



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 03:46 AM UTC

PDB ID : 6ZMO / pdb_00006zmo
EMDB ID : EMD-11299
Title : SARS-CoV-2 Nsp1 bound to the human LYAR-80S-eEF1a ribosome complex
Authors : Thoms, M.; Buschauer, R.; Ameismeier, M.; Denk, T.; Kratzat, H.; Mackens-Kiani, T.; Cheng, J.; Berninghausen, O.; Becker, T.; Beckmann, R.
Deposited on : 2020-07-03
Resolution : 3.10 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

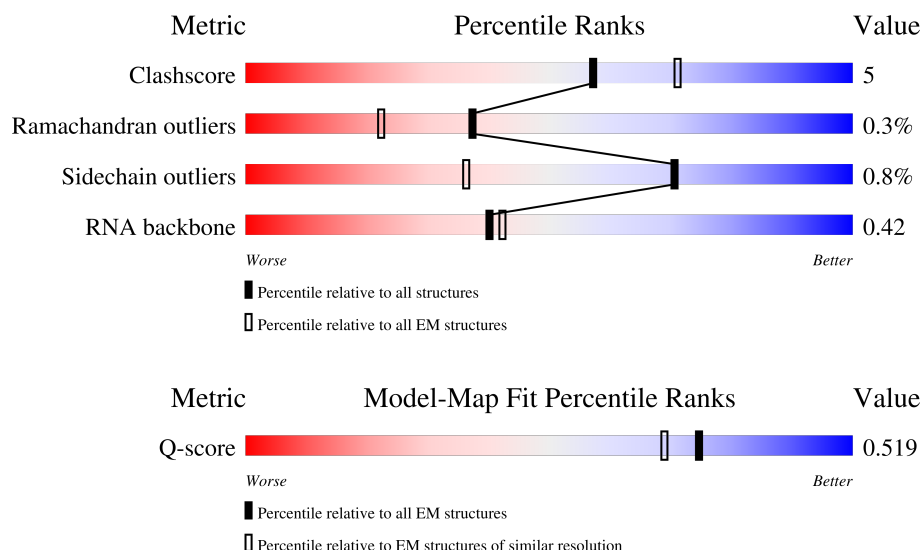
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.10 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.



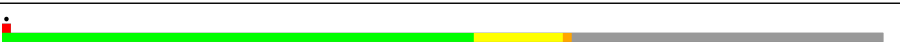
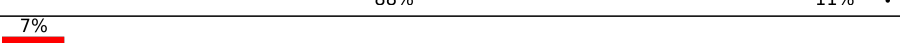
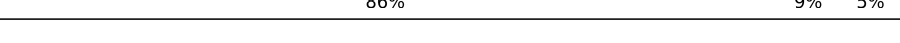
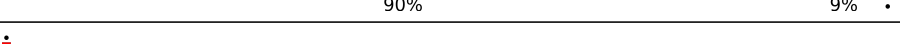
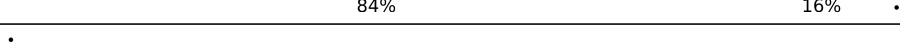
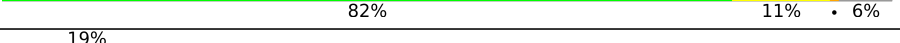
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	14724 (2.60 - 3.60)

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	5066	
2	L7	121	
3	L8	157	

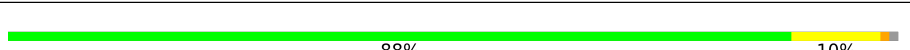
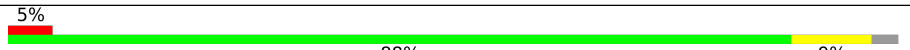
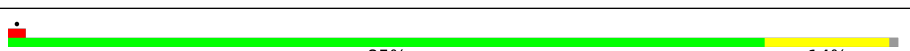
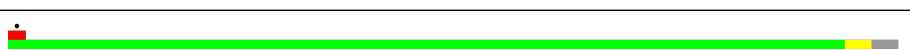
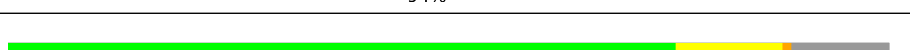
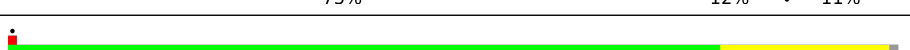
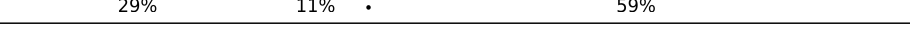
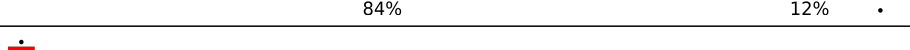
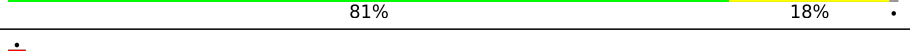
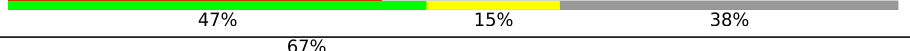
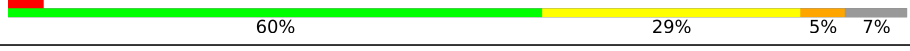
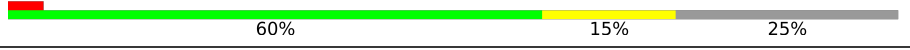
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Mol	Chain	Length	Quality of chain
4	LA	257	
5	LB	403	
6	LC	427	
7	LD	297	
8	LE	288	
9	LF	248	
10	LG	266	
11	LH	192	
12	LI	214	
13	LJ	178	
14	LL	211	
15	LM	215	
16	LN	204	
17	LO	203	
18	LP	184	
19	LQ	188	
20	LR	196	
21	LS	176	
22	LT	160	
23	LU	128	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

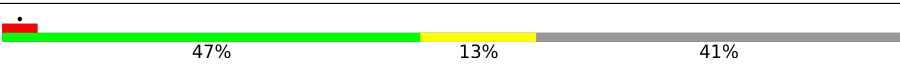
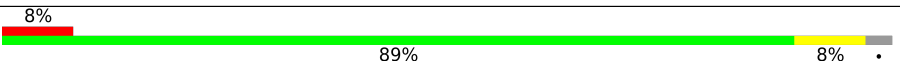
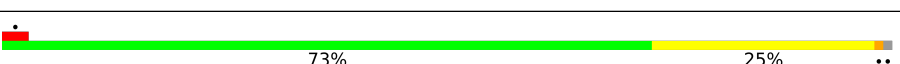
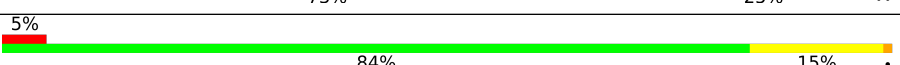
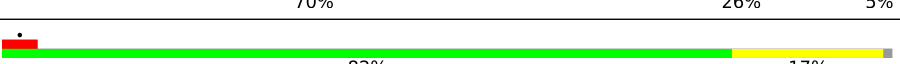
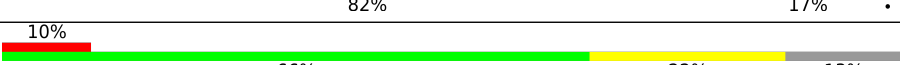
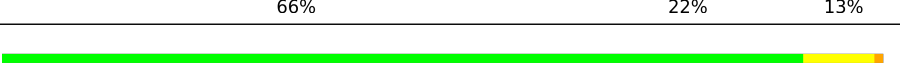
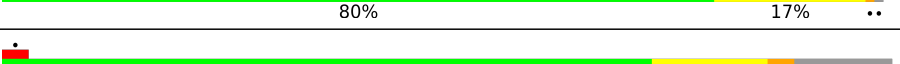
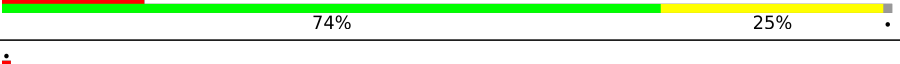
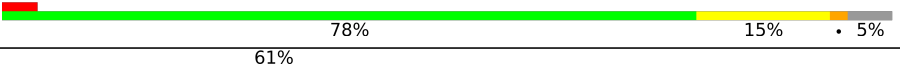
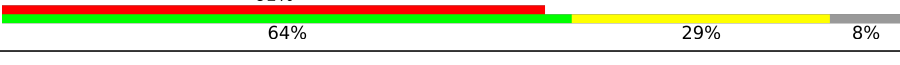
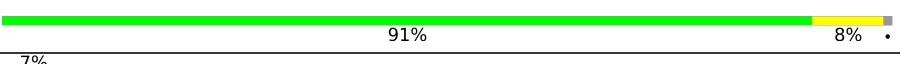
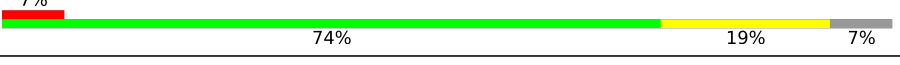
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Mol	Chain	Length	Quality of chain
29	La	148	
30	Lb	159	
31	Lc	115	
32	Ld	125	
33	Le	135	
34	Lf	110	
35	Lg	117	
36	Lh	123	
37	Li	105	
38	Lj	97	
39	Lk	70	
40	Ll	51	
41	Lm	128	
42	Ln	25	
43	Lo	106	
44	Lp	92	
45	Lr	137	
46	Ls	317	
47	Lt	165	
48	Lz	217	
49	S2	1869	
50	SA	295	
51	SB	264	
52	SD	243	
53	SE	263	

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Mol	Chain	Length	Quality of chain
54	SF	204	
55	SH	194	
56	SI	208	
57	SK	165	
58	SL	158	
59	SP	145	
60	SQ	146	
61	SR	135	
62	SS	152	
63	ST	145	
64	SU	119	
65	SV	83	
66	SX	143	
67	Sa	115	
68	Sc	69	
69	Sd	56	
70	Sg	317	
71	SC	293	
72	SG	249	
73	SJ	194	
74	SM	132	
75	SN	151	
76	SO	151	
77	SW	130	
78	SY	133	

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Mol	Chain	Length	Quality of chain
79	SZ	125	
80	Sb	84	
81	Se	59	
82	Sf	156	
83	CA	394	
84	CB	87	
85	CC	75	
86	CD	462	
87	CE	379	
88	i	180	

2 Entry composition

There are 90 unique types of molecules in this entry. The entry contains 230351 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 ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	L5	3773	Total	C	N	O	P	0	0
			80138	35655	14589	26122	3772		

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

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 ribosomal RNA.

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 acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Ls	196	Total	C	N	O	S	0	0
			1496	952	259	276	9		

- Molecule 47 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	Lt	141	Total	C	N	O	S	0	0
			1046	652	191	199	4		

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

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

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	1740	Total	C	N	O	P	0	0
			36899	16459	6598	12103	1739		

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

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

- Molecule 51 is a protein called 40S ribosomal protein S3a.

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

- Molecule 52 is a protein called 40S ribosomal protein S3.

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

- Molecule 53 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 54 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	SF	184	Total	C	N	O	S	0	0
			1461	914	276	264	7		

- Molecule 55 is a protein called 40S ribosomal protein S7.

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

- Molecule 56 is a protein called 40S ribosomal protein S8.

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

- Molecule 57 is a protein called 40S ribosomal protein S10.

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

- Molecule 58 is a protein called 40S ribosomal protein S11.

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

- Molecule 59 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	SP	129	Total	C	N	O	S	0	0
			1061	672	202	180	7		

- Molecule 60 is a protein called 40S ribosomal protein S16.

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

- Molecule 61 is a protein called 40S ribosomal protein S17.

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

- Molecule 62 is a protein called 40S ribosomal protein S18.

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

- Molecule 63 is a protein called 40S ribosomal protein S19.

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

- Molecule 64 is a protein called 40S ribosomal protein S20.

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

- Molecule 65 is a protein called 40S ribosomal protein S21.

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

- Molecule 66 is a protein called 40S ribosomal protein S23.

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

- Molecule 67 is a protein called 40S ribosomal protein S26.

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

- Molecule 68 is a protein called 40S ribosomal protein S28.

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

- Molecule 69 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Sd	55	Total	C	N	O	S	0	0
			459	286	94	74	5		

- Molecule 70 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 71 is a protein called 40S ribosomal protein S2.

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

- Molecule 72 is a protein called 40S ribosomal protein S6.

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

- Molecule 73 is a protein called 40S ribosomal protein S9.

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

- Molecule 74 is a protein called 40S ribosomal protein S12.

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

- Molecule 75 is a protein called 40S ribosomal protein S13.

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

- Molecule 76 is a protein called 40S ribosomal protein S14.

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

- Molecule 77 is a protein called 40S ribosomal protein S15a.

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

- Molecule 78 is a protein called 40S ribosomal protein S24.

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

- Molecule 79 is a protein called 40S ribosomal protein S25.

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

- Molecule 80 is a protein called 40S ribosomal protein S27.

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

- Molecule 81 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	Se	58	Total	C	N	O	S	0	0
			443	271	98	73	1		

- Molecule 82 is a protein called Ubiquitin-40S ribosomal protein S27a.

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

- Molecule 83 is a protein called Proliferation-associated protein 2G4.

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

- Molecule 84 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	CB	87	Total	C	N	O	P	0	0
			1858	828	332	611	87		

- Molecule 85 is a RNA chain called tRNA.

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

- Molecule 86 is a protein called Elongation factor 1-alpha 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	CD	440	Total	C	N	O	S	0	0
			3371	2143	581	630	17		

- Molecule 87 is a protein called Cell growth-regulating nucleolar protein.

Mol	Chain	Residues	Atoms				AltConf	Trace
87	CE	72	Total	C	N	O	0	0
			603	395	105	103		

- Molecule 88 is a protein called Non-structural protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
88	i	33	Total	C	N	O	S	0	0
			263	160	47	55	1		

- Molecule 89 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
89	L5	212	Total	Mg	0
			212	212	
89	L7	3	Total	Mg	0
			3	3	
89	L8	4	Total	Mg	0
			4	4	
89	LA	1	Total	Mg	0
			1	1	
89	LI	1	Total	Mg	0
			1	1	
89	LP	1	Total	Mg	0
			1	1	

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Mol	Chain	Residues	Atoms		AltConf
89	LV	1	Total 1	Mg 1	0
89	Le	2	Total 2	Mg 2	0
89	Lg	1	Total 1	Mg 1	0
89	S2	28	Total 28	Mg 28	0
89	SG	1	Total 1	Mg 1	0
89	SO	1	Total 1	Mg 1	0

- Molecule 90 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

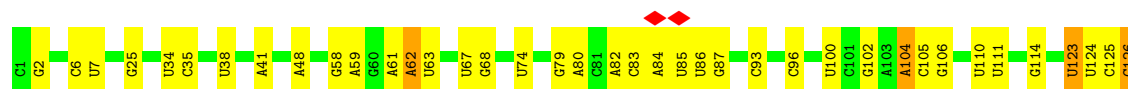




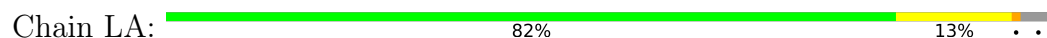




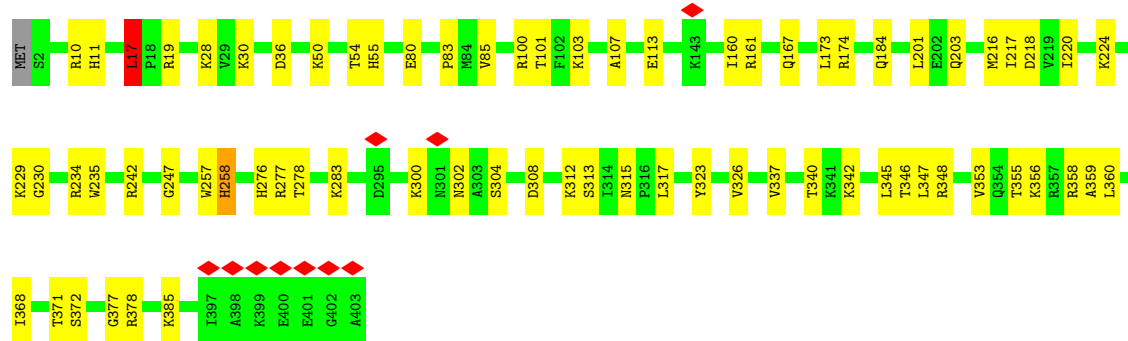
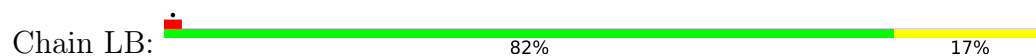
• Molecule 3: 5.8S ribosomal RNA



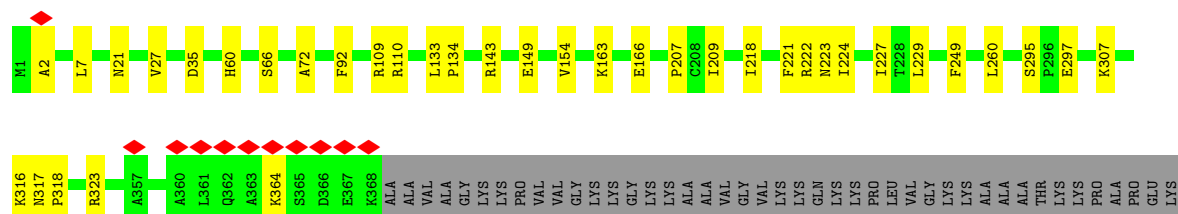
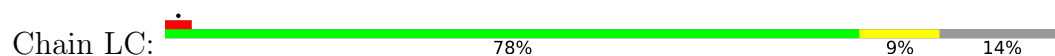
• Molecule 4: 60S ribosomal protein L8



• Molecule 5: 60S ribosomal protein L3



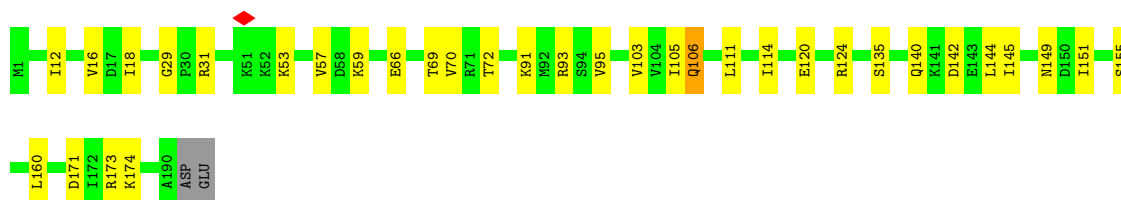
• Molecule 6: 60S ribosomal protein L4





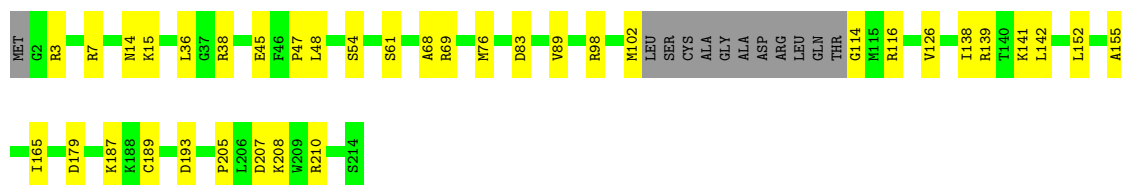
- Molecule 11: 60S ribosomal protein L9

Chain LH: 81% 17% ..



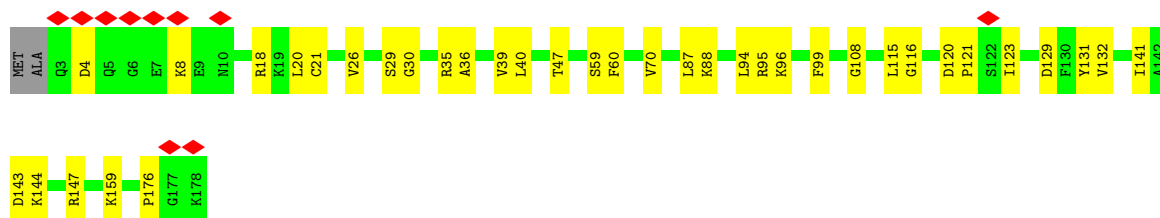
- Molecule 12: 60S ribosomal protein L10-like

Chain LI: 78% 17% 6%



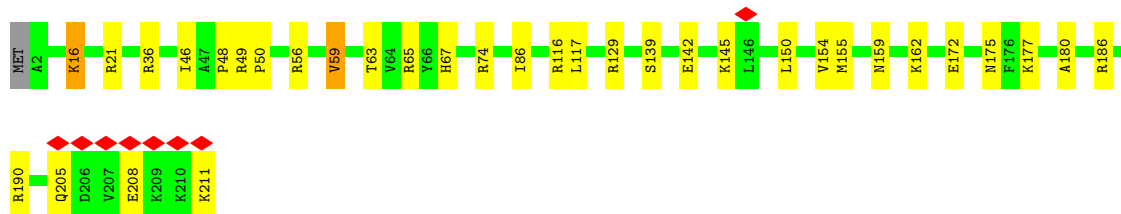
- Molecule 13: 60S ribosomal protein L11

Chain LJ: 6% 78% 21% .



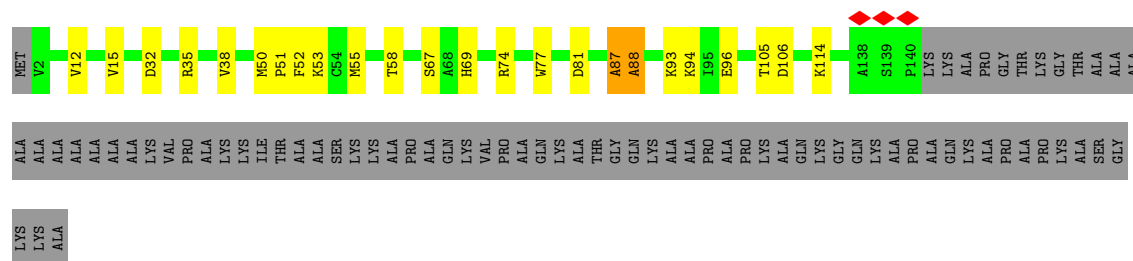
- Molecule 14: 60S ribosomal protein L13

Chain LL: 83% 15% .



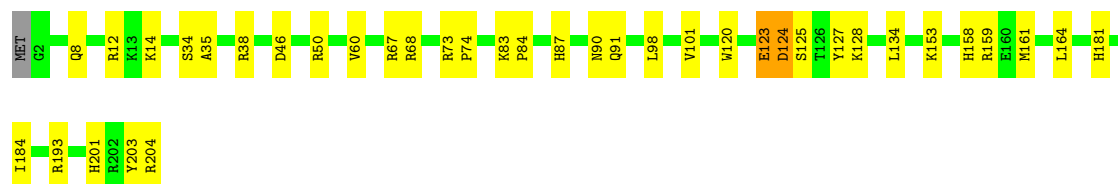
- Molecule 15: 60S ribosomal protein L14

Chain LM: 53% 10% 35%



- Molecule 16: 60S ribosomal protein L15

Chain LN: 81% 18% .



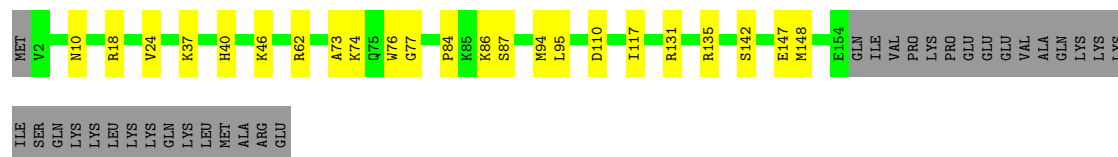
- Molecule 17: 60S ribosomal protein L13a

Chain LO: 88% 11% .



- Molecule 18: 60S ribosomal protein L17

Chain LP: 71% 12% 17%



- Molecule 19: 60S ribosomal protein L18

Chain LQ: 88% 11% .



- Molecule 20: 60S ribosomal protein L19

Chain LR: 7% 86% 9% 5%



- | | | | | | | | |
|------|------|------|------|------|------|------|------|
| MET | ALA | PRO | LYS | ALA | LYS | LYS | GLU | GLU | PRO | PRO | ALA | ALA | PRO | LYS | LYS | ALA | ALA | GLU | LYS | ALA | LYS | LYS | ALA | ALA | VAL | LYS | LYS | GLY | VAL | HIS | SER | HIS | LYS | LYS | K37 | K38 | K50 | Y60 | P61 | G62 | D72 | V100 | A104 | R129 | G132 | E133 | K134 | K135 | L147 |
|------|------|------|------|------|------|------|------|



- Molecule 27: 60S ribosomal protein L26

Chain LY: 81% 12% 8%



- Molecule 28: 60S ribosomal protein L27

Chain LZ: 82% 17% .



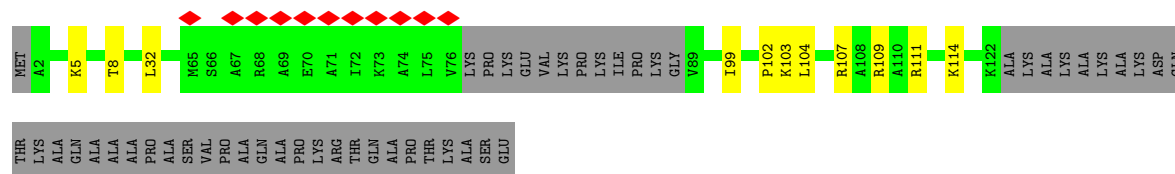
- Molecule 29: 60S ribosomal protein L27a

Chain La: 86% 14% .



- Molecule 30: 60S ribosomal protein L29

Chain Lb: 7% 62% 7% 31%



- Molecule 31: 60S ribosomal protein L30

Chain Lc: 70% 15% 15%



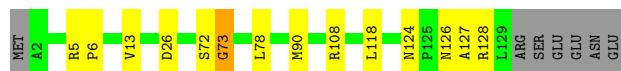
- Molecule 32: 60S ribosomal protein L31

Chain Ld: 70% 15% 14%



- Molecule 33: 60S ribosomal protein L32

Chain Le:  84% 10% 5%



- Molecule 34: 60S ribosomal protein L35a

Chain Lf:  88% 10% ..



- Molecule 35: 60S ribosomal protein L34

Chain Lg:  5% 88% 9% .



- Molecule 36: 60S ribosomal protein L35

Chain Lh:  85% 14% .



- Molecule 37: 60S ribosomal protein L36

Chain Li:  94% . .



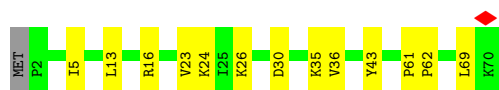
- Molecule 38: 60S ribosomal protein L37

Chain Lj:  75% 12% 11%



- Molecule 39: 60S ribosomal protein L38

Chain Lk:  80% 19% .



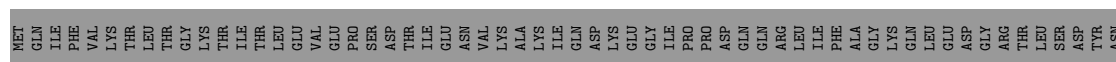
- Molecule 40: 60S ribosomal protein L39

Chain Ll: 90% 8%



- Molecule 41: Ubiquitin-60S ribosomal protein L40

Chain Lm: 29% 11% 59%



- Molecule 42: 60S ribosomal protein L41

Chain Ln: 84% 12%



- Molecule 43: 60S ribosomal protein L36a

Chain Lo: 81% 18%



- Molecule 44: 60S ribosomal protein L37a

Chain Lp: 86% 13%

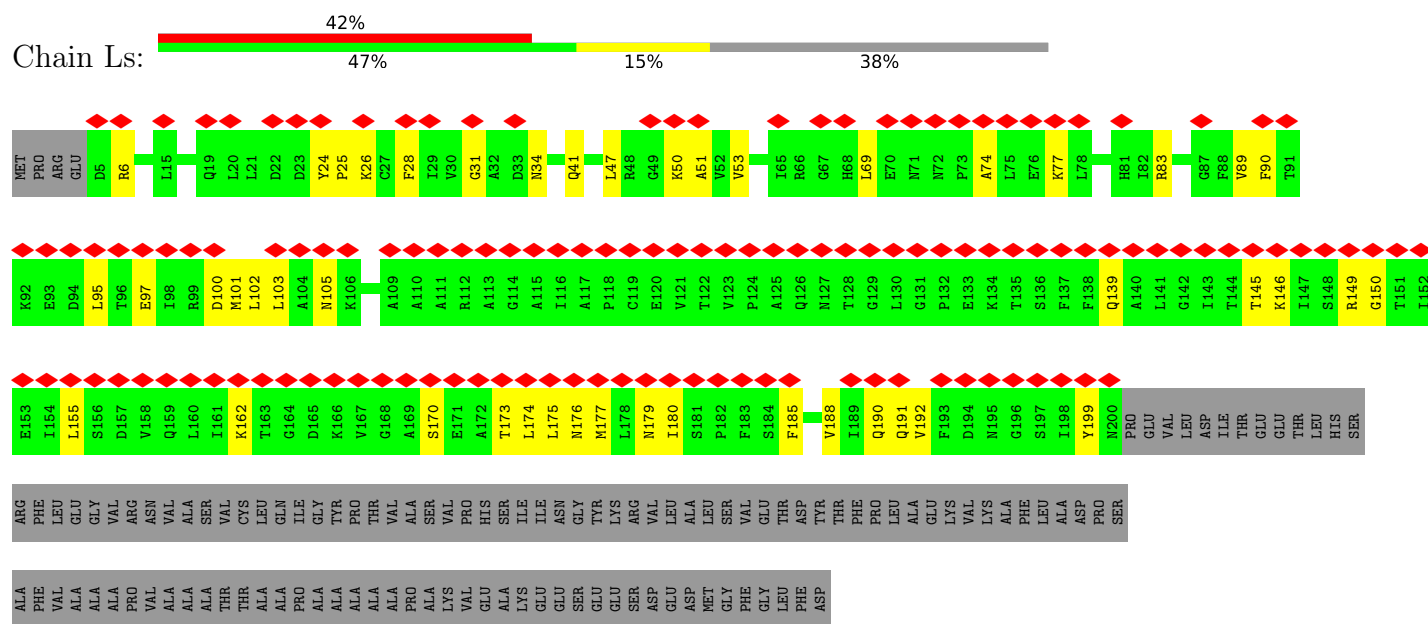


- Molecule 45: 60S ribosomal protein L28

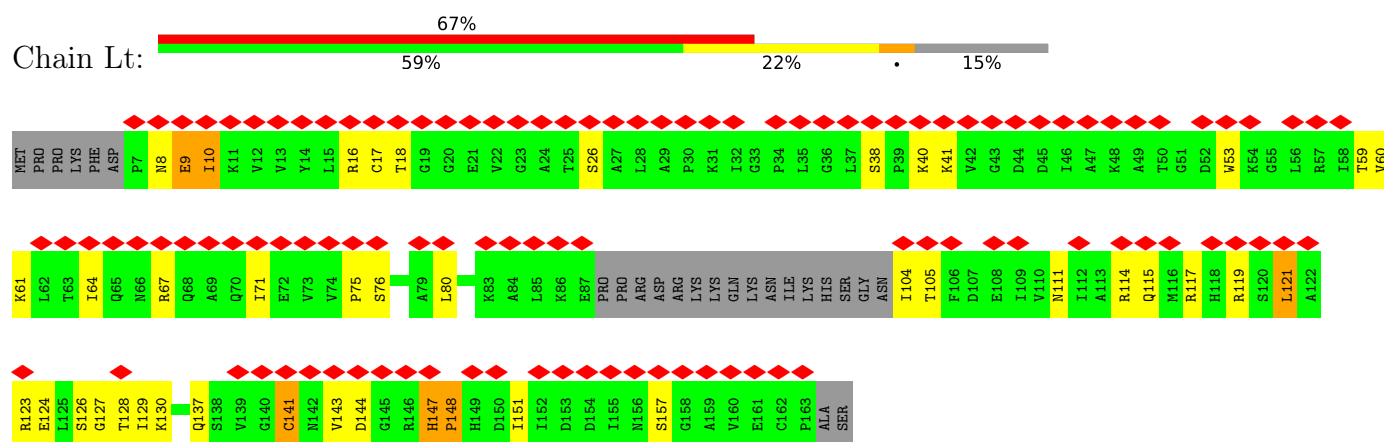
Chain Lr: 79% 12% 9%



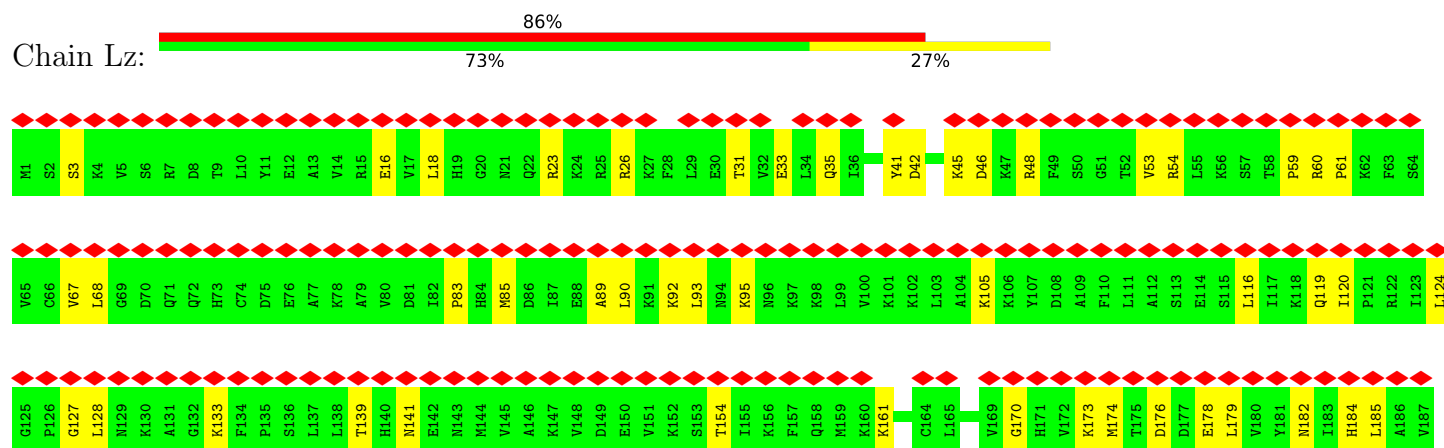
• Molecule 46: 60S acidic ribosomal protein P0

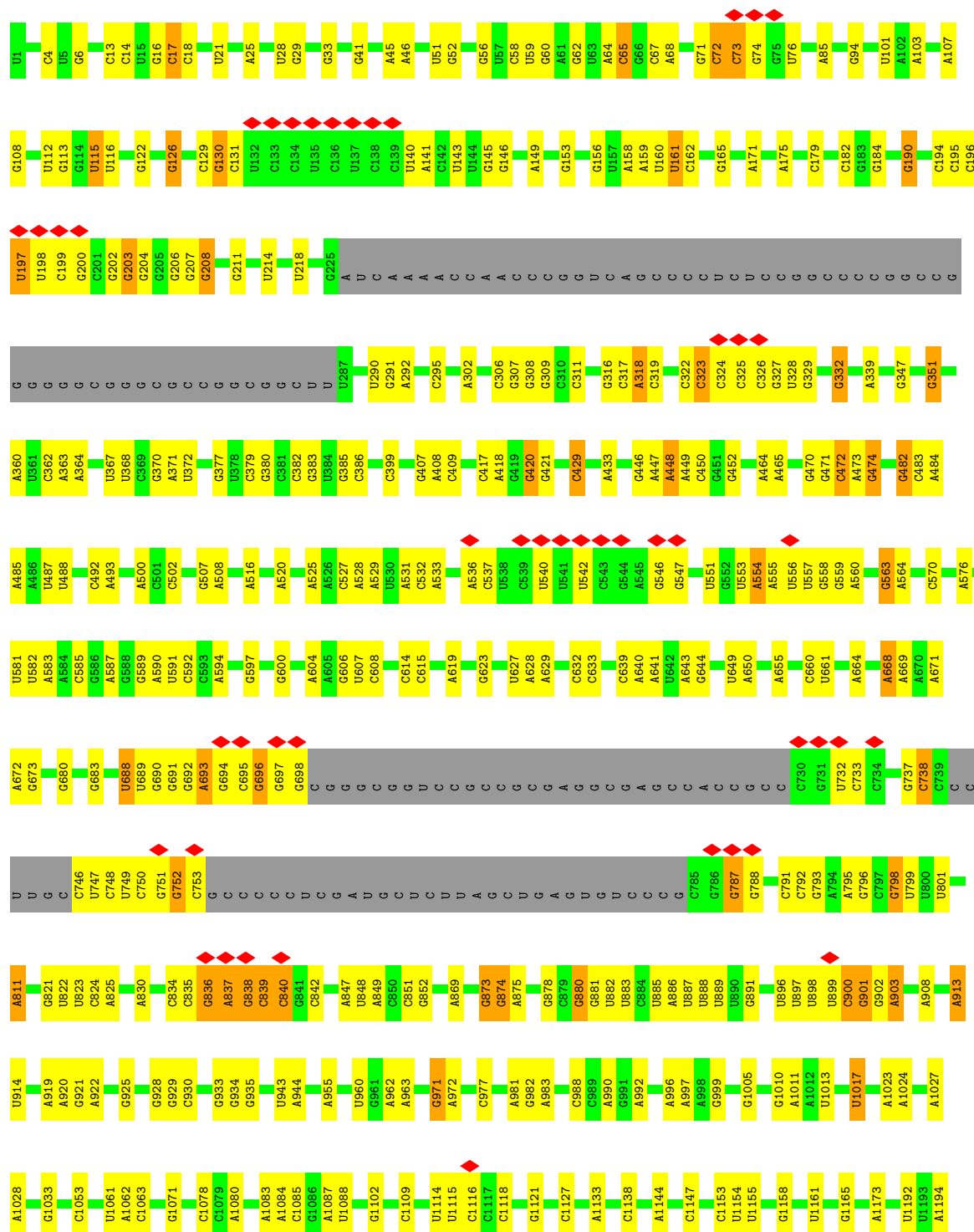


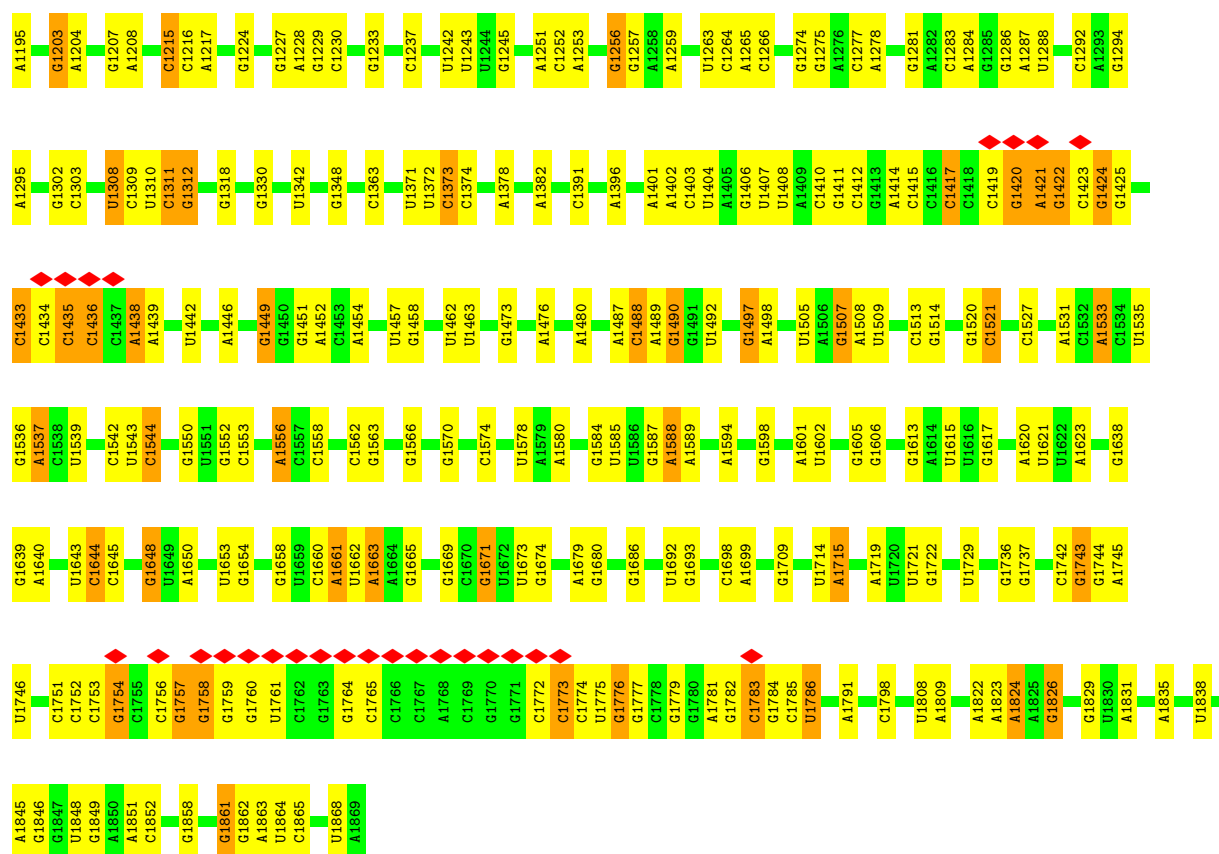
• Molecule 47: 60S ribosomal protein L12



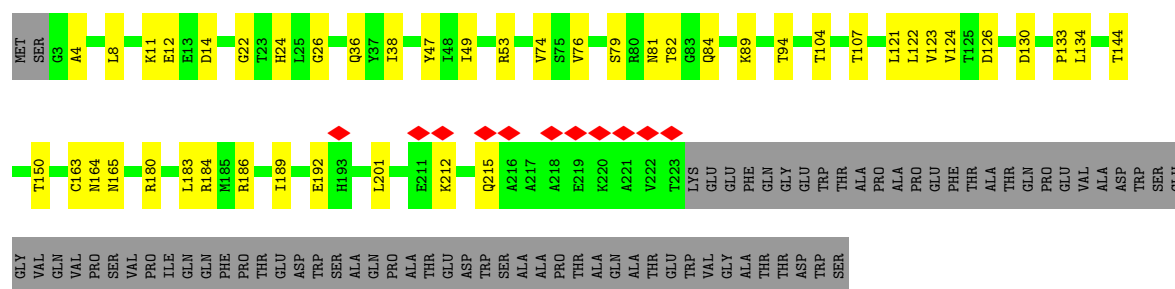
• Molecule 48: 60S ribosomal protein L10a



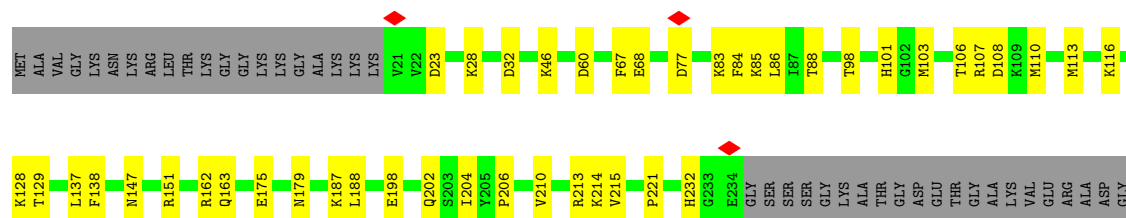




• Molecule 50: 40S ribosomal protein SA

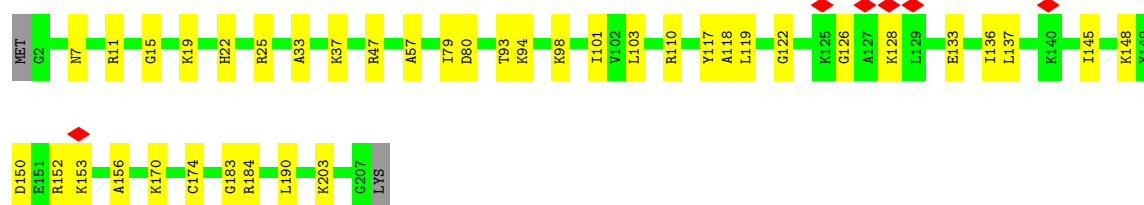


• Molecule 51: 40S ribosomal protein S3a



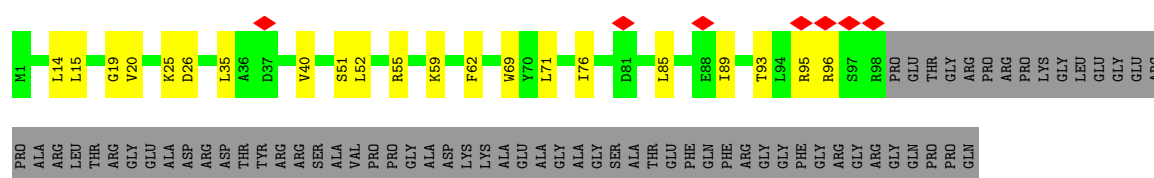
- Molecule 56: 40S ribosomal protein S8

Chain SI:  80% 19%

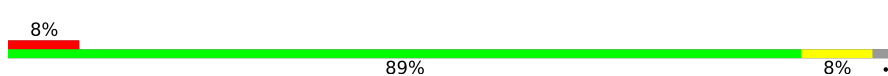


- Molecule 57: 40S ribosomal protein S10

Chain SK:  47% 13% 41%



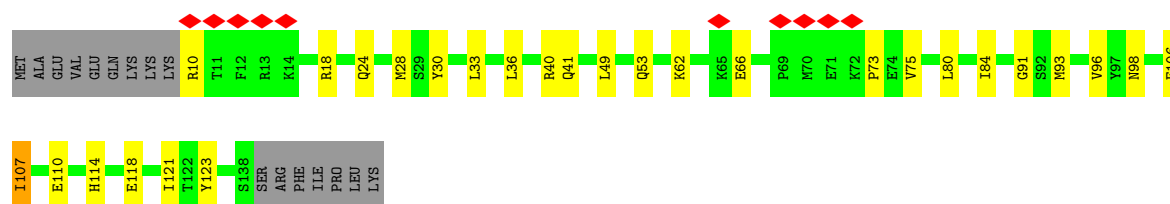
- Molecule 58: 40S ribosomal protein S11

Chain SL:  8% 89% 8%



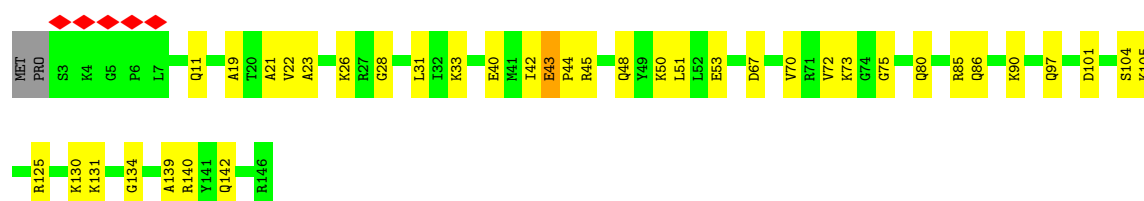
- Molecule 59: 40S ribosomal protein S15

Chain SP:  7% 70% 19% 11%

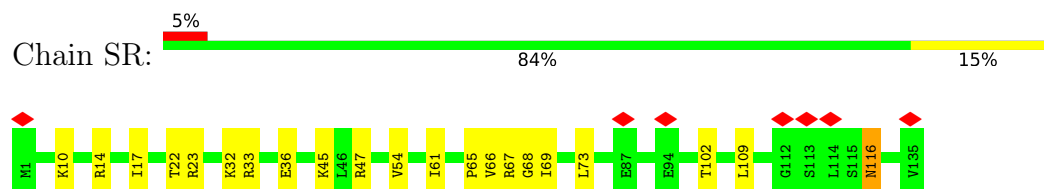


- Molecule 60: 40S ribosomal protein S16

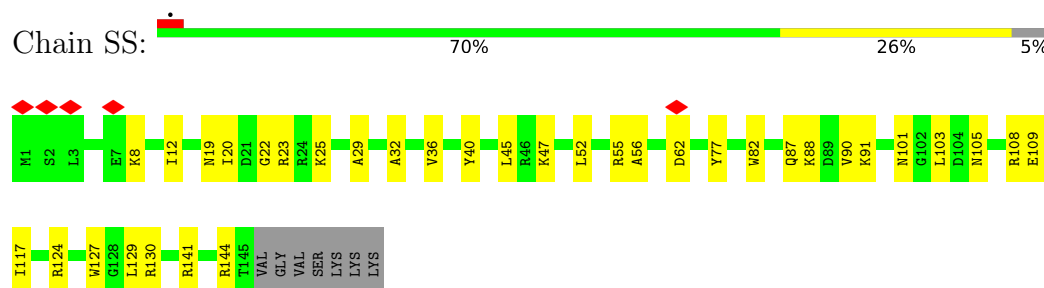
Chain SQ:  73% 25%



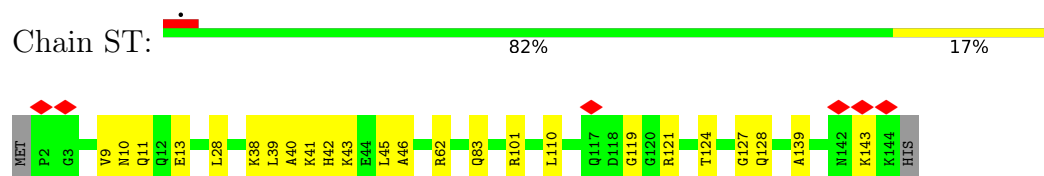
- Molecule 61: 40S ribosomal protein S17



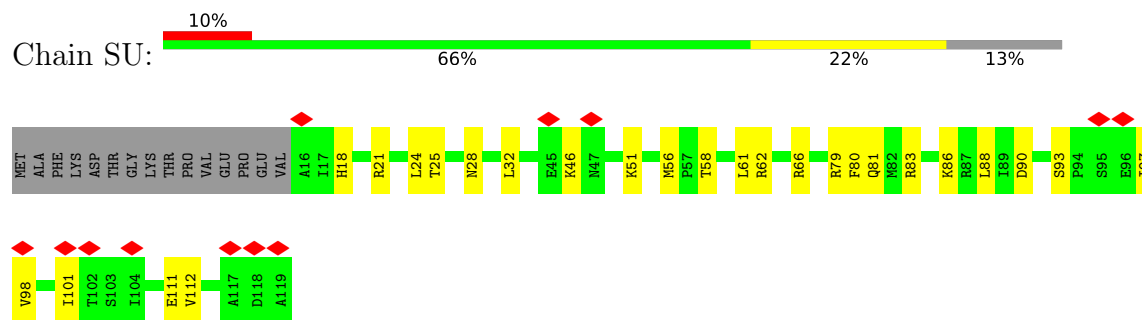
- Molecule 62: 40S ribosomal protein S18



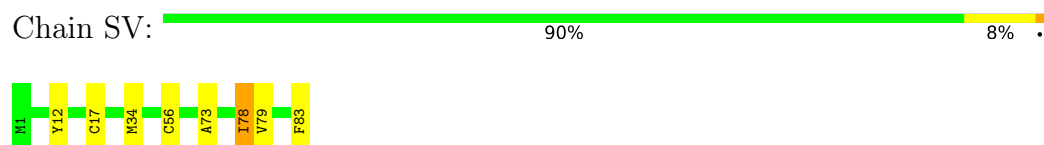
- Molecule 63: 40S ribosomal protein S19



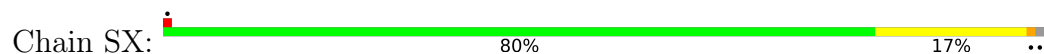
- Molecule 64: 40S ribosomal protein S20

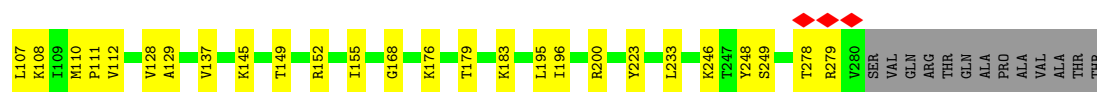


- Molecule 65: 40S ribosomal protein S21

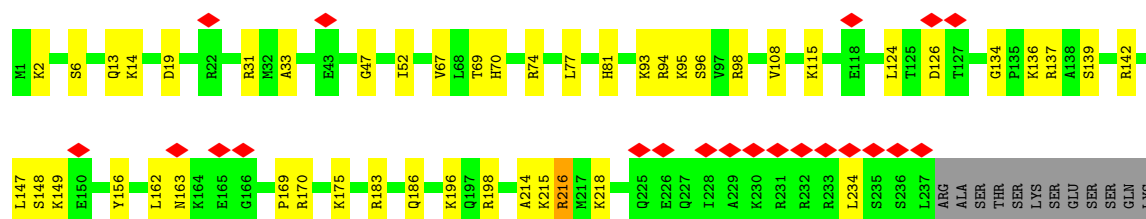
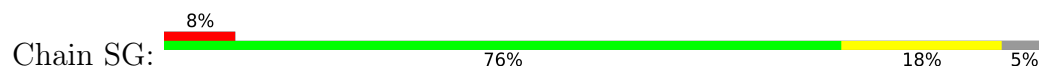


- Molecule 66: 40S ribosomal protein S23

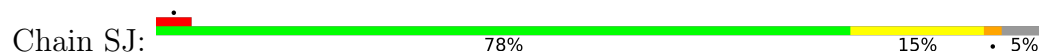




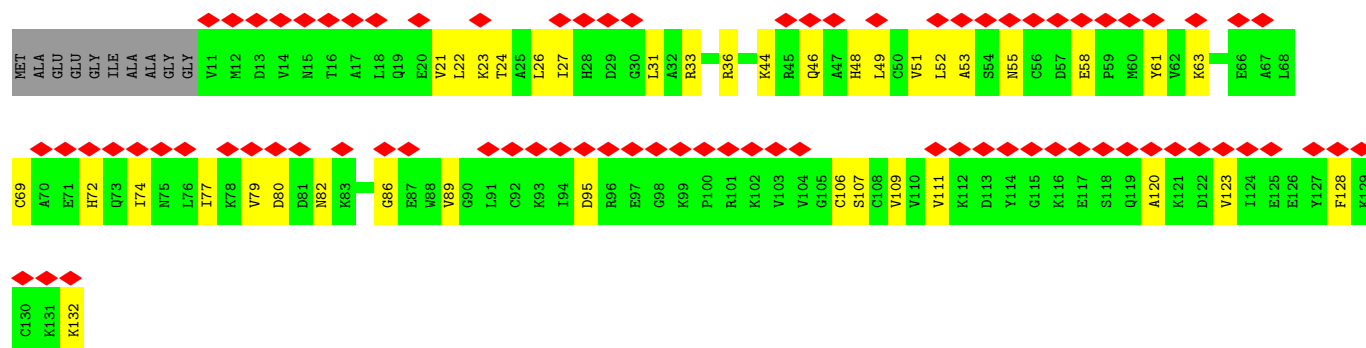
- Molecule 72: 40S ribosomal protein S6



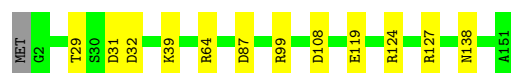
- Molecule 73: 40S ribosomal protein S9



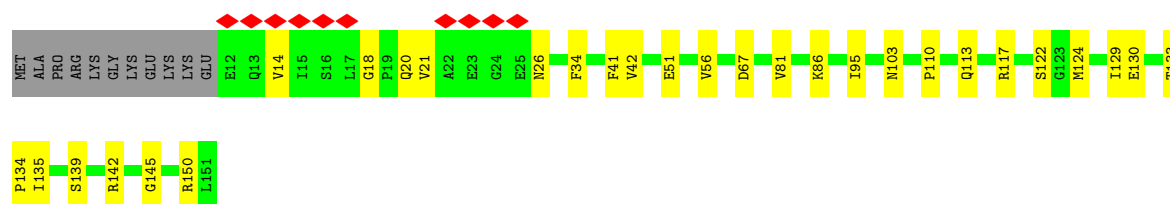
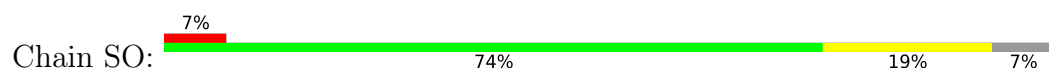
- Molecule 74: 40S ribosomal protein S12



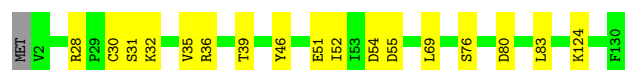
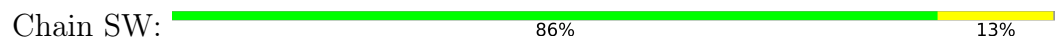
- Molecule 75: 40S ribosomal protein S13



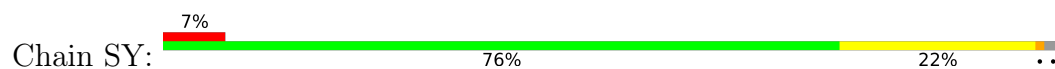
- Molecule 76: 40S ribosomal protein S14



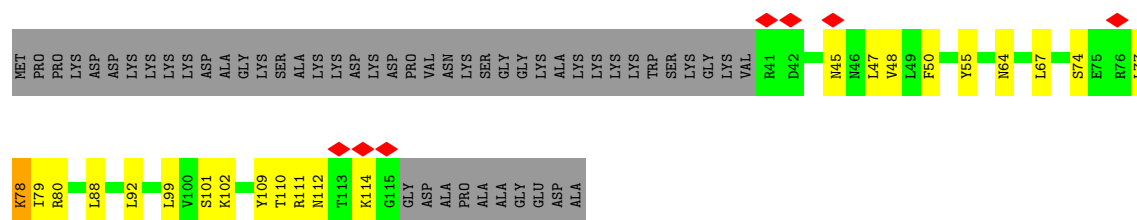
- Molecule 77: 40S ribosomal protein S15a



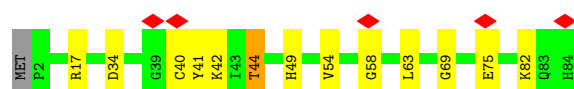
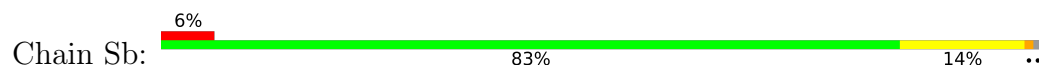
- Molecule 78: 40S ribosomal protein S24



- Molecule 79: 40S ribosomal protein S25

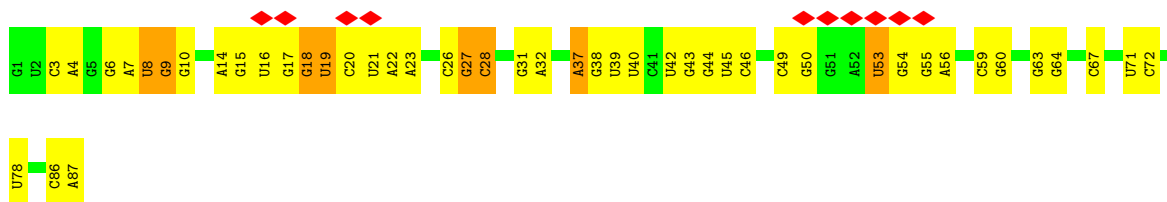


- Molecule 80: 40S ribosomal protein S27



- Molecule 81: 40S ribosomal protein S30

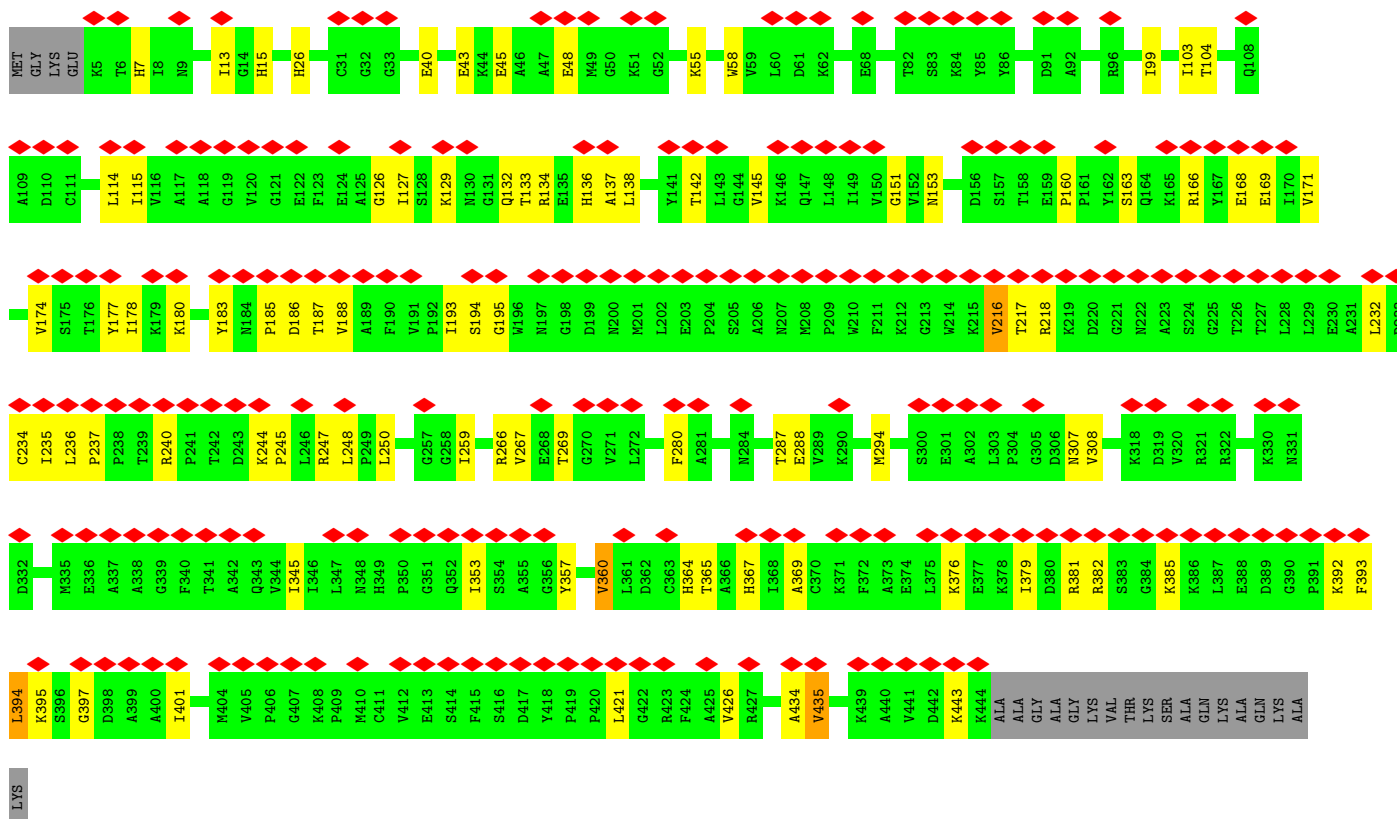
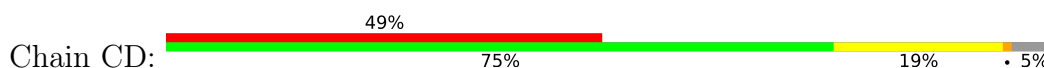




• Molecule 85: tRNA



• Molecule 86: Elongation factor 1-alpha 1





- Molecule 88: Non-structural protein 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	11417	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 ($e^-/\text{\AA}^2$)	44.8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.445	Depositor
Minimum map value	-0.150	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.018	Depositor
Recommended contour level	0.05	Depositor
Map size (Å)	423.6, 423.6, 423.6	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.059, 1.059, 1.059	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	0/89595	0.48	11/139686 (0.0%)
2	L7	0.46	0/2861	0.42	0/4459
3	L8	0.53	0/3701	0.44	0/5766
4	LA	0.57	0/1936	0.77	2/2596 (0.1%)
5	LB	0.49	0/3306	0.70	3/4424 (0.1%)
6	LC	0.50	0/2981	0.67	2/4002 (0.0%)
7	LD	0.38	0/2428	0.61	0/3252
8	LE	0.37	0/1942	0.62	0/2606
9	LF	0.50	0/1905	0.64	0/2539
10	LG	0.40	0/1960	0.66	0/2637
11	LH	0.41	0/1537	0.58	0/2066
12	LI	0.44	0/1673	0.64	0/2233
13	LJ	0.34	0/1433	0.71	1/1915 (0.1%)
14	LL	0.44	0/1732	0.63	1/2315 (0.0%)
15	LM	0.45	0/1161	0.69	2/1554 (0.1%)
16	LN	0.55	0/1746	0.74	2/2338 (0.1%)
17	LO	0.49	0/1682	0.58	0/2250
18	LP	0.50	0/1268	0.62	0/1701
19	LQ	0.53	0/1537	0.62	0/2052
20	LR	0.44	0/1582	0.62	2/2091 (0.1%)
21	LS	0.49	0/1493	0.58	0/2003
22	LT	0.46	0/1326	0.66	0/1770
23	LU	0.35	0/839	0.78	1/1126 (0.1%)
24	LV	0.49	0/993	0.64	0/1332
25	LW	0.39	0/1030	0.62	1/1364 (0.1%)
26	LX	0.44	0/1002	0.56	0/1345
27	LY	0.45	0/1132	0.61	0/1504
28	LZ	0.42	0/1130	0.61	0/1507
29	La	0.54	0/1191	0.66	2/1591 (0.1%)
30	Lb	0.38	0/889	0.68	0/1175
31	Lc	0.48	0/774	0.65	0/1038
32	Ld	0.44	0/903	0.61	0/1216

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Le	0.55	0/1071	0.66	0/1429
34	Lf	0.56	0/895	0.71	0/1198
35	Lg	0.50	0/916	0.65	0/1220
36	Lh	0.40	0/1023	0.61	0/1351
37	Li	0.37	0/843	0.57	0/1115
38	Lj	0.55	0/720	0.72	0/952
39	Lk	0.36	0/575	0.54	0/761
40	Ll	0.51	0/454	0.70	0/599
41	Lm	0.47	0/435	0.66	0/575
42	Ln	0.46	0/231	0.66	0/294
43	Lo	0.44	0/876	0.62	1/1156 (0.1%)
44	Lp	0.49	0/718	0.60	0/953
45	Lr	0.44	0/1017	0.60	0/1364
46	Ls	0.25	0/1519	0.63	0/2052
47	Lt	0.32	0/1058	0.91	4/1430 (0.3%)
48	Lz	0.25	0/1769	0.67	0/2371
49	S2	0.47	0/41245	0.46	3/64265 (0.0%)
50	SA	0.41	0/1778	0.63	0/2416
51	SB	0.38	0/1765	0.59	0/2362
52	SD	0.33	0/1793	0.66	2/2414 (0.1%)
53	SE	0.40	0/2118	0.61	0/2849
54	SF	0.36	0/1481	0.65	0/1988
55	SH	0.36	0/1519	0.72	0/2033
56	SI	0.45	0/1715	0.65	0/2287
57	SK	0.29	0/851	0.55	0/1147
58	SL	0.48	0/1268	0.60	0/1696
59	SP	0.28	0/1082	0.69	2/1446 (0.1%)
60	SQ	0.35	0/1160	0.67	0/1553
61	SR	0.32	0/1105	0.62	0/1484
62	SS	0.29	0/1216	0.58	1/1628 (0.1%)
63	ST	0.34	0/1131	0.65	0/1515
64	SU	0.35	0/831	0.67	0/1115
65	SV	0.38	0/643	0.55	0/860
66	SX	0.47	0/1116	0.71	1/1490 (0.1%)
67	Sa	0.47	0/836	0.67	0/1121
68	Sc	0.34	0/508	0.83	0/680
69	Sd	0.41	0/470	0.66	0/623
70	Sg	0.29	0/2493	0.68	2/3394 (0.1%)
71	SC	0.47	0/1762	0.71	0/2381
72	SG	0.31	0/1946	0.62	4/2590 (0.2%)
73	SJ	0.41	0/1550	0.63	0/2069
74	SM	0.25	0/950	0.70	0/1275
75	SN	0.43	0/1232	0.53	0/1656

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SO	0.43	0/1062	0.73	2/1425 (0.1%)
77	SW	0.49	0/1051	0.64	0/1406
78	SY	0.33	0/1083	0.59	0/1438
79	SZ	0.29	0/604	0.73	0/810
80	Sb	0.38	0/665	0.61	0/891
81	Se	0.31	0/448	0.56	0/592
82	Sf	0.26	0/560	0.75	0/745
83	CA	0.29	0/2810	0.76	1/3780 (0.0%)
84	CB	0.19	0/2076	0.36	0/3235
85	CC	0.23	0/1773	0.39	1/2759 (0.0%)
86	CD	0.23	0/3441	0.58	1/4657 (0.0%)
87	CE	0.31	0/613	0.61	0/819
88	i	0.37	0/268	0.56	0/361
All	All	0.47	0/246806	0.55	55/361528 (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	3
5	LB	0	2
9	LF	0	1
10	LG	0	1
11	LH	0	1
12	LI	0	3
13	LJ	0	2
14	LL	0	1
15	LM	0	2
17	LO	0	1
18	LP	0	1
22	LT	0	3
29	La	0	1
34	Lf	0	2
36	Lh	0	1
38	Lj	0	1
46	Ls	0	1
47	Lt	0	6
51	SB	0	1
52	SD	0	1
54	SF	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
55	SH	0	1
60	SQ	0	1
63	ST	0	1
65	SV	0	1
66	SX	0	3
67	Sa	0	1
68	Sc	0	1
73	SJ	0	2
77	SW	0	1
80	Sb	0	1
All	All	0	50

There are no bond length outliers.

The worst 5 of 55 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	SP	107	ILE	CA-C-N	8.86	149.53	121.98
59	SP	107	ILE	C-N-CA	8.86	149.53	121.98
83	CA	12	ILE	N-CA-C	-7.82	105.09	112.83
1	L5	4911	A	C2'-C3'-O3'	-7.26	98.61	109.50
6	LC	2	ALA	CA-C-N	7.16	134.58	121.70

There are no chirality outliers.

5 of 50 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
4	LA	110	GLY	Peptide
4	LA	244	GLY	Peptide
4	LA	54	ARG	Peptide
5	LB	17	LEU	Peptide
5	LB	258	HIS	Peptide

5.2 Too-close contacts [i](#)

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.

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	L5	80138	0	40376	403	0
2	L7	2561	0	1295	7	0
3	L8	3314	0	1683	16	0
4	LA	1898	0	1993	20	0
5	LB	3238	0	3376	41	0
6	LC	2927	0	3104	26	0
7	LD	2382	0	2410	29	0
8	LE	1904	0	2055	30	0
9	LF	1870	0	1996	19	0
10	LG	1927	0	2074	28	0
11	LH	1518	0	1601	24	0
12	LI	1634	0	1670	22	0
13	LJ	1410	0	1441	22	0
14	LL	1701	0	1818	23	0
15	LM	1138	0	1204	16	0
16	LN	1701	0	1749	26	0
17	LO	1650	0	1794	14	0
18	LP	1242	0	1269	17	0
19	LQ	1513	0	1628	13	0
20	LR	1566	0	1729	13	0
21	LS	1453	0	1490	12	0
22	LT	1298	0	1366	13	0
23	LU	825	0	850	8	0
24	LV	979	0	1039	11	0
25	LW	1015	0	1079	17	0
26	LX	985	0	1066	12	0
27	LY	1115	0	1205	12	0
28	LZ	1107	0	1182	16	0
29	La	1162	0	1213	12	0
30	Lb	876	0	948	8	0
31	Lc	764	0	804	11	0
32	Ld	888	0	930	12	0
33	Le	1053	0	1147	11	0
34	Lf	876	0	912	6	0
35	Lg	906	0	998	7	0
36	Lh	1015	0	1148	12	0
37	Li	832	0	917	2	0
38	Lj	705	0	738	10	0
39	Lk	569	0	637	8	0
40	Ll	444	0	483	3	0
41	Lm	429	0	465	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	Ln	230	0	276	3	0
43	Lo	862	0	929	11	0
44	Lp	708	0	756	6	0
45	Lr	1002	0	1068	12	0
46	Ls	1496	0	1540	30	0
47	Lt	1046	0	1076	23	0
48	Lz	1741	0	1854	35	0
49	S2	36899	0	18602	249	0
50	SA	1741	0	1746	28	0
51	SB	1738	0	1809	33	0
52	SD	1765	0	1865	21	0
53	SE	2076	0	2177	24	0
54	SF	1461	0	1511	21	0
55	SH	1497	0	1590	39	0
56	SI	1686	0	1772	29	0
57	SK	827	0	854	13	0
58	SL	1247	0	1323	7	0
59	SP	1061	0	1107	18	0
60	SQ	1142	0	1213	23	0
61	SR	1090	0	1149	13	0
62	SS	1198	0	1261	31	0
63	ST	1112	0	1146	15	0
64	SU	821	0	883	19	0
65	SV	636	0	637	6	0
66	SX	1098	0	1167	14	0
67	Sa	821	0	870	14	0
68	Sc	506	0	536	10	0
69	Sd	459	0	449	10	0
70	Sg	2436	0	2393	45	0
71	SC	1725	0	1813	14	0
72	SG	1923	0	2089	37	0
73	SJ	1525	0	1640	20	0
74	SM	940	0	965	27	0
75	SN	1208	0	1294	11	0
76	SO	1049	0	1073	21	0
77	SW	1034	0	1080	12	0
78	SY	1065	0	1142	24	0
79	SZ	598	0	656	17	0
80	Sb	651	0	672	7	0
81	Se	443	0	469	4	0
82	Sf	548	0	553	12	0
83	CA	2764	0	2779	49	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
84	CB	1858	0	939	29	0
85	CC	1589	0	810	15	0
86	CD	3371	0	3428	55	0
87	CE	603	0	660	5	0
88	i	263	0	234	2	0
89	L5	212	0	0	0	0
89	L7	3	0	0	0	0
89	L8	4	0	0	0	0
89	LA	1	0	0	0	0
89	LI	1	0	0	0	0
89	LP	1	0	0	0	0
89	LV	1	0	0	0	0
89	Le	2	0	0	0	0
89	Lg	1	0	0	0	0
89	S2	28	0	0	0	0
89	SG	1	0	0	0	0
89	SO	1	0	0	0	0
90	Lg	1	0	0	0	0
90	Lj	1	0	0	0	0
90	Lm	1	0	0	0	0
90	Lo	1	0	0	0	0
90	Lp	1	0	0	0	0
90	Sa	1	0	0	0	0
90	Sd	1	0	0	0	0
90	Sf	1	0	0	0	0
All	All	230351	0	172737	1855	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 5.

The worst 5 of 1855 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:L5:1176:C:H42	1:L5:1184:A:N6	1.53	1.05
49:S2:1756:C:H42	49:S2:1776:G:N2	1.54	1.04
1:L5:1095:A:H2	1:L5:1200:G:H1	1.08	1.02
49:S2:1756:C:N4	49:S2:1776:G:H22	1.58	1.01
1:L5:1176:C:N4	1:L5:1184:A:H61	1.57	1.01

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%)	222 (90%)	23 (9%)	1 (0%)	30	61
5	LB	400/403 (99%)	374 (94%)	24 (6%)	2 (0%)	24	57
6	LC	366/427 (86%)	329 (90%)	37 (10%)	0	100	100
7	LD	291/297 (98%)	267 (92%)	24 (8%)	0	100	100
8	LE	232/288 (81%)	212 (91%)	20 (9%)	0	100	100
9	LF	223/248 (90%)	211 (95%)	12 (5%)	0	100	100
10	LG	239/266 (90%)	218 (91%)	21 (9%)	0	100	100
11	LH	188/192 (98%)	170 (90%)	18 (10%)	0	100	100
12	LI	198/214 (92%)	182 (92%)	16 (8%)	0	100	100
13	LJ	174/178 (98%)	160 (92%)	14 (8%)	0	100	100
14	LL	208/211 (99%)	194 (93%)	14 (7%)	0	100	100
15	LM	137/215 (64%)	127 (93%)	9 (7%)	1 (1%)	18	49
16	LN	201/204 (98%)	188 (94%)	11 (6%)	2 (1%)	12	41
17	LO	199/203 (98%)	188 (94%)	11 (6%)	0	100	100
18	LP	151/184 (82%)	138 (91%)	12 (8%)	1 (1%)	18	49
19	LQ	185/188 (98%)	175 (95%)	10 (5%)	0	100	100
20	LR	185/196 (94%)	178 (96%)	7 (4%)	0	100	100
21	LS	173/176 (98%)	159 (92%)	14 (8%)	0	100	100
22	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
23	LU	99/128 (77%)	84 (85%)	15 (15%)	0	100	100
24	LV	129/140 (92%)	120 (93%)	9 (7%)	0	100	100
25	LW	122/157 (78%)	111 (91%)	11 (9%)	0	100	100
26	LX	118/156 (76%)	111 (94%)	7 (6%)	0	100	100
27	LY	132/145 (91%)	120 (91%)	12 (9%)	0	100	100
28	LZ	133/136 (98%)	123 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	La	145/148 (98%)	136 (94%)	8 (6%)	1 (1%)	18	49
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%)	98 (93%)	7 (7%)	0	100	100
33	Le	126/135 (93%)	118 (94%)	7 (6%)	1 (1%)	16	47
34	Lf	107/110 (97%)	94 (88%)	11 (10%)	2 (2%)	6	27
35	Lg	112/117 (96%)	105 (94%)	7 (6%)	0	100	100
36	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
37	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
38	Lj	84/97 (87%)	77 (92%)	6 (7%)	1 (1%)	10	37
39	Lk	67/70 (96%)	61 (91%)	6 (9%)	0	100	100
40	Ll	48/51 (94%)	45 (94%)	3 (6%)	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%)	96 (93%)	7 (7%)	0	100	100
44	Lp	89/92 (97%)	83 (93%)	6 (7%)	0	100	100
45	Lr	123/137 (90%)	115 (94%)	8 (6%)	0	100	100
46	Ls	194/317 (61%)	175 (90%)	18 (9%)	1 (0%)	24	57
47	Lt	137/165 (83%)	107 (78%)	26 (19%)	4 (3%)	3	19
48	Lz	215/217 (99%)	172 (80%)	43 (20%)	0	100	100
50	SA	219/295 (74%)	198 (90%)	20 (9%)	1 (0%)	24	57
51	SB	212/264 (80%)	198 (93%)	14 (7%)	0	100	100
52	SD	225/243 (93%)	200 (89%)	25 (11%)	0	100	100
53	SE	260/263 (99%)	241 (93%)	19 (7%)	0	100	100
54	SF	180/204 (88%)	160 (89%)	20 (11%)	0	100	100
55	SH	182/194 (94%)	154 (85%)	27 (15%)	1 (0%)	24	57
56	SI	204/208 (98%)	191 (94%)	13 (6%)	0	100	100
57	SK	96/165 (58%)	86 (90%)	10 (10%)	0	100	100
58	SL	151/158 (96%)	140 (93%)	11 (7%)	0	100	100
59	SP	127/145 (88%)	118 (93%)	9 (7%)	0	100	100
60	SQ	142/146 (97%)	123 (87%)	18 (13%)	1 (1%)	18	49

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
61	SR	133/135 (98%)	117 (88%)	16 (12%)	0	100	100
62	SS	143/152 (94%)	127 (89%)	16 (11%)	0	100	100
63	ST	141/145 (97%)	128 (91%)	11 (8%)	2 (1%)	9	34
64	SU	102/119 (86%)	91 (89%)	11 (11%)	0	100	100
65	SV	81/83 (98%)	71 (88%)	10 (12%)	0	100	100
66	SX	139/143 (97%)	126 (91%)	9 (6%)	4 (3%)	3	19
67	Sa	100/115 (87%)	91 (91%)	8 (8%)	1 (1%)	12	41
68	Sc	62/69 (90%)	51 (82%)	11 (18%)	0	100	100
69	Sd	53/56 (95%)	48 (91%)	4 (8%)	1 (2%)	6	27
70	Sg	311/317 (98%)	267 (86%)	44 (14%)	0	100	100
71	SC	220/293 (75%)	202 (92%)	18 (8%)	0	100	100
72	SG	235/249 (94%)	218 (93%)	17 (7%)	0	100	100
73	SJ	183/194 (94%)	170 (93%)	11 (6%)	2 (1%)	11	39
74	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100
75	SN	148/151 (98%)	141 (95%)	7 (5%)	0	100	100
76	SO	138/151 (91%)	125 (91%)	13 (9%)	0	100	100
77	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
78	SY	129/133 (97%)	121 (94%)	8 (6%)	0	100	100
79	SZ	73/125 (58%)	60 (82%)	11 (15%)	2 (3%)	4	20
80	Sb	81/84 (96%)	68 (84%)	13 (16%)	0	100	100
81	Se	56/59 (95%)	52 (93%)	4 (7%)	0	100	100
82	Sf	65/156 (42%)	56 (86%)	9 (14%)	0	100	100
83	CA	350/394 (89%)	330 (94%)	20 (6%)	0	100	100
86	CD	438/462 (95%)	419 (96%)	19 (4%)	0	100	100
87	CE	70/379 (18%)	67 (96%)	3 (4%)	0	100	100
88	i	31/180 (17%)	29 (94%)	2 (6%)	0	100	100
All	All	12761/14802 (86%)	11677 (92%)	1052 (8%)	32 (0%)	37	67

5 of 32 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
16	LN	124	ASP
47	Lt	147	HIS

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Mol	Chain	Res	Type
66	SX	127	ASN
34	Lf	80	ASN
47	Lt	148	PRO

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%)	186 (98%)	4 (2%)	47	71
5	LB	348/349 (100%)	343 (99%)	5 (1%)	59	76
6	LC	306/348 (88%)	305 (100%)	1 (0%)	86	87
7	LD	246/250 (98%)	244 (99%)	2 (1%)	73	81
8	LE	209/252 (83%)	205 (98%)	4 (2%)	50	73
9	LF	194/215 (90%)	193 (100%)	1 (0%)	81	85
10	LG	203/223 (91%)	202 (100%)	1 (0%)	81	85
11	LH	169/171 (99%)	168 (99%)	1 (1%)	78	83
12	LI	172/181 (95%)	171 (99%)	1 (1%)	78	83
13	LJ	148/149 (99%)	146 (99%)	2 (1%)	59	76
14	LL	176/177 (99%)	173 (98%)	3 (2%)	53	74
15	LM	118/161 (73%)	117 (99%)	1 (1%)	73	81
16	LN	171/172 (99%)	171 (100%)	0	100	100
17	LO	173/174 (99%)	169 (98%)	4 (2%)	44	70
18	LP	134/163 (82%)	134 (100%)	0	100	100
19	LQ	164/165 (99%)	161 (98%)	3 (2%)	51	73
20	LR	166/175 (95%)	165 (99%)	1 (1%)	78	83
21	LS	156/157 (99%)	156 (100%)	0	100	100
22	LT	139/140 (99%)	137 (99%)	2 (1%)	59	76
23	LU	91/115 (79%)	91 (100%)	0	100	100
24	LV	101/107 (94%)	99 (98%)	2 (2%)	48	72

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	LW	103/126 (82%)	103 (100%)	0	100	100
26	LX	108/133 (81%)	108 (100%)	0	100	100
27	LY	124/135 (92%)	123 (99%)	1 (1%)	73	81
28	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	80
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%)	83 (100%)	0	100	100
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%)	97 (99%)	1 (1%)	68	79
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	71
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%)	73 (99%)	1 (1%)	59	76
45	Lr	109/121 (90%)	107 (98%)	2 (2%)	51	73
46	Ls	162/258 (63%)	162 (100%)	0	100	100
47	Lt	112/137 (82%)	110 (98%)	2 (2%)	51	73
48	Lz	195/196 (100%)	194 (100%)	1 (0%)	81	85
50	SA	183/243 (75%)	178 (97%)	5 (3%)	39	67
51	SB	195/231 (84%)	195 (100%)	0	100	100
52	SD	190/202 (94%)	189 (100%)	1 (0%)	81	85
53	SE	224/225 (100%)	220 (98%)	4 (2%)	51	73
54	SF	156/170 (92%)	155 (99%)	1 (1%)	78	83
55	SH	166/174 (95%)	165 (99%)	1 (1%)	78	83
56	SI	178/180 (99%)	178 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
57	SK	89/136 (65%)	88 (99%)	1 (1%)	65	78
58	SL	137/142 (96%)	137 (100%)	0	100	100
59	SP	115/130 (88%)	114 (99%)	1 (1%)	70	80
60	SQ	119/121 (98%)	118 (99%)	1 (1%)	73	81
61	SR	122/122 (100%)	119 (98%)	3 (2%)	42	69
62	SS	126/132 (96%)	125 (99%)	1 (1%)	73	81
63	ST	113/115 (98%)	113 (100%)	0	100	100
64	SU	94/107 (88%)	94 (100%)	0	100	100
65	SV	67/67 (100%)	67 (100%)	0	100	100
66	SX	113/115 (98%)	113 (100%)	0	100	100
67	Sa	89/98 (91%)	87 (98%)	2 (2%)	45	71
68	Sc	57/62 (92%)	56 (98%)	1 (2%)	51	73
69	Sd	48/49 (98%)	48 (100%)	0	100	100
70	Sg	272/275 (99%)	268 (98%)	4 (2%)	57	75
71	SC	188/225 (84%)	186 (99%)	2 (1%)	65	78
72	SG	207/218 (95%)	207 (100%)	0	100	100
73	SJ	161/168 (96%)	159 (99%)	2 (1%)	63	78
74	SM	102/108 (94%)	102 (100%)	0	100	100
75	SN	130/131 (99%)	130 (100%)	0	100	100
76	SO	110/119 (92%)	109 (99%)	1 (1%)	70	80
77	SW	112/113 (99%)	112 (100%)	0	100	100
78	SY	113/115 (98%)	111 (98%)	2 (2%)	51	73
79	SZ	66/103 (64%)	66 (100%)	0	100	100
80	Sb	75/76 (99%)	74 (99%)	1 (1%)	61	77
81	Se	43/48 (90%)	43 (100%)	0	100	100
82	Sf	60/140 (43%)	60 (100%)	0	100	100
83	CA	303/336 (90%)	303 (100%)	0	100	100
86	CD	366/379 (97%)	362 (99%)	4 (1%)	65	78
87	CE	68/338 (20%)	68 (100%)	0	100	100
88	i	28/151 (18%)	28 (100%)	0	100	100
All	All	11095/12596 (88%)	11004 (99%)	91 (1%)	70	81

5 of 91 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	SA	192	GLU
62	SS	103	LEU
53	SE	69	PHE
57	SK	40	VAL
70	Sg	10	THR

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

Mol	Chain	Res	Type
55	SH	165	ASN
71	SC	277	HIS
56	SI	116	HIS
61	SR	93	GLN
74	SM	46	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	L5	3705/5066 (73%)	938 (25%)	20 (0%)
2	L7	119/121 (98%)	10 (8%)	0
3	L8	155/157 (98%)	33 (21%)	1 (0%)
49	S2	1715/1869 (91%)	414 (24%)	12 (0%)
84	CB	86/87 (98%)	25 (29%)	1 (1%)
85	CC	74/75 (98%)	24 (32%)	1 (1%)
All	All	5854/7375 (79%)	1444 (24%)	35 (0%)

5 of 1444 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	L5	2	G
1	L5	17	A
1	L5	19	G
1	L5	20	U
1	L5	25	A

5 of 35 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
49	S2	668	A

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Mol	Chain	Res	Type
49	S2	688	U
49	S2	1434	C
1	L5	2786	C
1	L5	2760	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 [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

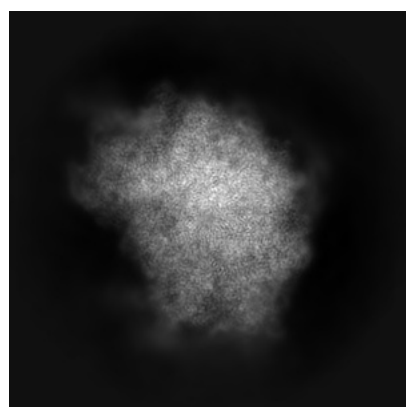
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-11299. These allow visual inspection of the internal detail of the map and identification of artifacts.

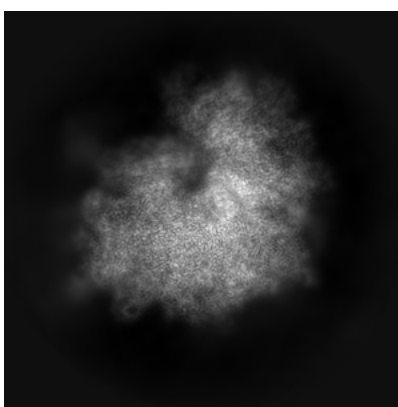
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

6.1.1 Primary map



X



Y

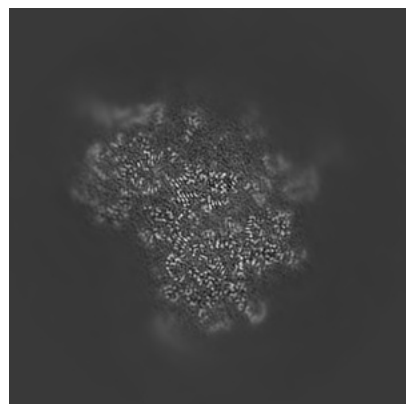


Z

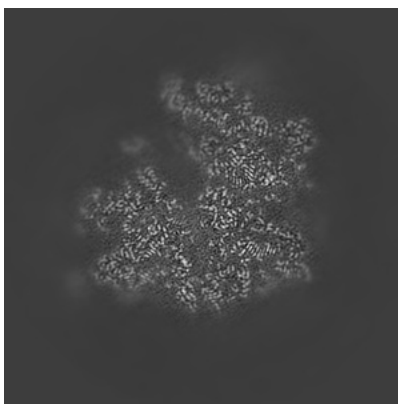
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

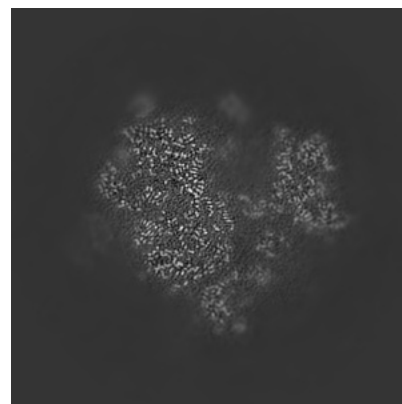
6.2.1 Primary map



X Index: 200



Y Index: 200

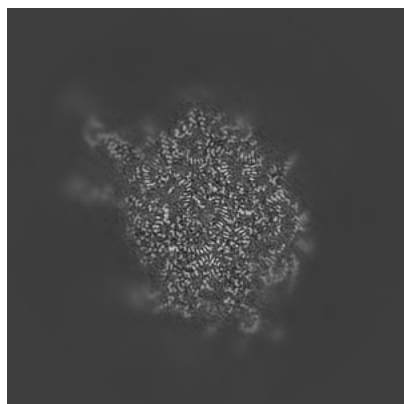


Z Index: 200

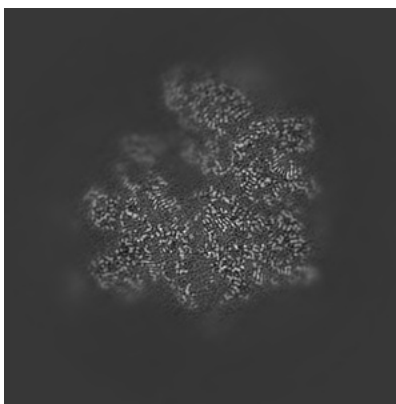
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

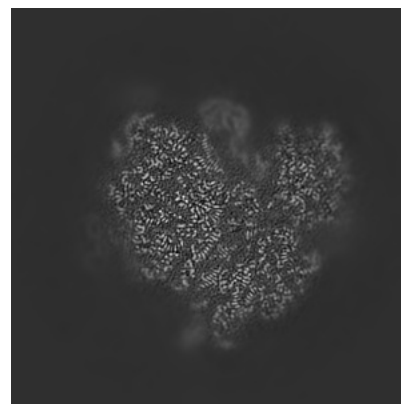
6.3.1 Primary map



X Index: 178



Y Index: 194

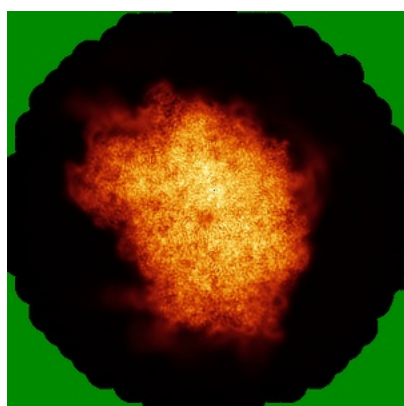


Z Index: 224

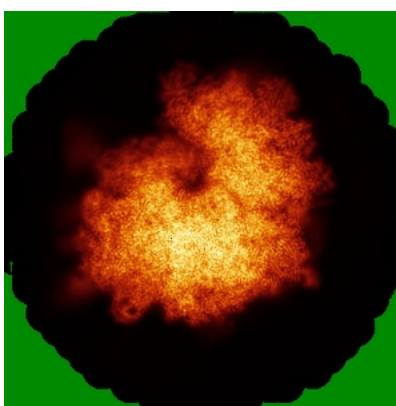
The images above show the largest variance slices of the map in three orthogonal directions.

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

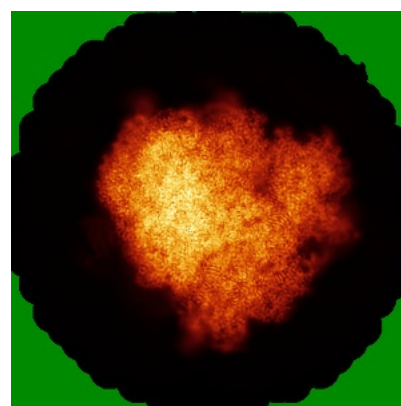
6.4.1 Primary map



X



Y

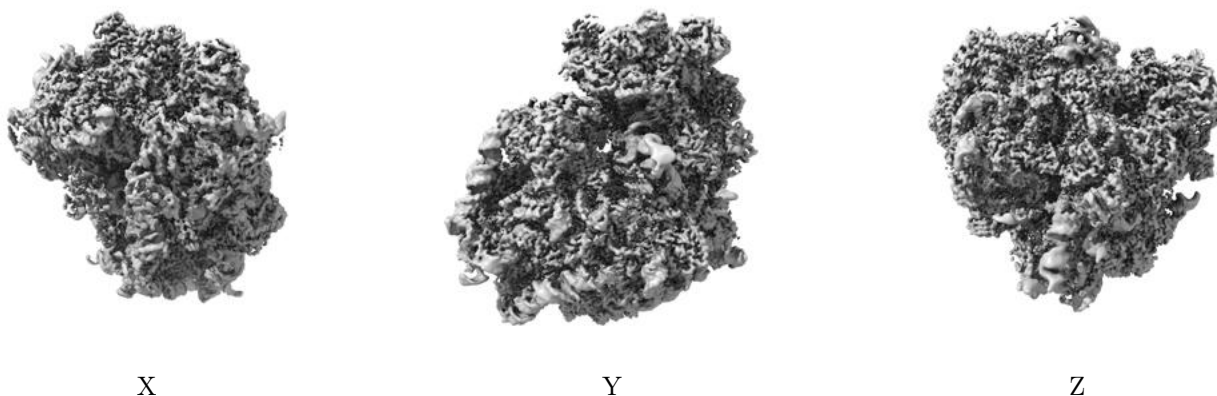


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.05. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

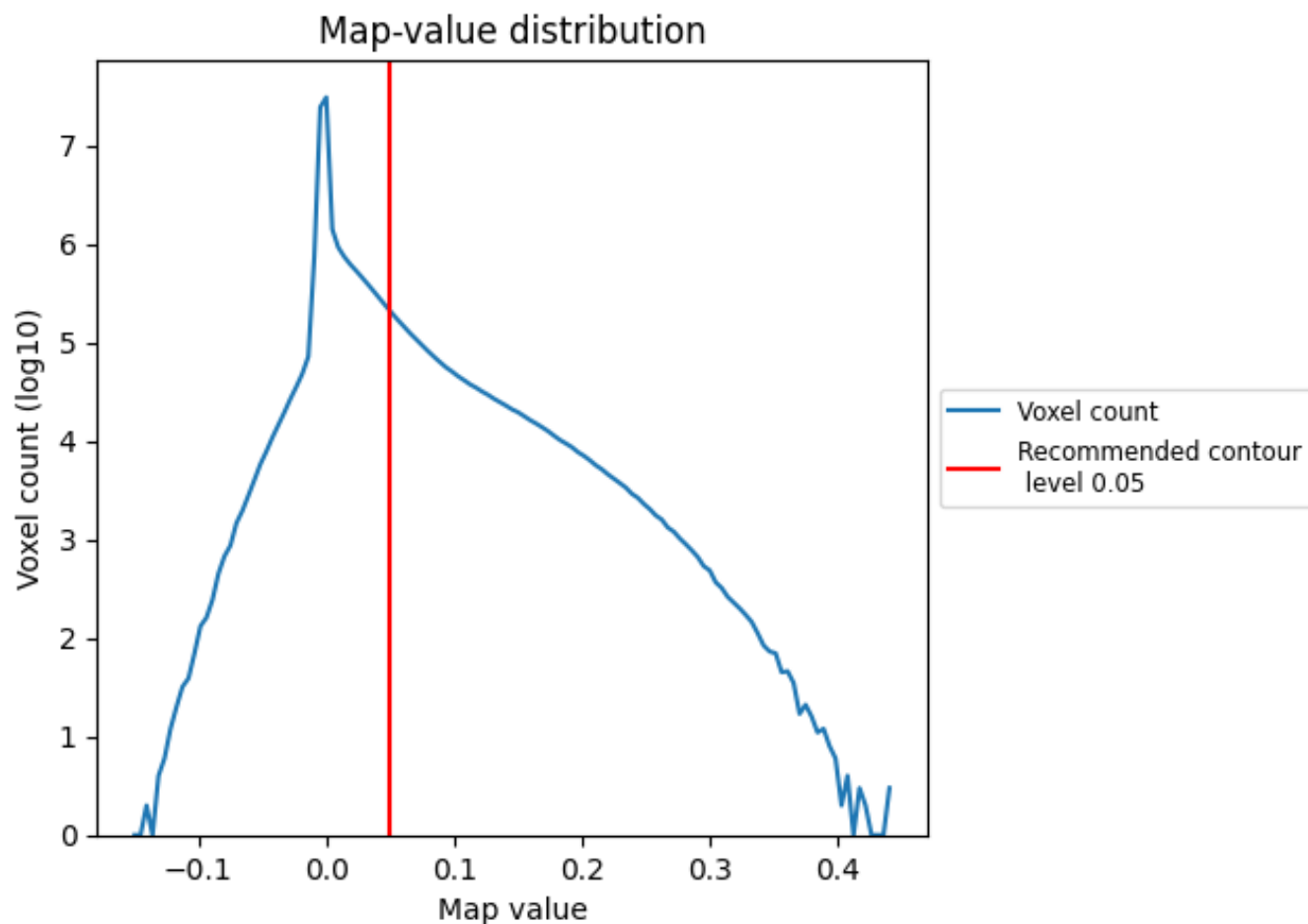
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

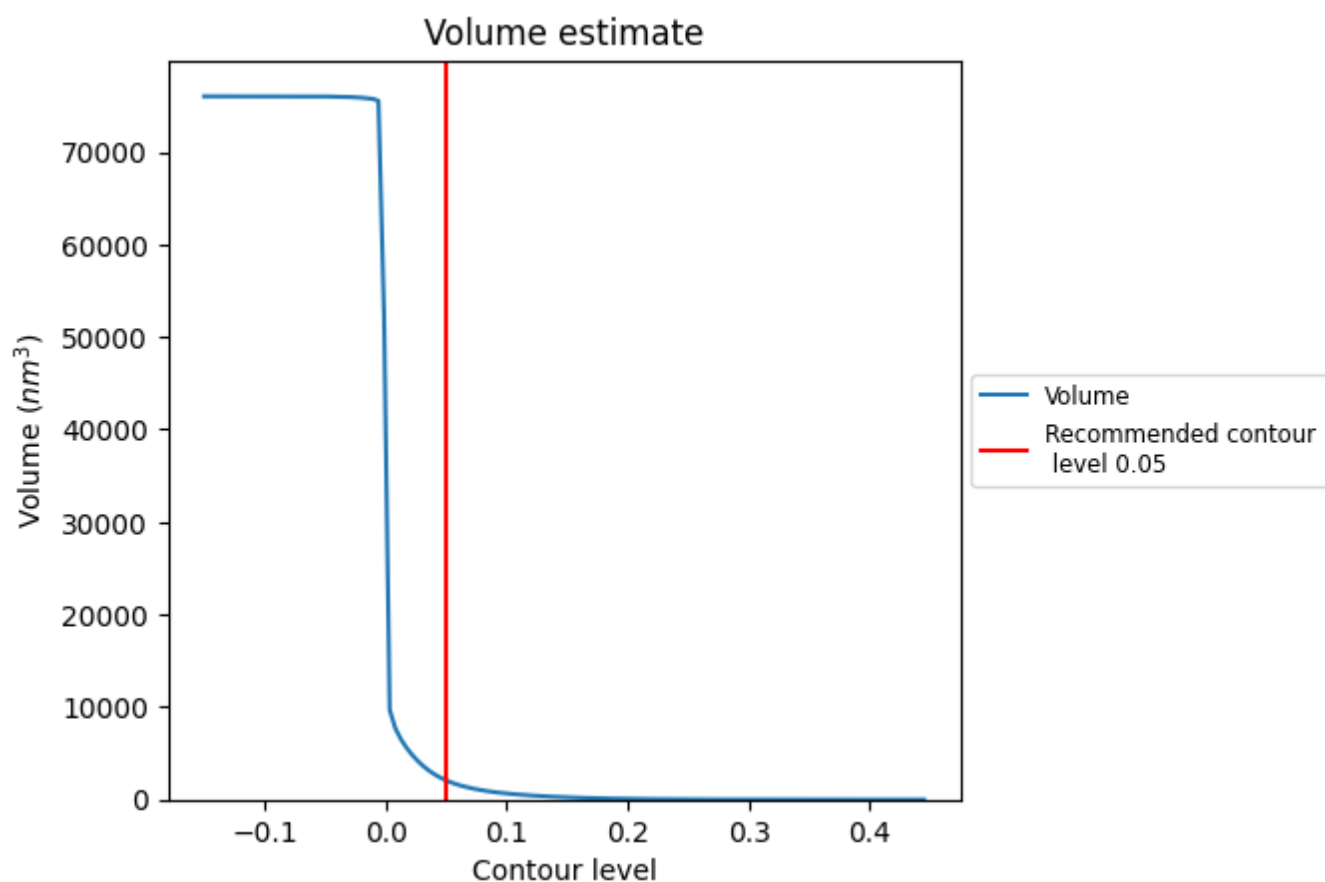
This section contains the results of statistical analysis of the map.

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.

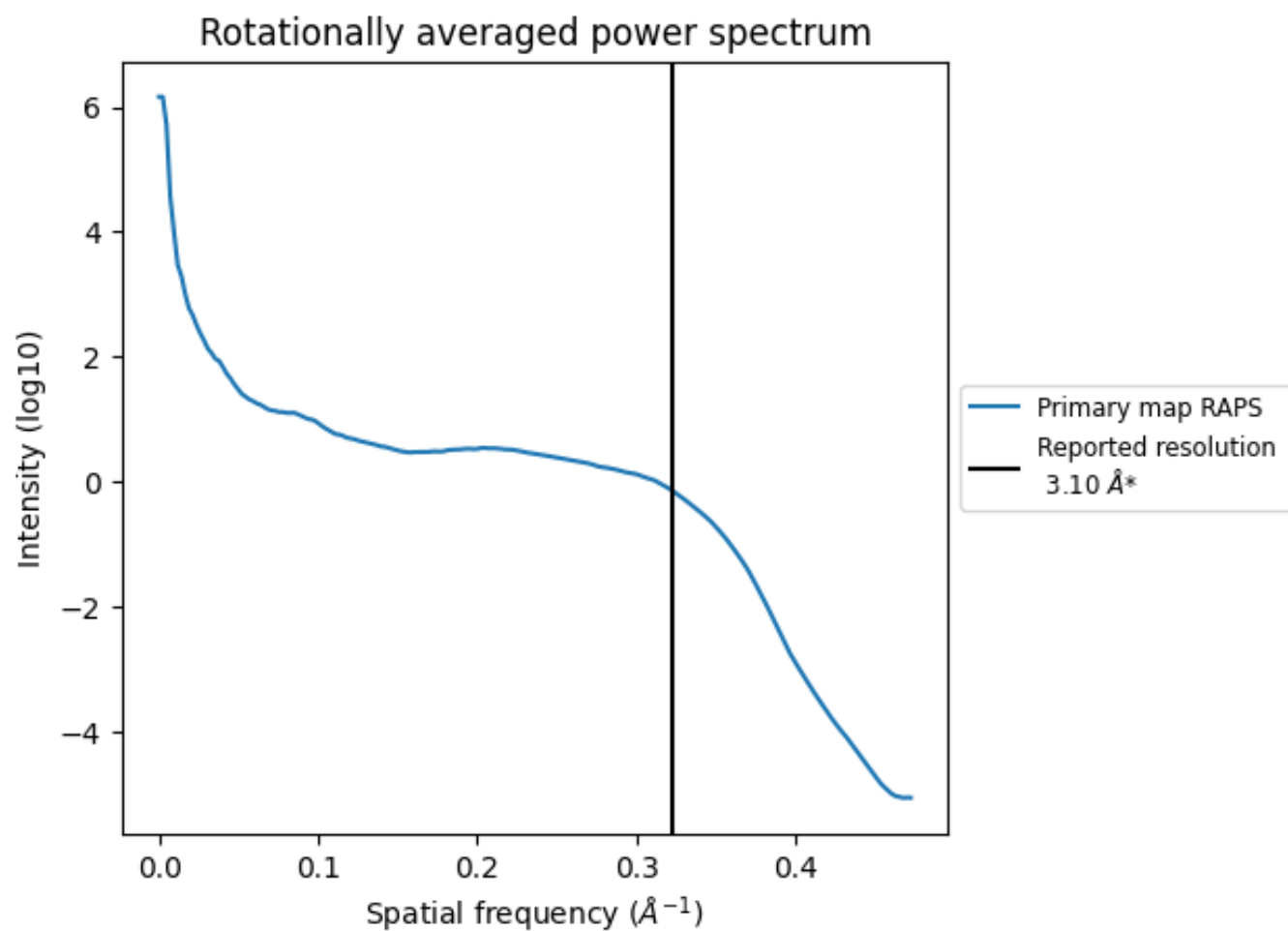
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2071 nm³; this corresponds to an approximate mass of 1871 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 ⓘ

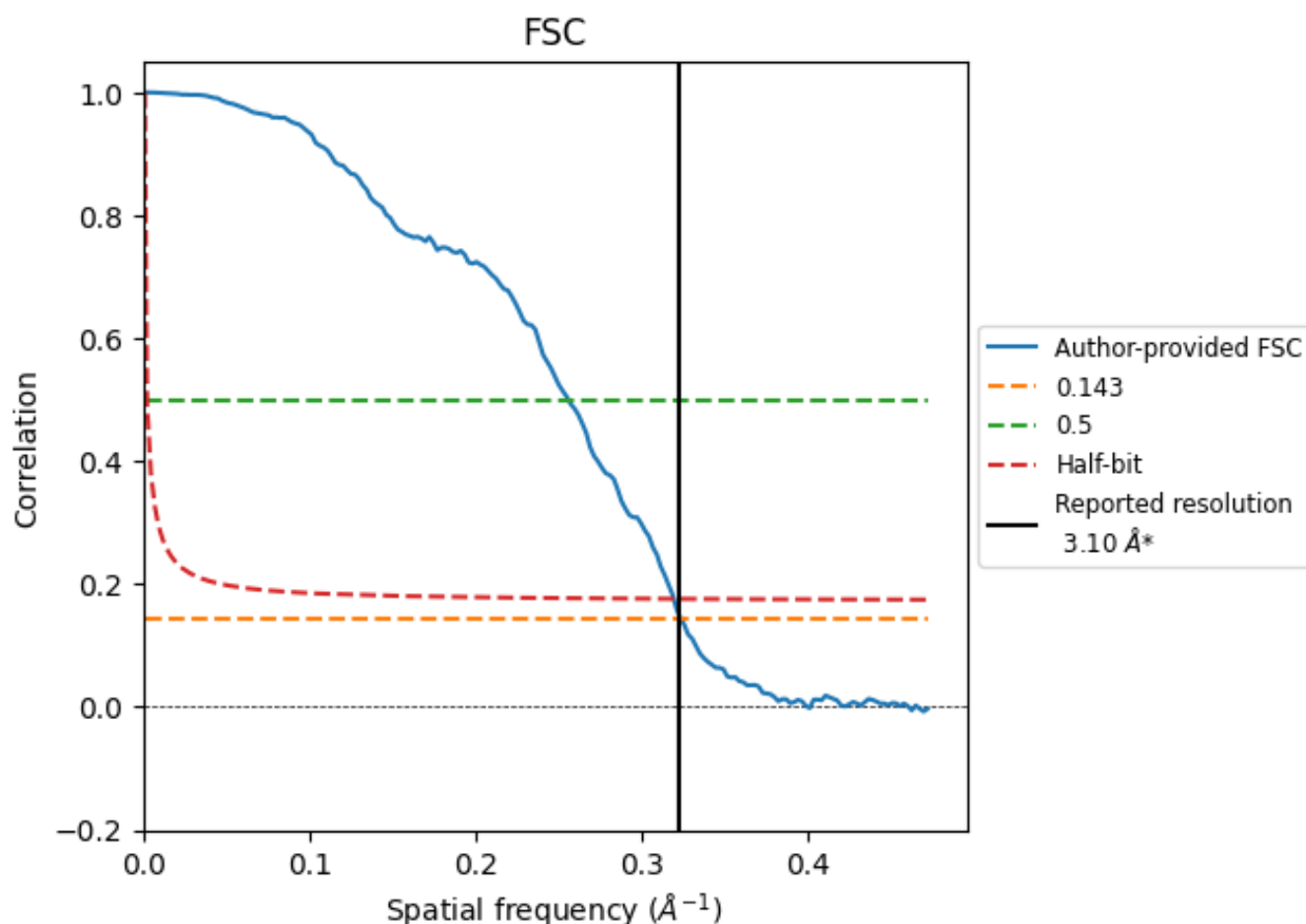


*Reported resolution corresponds to spatial frequency of 0.323 Å⁻¹

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	3.91	3.13
Unmasked-calculated*	-	-	-

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

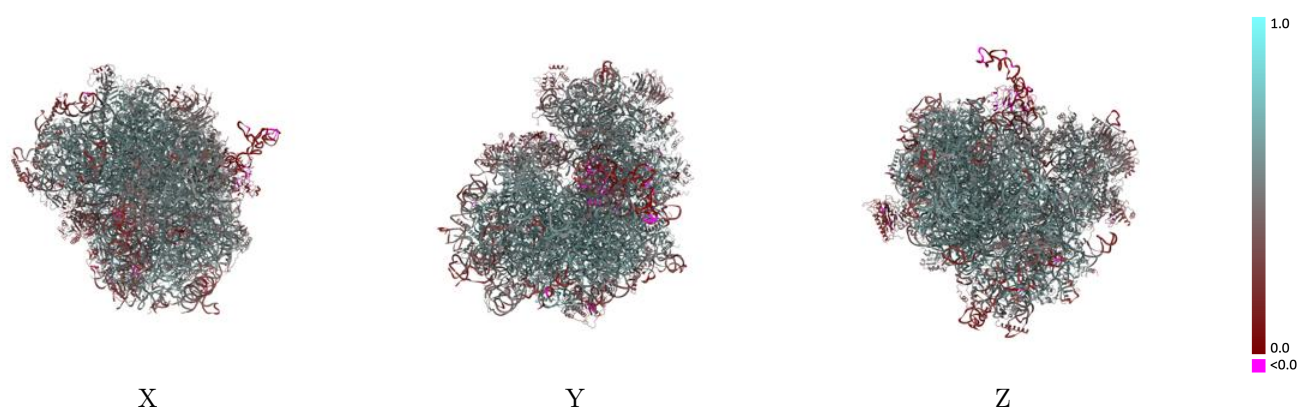
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-11299 and PDB model 6ZMO. Per-residue inclusion information can be found in section 3 on page 21.

9.1 Map-model overlay [i](#)

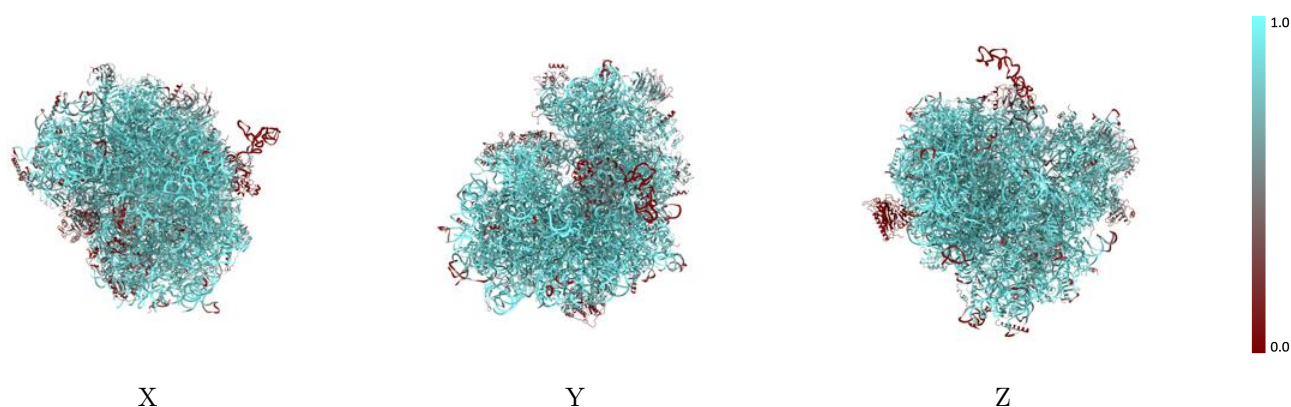
This section was not generated.

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



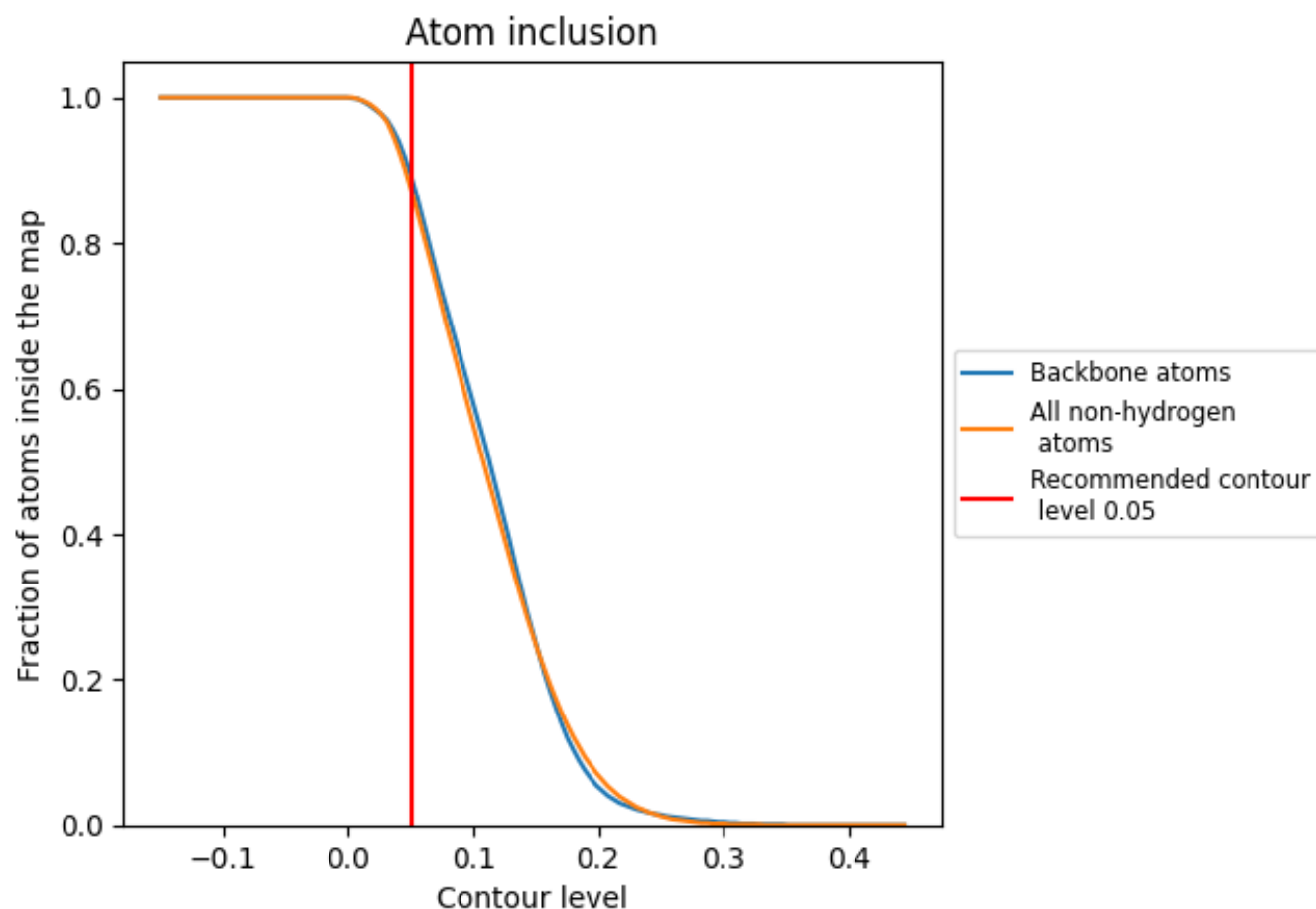
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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 (0.05).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 88% 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 (0.05) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8750	 0.5190
CA	 0.0180	 0.2200
CB	 0.7910	 0.2960
CC	 0.8540	 0.3030
CD	 0.3780	 0.3160
CE	 0.8810	 0.5060
L5	 0.9320	 0.5390
L7	 0.9890	 0.5720
L8	 0.9640	 0.5690
LA	 0.9850	 0.6230
LB	 0.9280	 0.5880
LC	 0.9350	 0.5790
LD	 0.8690	 0.5140
LE	 0.8300	 0.5080
LF	 0.9570	 0.5810
LG	 0.8080	 0.5080
LH	 0.9050	 0.5530
LI	 0.9340	 0.5600
LJ	 0.7760	 0.4480
LL	 0.8750	 0.5480
LM	 0.9070	 0.5440
LN	 0.9880	 0.6250
LO	 0.9470	 0.5890
LP	 0.9520	 0.6010
LQ	 0.9730	 0.6040
LR	 0.8730	 0.5490
LS	 0.9660	 0.5850
LT	 0.9170	 0.5630
LU	 0.7940	 0.4810
LV	 0.9550	 0.5920
LW	 0.6800	 0.4390
LX	 0.9350	 0.5740
LY	 0.9020	 0.5650
LZ	 0.9120	 0.5580
La	 0.9560	 0.6040



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Chain	Atom inclusion	Q-score
Lb	 0.8300	 0.4980
Lc	 0.9090	 0.5480
Ld	 0.9180	 0.5670
Le	 0.9750	 0.6090
Lf	 0.9800	 0.6120
Lg	 0.9180	 0.5840
Lh	 0.9100	 0.5520
Li	 0.9020	 0.5540
Lj	 0.9850	 0.6200
Lk	 0.7900	 0.5130
Ll	 0.9760	 0.5930
Lm	 0.9470	 0.5700
Ln	 0.9810	 0.6100
Lo	 0.9250	 0.5710
Lp	 0.9510	 0.5950
Lr	 0.9460	 0.5720
Ls	 0.2810	 0.2370
Lt	 0.1910	 0.2000
Lz	 0.1180	 0.1240
S2	 0.9400	 0.5330
SA	 0.8580	 0.5210
SB	 0.8750	 0.5420
SC	 0.9220	 0.5620
SD	 0.7980	 0.4700
SE	 0.9110	 0.5420
SF	 0.8530	 0.4930
SG	 0.7670	 0.4450
SH	 0.7000	 0.4450
SI	 0.8850	 0.5340
SJ	 0.8880	 0.5340
SK	 0.7630	 0.4390
SL	 0.8820	 0.5650
SM	 0.2740	 0.2330
SN	 0.9370	 0.5720
SO	 0.8820	 0.5320
SP	 0.7620	 0.4450
SQ	 0.8320	 0.4960
SR	 0.7770	 0.4790
SS	 0.7960	 0.4620
ST	 0.8350	 0.4870
SU	 0.7600	 0.4490
SV	 0.8750	 0.5330

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Chain	Atom inclusion	Q-score
SW	 0.9650	 0.5810
SX	 0.9550	 0.5820
SY	 0.7970	 0.4810
SZ	 0.6840	 0.4160
Sa	 0.8960	 0.5480
Sb	 0.8230	 0.5260
Sc	 0.7690	 0.4630
Sd	 0.9500	 0.5490
Se	 0.8060	 0.5050
Sf	 0.4080	 0.2950
Sg	 0.6350	 0.4060
i	 0.9070	 0.5520