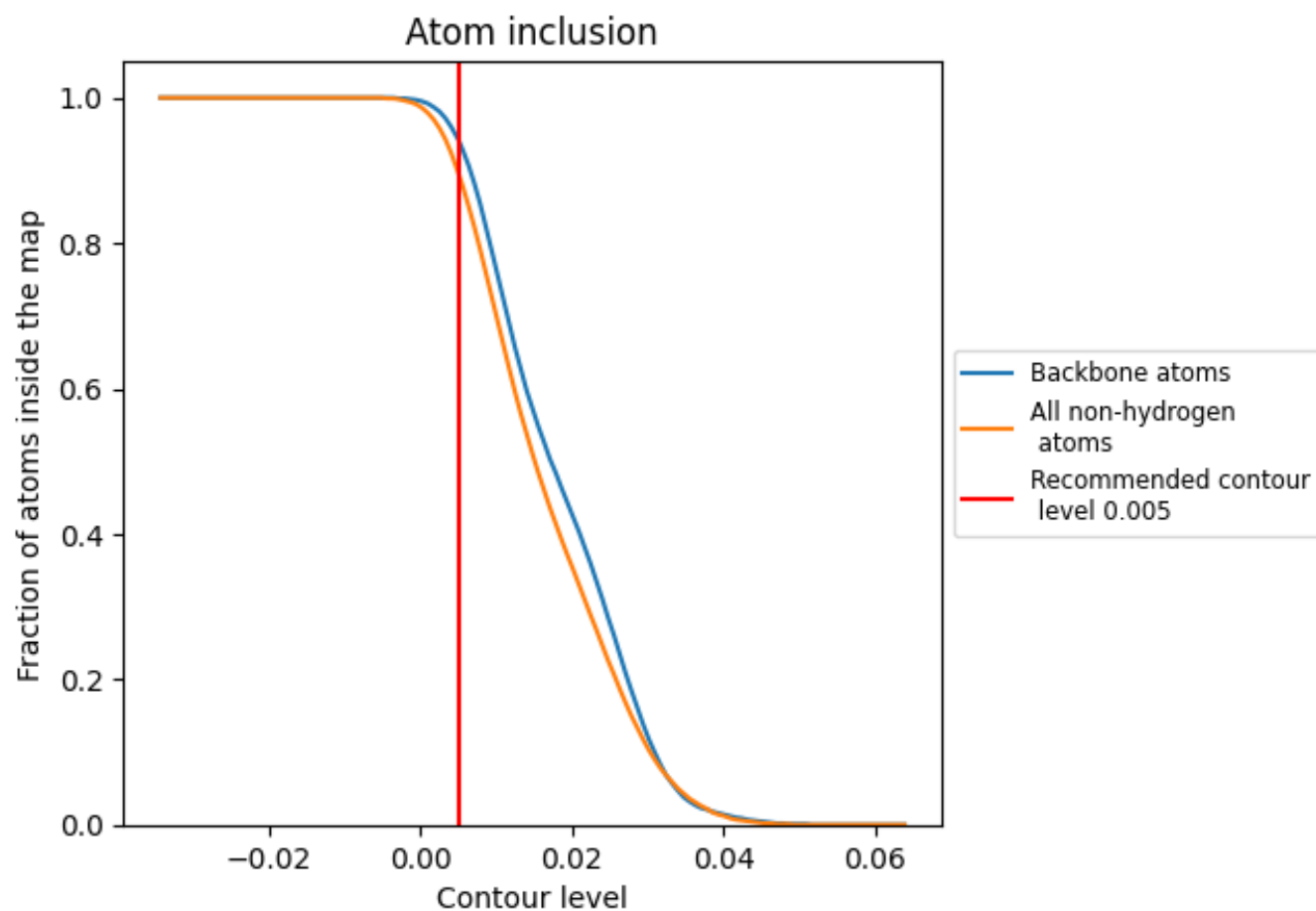
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.005).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8960	 0.5050
5	 0.5500	 0.4350
CB	 0.5540	 0.3760
L5	 0.9600	 0.5390
L7	 0.9970	 0.5850
L8	 0.9770	 0.5620
LA	 0.9420	 0.6020
LB	 0.9430	 0.5830
LC	 0.9500	 0.5860
LD	 0.9480	 0.5590
LE	 0.8960	 0.5330
LF	 0.9250	 0.5840
LG	 0.9260	 0.5470
LH	 0.9410	 0.5760
LI	 0.9420	 0.5760
LJ	 0.8700	 0.4970
LL	 0.9310	 0.5630
LM	 0.9330	 0.5610
LN	 0.9470	 0.6080
LO	 0.9440	 0.5870
LP	 0.9520	 0.5930
LQ	 0.9530	 0.6060
LR	 0.8860	 0.5330
LS	 0.9570	 0.5980
LT	 0.9300	 0.5730
LU	 0.9190	 0.5030
LV	 0.9460	 0.5920
LW	 0.9330	 0.5930
LX	 0.9270	 0.5840
LY	 0.9370	 0.5790
LZ	 0.9380	 0.5720
La	 0.9590	 0.6050
Lb	 0.8230	 0.5000
Lc	 0.9170	 0.5390
Ld	 0.9450	 0.5680



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Chain	Atom inclusion	Q-score
Le	 0.9430	 0.5970
Lf	 0.9540	 0.6040
Lg	 0.9100	 0.5710
Lh	 0.9290	 0.5710
Li	 0.9290	 0.5610
Lj	 0.9570	 0.6040
Lk	 0.9080	 0.5390
Ll	 0.9170	 0.5850
Lm	 0.9110	 0.5780
Ln	 0.8610	 0.5680
Lo	 0.9440	 0.5850
Lp	 0.9380	 0.5850
Lr	 0.9540	 0.5840
Lz	 0.4630	 0.3770
S	 0.5140	 0.3990
S2	 0.9190	 0.4440
SA	 0.8320	 0.4690
SB	 0.7360	 0.3740
SC	 0.8830	 0.5310
SD	 0.7550	 0.4260
SE	 0.7970	 0.4830
SF	 0.6470	 0.3310
SG	 0.7420	 0.3760
SH	 0.7820	 0.4040
SI	 0.7580	 0.4340
SJ	 0.8260	 0.4720
SK	 0.6980	 0.3550
SL	 0.7950	 0.4910
SN	 0.7880	 0.4600
SO	 0.7170	 0.4020
SP	 0.7410	 0.3600
SQ	 0.6300	 0.3740
SR	 0.7340	 0.4060
SS	 0.7420	 0.3670
ST	 0.6750	 0.3810
SU	 0.6910	 0.3870
SV	 0.8810	 0.5010
SW	 0.8560	 0.5460
SX	 0.8530	 0.5360
SY	 0.7510	 0.3880
SZ	 0.6810	 0.3000
Sa	 0.7700	 0.4460

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Chain	Atom inclusion	Q-score
Sb	 0.7710	 0.3780
Sc	 0.6960	 0.3230
Sd	 0.7000	 0.4460
Se	 0.7050	 0.4390
Sg	 0.7130	 0.3450