



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 01:46 PM UTC

PDB ID : 6Z6N / pdb_00006z6n
EMDB ID : EMD-11100
Title : Cryo-EM structure of human EBP1-80S ribosomes (focus on EBP1)
Authors : Wells, J.N.; Buschauer, R.; Mackens-Kiani, T.; Best, K.; Kratzat, H.; Berninghausen, O.; Becker, T.; Cheng, J.; Beckmann, R.
Deposited on : 2020-05-28
Resolution : 2.90 Å(reported)
Based on initial model : 6EK0

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

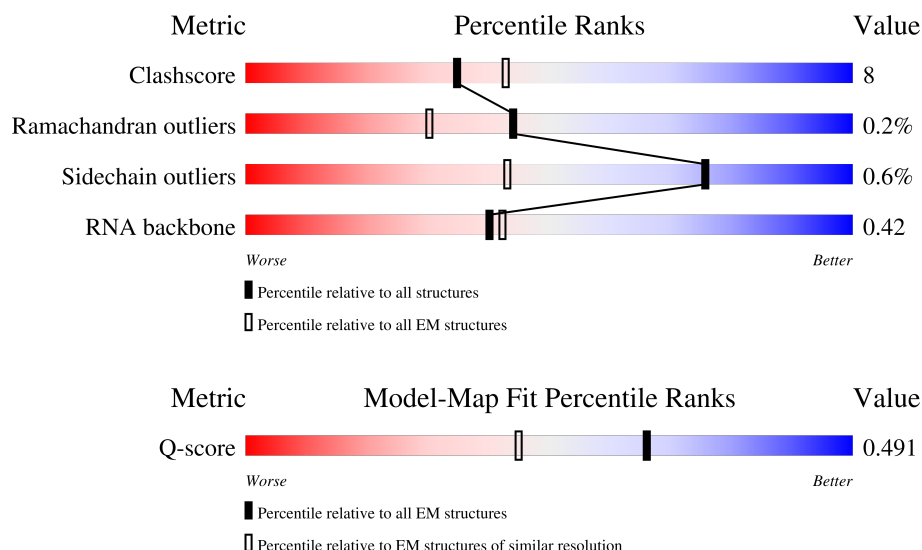
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 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.



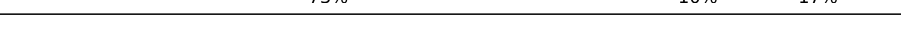
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13054 (2.40 - 3.40)

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	

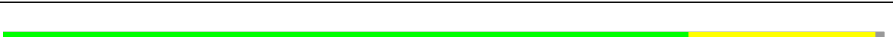
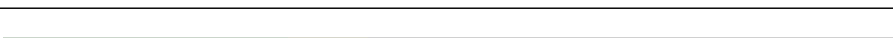
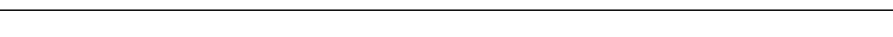
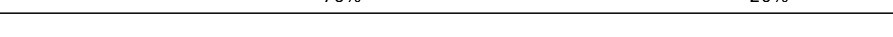
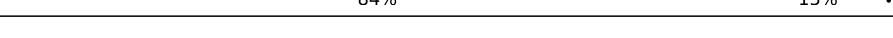
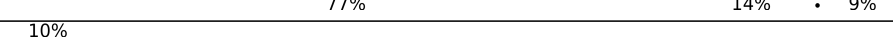
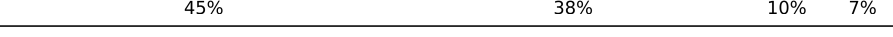
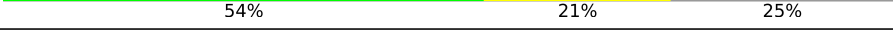
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

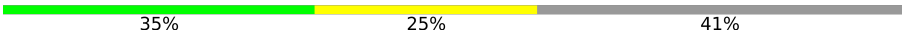
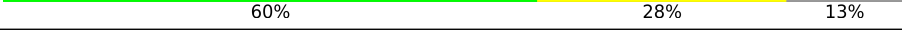
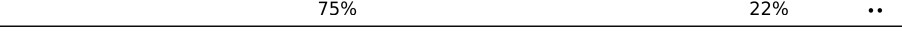
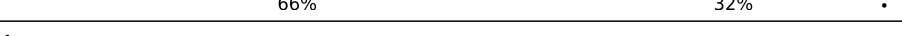
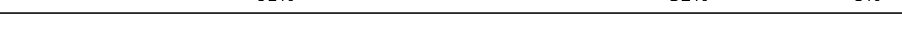
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Lz	217	
47	S2	1869	
48	SA	295	
49	SB	264	
50	SD	243	
51	SE	263	
52	SF	204	
53	SH	194	

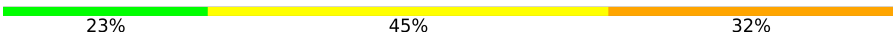
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Mol	Chain	Length	Quality of chain
54	SI	208	 77% 22% .
55	SK	165	 35% 25% 41%
56	SL	158	 6% 75% 22% .
57	SP	145	 63% 24% 12%
58	SQ	146	 62% 36% ..
59	SR	135	 75% 25%
60	SS	152	 66% 29% . 5%
61	ST	145	 72% 26% ..
62	SU	119	 60% 28% 13%
63	SV	83	 80% 18% .
64	SX	143	 75% 22% ..
65	Sa	115	 64% 23% . 11%
66	Sc	69	 55% 38% 7%
67	Sd	56	 66% 32% .
68	Sg	317	 65% 34% .
69	SC	293	 56% 19% . 24%
70	SG	249	 65% 30% 5%
71	SJ	194	 71% 25% 5%
72	SM	132	 6% 61% 32% 8%
73	SN	151	 84% 15% .
74	SO	151	 69% 23% . 7%
75	SW	130	 82% 17% .
76	SY	133	 74% 24% .
77	SZ	125	 38% 22% 40%
78	Sb	84	 76% 23% .

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Mol	Chain	Length	Quality of chain
79	Se	59	 81% 17%
80	Sf	156	 33% 10% 57%
81	CA	394	 65% 24% 10%
82	CB	858	 7% 74% 24%
83	CC	75	 23% 45% 32%
84	CD	408	 6% 92%

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 228566 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	3772	Total	C	N	O	P	0	0
			80116	35645	14585	26115	3771		

- 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	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- 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	236	Total	C	N	O	S	0	0
			1904	1222	361	317	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	241	Total	C	N	O	S	0	0
			1927	1228	371	324	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	176	Total	C	N	O	S	0	0
			1410	888	263	253	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	187	Total	C	N	O	S	0	0
			1566	971	336	250	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	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	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	105	Total	C	N	O	S	0	0
			862	542	175	139	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 protein called 60S ribosomal protein L10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lz	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6599	12101	1739		

- Molecule 48 is a protein called 40S ribosomal protein SA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	SA	221	Total	C	N	O	S	0	0
			1741	1106	305	322	8		

- Molecule 49 is a protein called 40S ribosomal protein S3a.

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

- Molecule 50 is a protein called 40S ribosomal protein S3.

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

- Molecule 51 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 52 is a protein called 40S ribosomal protein S5.

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

- Molecule 53 is a protein called 40S ribosomal protein S7.

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

- Molecule 54 is a protein called 40S ribosomal protein S8.

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

- Molecule 55 is a protein called 40S ribosomal protein S10.

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

- Molecule 56 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	SL	153	Total	C	N	O	S	0	0
			1247	793	234	214	6		

- Molecule 57 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	SP	127	Total	C	N	O	S	0	0
			1045	663	198	177	7		

- Molecule 58 is a protein called 40S ribosomal protein S16.

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

- Molecule 59 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SR	135	Total	C	N	O	S	0	0
			1090	685	202	198	5		

- Molecule 60 is a protein called 40S ribosomal protein S18.

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

- Molecule 61 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	ST	143	Total	C	N	O	S	0	0
			1112	697	214	198	3		

- Molecule 62 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SU	104	Total	C	N	O	S	0	0
			821	514	155	148	4		

- Molecule 63 is a protein called 40S ribosomal protein S21.

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

- Molecule 64 is a protein called 40S ribosomal protein S23.

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

- Molecule 65 is a protein called 40S ribosomal protein S26.

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

- 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	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 68 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 69 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	SC	222	Total	C	N	O	S	0	0
			1725	1115	298	302	10		

- Molecule 70 is a protein called 40S ribosomal protein S6.

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

- Molecule 71 is a protein called 40S ribosomal protein S9.

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

- Molecule 72 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	SM	122	Total	C	N	O	S	0	0
			940	590	164	177	9		

- Molecule 73 is a protein called 40S ribosomal protein S13.

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

- Molecule 74 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SO	140	Total	C	N	O	S	0	0
			1049	642	204	197	6		

- Molecule 75 is a protein called 40S ribosomal protein S15a.

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

- Molecule 76 is a protein called 40S ribosomal protein S24.

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

- Molecule 77 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	SZ	75	Total	C	N	O	S	0	0
			598	382	111	104	1		

- Molecule 78 is a protein called 40S ribosomal protein S27.

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

- Molecule 79 is a protein called 40S ribosomal protein S30.

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

- Molecule 80 is a protein called Ubiquitin-40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Sf	67	Total	C	N	O	S	0	0
			548	346	102	93	7		

- Molecule 81 is a protein called Proliferation-associated protein 2G4.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CA	354	Total	C	N	O	S	4	0
			2764	1744	475	528	17		

- Molecule 82 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CB	846	Total	C	N	O	S	0	0
			6609	4195	1136	1234	44		

- Molecule 83 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CC	75	Total	C	N	O	P	0	0
			1589	710	279	525	75		

- Molecule 84 is a protein called Plasminogen activator inhibitor 1 RNA-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CD	32	Total	C	N	O	S	0	0
			232	135	59	37	1		

- Molecule 85 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
85	L5	211	Total	Mg	0
			211	211	
85	L7	3	Total	Mg	0
			3	3	
85	L8	4	Total	Mg	0
			4	4	
85	LA	1	Total	Mg	0
			1	1	
85	LI	1	Total	Mg	0
			1	1	
85	LP	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	2	Total	Mg	0
			2	2	
85	Lg	1	Total	Mg	0
			1	1	
85	S2	30	Total	Mg	0
			30	30	
85	SG	1	Total	Mg	0
			1	1	

- Molecule 86 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

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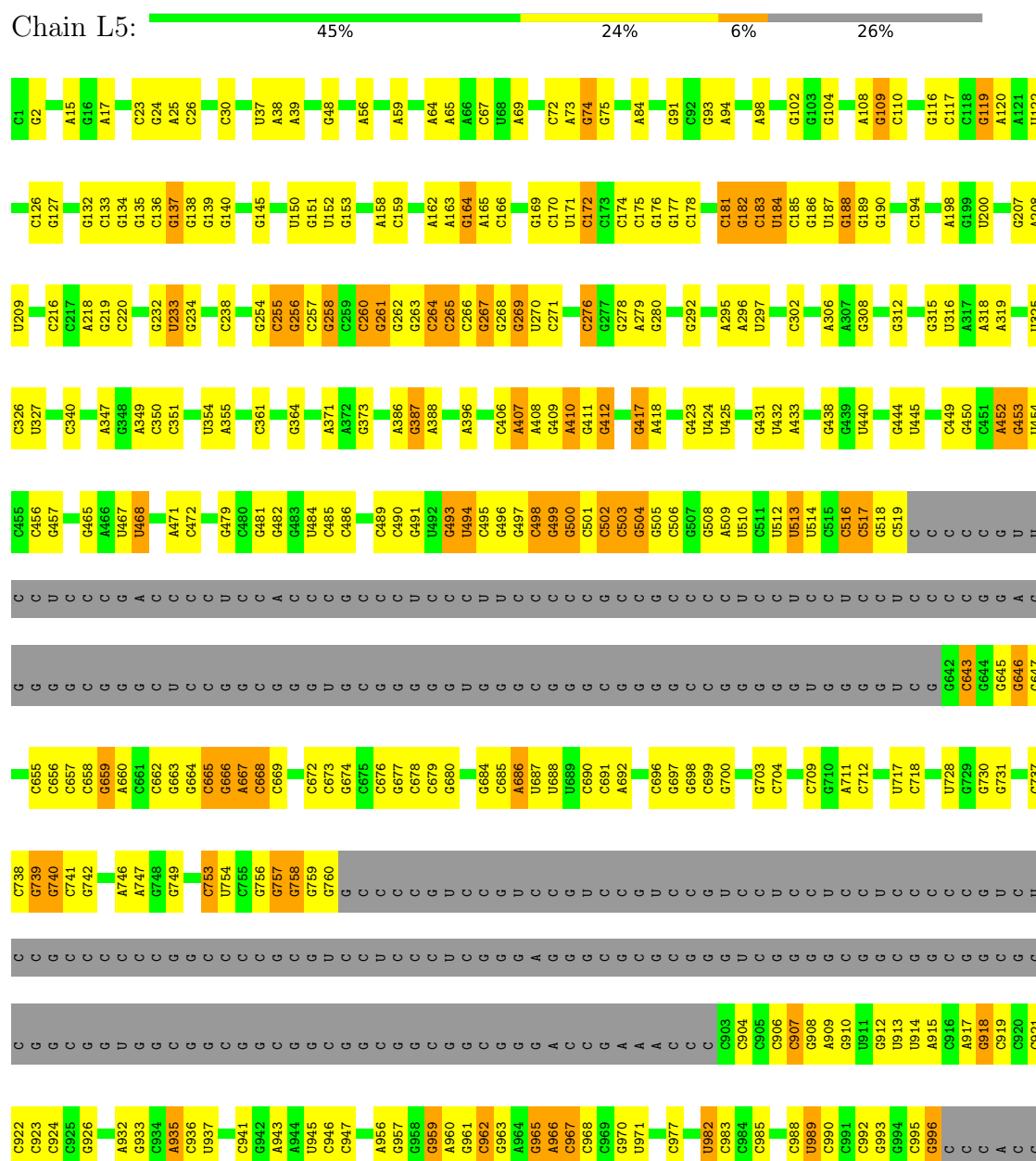
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Mol	Chain	Residues	Atoms		AltConf
86	Sd	1	Total 1	Zn 1	0
86	Sf	1	Total 1	Zn 1	0

3 Residue-property plots

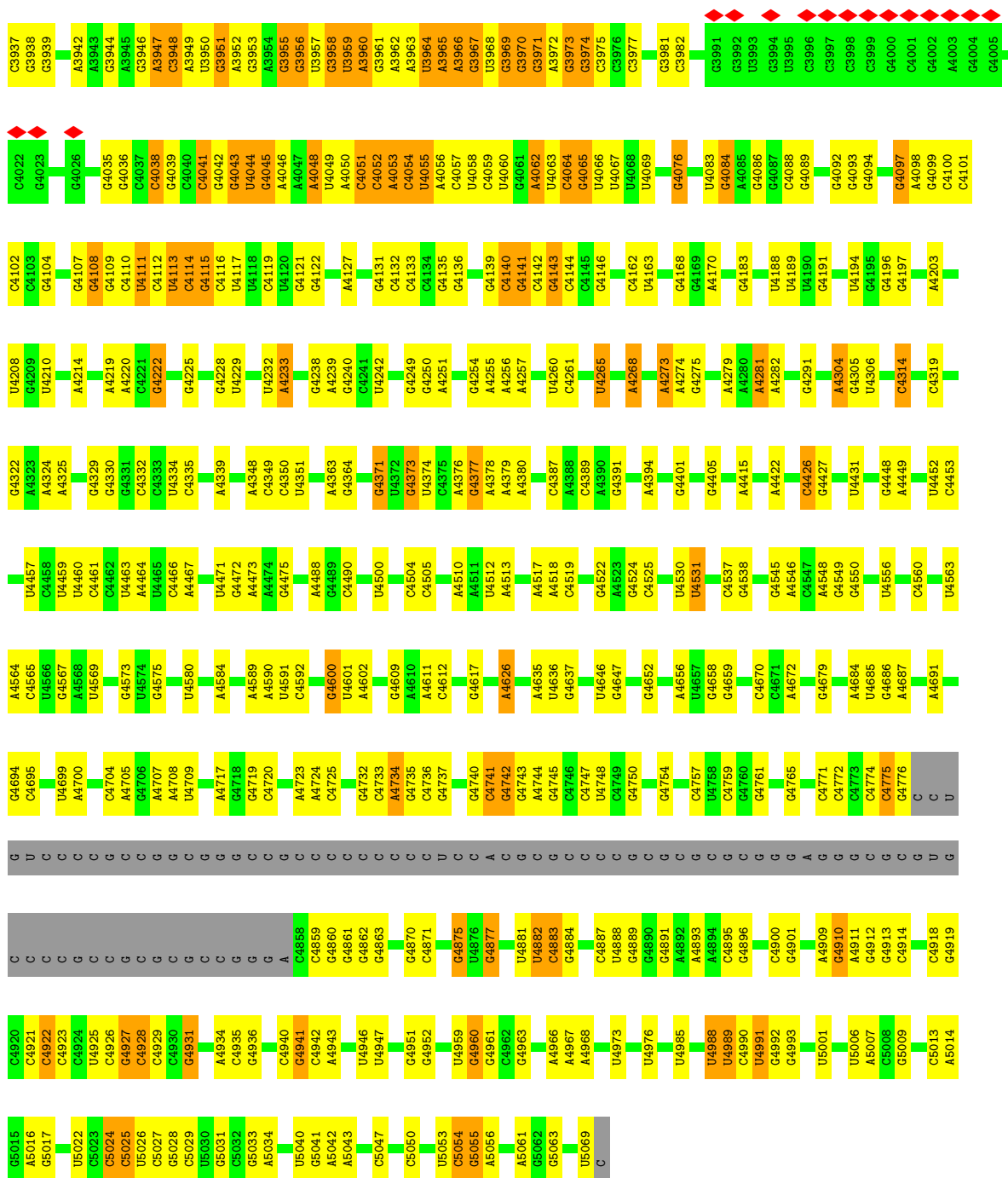
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 28S rRNA

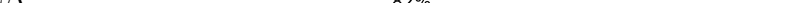


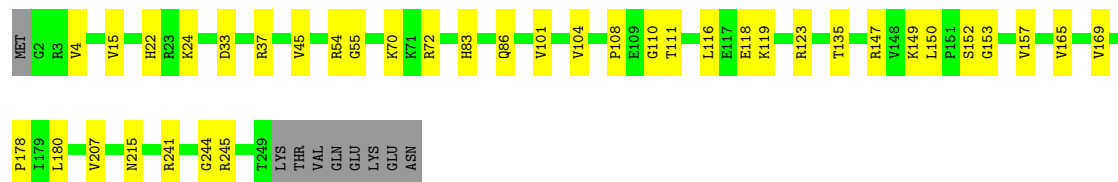






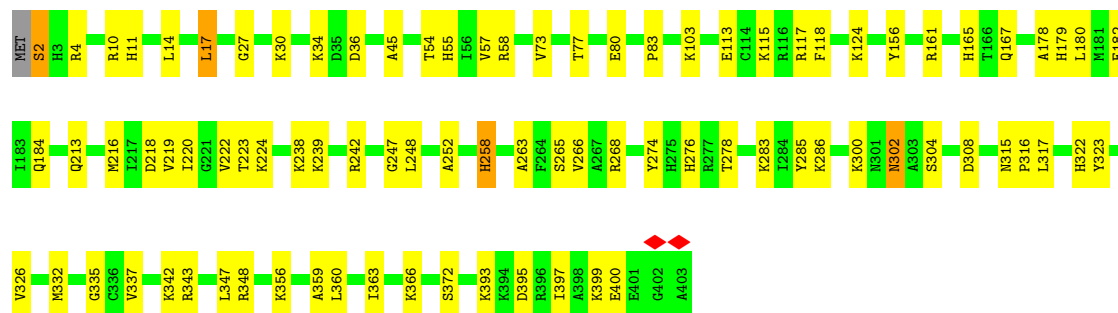
- Molecule 4: 60S ribosomal protein L8

Chain LA:  82% 15% 3%

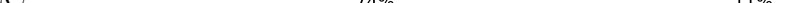


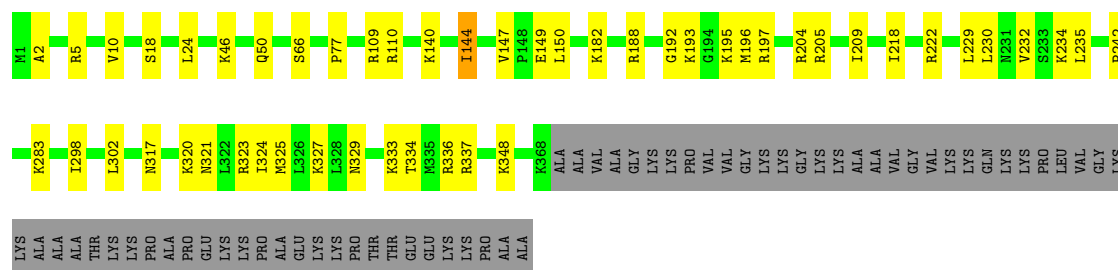
- Molecule 5: 60S ribosomal protein L3

Chain LB:  78% 21%

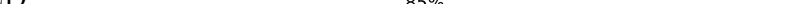


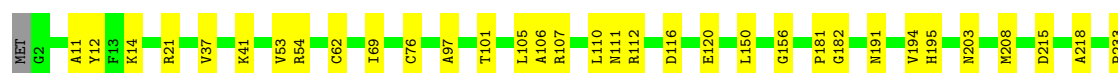
- Molecule 6: 60S ribosomal protein L4

Chain LC: 



- Molecule 7: 60S ribosomal protein L5

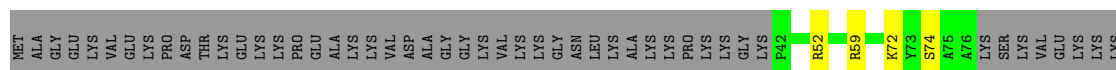
Chain LD:  85% 14%





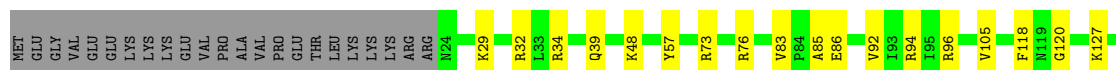
- Molecule 8: 60S ribosomal protein L6

Chain LE: 65% 16% 18%



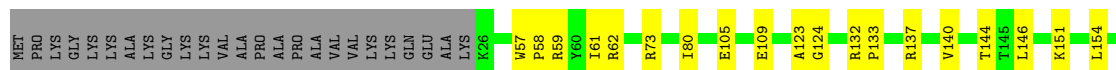
- Molecule 9: 60S ribosomal protein L7

Chain LF: 74% 17% 9%



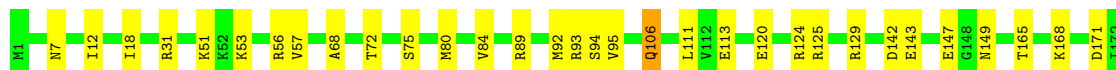
- Molecule 10: 60S ribosomal protein L7a

Chain LG: 79% 12% 9%



- Molecule 11: 60S ribosomal protein L9

Chain LH: 79% 19% ..



- Molecule 12: 60S ribosomal protein L10-like

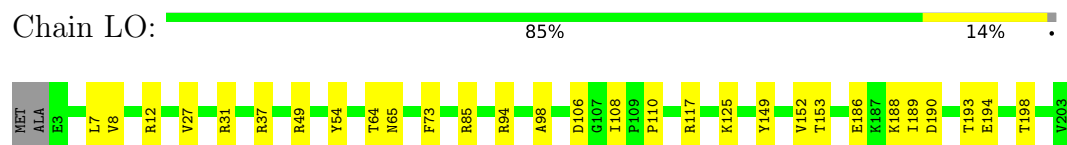
- Molecule 13: 60S ribosomal protein L11

- Molecule 14: 60S ribosomal protein L13

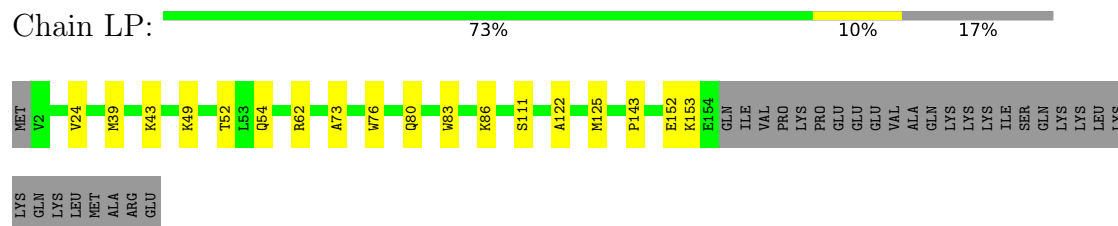
- Molecule 15: 60S ribosomal protein L14

- Molecule 16: 60S ribosomal protein L15

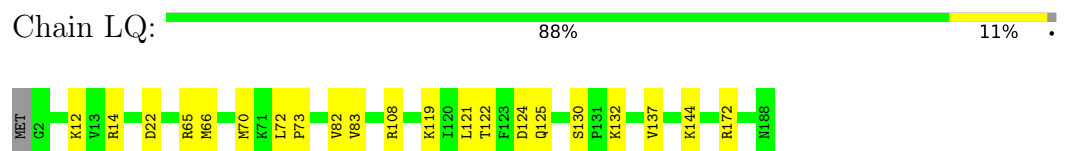
- Molecule 17: 60S ribosomal protein L13a



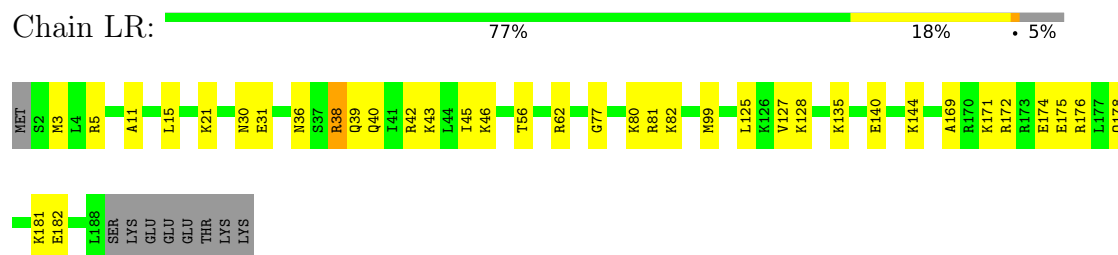
- Molecule 18: 60S ribosomal protein L17



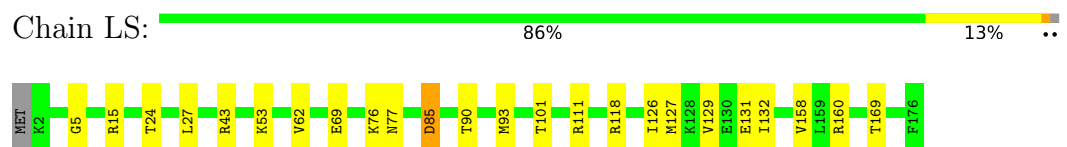
- Molecule 19: 60S ribosomal protein L18



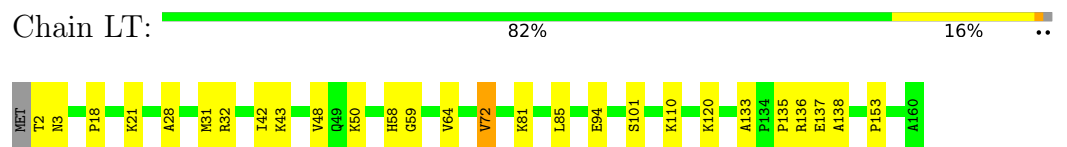
- Molecule 20: 60S ribosomal protein L19



- Molecule 21: 60S ribosomal protein L18a



- Molecule 22: 60S ribosomal protein L21



- Molecule 23: 60S ribosomal protein L22





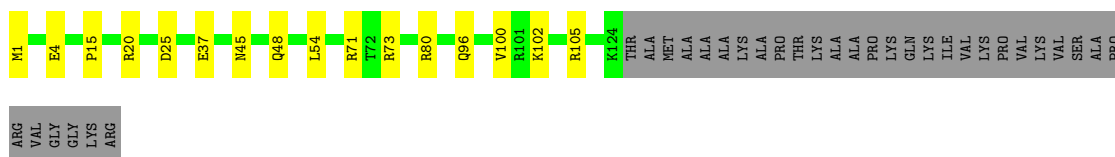
- Molecule 24: 60S ribosomal protein L23

Chain LV: 79% 14% 6%



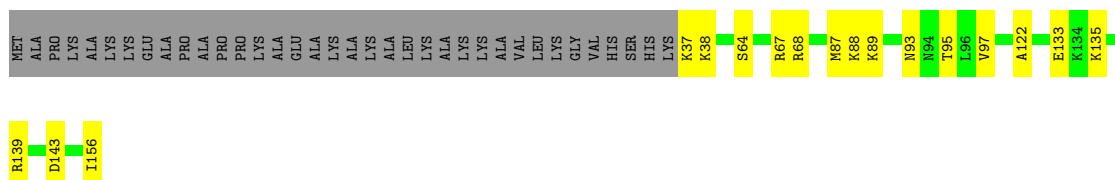
- Molecule 25: 60S ribosomal protein L24

Chain LW: 69% 10% 21%



- Molecule 26: 60S ribosomal protein L23a

Chain LX: 66% 11% 23%



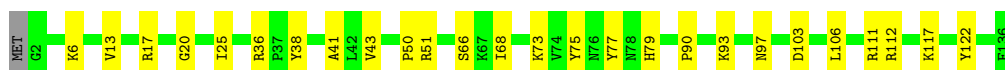
- Molecule 27: 60S ribosomal protein L26

Chain LY: 74% 18% 8%



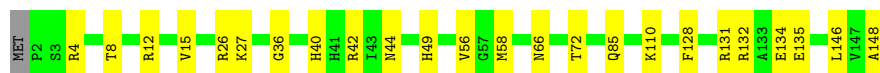
- Molecule 28: 60S ribosomal protein L27

Chain LZ: 80% 19% 1%



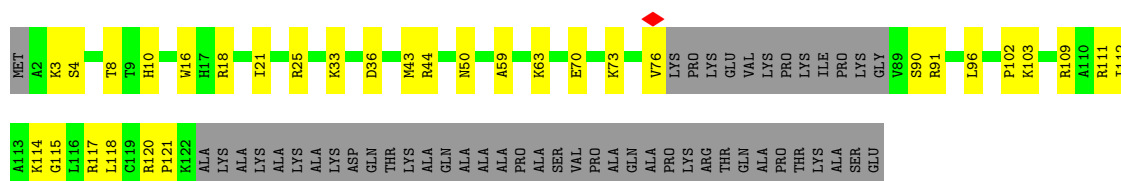
- Molecule 29: 60S ribosomal protein L27a

Chain La:  83% 16% .



- Molecule 30: 60S ribosomal protein L29

Chain Lb:  48% 20% 31%



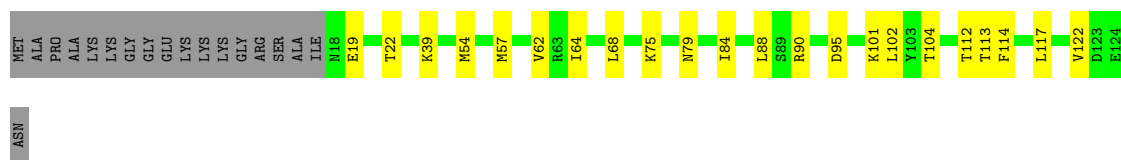
- Molecule 31: 60S ribosomal protein L30

Chain Lc:  73% 12% 15%



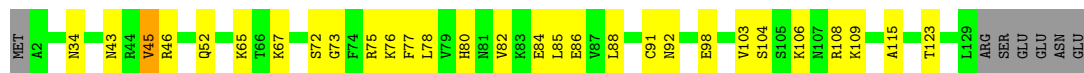
- Molecule 32: 60S ribosomal protein L31

Chain Ld:  68% 18% 14%



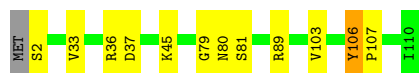
- Molecule 33: 60S ribosomal protein L32

Chain Le:  73% 21% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  88% 10% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg:  89% 9% .



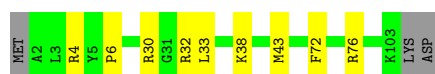
- Molecule 36: 60S ribosomal protein L35

Chain Lh: 86% 13%



- Molecule 37: 60S ribosomal protein L36

Chain Li: 89% 9%



- Molecule 38: 60S ribosomal protein L37

Chain Lj: 74% 12% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk: 77% 21%



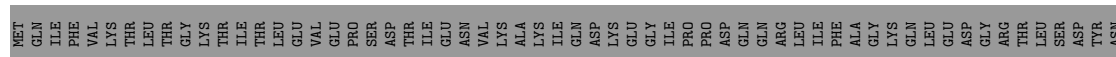
- Molecule 40: 60S ribosomal protein L39

Chain Ll: 82% 16%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm: 32% 9% 59%



- Molecule 42: 60S ribosomal protein L41

Chain Ln:  76% 20% .



- Molecule 43: 60S ribosomal protein L36a

Chain Lo:  84% 15% .



- Molecule 44: 60S ribosomal protein L37a

Chain Lp:  88% 11% .



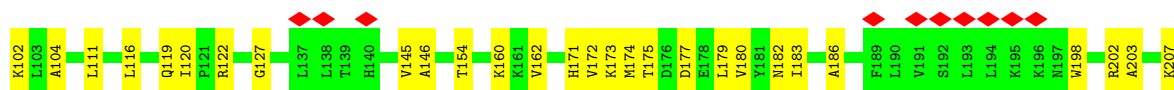
- Molecule 45: 60S ribosomal protein L28

Chain Lr:  77% 14% 9% .

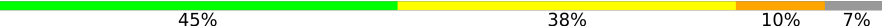


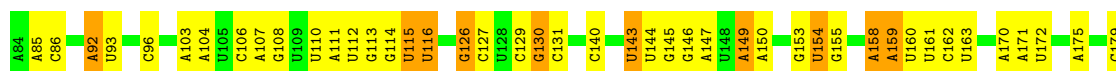
- Molecule 46: 60S ribosomal protein L10a

Chain Lz:  10% 71% 28% .

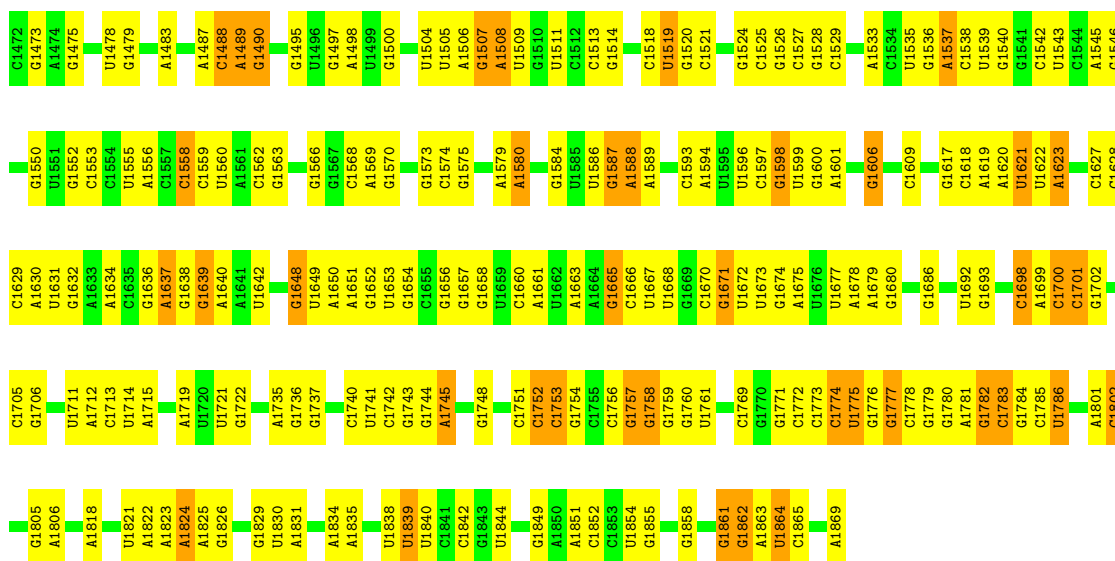


- Molecule 47: 18S rRNA

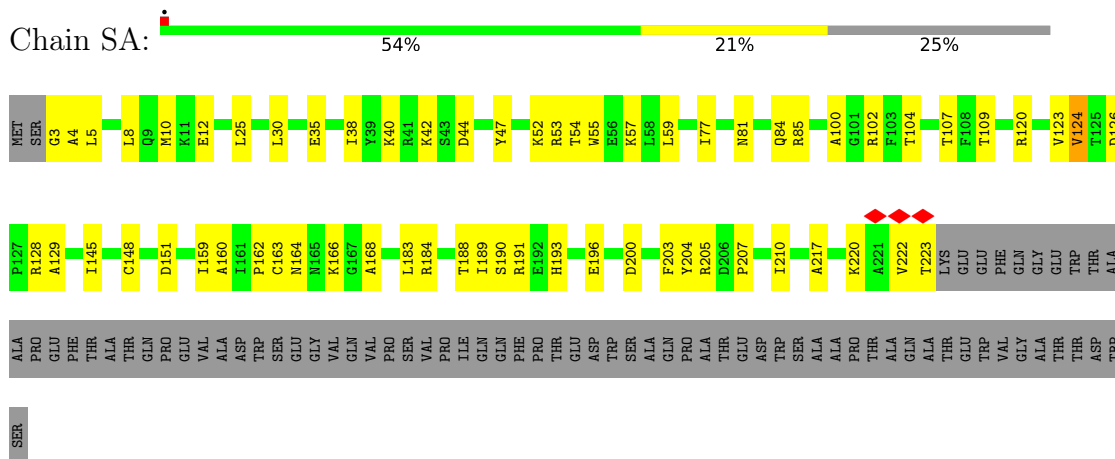
Chain S2:  45% 38% 10% 7% .



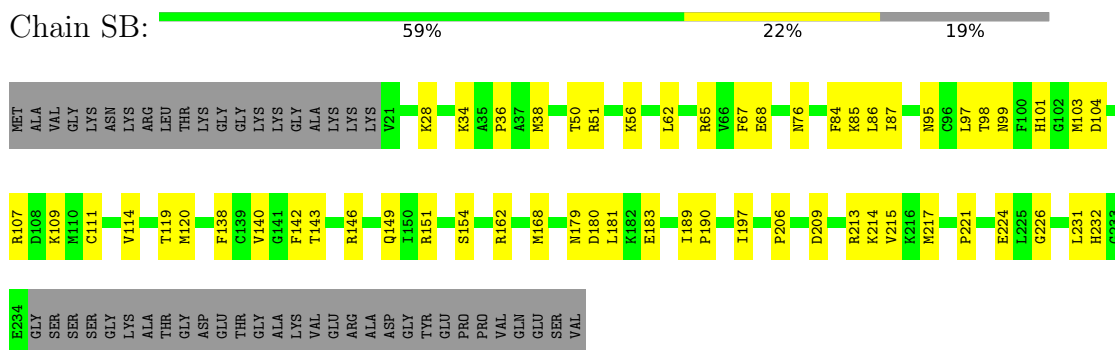
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U1120	G1121	A1122	G1126	U1127	G1128	G1129	G1133	U1136	U1137	C1138	C1139	G1142	G1143	A1144	A1145	A1148	A1149	A1150	C1153	U1154	U1155	U1156	U1160	U1161	G1171	G1187	A1188	A1189	A1190	A1194	A1195	A1196	G1203	A1204	C1205	G1206	G1207	A1208	C1215	C1216	A1217	C1218	G1221	G1222	A1223	G1224	G1226	G1227	A1228	G1229	C1230	C1231	U1232	G1233	C1237	A1240	A1241	U1242	U1243	U1248	C1249	A1250	A1251	C1252	A1253	C1254	G1255	G1256	G1257	A1258	A1259	A1260	C1261	C1264	A1265	A1266	C1267	G1270	C1271	G1274	G1275	A1276	C1277	A1278	C1283	A1284	G1285	G1286	A1287	A1293	G1294	A1295	G1296	U1297	G1298	A1301																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																				
G1302	C1303	U1304	C1305	U1306	U1307	U1308	C1309	U1310	C1311	G1312	G1317	G1318	G1324	U1329	A1332	U1333	C1337	G1338	U1342	U1343	U1346	U1347	G1348	G1349	U1350	G1351	G1354	A1357	U1362	U1371	U1372	C1373	U1377	A1378	A1382	A1455	G1385	U1390	C1391	U1392	G1393	G1394	C1395	A1396	U1397	G1398	C1401	A1402	G1403	G1404	G1405	G1406	G1407	G1408	G1409	G1410	G1411	G1412	G1415	G1416	G1417	G1418	G1419	G1420	G1421	G1422	G1423	G1424	G1430	G1431	G1432	G1433	G1434	G1435	G1436	G1437	G1438	G1439	G1441	G1442	G1443	G1444	G1445	G1446	G1447	G1448	G1449	G1452	G1453	G1454	G1455	G1456	G1457	G1458	G1461	G1462	G1463	G1464	G1465	G1471																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																																
U852	G857	U857	A862	A869	A870	U871	G873	G874	A875	C876	G877	G878	C879	G880	G881	U882	U883	C884	U885	A886	U887	U888	U889	U890	G891	U892	U896	U897	U898	U899	C900	G901	G902	A903	U906	G907	A908	G909	G910	A913	U914	G915	A916	A919	A920	G921	C1006	C1007	A1008	A1009	G1010	A1011	G929	C930	C931	G932	G933	G934	U940	C941	G942	U943	C948	G949	C950	U954	G958	G959	U960	G961	A962	A963	U969	G970	A971	A972	G975	A980	A981	G982	A983	C984	G985	A987	A990	G991	A992	G995	A996	A997	A998	G999	U1002	G1005	C1006	C1007	A1008	A1009	G1010	A1011	G829	C830	C831	G832	G833	G834	U835	A836	U837	G838	C839	C840	G841	C842	C843	U844	C845	C846	A847	U848	A849	C850	C851	U852	C853	C854	U855	A856	C857	C858	C859	C860	U861	C862	C863	C864	C865	C866	C867	C868	C869	C870	C871	C872	C873	C874	C875	C876	C877	C878	C879	C880	C881	C882	C883	C884	C885	C886	C887	C888	C889	C890	C891	C892	C893	C894	C895	C896	C897	C898	C899	C900	C901	C902	C903	C904	C905	C906	C907	C908	C909	C910	C911	C912	C913	C914	C915	C916	C917	C918	C919	C920	C921	C922	C923	C924	C925	C926	C927	C928	C929	C930	C931	C932	C933	C934	C935	C936	C937	C938	C939	C940	C941	C942	C943	C944	C945	C946	C947	C948	C949	C950	C951	C952	C953	C954	C955	C956	C957	C958	C959	C960	C961	C962	C963	C964	C965	C966	C967	C968	C969	C970	C971	C972	C973	C974	C975	C976	C977	C978	C979	C980	C981	C982	C983	C984	C985	C986	C987	C988	C989	C990	C991	C992	C993	C994	C995	C996	C997	C998	C999	G000	G001	G002	G003	G004	G005	G006	G007	G008	G009	G010	G011	G012	G013	G014	G015	G016	G017	G018	G019	G020	G021	G022	G023	G024	G025	G026	G027	G028	G029	G030	G031	G032	G033	G034	G035	G036	G037	G038	G039	G040	G041	G042	G043	G044	G045	G046	G047	G048	G049	G050	G051	G052	G053	G054	G055	G056	G057	G058	G059	G060	G061	G062	G063	G064	G065	G066	G067	G068	G069	G070	G071	G072	G073	G074	G075	G076	G077	G078	G079	G080	G081	G082	G083	G084	G085	G086	G087	G088	G089	G090	G091	G092	G093	G094	G095	G096	G097	G098	G099	G100	G101	G102	G103	G104	G105	G106	G107	G108	G109	G110	G111	G112	G113	G114	G115	G116	G117	G118	G119	G120	G121	G122	G123	G124	G125	G126	G127	G128	G129	G130	G131	G132	G133	G134	G135	G136	G137	G138	G139	G140	G141	G142	G143	G144	G145	G146	G147	G148	G149	G150	G151	G152	G153	G154	G155	G156	G157	G158	G159	G160	G161	G162	G163	G164	G165	G166	G167	G168	G169	G170	G171	G172	G173	G174	G175	G176	G177	G178	G179	G180	G181	G182	G183	G184	G185	G186	G187	G188	G189	G190	G191	G192	G193	G194	G195	G196	G197	G198	G199	G200	G201	G202	G203	G204	G205	G206	G207	G208	G209	G210	G211	G212	G213	G214	G215	G216	G217	G218	G219	G220	G221	G222	G223	G224	G225	G226	G227	G228	G229	G230	G231	G232	G233	G234	G235	G236	G237	G238	G239	G240	G241	G242	G243	G244	G245	G246	G247	G248	G249	G250	G251	G252	G253	G254	G255	G256	G257	G258	G259	G260	G261	G262	G263	G264	G265	G266	G267	G268	G269	G270	G271	G272	G273	G274	G275	G276	G277	G278	G279	G280	G281	G282	G283	G284	G285	G286	G287	G288	G289	G290	G291	G292	G293	G294	G295	G296	G297	G298	G299	G300	G301	G302	G303	G304	G305	G306	G307	G308	G309	G310	G311	G312	G313	G314	G315	G316	G317	G318	G319	G320	G321	G322	G323	G324	G325	G326	G327	G328	G329	G330	G331	G332	G333	G334	G335	G336	G337	G338	G339	G340	G341	G342	G343	G344	G345	G346	G347	G348	G349	G350	G351	G352	G353	G354	G355	G356	G357	G358	G359	G360	G361	G362	G363	G364	G365	G366	G367	G368	G369	G370	G371	G372	G373	G374	G375	G376	G377	G378	G379	G380	G381	G382	G383	G384	G385	G386	G387	G388	G389	G390	G391	G392	G393	G394	G395	G396	G397	G398	G399	G400	G401	G402	G403	G404	G405	G406	G407	G408	G409	G410	G411	G412	G413	G414	G415	G416	G417	G418	G419	G420	G421	G422	G423	G424	G425	G426	G427	G428	G429	G430	G431	G432	G433	G434	G435	G436	G437	G438	G439	G440	G441	G442	G443	G444	G445	G446	G447	G448	G449	G450	G451	G452	G453	G454	G455	G456	G457	G458	G459	G460	G461	G462	G463	G464	G465	G466	G467	G468	G469	G470	G471	G472	G473	G474	G475	G476	G477	G478	G479	G480	G481	G482	G483	G484	G485	G486	G487	G488	G489	G490	G491	G492	G493	G494	G495	G496	G497	G498	G499	G500	G501	G502	G503	G504	G505	G506	G507	G508	G509	G510	G511	G512	G513	G514	G515	G516	G517	G518	G519	G520	G521	G522	G523	G524	G525	G526	G527	G528	G529	G530	G531	G532	G533	G534	G535	G536	G537	G538	G539	G540	G541	G542	G543	G544	G545	G546	G547	G548	G549	G550	G551	G552	G553	G554	G555	G556	G557	G558	G559	G560	G561	G562	G563	G564	G565	G566	G567	G568	G569	G570	G571	G572	G573	G574	G575	G576	G577	G578	G579	G580	G581	G582	G583	G584	G585	G586	G587	G588	G589	G590	G591	G592	G593	G594	G595	G596	G597	G598	G599	G600	G601	G602	G603	G604	G605	G606	G607	G608	G609	G610	G611	G612	G613	G614	G615	G616	G617	G618	G619	G620	G621	G622	G623	G624	G625	G626	G627	G628	G629	G630	G631	G632	G633	G634	G635	G636	G637	G638	G639	G640	G641	G642	G643	G644	G645	G646	G647	G648	G649	G650	G651	G652	G653	G654	G655	G656	G657	G658	G659	G660	G661	G662	G663	G664	G665	G666	G667	G668	G669	G670	G671	G672	G673	G674	G675	G676	G677	G678	G679	G680	G681	G682	G683	G684	G685	G686	G687	G688	G689	G690	G691	G692	G693	G694	G695	G696	G697	G698	G699	G700	G701	G702	G703	G704	G705	G706	G707	G708	G709	G710	G711	G712	G713	G714	G715	G716	G717	G718	G719	G720	G721	G722	G723	G724	G725	G726	G727	G728	G729	G730	G731	G732	G733	G734	G735	G736	G737	G738	G739	G740	G741	G742	G743	G744	G745	G746	G747	G748	G749	G750	G751	G752	G753	G754	G755	G756	G757	G758	G759	G760	G761	G762	G763	G764	G765	G766	G767	G768	G769	G770	G771	G772	G773	G774	G775	G776	G777	G778	G779	G780	G781	G782	G783	G784	G785	G786	G787	G788	G789	G790	G791	G792	G793	G794	G795	G796	G797	G798	G799	G800	G801	G802	G803	G804	G805	G806	G807	G808	G809	G810	G811	G812	G813	G814	G815	G816	G817	G818	G819	G820	G821	G822	G823	G824	G825	G826	G827	G828	G829	G830	G831	G832	G833	G834	G835	G836	G837	G838	G839	G840	G841	G842	G843	G844	G845	G846	G847	G848	G849	G850	G851	G852	G853	G854	G855	G856	G857	G858	G859	G860	G861	G862	G863	G864	G865	G866	G867	G868	G869	G870	G871	G872	G873	G874	G875	G876	G877	G878	G879	G880	G881	G882	G883	G884	G885	G886	G887	G888	G889	G890	G891	G892	G893	G894	G895	G896	G897	G898	G899	G900	G901	G902	G903	G904	G905	G906	G907	G908	G909	G910	G911	G912	G913	G914	G915	G916	G917	G918	G919	G920	G921	G922	G923	G924	G925	G926	G927	G928	G929	G930	G931	G932	G933	G934	G935	G936	G937	G938	G939	G940	G941	G942	G943	G944	G945	G946	G947	G948	G949	G950	G951	G952	G953	G954	G955	G956	G957	G958	G959	G960	G961	G962	G963	G964



- Molecule 48: 40S ribosomal protein SA

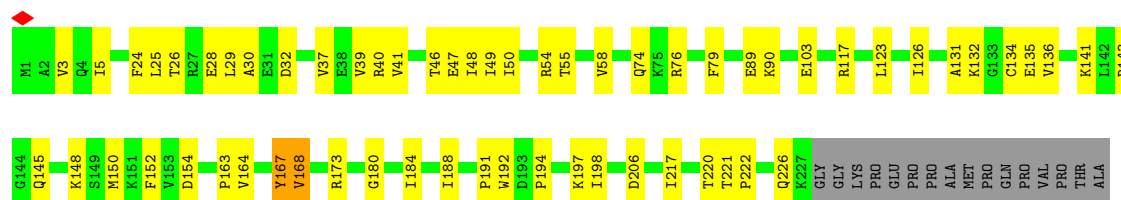


- Molecule 49: 40S ribosomal protein S3a



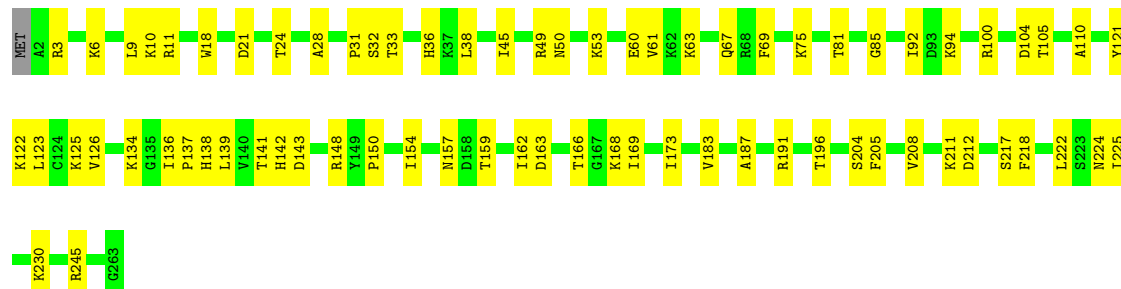
- Molecule 50: 40S ribosomal protein S3





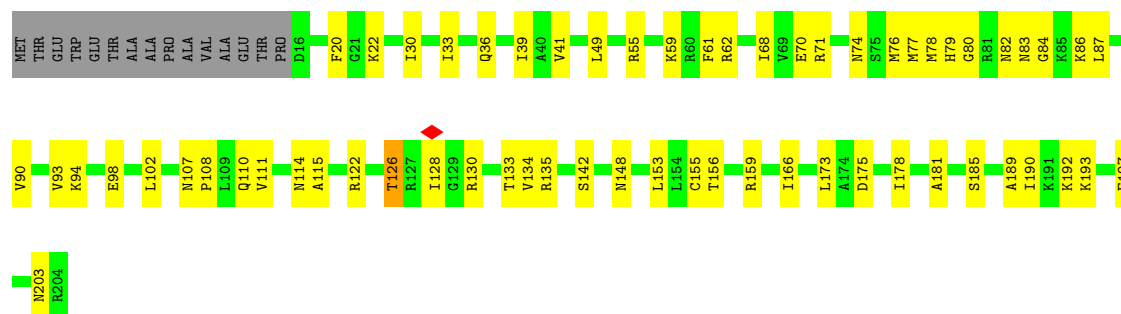
- Molecule 51: 40S ribosomal protein S4, X isoform

Chain SE:



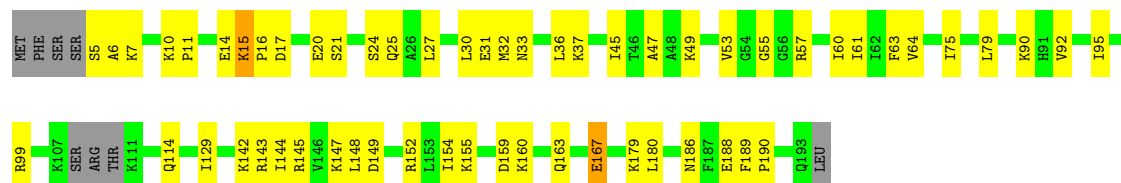
- Molecule 52: 40S ribosomal protein S5

Chain SF:



- Molecule 53: 40S ribosomal protein S7

Chain SH:



- Molecule 54: 40S ribosomal protein S8

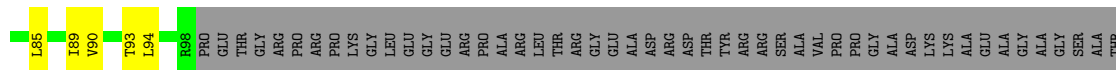
Chain SI:





- Molecule 55: 40S ribosomal protein S10

Chain SK: 35% 25% 41%



Chain SR:  75% 25%



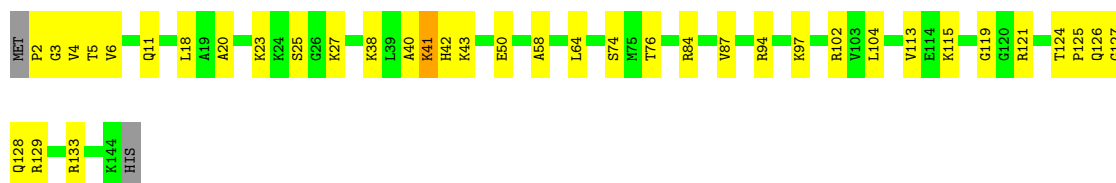
- Molecule 60: 40S ribosomal protein S18

Chain SS:  66% 29% 5%



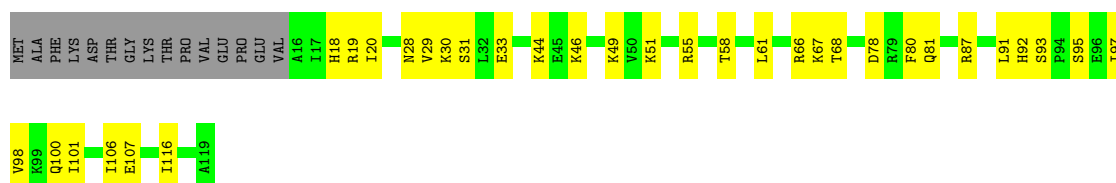
- Molecule 61: 40S ribosomal protein S19

Chain ST:  72% 26% ..



- Molecule 62: 40S ribosomal protein S20

Chain SU:  60% 28% 13%



- Molecule 63: 40S ribosomal protein S21

Chain SV:  80% 18% .



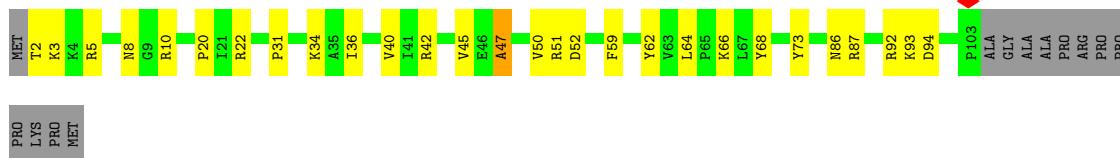
- Molecule 64: 40S ribosomal protein S23

Chain SX:  75% 22% ..





- Molecule 65: 40S ribosomal protein S26



- Molecule 66: 40S ribosomal protein S28



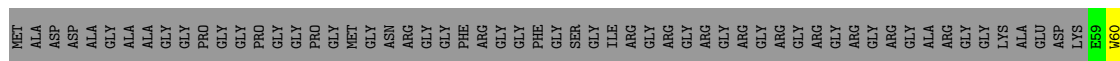
- Molecule 67: 40S ribosomal protein S29

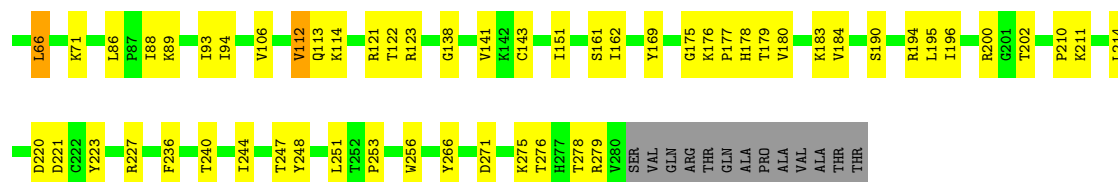


- Molecule 68: Receptor of activated protein C kinase 1



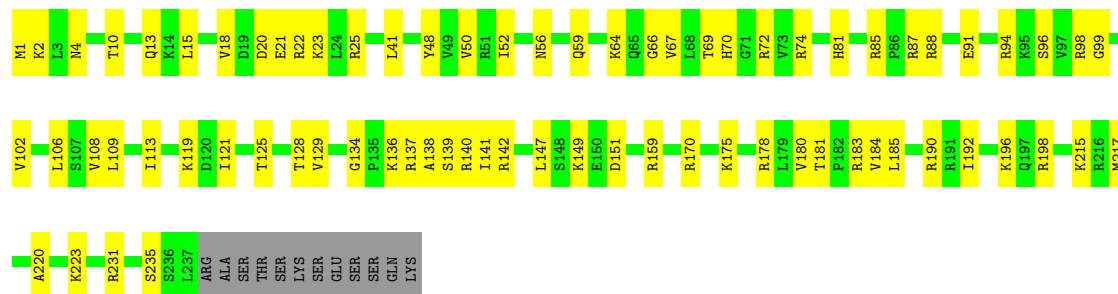
- Molecule 69: 40S ribosomal protein S2





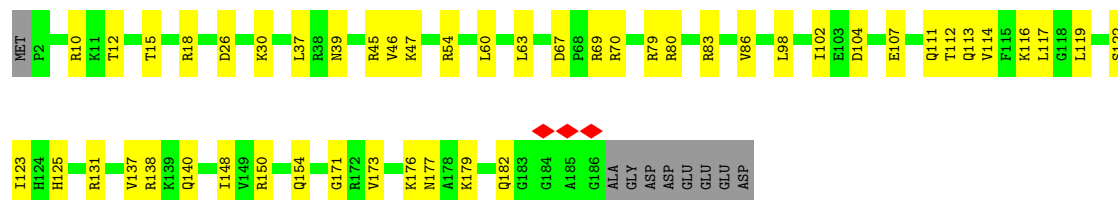
- Molecule 70: 40S ribosomal protein S6

Chain SG: 65% 30% 5%



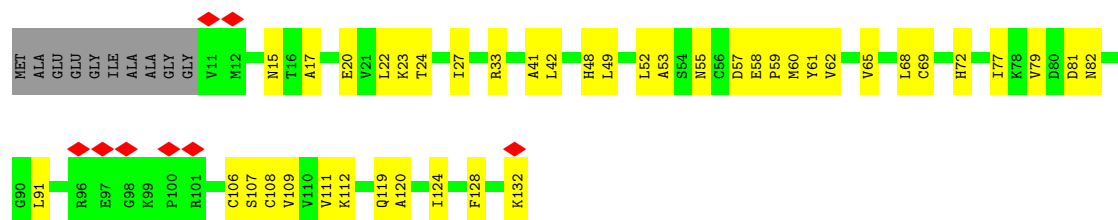
- Molecule 71: 40S ribosomal protein S9

Chain SJ: 71% 25% 5%



- Molecule 72: 40S ribosomal protein S12

Chain SM: 6% 61% 32% 8%



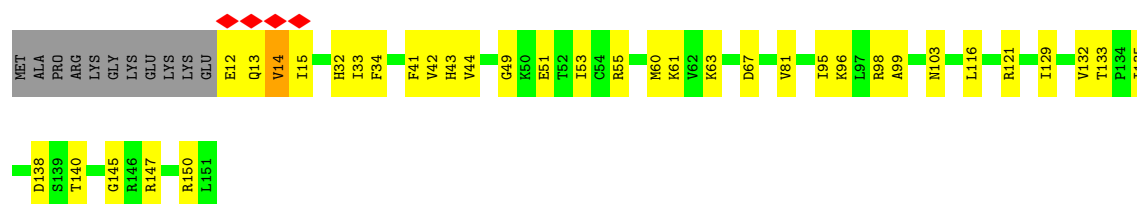
- Molecule 73: 40S ribosomal protein S13

Chain SN: 84% 15%



- Molecule 74: 40S ribosomal protein S14

Chain SO:  69% 23% 7%



- Molecule 75: 40S ribosomal protein S15a

Chain SW:  82% 17%

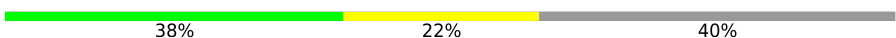


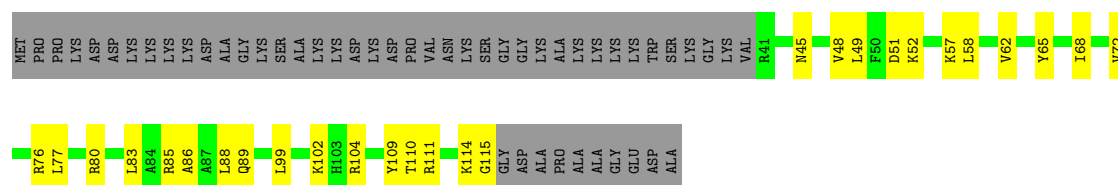
- Molecule 76: 40S ribosomal protein S24

Chain SY:  74% 24%



- Molecule 77: 40S ribosomal protein S25

Chain SZ:  38% 22% 40%



- Molecule 78: 40S ribosomal protein S27

Chain Sb:  76% 23%



- Molecule 79: 40S ribosomal protein S30

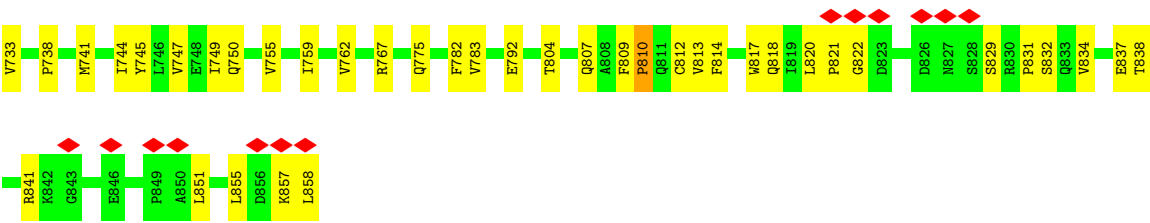
Chain Se:  81% 17%



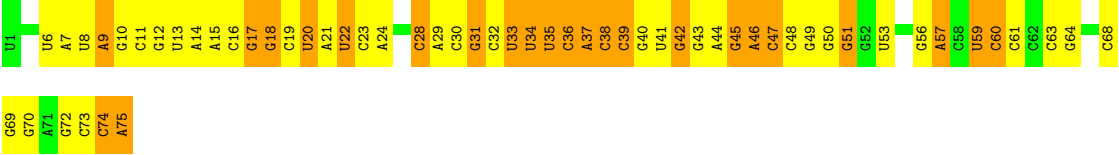
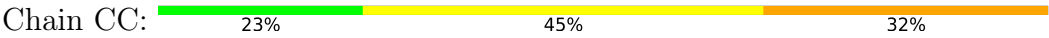
- Molecule 80: Ubiquitin-40S ribosomal protein S27a

Chain Sf:  33% 10% 57%

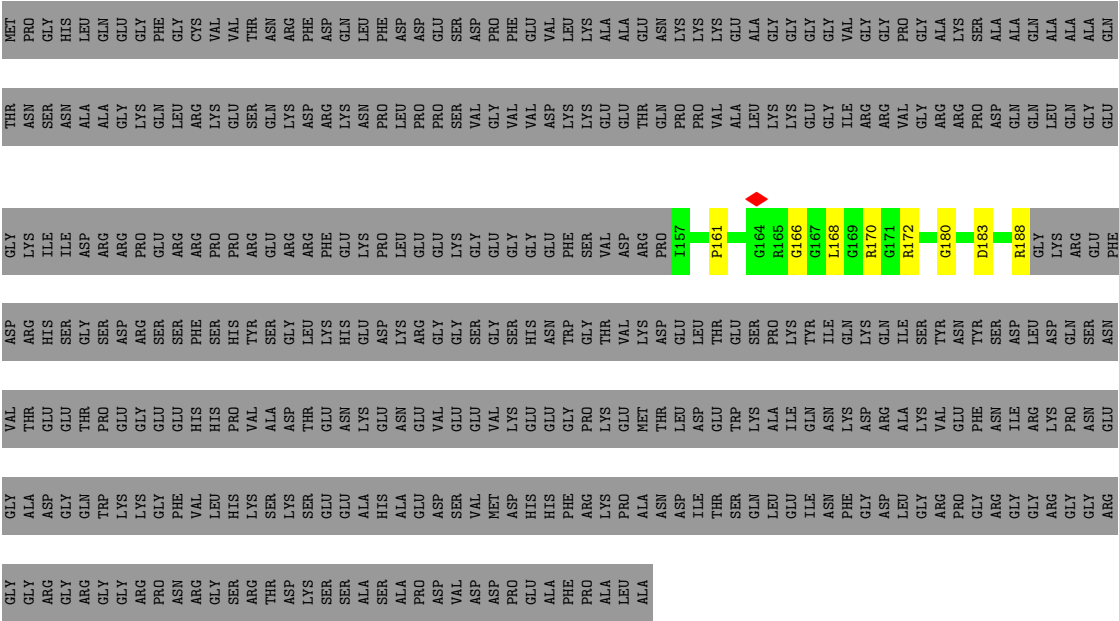




• Molecule 83: tRNA



• Molecule 84: Plasminogen activator inhibitor 1 RNA-binding protein



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	127706	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 ($e^-/\text{\AA}^2$)	28	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.277	Depositor
Minimum map value	-0.092	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.010	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	477.44998, 477.44998, 477.44998	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.061, 1.061, 1.061	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	L5	0.55	0/89570	0.44	1/139647 (0.0%)
2	L7	0.54	0/2861	0.37	0/4459
3	L8	0.55	0/3701	0.41	0/5766
4	LA	0.54	0/1936	0.68	0/2596
5	LB	0.51	0/3306	0.66	0/4424
6	LC	0.50	0/2981	0.65	4/4002 (0.1%)
7	LD	0.41	0/2428	0.56	0/3252
8	LE	0.41	0/1942	0.61	2/2606 (0.1%)
9	LF	0.52	0/1905	0.63	0/2539
10	LG	0.42	0/1960	0.63	1/2637 (0.0%)
11	LH	0.46	0/1537	0.62	0/2066
12	LI	0.49	0/1673	0.59	0/2233
13	LJ	0.38	0/1433	0.74	0/1915
14	LL	0.44	0/1732	0.63	0/2315
15	LM	0.45	0/1161	0.62	2/1554 (0.1%)
16	LN	0.56	0/1746	0.66	0/2338
17	LO	0.50	0/1682	0.54	0/2250
18	LP	0.50	0/1268	0.59	0/1701
19	LQ	0.53	0/1537	0.59	0/2052
20	LR	0.45	0/1582	0.60	2/2091 (0.1%)
21	LS	0.52	0/1493	0.55	0/2003
22	LT	0.49	0/1326	0.64	0/1770
23	LU	0.40	0/839	0.69	0/1126
24	LV	0.50	0/993	0.60	0/1332
25	LW	0.40	0/1030	0.59	0/1364
26	LX	0.44	0/1002	0.53	0/1345
27	LY	0.46	0/1132	0.58	0/1504
28	LZ	0.44	0/1130	0.56	0/1507
29	La	0.51	0/1191	0.59	0/1591
30	Lb	0.40	0/889	0.65	0/1175
31	Lc	0.45	0/774	0.58	0/1038
32	Ld	0.50	0/903	0.63	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.54	0/1071	0.62	0/1429
34	Lf	0.54	0/895	0.63	0/1198
35	Lg	0.48	0/916	0.57	0/1220
36	Lh	0.41	0/1023	0.54	0/1351
37	Li	0.37	0/843	0.50	0/1115
38	Lj	0.55	0/720	0.71	0/952
39	Lk	0.37	0/575	0.59	0/761
40	Ll	0.55	0/454	0.60	0/599
41	Lm	0.46	0/435	0.61	0/575
42	Ln	0.40	0/231	0.61	0/294
43	Lo	0.47	0/876	0.56	0/1156
44	Lp	0.48	0/718	0.55	0/953
45	Lr	0.50	0/1017	0.59	0/1364
46	Lz	0.25	0/1769	0.64	0/2371
47	S2	0.32	0/41244	0.40	1/64263 (0.0%)
48	SA	0.33	0/1778	0.63	0/2416
49	SB	0.28	0/1765	0.58	0/2362
50	SD	0.26	0/1793	0.66	0/2414
51	SE	0.28	0/2118	0.58	0/2849
52	SF	0.25	0/1516	0.58	0/2037
53	SH	0.29	0/1519	0.67	1/2033 (0.0%)
54	SI	0.30	0/1715	0.63	0/2287
55	SK	0.21	0/851	0.51	0/1147
56	SL	0.32	0/1268	0.56	0/1696
57	SP	0.23	0/1065	0.59	0/1423
58	SQ	0.24	0/1160	0.62	0/1553
59	SR	0.26	0/1105	0.65	0/1484
60	SS	0.23	0/1216	0.57	0/1628
61	ST	0.24	0/1131	0.56	0/1515
62	SU	0.26	0/831	0.65	0/1115
63	SV	0.30	0/643	0.63	0/860
64	SX	0.35	0/1116	0.65	0/1490
65	Sa	0.35	0/836	0.62	0/1121
66	Sc	0.28	0/508	0.69	0/680
67	Sd	0.24	0/470	0.57	0/623
68	Sg	0.23	0/2493	0.61	0/3394
69	SC	0.37	0/1762	0.61	0/2381
70	SG	0.23	0/1946	0.59	1/2590 (0.0%)
71	SJ	0.29	0/1550	0.61	0/2069
72	SM	0.26	0/950	0.77	2/1275 (0.2%)
73	SN	0.31	0/1232	0.55	0/1656
74	SO	0.31	0/1062	0.67	2/1425 (0.1%)
75	SW	0.34	0/1051	0.57	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SY	0.26	0/1083	0.57	1/1438 (0.1%)
77	SZ	0.25	0/604	0.71	0/810
78	Sb	0.27	0/665	0.58	0/891
79	Se	0.26	0/465	0.56	0/612
80	Sf	0.22	0/560	0.67	0/745
81	CA	0.25	0/2810	0.57	0/3780
82	CB	0.25	0/6738	0.64	0/9099
83	CC	0.27	0/1773	0.46	1/2759 (0.0%)
84	CD	0.27	0/233	0.90	0/302
All	All	0.45	0/244811	0.51	21/358380 (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	2
5	LB	0	3
8	LE	0	2
11	LH	0	2
12	LI	0	1
13	LJ	0	1
14	LL	0	1
15	LM	0	2
16	LN	0	1
17	LO	0	1
21	LS	0	1
22	LT	0	1
33	Le	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
45	Lr	0	1
49	SB	0	1
50	SD	0	1
52	SF	0	1
53	SH	0	1
58	SQ	0	3
63	SV	0	1
64	SX	0	3
66	Sc	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
82	CB	0	2
84	CD	0	1
All	All	0	39

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
70	SG	139	SER	N-CA-C	-8.45	104.99	114.62
15	LM	87	ALA	CA-C-N	6.68	134.29	121.54
15	LM	87	ALA	C-N-CA	6.68	134.29	121.54
47	S2	1417	C	N3-C4-N4	-6.41	98.76	118.00
6	LC	2	ALA	CA-C-N	6.33	133.09	121.70

There are no chirality outliers.

5 of 39 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	110	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	2	SER	Peptide
5	LB	258	HIS	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	80116	0	40364	765	0
2	L7	2561	0	1295	10	0
3	L8	3314	0	1683	27	0
4	LA	1898	0	1993	23	0
5	LB	3238	0	3376	61	0
6	LC	2927	0	3104	38	0
7	LD	2382	0	2410	31	0
8	LE	1904	0	2055	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	LF	1870	0	1996	31	0
10	LG	1927	0	2074	20	0
11	LH	1518	0	1601	25	0
12	LI	1634	0	1670	30	0
13	LJ	1410	0	1441	27	0
14	LL	1701	0	1818	34	0
15	LM	1138	0	1204	17	0
16	LN	1701	0	1749	22	0
17	LO	1650	0	1794	20	0
18	LP	1242	0	1269	12	0
19	LQ	1513	0	1628	17	0
20	LR	1566	0	1729	30	0
21	LS	1453	0	1490	15	0
22	LT	1298	0	1366	21	0
23	LU	825	0	850	17	0
24	LV	979	0	1039	14	0
25	LW	1015	0	1079	11	0
26	LX	985	0	1066	15	0
27	LY	1115	0	1205	17	0
28	LZ	1107	0	1182	17	0
29	La	1162	0	1213	21	0
30	Lb	876	0	948	24	0
31	Lc	764	0	804	9	0
32	Ld	888	0	930	15	0
33	Le	1053	0	1147	18	0
34	Lf	876	0	912	7	0
35	Lg	906	0	1000	7	0
36	Lh	1015	0	1148	11	0
37	Li	832	0	917	7	0
38	Lj	705	0	737	12	0
39	Lk	569	0	637	12	0
40	Ll	444	0	483	8	0
41	Lm	429	0	465	7	0
42	Ln	230	0	276	5	0
43	Lo	862	0	930	12	0
44	Lp	708	0	756	8	0
45	Lr	1002	0	1068	16	0
46	Lz	1741	0	1854	51	0
47	S2	36898	0	18601	610	0
48	SA	1741	0	1746	45	0
49	SB	1738	0	1809	40	0
50	SD	1765	0	1865	43	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
51	SE	2076	0	2177	51	0
52	SF	1495	0	1549	52	0
53	SH	1497	0	1590	44	0
54	SI	1686	0	1772	40	0
55	SK	827	0	854	32	0
56	SL	1247	0	1323	25	0
57	SP	1045	0	1095	28	0
58	SQ	1142	0	1213	39	0
59	SR	1090	0	1149	24	0
60	SS	1198	0	1261	39	0
61	ST	1112	0	1146	32	0
62	SU	821	0	883	26	0
63	SV	636	0	637	14	0
64	SX	1098	0	1167	26	0
65	Sa	821	0	870	21	0
66	Sc	506	0	536	22	0
67	Sd	459	0	449	19	0
68	Sg	2436	0	2393	72	0
69	SC	1725	0	1813	42	0
70	SG	1923	0	2089	56	0
71	SJ	1525	0	1640	39	0
72	SM	940	0	965	25	0
73	SN	1208	0	1294	19	0
74	SO	1049	0	1073	32	0
75	SW	1034	0	1080	16	0
76	SY	1065	0	1142	23	0
77	SZ	598	0	656	20	0
78	Sb	651	0	672	15	0
79	Se	459	0	503	10	0
80	Sf	548	0	554	11	0
81	CA	2764	0	2779	64	0
82	CB	6609	0	6685	132	0
83	CC	1589	0	810	62	0
84	CD	232	0	236	8	0
85	L5	211	0	0	0	0
85	L7	3	0	0	0	0
85	L8	4	0	0	0	0
85	LA	1	0	0	0	0
85	LI	1	0	0	0	0
85	LP	1	0	0	0	0
85	LV	1	0	0	0	0
85	Le	2	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	Lg	1	0	0	0	0
85	S2	30	0	0	0	0
85	SG	1	0	0	0	0
86	Lg	1	0	0	0	0
86	Lj	1	0	0	0	0
86	Lm	1	0	0	0	0
86	Lo	1	0	0	0	0
86	Lp	1	0	0	0	0
86	Sa	1	0	0	0	0
86	Sd	1	0	0	0	0
86	Sf	1	0	0	0	0
All	All	228566	0	171831	3047	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 8.

The worst 5 of 3047 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:L5:493:G:N1	1:L5:660:A:C2	2.16	1.14
1:L5:1443:A:C2	1:L5:2103:G:N1	2.16	1.14
1:L5:493:G:N1	1:L5:660:A:H2	1.45	1.13
47:S2:1455:A:H61	47:S2:1471:C:N4	1.46	1.10
57:SP:24:GLN:O	57:SP:28:MET:HB2	1.56	1.06

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
4	LA	246/257 (96%)	221 (90%)	24 (10%)	1 (0%)	30 59

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	LB	400/403 (99%)	374 (94%)	24 (6%)	2 (0%)	24	54
6	LC	366/427 (86%)	335 (92%)	31 (8%)	0	100	100
7	LD	291/297 (98%)	273 (94%)	18 (6%)	0	100	100
8	LE	232/288 (81%)	208 (90%)	24 (10%)	0	100	100
9	LF	223/248 (90%)	213 (96%)	10 (4%)	0	100	100
10	LG	239/266 (90%)	221 (92%)	18 (8%)	0	100	100
11	LH	188/192 (98%)	169 (90%)	19 (10%)	0	100	100
12	LI	198/214 (92%)	181 (91%)	17 (9%)	0	100	100
13	LJ	174/178 (98%)	154 (88%)	20 (12%)	0	100	100
14	LL	208/211 (99%)	192 (92%)	16 (8%)	0	100	100
15	LM	137/215 (64%)	127 (93%)	9 (7%)	1 (1%)	18	48
16	LN	201/204 (98%)	189 (94%)	10 (5%)	2 (1%)	12	39
17	LO	199/203 (98%)	190 (96%)	9 (4%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	174 (94%)	11 (6%)	0	100	100
20	LR	185/196 (94%)	179 (97%)	6 (3%)	0	100	100
21	LS	173/176 (98%)	159 (92%)	14 (8%)	0	100	100
22	LT	157/160 (98%)	146 (93%)	10 (6%)	1 (1%)	21	51
23	LU	99/128 (77%)	85 (86%)	13 (13%)	1 (1%)	12	39
24	LV	129/140 (92%)	121 (94%)	8 (6%)	0	100	100
25	LW	122/157 (78%)	117 (96%)	5 (4%)	0	100	100
26	LX	118/156 (76%)	112 (95%)	6 (5%)	0	100	100
27	LY	132/145 (91%)	120 (91%)	12 (9%)	0	100	100
28	LZ	133/136 (98%)	125 (94%)	8 (6%)	0	100	100
29	La	145/148 (98%)	136 (94%)	9 (6%)	0	100	100
30	Lb	105/159 (66%)	99 (94%)	6 (6%)	0	100	100
31	Lc	96/115 (84%)	89 (93%)	7 (7%)	0	100	100
32	Ld	105/125 (84%)	97 (92%)	8 (8%)	0	100	100
33	Le	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	16	44
34	Lf	107/110 (97%)	96 (90%)	9 (8%)	2 (2%)	6	23
35	Lg	112/117 (96%)	110 (98%)	2 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	98 (98%)	2 (2%)	0	100	100
38	Lj	84/97 (87%)	77 (92%)	6 (7%)	1 (1%)	10	34
39	Lk	67/70 (96%)	62 (92%)	5 (8%)	0	100	100
40	Ll	48/51 (94%)	45 (94%)	3 (6%)	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	103/106 (97%)	94 (91%)	9 (9%)	0	100	100
44	Lp	89/92 (97%)	84 (94%)	5 (6%)	0	100	100
45	Lr	123/137 (90%)	114 (93%)	9 (7%)	0	100	100
46	Lz	215/217 (99%)	171 (80%)	43 (20%)	1 (0%)	24	54
48	SA	219/295 (74%)	197 (90%)	21 (10%)	1 (0%)	24	54
49	SB	212/264 (80%)	197 (93%)	15 (7%)	0	100	100
50	SD	225/243 (93%)	201 (89%)	24 (11%)	0	100	100
51	SE	260/263 (99%)	243 (94%)	17 (6%)	0	100	100
52	SF	187/204 (92%)	166 (89%)	21 (11%)	0	100	100
53	SH	182/194 (94%)	162 (89%)	20 (11%)	0	100	100
54	SI	204/208 (98%)	195 (96%)	9 (4%)	0	100	100
55	SK	96/165 (58%)	87 (91%)	9 (9%)	0	100	100
56	SL	151/158 (96%)	138 (91%)	13 (9%)	0	100	100
57	SP	125/145 (86%)	111 (89%)	14 (11%)	0	100	100
58	SQ	142/146 (97%)	123 (87%)	19 (13%)	0	100	100
59	SR	133/135 (98%)	120 (90%)	13 (10%)	0	100	100
60	SS	143/152 (94%)	128 (90%)	15 (10%)	0	100	100
61	ST	141/145 (97%)	132 (94%)	8 (6%)	1 (1%)	18	48
62	SU	102/119 (86%)	92 (90%)	10 (10%)	0	100	100
63	SV	81/83 (98%)	74 (91%)	6 (7%)	1 (1%)	10	34
64	SX	139/143 (97%)	125 (90%)	12 (9%)	2 (1%)	9	30
65	Sa	100/115 (87%)	91 (91%)	8 (8%)	1 (1%)	12	39
66	Sc	62/69 (90%)	54 (87%)	8 (13%)	0	100	100
67	Sd	53/56 (95%)	47 (89%)	6 (11%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Sg	311/317 (98%)	272 (88%)	39 (12%)	0	100	100
69	SC	220/293 (75%)	205 (93%)	15 (7%)	0	100	100
70	SG	235/249 (94%)	218 (93%)	17 (7%)	0	100	100
71	SJ	183/194 (94%)	170 (93%)	13 (7%)	0	100	100
72	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
73	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
74	SO	138/151 (91%)	123 (89%)	15 (11%)	0	100	100
75	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
76	SY	129/133 (97%)	117 (91%)	12 (9%)	0	100	100
77	SZ	73/125 (58%)	60 (82%)	12 (16%)	1 (1%)	9	30
78	Sb	81/84 (96%)	73 (90%)	8 (10%)	0	100	100
79	Se	56/59 (95%)	54 (96%)	2 (4%)	0	100	100
80	Sf	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
81	CA	350/394 (89%)	337 (96%)	13 (4%)	0	100	100
82	CB	842/858 (98%)	787 (94%)	52 (6%)	3 (0%)	30	59
84	CD	30/408 (7%)	19 (63%)	11 (37%)	0	100	100
All	All	12768/14565 (88%)	11751 (92%)	994 (8%)	23 (0%)	44	72

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
64	SX	127	ASN
33	Le	73	GLY
61	ST	41	LYS
77	SZ	45	ASN

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%)	185 (97%)	5 (3%)	40	73
5	LB	348/349 (100%)	346 (99%)	2 (1%)	78	93
6	LC	306/348 (88%)	305 (100%)	1 (0%)	86	96
7	LD	246/250 (98%)	245 (100%)	1 (0%)	84	94
8	LE	209/252 (83%)	207 (99%)	2 (1%)	68	89
9	LF	194/215 (90%)	194 (100%)	0	100	100
10	LG	203/223 (91%)	203 (100%)	0	100	100
11	LH	169/171 (99%)	168 (99%)	1 (1%)	78	93
12	LI	172/181 (95%)	171 (99%)	1 (1%)	78	93
13	LJ	148/149 (99%)	145 (98%)	3 (2%)	48	78
14	LL	176/177 (99%)	175 (99%)	1 (1%)	78	93
15	LM	118/161 (73%)	116 (98%)	2 (2%)	53	82
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	172 (99%)	1 (1%)	78	93
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	162 (99%)	2 (1%)	63	86
20	LR	166/175 (95%)	166 (100%)	0	100	100
21	LS	156/157 (99%)	151 (97%)	5 (3%)	34	68
22	LT	139/140 (99%)	137 (99%)	2 (1%)	59	85
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	100 (99%)	1 (1%)	68	89
25	LW	103/126 (82%)	102 (99%)	1 (1%)	68	89
26	LX	108/133 (81%)	107 (99%)	1 (1%)	70	90
27	LY	124/135 (92%)	123 (99%)	1 (1%)	73	90
28	LZ	117/118 (99%)	117 (100%)	0	100	100
29	La	120/121 (99%)	119 (99%)	1 (1%)	73	90
30	Lb	88/126 (70%)	87 (99%)	1 (1%)	65	88
31	Lc	83/97 (86%)	82 (99%)	1 (1%)	63	86
32	Ld	98/110 (89%)	98 (100%)	0	100	100
33	Le	114/121 (94%)	113 (99%)	1 (1%)	70	90
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	88
35	Lg	98/100 (98%)	96 (98%)	2 (2%)	48	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
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%)	47 (98%)	1 (2%)	47	77
42	Ln	23/24 (96%)	23 (100%)	0	100	100
43	Lo	93/94 (99%)	93 (100%)	0	100	100
44	Lp	74/75 (99%)	74 (100%)	0	100	100
45	Lr	109/121 (90%)	108 (99%)	1 (1%)	70	90
46	Lz	195/196 (100%)	194 (100%)	1 (0%)	81	93
48	SA	183/243 (75%)	182 (100%)	1 (0%)	81	93
49	SB	195/231 (84%)	193 (99%)	2 (1%)	68	89
50	SD	190/202 (94%)	187 (98%)	3 (2%)	55	83
51	SE	224/225 (100%)	223 (100%)	1 (0%)	84	94
52	SF	159/170 (94%)	158 (99%)	1 (1%)	78	93
53	SH	166/174 (95%)	164 (99%)	2 (1%)	63	86
54	SI	178/180 (99%)	178 (100%)	0	100	100
55	SK	89/136 (65%)	89 (100%)	0	100	100
56	SL	137/142 (96%)	136 (99%)	1 (1%)	76	92
57	SP	113/130 (87%)	113 (100%)	0	100	100
58	SQ	119/121 (98%)	119 (100%)	0	100	100
59	SR	122/122 (100%)	122 (100%)	0	100	100
60	SS	126/132 (96%)	125 (99%)	1 (1%)	73	90
61	ST	113/115 (98%)	113 (100%)	0	100	100
62	SU	94/107 (88%)	93 (99%)	1 (1%)	65	88
63	SV	67/67 (100%)	66 (98%)	1 (2%)	57	84
64	SX	113/115 (98%)	112 (99%)	1 (1%)	70	90
65	Sa	89/98 (91%)	89 (100%)	0	100	100
66	Sc	57/62 (92%)	57 (100%)	0	100	100
67	Sd	48/49 (98%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Sg	272/275 (99%)	272 (100%)	0	100	100
69	SC	188/225 (84%)	185 (98%)	3 (2%)	55	83
70	SG	207/218 (95%)	207 (100%)	0	100	100
71	SJ	161/168 (96%)	160 (99%)	1 (1%)	78	93
72	SM	102/108 (94%)	102 (100%)	0	100	100
73	SN	130/131 (99%)	130 (100%)	0	100	100
74	SO	110/119 (92%)	110 (100%)	0	100	100
75	SW	112/113 (99%)	112 (100%)	0	100	100
76	SY	113/115 (98%)	113 (100%)	0	100	100
77	SZ	66/103 (64%)	66 (100%)	0	100	100
78	Sb	75/76 (99%)	75 (100%)	0	100	100
79	Se	47/48 (98%)	47 (100%)	0	100	100
80	Sf	60/140 (43%)	60 (100%)	0	100	100
81	CA	303/336 (90%)	303 (100%)	0	100	100
82	CB	723/730 (99%)	721 (100%)	2 (0%)	86	96
84	CD	19/328 (6%)	19 (100%)	0	100	100
All	All	11106/12391 (90%)	11042 (99%)	64 (1%)	76	93

5 of 64 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
64	SX	112	VAL
69	SC	112	VAL
21	LS	126	ILE
21	LS	85	ASP
69	SC	141	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 195 such sidechains are listed below:

Mol	Chain	Res	Type
52	SF	118	ASN
63	SV	35	ASN
53	SH	114	GLN
57	SP	24	GLN
68	Sg	117	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3704/5070 (73%)	968 (26%)	19 (0%)
2	L7	119/121 (98%)	15 (12%)	0
3	L8	155/157 (98%)	33 (21%)	1 (0%)
47	S2	1715/1869 (91%)	467 (27%)	8 (0%)
83	CC	74/75 (98%)	29 (39%)	3 (4%)
All	All	5767/7292 (79%)	1512 (26%)	31 (0%)

5 of 1512 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	15	A
1	L5	17	A
1	L5	25	A
1	L5	26	C

5 of 31 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	3614	G
47	S2	1434	C
1	L5	4378	A
83	CC	37	A
47	S2	563	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 264 ligands modelled in this entry, 264 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.

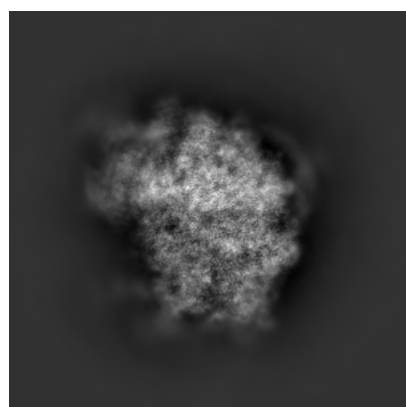
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11100. These allow visual inspection of the internal detail of the map and identification of artifacts.

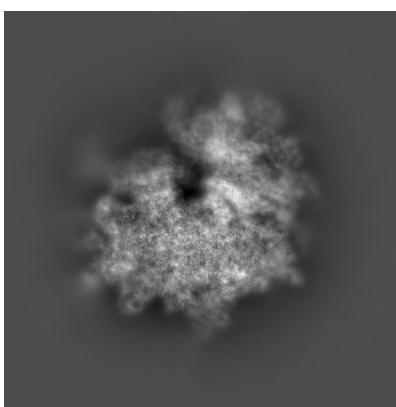
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

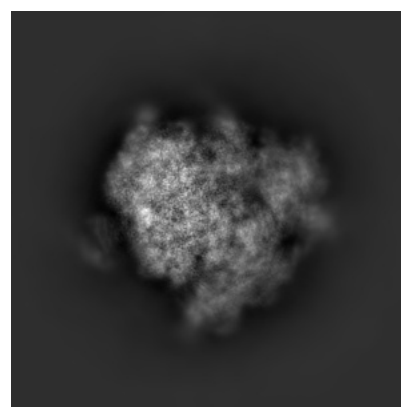
6.1.1 Primary map



X



Y

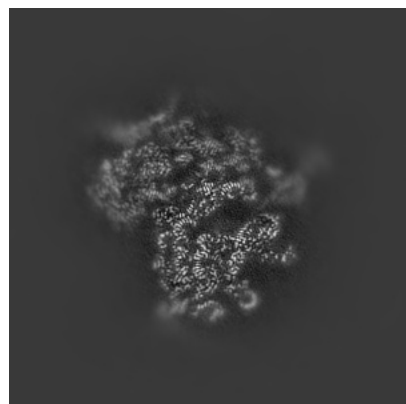


Z

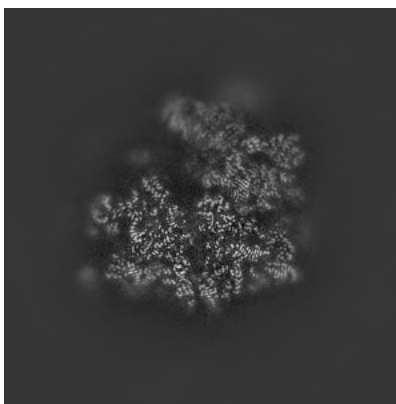
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

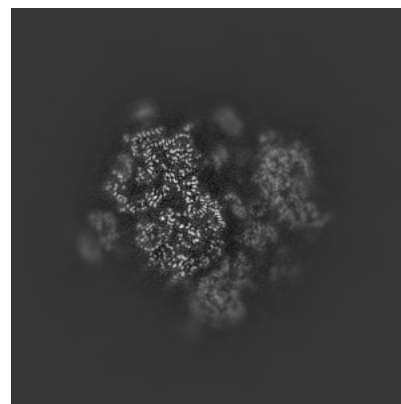
6.2.1 Primary map



X Index: 225



Y Index: 225

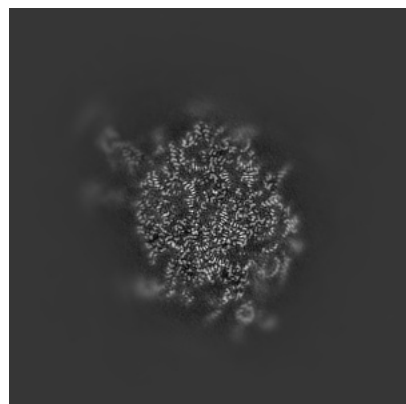


Z Index: 225

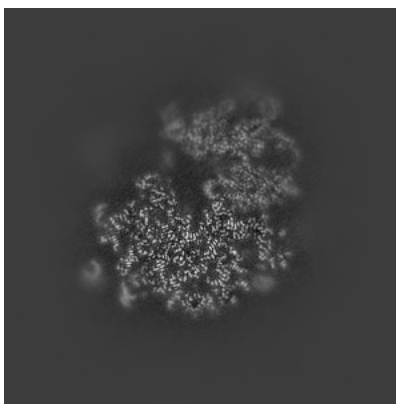
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

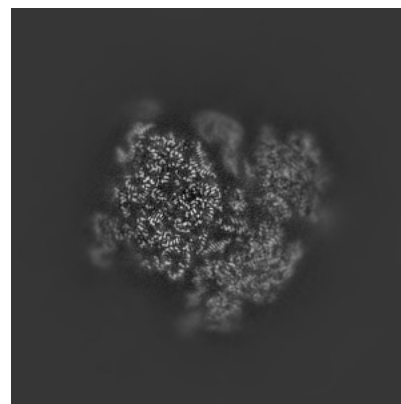
6.3.1 Primary map



X Index: 195



Y Index: 239

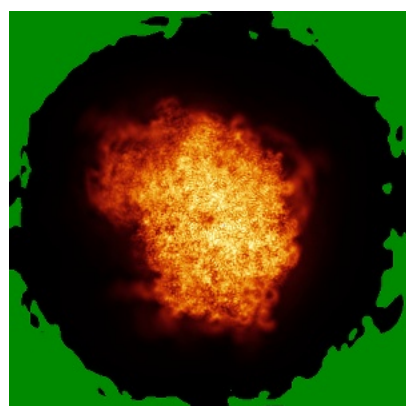


Z Index: 245

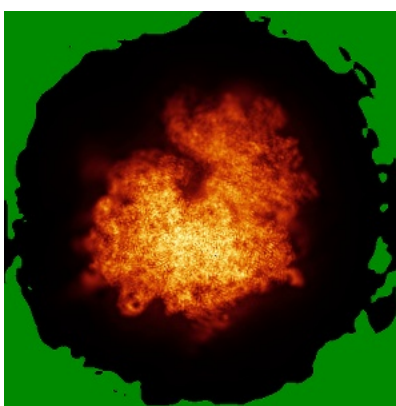
The images above show the largest variance slices of the map in three orthogonal directions.

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

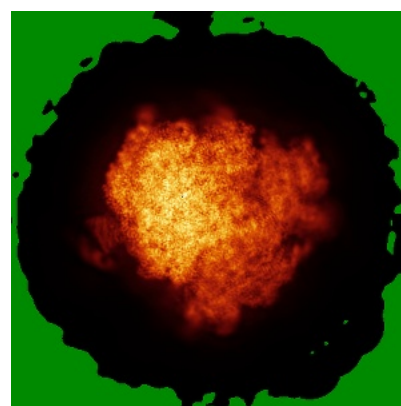
6.4.1 Primary map



X



Y

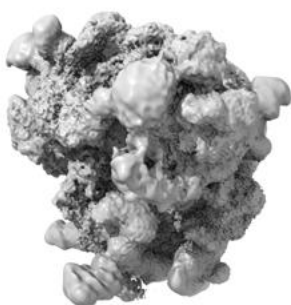


Z

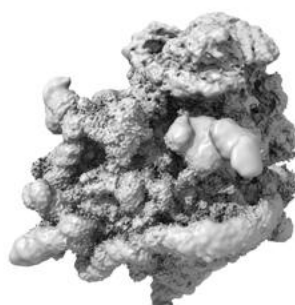
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

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.

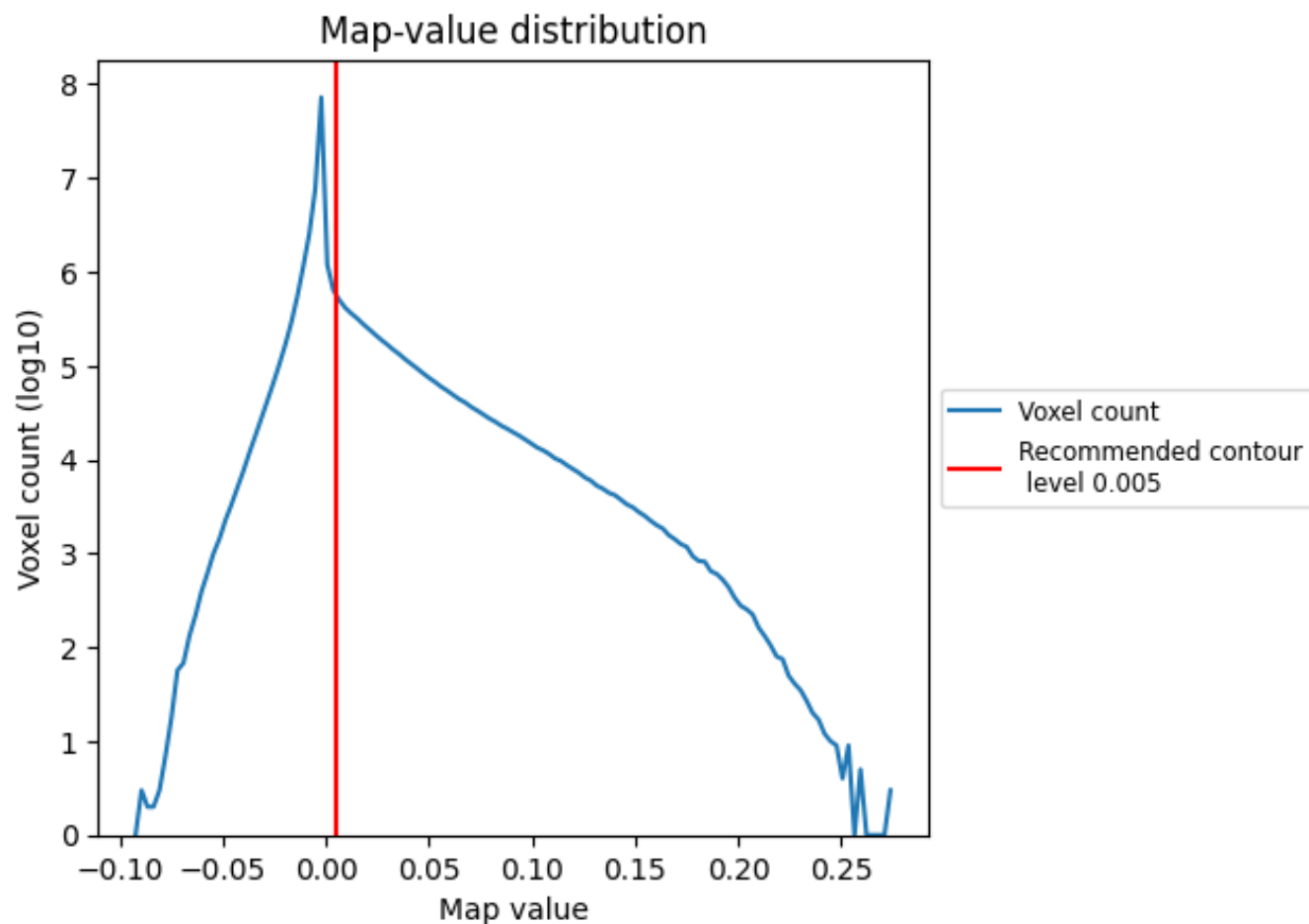
6.6 Mask visualisation [i](#)

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

7 Map analysis ⓘ

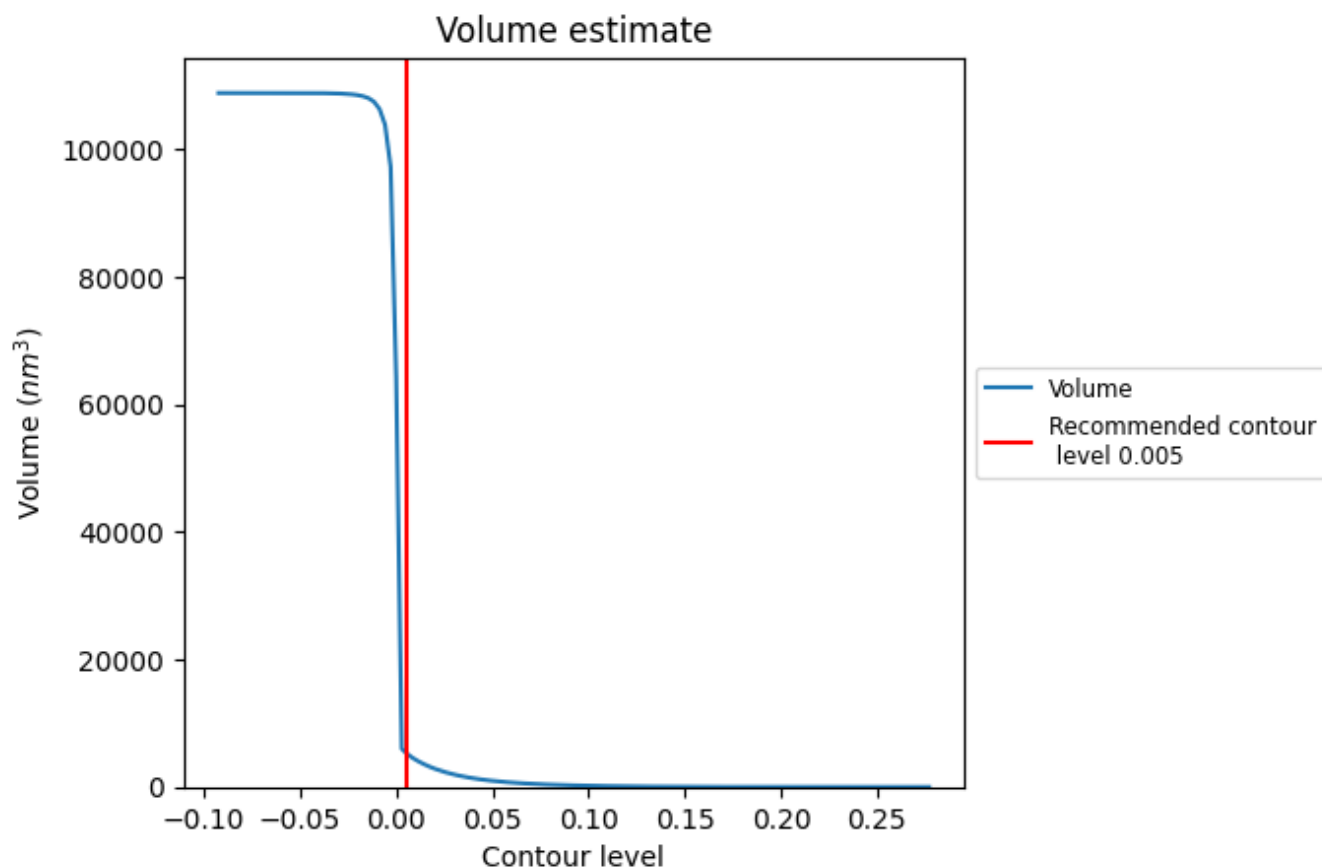
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution ⓘ



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

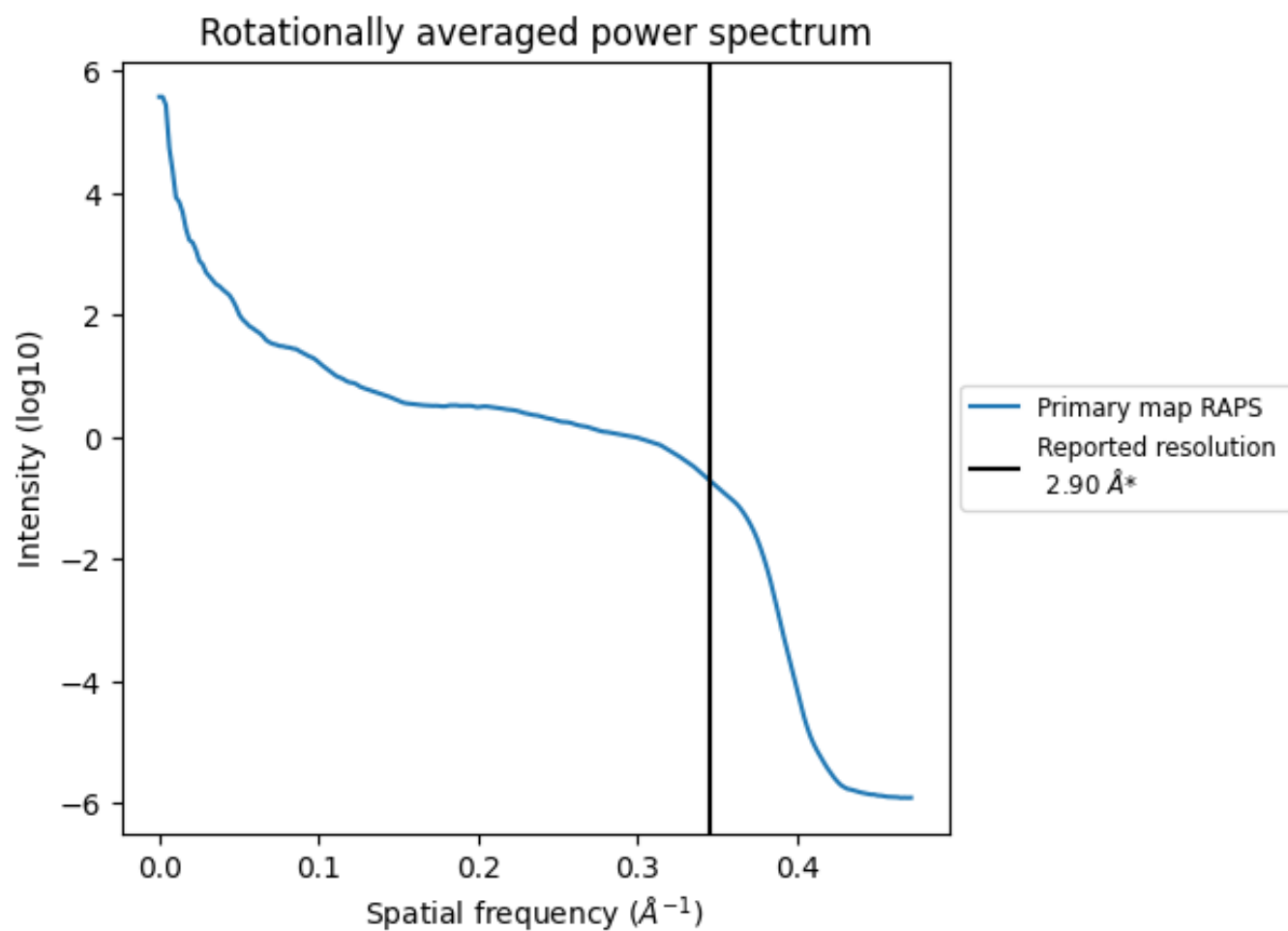
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5376 nm³; this corresponds to an approximate mass of 4856 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 ⓘ

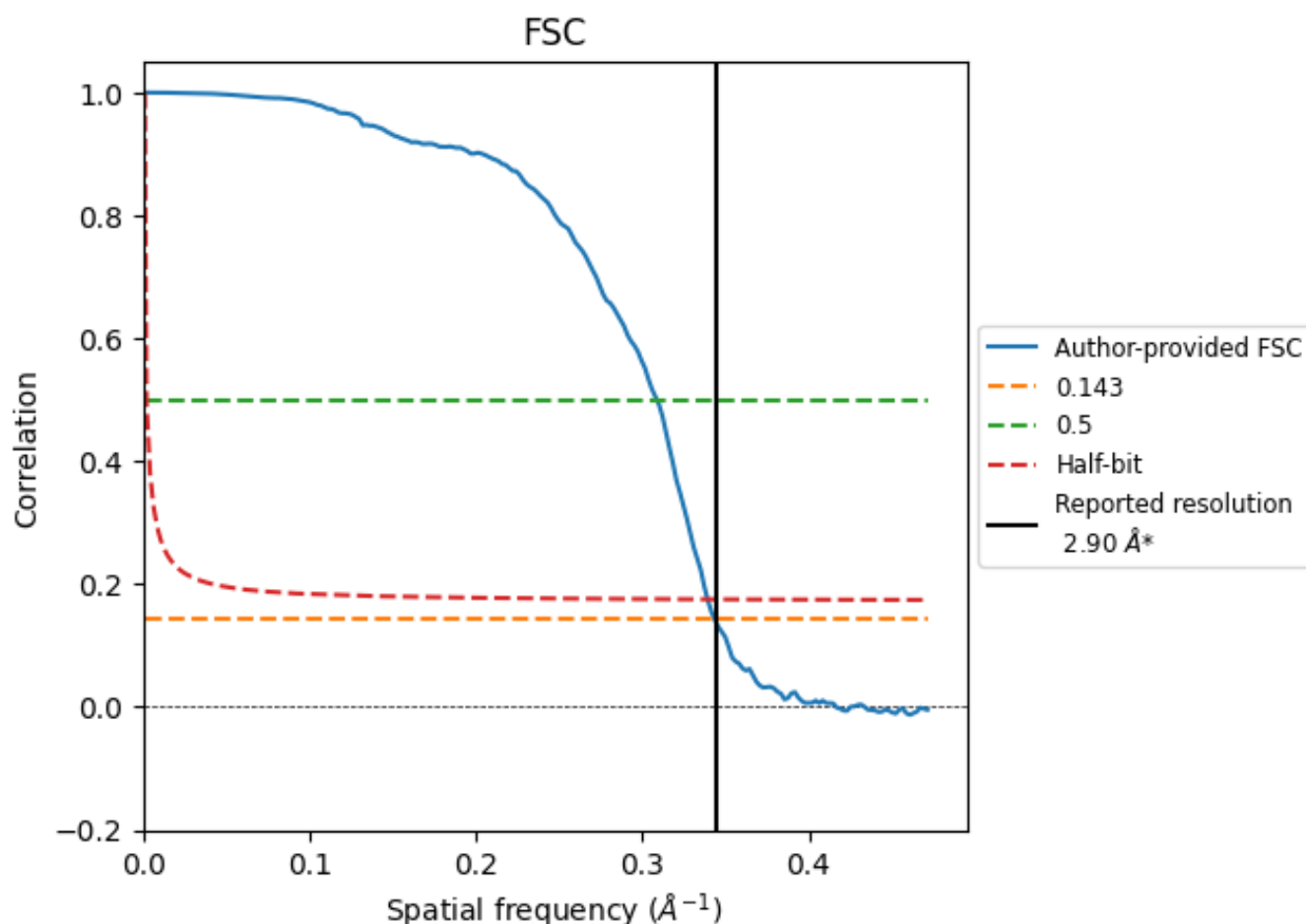


*Reported resolution corresponds to spatial frequency of 0.345 $\text{\AA}^{-1}$

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 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

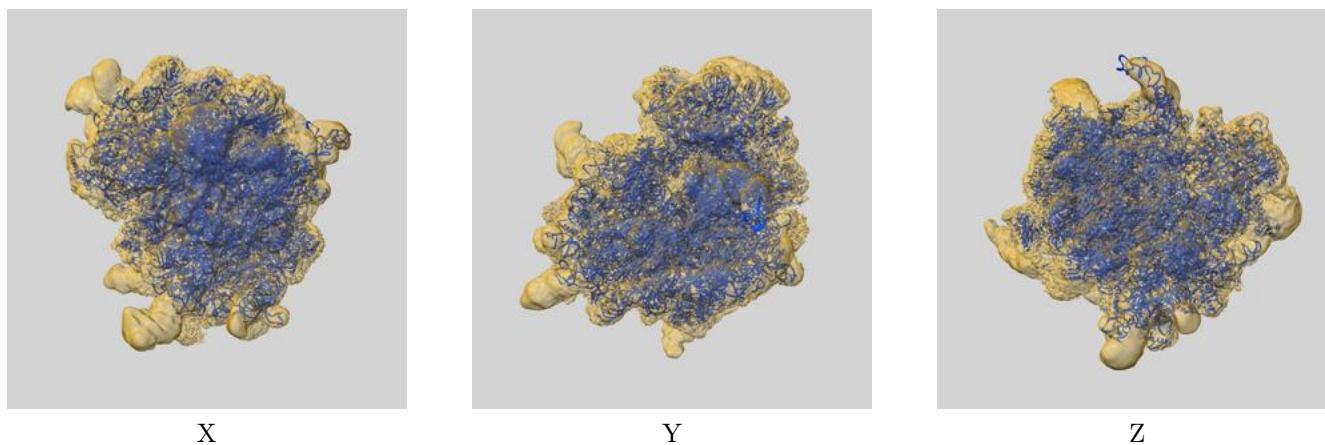
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	2.91	3.24	2.95
Unmasked-calculated*	-	-	-

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

9 Map-model fit [i](#)

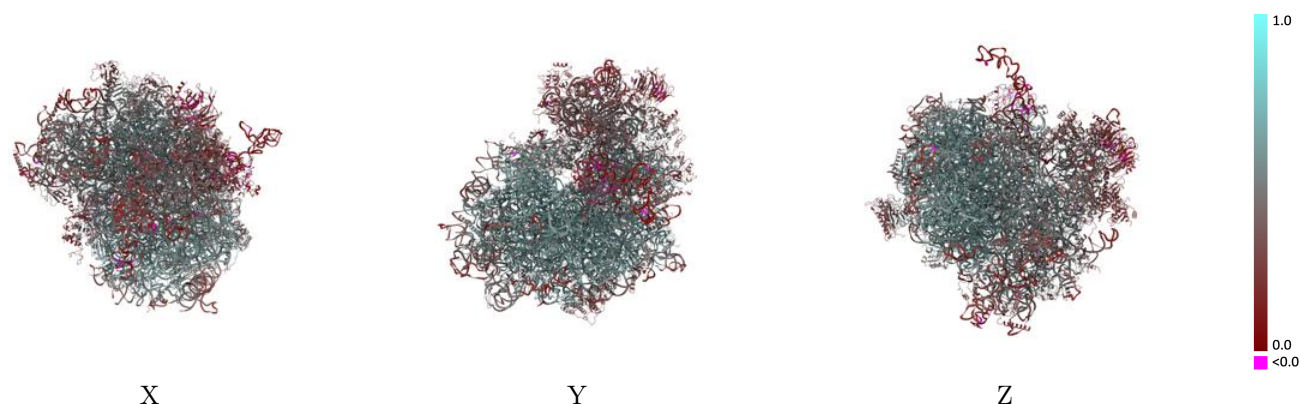
This section contains information regarding the fit between EMDB map EMD-11100 and PDB model 6Z6N. Per-residue inclusion information can be found in section [3](#) on page [21](#).

9.1 Map-model overlay [i](#)



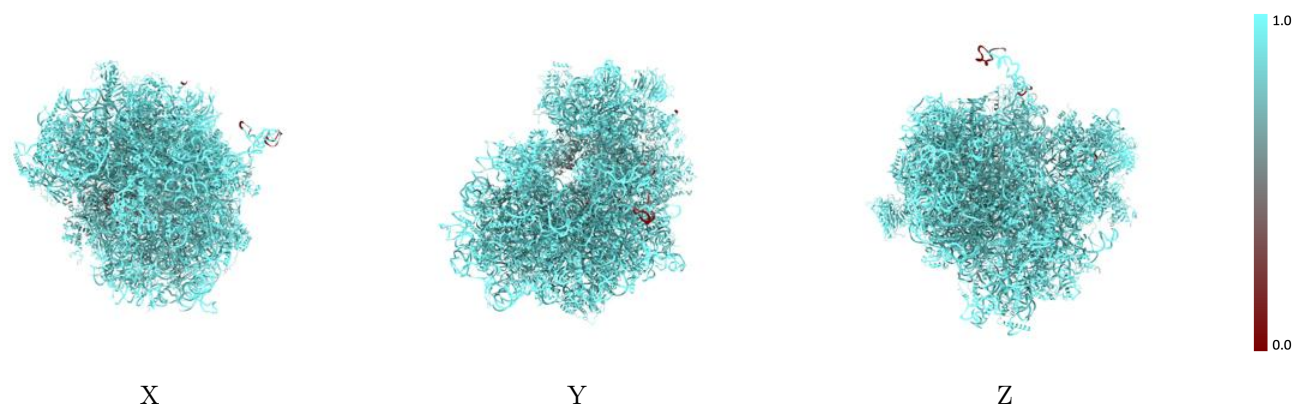
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



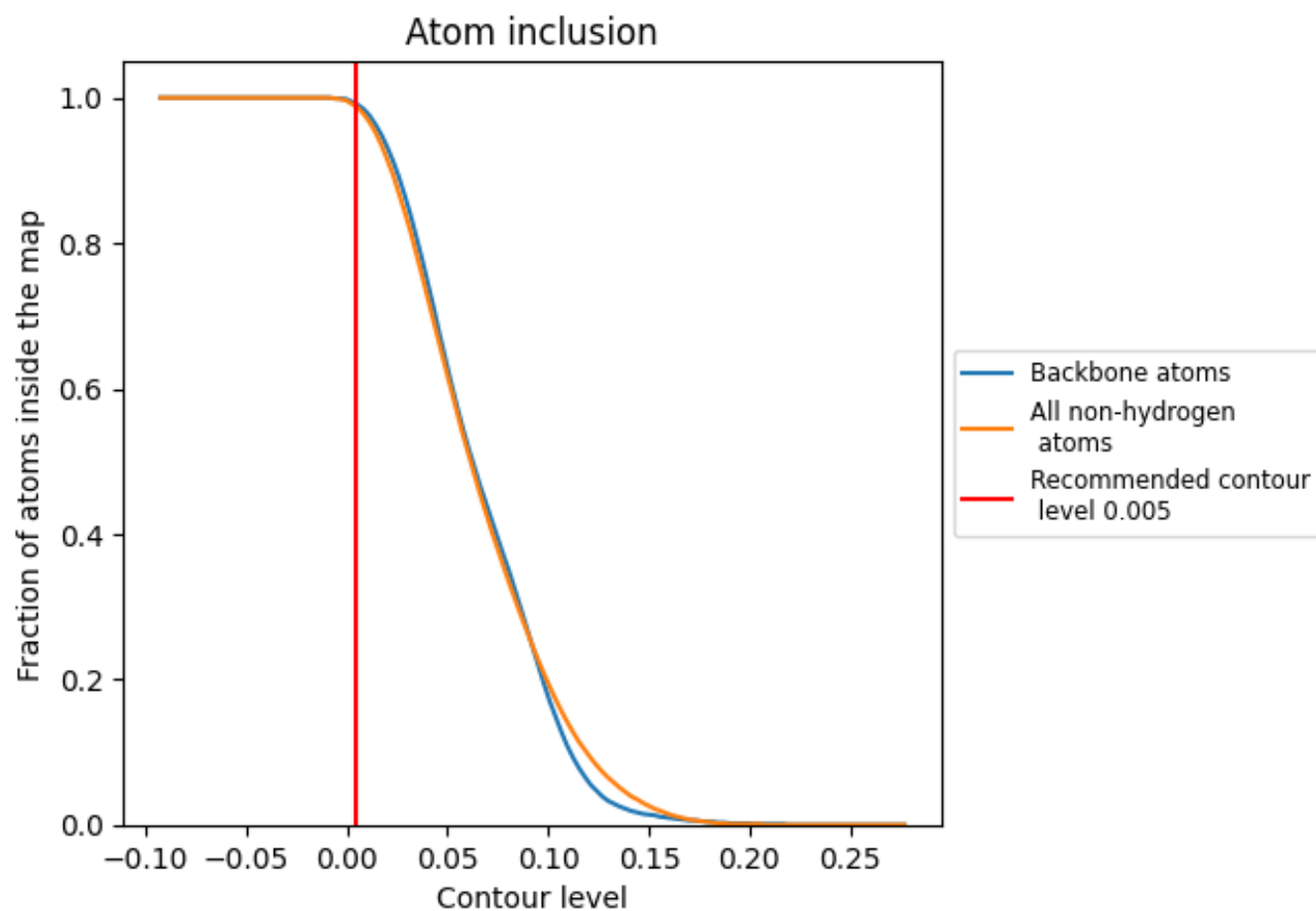
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 99% of all backbone atoms, 99% 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	 0.9870	 0.4910
CA	 0.9930	 0.3530
CB	 0.7870	 0.3720
CC	 0.9880	 0.2560
CD	 0.8690	 0.2290
L5	 0.9980	 0.5420
L7	 1.0000	 0.5960
L8	 0.9990	 0.5750
LA	 0.9920	 0.6150
LB	 0.9960	 0.5850
LC	 0.9970	 0.5800
LD	 0.9990	 0.5320
LE	 0.9960	 0.5020
LF	 0.9930	 0.5850
LG	 0.9920	 0.5020
LH	 0.9970	 0.5530
LI	 0.9910	 0.5740
LJ	 0.9920	 0.4600
LL	 0.9930	 0.5450
LM	 0.9970	 0.5460
LN	 0.9970	 0.6200
LO	 0.9960	 0.5950
LP	 0.9980	 0.6000
LQ	 0.9930	 0.6060
LR	 0.9830	 0.5280
LS	 0.9960	 0.6020
LT	 0.9930	 0.5750
LU	 0.9990	 0.4670
LV	 0.9900	 0.5980
LW	 0.9880	 0.4130
LX	 0.9960	 0.5670
LY	 0.9970	 0.5590
LZ	 1.0000	 0.5470
La	 0.9970	 0.6090
Lb	 0.9790	 0.5060



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Chain	Atom inclusion	Q-score
Lc	 0.9840	 0.5440
Ld	 0.9990	 0.5660
Le	 0.9920	 0.6120
Lf	 0.9980	 0.6140
Lg	 0.9970	 0.5780
Lh	 0.9930	 0.5440
Li	 0.9960	 0.5470
Lj	 0.9970	 0.6200
Lk	 0.9930	 0.5090
Ll	 0.9880	 0.6050
Lm	 0.9860	 0.5780
Ln	 0.9860	 0.5750
Lo	 0.9850	 0.5810
Lp	 0.9860	 0.5940
Lr	 0.9990	 0.5800
Lz	 0.9000	 0.1130
S2	 0.9990	 0.4420
SA	 0.9840	 0.4150
SB	 0.9940	 0.4580
SC	 0.9910	 0.4750
SD	 0.9840	 0.3170
SE	 0.9930	 0.4640
SF	 0.9790	 0.3610
SG	 0.9950	 0.3550
SH	 0.9860	 0.3570
SI	 0.9740	 0.4610
SJ	 0.9850	 0.4280
SK	 0.9980	 0.2590
SL	 0.9140	 0.5030
SM	 0.9180	 0.1690
SN	 0.9870	 0.5020
SO	 0.9420	 0.4720
SP	 0.9820	 0.2620
SQ	 0.9980	 0.3290
SR	 0.9870	 0.3540
SS	 0.9920	 0.3120
ST	 0.9920	 0.3090
SU	 0.9980	 0.2920
SV	 0.9980	 0.4250
SW	 0.9900	 0.5000
SX	 0.9830	 0.4770
SY	 0.9990	 0.3810

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Chain	Atom inclusion	Q-score
SZ	 0.9850	 0.2400
Sa	 0.9840	 0.5000
Sb	 0.9910	 0.4460
Sc	 0.9710	 0.3510
Sd	 0.9840	 0.3890
Se	 0.9820	 0.3920
Sf	 0.9960	 0.1540
Sg	 0.9830	 0.2050