



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:07 PM UTC

PDB ID : 8Y0X / pdb_00008y0x
EMDB ID : EMD-37992
Title : Dormant ribosome with SERBP1
Authors : Du, M.; Zeng, F.
Deposited on : 2024-01-23
Resolution : 3.30 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

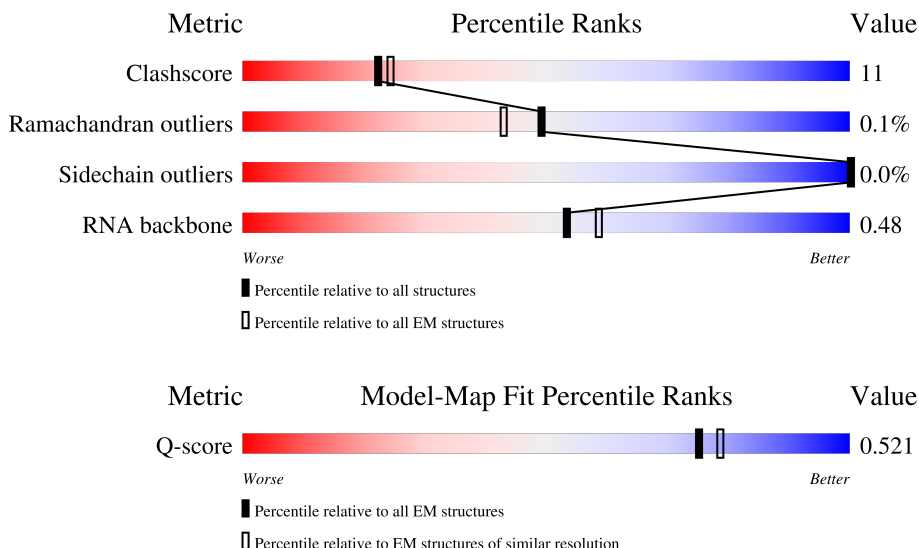
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.30 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.



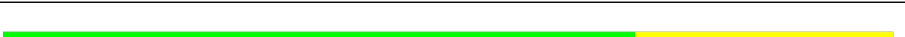
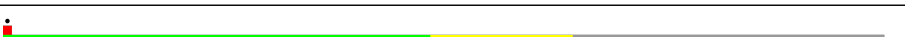
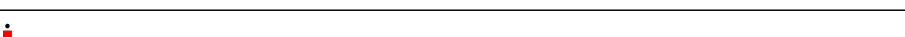
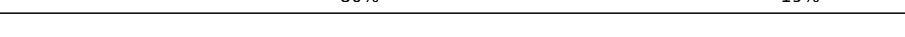
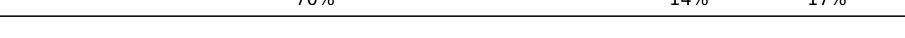
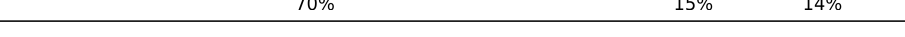
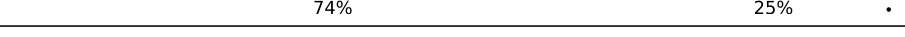
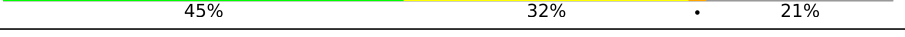
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 (2.80 - 3.80)

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	L5	5070	
2	L7	121	
3	L8	157	

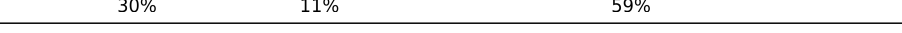
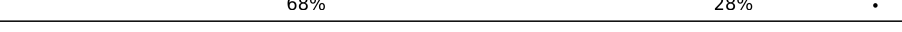
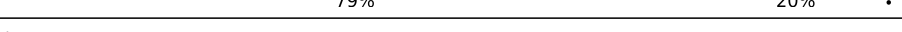
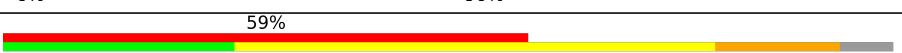
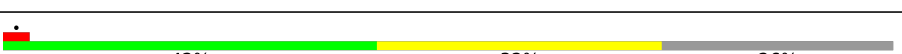
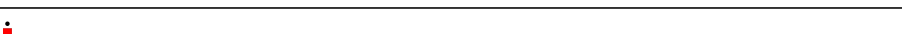
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	
24	LV	140	
25	LW	157	
26	LX	156	
27	LY	145	
28	LZ	136	

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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	S2	1869	
47	S	402	
48	E	85	
49	SA	295	
50	SB	264	
51	SN	151	
52	SO	151	
53	SP	145	

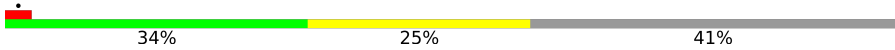
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Mol	Chain	Length	Quality of chain
54	SQ	146	
55	SR	135	
56	SS	152	
57	ST	145	
58	SU	119	
59	SV	83	
60	SW	130	
61	SX	143	
62	SY	133	
63	SZ	125	
64	Sa	115	
65	Sb	84	
66	Sc	69	
67	Sd	56	
68	Se	59	
69	Sg	317	
70	CB	858	
71	SG	249	
72	SJ	194	
73	SC	293	
74	SF	204	
75	SH	194	
76	SD	243	
77	SE	263	
78	SI	208	

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Mol	Chain	Length	Quality of chain
79	SK	165	
80	SL	158	

2 Entry composition

There are 82 unique types of molecules in this entry. The entry contains 218903 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3658	Total	C	N	O	P	0	0
			78419	34920	14351	25491	3657		

- Molecule 2 is a RNA chain called 5S rRNA.

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

- Molecule 3 is a RNA chain called 5.8S rRNA.

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

- Molecule 4 is a protein called 60S ribosomal protein L8.

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

- Molecule 5 is a protein called 60S ribosomal protein L3.

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

- Molecule 6 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LC	365	Total	C	N	O	S	0	0
			2908	1829	580	486	13		

- Molecule 7 is a protein called 60S ribosomal protein L5.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	LE	219	Total	C	N	O	S	0	0
			1764	1136	334	290	4		

- Molecule 9 is a protein called 60S ribosomal protein L7.

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

- Molecule 10 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	LG	231	Total	C	N	O	S	0	0
			1867	1191	359	313	4		

- Molecule 11 is a protein called 60S ribosomal protein L9.

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

- Molecule 12 is a protein called 60S ribosomal protein L10-like.

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

- Molecule 13 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LJ	172	Total	C	N	O	S	0	0
			1381	868	258	249	6		

- Molecule 14 is a protein called 60S ribosomal protein L13.

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

- Molecule 15 is a protein called 60S ribosomal protein L14.

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

- Molecule 16 is a protein called 60S ribosomal protein L15.

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

- Molecule 17 is a protein called 60S ribosomal protein L13a.

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

- Molecule 18 is a protein called 60S ribosomal protein L17.

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

- Molecule 19 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	LQ	187	Total	C	N	O	S	0	0
			1513	944	314	250	5		

- Molecule 20 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	LR	168	Total	C	N	O	S	0	0
			1397	867	300	221	9		

- Molecule 21 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	LS	175	Total	C	N	O	S	0	0
			1453	925	283	235	10		

- Molecule 22 is a protein called 60S ribosomal protein L21.

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

- Molecule 23 is a protein called 60S ribosomal protein L22.

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

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

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

- Molecule 25 is a protein called 60S ribosomal protein L24.

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

- Molecule 26 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	117	Total	C	N	O	S	0	0
			958	612	179	166	1		

- Molecule 27 is a protein called 60S ribosomal protein L26.

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

- Molecule 28 is a protein called 60S ribosomal protein L27.

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

- Molecule 29 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	La	147	Total	C	N	O	S	0	0
			1162	736	237	186	3		

- Molecule 30 is a protein called 60S ribosomal protein L29.

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

- Molecule 31 is a protein called 60S ribosomal protein L30.

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

- Molecule 32 is a protein called 60S ribosomal protein L31.

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

- Molecule 33 is a protein called 60S ribosomal protein L32.

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

- Molecule 34 is a protein called 60S ribosomal protein L35a.

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

- Molecule 35 is a protein called 60S ribosomal protein L34.

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

- Molecule 36 is a protein called 60S ribosomal protein L35.

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

- Molecule 37 is a protein called 60S ribosomal protein L36.

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

- Molecule 38 is a protein called 60S ribosomal protein L37.

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

- Molecule 39 is a protein called 60S ribosomal protein L38.

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

- Molecule 40 is a protein called 60S ribosomal protein L39.

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

- Molecule 41 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 42 is a protein called 60S ribosomal protein L41.

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

- Molecule 43 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	Lo	98	Total	C	N	O	S	0	0
			805	504	165	130	6		

- Molecule 44 is a protein called 60S ribosomal protein L37a.

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

- Molecule 45 is a protein called 60S ribosomal protein L28.

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

- Molecule 46 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	S2	1739	Total	C	N	O	P	0	0
			36875	16449	6594	12094	1738		

- Molecule 47 is a protein called Isoform 2 of SERPINE1 mRNA-binding protein 1.

Mol	Chain	Residues	Atoms				AltConf	Trace
47	S	40	Total	C	N	O	0	0
			318	188	65	65		

- Molecule 48 is a RNA chain called EtRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	E	80	Total	C	N	O	P	0	0
			1708	761	305	562	80		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	34	U	A	variant	GB 2634358191
E	83	C	U	variant	GB 2634358191

- Molecule 49 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	SA	219	Total	C	N	O	S	0	0
			1733	1102	303	320	8		

- Molecule 50 is a protein called 40S ribosomal protein S3a.

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

- Molecule 51 is a protein called 40S ribosomal protein S13.

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

- Molecule 52 is a protein called 40S ribosomal protein S14.

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

- Molecule 53 is a protein called 40S ribosomal protein S15.

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

- Molecule 54 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SQ	140	Total	C	N	O	S	0	0
			1107	704	209	191	3		

- Molecule 55 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	SR	131	Total	C	N	O	S	0	0
			1060	666	195	194	5		

- Molecule 56 is a protein called 40S ribosomal protein S18.

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

- Molecule 57 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	ST	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 58 is a protein called 40S ribosomal protein S20.

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

- Molecule 59 is a protein called 40S ribosomal protein S21.

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

- Molecule 60 is a protein called 40S ribosomal protein S15a.

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

- Molecule 61 is a protein called 40S ribosomal protein S23.

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

- Molecule 62 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SY	131	Total	C	N	O	S	0	0
			1065	673	209	178	5		

- Molecule 63 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	SZ	62	Total	C	N	O	S	0	0
			480	308	84	87	1		

- Molecule 64 is a protein called 40S ribosomal protein S26.

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

- Molecule 65 is a protein called 40S ribosomal protein S27.

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

- Molecule 66 is a protein called 40S ribosomal protein S28.

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

- Molecule 67 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Sd	52	Total	C	N	O	S	0	0
			436	273	88	70	5		

- Molecule 68 is a protein called 40S ribosomal protein S30.

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

- Molecule 69 is a protein called Receptor of activated protein C kinase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sg	313	Total	C	N	O	S	0	0
			2436	1535	424	465	12		

- Molecule 70 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	CB	755	Total	C	N	O	S	0	0
			5904	3753	1014	1099	38		

- Molecule 71 is a protein called 40S ribosomal protein S6.

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

- Molecule 72 is a protein called 40S ribosomal protein S9.

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

- Molecule 73 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SC	219	Total	C	N	O	S	0	0
			1700	1100	292	298	10		

- Molecule 74 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SF	181	Total	C	N	O	S	0	0
			1438	900	270	261	7		

- Molecule 75 is a protein called 40S ribosomal protein S7.

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

- Molecule 76 is a protein called 40S ribosomal protein S3.

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

- Molecule 77 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 78 is a protein called 40S ribosomal protein S8.

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

- Molecule 79 is a protein called 40S ribosomal protein S10.

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

- Molecule 80 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	SL	147	Total	C	N	O	S	0	0
			1205	769	227	203	6		

- Molecule 81 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

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

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Mol	Chain	Residues	Atoms		AltConf
81	LV	1	Total 1	Mg 1	0
81	La	1	Total 1	Mg 1	0
81	Le	1	Total 1	Mg 1	0
81	Lg	1	Total 1	Mg 1	0
81	S2	29	Total 29	Mg 29	0

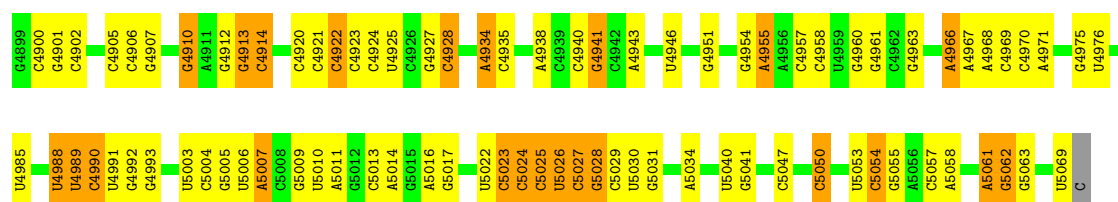
- Molecule 82 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
82	Lg	1	Total 1	Zn 1	0
82	Lj	1	Total 1	Zn 1	0
82	Lm	1	Total 1	Zn 1	0
82	Lo	1	Total 1	Zn 1	0
82	Lp	1	Total 1	Zn 1	0
82	Sa	1	Total 1	Zn 1	0
82	Sd	1	Total 1	Zn 1	0



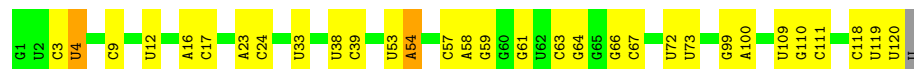






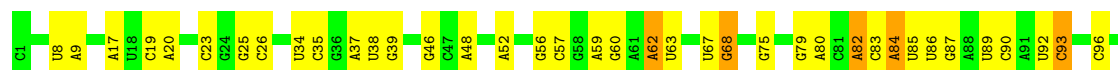
- Molecule 2: 5S rRNA

Chain L7: 74% 24% ..



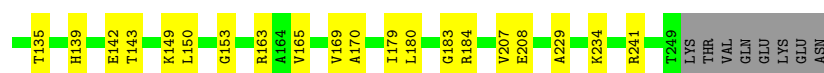
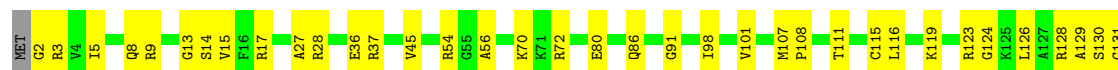
- Molecule 3: 5.8S rRNA

Chain L8: 55% 37% 7% .



- Molecule 4: 60S ribosomal protein L8

Chain LA: 75% 22% .



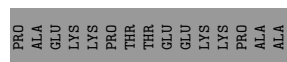
- Molecule 5: 60S ribosomal protein L3

Chain LB: 76% 23%



- Molecule 6: 60S ribosomal protein L4

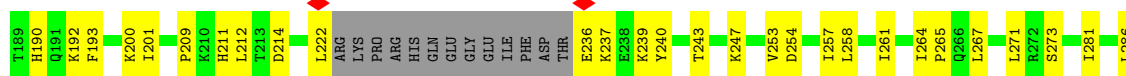
15%



- 21%



- 24%

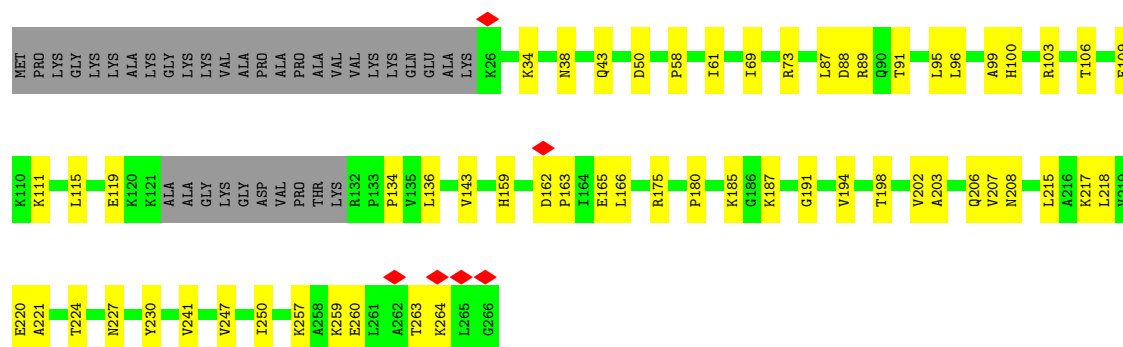


- 9%

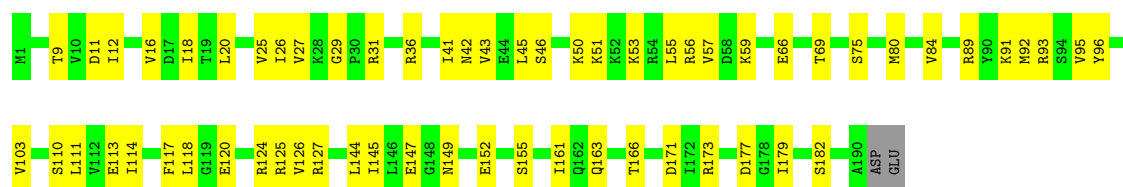




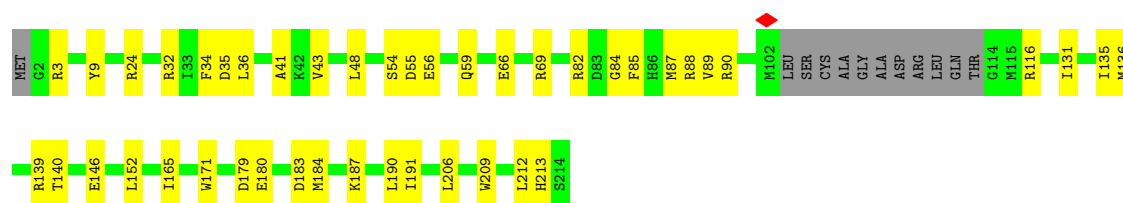
- Molecule 10: 60S ribosomal protein L7a



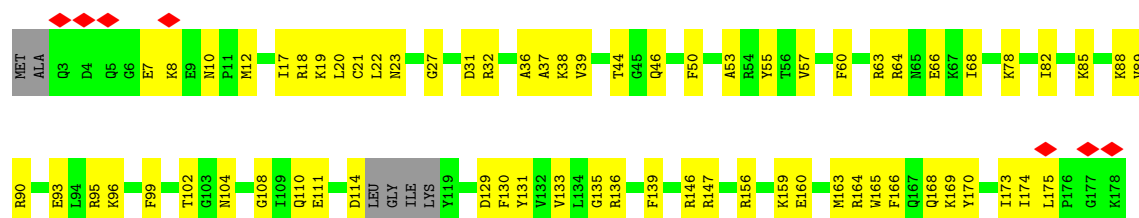
- Molecule 11: 60S ribosomal protein L9

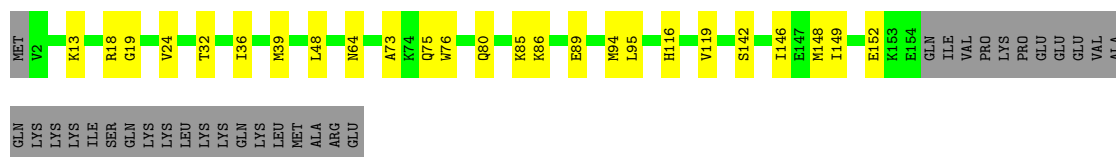


- Molecule 12: 60S ribosomal protein L10-like



- Molecule 13: 60S ribosomal protein L11





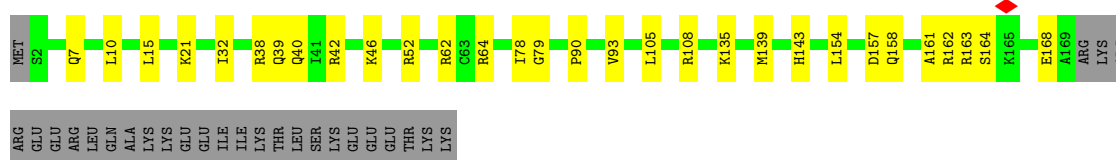
- Molecule 19: 60S ribosomal protein L18

Chain LQ: 85% 15% .



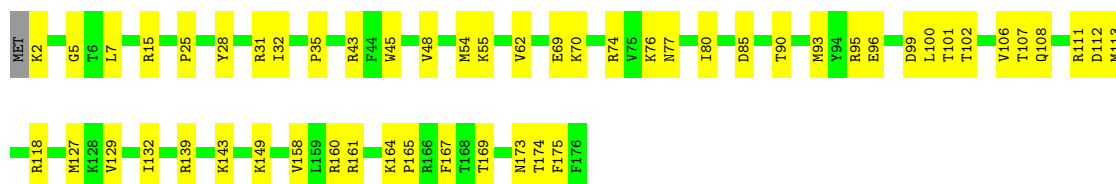
- Molecule 20: 60S ribosomal protein L19

Chain LR: 70% 15% 14% .



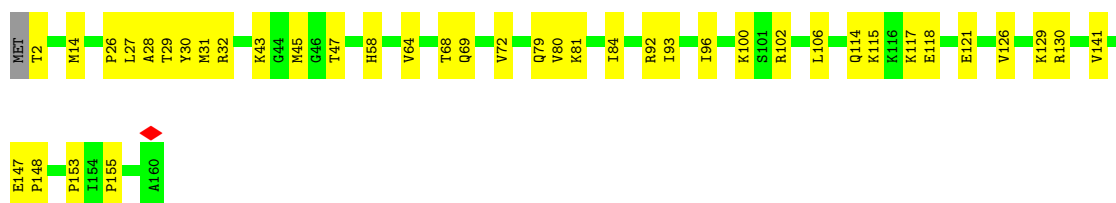
- Molecule 21: 60S ribosomal protein L18a

Chain LS: 69% 30% .



- Molecule 22: 60S ribosomal protein L21

Chain LT: 74% 25% .

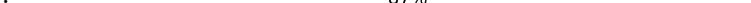


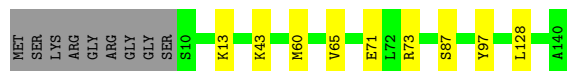
- Molecule 23: 60S ribosomal protein L22

Chain LU: 45% 32% 21% .



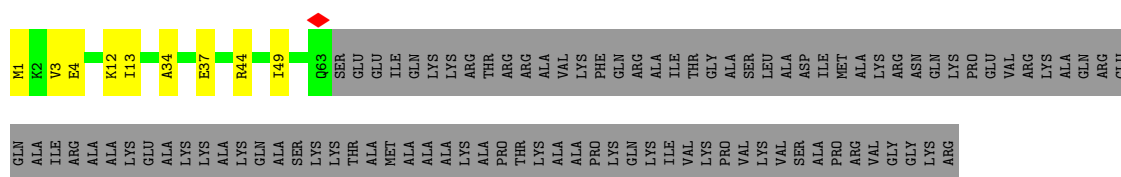
- Molecule 24: 60S ribosomal protein L23

Chain LV:  87% 6% 6%

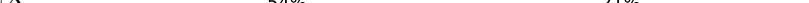


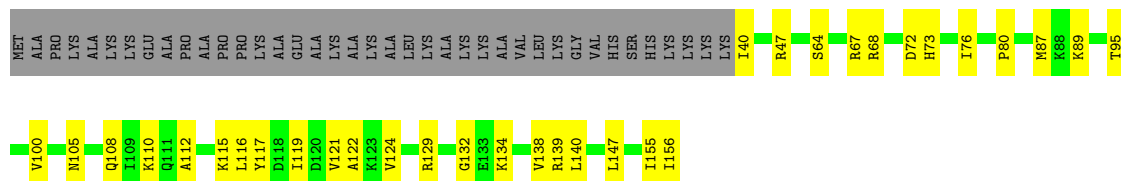
- Molecule 25: 60S ribosomal protein L24

Chain LW:

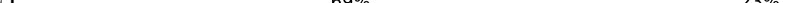


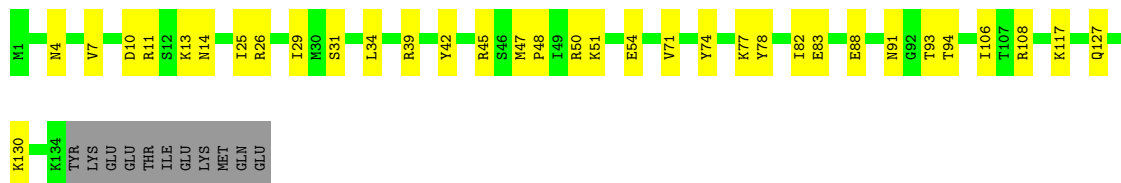
- Molecule 26: 60S ribosomal protein L23a

Chain LX: 

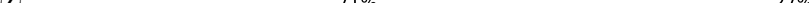


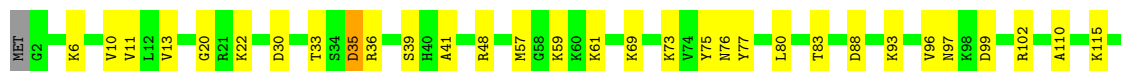
- Molecule 27: 60S ribosomal protein L26

Chain LY: 



- Molecule 28: 60S ribosomal protein L27

Chain LZ:  71% 27% ..





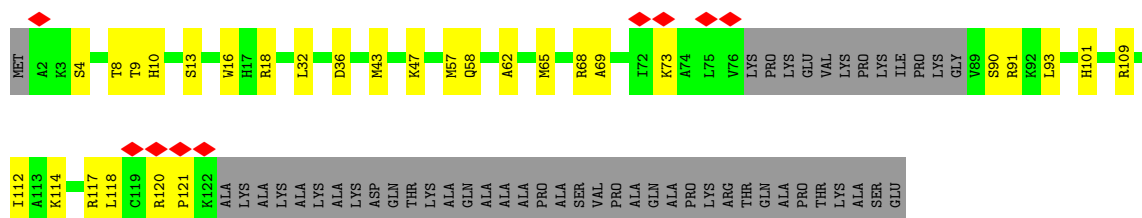
- Molecule 29: 60S ribosomal protein L27a

Chain La: 80% 20% .



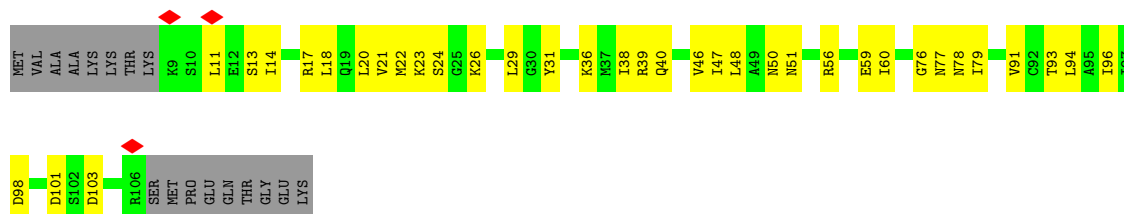
- Molecule 30: 60S ribosomal protein L29

Chain Lb: 6% 50% 18% 31%



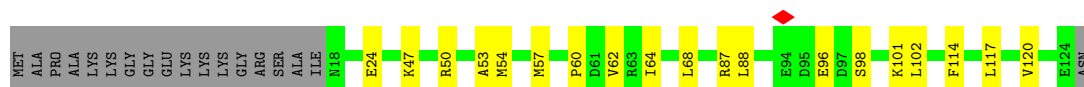
- Molecule 31: 60S ribosomal protein L30

Chain Lc: 54% 31% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld: 70% 15% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le: 75% 20% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  78% 19% ..



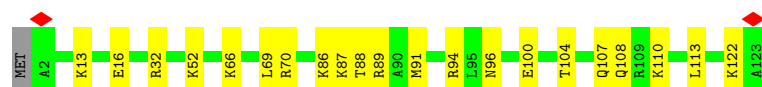
- Molecule 35: 60S ribosomal protein L34

Chain Lg:  79% 18% .



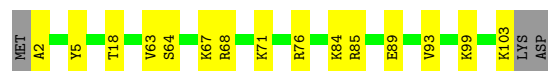
- Molecule 36: 60S ribosomal protein L35

Chain Lh:  82% 17% .



- Molecule 37: 60S ribosomal protein L36

Chain Li:  83% 14% .



- Molecule 38: 60S ribosomal protein L37

Chain Lj:  71% 18% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  60% 39% .



- Molecule 40: 60S ribosomal protein L39

Chain Ll:  59% 39% .



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm:  30% 11% 59%

MET GLN ILE PHE VAL SER THR LEU THR LEU GLY LYS THR ILE THR LEU VAL GLU PRO SER ASP THR ILE ILE GLN ASP LYS GLY ILE PRO PRO ASP GLN ARG LEU ILE PHE ALA GLY LYS GLN LEU GLU ASP GLY ARG THR SER ASP ASN

ILE GLN LYS SER THR LEU HIS LEU VAL LEU ARG LEU ARG GLY I77 I78 E79 P80 S81 L82 R83 Q84 Q87 K88 Y89 M94 Y100 P105 K124 K125 K126 V127 K128

- Molecule 42: 60S ribosomal protein L41

Chain Ln:  68% 28%

M1 R2 A3 R6 K7 R11 R12 R15 S24 LYS

- Molecule 43: 60S ribosomal protein L36a

Chain Lo:  64% 28% 8%

MET V2 T10 F11 C12 C15 G16 K17 H18 Q19 P20 H21 K22 V23 T24 Q25 V26 K27 K30 D31 S32 L33 Y34 A35 Q36 G37 K38 R39 R40 P54 I55 F56 B57 T63 R69 E74 P75 N76 C77 K80 R87 D96 R99 LYS GLY GLN VAL ILE GLN PHE

- Molecule 44: 60S ribosomal protein L37a

Chain Lp:  79% 20%

MET A2 T16 R17 Y18 L22 R23 V26 T38 T45 K46 M47 C57 G58 S59 T70 Y71 N72 T73 T74 S75 A76 V77 T78 V79 K80 Q92

- Molecule 45: 60S ribosomal protein L28

Chain Lr:  66% 25% 9%

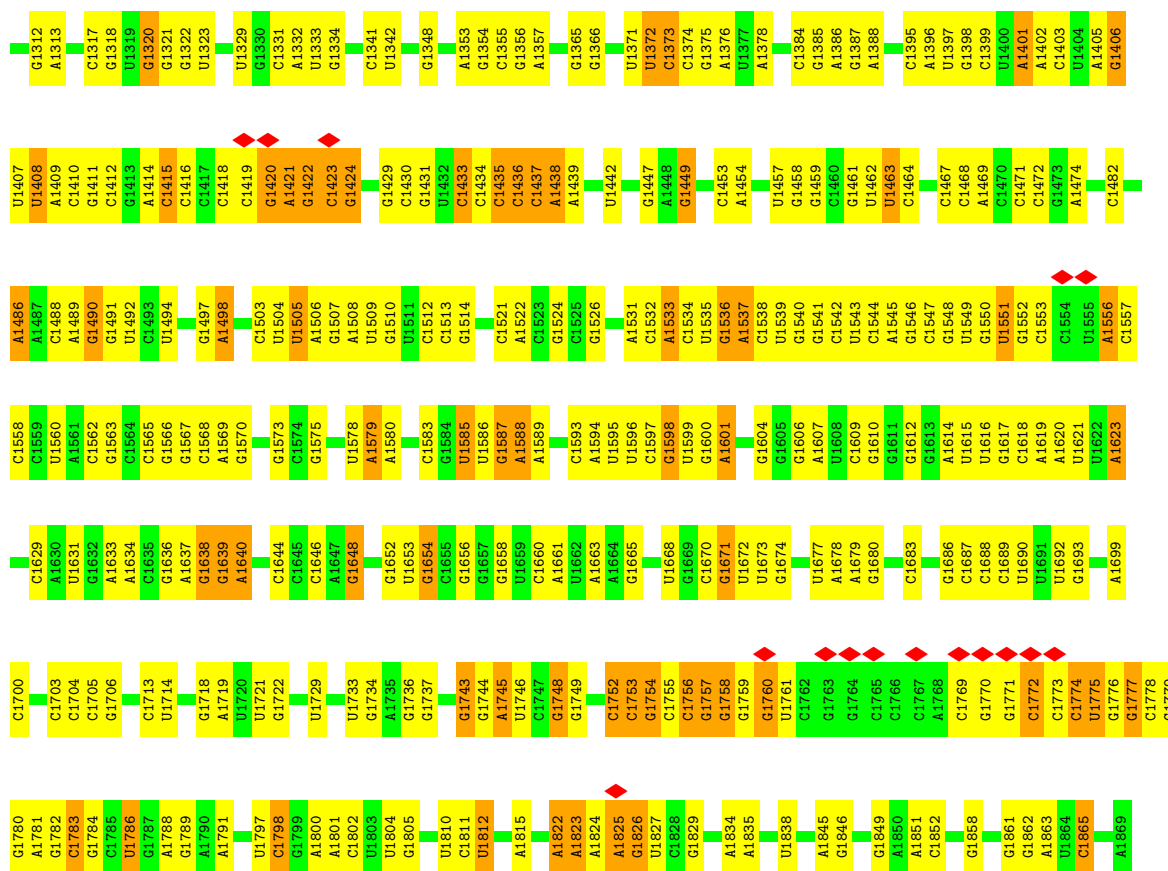
MET S2 A3 H4 L5 Q6 W7 M8 V9 V10 R11 R12 C13 K19 S26 T27 E28 N31 L32 K33 A34 S37 K47 T48 V49 A54 V61 I64 K65 R66 R67 I82 N85 T89 M96 I97 R98 Y102 R103 R107 M108 I111 R112 K122 M125 V126 LYS ARG LYS ARG THR PRO THR LYS SER SER

- Molecule 46: 18S rRNA

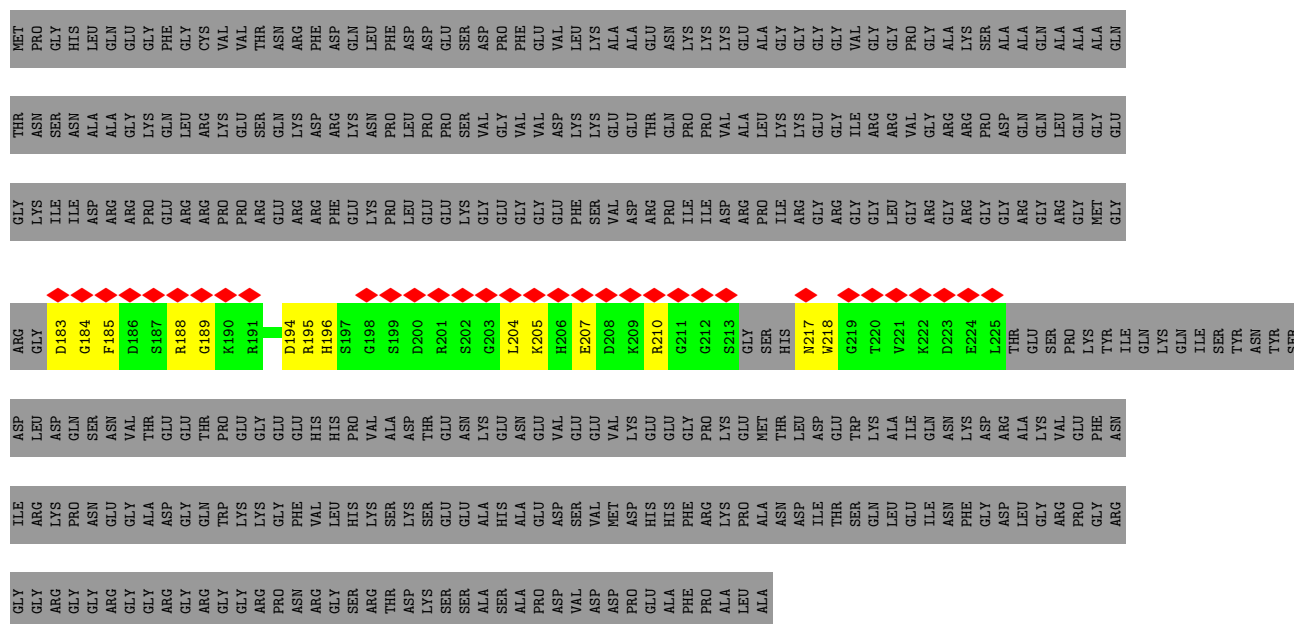
Chain S2:  44% 38% 11% 7%

U1 A2 C3 C4 U5 G6 U12 C13 C14 U15 U16 G16 C17 C18 C24 A25 U28 C29 C30 G33 A38 G41 U44 A45 A46 U51 G52 G56 U57 C58 U59 A64 C65 G66 G67 A68 G71 C72 C73 C74 G75 U76 A77 C78 A84 A85 G90 A91

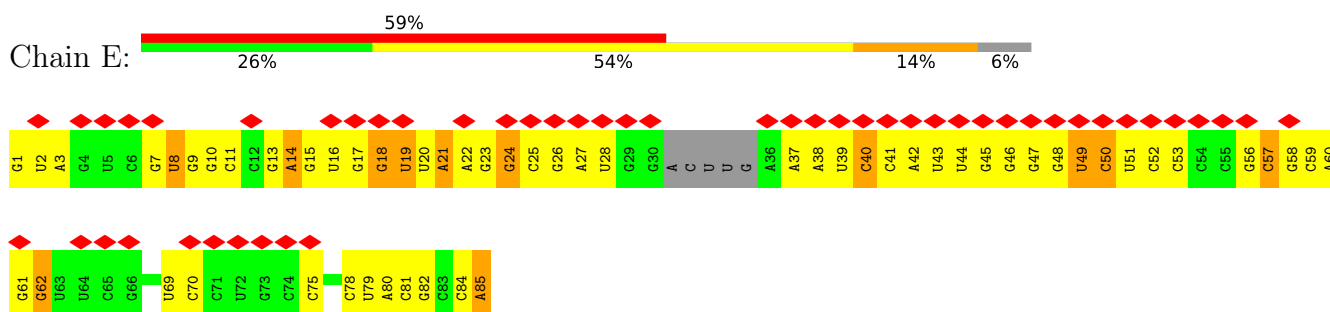
U1238	C1138	A1012	G934	A864	C	A650	G559	C492	G383	G307	A175	A92
U1239	C1139	U1013	C941	A865	C	G856	A560	A493	U384	G308	U176	U93
A1240	G1140	U1014	C942	G866	C	U857	U562	C494	C385	G309	C177	G94
U1241	G1141	U1015	G	U867	A	U858	U561	U495	C386	C310	C178	
U1242	G1142	U1016	C785	G868	C	G859	A564	C496	C390	C311	C179	A103
U1243	G1143	U1017	G786	G869	C	G860	U565	C497	G407	G312	G182	U105
U1244	A1143	U1018	G787	C861	C	U861	U566	C498	G408	G313	G183	C106
G1245	A1144	U871	G788	G862	C	G862	C567	G499	C409	A318	G184	U107
A1246	A1145	A872		C863		A864	A569	C502	C319	C319	G185	G108
C1247		G		A865			C570	G503	C417	C322	U112	U112
A1251	C1247	G874	C791	A866		A868	A575	G507	G418	C323	G113	G113
C1252	A1148	A875	C792	A869		A869	A576	G507	G419	C324	U115	U115
A1253	A1149	C876	G793	A870		A871	A577	G508	G420	C325	U116	U116
C1254	C1153	C877	A794	A871		A872	U582	G509	G421	C326	C192	C192
U1255	U1154	C878	G795	A872		G873	U583	G510	G431	C327	C193	C193
G1256	U1155	C879	C797	A873		C874	A582	U511	G438	U328	C194	C125
G1257	U1156	G880	G798	C874		U875	A587	A512		G330	C195	G126
A1258	G1157	U882	U799	U876		G877	G588	A516		G331	C196	
A1259	G1158		U800	G877		G878	G589	A517		G332	C197	
A1260	G1164	A963	U804	G879		G880	A590	A521		G333	U198	
C1261	G1165	A964	U805	G881		G882	U591	A522		G334	U199	
A1264	G1166	G970	A809	G883		G884	C592	A523		G335	G200	
A1265	G1171	G971	A810	U886		U887	C593	A524		G336	C201	
G1269	G1187	G976	U815	C887		U888	A594	A525		G337	G202	
G1270	G1188	C977	A816	U889		U889	U595	A526		G338	G203	
C1271	U1192		U819	G890		G891	U596	C527		G339	G204	
C1272	U1193	A980	G820	G892		G893	U597	A528		G340	G205	
C1273	A1194	A981	G821	G894		G895	G606	A529		U344	G206	
G1274	A1195	G982	U822	G896		G897	G607	U530		U345	G207	
G1275		A983	U823	G898		G899	U609	U531		G346	G208	
A1276	A1199	G984	C924	G899		G900	G610	A533		G347	A209	
A1277		G985		G901		G902	C614	A534		A348	U210	
A1278	U1201	G986	C829	G903		G904	G617	G535		A349	G211	
C1279	U1202	C987	A830	A904		G905	U623	A536		C350	C212	
A1284	G1203	C988	C834	A905		G906	G624	C537		C356	G213	
G1285	A1204	G989	C835	C906		G907	C625	U538		A360	U214	
G1286	G1207	A990	G836	U906		G908	G626	C539		U361	G215	
	A1208	G991	A837	G907		G909	A628	U540		C362	C216	
U1289	C1213	G992	G838	A908		G910	U629	U541		A363	C223	
G1290	C1214	G993	C839	A909		G911	U630	G542		A364	A224	
	A1215	A996	C840	C905		G912	U631	G543		U367	G225	
G1294	C1216	A997	C841	C906		G913	U632	A544		U368	A	
A1295	A1217	G998	C842	U907		G914	C633	G545		C369	U	
	C1218	C1000	C843	G908		G915	U637	C546		U370	A	
G1298	G1221	A1001	U844	A920		G916	C634	G547		G371	A	
A1301	G1222	U1004	G845	G921		G917	U638	C548		G374	A	
G1302	G1223	G1005	G846	G925		G918	C635	U551		U375	A	
C1303	G1224	U1006	A847	G926		G919	U639	G552		A376	A	
U1304	G1225	C1007	C851	G927		G920	A640	U553		G377	A	
C1305	G1226	A1008	G852	G928		G921	A641	A554			C	
U1306	G1227	A1009	G860	G929		G922	U642	A555			C	
U1307	G1228	G1010	U861	G930		G923	A644	U556			C	
U1308	G1229	U1011	U863	G933		G924	G644	U557			C	
C1309	G1230					G925		G558			C	



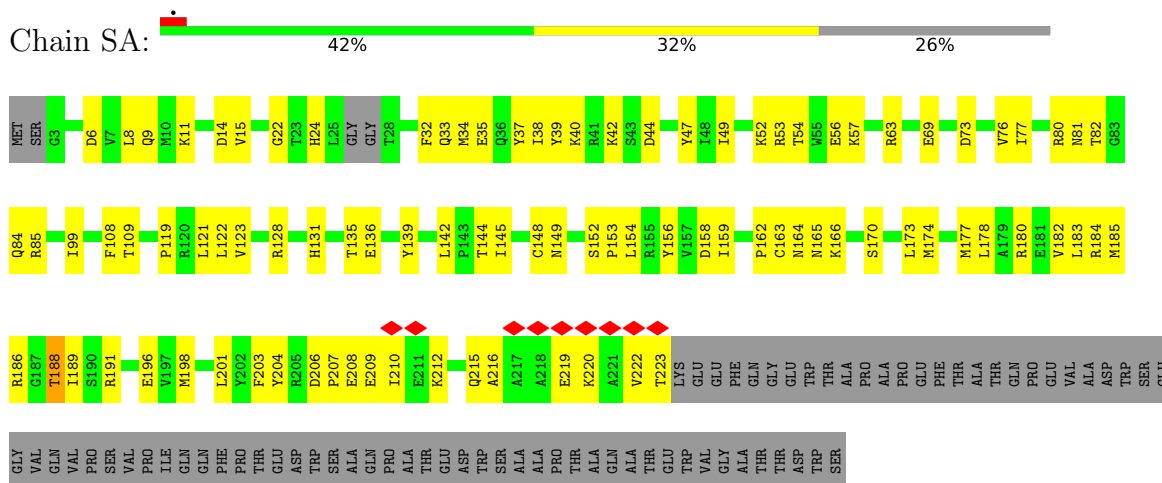
• Molecule 47: Isoform 2 of SERPINE1 mRNA-binding protein 1



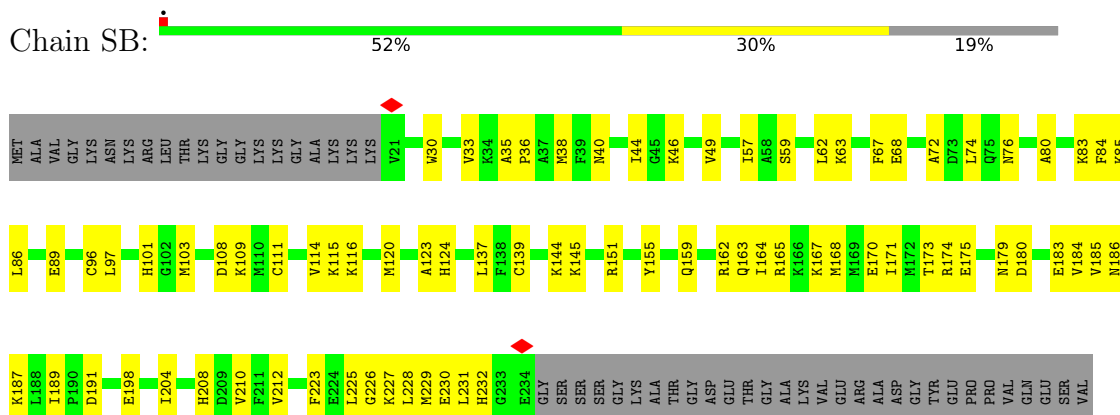
• Molecule 48: EtRNA



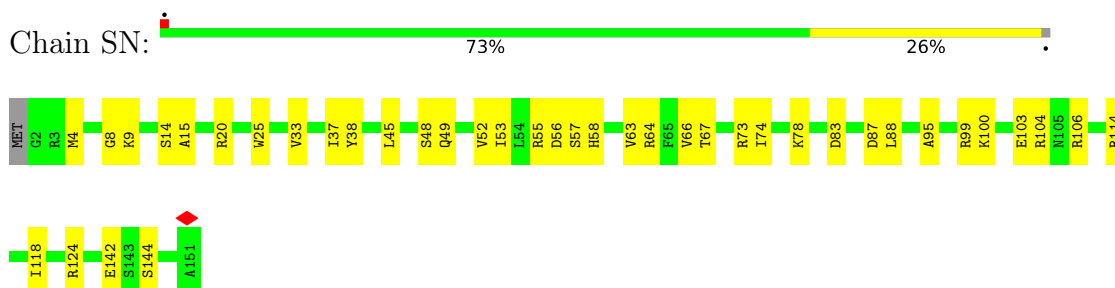
- Molecule 49: 40S ribosomal protein SA



- Molecule 50: 40S ribosomal protein S3a

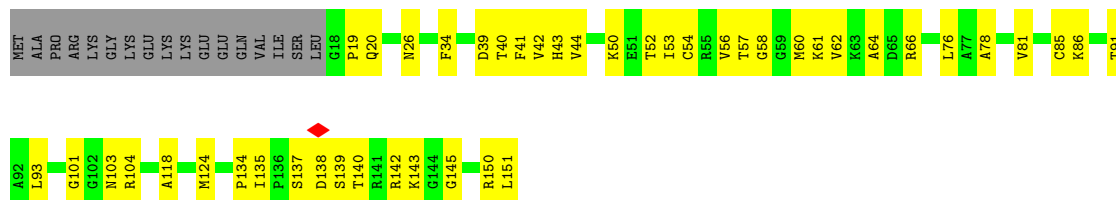


- Molecule 51: 40S ribosomal protein S13



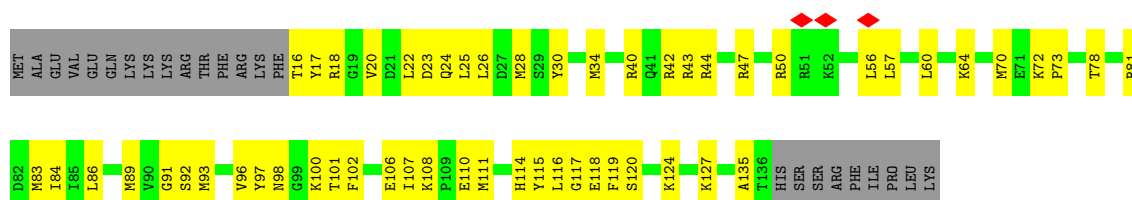
- Molecule 52: 40S ribosomal protein S14

Chain SO: 



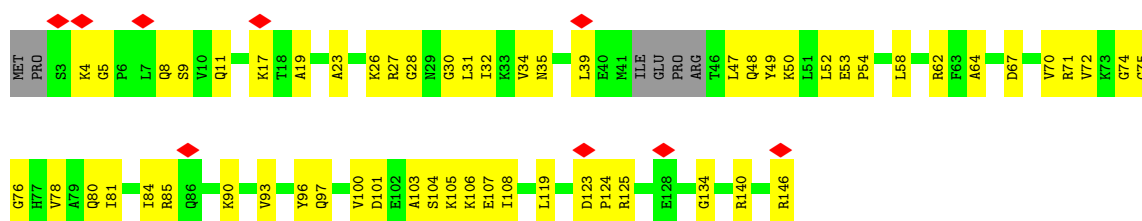
- Molecule 53: 40S ribosomal protein S15

Chain SP: 



- Molecule 54: 40S ribosomal protein S16

Chain SQ: 



- Molecule 55: 40S ribosomal protein S17

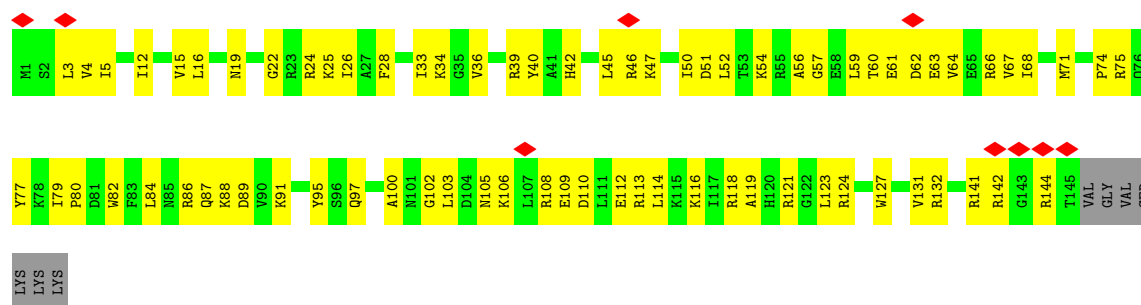
Chain SR: 



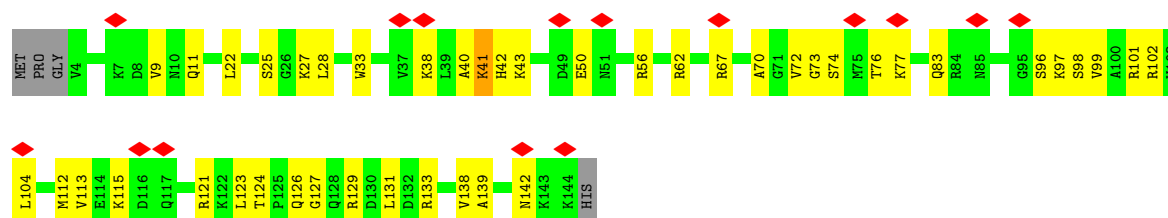
- Molecule 56: 40S ribosomal protein S18

Chain SS: 

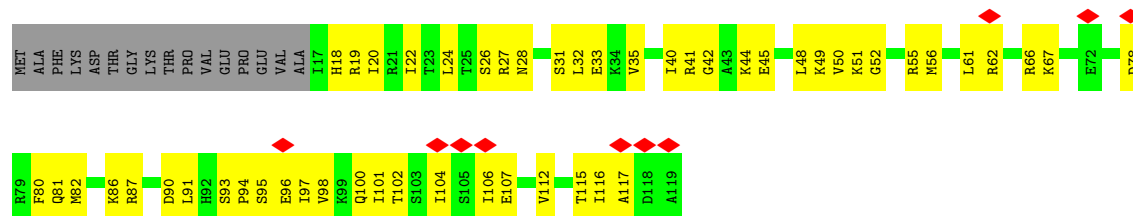
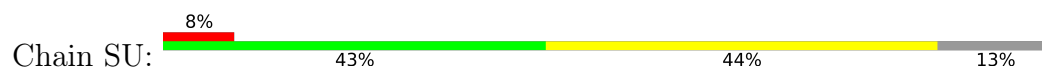




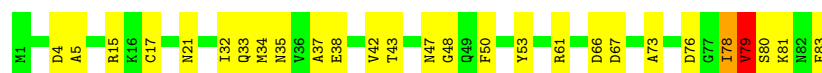
- Molecule 57: 40S ribosomal protein S19



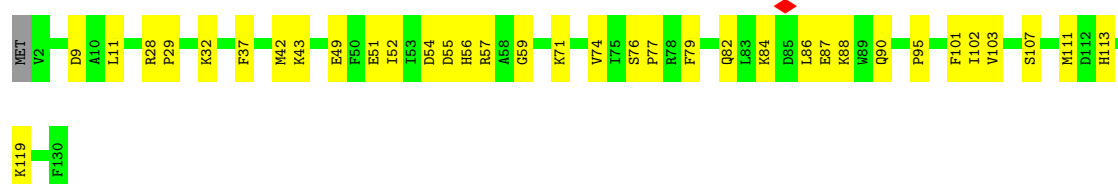
- Molecule 58: 40S ribosomal protein S20



- Molecule 59: 40S ribosomal protein S21

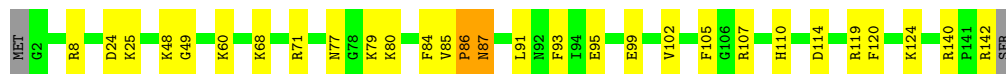


- Molecule 60: 40S ribosomal protein S15a



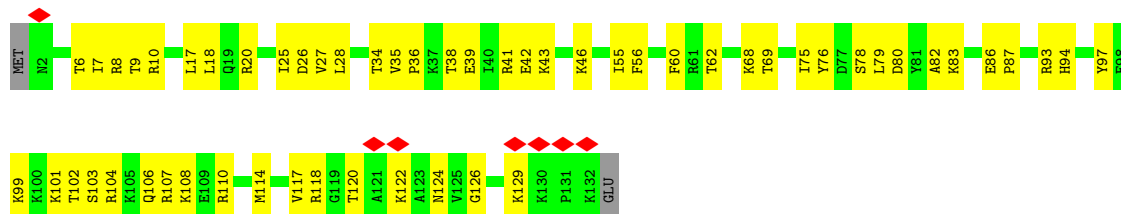
- Molecule 61: 40S ribosomal protein S23

Chain SX:  78% 19% ..



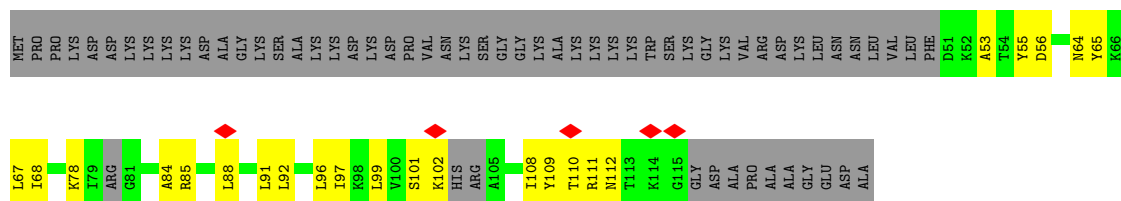
- Molecule 62: 40S ribosomal protein S24

Chain SY:  5% 56% 42% .



- Molecule 63: 40S ribosomal protein S25

Chain SZ:  31% 18% 50%



- Molecule 64: 40S ribosomal protein S26

Chain Sa:  63% 25% 11%



- Molecule 65: 40S ribosomal protein S27

Chain Sb:  63% 36% .

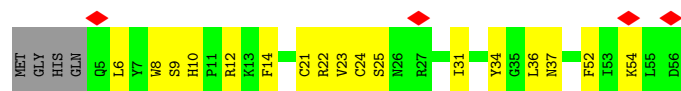


- Molecule 66: 40S ribosomal protein S28

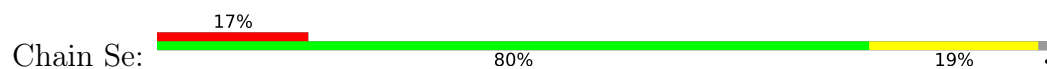
Chain Sc:  10% 49% 43% 7%



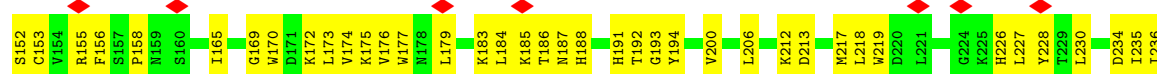
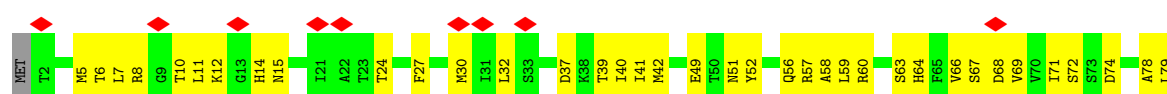
- Molecule 67: 40S ribosomal protein S29



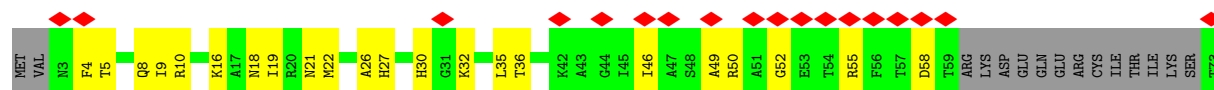
- Molecule 68: 40S ribosomal protein S30

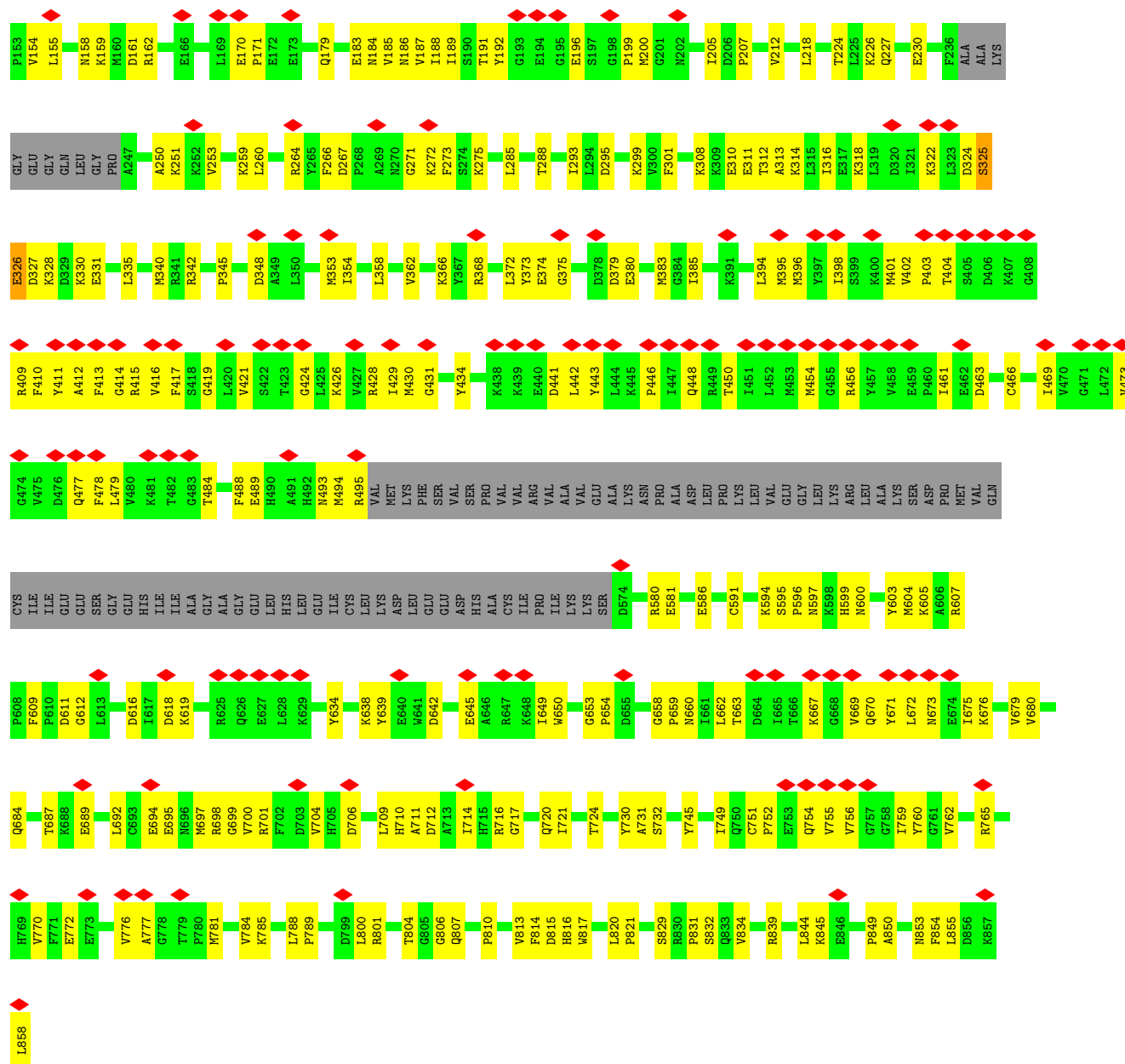


- Molecule 69: Receptor of activated protein C kinase 1



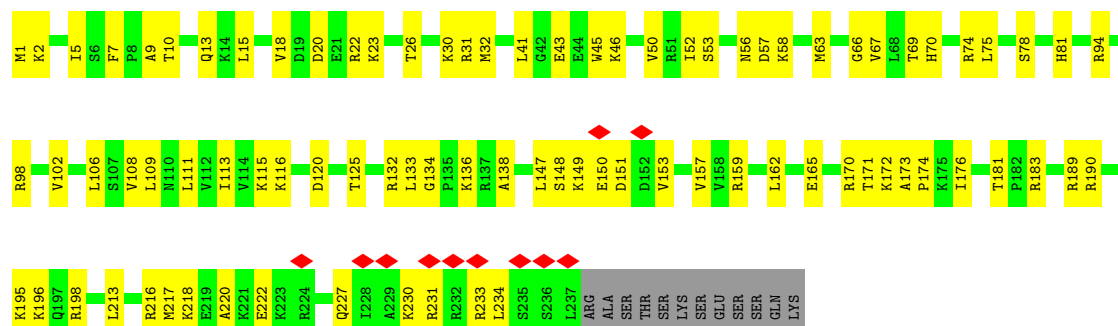
- Molecule 70: Elongation factor 2



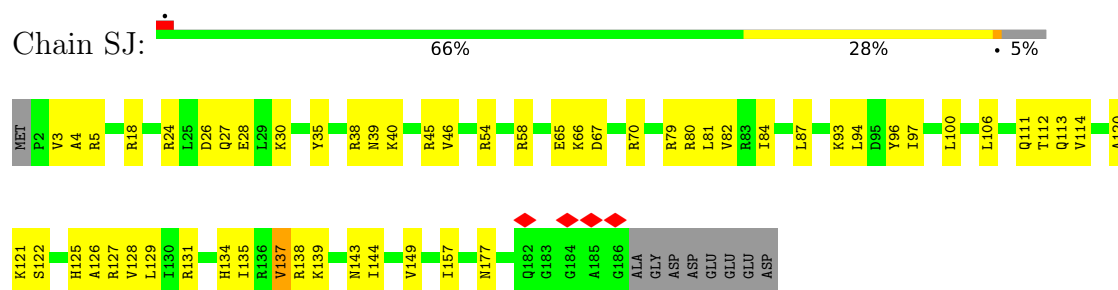


• Molecule 71: 40S ribosomal protein S6

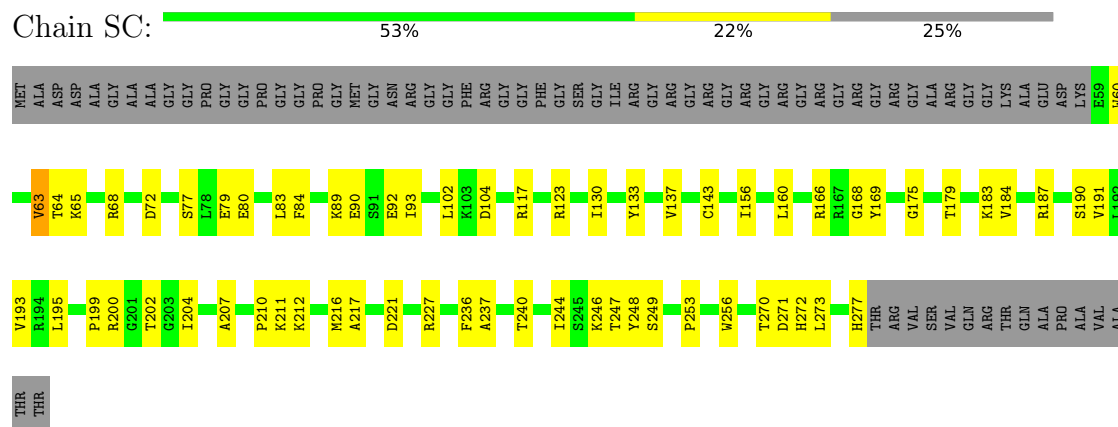
Chain SG: 60% 35% 5%



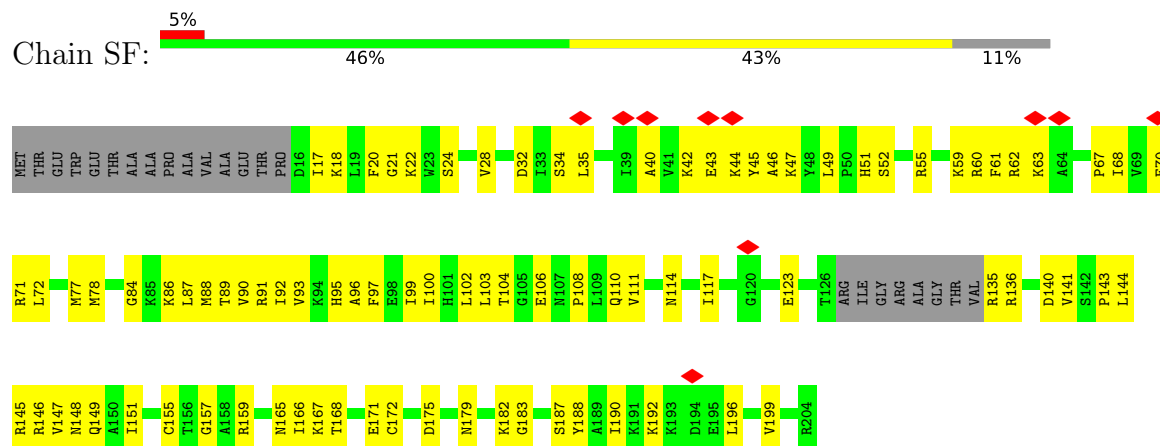
- Molecule 72: 40S ribosomal protein S9



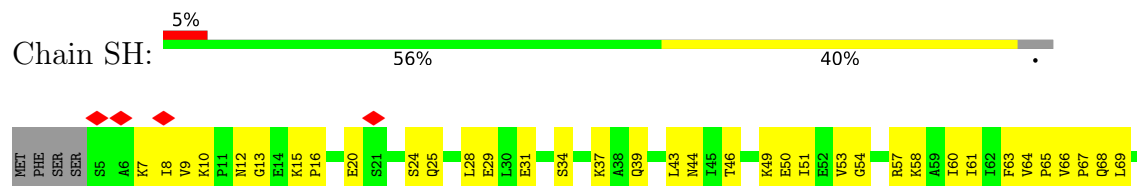
- Molecule 73: 40S ribosomal protein S2

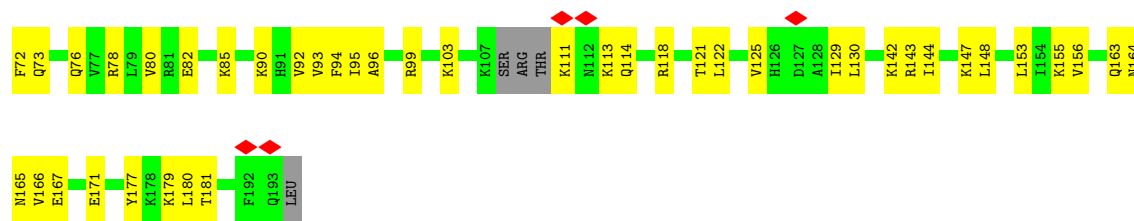


- Molecule 74: 40S ribosomal protein S5

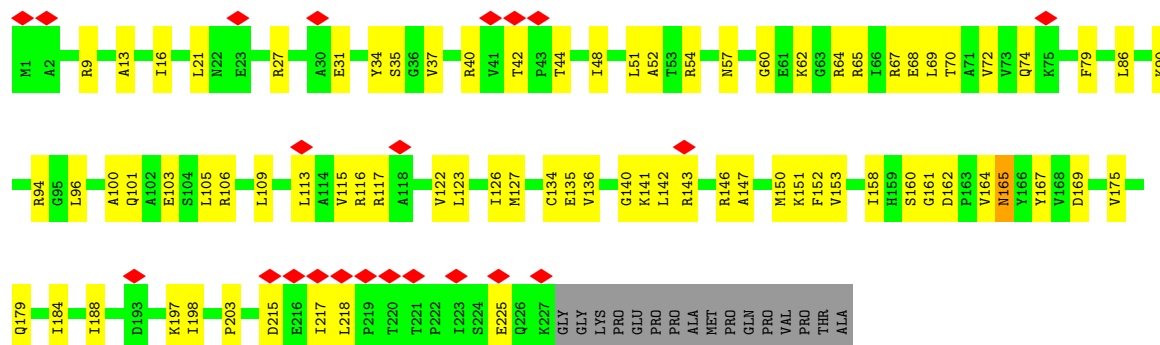


- Molecule 75: 40S ribosomal protein S7

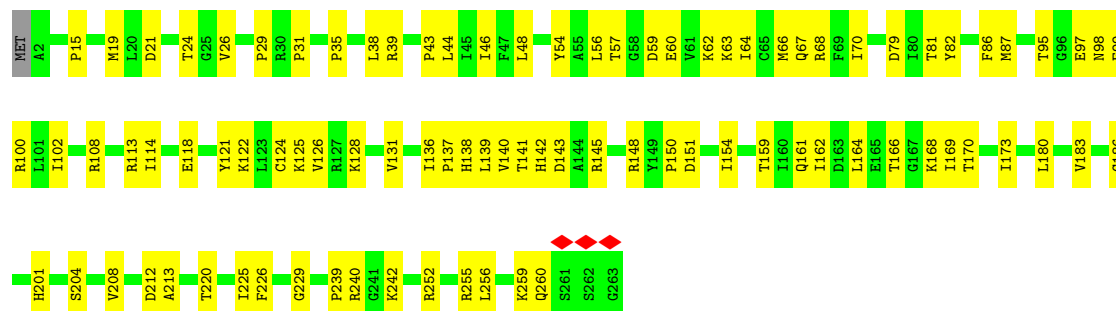




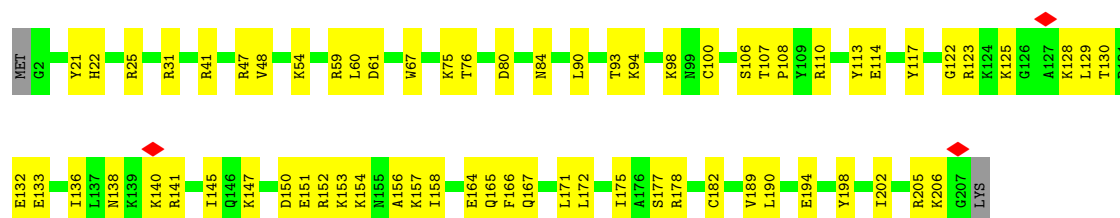
• Molecule 76: 40S ribosomal protein S3



• Molecule 77: 40S ribosomal protein S4, X isoform

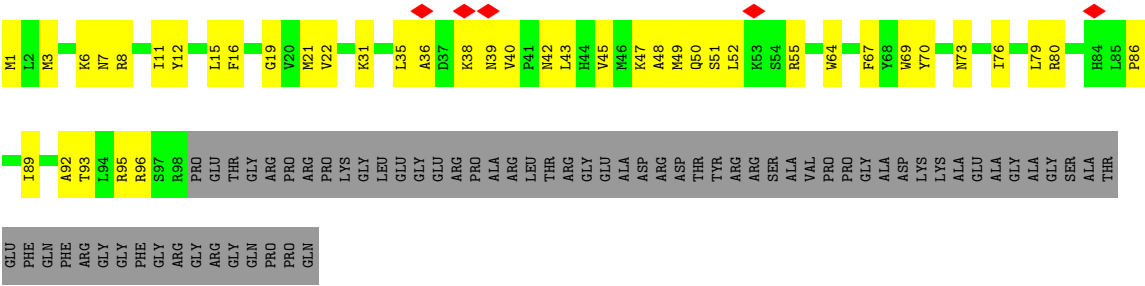


• Molecule 78: 40S ribosomal protein S8

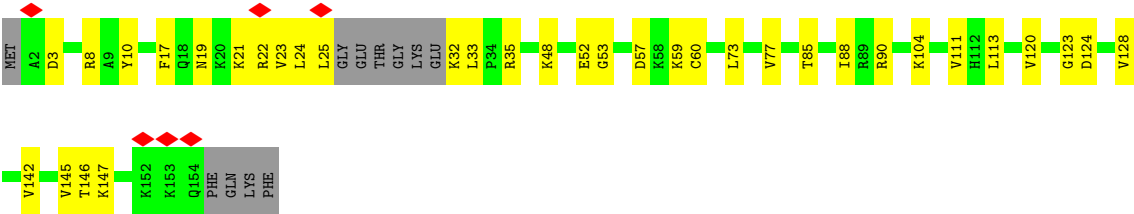


• Molecule 79: 40S ribosomal protein S10





• Molecule 80: 40S ribosomal protein S11



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	85947	Depositor
Resolution determination method	FSC 0.33 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	0.063	Depositor
Minimum map value	-0.036	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	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	L5	0.34	0/87719	0.33	0/136834
2	L7	0.35	0/2861	0.27	0/4459
3	L8	0.34	0/3701	0.29	0/5766
4	LA	0.38	0/1936	0.55	0/2596
5	LB	0.36	0/3306	0.54	0/4424
6	LC	0.38	0/2962	0.53	0/3977
7	LD	0.33	0/2428	0.50	0/3252
8	LE	0.33	0/1797	0.55	0/2408
9	LF	0.38	0/1905	0.54	0/2539
10	LG	0.32	0/1898	0.51	0/2552
11	LH	0.35	0/1537	0.54	0/2066
12	LI	0.33	0/1673	0.54	0/2233
13	LJ	0.30	0/1403	0.58	0/1874
14	LL	0.34	0/1732	0.51	0/2315
15	LM	0.34	0/1161	0.56	0/1554
16	LN	0.38	0/1746	0.57	0/2338
17	LO	0.36	0/1682	0.51	0/2250
18	LP	0.37	0/1268	0.48	0/1701
19	LQ	0.39	0/1537	0.56	0/2052
20	LR	0.35	0/1413	0.53	0/1870
21	LS	0.38	0/1493	0.52	0/2003
22	LT	0.36	0/1326	0.48	0/1770
23	LU	0.30	0/839	0.67	1/1126 (0.1%)
24	LV	0.34	0/993	0.48	0/1332
25	LW	0.34	0/541	0.46	0/720
26	LX	0.36	0/975	0.51	0/1312
27	LY	0.35	0/1132	0.48	0/1504
28	LZ	0.34	0/1130	0.54	1/1507 (0.1%)
29	La	0.37	0/1191	0.53	0/1591
30	Lb	0.29	0/889	0.54	0/1175
31	Lc	0.35	0/774	0.54	0/1038
32	Ld	0.37	0/903	0.51	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.38	0/1071	0.53	0/1429
34	Lf	0.38	0/895	0.56	0/1198
35	Lg	0.35	0/916	0.50	0/1220
36	Lh	0.32	0/1023	0.46	0/1351
37	Li	0.30	0/843	0.45	0/1115
38	Lj	0.38	0/720	0.60	0/952
39	Lk	0.30	0/575	0.54	0/761
40	Ll	0.35	0/454	0.50	0/599
41	Lm	0.32	0/435	0.50	0/575
42	Ln	0.33	0/231	0.50	0/294
43	Lo	0.35	0/818	0.50	0/1079
44	Lp	0.34	0/718	0.44	0/953
45	Lr	0.37	0/1017	0.51	0/1364
46	S2	0.26	0/41217	0.31	0/64218
47	S	0.15	0/322	0.42	0/423
48	E	0.13	0/1907	0.28	0/2969
49	SA	0.29	0/1769	0.59	2/2403 (0.1%)
50	SB	0.29	0/1765	0.53	0/2362
51	SN	0.29	0/1232	0.45	0/1656
52	SO	0.31	0/1015	0.53	0/1361
53	SP	0.24	0/1003	0.57	0/1342
54	SQ	0.22	0/1123	0.57	0/1501
55	SR	0.24	0/1074	0.59	0/1441
56	SS	0.23	0/1216	0.52	0/1628
57	ST	0.20	0/1119	0.47	0/1499
58	SU	0.23	0/827	0.59	0/1110
59	SV	0.28	0/643	0.58	0/860
60	SW	0.32	0/1051	0.50	0/1406
61	SX	0.32	0/1116	0.58	0/1490
62	SY	0.27	0/1083	0.58	0/1438
63	SZ	0.20	0/482	0.51	0/644
64	Sa	0.32	0/836	0.59	0/1121
65	Sb	0.30	0/665	0.60	0/891
66	Sc	0.24	0/508	0.62	0/680
67	Sd	0.22	0/446	0.47	0/591
68	Se	0.23	0/465	0.59	0/612
69	Sg	0.22	0/2493	0.57	2/3394 (0.1%)
70	CB	0.21	0/6022	0.51	0/8133
71	SG	0.23	0/1946	0.49	0/2590
72	SJ	0.28	0/1550	0.51	1/2069 (0.0%)
73	SC	0.31	0/1737	0.59	2/2347 (0.1%)
74	SF	0.23	0/1458	0.54	0/1958
75	SH	0.28	0/1519	0.61	0/2033

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SD	0.22	0/1793	0.52	1/2414 (0.0%)
77	SE	0.27	0/2118	0.54	0/2849
78	SI	0.29	0/1715	0.53	0/2287
79	SK	0.24	0/851	0.56	0/1147
80	SL	0.30	0/1225	0.48	0/1638
All	All	0.32	0/234878	0.41	10/344749 (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
4	LA	0	1
34	Lf	0	1
36	Lh	0	1
59	SV	0	2
All	All	0	5

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
23	LU	18	VAL	N-CA-C	-8.01	104.78	111.91
76	SD	165	ASN	N-CA-C	-6.80	106.17	114.75
69	Sg	124	SER	CA-C-N	5.75	129.80	120.60
69	Sg	124	SER	C-N-CA	5.75	129.80	120.60
49	SA	73	ASP	N-CA-C	-5.59	107.71	114.75

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	13	GLY	Peptide
34	Lf	106	TYR	Peptide
36	Lh	86	LYS	Peptide
59	SV	78	ILE	Peptide
59	SV	79	VAL	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	L5	78419	0	39630	1092	0
2	L7	2561	0	1295	18	0
3	L8	3314	0	1683	43	0
4	LA	1898	0	1993	47	0
5	LB	3238	0	3376	73	0
6	LC	2908	0	3082	57	0
7	LD	2382	0	2410	50	0
8	LE	1764	0	1919	52	0
9	LF	1870	0	1996	38	0
10	LG	1867	0	2013	44	0
11	LH	1518	0	1601	44	0
12	LI	1634	0	1671	39	0
13	LJ	1381	0	1402	52	0
14	LL	1701	0	1818	46	0
15	LM	1138	0	1204	25	0
16	LN	1701	0	1749	50	0
17	LO	1650	0	1794	32	0
18	LP	1242	0	1269	19	0
19	LQ	1513	0	1628	24	0
20	LR	1397	0	1537	28	0
21	LS	1453	0	1490	40	0
22	LT	1298	0	1366	31	0
23	LU	825	0	850	36	0
24	LV	979	0	1039	5	0
25	LW	528	0	541	8	0
26	LX	958	0	1027	26	0
27	LY	1115	0	1205	23	0
28	LZ	1107	0	1182	28	0
29	La	1162	0	1213	24	0
30	Lb	876	0	948	24	0
31	Lc	764	0	804	25	0
32	Ld	888	0	930	14	0
33	Le	1053	0	1147	19	0
34	Lf	876	0	912	15	0
35	Lg	906	0	999	13	0
36	Lh	1015	0	1148	18	0
37	Li	832	0	917	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	Lj	705	0	736	12	0
39	Lk	569	0	637	17	0
40	Ll	444	0	483	15	0
41	Lm	429	0	465	11	0
42	Ln	230	0	276	5	0
43	Lo	805	0	869	21	0
44	Lp	708	0	756	15	0
45	Lr	1002	0	1068	26	0
46	S2	36875	0	18593	719	0
47	S	318	0	289	15	0
48	E	1708	0	865	49	0
49	SA	1733	0	1739	76	0
50	SB	1738	0	1809	62	0
51	SN	1208	0	1294	32	0
52	SO	1002	0	1023	38	0
53	SP	985	0	1031	56	0
54	SQ	1107	0	1175	48	0
55	SR	1060	0	1112	46	0
56	SS	1198	0	1261	74	0
57	ST	1101	0	1135	46	0
58	SU	817	0	882	41	0
59	SV	636	0	637	23	0
60	SW	1034	0	1080	32	0
61	SX	1098	0	1167	25	0
62	SY	1065	0	1142	53	0
63	SZ	480	0	528	21	0
64	Sa	821	0	870	22	0
65	Sb	651	0	672	26	0
66	Sc	506	0	536	35	0
67	Sd	436	0	433	15	0
68	Se	459	0	503	8	0
69	Sg	2436	0	2393	124	0
70	CB	5904	0	5943	226	0
71	SG	1923	0	2089	84	0
72	SJ	1525	0	1640	52	0
73	SC	1700	0	1784	55	0
74	SF	1438	0	1484	74	0
75	SH	1497	0	1590	68	0
76	SD	1765	0	1865	59	0
77	SE	2076	0	2177	72	0
78	SI	1686	0	1772	57	0
79	SK	827	0	854	44	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
80	SL	1205	0	1284	29	0
81	L5	211	0	0	0	0
81	L7	3	0	0	0	0
81	L8	5	0	0	0	0
81	LA	1	0	0	0	0
81	LI	1	0	0	0	0
81	LP	1	0	0	0	0
81	LV	1	0	0	0	0
81	La	1	0	0	0	0
81	Le	1	0	0	0	0
81	Lg	1	0	0	0	0
81	S2	29	0	0	0	0
82	Lg	1	0	0	0	0
82	Lj	1	0	0	0	0
82	Lm	1	0	0	0	0
82	Lo	1	0	0	0	0
82	Lp	1	0	0	0	0
82	Sa	1	0	0	0	0
82	Sd	1	0	0	0	0
All	All	218903	0	162729	4277	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 11.

The worst 5 of 4277 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)
1:L5:1762:C:N4	1:L5:1770:A:C2	2.08	1.21
46:S2:886:A:N6	46:S2:901:G:C4	2.09	1.19
1:L5:1443:A:N6	1:L5:2104:G:H21	1.39	1.19
1:L5:1176:C:N4	1:L5:1184:A:H61	1.41	1.17
1:L5:1176:C:H42	1:L5:1184:A:N6	1.41	1.17

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	
4	LA	246/257 (96%)	225 (92%)	21 (8%)	0	100	100
5	LB	400/403 (99%)	373 (93%)	27 (7%)	0	100	100
6	LC	363/427 (85%)	330 (91%)	33 (9%)	0	100	100
7	LD	291/297 (98%)	269 (92%)	22 (8%)	0	100	100
8	LE	211/288 (73%)	193 (92%)	18 (8%)	0	100	100
9	LF	223/248 (90%)	213 (96%)	10 (4%)	0	100	100
10	LG	227/266 (85%)	214 (94%)	13 (6%)	0	100	100
11	LH	188/192 (98%)	169 (90%)	19 (10%)	0	100	100
12	LI	198/214 (92%)	184 (93%)	14 (7%)	0	100	100
13	LJ	168/178 (94%)	153 (91%)	15 (9%)	0	100	100
14	LL	208/211 (99%)	191 (92%)	17 (8%)	0	100	100
15	LM	137/215 (64%)	125 (91%)	12 (9%)	0	100	100
16	LN	201/204 (98%)	185 (92%)	15 (8%)	1 (0%)	24	55
17	LO	199/203 (98%)	191 (96%)	8 (4%)	0	100	100
18	LP	151/184 (82%)	142 (94%)	9 (6%)	0	100	100
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	166/196 (85%)	158 (95%)	8 (5%)	0	100	100
21	LS	173/176 (98%)	158 (91%)	15 (9%)	0	100	100
22	LT	157/160 (98%)	150 (96%)	7 (4%)	0	100	100
23	LU	99/128 (77%)	81 (82%)	17 (17%)	1 (1%)	12	40
24	LV	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
25	LW	61/157 (39%)	57 (93%)	4 (7%)	0	100	100
26	LX	115/156 (74%)	112 (97%)	3 (3%)	0	100	100
27	LY	132/145 (91%)	121 (92%)	11 (8%)	0	100	100
28	LZ	133/136 (98%)	122 (92%)	11 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
30	Lb	105/159 (66%)	98 (93%)	7 (7%)	0	100	100
31	Lc	96/115 (84%)	88 (92%)	8 (8%)	0	100	100
32	Ld	105/125 (84%)	98 (93%)	7 (7%)	0	100	100
33	Le	126/135 (93%)	116 (92%)	10 (8%)	0	100	100
34	Lf	107/110 (97%)	97 (91%)	9 (8%)	1 (1%)	14	43
35	Lg	112/117 (96%)	108 (96%)	4 (4%)	0	100	100
36	Lh	120/123 (98%)	116 (97%)	4 (3%)	0	100	100
37	Li	100/105 (95%)	95 (95%)	5 (5%)	0	100	100
38	Lj	84/97 (87%)	78 (93%)	6 (7%)	0	100	100
39	Lk	67/70 (96%)	63 (94%)	4 (6%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	50/128 (39%)	50 (100%)	0	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	96/106 (91%)	93 (97%)	3 (3%)	0	100	100
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
47	S	36/402 (9%)	35 (97%)	1 (3%)	0	100	100
49	SA	215/295 (73%)	191 (89%)	24 (11%)	0	100	100
50	SB	212/264 (80%)	200 (94%)	12 (6%)	0	100	100
51	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
52	SO	132/151 (87%)	120 (91%)	12 (9%)	0	100	100
53	SP	119/145 (82%)	105 (88%)	14 (12%)	0	100	100
54	SQ	136/146 (93%)	125 (92%)	11 (8%)	0	100	100
55	SR	127/135 (94%)	115 (91%)	12 (9%)	0	100	100
56	SS	143/152 (94%)	129 (90%)	14 (10%)	0	100	100
57	ST	139/145 (96%)	124 (89%)	14 (10%)	1 (1%)	18	49
58	SU	101/119 (85%)	92 (91%)	9 (9%)	0	100	100
59	SV	81/83 (98%)	71 (88%)	9 (11%)	1 (1%)	10	37
60	SW	127/130 (98%)	123 (97%)	4 (3%)	0	100	100
61	SX	139/143 (97%)	123 (88%)	14 (10%)	2 (1%)	9	33

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
62	SY	129/133 (97%)	117 (91%)	12 (9%)	0	100	100
63	SZ	56/125 (45%)	50 (89%)	6 (11%)	0	100	100
64	Sa	100/115 (87%)	87 (87%)	13 (13%)	0	100	100
65	Sb	81/84 (96%)	70 (86%)	11 (14%)	0	100	100
66	Sc	62/69 (90%)	48 (77%)	14 (23%)	0	100	100
67	Sd	50/56 (89%)	46 (92%)	4 (8%)	0	100	100
68	Se	56/59 (95%)	49 (88%)	7 (12%)	0	100	100
69	Sg	311/317 (98%)	270 (87%)	41 (13%)	0	100	100
70	CB	747/858 (87%)	693 (93%)	52 (7%)	2 (0%)	36	65
71	SG	235/249 (94%)	221 (94%)	14 (6%)	0	100	100
72	SJ	183/194 (94%)	168 (92%)	15 (8%)	0	100	100
73	SC	217/293 (74%)	203 (94%)	14 (6%)	0	100	100
74	SF	177/204 (87%)	161 (91%)	16 (9%)	0	100	100
75	SH	182/194 (94%)	151 (83%)	31 (17%)	0	100	100
76	SD	225/243 (93%)	199 (88%)	26 (12%)	0	100	100
77	SE	260/263 (99%)	244 (94%)	16 (6%)	0	100	100
78	SI	204/208 (98%)	195 (96%)	9 (4%)	0	100	100
79	SK	96/165 (58%)	79 (82%)	17 (18%)	0	100	100
80	SL	143/158 (90%)	133 (93%)	10 (7%)	0	100	100
All	All	11725/13660 (86%)	10797 (92%)	919 (8%)	9 (0%)	49	75

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
23	LU	55	ASN
61	SX	87	ASN
59	SV	79	VAL
70	CB	326	GLU

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	
4	LA	190/199 (96%)	190 (100%)	0	100	100
5	LB	348/349 (100%)	348 (100%)	0	100	100
6	LC	304/348 (87%)	304 (100%)	0	100	100
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	194/252 (77%)	194 (100%)	0	100	100
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	199/223 (89%)	199 (100%)	0	100	100
11	LH	169/171 (99%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	172 (100%)	0	100	100
13	LJ	145/149 (97%)	145 (100%)	0	100	100
14	LL	176/177 (99%)	176 (100%)	0	100	100
15	LM	118/161 (73%)	118 (100%)	0	100	100
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	173 (100%)	0	100	100
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	164 (100%)	0	100	100
20	LR	148/175 (85%)	148 (100%)	0	100	100
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	90 (99%)	1 (1%)	65	76
24	LV	101/107 (94%)	101 (100%)	0	100	100
25	LW	55/126 (44%)	55 (100%)	0	100	100
26	LX	105/133 (79%)	105 (100%)	0	100	100
27	LY	124/135 (92%)	124 (100%)	0	100	100
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	120 (100%)	0	100	100
30	Lb	88/126 (70%)	88 (100%)	0	100	100
31	Lc	83/97 (86%)	83 (100%)	0	100	100
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	114 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Lf	88/89 (99%)	88 (100%)	0	100	100
35	Lg	98/100 (98%)	98 (100%)	0	100	100
36	Lh	109/110 (99%)	109 (100%)	0	100	100
37	Li	86/89 (97%)	86 (100%)	0	100	100
38	Lj	73/80 (91%)	73 (100%)	0	100	100
39	Lk	64/65 (98%)	64 (100%)	0	100	100
40	Ll	47/48 (98%)	47 (100%)	0	100	100
41	Lm	48/116 (41%)	48 (100%)	0	100	100
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	87/94 (93%)	87 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	109 (100%)	0	100	100
47	S	33/322 (10%)	33 (100%)	0	100	100
49	SA	183/243 (75%)	183 (100%)	0	100	100
50	SB	195/231 (84%)	195 (100%)	0	100	100
51	SN	130/131 (99%)	130 (100%)	0	100	100
52	SO	104/119 (87%)	104 (100%)	0	100	100
53	SP	107/130 (82%)	107 (100%)	0	100	100
54	SQ	115/121 (95%)	115 (100%)	0	100	100
55	SR	119/122 (98%)	119 (100%)	0	100	100
56	SS	126/132 (96%)	126 (100%)	0	100	100
57	ST	112/115 (97%)	112 (100%)	0	100	100
58	SU	94/107 (88%)	94 (100%)	0	100	100
59	SV	67/67 (100%)	67 (100%)	0	100	100
60	SW	112/113 (99%)	112 (100%)	0	100	100
61	SX	113/115 (98%)	113 (100%)	0	100	100
62	SY	113/115 (98%)	113 (100%)	0	100	100
63	SZ	53/103 (52%)	53 (100%)	0	100	100
64	Sa	89/98 (91%)	89 (100%)	0	100	100
65	Sb	75/76 (99%)	75 (100%)	0	100	100
66	Sc	57/62 (92%)	57 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
67	Sd	46/49 (94%)	46 (100%)	0	100	100
68	Se	47/48 (98%)	47 (100%)	0	100	100
69	Sg	272/275 (99%)	272 (100%)	0	100	100
70	CB	642/730 (88%)	642 (100%)	0	100	100
71	SG	207/218 (95%)	207 (100%)	0	100	100
72	SJ	161/168 (96%)	161 (100%)	0	100	100
73	SC	185/225 (82%)	185 (100%)	0	100	100
74	SF	154/170 (91%)	154 (100%)	0	100	100
75	SH	166/174 (95%)	166 (100%)	0	100	100
76	SD	190/202 (94%)	190 (100%)	0	100	100
77	SE	224/225 (100%)	224 (100%)	0	100	100
78	SI	178/180 (99%)	178 (100%)	0	100	100
79	SK	89/136 (65%)	89 (100%)	0	100	100
80	SL	133/142 (94%)	133 (100%)	0	100	100
All	All	10233/11605 (88%)	10232 (100%)	1 (0%)	100	100

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
23	LU	17	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 104 such sidechains are listed below:

Mol	Chain	Res	Type
55	SR	83	ASN
68	Se	15	GLN
77	SE	201	HIS
55	SR	118	GLN
60	SW	120	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3644/5070 (71%)	814 (22%)	20 (0%)
2	L7	119/121 (98%)	11 (9%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	L8	155/157 (98%)	30 (19%)	0
46	S2	1713/1869 (91%)	408 (23%)	8 (0%)
48	E	78/85 (91%)	26 (33%)	1 (1%)
All	All	5709/7302 (78%)	1289 (22%)	29 (0%)

5 of 1289 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	25	A
1	L5	26	C
1	L5	39	A
1	L5	42	A

5 of 29 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	2786	C
46	S2	1551	U
1	L5	4699	U
46	S2	563	G
1	L5	3673	C

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 262 ligands modelled in this entry, 262 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

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

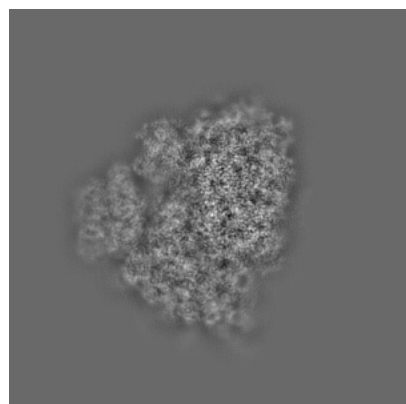
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-37992. These allow visual inspection of the internal detail of the map and identification of artifacts.

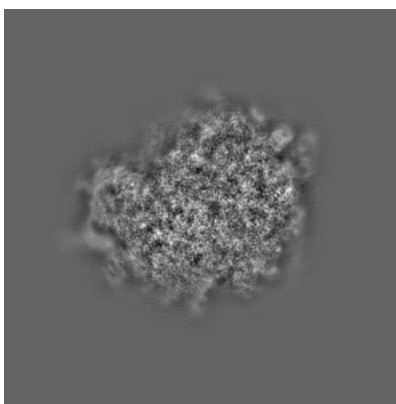
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

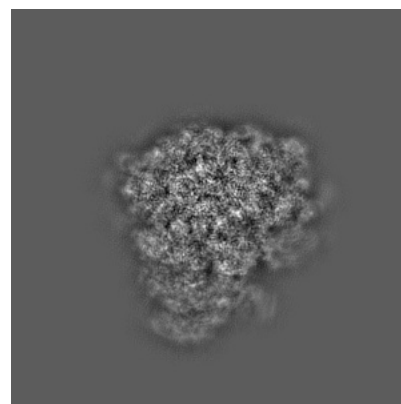
6.1.1 Primary map



X

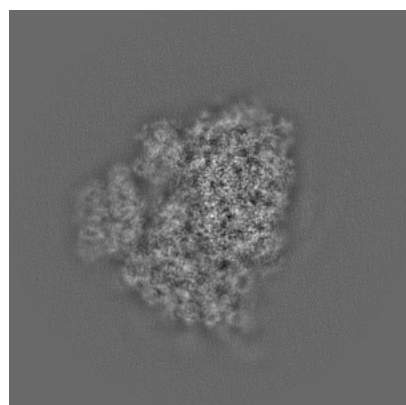


Y

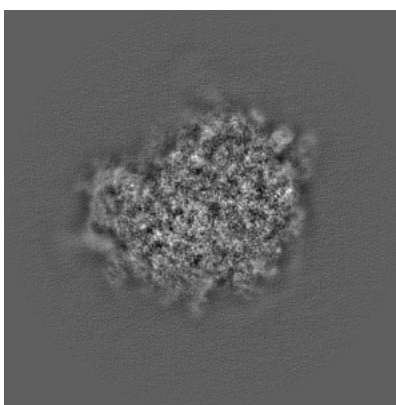


Z

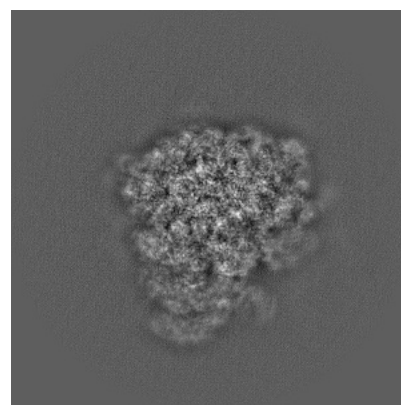
6.1.2 Raw map



X



Y

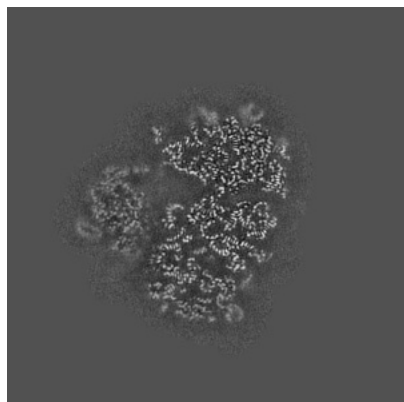


Z

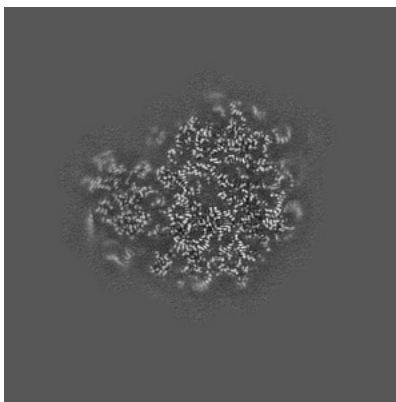
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

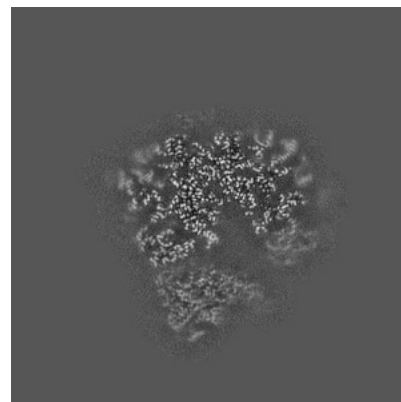
6.2.1 Primary map



X Index: 224

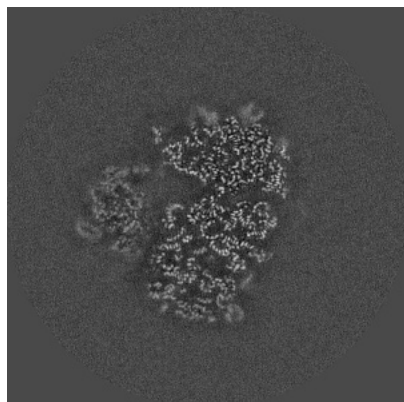


Y Index: 224

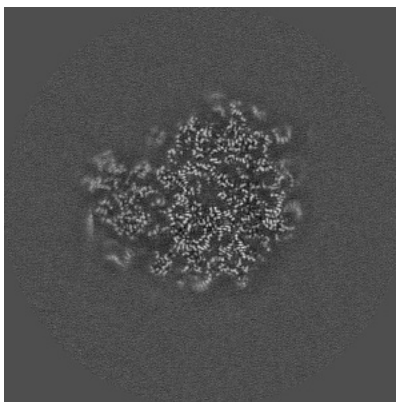


Z Index: 224

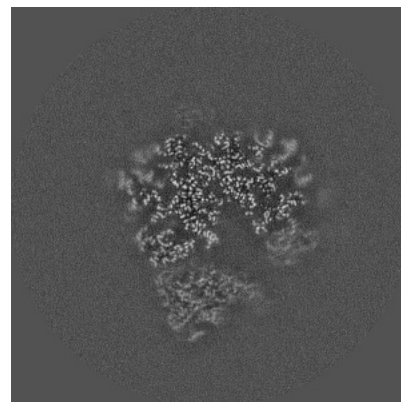
6.2.2 Raw map



X Index: 224



Y Index: 224

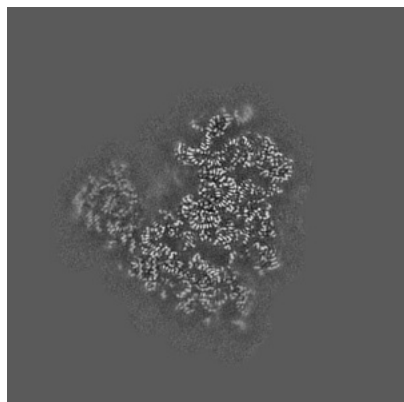


Z Index: 224

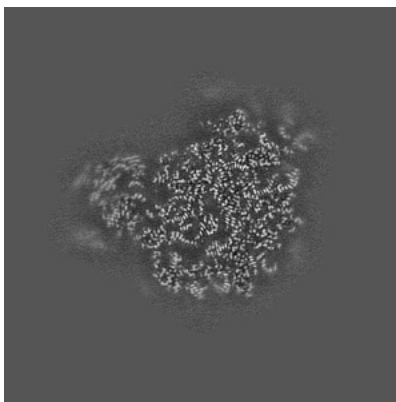
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

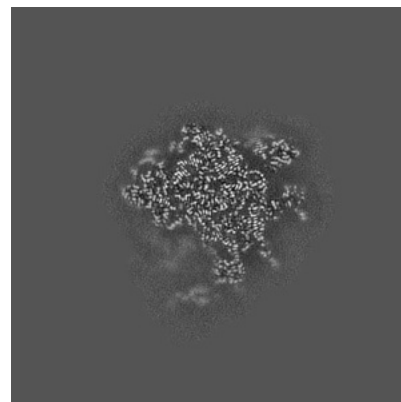
6.3.1 Primary map



X Index: 207

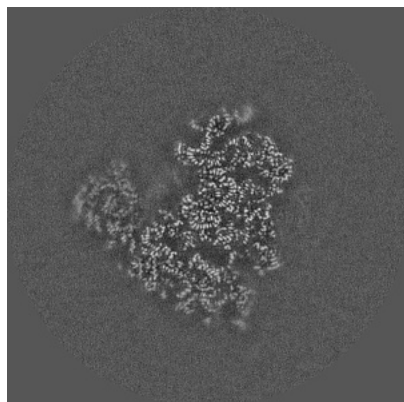


Y Index: 243

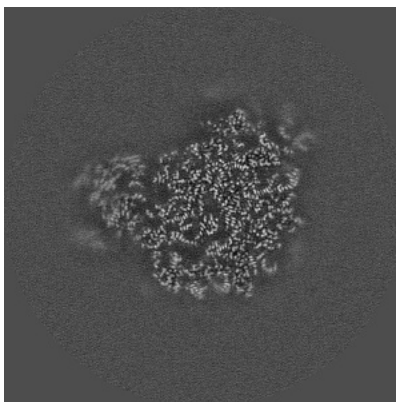


Z Index: 271

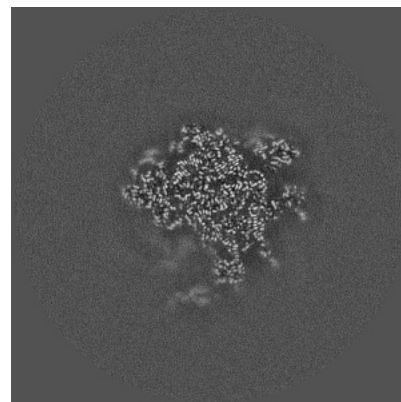
6.3.2 Raw map



X Index: 207



Y Index: 243

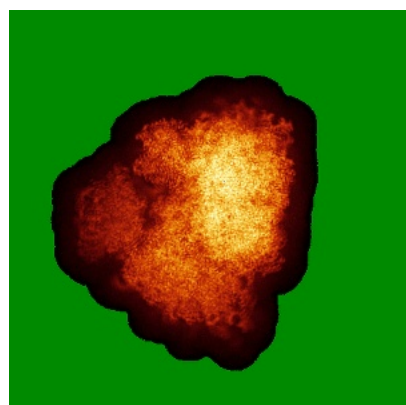


Z Index: 271

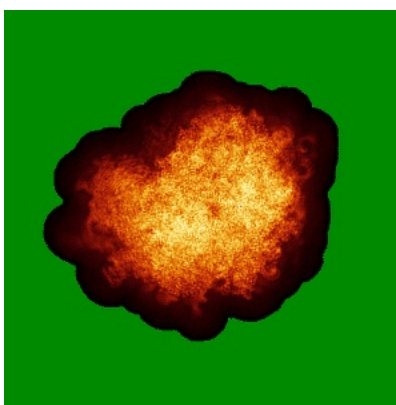
The images above show the largest variance slices of the map in three orthogonal directions.

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

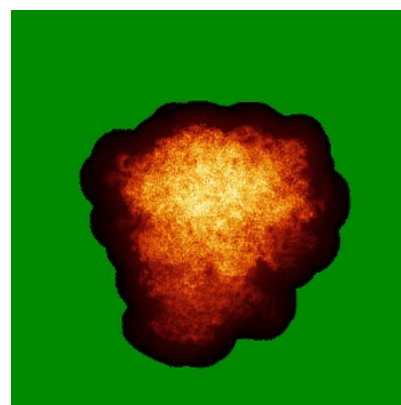
6.4.1 Primary map



X

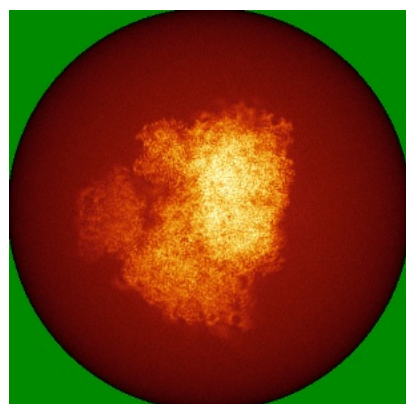


Y

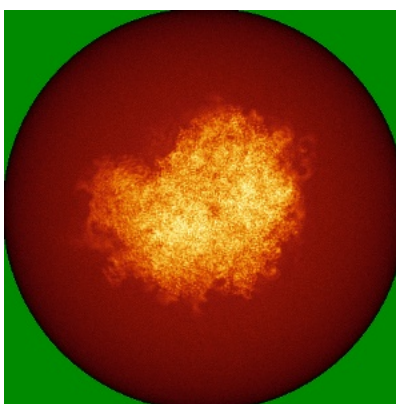


Z

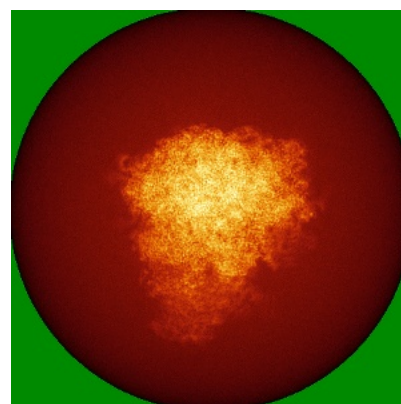
6.4.2 Raw map



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](#)

This section was not generated.

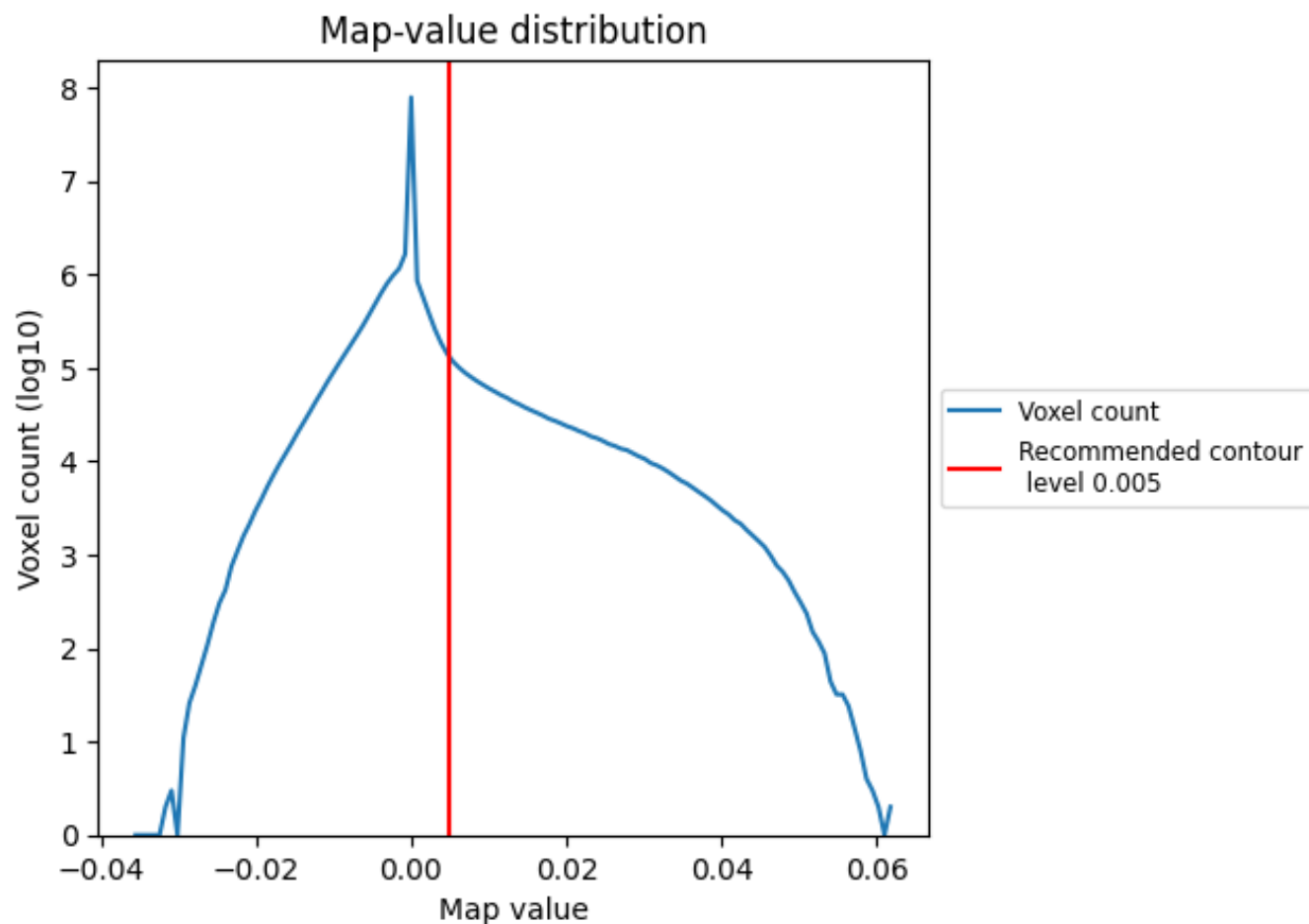
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

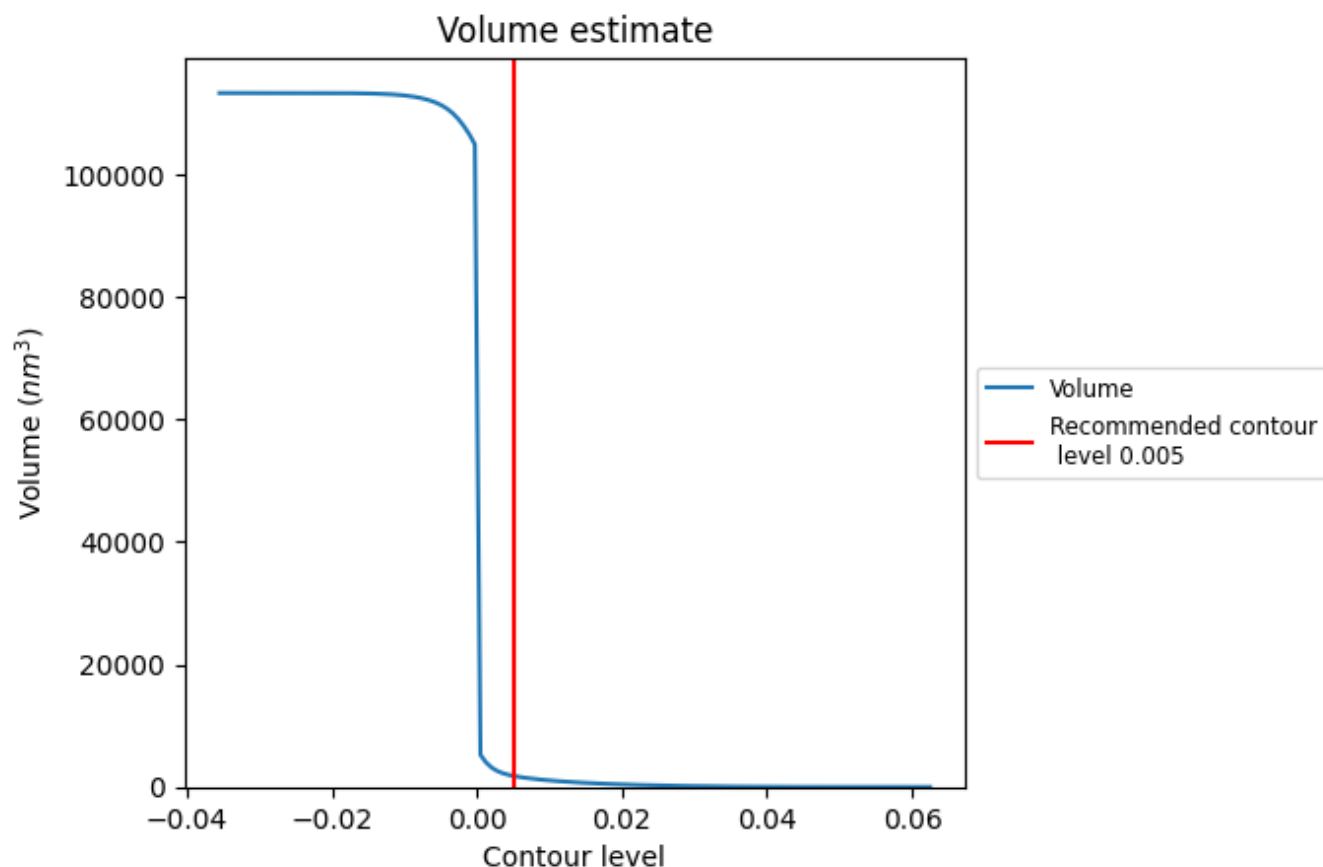
This section contains the results of statistical analysis of the map.

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.

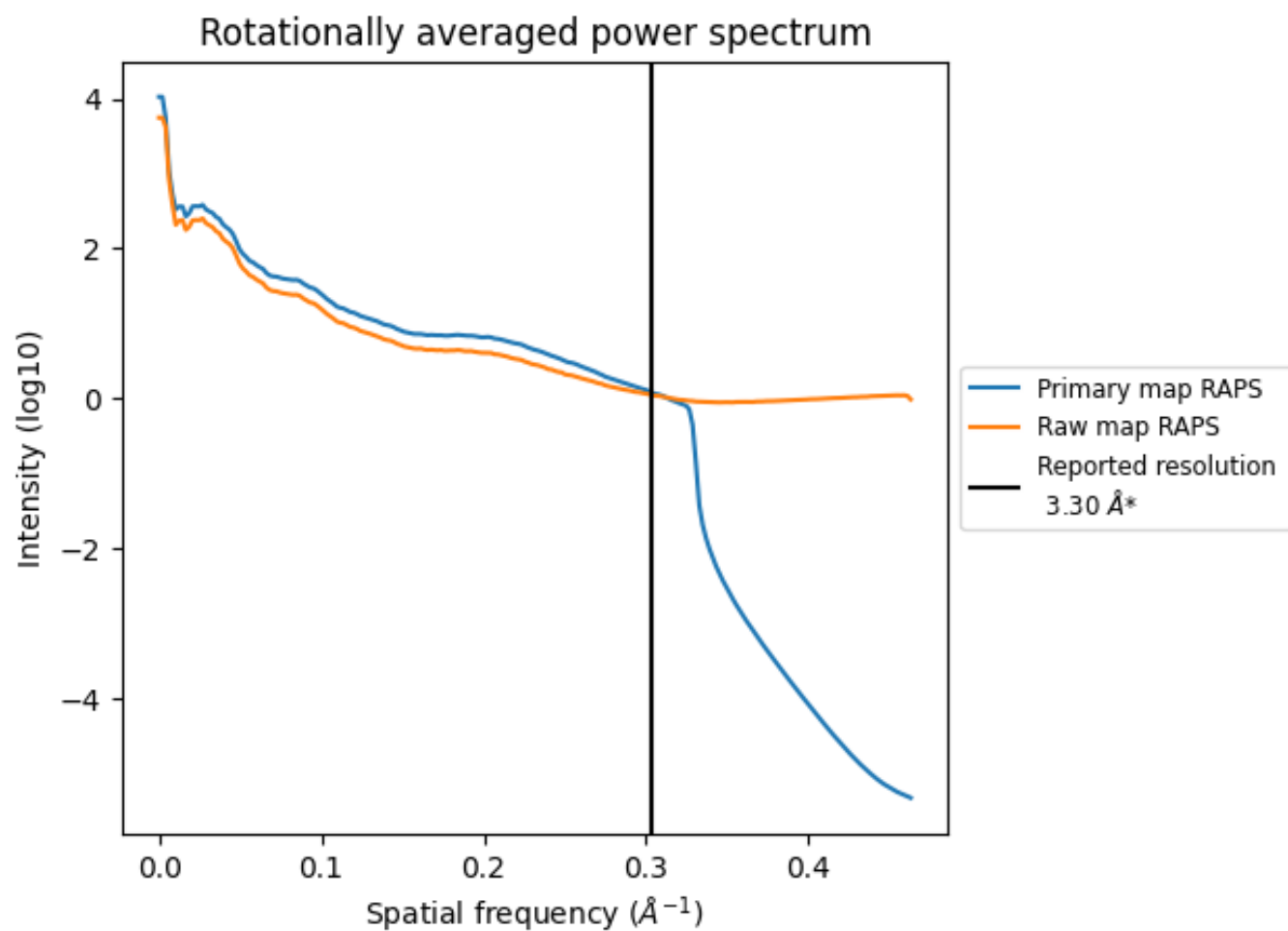
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1813 nm³; this corresponds to an approximate mass of 1637 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 ⓘ

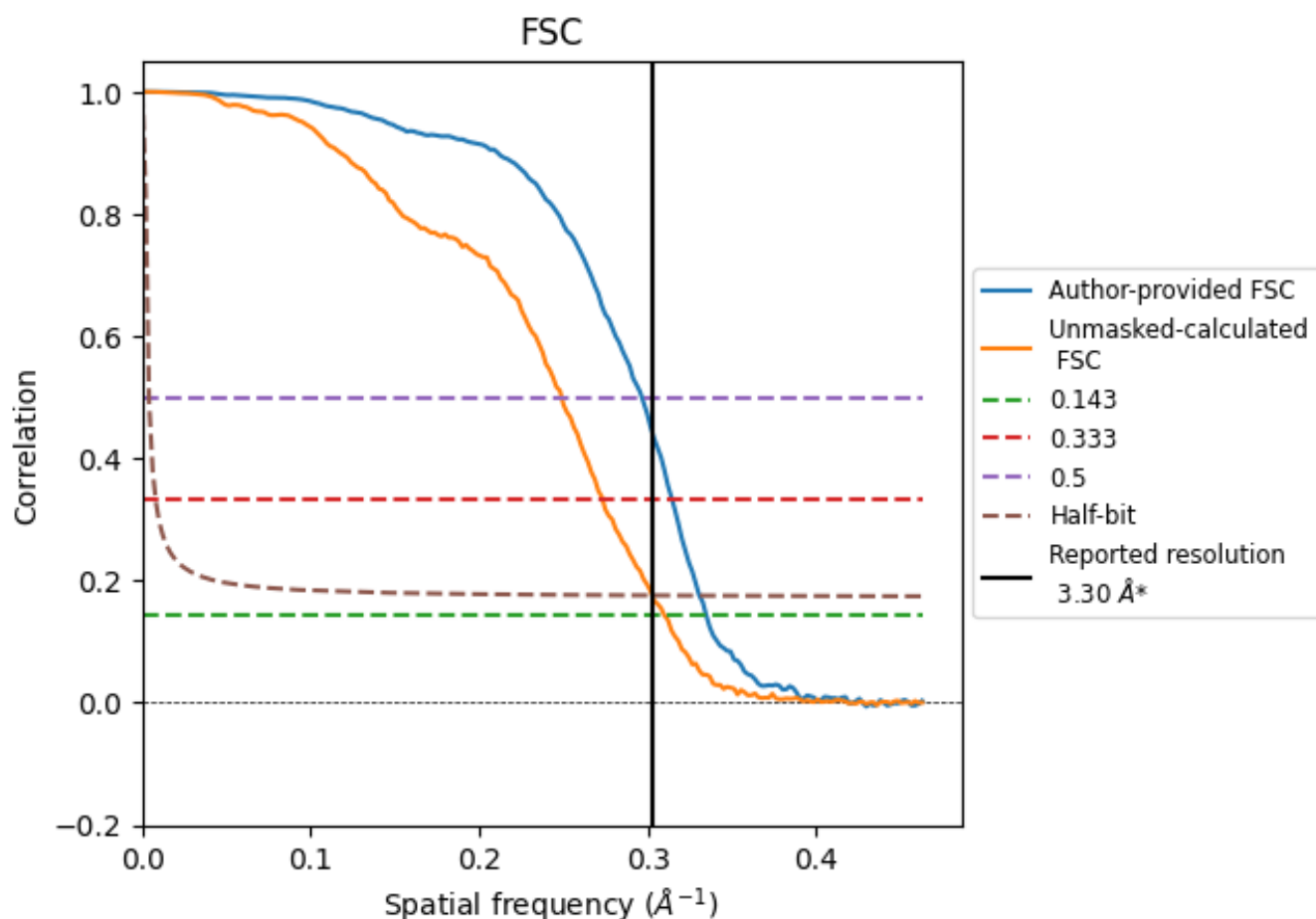


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

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 $0.303 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

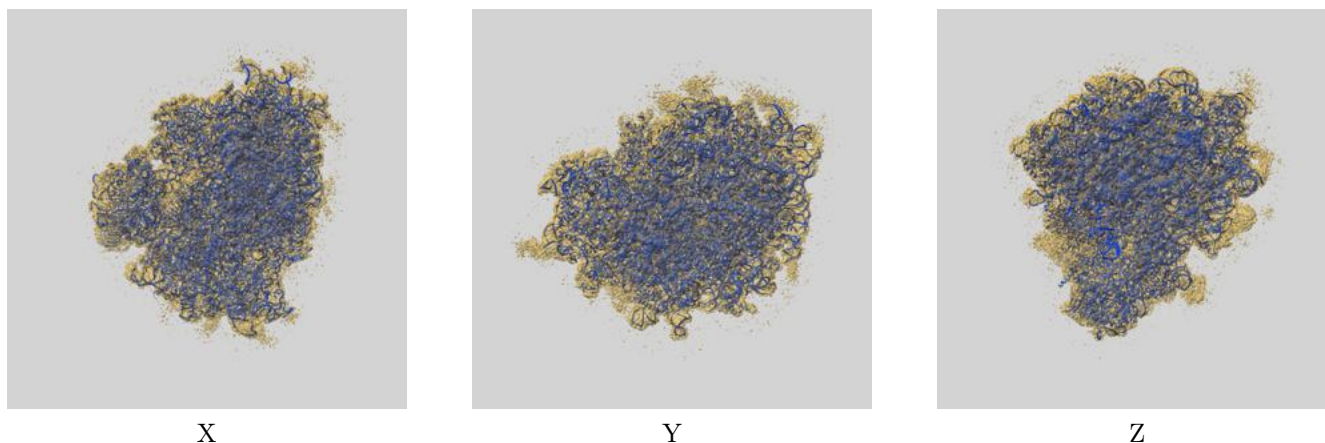
Resolution estimate (Å)	Estimation criterion (FSC cut-off)			
	0.143	0.5	Half-bit	0.333
Reported by author	-	-	-	3.30
Author-provided FSC curve	2.99	3.37	3.02	3.18
Unmasked-calculated*	3.23	4.02	3.30	3.66

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.33 CUT-OFF 3.66 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

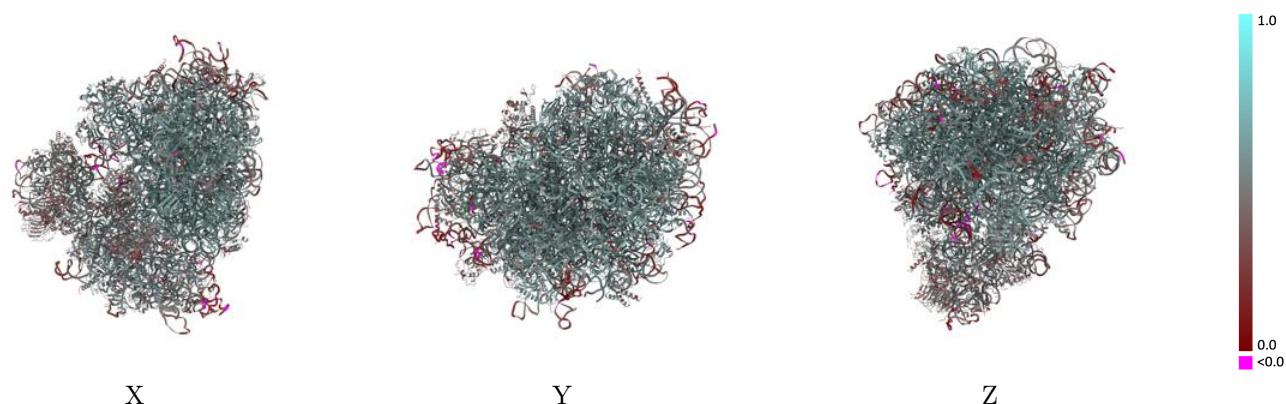
This section contains information regarding the fit between EMDB map EMD-37992 and PDB model 8Y0X. Per-residue inclusion information can be found in [section 3](#) on [page 20](#).

9.1 Map-model overlay [i](#)



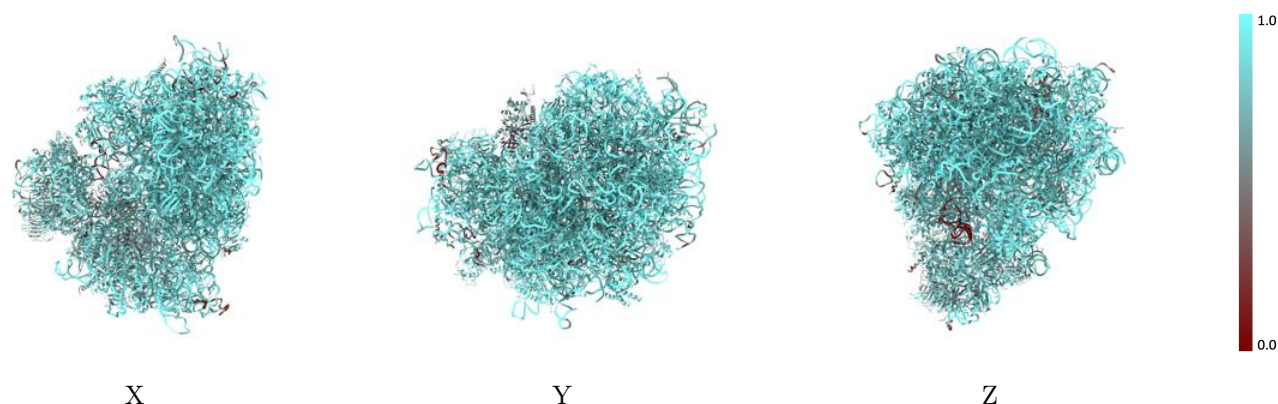
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



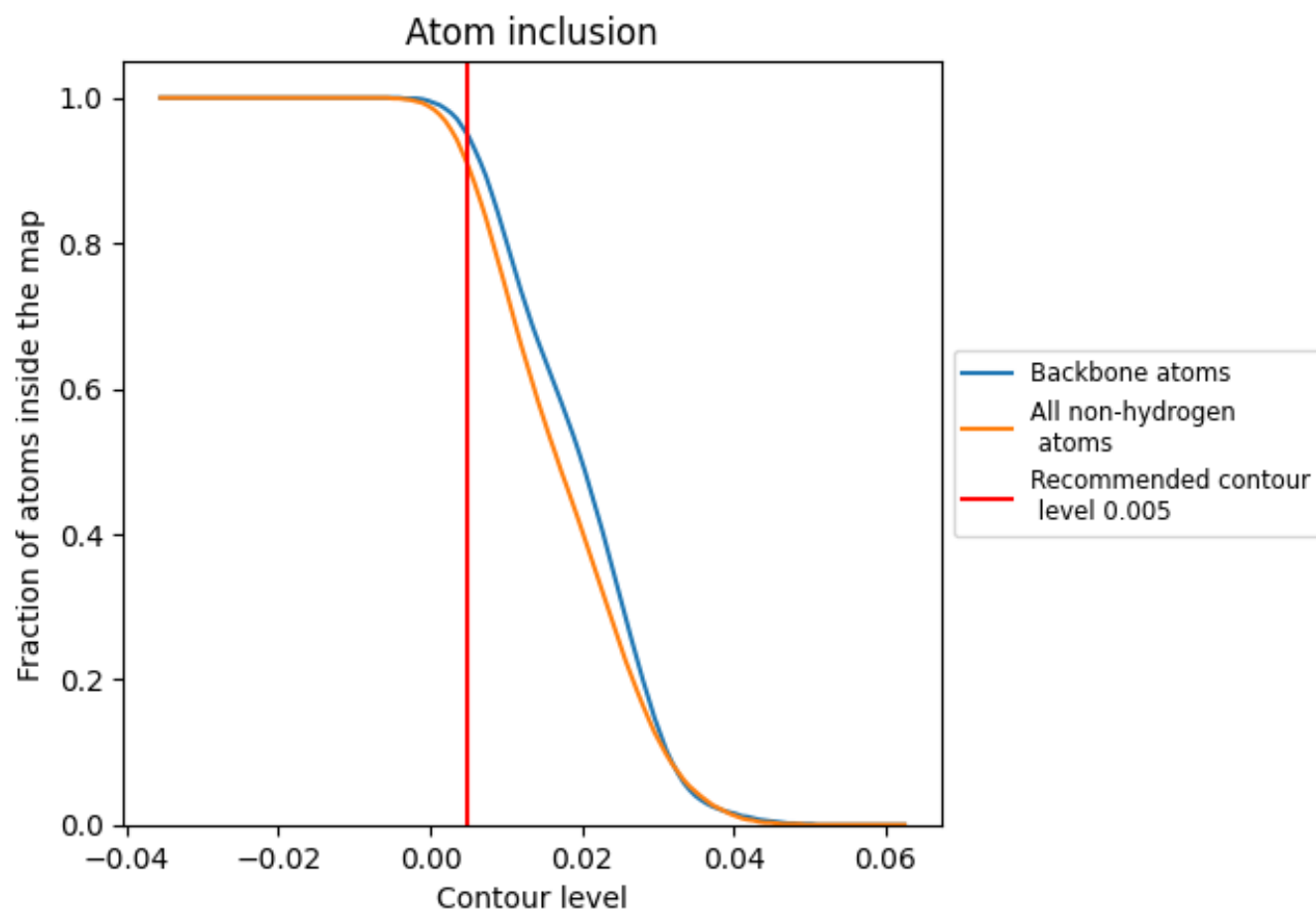
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 95% of all backbone atoms, 91% 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	 0.9070	 0.5210
CB	 0.5820	 0.3940
E	 0.3000	 0.1720
L5	 0.9570	 0.5340
L7	 0.9980	 0.5880
L8	 0.9760	 0.5580
LA	 0.9410	 0.5980
LB	 0.9390	 0.5780
LC	 0.9390	 0.5720
LD	 0.9420	 0.5540
LE	 0.9090	 0.5420
LF	 0.9190	 0.5770
LG	 0.9070	 0.5290
LH	 0.9380	 0.5700
LI	 0.9420	 0.5800
LJ	 0.8850	 0.5010
LL	 0.9190	 0.5530
LM	 0.9360	 0.5620
LN	 0.9280	 0.5980
LO	 0.9360	 0.5820
LP	 0.9450	 0.5850
LQ	 0.9430	 0.5990
LR	 0.9180	 0.5540
LS	 0.9520	 0.5890
LT	 0.9260	 0.5690
LU	 0.9220	 0.5000
LV	 0.9430	 0.5930
LW	 0.9210	 0.5850
LX	 0.9170	 0.5710
LY	 0.9220	 0.5710
LZ	 0.9360	 0.5680
La	 0.9470	 0.5950
Lb	 0.8040	 0.5000
Lc	 0.9260	 0.5480
Ld	 0.9330	 0.5640



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Chain	Atom inclusion	Q-score
Le	 0.9340	 0.5910
Lf	 0.9500	 0.5990
Lg	 0.9040	 0.5680
Lh	 0.9130	 0.5600
Li	 0.9340	 0.5550
Lj	 0.9290	 0.5910
Lk	 0.8920	 0.5210
Ll	 0.8890	 0.5680
Lm	 0.8990	 0.5760
Ln	 0.8900	 0.5740
Lo	 0.9530	 0.5840
Lp	 0.9200	 0.5750
Lr	 0.9490	 0.5790
S	 0.2080	 0.3590
S2	 0.9390	 0.5010
SA	 0.8760	 0.5080
SB	 0.8900	 0.5210
SC	 0.9030	 0.5390
SD	 0.7300	 0.4300
SE	 0.8590	 0.5230
SF	 0.7300	 0.4440
SG	 0.8150	 0.4380
SH	 0.8280	 0.4480
SI	 0.8750	 0.5160
SJ	 0.8590	 0.5080
SK	 0.6980	 0.3910
SL	 0.8740	 0.5540
SN	 0.8870	 0.5500
SO	 0.8890	 0.5340
SP	 0.7830	 0.4370
SQ	 0.7190	 0.4540
SR	 0.7690	 0.4440
SS	 0.7440	 0.4230
ST	 0.7300	 0.4460
SU	 0.7340	 0.4080
SV	 0.9050	 0.5300
SW	 0.8980	 0.5610
SX	 0.8900	 0.5470
SY	 0.8280	 0.4650
SZ	 0.6900	 0.3610
Sa	 0.8800	 0.5390
Sb	 0.8550	 0.4670

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Chain	Atom inclusion	Q-score
Sc	 0.6810	 0.4260
Sd	 0.7520	 0.4980
Se	 0.7120	 0.4450
Sg	 0.7010	 0.3820