



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:04 AM UTC

PDB ID : 6Z6M / pdb_00006z6m
EMDB ID : EMD-11099
Title : Cryo-EM structure of human 80S ribosomes bound to EBP1, eEF2 and SERBP1
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 : 3.10 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:

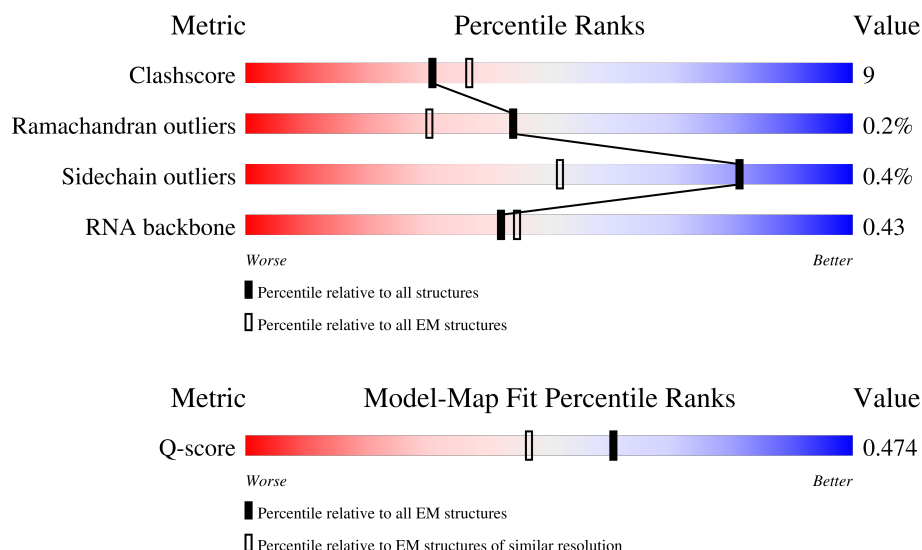
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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 3.10 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.



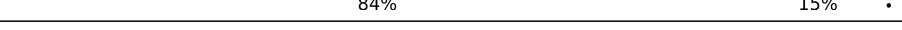
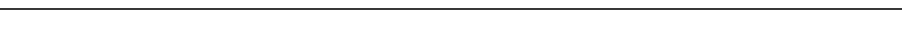
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	

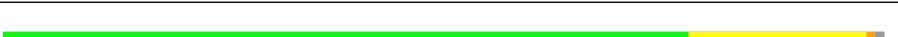
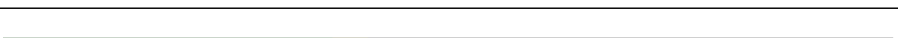
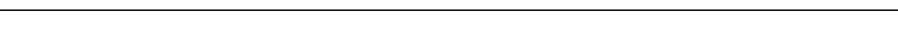
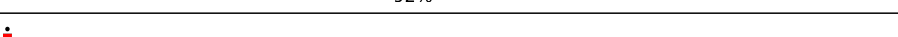
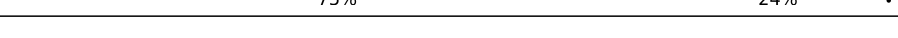
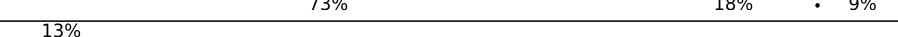
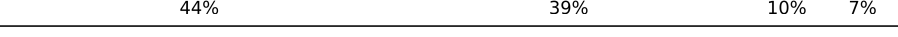
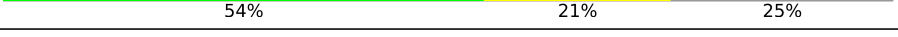
Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
4	LA	257	 83% 14% .
5	LB	403	 80% 19%
6	LC	427	 74% 12% 14%
7	LD	297	 81% 18% .
8	LE	288	 61% 21% 18%
9	LF	248	 73% 18% 9%
10	LG	266	 76% 15% 9%
11	LH	192	 77% 21% ..
12	LI	214	 70% 24% 6%
13	LJ	178	 74% 25% .
14	LL	211	 82% 18%
15	LM	215	 48% 15% . 35%
16	LN	204	 84% 15%
17	LO	203	 84% 15% .
18	LP	184	 71% 12% 17%
19	LQ	188	 84% 15% .
20	LR	196	 79% 16% . 5%
21	LS	176	 88% 11% .
22	LT	160	 82% 17% .
23	LU	128	 58% 21% 21%
24	LV	140	 75% 18% . 6%
25	LW	157	 59% 17% 25%
26	LX	156	 61% 16% 23%
27	LY	145	 72% 20% 8%
28	LZ	136	 74% 26% .

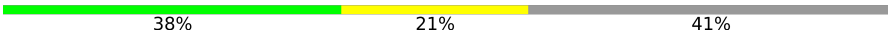
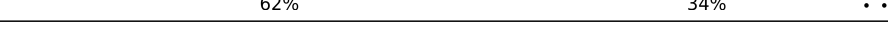
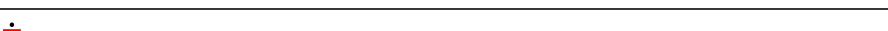
Continued on next page...

Continued from previous page...

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	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
54	SI	208	 80% 18% .
55	SK	165	 38% 21% 41%
56	SL	158	 73% 23% .
57	SP	145	 59% 23% . 17%
58	SQ	146	 64% 34% ..
59	SR	135	 76% 24%
60	SS	152	 59% 36% 5%
61	ST	145	 70% 29% .
62	SU	119	 65% 23% 13%
63	SV	83	 82% 17% .
64	SX	143	 80% 18% ..
65	Sa	115	 66% 22% . 11%
66	Sc	69	 46% 46% 7%
67	Sd	56	 62% 34% ..
68	Sg	317	 65% 33% .
69	SC	293	 59% 17% 24%
70	SG	249	 66% 29% 5%
71	SJ	194	 69% 27% 5%
72	SM	132	 56% 36% 8%
73	SN	151	 77% 23% .
74	SO	151	 75% 18% 7%
75	SW	130	 77% 22% .
76	SY	133	 71% 28% .
77	SZ	125	 41% 19% 40%
78	Sb	84	 80% 19% .

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
79	Se	59	 90%8%
80	Sf	156	 30%13%57%
81	CA	394	 63%26%10%
82	CB	858	 71%27%
83	CC	85	 51%34%15%
84	CD	408	 9%5%87%

2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 228884 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		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	2113	C	G	conflict	GB 86475748

- 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	118	Total	C	N	O	S	0	0
			965	604	199	158	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	121	Total	C	N	O	S	0	0
			985	623	185	170	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
			6605	4193	1136	1232	44		

- Molecule 83 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	CC	85	Total	C	N	O	P	0	0
			1813	808	322	598	85		

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

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

- 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	5	Total	Mg	0
			5	5	
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	LT	1	Total	Mg	0
			1	1	
85	LV	1	Total	Mg	0
			1	1	
85	Le	1	Total	Mg	0
			1	1	
85	Lg	1	Total	Mg	0
			1	1	
85	S2	29	Total	Mg	0
			29	29	
85	CC	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	

Continued on next page...

Continued from previous page...

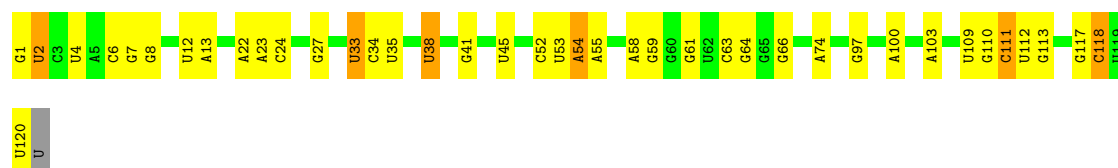
Mol	Chain	Residues	Atoms		AltConf
86	Lj	1	Total 1	Zn 1	0
86	Lm	1	Total 1	Zn 1	0
86	Lo	1	Total 1	Zn 1	0
86	Lp	1	Total 1	Zn 1	0
86	Sa	1	Total 1	Zn 1	0
86	Sd	1	Total 1	Zn 1	0
86	SM	1	Total 1	Zn 1	0





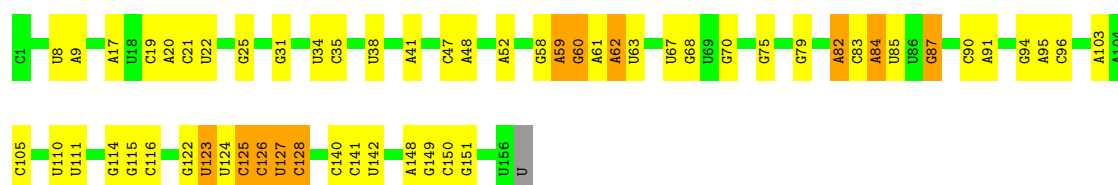
C5024	C4935	C4858	C4719	U4580	G4472	G4373	A4257	G4151	A4085	C3977	C3896	A3784	U3697
C5025	C4936	C4859	C4720	U4589	A4473	U4374	A4257	G4152	G4086	C3981	G3897	A3785	U3698
U5026	C4937	G4860	C4721	U4590	A4474	C4375	C4258	G4156	G4087	C3982	A3901	U3786	
C5027	C4940	G4861	A4723	U4591	A4475	A4376	C4259	A4156	G4088	C3983	A3906	G3787	U3709
G5028	C4941	G4862	A4724	U4592	C4476	C4377	U4260	C4162	G4089	C3984	A3907	G3788	G3710
C5029	G4942	G4863	G4725	U4593	A4477	A4378	C4261	U4163	G4090	G3985	G3908	A3711	A3711
U5030	C4943	G4864	G4726	U4594	G4478	A4379	U4262	U4164	G4091	G3986	G3909	U3712	
G5031	A4943	U4865	C4727	U4595	G4479	A4380	U4263	G4165	G4092	G3987	C3910	U3713	U3713
C5032	C4944	U4866	C4728	U4596	A4480	C4381	A4264	G4166	G4093	G3988	C3911	G3714	G3714
G5033	U4945	G4867	G4729	U4597	C4481	A4382	G4265	G4167	G4094	C3989	U3915	A3718	
A5034	U4946	C4871	G4730	U4598	C4482	A4383	U4266	U4168	G4095	C3990	G3916	A3719	
U5040	G4951	G4872	G4731	U4599	U4500	C4389	U4267	C4171	G4096	C3991	U3917	A3720	
G5041	C4952	U4873	C4732	U4600	C4504	A4390	G4268	G4172	G4097	G3992	U3918	A3721	
C5042	G4953	U4874	A4733	U4601	C4505	C4391	G4269	G4173	G4098	C3993	U3919	A3722	
U5043	U4954	G4875	G4734	C4602	C4506	A4392	U4270	G4174	G4099	C3994	U3920	A3723	
A5044	G4955	C4876	G4735	C4603	C4507	A4393	G4271	G4175	G4100	C3995	U3921	A3724	
C5045	U4956	U4877	G4736	G4604	U4508	G4401	U4272	G4176	G4101	C4000	U3922	G3725	
G5046	G4957	C4878	G4737	U4605	U4509	G4402	U4273	G4177	G4102	C4001	U3923	A3726	
U5047	C4958	U4879	G4738	U4606	C4510	G4403	U4274	G4178	G4103	C4002	U3924	A3727	
C5048	U4959	G4880	G4739	U4607	U4511	G4404	U4275	G4179	G4104	C4003	U3925	A3728	
U5049	C4960	U4881	C4740	U4608	U4512	G4405	U4276	G4180	G4105	U4004	U3926	U3729	
C5050	U4961	U4882	G4741	G4609	A4513	G4406	U4277	G4181	G4106	U4005	U3927		
U5051	C4962	C4883	A4742	U4610	A4514	G4407	U4278	G4182	G4107				
G5052	U4963	U4884	G4743	A4611	C4515	G4408	U4279	G4183	G4108				
C5053	U4964	G4885	G4744	G4612	C4516	G4409	U4280	G4184	G4109				
G5054	U4965	U4886	C4745	U4613	U4517	U4410	U4281	G4185	G4110				
U5055	C4966	C4887	G4746	U4614	A4518	U4411	U4282	G4186	U4111				
C5056	U4967	U4888	G4747	U4615	C4519	G4412	U4283	G4187	U4112				
G5057	C4968	C4889	C4748	U4616	U4520	G4413	U4284	G4188	U4113				
A5058	U4969	G4890	G4749	U4617	C4521	U4414	U4285	G4189	U4114				
U5059	C4970	U4891	C4750	U4618	U4522	G4415	U4286	G4190	U4115				
C5060	U4971	C4892	G4751	U4619	G4523	G4416	U4287	G4191	U4116				
U5061	C4972	U4893	G4752	U4620	U4524	U4417	U4288	G4192	U4117				
G5062	U4973	C4894	A4753	U4621	C4525	U4418	U4289	G4193	U4118				
C5063	C4974	U4895	G4754	U4622	U4526	U4419	U4290	G4194	U4119				
U5064	U4975	G4896	G4755	U4623	G4527	U4420	U4291	G4195	U4120				
C	C4976	C4897	C4756	U4624	U4528	U4421	U4292	G4196	U4121				
	G4981	G4900	G4757	U4625	U4529	U4422	U4293	G4197	U4122				
	U4982	C4901	C4758	U4626	U4530	U4423	U4294	G4198					
	U4983	C4902	G4759	U4627	U4531	U4424	U4295	G4199					
	U4984	C4903	G4760	U4628	U4532	U4425	U4296	G4200					
	U4985	C4904	C4761	U4629	U4533	U4426	U4297	G4201					
	U4986	C4905	G4762	U4630	U4534	U4427	U4298	G4202					
	U4987	C4906	G4763	U4631	U4535	U4428	U4299	G4203					
	U4988	C4907	C4764	U4632	U4536	U4429	U4300	G4204					
	U4989	C4908	C4765	U4633	U4537	U4430	U4301	G4205					
	U4990	C4909	C4766	U4634	U4538	U4431	U4302	G4206					
	U4991	C4910	C4767	U4635	U4539	U4432	U4303	G4207					
	U4992	C4911	C4768	U4636	U4540	U4433	U4304	G4208					
	C4993	C4912	C4769	U4637	U4541	U4434	U4305	G4209					
	U4994	C4913	U4770	U4638	U4542	U4435	U4306	G4210					
	U4995	C4914	C4771	U4639	U4543	U4436	U4307	G4211					
	U5006	C4915	C4772	U4640	U4544	U4437	U4308	G4212					
	A5007	C4916	C4773	U4641	U4545	U4438	U4309	G4213					
	C5013	C4917	C4774	U4642	U4546	U4439	U4310	G4214					
	A5014	C4918	C4775	U4643	U4547	U4440	U4311	G4215					
	G5015	C4919	C4776	U4644	U4548	U4441	U4312	G4216					
	A5016	C4920	C4777	U4645	U4549	U4442	U4313	G4217					
	G5017	C4921	C4778	U4646	U4550	U4443	U4314	G4218					
	C5018	C4922	C4779	U4647	U4551	U4444	U4315	G4219					
	A5019	C4923	C4780	U4648	U4552	U4445	U4316	G4220					
	U5022	C4924	C4781	U4649	U4553	U4446	U4317	G4221					
	C5023	C4925	C4782	U4650	U4554	U4447	U4318	G4222					
		C4926	C4783	U4651	U4555	U4448	U4319	G4223					
		U4927	C4784	U4652	U4556	U4449	U4320	G4224					
		C4928	C4785	U4653	U4557	U4450	U4321	G4225					
		C4929	C4786	U4654	U4558	U4451	U4322	G4226					
		C4930	C4787	U4655	U4559	U4452	U4323	G4227					
		U4931	C4788	U4656	U4560	U4453	U4324	G4228					
		C4932	C4789	U4657	U4561	U4454	U4325	G4229					
		C4933	C4790	U4658	U4562	U4455	U4326	G4230					
		C4934	C4791	U4659	U4563	U4456	U4327	G4231					
		C4935	C4792	U4660	U4564	U4457	U4328	G4232					
		C4936	C4793	U4661	U4565	U4458	U4329	G4233					
		C4937	C4794	U4662	U4566	U4459	U4330	G4234					
		C4938	C4795	U4663	U4567	U4460	U4331	G4235					
		C4939	C4796	U4664	U4568	U4461	U4332	G4236					
		C4940	C4797	U4665	U4569	U4462	U4333	G4237					
		C4941	C4798	U4666	U4570	U4463	U4334	G4238					
		C4942	C4799	U4667	U4571	U4464	U4335	G4239					
		C4943	C4800	U4668	U4572	U4465	U4336	G4240					
		C4944	U4601	U4669	U4573	U4466	U4337	G4241					
		C4945	U4602	U4670	U4574	U4467	U4338	G4242					
		C4946	C4603	U4671	U4575	U4468	U4339	G4243					
		C4947	G4604	U4672	U4576	U4469	U4340	G4244					
		C4948	U4605	U4673	U4577	U4470	U4341	G4245					
		C4949	U4606	U4674	U4578	U4471	U4342	G4246					
		C4950	U4607	U4675	U4579	U4472	U4343	G4247					
		C4951	U4608	U4676	U4580	U4473	U4344	G4248					
		C4952	U4609	U4677	U4581	U4474	U4345	G4249					
		C4953	U4610	U4678	U4582	U4475	U4346	G4250					
		C4954	U4611	U4679	U4583	U4476	U4347	G4251					
		C4955	U4612	U4680	U4584	U4477	U4348	G4252					
		C4956	U4613	U4681	U4585	U4478	U4349	G4253					
		C4957	U4614	U4682	U4586	U4479	U4350	G4254					
		C4958	U4615	U4683	U4587	U4480	U4351	G4255					
		C4959	U4616	U4684	U4588	U4481	U4352	G4256					
		C4960	U4617	U4685	U4589	U4482	U4353	G4257					
		C4961	U4618	U4686	U4590	U4483	U4354	G4258					
		C4962	U4619	U4687	U4591	U4484	U4355	G4259					
		C4963	U4620	U4688	U4592	U4485	U4356	G4260					
		C4964	U4621	U4689	U4593	U4486	U4357	G4261					
		C4965	U4622	U4690	U4594	U4487	U4358	G4262					
		C4966	U4623	U4691	U4595	U4488	U4359	G4263					
		C4967	U4624	U4692	U4596	U4489	U4360	G4264					
		C4968	U4625	U4693	U4597	U4490	U4361	G4265					
		C4969	U4626	U4694	U4598	U4491	U4362	G4266					
		C4970	U4627	U4695	U4599	U4492	U4363	G4267					
		C4971	U4628	U4696	U4600	U4493	U4364	G4268					
		C4972	U4629	U4697	U4601	U4494	U4365	G4269					
		C4973	U4630	U4698	U4602	U4495	U4366	G4270					
		C4974	U4631	U4699	U46								

Chain L7:  66% 28% 5% .



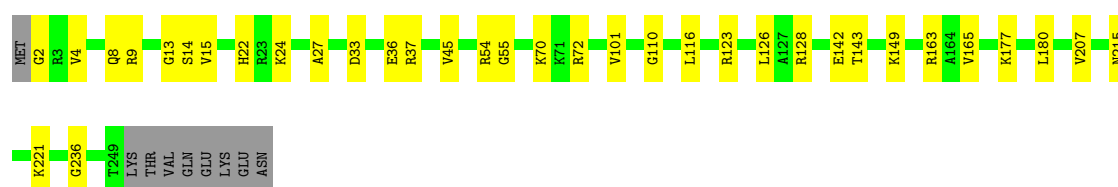
• Molecule 3: 5.8S rRNA

Chain L8:  62% 30% 7% .



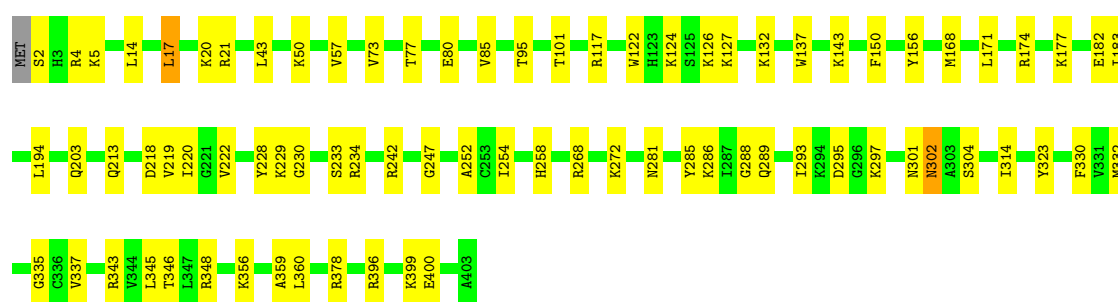
• Molecule 4: 60S ribosomal protein L8

Chain LA:  83% 14% .



• Molecule 5: 60S ribosomal protein L3

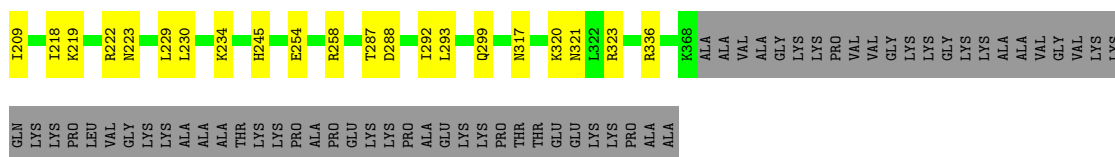
Chain LB:  80% 19% .



• Molecule 6: 60S ribosomal protein L4

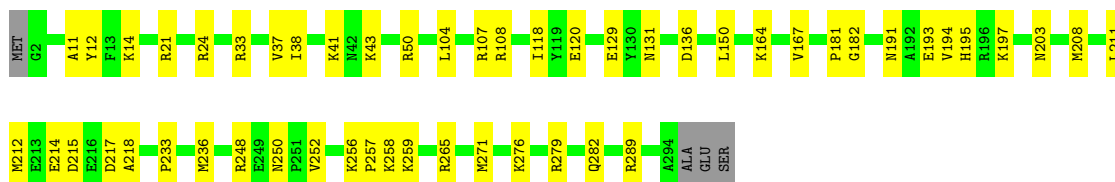
Chain LC:  74% 12% 14% .





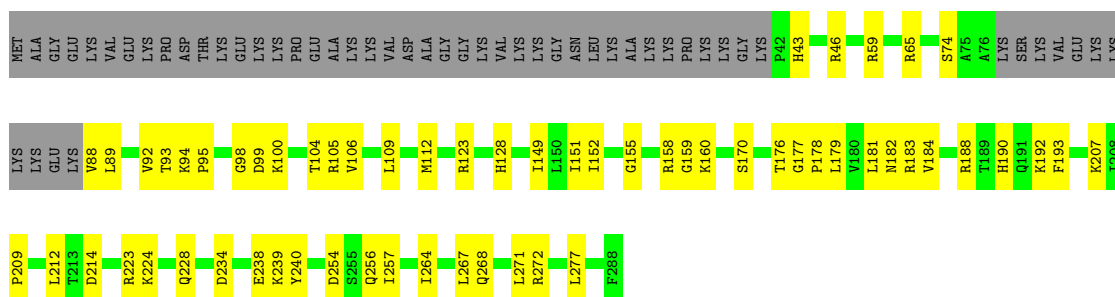
- Molecule 7: 60S ribosomal protein L5

Chain LD: 81% 18% .



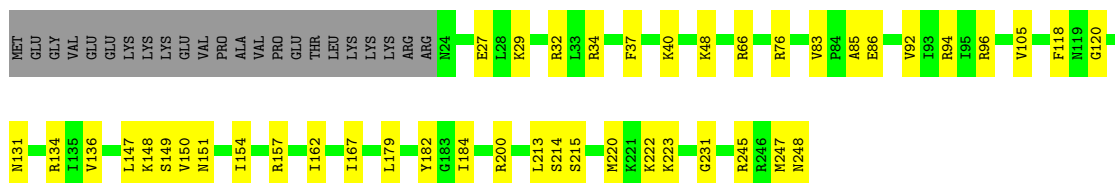
- Molecule 8: 60S ribosomal protein L6

Chain LE: 61% 21% 18%



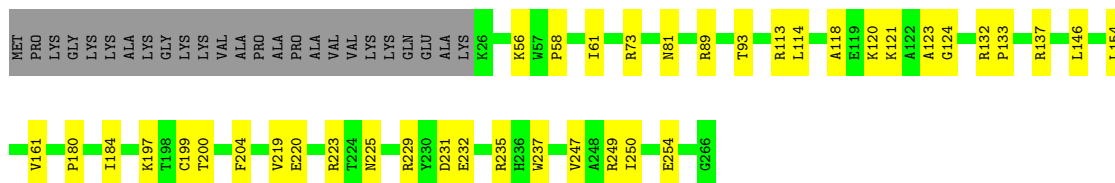
- Molecule 9: 60S ribosomal protein L7

Chain LF: 73% 18% 9%



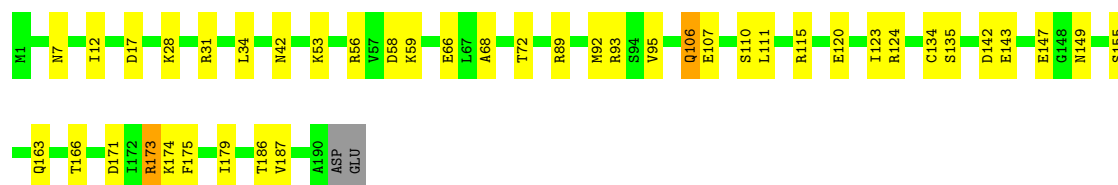
- Molecule 10: 60S ribosomal protein L7a

Chain LG: 76% 15% 9%



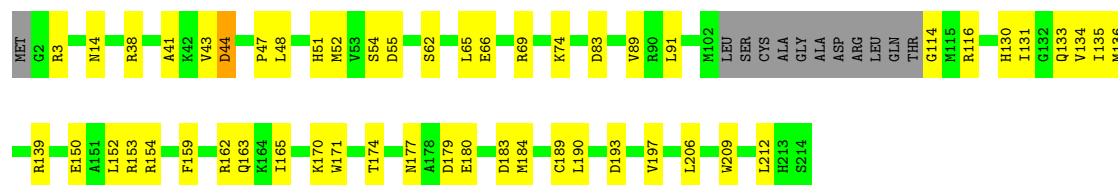
- Molecule 11: 60S ribosomal protein L9

Chain LH:  77% 21% ..



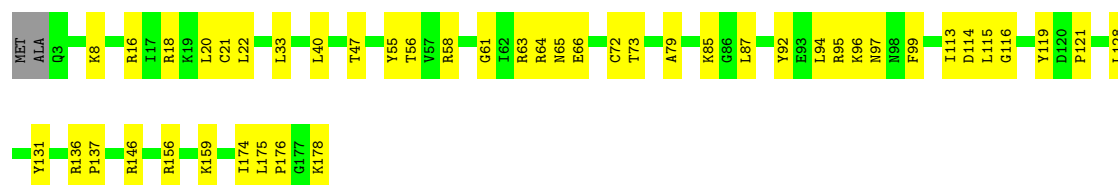
- Molecule 12: 60S ribosomal protein L10-like

Chain LI:  70% 24% 6%



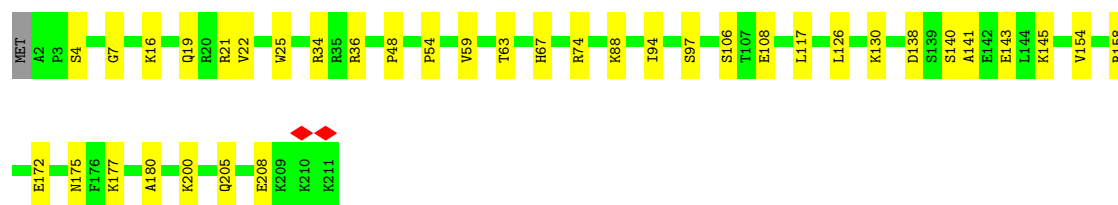
- Molecule 13: 60S ribosomal protein L11

Chain LJ:  74% 25% .



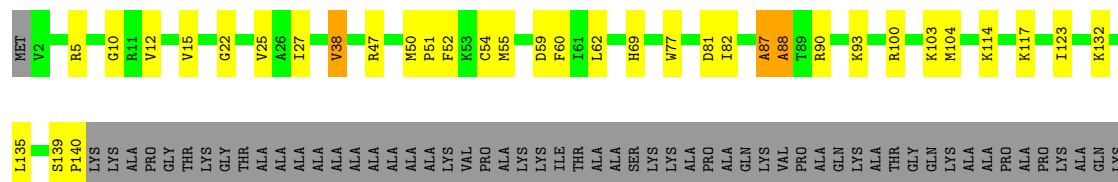
- Molecule 14: 60S ribosomal protein L13

Chain LL:  82% 18%



- Molecule 15: 60S ribosomal protein L14

Chain LM:  48% 15% 35%



GLY
GLN
LYS
ALA
PRO
ALA
GLN
LYS
ALA
PRO
ALA
LYS
LYS
ALA
SER
GLY
LYS
LYS
ALA

- Molecule 16: 60S ribosomal protein L15

Chain LN:  84% 15%

MET G2 A3 I7 Q8 E9 L10 K13 D17 K83 P84 V85 H86 H87 E103 L116 N117 S118 Y119 E123 D124 S125 T126 Y127 K128 E131 I135 I151 R162 H178 Y192 R193 N196 T197 L198 Q199 L200 Y203 R204

- Molecule 17: 60S ribosomal protein L13a

Chain LO:  84% 15%

MET ALA E3 V4 Q5 K25 R49 Y54 M65 P66 S67 F73 F80 T83 V84 R85 R94 D106 P110 P111 Y112 D113 K114 K115 L124 P131 V145 L174 M175 R176 L177 E186 K187 K188 I189 D190 K191 H199 L202 Y203

- Molecule 18: 60S ribosomal protein L17

Chain LP:  71% 12% 17%

MET V2 L6 D7 S14 T36 L53 R62 C70 A71 Q72 A73 K74 Q75 W76 K85 E89 F90 L91 L95 D108 A122 M125 R131 R135 M140 P143 L150 E154 G156 T157 L158 V159 P160 L161 G162 T163 L164 V165 L166 L167 L168 L169 L170 L171 L172 L173 L174 L175 L176 L177 L178 L179 L180 L181 L182 L183 L184 L185 L186 L187 L188 L189 L190 L191 L192 L193 L194 L195 L196 L197 L198 L199 L200 L201 L202 L203 L204 L205 L206 L207 L208 L209 L210 L211 L212 L213 L214 L215 L216 L217 L218 L219 L220 L221 L222 L223 L224 L225 L226 L227 L228 L229 L230 L231 L232 L233 L234 L235 L236 L237 L238 L239 L240 L241 L242 L243 L244 L245 L246 L247 L248 L249 L250 L251 L252 L253 L254 L255 L256 L257 L258 L259 L260 L261 L262 L263 L264 L265 L266 L267 L268 L269 L270 L271 L272 L273 L274 L275 L276 L277 L278 L279 L280 L281 L282 L283 L284 L285 L286 L287 L288 L289 L290 L291 L292 L293 L294 L295 L296 L297 L298 L299 L300 L301 L302 L303 L304 L305 L306 L307 L308 L309 L310 L311 L312 L313 L314 L315 L316 L317 L318 L319 L320 L321 L322 L323 L324 L325 L326 L327 L328 L329 L330 L331 L332 L333 L334 L335 L336 L337 L338 L339 L340 L341 L342 L343 L344 L345 L346 L347 L348 L349 L350 L351 L352 L353 L354 L355 L356 L357 L358 L359 L360 L361 L362 L363 L364 L365 L366 L367 L368 L369 L370 L371 L372 L373 L374 L375 L376 L377 L378 L379 L380 L381 L382 L383 L384 L385 L386 L387 L388 L389 L390 L391 L392 L393 L394 L395 L396 L397 L398 L399 L400 L401 L402 L403 L404 L405 L406 L407 L408 L409 L410 L411 L412 L413 L414 L415 L416 L417 L418 L419 L420 L421 L422 L423 L424 L425 L426 L427 L428 L429 L430 L431 L432 L433 L434 L435 L436 L437 L438 L439 L440 L441 L442 L443 L444 L445 L446 L447 L448 L449 L450 L451 L452 L453 L454 L455 L456 L457 L458 L459 L460 L461 L462 L463 L464 L465 L466 L467 L468 L469 L470 L471 L472 L473 L474 L475 L476 L477 L478 L479 L480 L481 L482 L483 L484 L485 L486 L487 L488 L489 L490 L491 L492 L493 L494 L495 L496 L497 L498 L499 L500 L501 L502 L503 L504 L505 L506 L507 L508 L509 L510 L511 L512 L513 L514 L515 L516 L517 L518 L519 L520 L521 L522 L523 L524 L525 L526 L527 L528 L529 L530 L531 L532 L533 L534 L535 L536 L537 L538 L539 L540 L541 L542 L543 L544 L545 L546 L547 L548 L549 L550 L551 L552 L553 L554 L555 L556 L557 L558 L559 L560 L561 L562 L563 L564 L565 L566 L567 L568 L569 L570 L571 L572 L573 L574 L575 L576 L577 L578 L579 L580 L581 L582 L583 L584 L585 L586 L587 L588 L589 L590 L591 L592 L593 L594 L595 L596 L597 L598 L599 L600 L601 L602 L603 L604 L605 L606 L607 L608 L609 L610 L611 L612 L613 L614 L615 L616 L617 L618 L619 L620 L621 L622 L623 L624 L625 L626 L627 L628 L629 L630 L631 L632 L633 L634 L635 L636 L637 L638 L639 L640 L641 L642 L643 L644 L645 L646 L647 L648 L649 L650 L651 L652 L653 L654 L655 L656 L657 L658 L659 L660 L661 L662 L663 L664 L665 L666 L667 L668 L669 L670 L671 L672 L673 L674 L675 L676 L677 L678 L679 L680 L681 L682 L683 L684 L685 L686 L687 L688 L689 L690 L691 L692 L693 L694 L695 L696 L697 L698 L699 L700 L701 L702 L703 L704 L705 L706 L707 L708 L709 L710 L711 L712 L713 L714 L715 L716 L717 L718 L719 L720 L721 L722 L723 L724 L725 L726 L727 L728 L729 L730 L731 L732 L733 L734 L735 L736 L737 L738 L739 L740 L741 L742 L743 L744 L745 L746 L747 L748 L749 L750 L751 L752 L753 L754 L755 L756 L757 L758 L759 L760 L761 L762 L763 L764 L765 L766 L767 L768 L769 L770 L771 L772 L773 L774 L775 L776 L777 L778 L779 L780 L781 L782 L783 L784 L785 L786 L787 L788 L789 L790 L791 L792 L793 L794 L795 L796 L797 L798 L799 L800 L801 L802 L803 L804 L805 L806 L807 L808 L809 L810 L811 L812 L813 L814 L815 L816 L817 L818 L819 L820 L821 L822 L823 L824 L825 L826 L827 L828 L829 L830 L831 L832 L833 L834 L835 L836 L837 L838 L839 L840 L841 L842 L843 L844 L845 L846 L847 L848 L849 L850 L851 L852 L853 L854 L855 L856 L857 L858 L859 L860 L861 L862 L863 L864 L865 L866 L867 L868 L869 L870 L871 L872 L873 L874 L875 L876 L877 L878 L879 L880 L881 L882 L883 L884 L885 L886 L887 L888 L889 L890 L891 L892 L893 L894 L895 L896 L897 L898 L899 L900 L901 L902 L903 L904 L905 L906 L907 L908 L909 L910 L911 L912 L913 L914 L915 L916 L917 L918 L919 L920 L921 L922 L923 L924 L925 L926 L927 L928 L929 L930 L931 L932 L933 L934 L935 L936 L937 L938 L939 L940 L941 L942 L943 L944 L945 L946 L947 L948 L949 L950 L951 L952 L953 L954 L955 L956 L957 L958 L959 L960 L961 L962 L963 L964 L965 L966 L967 L968 L969 L970 L971 L972 L973 L974 L975 L976 L977 L978 L979 L980 L981 L982 L983 L984 L985 L986 L987 L988 L989 L990 L991 L992 L993 L994 L995 L996 L997 L998 L999 L1000

- Molecule 19: 60S ribosomal protein L18

Chain LQ:  84% 15%

MET G2 R14 L35 R65 M66 L72 P73 T79 V83 D89 V90 R91 L103 R108 T122 F123 D124 Q125 T136 R143 K144 G145 R146 Y149 A155 T158 P159 H160 R172 K173 N188

- Molecule 20: 60S ribosomal protein L19

Chain LR:  79% 16% 5%

MET S2 M3 L4 R5 S13 Y14 L15 K20 K21 N30 N34 R38 I45 K46 R52 V55 K82 R103 R104 L105 L106 D116 K128 M134 L138 H143 R163 A169 R170 K171 R172 R173 R174 E175 R176 L177 Q178 A179 K180 K181 I185

K186 T187 L188 SER LYS GLU GLU THR LYS LYS

- Molecule 21: 60S ribosomal protein L18a

Chain LS:  88% 11%



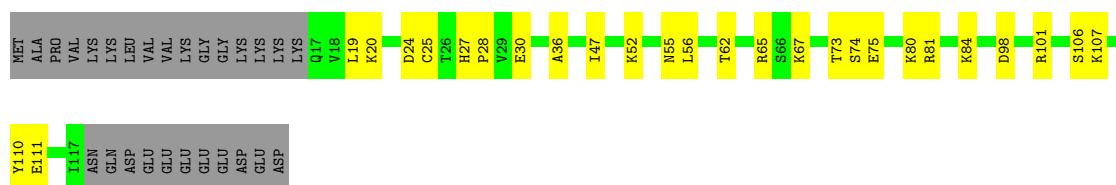
- Molecule 22: 60S ribosomal protein L21

Chain LT: 82% 17% .



- Molecule 23: 60S ribosomal protein L22

Chain LU: 58% 21% 21%



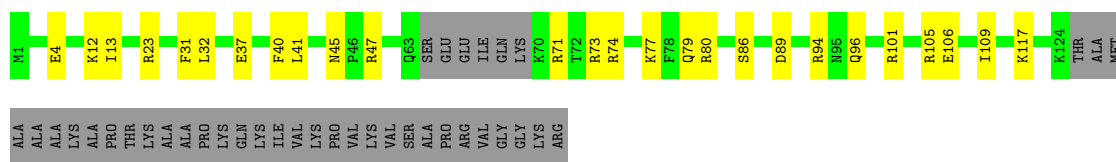
- Molecule 24: 60S ribosomal protein L23

Chain LV: 75% 18% 6%



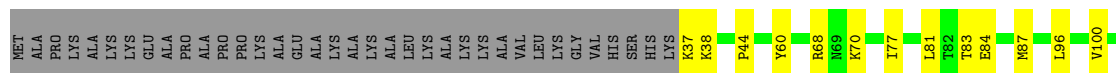
- Molecule 25: 60S ribosomal protein L24

Chain LW: 59% 17% 25%



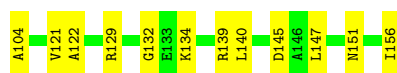
- Molecule 26: 60S ribosomal protein L23a

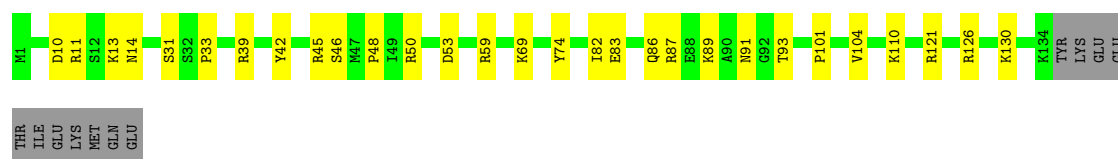
Chain LX: 61% 16% 23%



- Molecule 27: 60S ribosomal protein L26

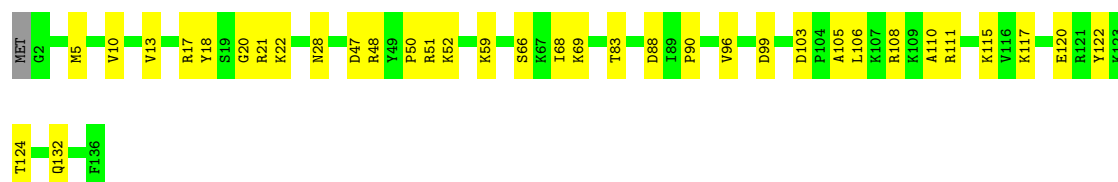
Chain LY: 72% 20% 8%





- Molecule 28: 60S ribosomal protein L27

Chain LZ: 74% 26%



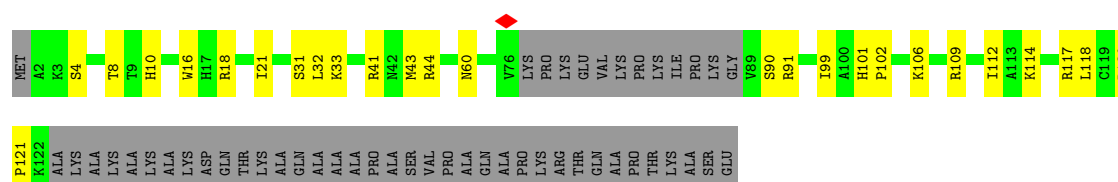
- Molecule 29: 60S ribosomal protein L27a

Chain La: 78% 21%



- Molecule 30: 60S ribosomal protein L29

Chain Lb: 52% 16% 31%



- Molecule 31: 60S ribosomal protein L30

Chain Lc: 69% 16% 15%



- Molecule 32: 60S ribosomal protein L31

Chain Ld: 69% 17% 14%



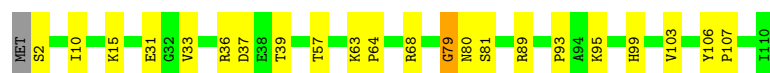
- Molecule 33: 60S ribosomal protein L32

Chain Le:  76% 16% 5%



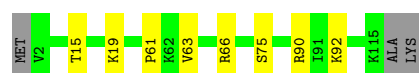
- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  79% 19% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg:  91% 7% .



- Molecule 36: 60S ribosomal protein L35

Chain Lh:  82% 17% .



- Molecule 37: 60S ribosomal protein L36

Chain Li:  85% 12% .



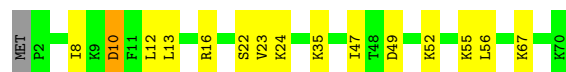
- Molecule 38: 60S ribosomal protein L37

Chain Lj:  66% 21% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  77% 20% ..



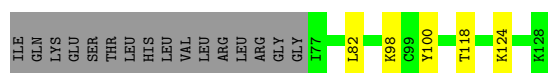
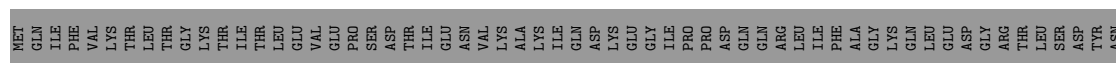
- Molecule 40: 60S ribosomal protein L39

Chain Ll:  76% 22% .



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm:  37% 59%



- Molecule 42: 60S ribosomal protein L41

Chain Ln:  92% . .



- Molecule 43: 60S ribosomal protein L36a

Chain Lo:  75% 24% .



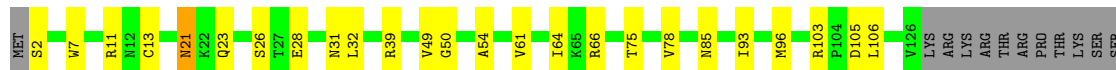
- Molecule 44: 60S ribosomal protein L37a

Chain Lp:  85% 14% .



- Molecule 45: 60S ribosomal protein L28

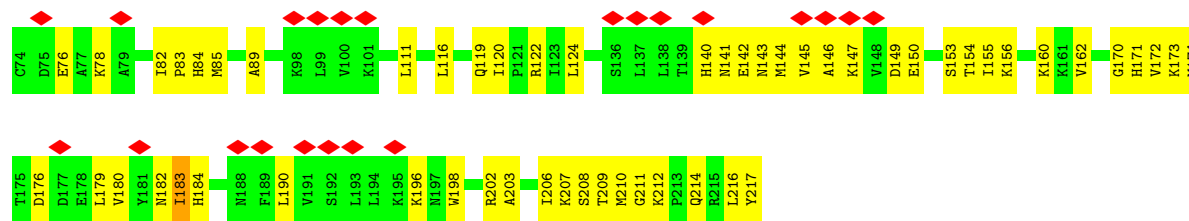
Chain Lr:  73% 18% 9%



- Molecule 46: 60S ribosomal protein L10a

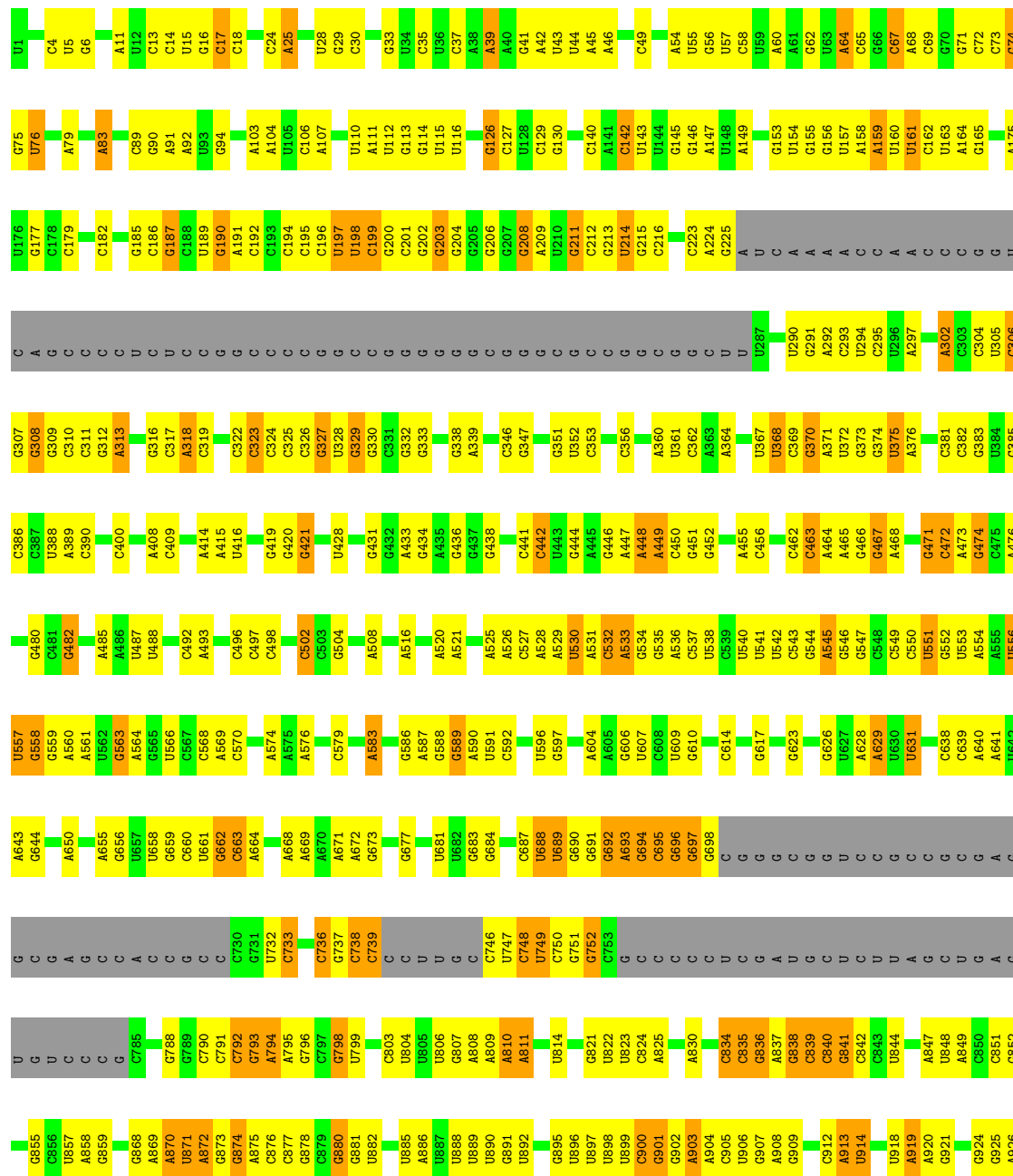
Chain Lz:  13% 59% 40%



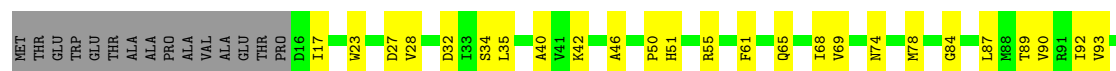


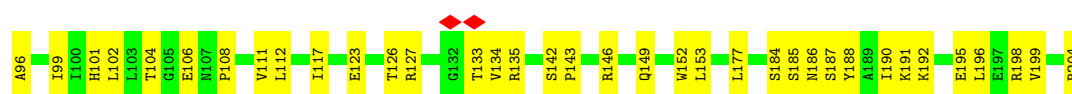
• Molecule 47: 18S rRNA

Chain S2: 44% 39% 10% 7%

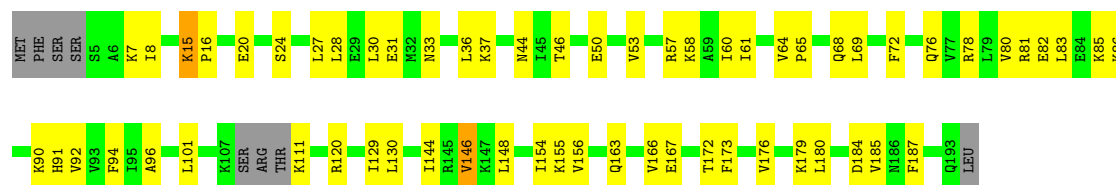




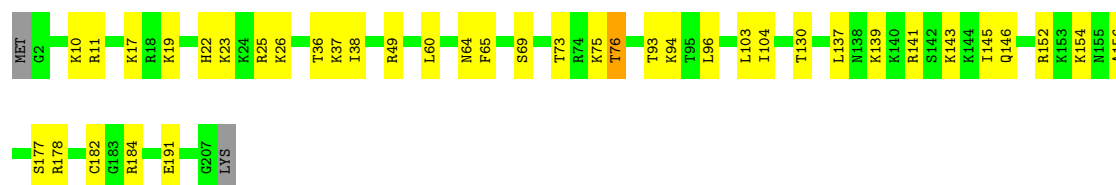
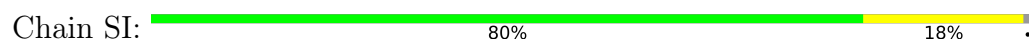




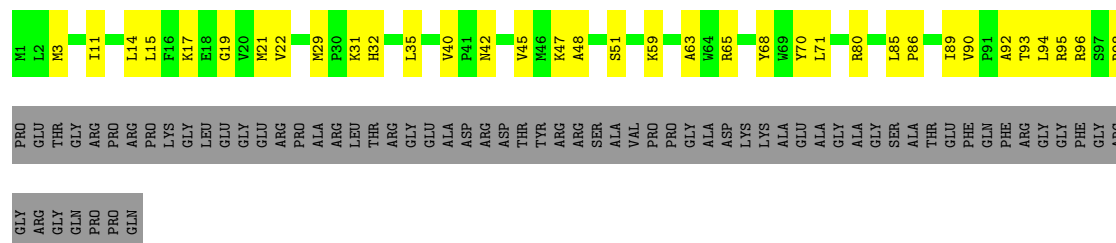
- Molecule 53: 40S ribosomal protein S7



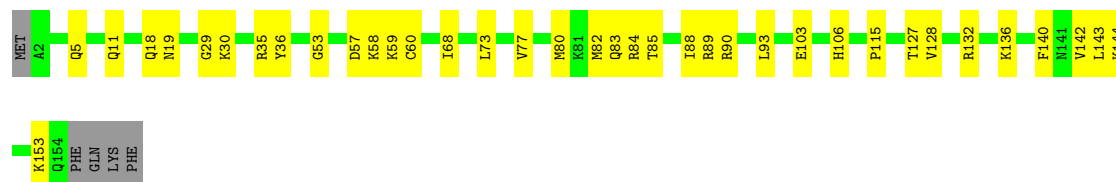
- Molecule 54: 40S ribosomal protein S8



- Molecule 55: 40S ribosomal protein S10

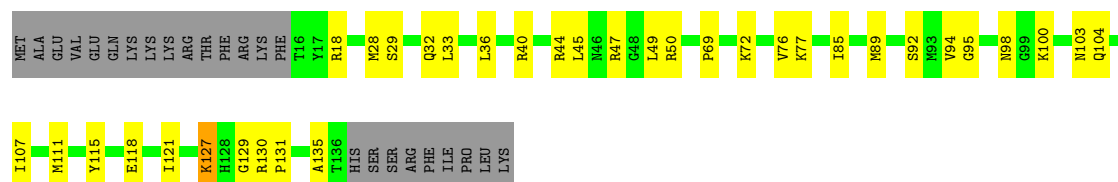


- Molecule 56: 40S ribosomal protein S11



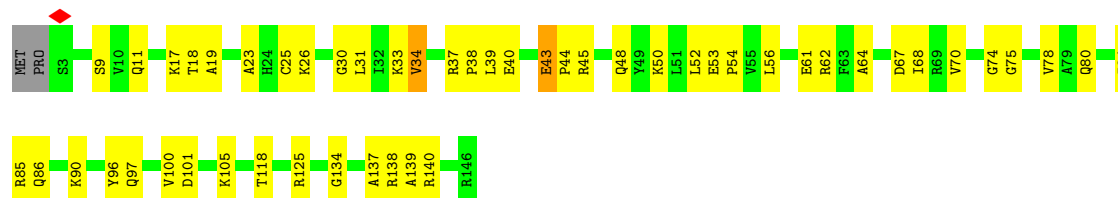
- Molecule 57: 40S ribosomal protein S15





- Molecule 58: 40S ribosomal protein S16

Chain SQ: 64% 34% ..



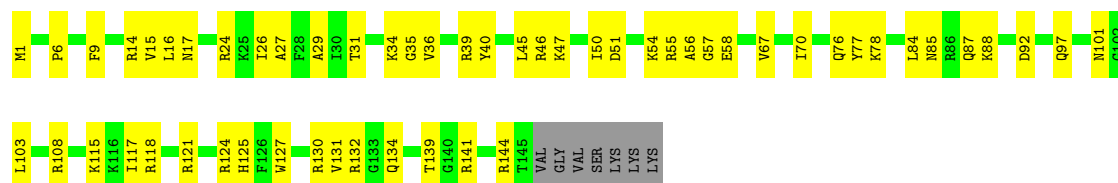
- Molecule 59: 40S ribosomal protein S17

Chain SR: 76% 24%



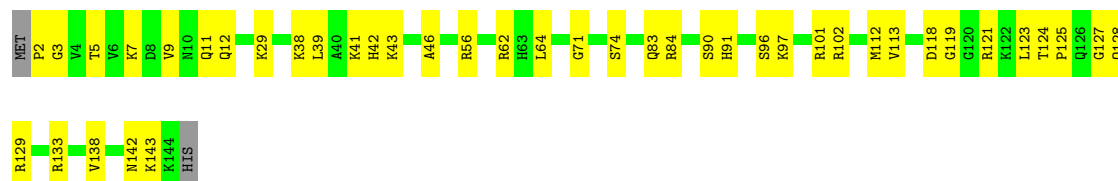
- Molecule 60: 40S ribosomal protein S18

Chain SS: 59% 36% 5%



- Molecule 61: 40S ribosomal protein S19

Chain ST: 70% 29%

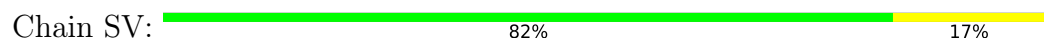


- Molecule 62: 40S ribosomal protein S20

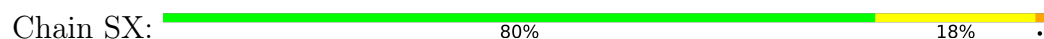
Chain SU: 65% 23% 13%



- Molecule 63: 40S ribosomal protein S21



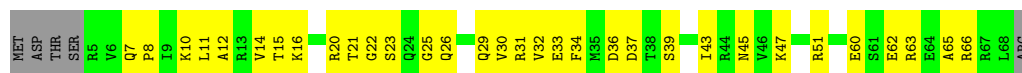
- Molecule 64: 40S ribosomal protein S23



- Molecule 65: 40S ribosomal protein S26



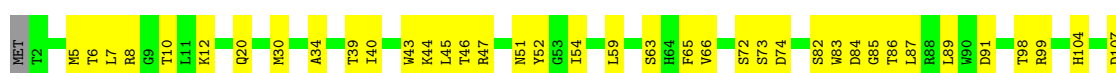
- Molecule 66: 40S ribosomal protein S28



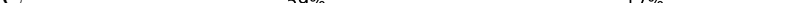
- Molecule 67: 40S ribosomal protein S29

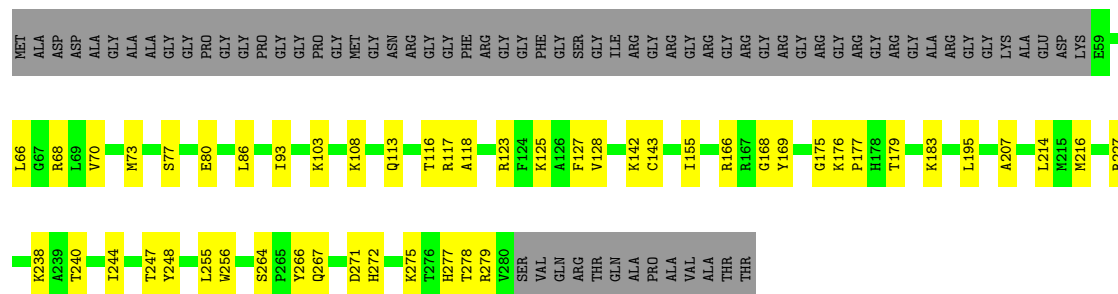


- Molecule 68: Receptor of activated protein C kinase 1

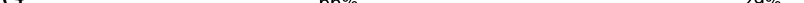


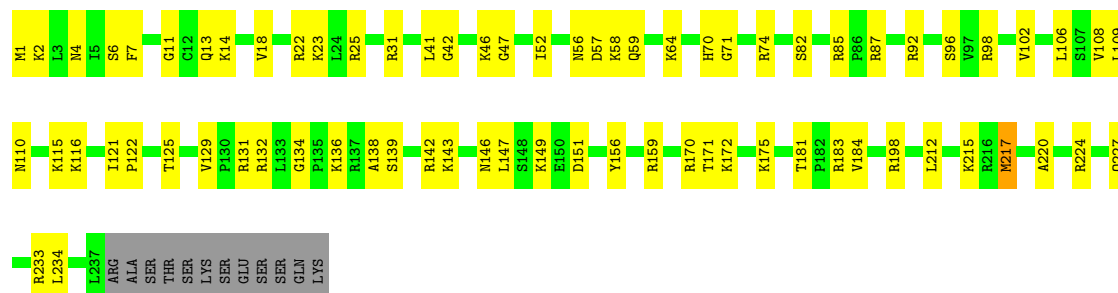
- Molecule 69: 40S ribosomal protein S2

Chain SC: 

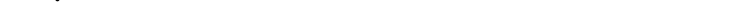


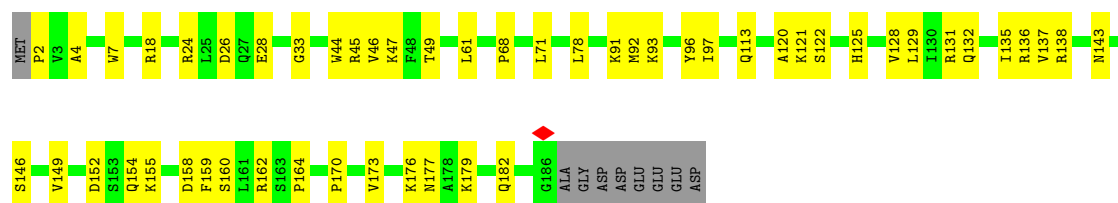
- Molecule 70: 40S ribosomal protein S6

Chain SG: 

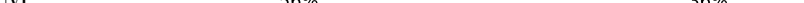


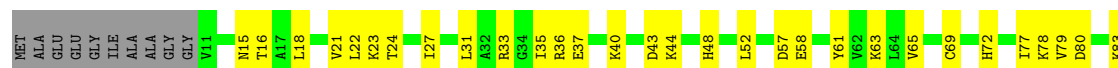
- Molecule 71: 40S ribosomal protein S9

Chain SJ:  69% 27% 5%

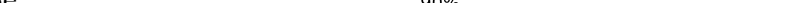


- Molecule 72: 40S ribosomal protein S12

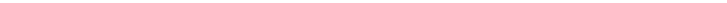
Chain SM: 



Met	P2	E14	R17	K18	H19	R23	L24	S27	Y31	D34	C40	Y41	T44	S48	H49	T67	G68	G69	K70	H84
-----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

- Chain Se: 

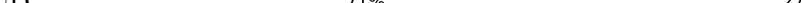
LYS
V2
L6
Y38
R41
F42
K53
S59

- Chain Sf: 

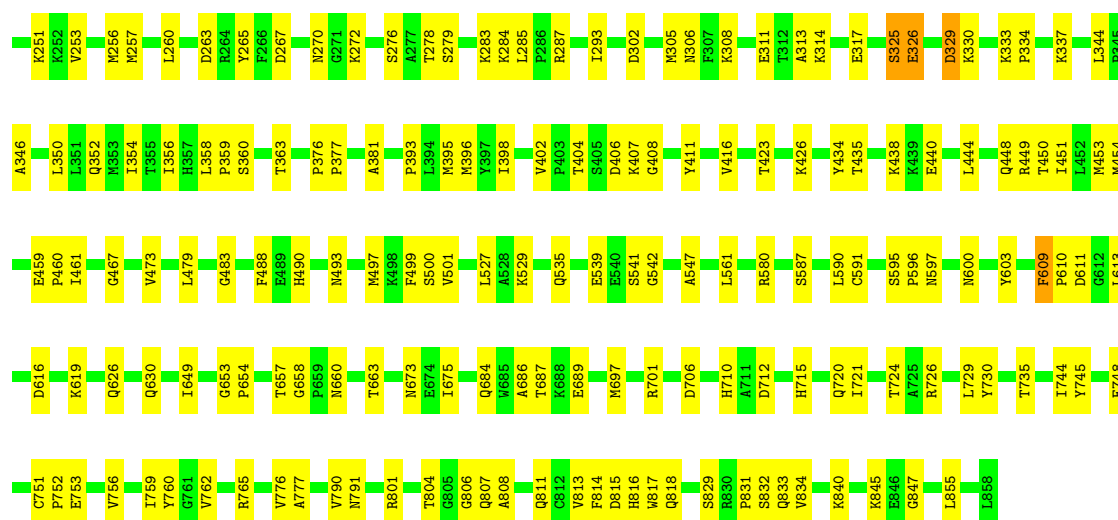
LYS	ILE	MET
PRO	GLN	GLN
GLU	LYS	ILE
ASP	GLU	PHE
LYS	SER	VAL
	THR	LYS
	LEU	THR
	HIS	LEU
	LEU	THR
	VAL	GLY
	LEU	LYS
	ARG	THR
	LEU	ILE
	ARG	THR
	GLY	LEU
	GLY	GLU
	ALA	VAL
	LYS	GLU
	LYS	PRO
	ARG	SER
	LYS	ASP
	LYS	THR
	SER	ILE
	SER	GLU
	T85	ASN
	T86	VAL
	T87	LYS
	P88	ALA
	K89	LYS
	K90	ILE
	R91	GLN
		ASP
	K97	LYS
	V98	GLU
	K99	GLY
		ILE
	L103	PRO
	K104	PRO
	Y105	ASP
		GLN
	V108	GLN
		ARG
		LEU
	R116	ILE
		PHE
	S123	ALA
		GLY
	C126	LYS
	G127	GLN
		LEU
	A133	GLU
	S134	GLY
	H135	ASP
		GLY
	H139	ARG
	Y140	THR
	C141	LEU
		SER
	L146	ASP
		TYR
	V151	ASN

- Chain CA: 63% 26% 10%

D36.1	G233	L105	MET
A352	R243	I108	SER
K355	L246	D109	GLU
A356	D250	V114	ASP
L357	G251	A122	GLU
L368	S252	V127	Q7
Q359	L257	B128	Q8
S360	K258	V129	E9
S361	M259	T136	T11
A362	K260	K139	T12
SER	R263	K144	T13
ARG	A264	L148	T19
THR	F265	E151	K20
LYS	E268	R155	M23
LYS	V269	N163	G24
LYS	E270	E167	G25
LYS	R271	E188	G26
LYS	R281	K172	I27
ALA	A282	S176	A28
ALA	F283	P181	N29
ASN	GLU	L190	R33
ALA	ASP	K199	V36
THR	E286	N204	S44
SER	R290	T205	V45
GLY	M291	D207	L46
GLY	M291	Q208	M55
THR	F305	Q209	E59
LEU	E310	H213	T60
GLU	E314	E217	G61
GLU	E314	H221	K62
ALA	A317	E222	I63
GLY	Q318	V223	E67
ASP	F319	D227	M70
	K320	L229	K71
	L325	V230	K72
	M326	D238	T78
	I333	L242	N83
	T334	K344	S90
	S335		P91
	E339		D97
	L342		I100

- Chain CB:  71% 27%

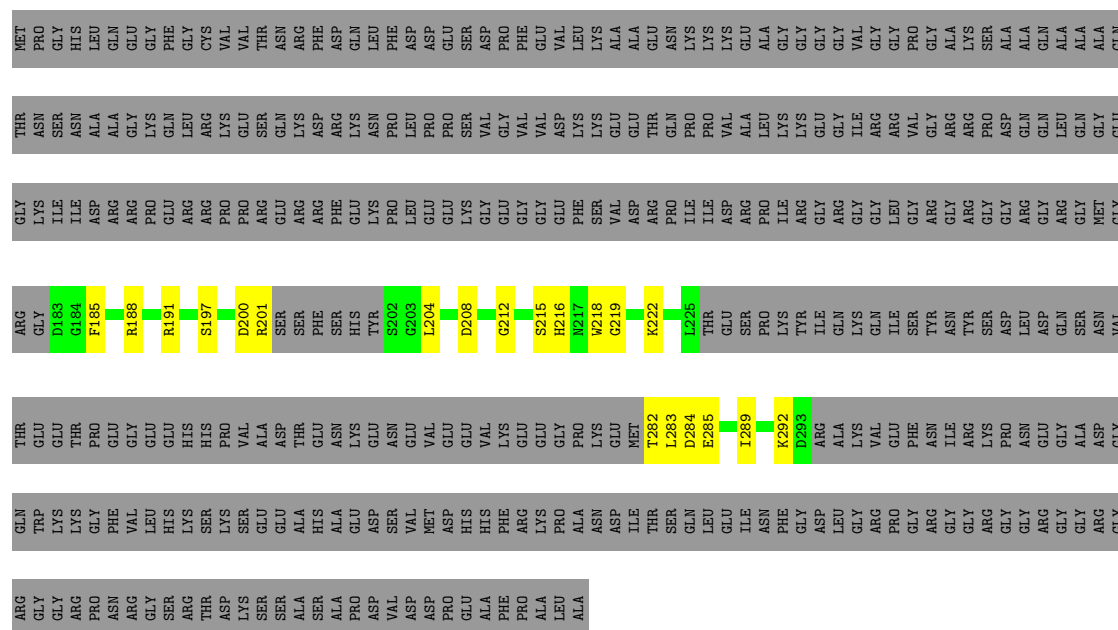
P106	P109	D110	F111	S112	S113	E114	V115	T116	L119	R120	V121	T122	Q138	I147	K159	M160	D161	R162	V185	I188	I189	D206	L209	V212	L218	F223	T224	Q227	F228	A229	Y232	K235	F236	ALA	ALA	LVS	GLY	GLU	GLY	GLN	GLN	I100	I101	D104	P107											
Met	Val	N3	F4	T5		Q8	I9	M13	K16	A17	M18	I19	A26	H27	V28		K32	L35	F36	D37		K42	A43	G44	I45	I46	A47		R55	F56	F57	D58		K61	D62		F63	Q64	S65	R66	O67	I68		S72		L77		Q91		D94		L99	I100		D104	P107



• 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	72367	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	0.229	Depositor
Minimum map value	-0.083	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.011	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	424.4, 424.4, 424.4	wwPDB
Map dimensions	400, 400, 400	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	0.53	0/89570	0.43	2/139647 (0.0%)
2	L7	0.51	0/2861	0.36	0/4459
3	L8	0.53	0/3701	0.38	0/5766
4	LA	0.52	0/1936	0.69	2/2596 (0.1%)
5	LB	0.47	0/3306	0.60	0/4424
6	LC	0.49	0/2981	0.60	2/4002 (0.0%)
7	LD	0.38	0/2428	0.53	1/3252 (0.0%)
8	LE	0.36	0/1942	0.58	0/2606
9	LF	0.51	0/1905	0.60	0/2539
10	LG	0.38	0/1960	0.57	0/2637
11	LH	0.44	0/1537	0.59	0/2066
12	LI	0.45	0/1673	0.59	0/2233
13	LJ	0.34	0/1433	0.63	0/1915
14	LL	0.41	0/1732	0.58	0/2315
15	LM	0.42	0/1161	0.60	2/1554 (0.1%)
16	LN	0.53	0/1746	0.64	0/2338
17	LO	0.48	0/1682	0.52	0/2250
18	LP	0.48	0/1268	0.56	0/1701
19	LQ	0.49	0/1537	0.59	0/2052
20	LR	0.42	0/1582	0.56	0/2091
21	LS	0.49	0/1493	0.52	0/2003
22	LT	0.46	0/1326	0.64	0/1770
23	LU	0.35	0/839	0.65	0/1126
24	LV	0.49	0/993	0.61	0/1332
25	LW	0.37	0/979	0.53	0/1295
26	LX	0.43	0/1002	0.52	0/1345
27	LY	0.43	0/1132	0.54	0/1504
28	LZ	0.40	0/1130	0.56	0/1507
29	La	0.49	0/1191	0.56	0/1591
30	Lb	0.37	0/889	0.61	0/1175
31	Lc	0.41	0/774	0.54	0/1038
32	Ld	0.46	0/903	0.56	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.51	0/1071	0.59	0/1429
34	Lf	0.51	0/895	0.61	0/1198
35	Lg	0.45	0/916	0.56	0/1220
36	Lh	0.38	0/1023	0.51	0/1351
37	Li	0.36	0/843	0.49	0/1115
38	Lj	0.53	0/720	0.66	0/952
39	Lk	0.35	0/575	0.53	0/761
40	Ll	0.49	0/454	0.59	0/599
41	Lm	0.45	0/435	0.53	0/575
42	Ln	0.39	0/231	0.55	0/294
43	Lo	0.45	0/876	0.52	0/1156
44	Lp	0.46	0/718	0.54	0/953
45	Lr	0.47	0/1017	0.55	0/1364
46	Lz	0.24	0/1769	0.63	0/2371
47	S2	0.37	0/41244	0.40	2/64263 (0.0%)
48	SA	0.34	0/1778	0.57	0/2416
49	SB	0.31	0/1765	0.58	0/2362
50	SD	0.31	0/1793	0.60	0/2414
51	SE	0.30	0/2118	0.55	0/2849
52	SF	0.24	0/1516	0.57	0/2037
53	SH	0.28	0/1519	0.62	0/2033
54	SI	0.30	0/1715	0.57	0/2287
55	SK	0.28	0/851	0.52	0/1147
56	SL	0.33	0/1268	0.49	0/1696
57	SP	0.30	0/1003	0.65	2/1342 (0.1%)
58	SQ	0.27	0/1160	0.65	1/1553 (0.1%)
59	SR	0.27	0/1105	0.59	0/1484
60	SS	0.25	0/1216	0.50	0/1628
61	ST	0.23	0/1131	0.52	0/1515
62	SU	0.26	0/831	0.56	0/1115
63	SV	0.34	0/643	0.60	0/860
64	SX	0.42	0/1116	0.62	2/1490 (0.1%)
65	Sa	0.36	0/836	0.61	0/1121
66	Sc	0.26	0/508	0.68	0/680
67	Sd	0.34	0/470	0.58	0/623
68	Sg	0.25	0/2493	0.57	0/3394
69	SC	0.38	0/1762	0.65	0/2381
70	SG	0.24	0/1946	0.54	0/2590
71	SJ	0.34	0/1550	0.61	0/2069
72	SM	0.22	0/950	0.66	0/1275
73	SN	0.32	0/1232	0.50	0/1656
74	SO	0.30	0/1062	0.62	0/1425
75	SW	0.36	0/1051	0.50	0/1406

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SY	0.27	0/1083	0.56	0/1438
77	SZ	0.23	0/604	0.63	0/810
78	Sb	0.29	0/665	0.57	0/891
79	Se	0.28	0/465	0.56	0/612
80	Sf	0.21	0/560	0.63	0/745
81	CA	0.24	0/2810	0.63	0/3780
82	CB	0.31	0/6734	0.60	0/9094
83	CC	0.26	0/2025	0.41	0/3155
84	CD	0.28	0/447	0.52	0/592
All	All	0.44	0/245160	0.49	16/358911 (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
1	L5	0	1
4	LA	0	3
5	LB	0	2
11	LH	0	2
12	LI	0	1
13	LJ	0	1
14	LL	0	1
15	LM	0	2
17	LO	0	1
18	LP	0	1
22	LT	0	1
28	LZ	0	1
33	Le	0	1
34	Lf	0	3
36	Lh	0	1
38	Lj	0	1
46	Lz	0	1
50	SD	0	1
52	SF	0	2
53	SH	0	1
57	SP	0	1
58	SQ	0	2
61	ST	0	1
63	SV	0	1
64	SX	0	3

Continued on next page...

Continued from previous page...

Mol	Chain	#Chirality outliers	#Planarity outliers
70	SG	0	1
77	SZ	0	1
82	CB	0	2
All	All	0	40

There are no bond length outliers.

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	LC	2	ALA	CA-C-N	6.42	133.26	121.70
6	LC	2	ALA	C-N-CA	6.42	133.26	121.70
15	LM	87	ALA	CA-C-N	6.04	133.07	121.54
15	LM	87	ALA	C-N-CA	6.04	133.07	121.54
58	SQ	18	THR	N-CA-C	-5.86	107.37	114.75

There are no chirality outliers.

5 of 40 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	L5	3948	C	Sidechain
4	LA	110	GLY	Peptide
4	LA	13	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	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	992	0
2	L7	2561	0	1295	23	0
3	L8	3314	0	1683	33	0
4	LA	1898	0	1993	22	0
5	LB	3238	0	3376	55	0
6	LC	2927	0	3104	37	0
7	LD	2382	0	2410	36	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	LE	1904	0	2055	45	0
9	LF	1870	0	1996	29	0
10	LG	1927	0	2074	25	0
11	LH	1518	0	1601	29	0
12	LI	1634	0	1670	36	0
13	LJ	1410	0	1441	29	0
14	LL	1701	0	1818	29	0
15	LM	1138	0	1204	20	0
16	LN	1701	0	1749	23	0
17	LO	1650	0	1794	26	0
18	LP	1242	0	1269	16	0
19	LQ	1513	0	1628	22	0
20	LR	1566	0	1729	28	0
21	LS	1453	0	1490	16	0
22	LT	1298	0	1366	21	0
23	LU	825	0	850	18	0
24	LV	979	0	1039	17	0
25	LW	965	0	1029	22	0
26	LX	985	0	1066	18	0
27	LY	1115	0	1205	23	0
28	LZ	1107	0	1182	22	0
29	La	1162	0	1213	23	0
30	Lb	876	0	948	19	0
31	Lc	764	0	804	12	0
32	Ld	888	0	930	16	0
33	Le	1053	0	1147	17	0
34	Lf	876	0	912	11	0
35	Lg	906	0	999	7	0
36	Lh	1015	0	1148	15	0
37	Li	832	0	917	9	0
38	Lj	705	0	737	17	0
39	Lk	569	0	637	13	0
40	Ll	444	0	483	8	0
41	Lm	429	0	465	4	0
42	Ln	230	0	276	1	0
43	Lo	862	0	930	20	0
44	Lp	708	0	756	10	0
45	Lr	1002	0	1068	17	0
46	Lz	1741	0	1854	68	0
47	S2	36898	0	18601	626	0
48	SA	1741	0	1746	43	0
49	SB	1738	0	1809	51	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
50	SD	1765	0	1865	45	0
51	SE	2076	0	2177	53	0
52	SF	1495	0	1549	41	0
53	SH	1497	0	1590	47	0
54	SI	1686	0	1772	29	0
55	SK	827	0	854	25	0
56	SL	1247	0	1323	25	0
57	SP	985	0	1031	26	0
58	SQ	1142	0	1213	33	0
59	SR	1090	0	1149	22	0
60	SS	1198	0	1261	40	0
61	ST	1112	0	1146	33	0
62	SU	821	0	883	18	0
63	SV	636	0	637	12	0
64	SX	1098	0	1167	18	0
65	Sa	821	0	870	20	0
66	Sc	506	0	536	28	0
67	Sd	459	0	452	18	0
68	Sg	2436	0	2393	82	0
69	SC	1725	0	1813	34	0
70	SG	1923	0	2089	54	0
71	SJ	1525	0	1640	35	0
72	SM	940	0	965	35	0
73	SN	1208	0	1294	26	0
74	SO	1049	0	1073	21	0
75	SW	1034	0	1080	24	0
76	SY	1065	0	1142	25	0
77	SZ	598	0	656	22	0
78	Sb	651	0	672	12	0
79	Se	459	0	503	5	0
80	Sf	548	0	555	15	0
81	CA	2764	0	2779	65	0
82	CB	6605	0	6681	154	0
83	CC	1813	0	917	33	0
84	CD	440	0	402	18	0
85	CC	1	0	0	0	0
85	L5	211	0	0	0	0
85	L7	3	0	0	0	0
85	L8	5	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

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
85	LT	1	0	0	0	0
85	LV	1	0	0	0	0
85	Le	1	0	0	0	0
85	Lg	1	0	0	0	0
85	S2	29	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	SM	1	0	0	0	0
86	Sa	1	0	0	0	0
86	Sd	1	0	0	0	0
All	All	228884	0	171989	3402	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 9.

The worst 5 of 3402 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)
47:S2:834:C:N4	47:S2:839:C:H42	1.06	1.47
47:S2:834:C:H42	47:S2:839:C:N4	1.22	1.35
1:L5:1762:C:N4	1:L5:1770:A:C2	1.96	1.34
1:L5:1443:A:C2	1:L5:2103:G:N1	2.03	1.26
1:L5:1762:C:N3	1:L5:1770:A:N1	1.84	1.24

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%)	221 (90%)	24 (10%)	1 (0%)	30	61
5	LB	400/403 (99%)	371 (93%)	27 (7%)	2 (0%)	24	57
6	LC	366/427 (86%)	335 (92%)	31 (8%)	0	100	100
7	LD	291/297 (98%)	266 (91%)	25 (9%)	0	100	100
8	LE	232/288 (81%)	210 (90%)	21 (9%)	1 (0%)	30	61
9	LF	223/248 (90%)	210 (94%)	13 (6%)	0	100	100
10	LG	239/266 (90%)	218 (91%)	21 (9%)	0	100	100
11	LH	188/192 (98%)	171 (91%)	17 (9%)	0	100	100
12	LI	198/214 (92%)	181 (91%)	17 (9%)	0	100	100
13	LJ	174/178 (98%)	155 (89%)	18 (10%)	1 (1%)	21	52
14	LL	208/211 (99%)	190 (91%)	18 (9%)	0	100	100
15	LM	137/215 (64%)	124 (90%)	12 (9%)	1 (1%)	18	49
16	LN	201/204 (98%)	185 (92%)	15 (8%)	1 (0%)	24	57
17	LO	199/203 (98%)	188 (94%)	11 (6%)	0	100	100
18	LP	151/184 (82%)	140 (93%)	11 (7%)	0	100	100
19	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
20	LR	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
21	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
22	LT	157/160 (98%)	143 (91%)	14 (9%)	0	100	100
23	LU	99/128 (77%)	83 (84%)	16 (16%)	0	100	100
24	LV	129/140 (92%)	119 (92%)	10 (8%)	0	100	100
25	LW	114/157 (73%)	108 (95%)	6 (5%)	0	100	100
26	LX	118/156 (76%)	110 (93%)	8 (7%)	0	100	100
27	LY	132/145 (91%)	121 (92%)	11 (8%)	0	100	100
28	LZ	133/136 (98%)	119 (90%)	14 (10%)	0	100	100
29	La	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
30	Lb	105/159 (66%)	96 (91%)	9 (9%)	0	100	100
31	Lc	96/115 (84%)	90 (94%)	6 (6%)	0	100	100
32	Ld	105/125 (84%)	96 (91%)	9 (9%)	0	100	100
33	Le	126/135 (93%)	119 (94%)	6 (5%)	1 (1%)	16	47
34	Lf	107/110 (97%)	98 (92%)	7 (6%)	2 (2%)	6	27
35	Lg	112/117 (96%)	109 (97%)	3 (3%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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%)	76 (90%)	8 (10%)	0	100	100
39	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
40	Ll	48/51 (94%)	46 (96%)	2 (4%)	0	100	100
41	Lm	50/128 (39%)	49 (98%)	1 (2%)	0	100	100
42	Ln	22/25 (88%)	22 (100%)	0	0	100	100
43	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
44	Lp	89/92 (97%)	85 (96%)	4 (4%)	0	100	100
45	Lr	123/137 (90%)	117 (95%)	6 (5%)	0	100	100
46	Lz	215/217 (99%)	159 (74%)	55 (26%)	1 (0%)	24	57
48	SA	219/295 (74%)	196 (90%)	23 (10%)	0	100	100
49	SB	212/264 (80%)	201 (95%)	11 (5%)	0	100	100
50	SD	225/243 (93%)	204 (91%)	21 (9%)	0	100	100
51	SE	260/263 (99%)	238 (92%)	22 (8%)	0	100	100
52	SF	187/204 (92%)	162 (87%)	25 (13%)	0	100	100
53	SH	182/194 (94%)	155 (85%)	27 (15%)	0	100	100
54	SI	204/208 (98%)	194 (95%)	10 (5%)	0	100	100
55	SK	96/165 (58%)	83 (86%)	13 (14%)	0	100	100
56	SL	151/158 (96%)	141 (93%)	10 (7%)	0	100	100
57	SP	119/145 (82%)	108 (91%)	11 (9%)	0	100	100
58	SQ	142/146 (97%)	125 (88%)	16 (11%)	1 (1%)	18	49
59	SR	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
60	SS	143/152 (94%)	127 (89%)	16 (11%)	0	100	100
61	ST	141/145 (97%)	127 (90%)	13 (9%)	1 (1%)	18	49
62	SU	102/119 (86%)	90 (88%)	12 (12%)	0	100	100
63	SV	81/83 (98%)	74 (91%)	7 (9%)	0	100	100
64	SX	139/143 (97%)	125 (90%)	11 (8%)	3 (2%)	5	24
65	Sa	100/115 (87%)	90 (90%)	9 (9%)	1 (1%)	12	41
66	Sc	62/69 (90%)	48 (77%)	14 (23%)	0	100	100
67	Sd	53/56 (95%)	50 (94%)	2 (4%)	1 (2%)	6	27

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
68	Sg	311/317 (98%)	265 (85%)	46 (15%)	0	100	100
69	SC	220/293 (75%)	204 (93%)	16 (7%)	0	100	100
70	SG	235/249 (94%)	220 (94%)	15 (6%)	0	100	100
71	SJ	183/194 (94%)	168 (92%)	15 (8%)	0	100	100
72	SM	120/132 (91%)	109 (91%)	11 (9%)	0	100	100
73	SN	148/151 (98%)	140 (95%)	8 (5%)	0	100	100
74	SO	138/151 (91%)	129 (94%)	9 (6%)	0	100	100
75	SW	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
76	SY	129/133 (97%)	120 (93%)	9 (7%)	0	100	100
77	SZ	73/125 (58%)	61 (84%)	12 (16%)	0	100	100
78	Sb	81/84 (96%)	69 (85%)	12 (15%)	0	100	100
79	Se	56/59 (95%)	47 (84%)	9 (16%)	0	100	100
80	Sf	65/156 (42%)	49 (75%)	16 (25%)	0	100	100
81	CA	350/394 (89%)	335 (96%)	15 (4%)	0	100	100
82	CB	842/858 (98%)	780 (93%)	59 (7%)	3 (0%)	30	61
84	CD	51/408 (12%)	47 (92%)	4 (8%)	0	100	100
All	All	12775/14565 (88%)	11678 (91%)	1076 (8%)	21 (0%)	44	73

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
64	SX	127	ASN
65	Sa	47	ALA
82	CB	56	PHE
82	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%)	187 (98%)	3 (2%)	55	75
5	LB	348/349 (100%)	347 (100%)	1 (0%)	86	87
6	LC	306/348 (88%)	305 (100%)	1 (0%)	86	87
7	LD	246/250 (98%)	246 (100%)	0	100	100
8	LE	209/252 (83%)	209 (100%)	0	100	100
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%)	169 (100%)	0	100	100
12	LI	172/181 (95%)	171 (99%)	1 (1%)	78	83
13	LJ	148/149 (99%)	147 (99%)	1 (1%)	76	82
14	LL	176/177 (99%)	176 (100%)	0	100	100
15	LM	118/161 (73%)	116 (98%)	2 (2%)	53	74
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%)	133 (99%)	1 (1%)	76	82
19	LQ	164/165 (99%)	163 (99%)	1 (1%)	78	83
20	LR	166/175 (95%)	165 (99%)	1 (1%)	78	83
21	LS	156/157 (99%)	155 (99%)	1 (1%)	78	83
22	LT	139/140 (99%)	139 (100%)	0	100	100
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	100 (99%)	1 (1%)	68	79
25	LW	97/126 (77%)	97 (100%)	0	100	100
26	LX	108/133 (81%)	107 (99%)	1 (1%)	70	80
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%)	119 (99%)	1 (1%)	73	81
30	Lb	88/126 (70%)	88 (100%)	0	100	100
31	Lc	83/97 (86%)	82 (99%)	1 (1%)	63	78
32	Ld	98/110 (89%)	97 (99%)	1 (1%)	68	79
33	Le	114/121 (94%)	112 (98%)	2 (2%)	51	73
34	Lf	88/89 (99%)	87 (99%)	1 (1%)	65	78
35	Lg	98/100 (98%)	98 (100%)	0	100	100

Continued on next page...

Continued from previous page...

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%)	72 (99%)	1 (1%)	59	76
39	Lk	64/65 (98%)	63 (98%)	1 (2%)	55	75
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	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	80
46	Lz	195/196 (100%)	195 (100%)	0	100	100
48	SA	183/243 (75%)	182 (100%)	1 (0%)	81	85
49	SB	195/231 (84%)	195 (100%)	0	100	100
50	SD	190/202 (94%)	190 (100%)	0	100	100
51	SE	224/225 (100%)	223 (100%)	1 (0%)	84	86
52	SF	159/170 (94%)	159 (100%)	0	100	100
53	SH	166/174 (95%)	164 (99%)	2 (1%)	63	78
54	SI	178/180 (99%)	176 (99%)	2 (1%)	65	78
55	SK	89/136 (65%)	89 (100%)	0	100	100
56	SL	137/142 (96%)	137 (100%)	0	100	100
57	SP	107/130 (82%)	107 (100%)	0	100	100
58	SQ	119/121 (98%)	117 (98%)	2 (2%)	53	74
59	SR	122/122 (100%)	122 (100%)	0	100	100
60	SS	126/132 (96%)	125 (99%)	1 (1%)	73	81
61	ST	113/115 (98%)	113 (100%)	0	100	100
62	SU	94/107 (88%)	94 (100%)	0	100	100
63	SV	67/67 (100%)	67 (100%)	0	100	100
64	SX	113/115 (98%)	112 (99%)	1 (1%)	70	80
65	Sa	89/98 (91%)	88 (99%)	1 (1%)	65	78
66	Sc	57/62 (92%)	57 (100%)	0	100	100
67	Sd	48/49 (98%)	48 (100%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
68	Sg	272/275 (99%)	272 (100%)	0	100	100
69	SC	188/225 (84%)	188 (100%)	0	100	100
70	SG	207/218 (95%)	205 (99%)	2 (1%)	68	79
71	SJ	161/168 (96%)	159 (99%)	2 (1%)	63	78
72	SM	102/108 (94%)	102 (100%)	0	100	100
73	SN	130/131 (99%)	129 (99%)	1 (1%)	73	81
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	722/730 (99%)	717 (99%)	5 (1%)	76	82
84	CD	46/328 (14%)	46 (100%)	0	100	100
All	All	11120/12391 (90%)	11075 (100%)	45 (0%)	81	86

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
54	SI	76	THR
70	SG	102	VAL
54	SI	130	THR
60	SS	103	LEU
71	SJ	61	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 173 such sidechains are listed below:

Mol	Chain	Res	Type
60	SS	10	GLN
75	SW	90	GLN
61	ST	85	ASN
68	Sg	64	HIS
78	Sb	65	GLN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3704/5070 (73%)	970 (26%)	17 (0%)
2	L7	119/121 (98%)	16 (13%)	0
3	L8	155/157 (98%)	29 (18%)	0
47	S2	1715/1869 (91%)	458 (26%)	7 (0%)
83	CC	84/85 (98%)	23 (27%)	2 (2%)
All	All	5777/7302 (79%)	1496 (25%)	26 (0%)

5 of 1496 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 26 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	L5	3673	C
47	S2	112	U
83	CC	18	G
1	L5	4913	G
47	S2	291	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.

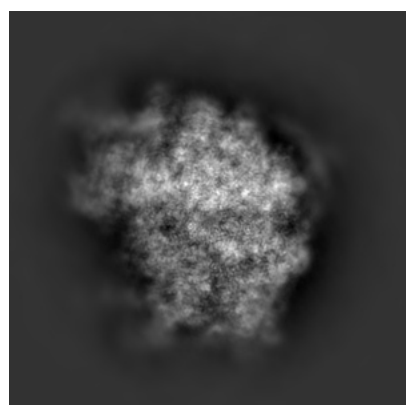
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11099. These allow visual inspection of the internal detail of the map and identification of artifacts.

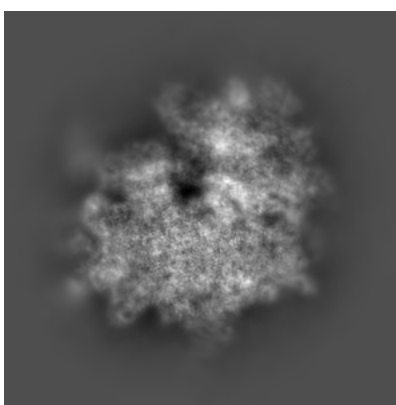
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

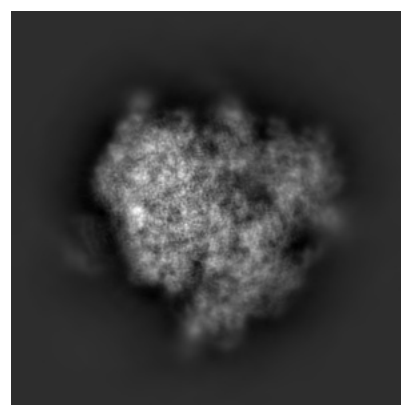
6.1.1 Primary map



X



Y

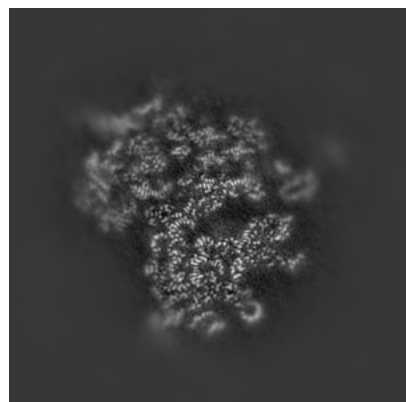


Z

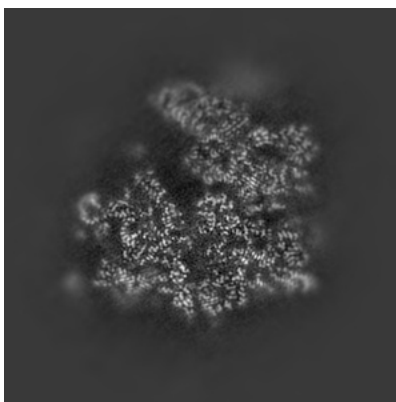
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

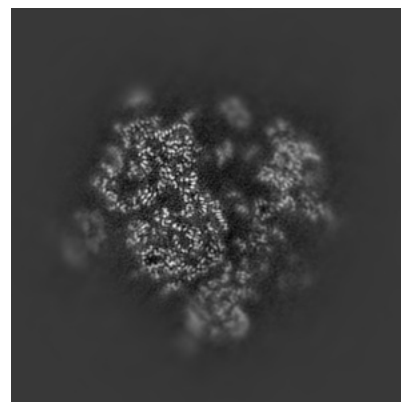
6.2.1 Primary map



X Index: 200



Y Index: 200

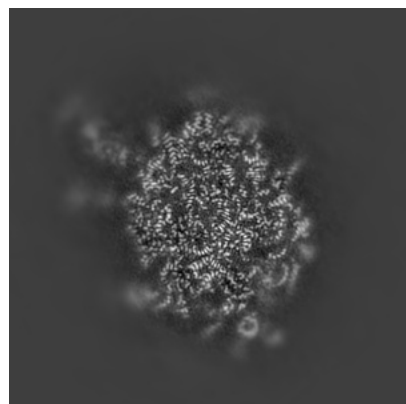


Z Index: 200

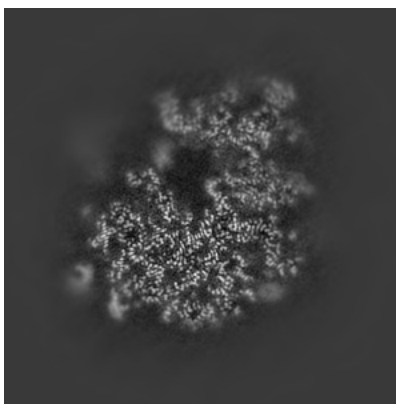
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

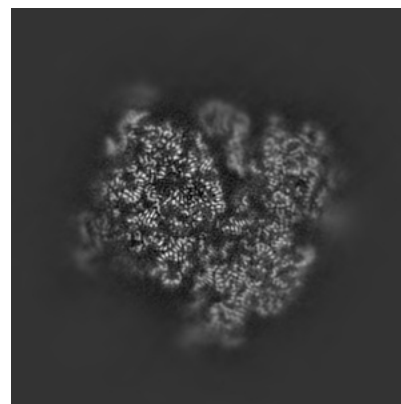
6.3.1 Primary map



X Index: 172



Y Index: 216

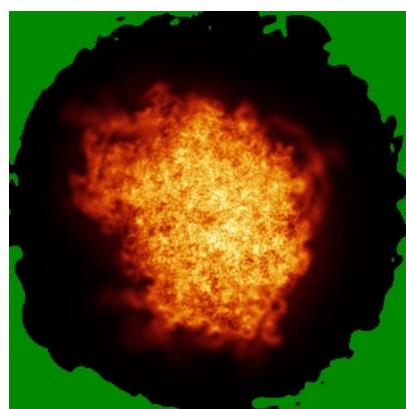


Z Index: 219

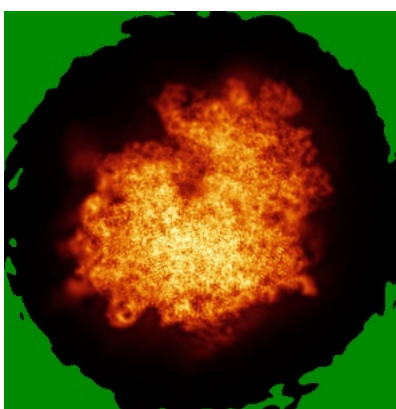
The images above show the largest variance slices of the map in three orthogonal directions.

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

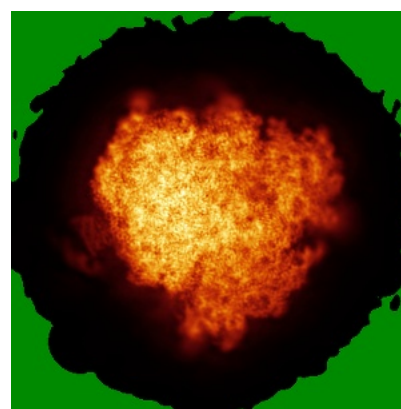
6.4.1 Primary map



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

This section was not generated.

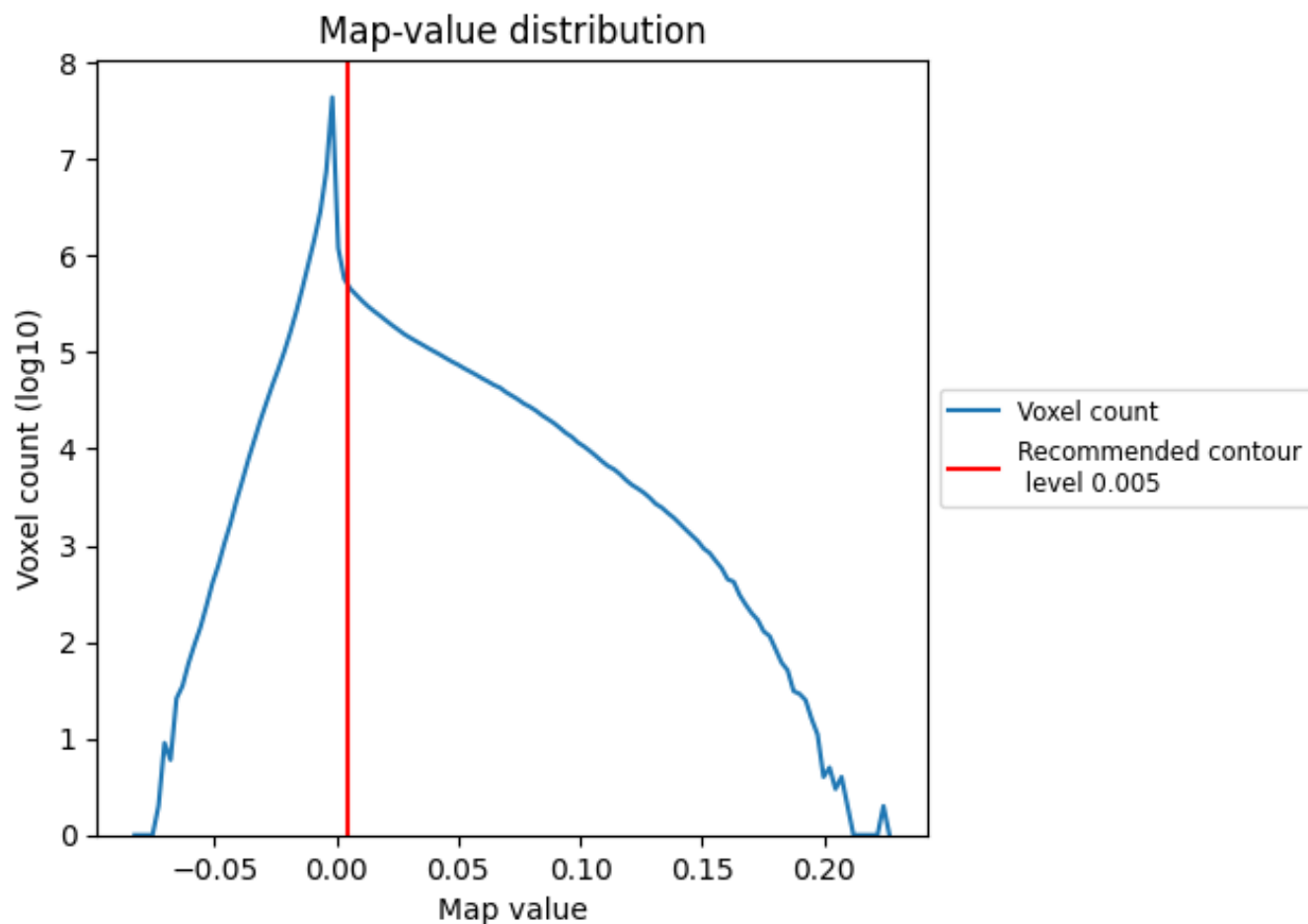
6.6 Mask visualisation

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

7 Map analysis [i](#)

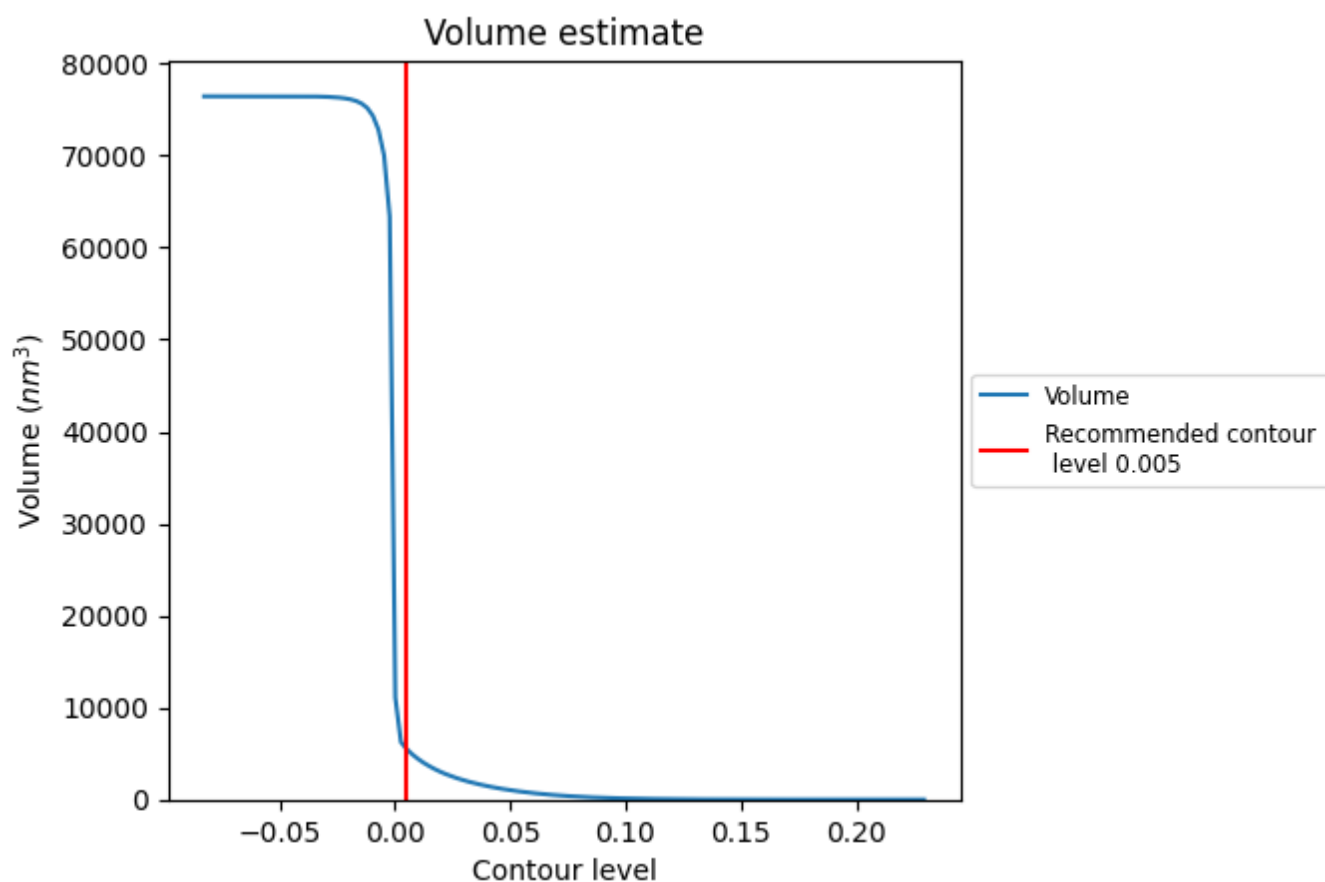
This section contains the results of statistical analysis of the map.

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.

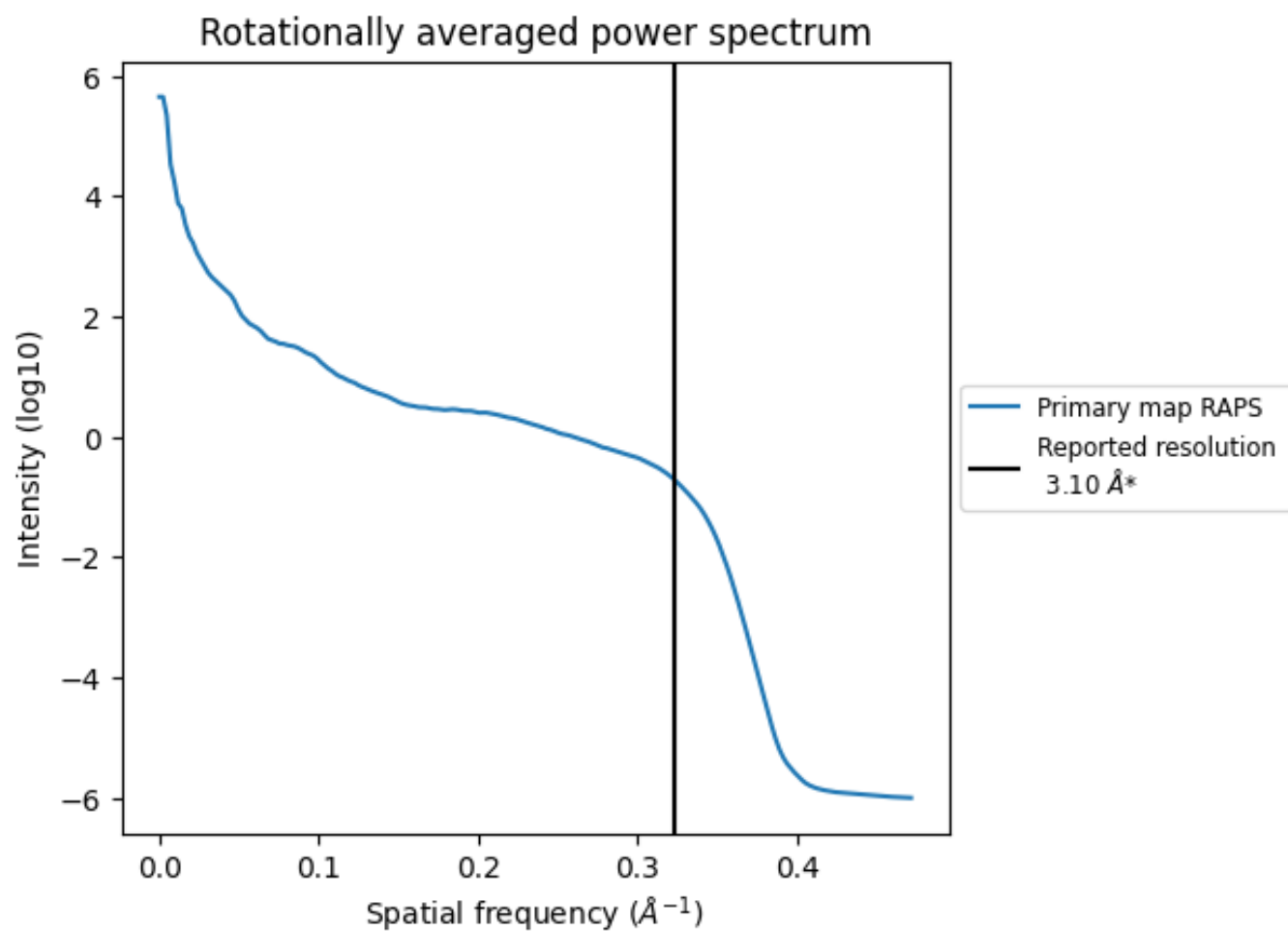
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 5515 nm^3 ; this corresponds to an approximate mass of 4981 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 ⓘ

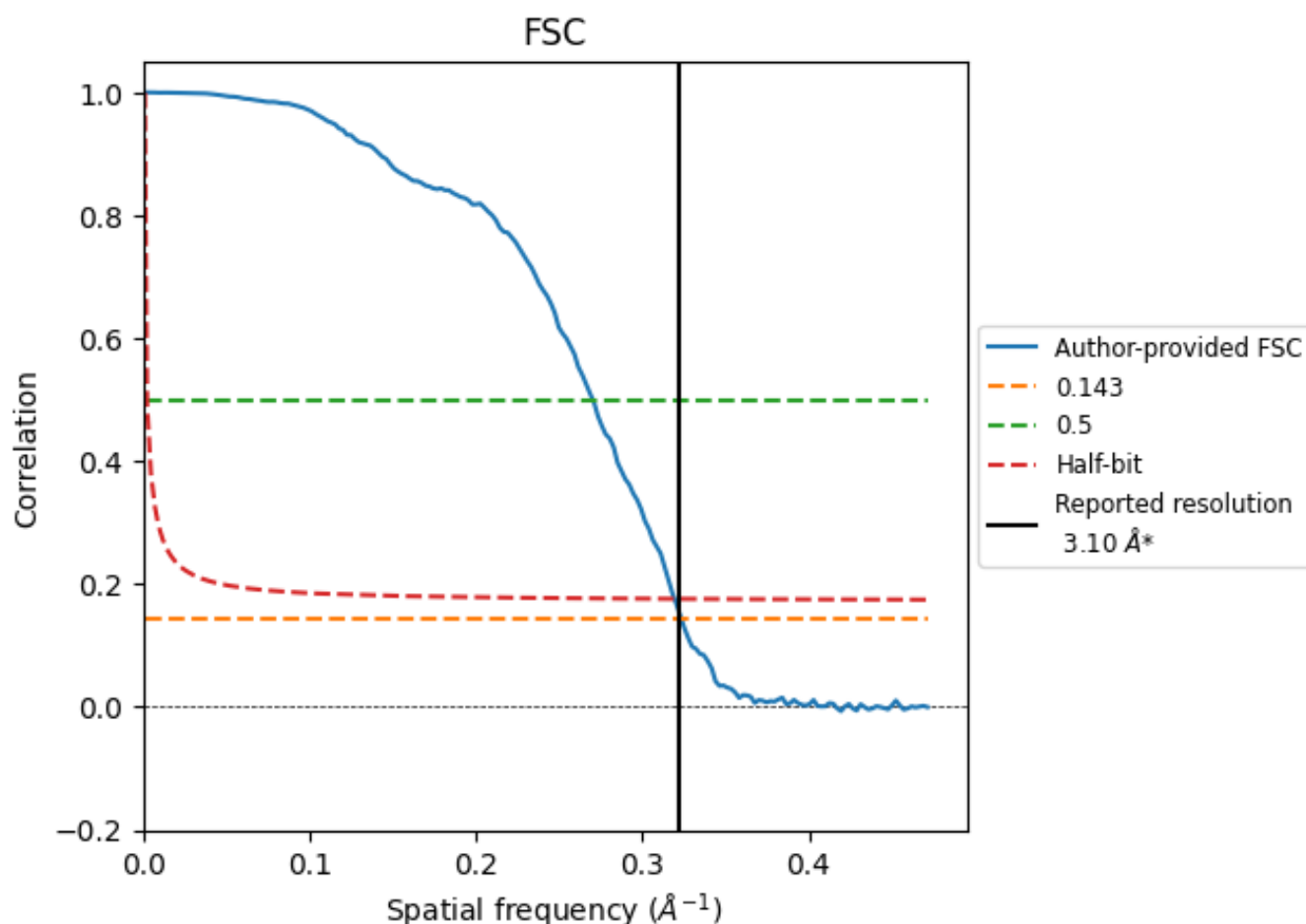


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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 0.323 Å⁻¹

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.10	-	-
Author-provided FSC curve	3.09	3.70	3.13
Unmasked-calculated*	-	-	-

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

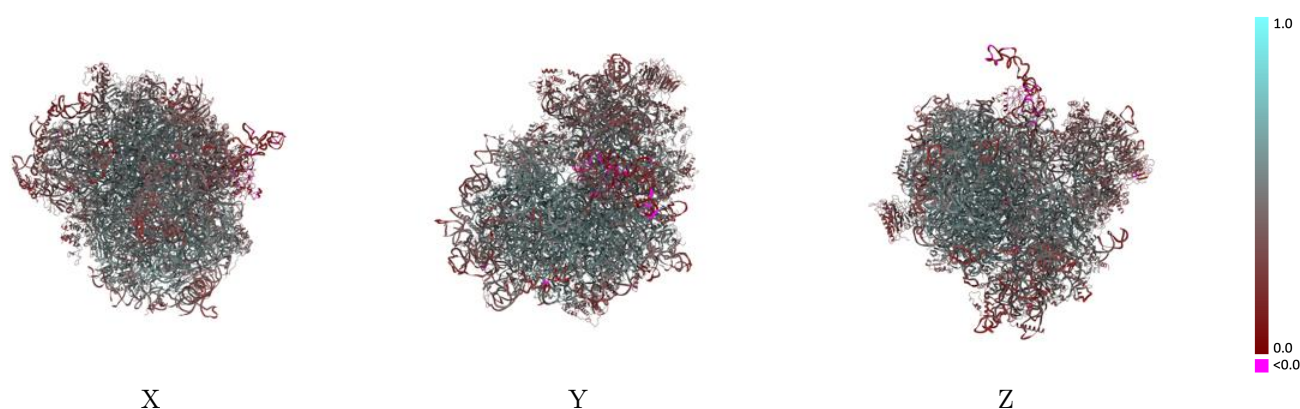
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11099 and PDB model 6Z6M. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

This section was not generated.

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

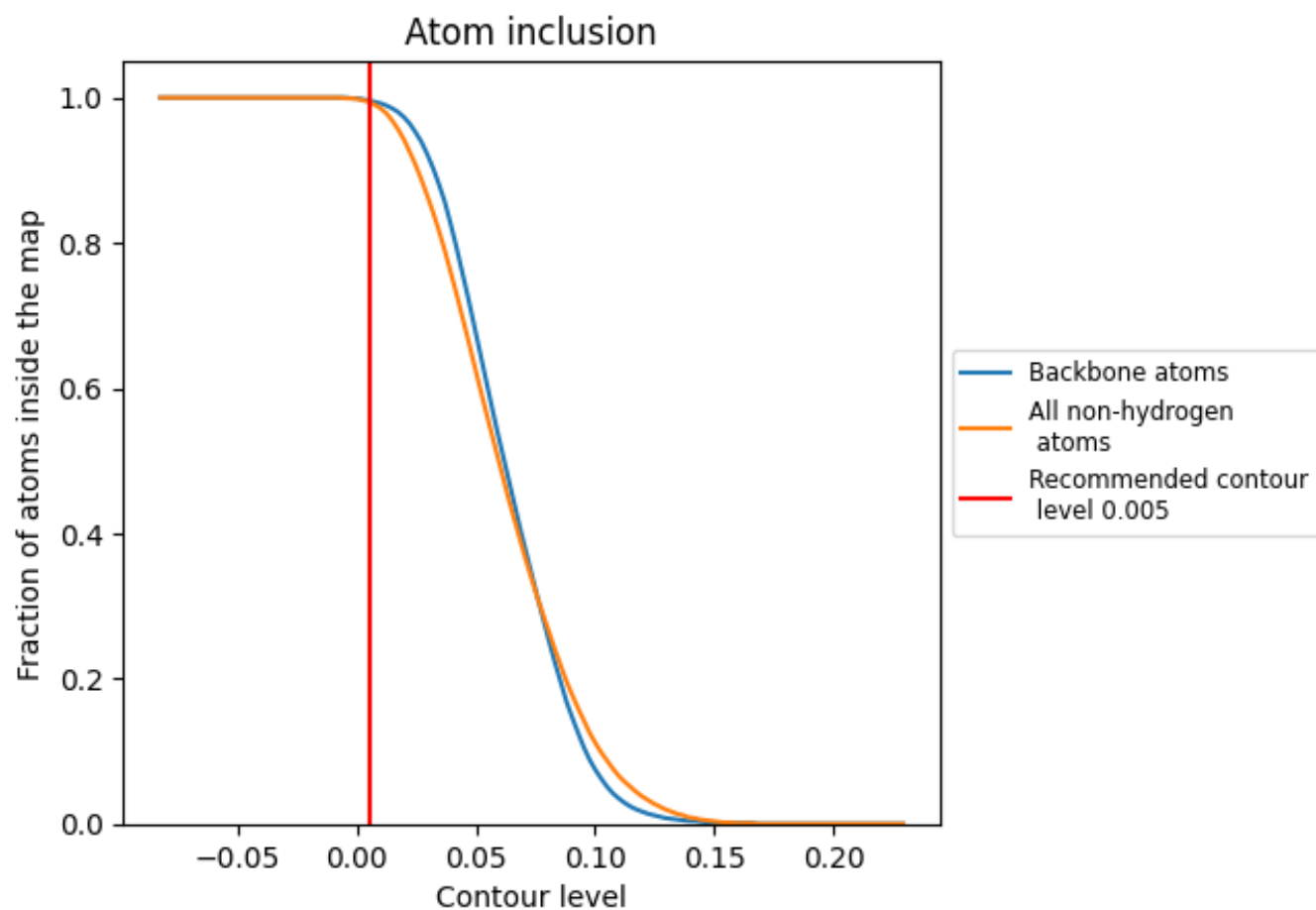


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% 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	 0.9940	 0.4740
CA	 0.9820	 0.3040
CB	 0.9720	 0.4230
CC	 0.9900	 0.3700
CD	 0.9910	 0.4420
L5	 0.9980	 0.5060
L7	 1.0000	 0.5410
L8	 0.9990	 0.5280
LA	 0.9900	 0.5770
LB	 0.9940	 0.5440
LC	 0.9950	 0.5390
LD	 1.0000	 0.4750
LE	 0.9960	 0.4540
LF	 0.9910	 0.5410
LG	 0.9910	 0.4600
LH	 0.9950	 0.5190
LI	 0.9920	 0.5400
LJ	 0.9960	 0.4270
LL	 0.9850	 0.4980
LM	 0.9980	 0.4950
LN	 0.9900	 0.5790
LO	 0.9910	 0.5510
LP	 0.9950	 0.5530
LQ	 0.9920	 0.5670
LR	 0.9840	 0.4820
LS	 0.9940	 0.5600
LT	 0.9910	 0.5310
LU	 0.9960	 0.4130
LV	 0.9840	 0.5580
LW	 0.9980	 0.4060
LX	 0.9930	 0.5250
LY	 0.9980	 0.5140
LZ	 0.9980	 0.4880
La	 0.9980	 0.5650
Lb	 0.9840	 0.4600



Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
Lc	 0.9770	 0.4810
Ld	 0.9950	 0.5230
Le	 0.9940	 0.5700
Lf	 0.9960	 0.5730
Lg	 0.9970	 0.5410
Lh	 0.9960	 0.4930
Li	 0.9990	 0.4950
Lj	 0.9990	 0.5790
Lk	 0.9960	 0.4510
Ll	 0.9910	 0.5530
Lm	 0.9830	 0.5460
Ln	 0.9900	 0.5700
Lo	 0.9810	 0.5380
Lp	 0.9810	 0.5560
Lr	 0.9940	 0.5320
Lz	 0.8510	 0.0960
S2	 0.9990	 0.4520
SA	 0.9900	 0.4270
SB	 0.9920	 0.4250
SC	 0.9930	 0.4760
SD	 0.9910	 0.4120
SE	 0.9980	 0.4500
SF	 0.9840	 0.3460
SG	 0.9950	 0.3300
SH	 0.9970	 0.3500
SI	 0.9910	 0.4130
SJ	 0.9930	 0.4360
SK	 1.0000	 0.3810
SL	 0.9930	 0.4760
SM	 0.9980	 0.2330
SN	 0.9870	 0.4680
SO	 0.9640	 0.4350
SP	 0.9980	 0.3730
SQ	 0.9910	 0.3900
SR	 0.9950	 0.3850
SS	 0.9970	 0.3450
ST	 1.0000	 0.3590
SU	 0.9990	 0.3690
SV	 0.9940	 0.4440
SW	 0.9900	 0.5080
SX	 0.9940	 0.5290
SY	 0.9750	 0.3840

Continued on next page...

Continued from previous page...

Chain	Atom inclusion	Q-score
SZ	 0.9880	 0.2750
Sa	 0.9920	 0.4930
Sb	 0.9950	 0.4290
Sc	 0.9750	 0.3490
Sd	 0.9930	 0.4670
Se	 0.9800	 0.4370
Sf	 1.0000	 0.2810
Sg	 0.9990	 0.3120