



wwPDB EM Validation Summary Report ⓘ

Sep 23, 2026 – 06:41 pm BST

PDB ID : 9T6D / pdb_00009t6d
EMDB ID : EMD-55613
Title : NAA40-NAC bound human 80S (combined translation states)
Authors : Guan, D.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-11-07
Resolution : 2.67 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:

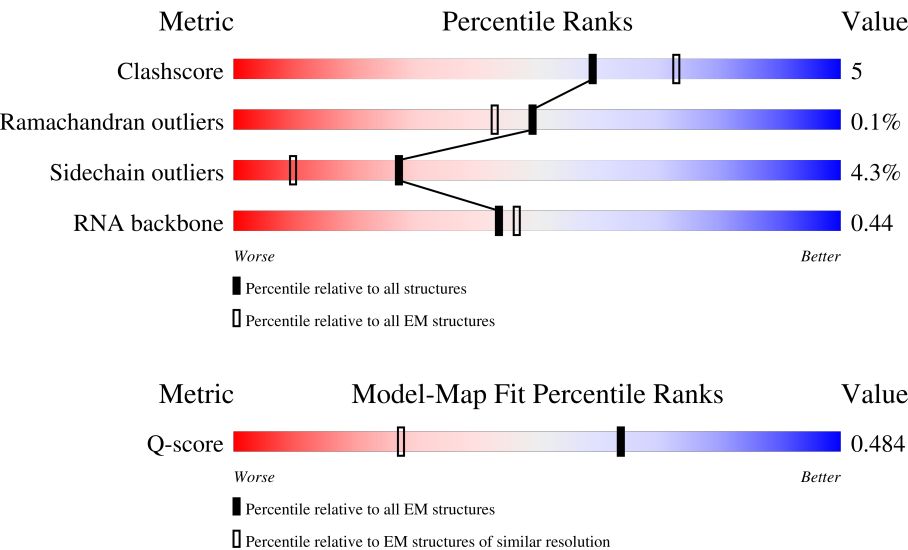
EMDB validation analysis : 0.0.1.dev133
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.50

1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:
ELECTRON MICROSCOPY

The reported resolution of this entry is 2.67 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.



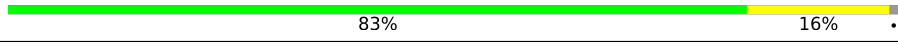
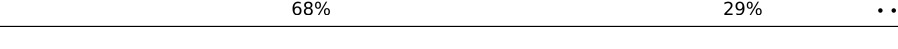
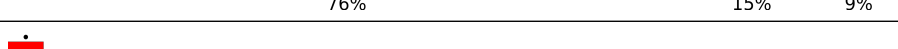
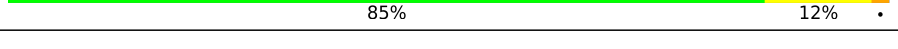
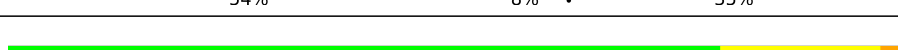
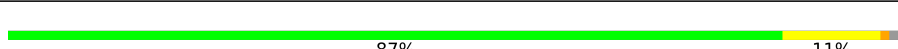
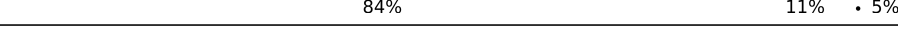
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	9182 (2.17 - 3.17)

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	CB	858	
2	CC	85	
3	CD	402	

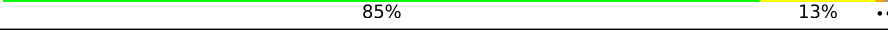
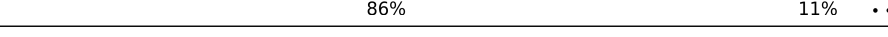
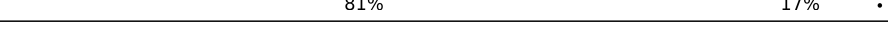
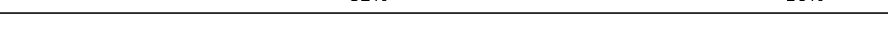
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Mol	Chain	Length	Quality of chain
4	L5	5070	
5	L7	121	
6	L8	157	
7	LA	257	
8	LB	403	
9	LC	427	
10	LD	297	
11	LE	288	
12	LF	248	
13	LG	266	
14	LH	192	
15	LI	214	
16	LJ	178	
17	LL	211	
18	LM	215	
19	LN	204	
20	LO	203	
21	LP	184	
22	LQ	188	
23	LR	196	
24	LS	176	
25	LT	160	
26	LU	128	
27	LV	140	
28	LW	157	

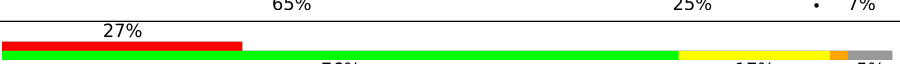
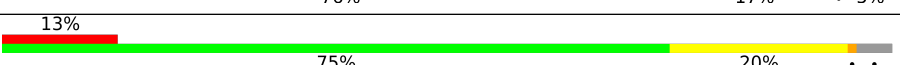
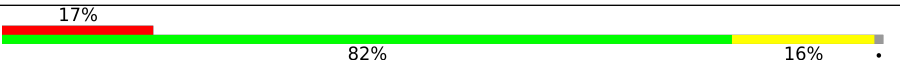
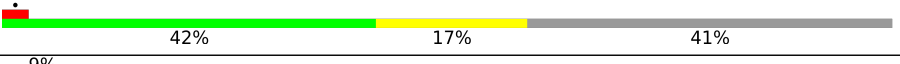
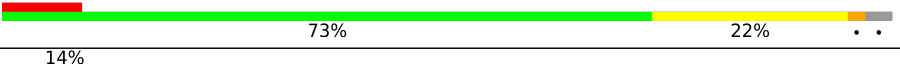
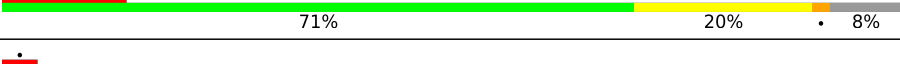
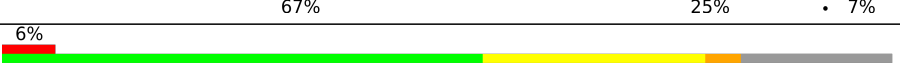
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Mol	Chain	Length	Quality of chain
29	LX	156	
30	LY	145	
31	LZ	136	
32	La	148	
33	Lb	159	
34	Lc	115	
35	Ld	125	
36	Le	135	
37	Lf	110	
38	Lg	117	
39	Lh	123	
40	Li	105	
41	Lj	97	
42	Lk	70	
43	Ll	51	
44	Lm	128	
45	Ln	25	
46	Lo	106	
47	Lp	92	
48	Lr	137	
49	Lz	217	
50	N4	237	
51	NA	215	
52	NB	206	
53	S2	1869	

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Mol	Chain	Length	Quality of chain
54	SA	295	
55	SB	264	
56	SC	293	
57	SD	243	
58	SE	263	
59	SF	204	
60	SG	249	
61	SH	194	
62	SI	208	
63	SJ	194	
64	SK	165	
65	SL	158	
66	SM	132	
67	SN	151	
68	SO	151	
69	SP	145	
70	SQ	146	
71	SR	135	
72	SS	152	
73	ST	145	
74	SU	119	
75	SV	83	
76	SW	130	
77	SX	143	
78	SY	133	

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Mol	Chain	Length	Quality of chain
79	SZ	125	
80	Sa	115	
81	Sb	84	
82	Sc	69	
83	Sd	56	
84	Se	133	
85	Sf	156	
86	Sg	317	

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 229537 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	CB	846	Total	C	N	O	S	0	0
			6605	4193	1136	1232	44		

- Molecule 2 is a RNA chain called E-site tRNA.

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

- Molecule 3 is a protein called Isoform 2 of SERPINE1 mRNA-binding protein 1.

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

- Molecule 4 is a RNA chain called 28S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L5	3772	Total	C	N	O	P	0	0
			80116	35645	14585	26115	3771		

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

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

- Molecule 6 is a RNA chain called 5.8S rRNA.

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

- Molecule 7 is a protein called 60S ribosomal protein L8.

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

- Molecule 8 is a protein called 60S ribosomal protein L3.

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

- Molecule 9 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	LC	368	Total	C	N	O	S	0	0
			2927	1840	583	489	15		

- Molecule 10 is a protein called 60S ribosomal protein L5.

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

- Molecule 11 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	LE	236	Total	C	N	O	S	0	0
			1904	1222	361	317	4		

- Molecule 12 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 13 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	LG	241	Total	C	N	O	S	0	0
			1927	1228	371	324	4		

- Molecule 14 is a protein called 60S ribosomal protein L9.

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

- Molecule 15 is a protein called Ribosomal protein uL16-like.

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

- Molecule 16 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	LJ	176	Total	C	N	O	S	0	0
			1410	888	263	253	6		

- Molecule 17 is a protein called Large ribosomal subunit protein eL13.

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

- Molecule 18 is a protein called 60S ribosomal protein L14.

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

- Molecule 19 is a protein called 60S ribosomal protein L15.

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

- Molecule 20 is a protein called 60S ribosomal protein L13a.

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

- Molecule 21 is a protein called 60S ribosomal protein L17.

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

- Molecule 22 is a protein called 60S ribosomal protein L18.

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

- Molecule 23 is a protein called 60S ribosomal protein L19.

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

- Molecule 24 is a protein called 60S ribosomal protein L18a.

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

- Molecule 25 is a protein called 60S ribosomal protein L21.

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

- Molecule 26 is a protein called 60S ribosomal protein L22.

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

- Molecule 27 is a protein called 60S ribosomal protein L23.

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

- Molecule 28 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	LW	118	Total	C	N	O	S	0	0
			965	604	199	158	4		

- Molecule 29 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	LX	120	Total	C	N	O	S	0	0
			985	630	185	169	1		

- Molecule 30 is a protein called 60S ribosomal protein L26.

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

- Molecule 31 is a protein called 60S ribosomal protein L27.

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

- Molecule 32 is a protein called 60S ribosomal protein L27a.

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

- Molecule 33 is a protein called 60S ribosomal protein L29.

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

- Molecule 34 is a protein called 60S ribosomal protein L30.

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

- Molecule 35 is a protein called 60S ribosomal protein L31.

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

- Molecule 36 is a protein called 60S ribosomal protein L32.

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

- Molecule 37 is a protein called 60S ribosomal protein L35a.

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

- Molecule 38 is a protein called 60S ribosomal protein L34.

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

- Molecule 39 is a protein called 60S ribosomal protein L35.

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

- Molecule 40 is a protein called 60S ribosomal protein L36.

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

- Molecule 41 is a protein called Large ribosomal subunit protein eL37.

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

- Molecule 42 is a protein called 60S ribosomal protein L38.

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

- Molecule 43 is a protein called 60S ribosomal protein L39.

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

- Molecule 44 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 45 is a protein called 60S ribosomal protein L41.

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

- Molecule 46 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	Lo	105	Total	C	N	O	S	0	0
			862	542	175	139	6		

- Molecule 47 is a protein called 60S ribosomal protein L37a.

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

- Molecule 48 is a protein called 60S ribosomal protein L28.

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

- Molecule 49 is a protein called 60S ribosomal protein L10a.

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

- Molecule 50 is a protein called N-alpha-acetyltransferase 40.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	N4	221	Total	C	N	O	S	0	0
			1795	1128	313	339	15		

- Molecule 51 is a protein called Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NA	105	Total	C	N	O	S	0	0
			817	511	148	154	4		

- Molecule 52 is a protein called Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	NB	104	Total	C	N	O	S	0	0
			805	503	151	149	2		

- Molecule 53 is a RNA chain called 18S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S2	1740	Total	C	N	O	P	0	0
			36898	16459	6598	12102	1739		

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

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

- Molecule 55 is a protein called 40S ribosomal protein S3a.

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

- Molecule 56 is a protein called 40S ribosomal protein S2.

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

- Molecule 57 is a protein called 40S ribosomal protein S3.

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

- Molecule 58 is a protein called Small ribosomal subunit protein eS4, X isoform.

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

- Molecule 59 is a protein called 40S ribosomal protein S5.

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

- Molecule 60 is a protein called 40S ribosomal protein S6.

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

- Molecule 61 is a protein called 40S ribosomal protein S7.

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

- Molecule 62 is a protein called 40S ribosomal protein S8.

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

- Molecule 63 is a protein called 40S ribosomal protein S9.

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

- Molecule 64 is a protein called 40S ribosomal protein S10.

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

- Molecule 65 is a protein called 40S ribosomal protein S11.

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

- Molecule 66 is a protein called 40S ribosomal protein S12.

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

- Molecule 67 is a protein called 40S ribosomal protein S13.

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

- Molecule 68 is a protein called 40S ribosomal protein S14.

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

- Molecule 69 is a protein called 40S ribosomal protein S15.

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

- Molecule 70 is a protein called 40S ribosomal protein S16.

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

- Molecule 71 is a protein called 40S ribosomal protein S17.

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

- Molecule 72 is a protein called 40S ribosomal protein S18.

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

- Molecule 73 is a protein called 40S ribosomal protein S19.

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

- Molecule 74 is a protein called 40S ribosomal protein S20.

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

- Molecule 75 is a protein called 40S ribosomal protein S21.

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

- Molecule 76 is a protein called 40S ribosomal protein S15a.

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

- Molecule 77 is a protein called 40S ribosomal protein S23.

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

- 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 S26.

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

- Molecule 81 is a protein called 40S ribosomal protein S27.

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

- Molecule 82 is a protein called 40S ribosomal protein S28.

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

- Molecule 83 is a protein called 40S ribosomal protein S29.

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

- Molecule 84 is a protein called Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein.

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

- Molecule 85 is a protein called Ubiquitin.

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

- Molecule 86 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 87 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	CC	1	Total	Mg	0
			1	1	
87	L5	214	Total	Mg	0
			214	214	
87	L7	3	Total	Mg	0
			3	3	
87	L8	3	Total	Mg	0
			3	3	
87	LA	1	Total	Mg	0
			1	1	
87	LI	1	Total	Mg	0
			1	1	
87	LP	1	Total	Mg	0
			1	1	
87	LV	1	Total	Mg	0
			1	1	
87	Le	1	Total	Mg	0
			1	1	
87	Lg	1	Total	Mg	0
			1	1	
87	S2	29	Total	Mg	0
			29	29	

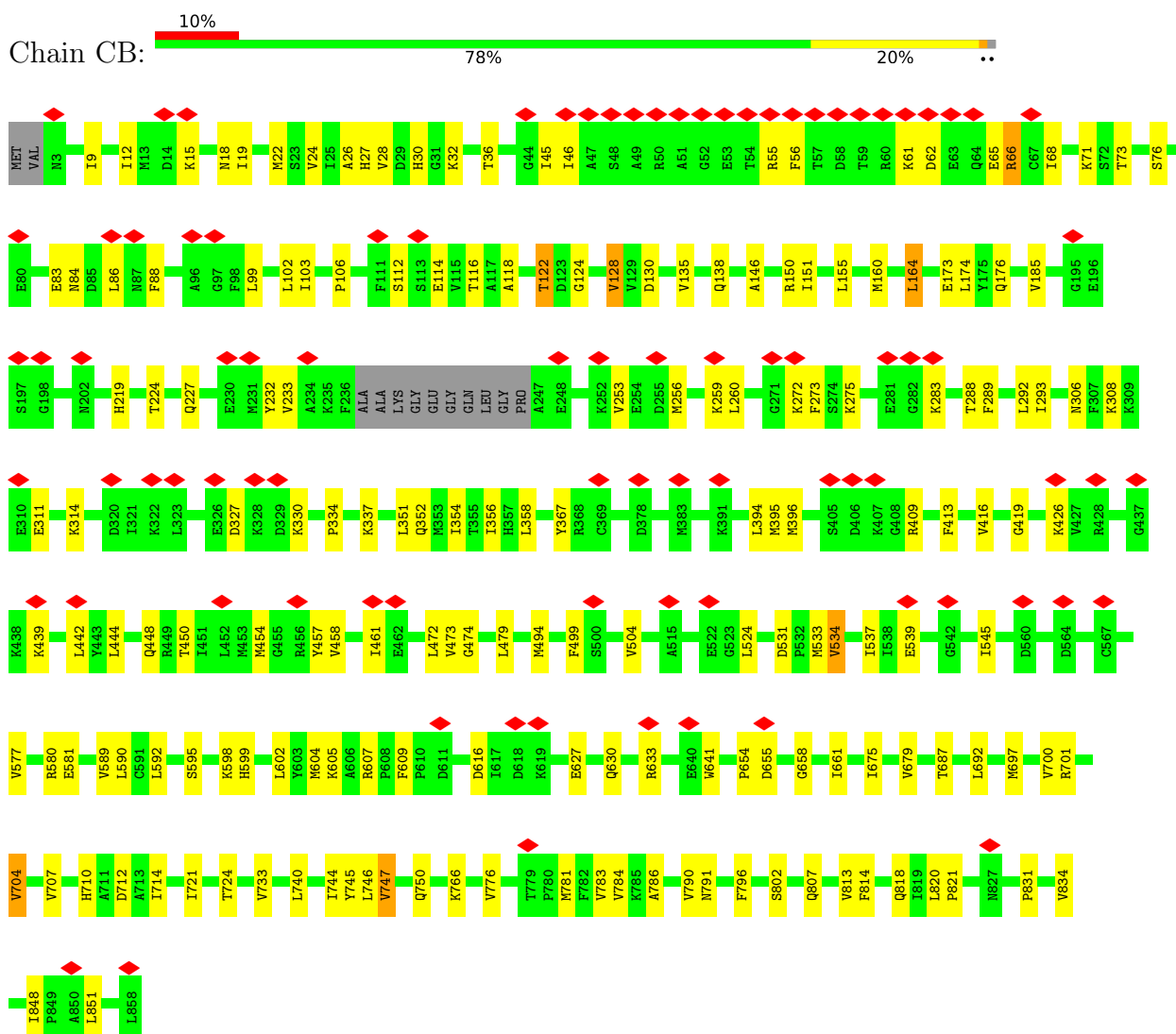
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Elongation factor 2



- Molecule 2: E-site tRNA









U5030	U4925	G	C4773	A4656	A4513	A4348	A4239	U4118	C4041	U3992	G3750	A3635
A5034	C4926	C	C4774	U4657	C4519	C4349	G4240	C4119	G4042	G3997	A3756	U3641
G5041	C4927	G	G4775	G4658	G4524	A4363	C4243	C4122	U4044	C3977	A3760	U3644
C5050	C4928	G	G4776	G4659	C4525	C4364	G4249	A4127	G4045	A3900	C3761	U3645
C5054	U4932	U	C	C4670	G4528	G4371	G4250	A4128	A4047	A3901	A3760	A3646
G5055	A4934	C	U	C4671	G4529	U4372	A4251	C4133	A4048	A3905	A3760	A3647
A5056	C4935	C	U	C4672	U4530	G4373	G4254	C4134	U4049	A3906	A3760	A3648
C5057	G4936	C	U	G4679	U4531	A4376	A4255	C4133	A4050	G3907	A3773	A3656
A5058	C4937	C	C	C4679	U4531	G4377	G4255	C4134	A4051	A3908	A3774	U3657
C4940	C	C	C	A4687	C4537	A4378	U4260	C4139	C4052	C3909	A3775	A3662
C4941	C	C	C	A4687	G4538	A4379	C4261	C4140	A4053	C3910	A3775	A3663
C4942	C	C	C	A4691	G4545	A4380	G4265	C4141	C4054	C3911	A3776	A3664
A4943	C	C	C	G4694	G4545	A4381	U4265	C4142	U4055	U3915	A3776	A3664
G4949	C	C	C	G4694	A4548	A4382	G4268	C4143	A4056	U3916	A3784	C3670
U4950	C	C	C	G4695	G4549	C4387	A4268	C4144	C4057	A3917	A3785	C3673
G4951	C	C	C	U4699	G4557	A4388	A4273	C4145	U4058	A3918	A3785	G3674
G4952	C	C	C	A4700	C4560	C4389	A4274	C4146	C4059	C3919	A3786	U3680
G4953	C	C	C	A4708	C4560	A4394	G4275	C4149	U4060	C3923	A3787	C3673
A4955	C	C	C	U4709	G4567	G4405	G4276	C4150	C4064	C3924	A3787	C3674
G4960	C	C	C	G4719	G4573	G4422	C4277	C4160	C4065	U3932	A3788	U3680
A4966	C	C	C	C4720	G4574	A4422	A4281	C4161	U4066	G3933	A3788	U3680
A4967	C	C	C	G4727	G4575	C4426	A4282	U4163	U4069	C3937	A3788	C3699
A4968	C	C	C	C4733	A4584	C4434	G4283	C4169	G4076	G3938	A3788	C3701
G4975	C	C	C	A4734	A4589	U4438	U4290	C4171	G4081	G3939	A3788	U3707
U4976	C	C	C	G4740	A4590	U4438	G4291	U4174	G4082	A3942	A3788	C3708
A4979	C	C	C	G4741	U4591	C4444	A4292	C4175	U4083	A3943	A3788	U3709
U4981	C	C	C	G4742	C4592	C4444	C4293	C4175	G4084	G3944	A3788	G3710
U4982	C	C	C	G4743	C4592	C4444	C4294	C4175	G4084	U3947	A3788	A3711
C4983	C	C	C	A4744	A4600	G4448	U4295	C4183	G4091	C3948	A3788	A3712
C4887	C	C	C	G4745	U4601	A4449	G4304	C4184	G4092	C3949	A3788	U3713
U4888	C	C	C	U4748	A4602	U4452	G4305	U4188	G4093	U3950	A3788	A3717
U4889	C	C	C	G4749	A4611	C4453	U4306	U4189	G4094	G3951	A3788	A3718
A4894	C	C	C	G4750	C4612	U4457	G4309	U4190	G4095	G3956	A3788	A3719
C4895	C	C	C	G4754	G4617	U4459	C4314	G4191	G4096	U3957	A3788	G3720
G4896	C	C	C	C4757	G4618	U4459	G4314	G4196	G4097	G3958	A3788	A3723
G4897	C	C	C	U4758	G4625	A4464	C4319	A4203	G4098	U3959	A3788	A3724
C4900	C	C	C	C4759	A4626	U4465	A4323	A4214	G4100	A3960	A3788	A3727
G4901	C	C	C	G4760	U4627	C4466	A4323	A4214	G4101	G3961	A3788	A3732
C4902	C	C	C	G4761	G4631	U4475	G4326	A4219	G4102	A3962	A3788	A3733
U4910	C	C	C	U4762	U4632	A4488	G4329	A4220	C4103	U3963	A3788	A3734
C4911	C	C	C	U4763	G4633	U4488	G4330	C4221	G4104	A3965	A3788	G3735
G4912	C	C	C	G4765	U4634	U4500	G4331	G4222	G4104	A3966	A3788	A3736
G4913	C	C	C	G4769	U4635	A4507	C4332	G4228	C4015	G3967	A3788	A3737
C4914	C	C	C	U4770	U4637	A4508	G4338	U4229	G4016	U3968	A3788	U3745
C4922	C	C	C	G4772	G4652	U4512	G4347	G4238	C4021	G3970	A3788	A3746
C5023	C	C	C	C4773	G4652	U4512	G4347	G4238	C4022	A3971	A3788	A3747
C5024	C	C	C	C4773	G4652	U4512	G4347	G4238	C4023	G3972	A3788	A3748
C5025	C	C	C	C4773	G4652	U4512	G4347	G4238	C4024	G3973	A3788	C3749
U5026	C	C	C	C4773	G4652	U4512	G4347	G4238	C4025	G3973	A3788	C3749
C5027	C	C	C	C4773	G4652	U4512	G4347	G4238	C4026	G3973	A3788	C3749
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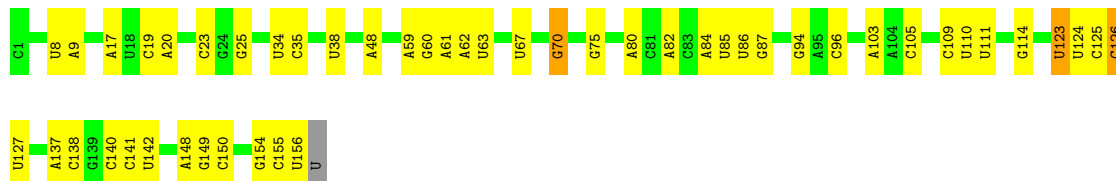
- Molecule 5: 5S rRNA

Chain L7:  83% 16%



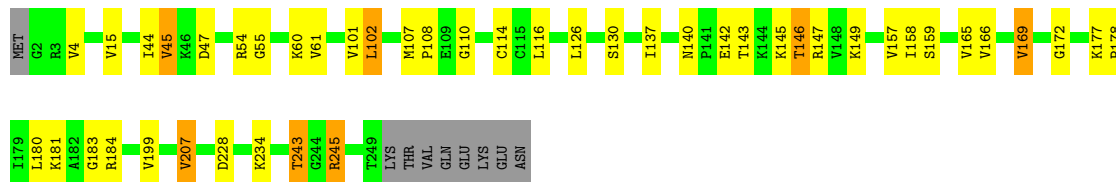
- Molecule 6: 5.8S rRNA

Chain L8:  68% 29%



- Molecule 7: 60S ribosomal protein L8

Chain LA:  79% 15%



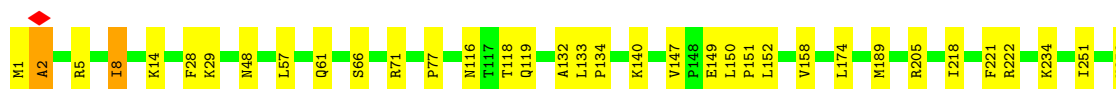
- Molecule 8: 60S ribosomal protein L3

Chain LB:  85% 14%



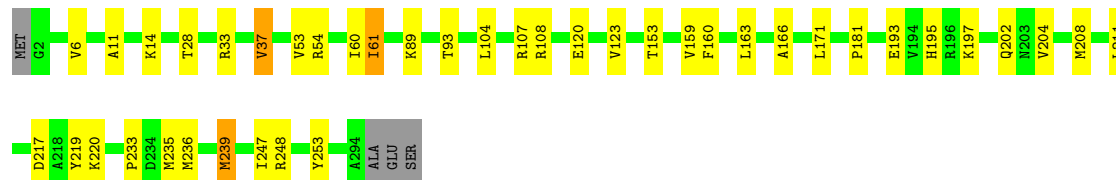
- Molecule 9: 60S ribosomal protein L4

Chain LC:  76% 10% 14%

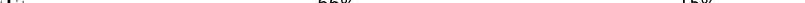


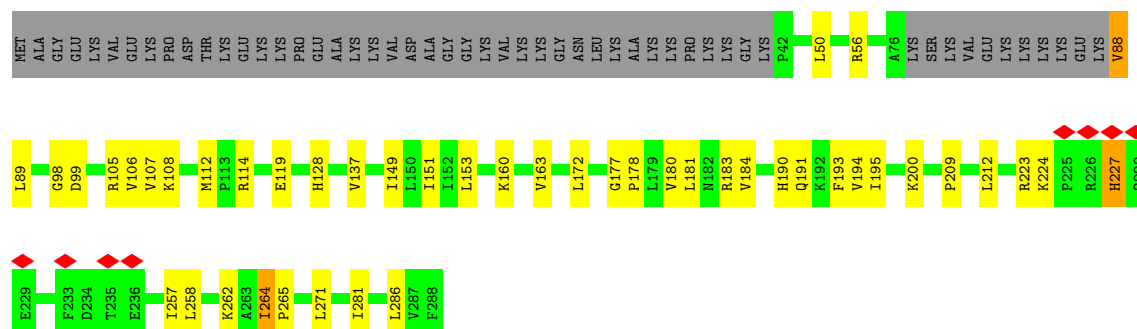
- Molecule 10: 60S ribosomal protein L5

Chain LD: 85% 13%

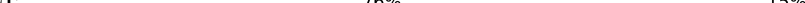


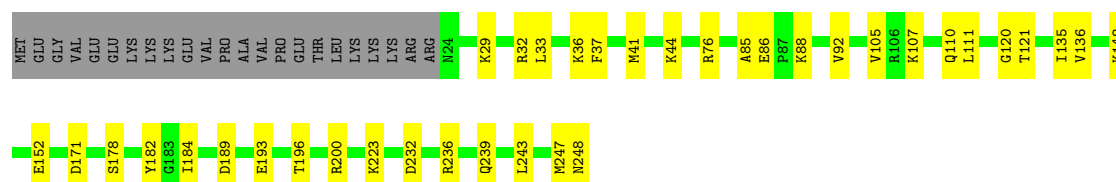
- Molecule 11: Large ribosomal subunit protein eL6

Chain LE: 



- Molecule 12: Large ribosomal subunit protein uL30

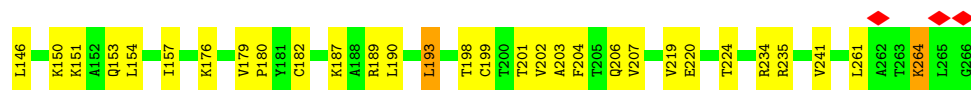
Chain LF: 



- Molecule 13: 60S ribosomal protein L7a

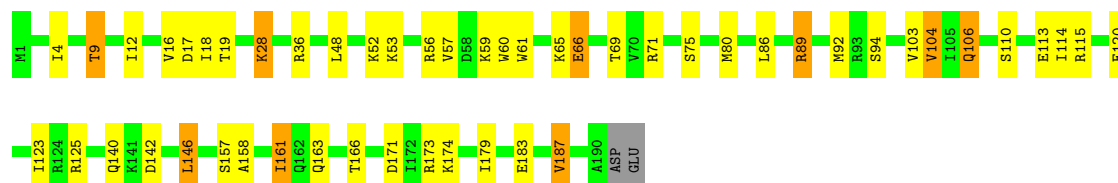
Chain LG: 74% 16% 9%





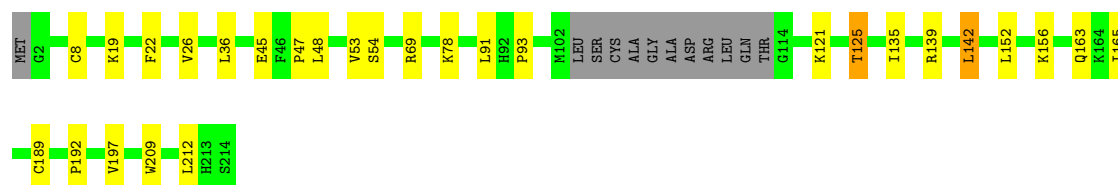
- Molecule 14: 60S ribosomal protein L9

Chain LH: 72% 22% 5%



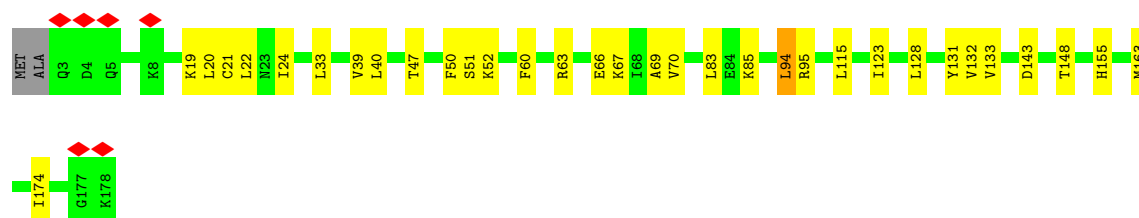
- Molecule 15: Ribosomal protein uL16-like

Chain LI: 81% 12% 6%



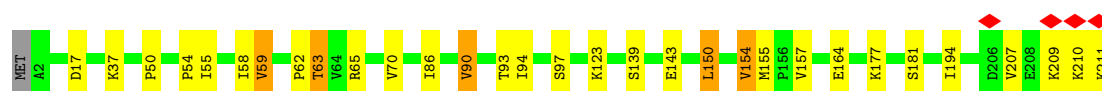
- Molecule 16: 60S ribosomal protein L11

Chain LJ: 80% 18% 2%



- Molecule 17: Large ribosomal subunit protein eL13

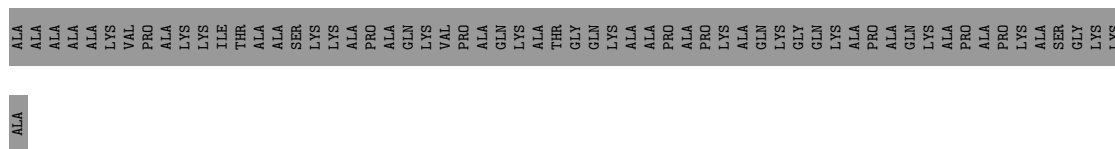
Chain LL: 85% 12% 3%



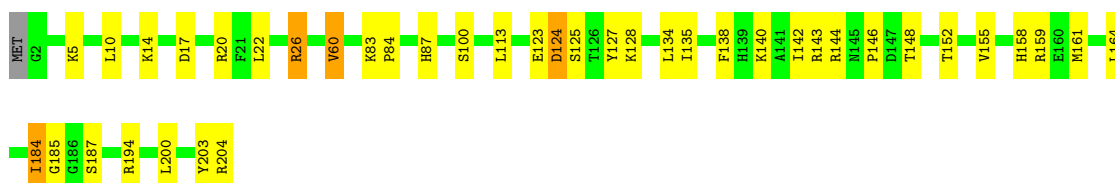
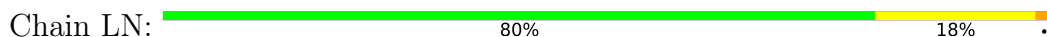
- Molecule 18: 60S ribosomal protein L14

Chain LM: 54% 8% 35%

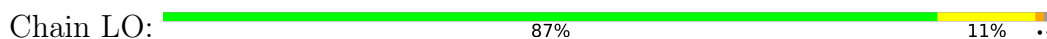




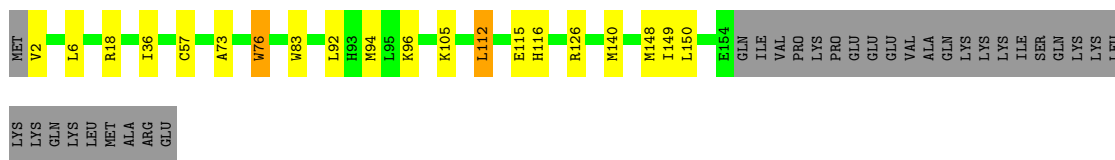
- Molecule 19: 60S ribosomal protein L15



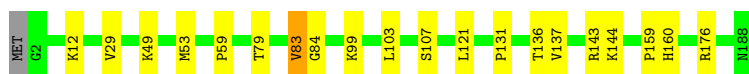
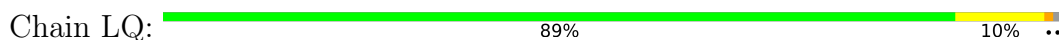
- Molecule 20: 60S ribosomal protein L13a



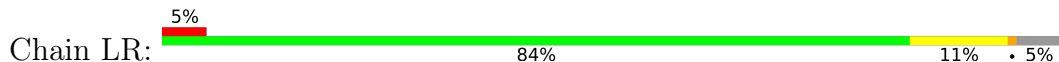
- Molecule 21: 60S ribosomal protein L17



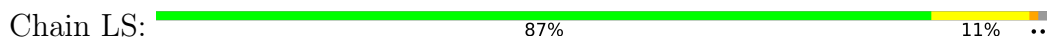
- Molecule 22: 60S ribosomal protein L18

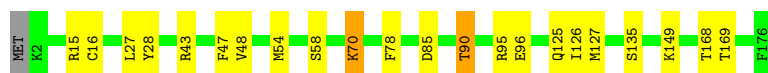


- Molecule 23: 60S ribosomal protein L19

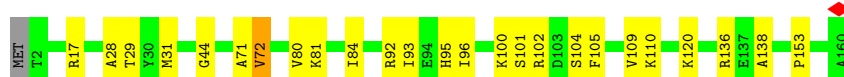
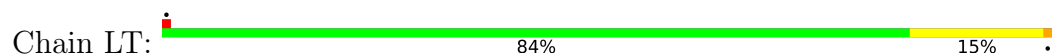


- Molecule 24: 60S ribosomal protein L18a

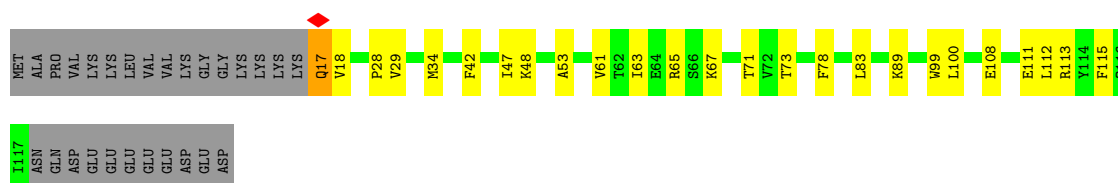




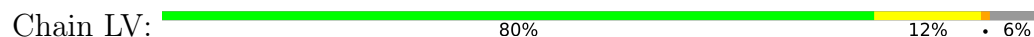
- Molecule 25: 60S ribosomal protein L21



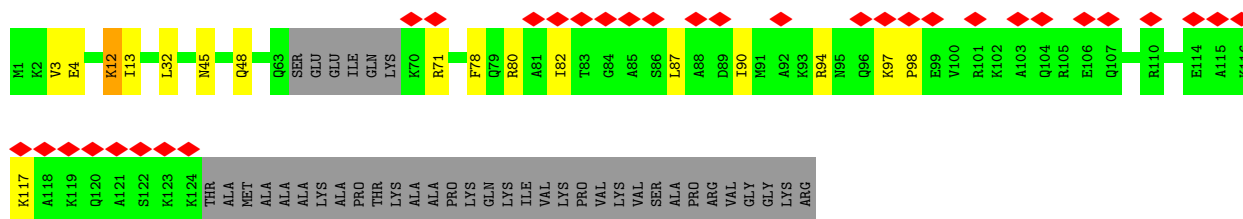
- Molecule 26: 60S ribosomal protein L22



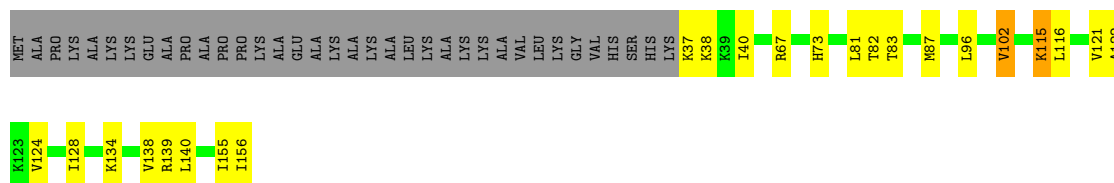
- Molecule 27: 60S ribosomal protein L23



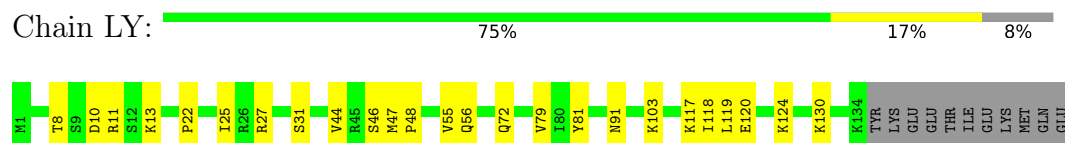
- Molecule 28: 60S ribosomal protein L24



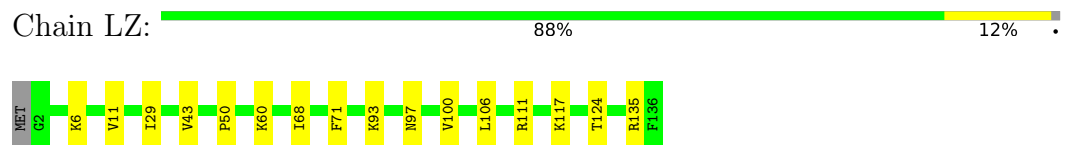
- Molecule 29: 60S ribosomal protein L23a



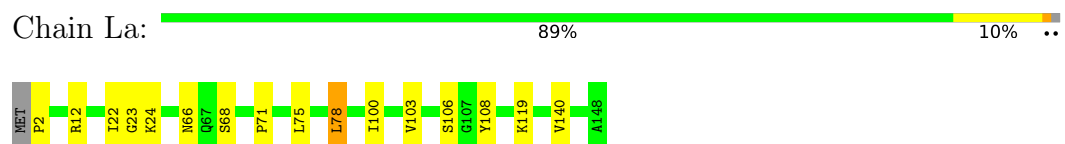
- Molecule 30: 60S ribosomal protein L26



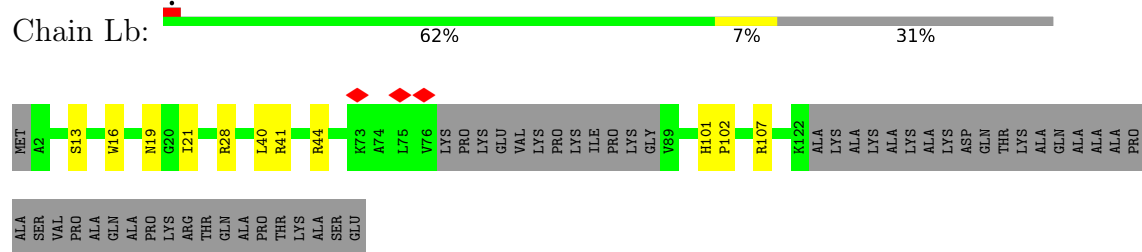
- Molecule 31: 60S ribosomal protein L27



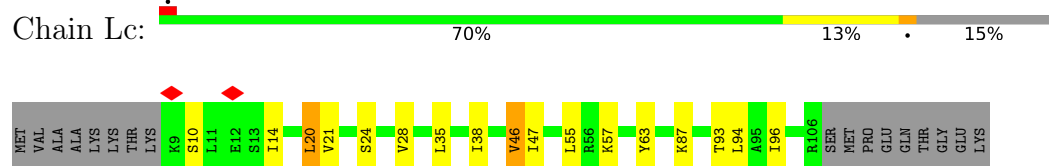
- Molecule 32: 60S ribosomal protein L27a



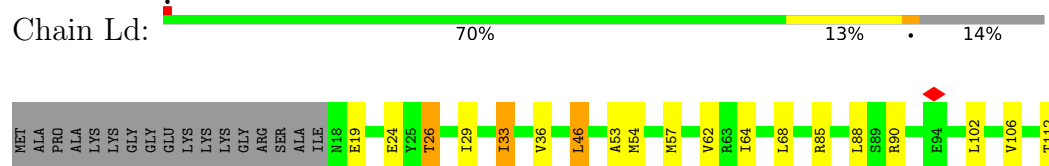
- Molecule 33: 60S ribosomal protein L29



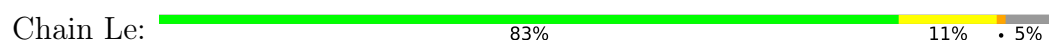
- Molecule 34: 60S ribosomal protein L30



- Molecule 35: 60S ribosomal protein L31



- Molecule 36: 60S ribosomal protein L32





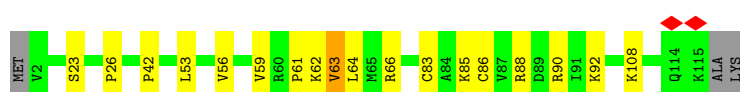
- Molecule 37: 60S ribosomal protein L35a

Chain Lf: 85% 13% ..



- Molecule 38: 60S ribosomal protein L34

Chain Lg: 82% 15% ..



- Molecule 39: 60S ribosomal protein L35

Chain Lh: 86% 11% ..



- Molecule 40: 60S ribosomal protein L36

Chain Li: 90% 8% .



- Molecule 41: Large ribosomal subunit protein eL37

Chain Lj: 76% 10% 11%



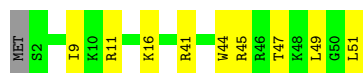
- Molecule 42: 60S ribosomal protein L38

Chain Lk: 81% 17% ..



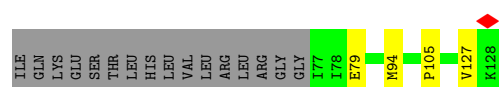
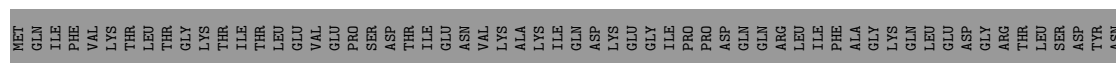
- Molecule 43: 60S ribosomal protein L39

Chain Ll:  80% 18% .



- Molecule 44: Ubiquitin-60S ribosomal protein L40

Chain Lm:  38% 59% .



- Molecule 45: 60S ribosomal protein L41

Chain Ln:  76% 20% .



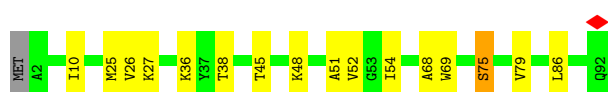
- Molecule 46: 60S ribosomal protein L36a

Chain Lo:  85% 13% ..



- Molecule 47: 60S ribosomal protein L37a

Chain Lp:  82% 16% ..



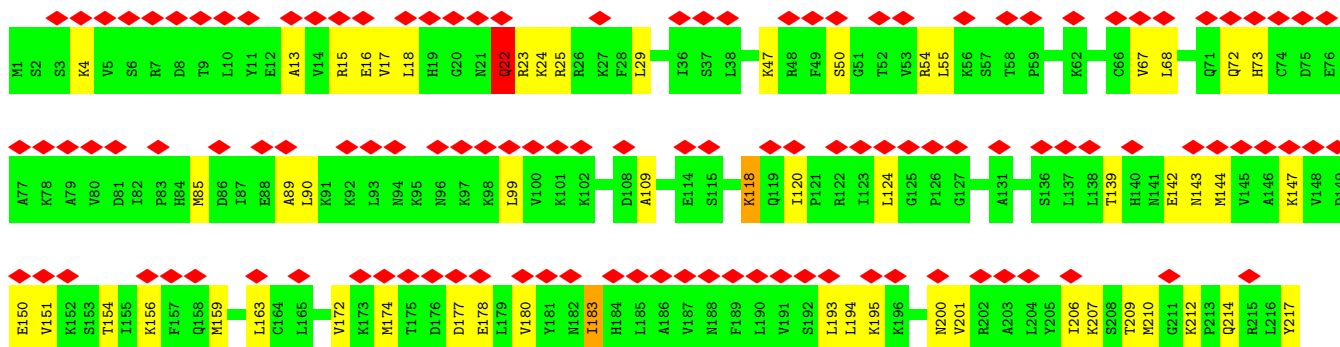
- Molecule 48: 60S ribosomal protein L28

Chain Lr:  84% 7% 9%

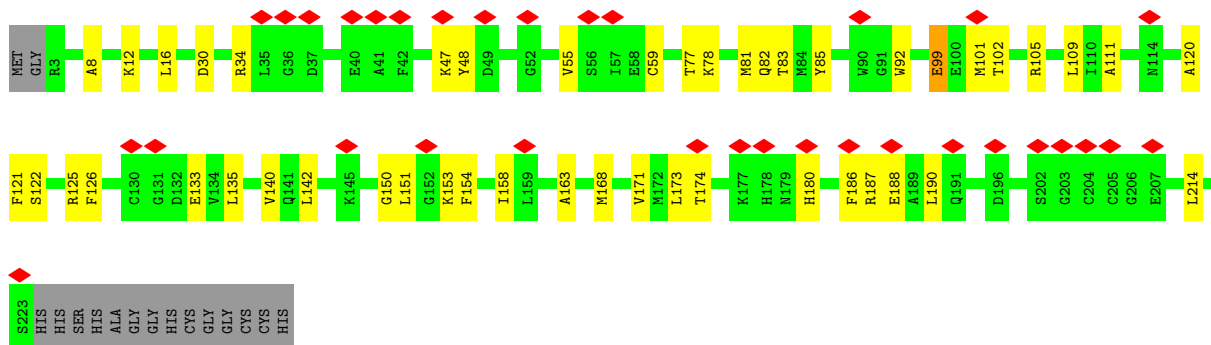


- Molecule 49: 60S ribosomal protein L10a

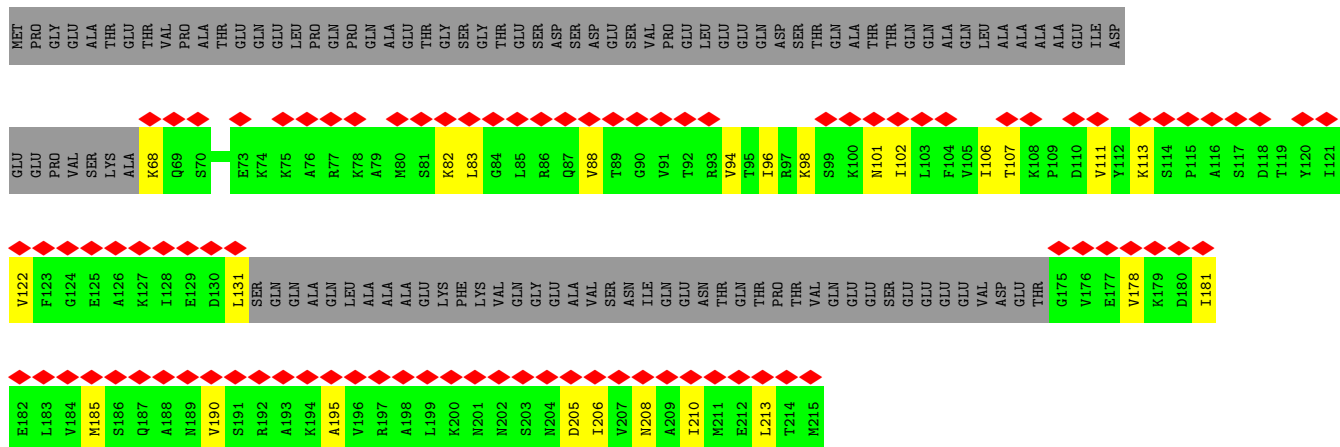
Chain Lz:  54% 74% 24% .



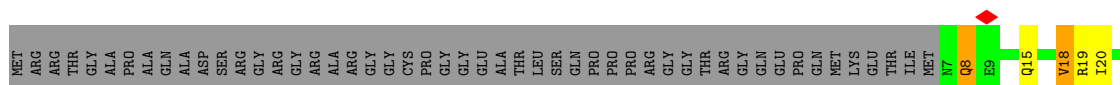
- Molecule 50: N-alpha-acetyltransferase 40



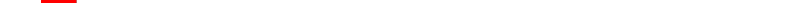
- Molecule 51: Nascent polypeptide-associated complex subunit alpha

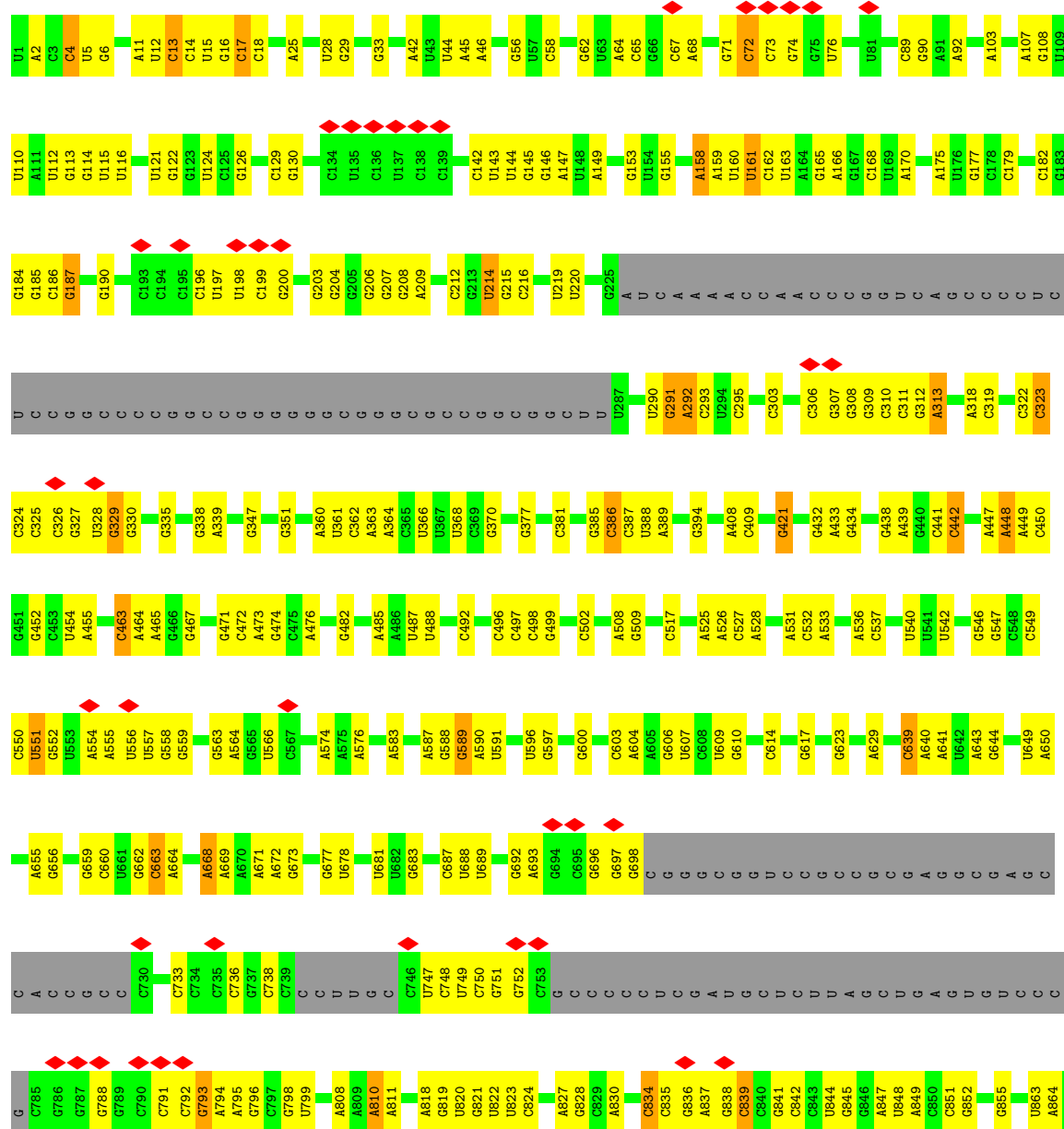


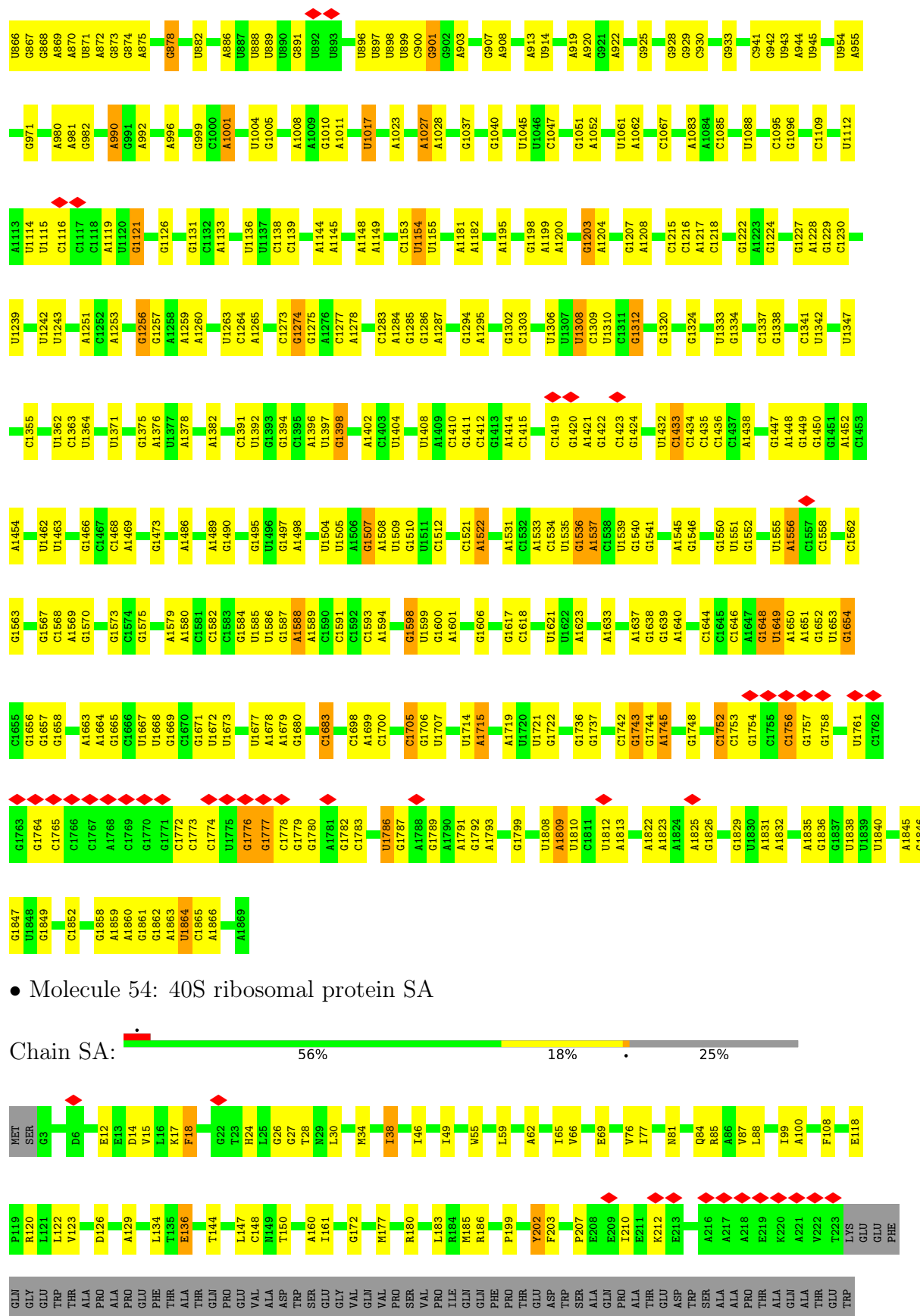
- Molecule 52: Transcription factor BTF3

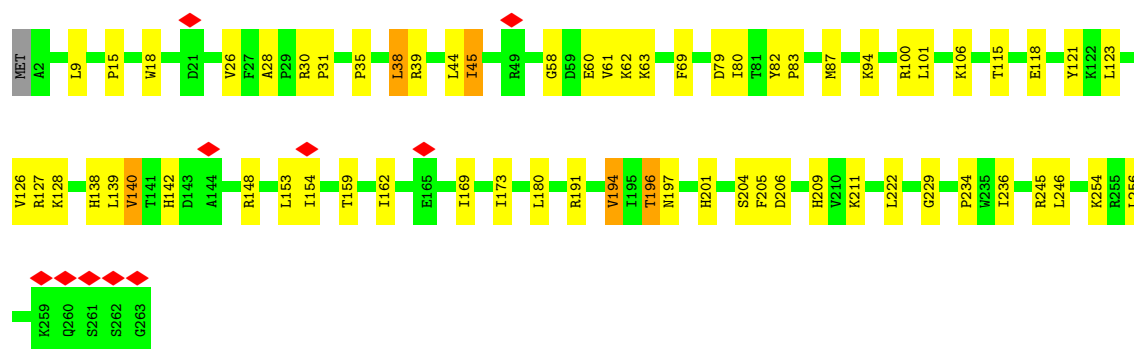


- Molecule 53: 18S rRNA

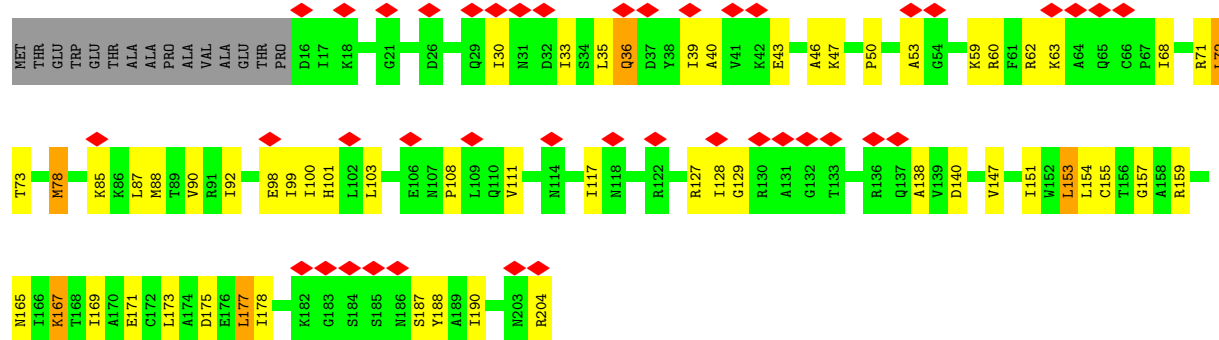
Chain S2:  57% 33% 7%



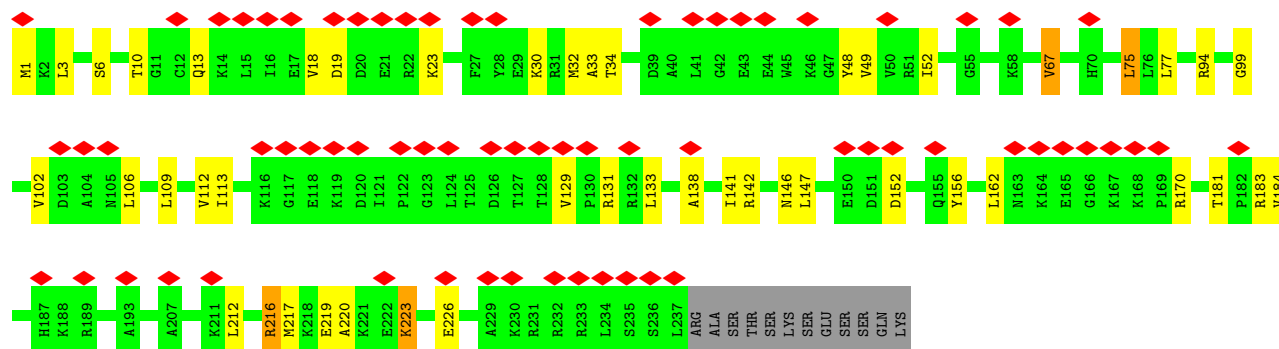
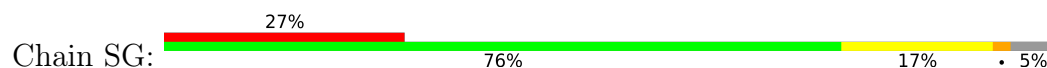




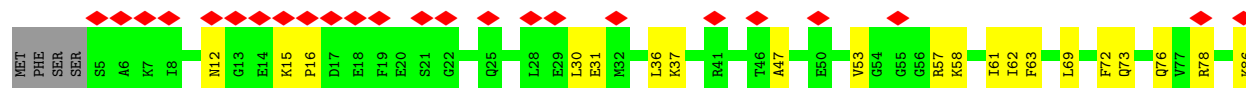
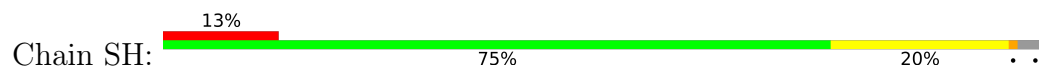
- Molecule 59: 40S ribosomal protein S5

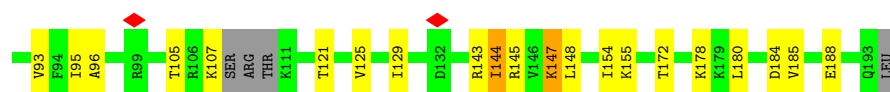


- Molecule 60: 40S ribosomal protein S6

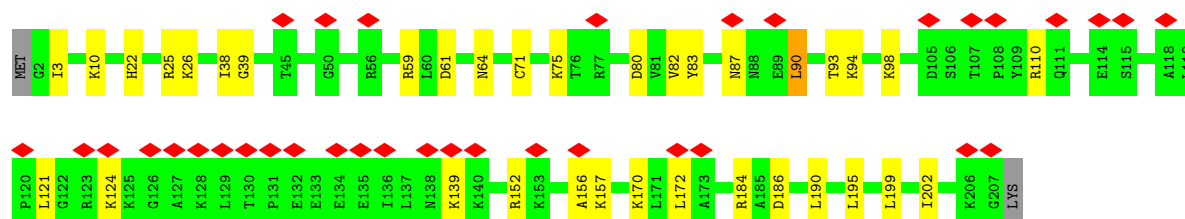
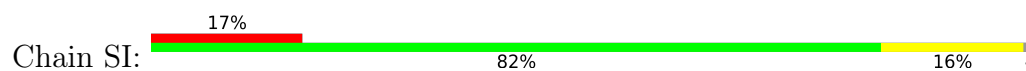


- Molecule 61: 40S ribosomal protein S7

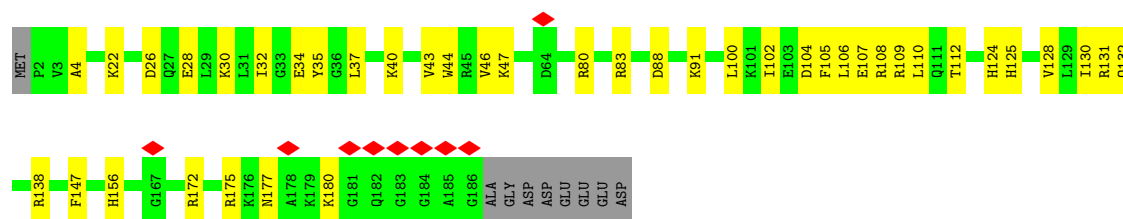
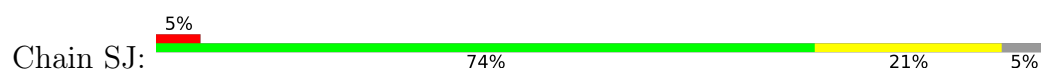




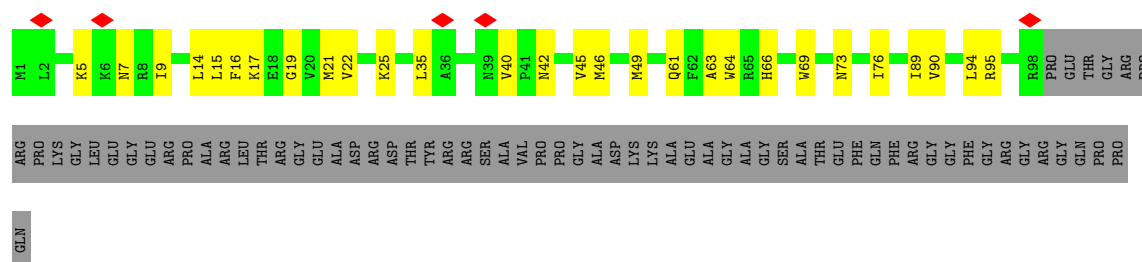
- Molecule 62: 40S ribosomal protein S8



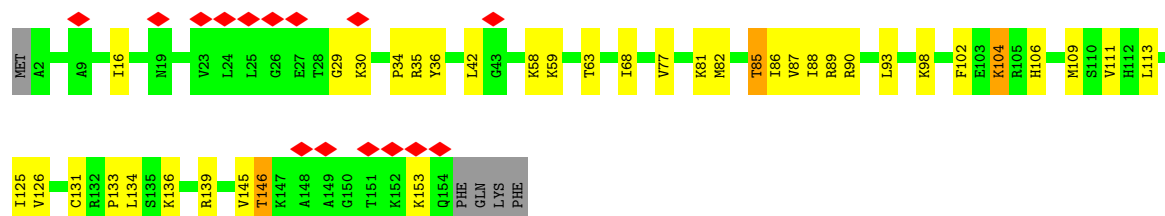
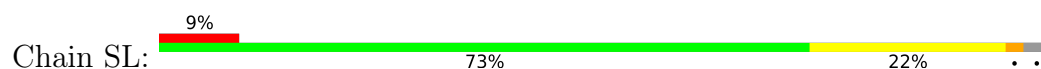
- Molecule 63: 40S ribosomal protein S9



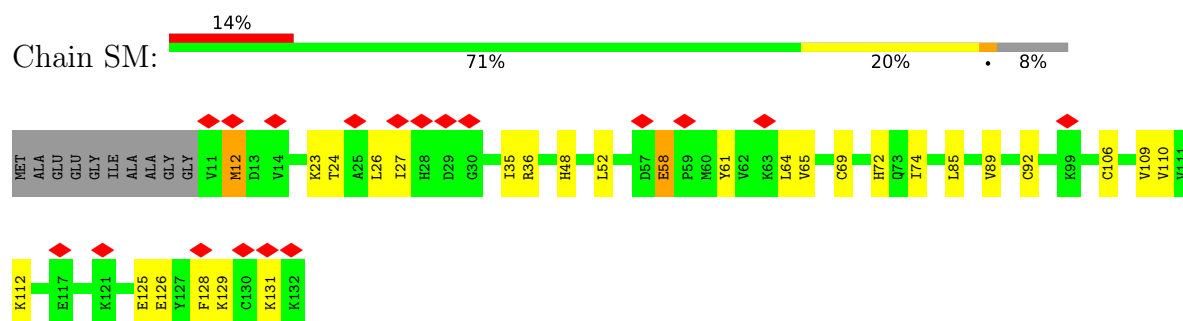
- Molecule 64: 40S ribosomal protein S10



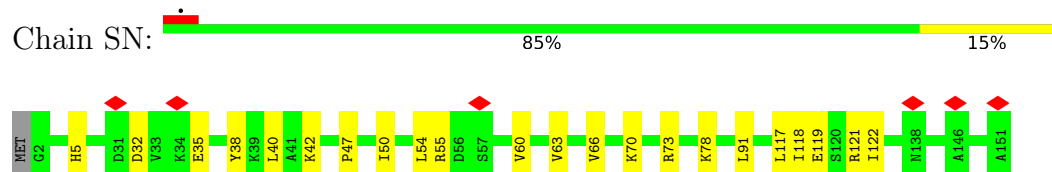
- Molecule 65: 40S ribosomal protein S11



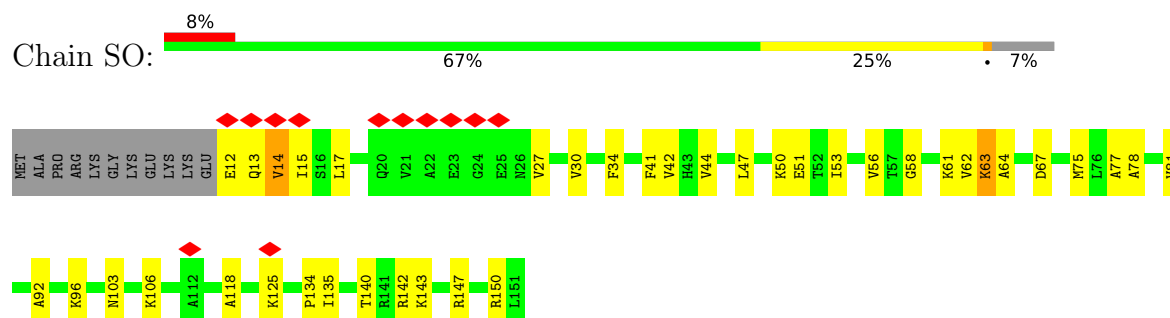
- Molecule 66: 40S ribosomal protein S12



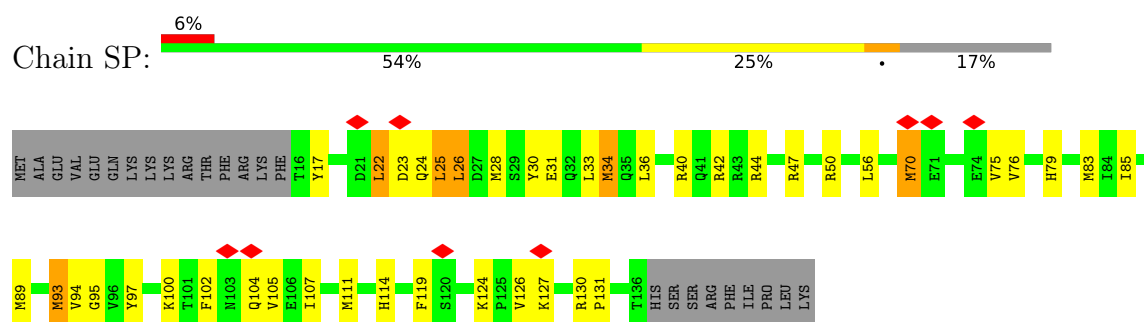
- Molecule 67: 40S ribosomal protein S13



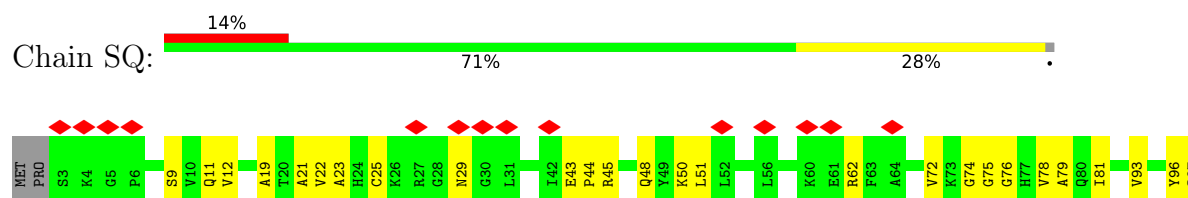
- Molecule 68: 40S ribosomal protein S14

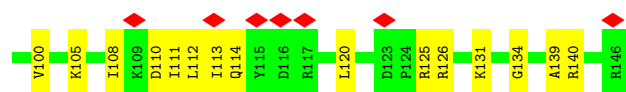


- Molecule 69: 40S ribosomal protein S15

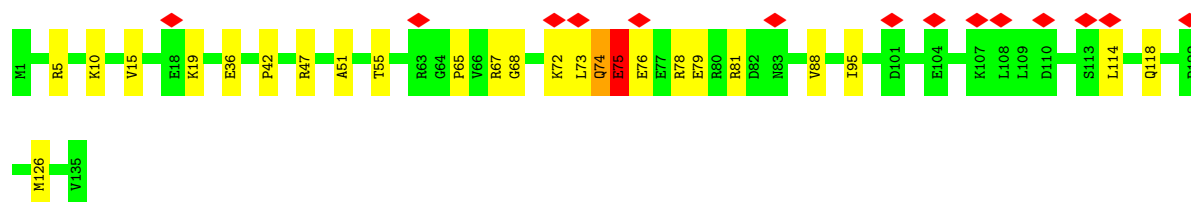
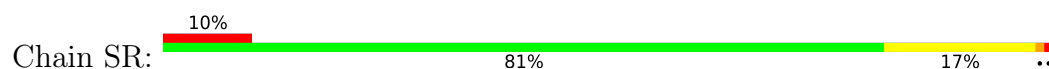


- Molecule 70: 40S ribosomal protein S16

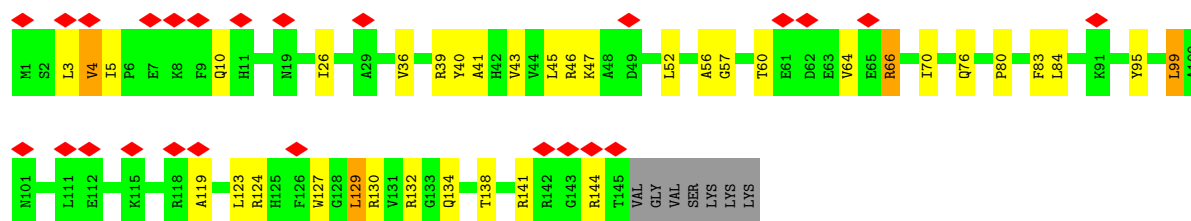




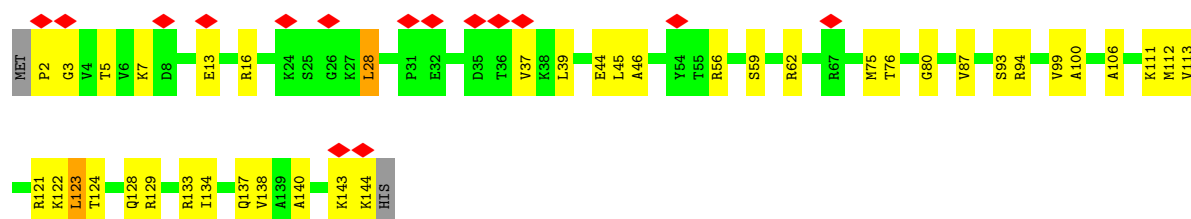
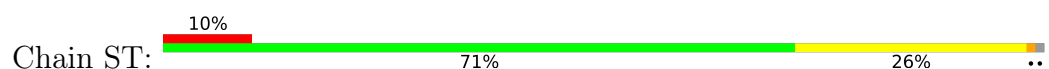
- Molecule 71: 40S ribosomal protein S17



- Molecule 72: 40S ribosomal protein S18



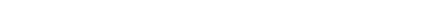
- Molecule 73: 40S ribosomal protein S19



- Molecule 74: 40S ribosomal protein S20



- Molecule 75: 40S ribosomal protein S21

Chain SV: 



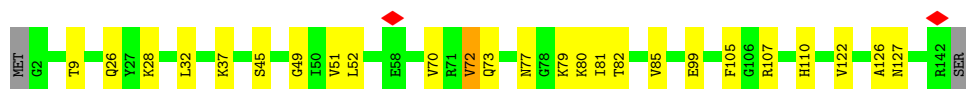
- Molecule 76: 40S ribosomal protein S15a

Chain SW: 

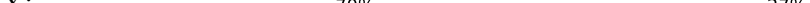


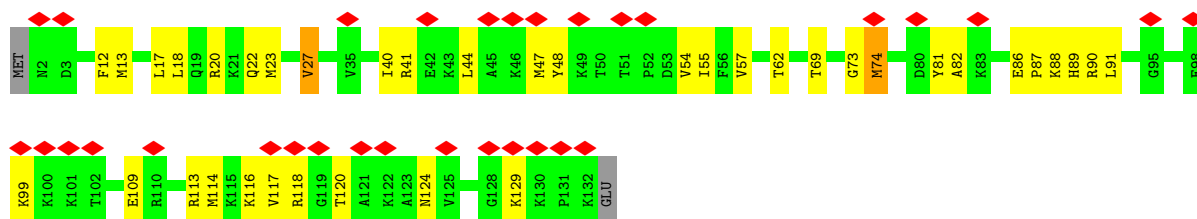
- Molecule 77: 40S ribosomal protein S23

Chain SX: 81% 17% ..

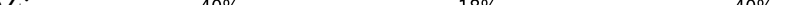


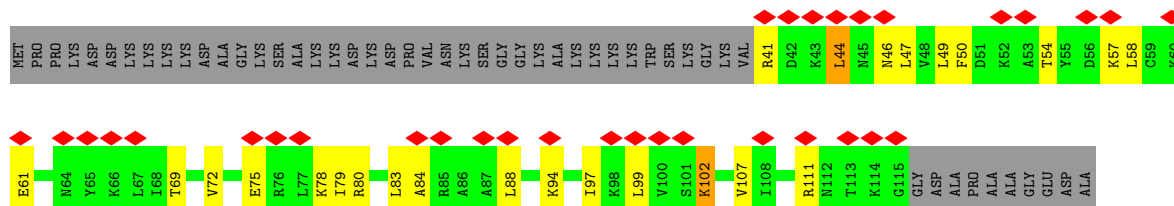
- Molecule 78: 40S ribosomal protein S24

Chain SY: 

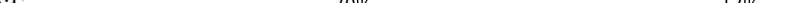


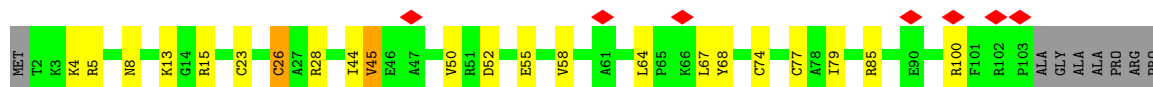
- Molecule 79: 40S ribosomal protein S25

Chain SZ: 



- Molecule 80: 40S ribosomal protein S26

Chain Sa: 



PRO
PRO
LYS
PRO
MET

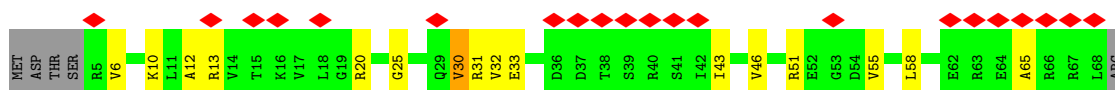
- Molecule 81: 40S ribosomal protein S27

Chain Sb:  8% 88% 10% ..



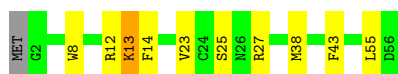
- Molecule 82: 40S ribosomal protein S28

Chain Sc:  30% 70% 22% 7%



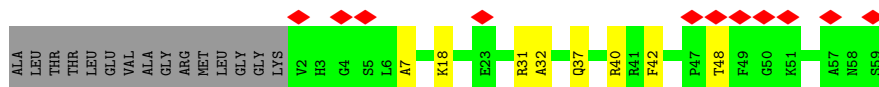
- Molecule 83: 40S ribosomal protein S29

Chain Sd:  80% 16% ..



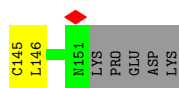
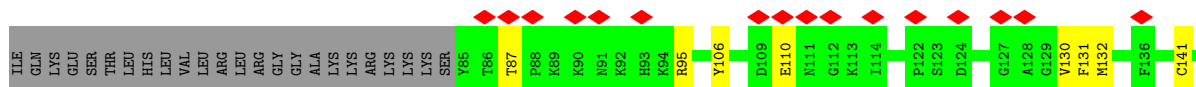
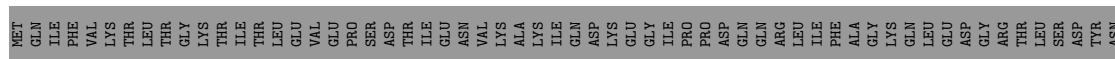
- Molecule 84: Ubiquitin-like FUBI-ribosomal protein eS30 fusion protein

Chain Se:  8% 38% 6% 56%

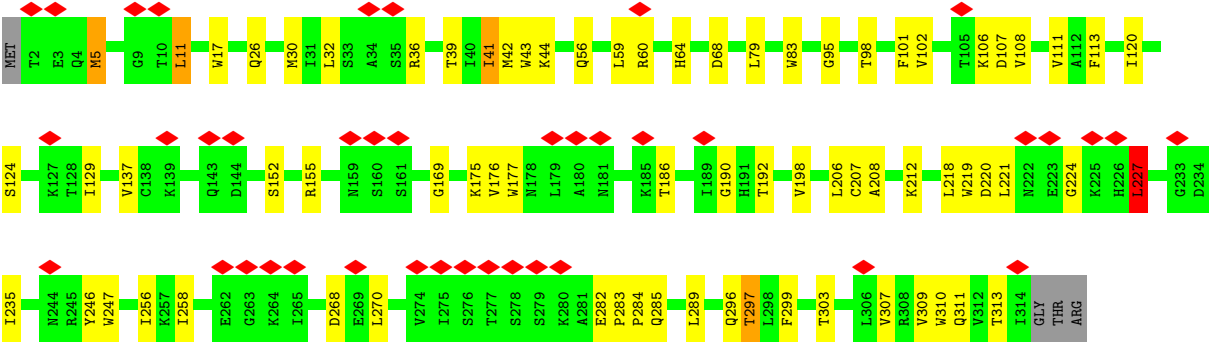
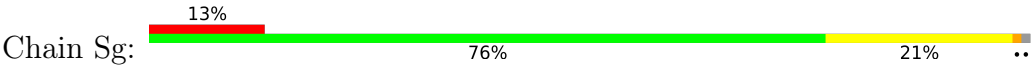


- Molecule 85: Ubiquitin

Chain Sf:  11% 37% 6% 57%



- Molecule 86: Receptor of activated protein C kinase 1



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	47197	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	FEI FALCON IV (4k x 4k)	Depositor
Maximum map value	4.817	Depositor
Minimum map value	-2.521	Depositor
Average map value	0.008	Depositor
Map value standard deviation	0.101	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	465.28, 465.28, 465.28	wwPDB
Map dimensions	640, 640, 640	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.727, 0.727, 0.727	Depositor

5 Model quality

5.1 Standard geometry

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	CB	0.22	0/6734	0.59	2/9094 (0.0%)
2	CC	0.15	0/2025	0.32	0/3155
3	CD	0.21	0/447	0.61	0/592
4	L5	0.25	0/89570	0.38	2/139647 (0.0%)
5	L7	0.24	0/2861	0.33	0/4459
6	L8	0.25	0/3701	0.34	0/5766
7	LA	0.27	0/1936	0.59	0/2596
8	LB	0.25	0/3306	0.55	0/4424
9	LC	0.27	0/2981	0.53	2/4002 (0.0%)
10	LD	0.24	0/2428	0.59	0/3252
11	LE	0.23	0/1942	0.56	0/2606
12	LF	0.27	0/1905	0.52	0/2539
13	LG	0.25	0/1960	0.57	0/2637
14	LH	0.28	0/1537	0.61	1/2066 (0.0%)
15	LI	0.23	0/1673	0.52	0/2233
16	LJ	0.26	0/1433	0.66	0/1915
17	LL	0.24	0/1732	0.49	0/2315
18	LM	0.25	0/1161	0.60	2/1554 (0.1%)
19	LN	0.28	0/1746	0.59	1/2338 (0.0%)
20	LO	0.25	0/1682	0.46	0/2250
21	LP	0.24	0/1268	0.49	0/1701
22	LQ	0.25	0/1537	0.51	0/2052
23	LR	0.22	0/1582	0.45	0/2091
24	LS	0.24	0/1493	0.44	0/2003
25	LT	0.24	0/1326	0.48	0/1770
26	LU	0.25	0/839	0.61	1/1126 (0.1%)
27	LV	0.23	0/993	0.50	0/1332
28	LW	0.22	0/979	0.49	0/1295
29	LX	0.23	0/1002	0.56	0/1345
30	LY	0.22	0/1132	0.46	0/1504
31	LZ	0.25	0/1130	0.60	2/1507 (0.1%)
32	La	0.25	0/1191	0.48	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lb	0.24	0/889	0.60	0/1175
34	Lc	0.23	0/774	0.56	0/1038
35	Ld	0.24	0/903	0.49	0/1216
36	Le	0.26	0/1071	0.53	0/1429
37	Lf	0.28	0/895	0.55	0/1198
38	Lg	0.24	0/916	0.50	0/1220
39	Lh	0.21	0/1023	0.45	0/1351
40	Li	0.20	0/843	0.48	0/1115
41	Lj	0.31	0/720	0.60	0/952
42	Lk	0.22	0/575	0.52	0/761
43	Ll	0.27	0/454	0.48	0/599
44	Lm	0.20	0/435	0.41	0/575
45	Ln	0.20	0/231	0.36	0/294
46	Lo	0.23	0/876	0.50	0/1156
47	Lp	0.26	0/718	0.52	0/953
48	Lr	0.25	0/1017	0.49	0/1364
49	Lz	0.24	0/1769	0.70	2/2371 (0.1%)
50	N4	0.22	0/1831	0.66	1/2456 (0.0%)
51	NA	0.20	0/821	0.56	0/1096
52	NB	0.23	0/813	0.61	1/1091 (0.1%)
53	S2	0.16	0/41244	0.34	0/64263
54	SA	0.25	0/1778	0.61	0/2416
55	SB	0.22	0/1765	0.64	1/2362 (0.0%)
56	SC	0.27	0/1762	0.71	1/2381 (0.0%)
57	SD	0.23	0/1793	0.67	0/2414
58	SE	0.21	0/2118	0.58	0/2849
59	SF	0.25	0/1516	0.71	2/2037 (0.1%)
60	SG	0.22	0/1946	0.64	4/2590 (0.2%)
61	SH	0.27	0/1519	0.68	2/2033 (0.1%)
62	SI	0.22	0/1715	0.58	1/2287 (0.0%)
63	SJ	0.24	0/1550	0.60	0/2069
64	SK	0.30	0/851	0.79	0/1147
65	SL	0.22	0/1268	0.53	0/1696
66	SM	0.22	0/950	0.70	2/1275 (0.2%)
67	SN	0.22	0/1232	0.59	0/1656
68	SO	0.24	0/1062	0.62	2/1425 (0.1%)
69	SP	0.33	0/1003	0.90	7/1342 (0.5%)
70	SQ	0.30	0/1160	0.76	2/1553 (0.1%)
71	SR	0.29	0/1105	0.85	4/1484 (0.3%)
72	SS	0.23	0/1216	0.63	1/1628 (0.1%)
73	ST	0.28	0/1131	0.76	2/1515 (0.1%)
74	SU	0.25	0/831	0.77	3/1115 (0.3%)
75	SV	0.23	0/643	0.64	0/860

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	SW	0.23	0/1051	0.51	0/1406
77	SX	0.22	0/1116	0.61	1/1490 (0.1%)
78	SY	0.23	0/1083	0.63	1/1438 (0.1%)
79	SZ	0.29	0/604	0.92	1/810 (0.1%)
80	Sa	0.29	0/836	0.57	0/1121
81	Sb	0.23	0/665	0.62	1/891 (0.1%)
82	Sc	0.27	0/508	0.82	0/680
83	Sd	0.22	0/470	0.69	2/623 (0.3%)
84	Se	0.23	0/465	0.63	0/612
85	Sf	0.25	0/560	0.81	1/745 (0.1%)
86	Sg	0.23	0/2493	0.71	4/3394 (0.1%)
All	All	0.24	0/245815	0.47	62/359774 (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	CB	0	1
7	LA	0	2
8	LB	0	2
14	LH	0	2
16	LJ	0	1
17	LL	0	1
18	LM	0	2
20	LO	0	1
25	LT	0	1
28	LW	0	1
31	LZ	0	1
37	Lf	0	1
39	Lh	0	1
41	Lj	0	1
49	Lz	0	1
57	SD	0	1
59	SF	0	1
60	SG	0	1
61	SH	0	1
69	SP	0	1
70	SQ	0	1
72	SS	0	1
73	ST	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
75	SV	0	1
77	SX	0	2
79	SZ	0	1
85	Sf	0	1
86	Sg	0	1
All	All	0	33

There are no bond length outliers.

The worst 5 of 62 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	NB	8	GLN	CA-CB-CG	6.62	127.34	114.10
56	SC	80	GLU	CA-CB-CG	6.36	126.83	114.10
19	LN	184	ILE	N-CA-C	-6.28	106.32	111.91
60	SG	223	LYS	CB-CG-CD	6.27	125.73	111.30
73	ST	112	MET	CB-CG-SD	6.26	131.49	112.70

There are no chirality outliers.

5 of 33 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	CB	807	GLN	Peptide
7	LA	110	GLY	Peptide
7	LA	54	ARG	Peptide
8	LB	17	LEU	Peptide
8	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.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	CB	6605	0	6681	94	0
2	CC	1813	0	917	6	0
3	CD	440	0	402	4	0
4	L5	80116	0	40368	331	0
5	L7	2561	0	1295	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	L8	3314	0	1683	15	0
7	LA	1898	0	1993	25	0
8	LB	3238	0	3376	33	0
9	LC	2927	0	3104	21	0
10	LD	2382	0	2410	19	0
11	LE	1904	0	2055	22	0
12	LF	1870	0	1996	18	0
13	LG	1927	0	2074	23	0
14	LH	1518	0	1601	28	0
15	LI	1634	0	1671	17	0
16	LJ	1410	0	1441	18	0
17	LL	1701	0	1818	18	0
18	LM	1138	0	1204	13	0
19	LN	1701	0	1749	24	0
20	LO	1650	0	1794	14	0
21	LP	1242	0	1269	12	0
22	LQ	1513	0	1628	10	0
23	LR	1566	0	1729	11	0
24	LS	1453	0	1490	9	0
25	LT	1298	0	1365	15	0
26	LU	825	0	850	15	0
27	LV	979	0	1039	10	0
28	LW	965	0	1029	11	0
29	LX	985	0	1066	13	0
30	LY	1115	0	1205	11	0
31	LZ	1107	0	1182	7	0
32	La	1162	0	1213	10	0
33	Lb	876	0	948	6	0
34	Lc	764	0	804	11	0
35	Ld	888	0	930	9	0
36	Le	1053	0	1147	7	0
37	Lf	876	0	912	6	0
38	Lg	906	0	998	13	0
39	Lh	1015	0	1148	13	0
40	Li	832	0	917	4	0
41	Lj	705	0	737	9	0
42	Lk	569	0	637	8	0
43	Ll	444	0	483	5	0
44	Lm	429	0	465	1	0
45	Ln	230	0	276	3	0
46	Lo	862	0	929	6	0
47	Lp	708	0	756	11	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	Lr	1002	0	1068	4	0
49	Lz	1741	0	1854	33	0
50	N4	1795	0	1754	25	0
51	NA	817	0	877	15	0
52	NB	805	0	847	17	0
53	S2	36898	0	18601	237	0
54	SA	1741	0	1746	33	0
55	SB	1738	0	1809	29	0
56	SC	1725	0	1813	37	0
57	SD	1765	0	1865	34	0
58	SE	2076	0	2177	41	0
59	SF	1495	0	1549	39	0
60	SG	1923	0	2089	28	0
61	SH	1497	0	1590	22	0
62	SI	1686	0	1772	23	0
63	SJ	1525	0	1640	24	0
64	SK	827	0	854	21	0
65	SL	1247	0	1323	23	0
66	SM	940	0	965	15	0
67	SN	1208	0	1294	13	0
68	SO	1049	0	1073	30	0
69	SP	985	0	1031	23	0
70	SQ	1142	0	1213	30	0
71	SR	1090	0	1149	16	0
72	SS	1198	0	1261	27	0
73	ST	1112	0	1146	20	0
74	SU	821	0	883	22	0
75	SV	636	0	637	9	0
76	SW	1034	0	1080	15	0
77	SX	1098	0	1167	13	0
78	SY	1065	0	1142	25	0
79	SZ	598	0	656	12	0
80	Sa	821	0	870	16	0
81	Sb	651	0	672	5	0
82	Sc	506	0	536	11	0
83	Sd	459	0	451	9	0
84	Se	459	0	503	6	0
85	Sf	548	0	555	4	0
86	Sg	2436	0	2393	39	0
87	CC	1	0	0	0	0
87	L5	214	0	0	0	0
87	L7	3	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
87	L8	3	0	0	0	0
87	LA	1	0	0	0	0
87	LI	1	0	0	0	0
87	LP	1	0	0	0	0
87	LV	1	0	0	0	0
87	Le	1	0	0	0	0
87	Lg	1	0	0	0	0
87	S2	29	0	0	0	0
88	Lg	1	0	0	0	0
88	Lj	1	0	0	0	0
88	Lm	1	0	0	0	0
88	Lo	1	0	0	0	0
88	Lp	1	0	0	0	0
88	SM	1	0	0	0	0
88	Sa	1	0	0	0	0
88	Sd	1	0	0	0	0
All	All	229537	0	172689	1830	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 1830 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)
4:L5:1176:C:H42	4:L5:1184:A:N6	1.49	1.10
4:L5:1176:C:N4	4:L5:1184:A:H61	1.51	1.08
53:S2:886:A:N6	53:S2:901:G:C4	2.21	1.07
4:L5:1269:G:N2	4:L5:1441:C:C2	2.25	1.04
59:SF:35:LEU:O	59:SF:39:ILE:HB	1.58	1.03

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	CB	842/858 (98%)	788 (94%)	54 (6%)	0	100	100
3	CD	51/402 (13%)	48 (94%)	3 (6%)	0	100	100
7	LA	246/257 (96%)	226 (92%)	19 (8%)	1 (0%)	30	51
8	LB	400/403 (99%)	376 (94%)	23 (6%)	1 (0%)	36	57
9	LC	366/427 (86%)	339 (93%)	27 (7%)	0	100	100
10	LD	291/297 (98%)	274 (94%)	17 (6%)	0	100	100
11	LE	232/288 (81%)	216 (93%)	16 (7%)	0	100	100
12	LF	223/248 (90%)	216 (97%)	7 (3%)	0	100	100
13	LG	239/266 (90%)	225 (94%)	14 (6%)	0	100	100
14	LH	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
15	LI	198/214 (92%)	185 (93%)	13 (7%)	0	100	100
16	LJ	174/178 (98%)	160 (92%)	14 (8%)	0	100	100
17	LL	208/211 (99%)	192 (92%)	16 (8%)	0	100	100
18	LM	137/215 (64%)	128 (93%)	8 (6%)	1 (1%)	18	37
19	LN	201/204 (98%)	191 (95%)	8 (4%)	2 (1%)	12	28
20	LO	199/203 (98%)	193 (97%)	6 (3%)	0	100	100
21	LP	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
22	LQ	185/188 (98%)	177 (96%)	8 (4%)	0	100	100
23	LR	185/196 (94%)	182 (98%)	3 (2%)	0	100	100
24	LS	173/176 (98%)	161 (93%)	12 (7%)	0	100	100
25	LT	157/160 (98%)	146 (93%)	11 (7%)	0	100	100
26	LU	99/128 (77%)	94 (95%)	5 (5%)	0	100	100
27	LV	129/140 (92%)	122 (95%)	7 (5%)	0	100	100
28	LW	114/157 (73%)	108 (95%)	6 (5%)	0	100	100
29	LX	118/156 (76%)	115 (98%)	3 (2%)	0	100	100
30	LY	132/145 (91%)	127 (96%)	5 (4%)	0	100	100
31	LZ	133/136 (98%)	121 (91%)	12 (9%)	0	100	100
32	La	145/148 (98%)	137 (94%)	8 (6%)	0	100	100
33	Lb	105/159 (66%)	97 (92%)	8 (8%)	0	100	100
34	Lc	96/115 (84%)	88 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Ld	105/125 (84%)	99 (94%)	6 (6%)	0	100	100
36	Le	126/135 (93%)	120 (95%)	6 (5%)	0	100	100
37	Lf	107/110 (97%)	99 (92%)	7 (6%)	1 (1%)	14	31
38	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
39	Lh	120/123 (98%)	117 (98%)	3 (2%)	0	100	100
40	Li	100/105 (95%)	96 (96%)	4 (4%)	0	100	100
41	Lj	84/97 (87%)	74 (88%)	10 (12%)	0	100	100
42	Lk	67/70 (96%)	64 (96%)	3 (4%)	0	100	100
43	Ll	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
44	Lm	50/128 (39%)	50 (100%)	0	0	100	100
45	Ln	22/25 (88%)	22 (100%)	0	0	100	100
46	Lo	103/106 (97%)	97 (94%)	6 (6%)	0	100	100
47	Lp	89/92 (97%)	86 (97%)	3 (3%)	0	100	100
48	Lr	123/137 (90%)	116 (94%)	7 (6%)	0	100	100
49	Lz	215/217 (99%)	164 (76%)	51 (24%)	0	100	100
50	N4	219/237 (92%)	213 (97%)	6 (3%)	0	100	100
51	NA	101/215 (47%)	96 (95%)	5 (5%)	0	100	100
52	NB	102/206 (50%)	99 (97%)	2 (2%)	1 (1%)	12	28
54	SA	219/295 (74%)	197 (90%)	22 (10%)	0	100	100
55	SB	212/264 (80%)	205 (97%)	7 (3%)	0	100	100
56	SC	220/293 (75%)	203 (92%)	17 (8%)	0	100	100
57	SD	225/243 (93%)	202 (90%)	23 (10%)	0	100	100
58	SE	260/263 (99%)	240 (92%)	20 (8%)	0	100	100
59	SF	187/204 (92%)	172 (92%)	15 (8%)	0	100	100
60	SG	235/249 (94%)	219 (93%)	16 (7%)	0	100	100
61	SH	182/194 (94%)	161 (88%)	21 (12%)	0	100	100
62	SI	204/208 (98%)	190 (93%)	14 (7%)	0	100	100
63	SJ	183/194 (94%)	169 (92%)	14 (8%)	0	100	100
64	SK	96/165 (58%)	85 (88%)	11 (12%)	0	100	100
65	SL	151/158 (96%)	139 (92%)	12 (8%)	0	100	100
66	SM	120/132 (91%)	113 (94%)	7 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	SN	148/151 (98%)	142 (96%)	6 (4%)	0	100	100
68	SO	138/151 (91%)	124 (90%)	14 (10%)	0	100	100
69	SP	119/145 (82%)	105 (88%)	14 (12%)	0	100	100
70	SQ	142/146 (97%)	131 (92%)	11 (8%)	0	100	100
71	SR	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
72	SS	143/152 (94%)	133 (93%)	10 (7%)	0	100	100
73	ST	141/145 (97%)	130 (92%)	11 (8%)	0	100	100
74	SU	102/119 (86%)	94 (92%)	8 (8%)	0	100	100
75	SV	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
76	SW	127/130 (98%)	122 (96%)	5 (4%)	0	100	100
77	SX	139/143 (97%)	124 (89%)	14 (10%)	1 (1%)	18	37
78	SY	129/133 (97%)	124 (96%)	5 (4%)	0	100	100
79	SZ	73/125 (58%)	58 (80%)	14 (19%)	1 (1%)	9	21
80	Sa	100/115 (87%)	88 (88%)	12 (12%)	0	100	100
81	Sb	81/84 (96%)	74 (91%)	7 (9%)	0	100	100
82	Sc	62/69 (90%)	52 (84%)	10 (16%)	0	100	100
83	Sd	53/56 (95%)	48 (91%)	5 (9%)	0	100	100
84	Se	56/133 (42%)	47 (84%)	9 (16%)	0	100	100
85	Sf	65/156 (42%)	53 (82%)	12 (18%)	0	100	100
86	Sg	311/317 (98%)	269 (86%)	42 (14%)	0	100	100
All	All	12847/14897 (86%)	11924 (93%)	914 (7%)	9 (0%)	49	71

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
52	NB	8	GLN
19	LN	124	ASP
18	LM	88	ALA
79	SZ	50	PHE
8	LB	302	ASN

5.3.2 Protein sidechains ⓘ

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

entries.

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	CB	722/730 (99%)	690 (96%)	32 (4%)	25	50
3	CD	46/322 (14%)	45 (98%)	1 (2%)	45	72
7	LA	190/199 (96%)	177 (93%)	13 (7%)	14	32
8	LB	348/349 (100%)	332 (95%)	16 (5%)	24	48
9	LC	306/348 (88%)	292 (95%)	14 (5%)	24	48
10	LD	246/250 (98%)	237 (96%)	9 (4%)	30	56
11	LE	209/252 (83%)	198 (95%)	11 (5%)	20	43
12	LF	194/215 (90%)	186 (96%)	8 (4%)	27	52
13	LG	203/223 (91%)	191 (94%)	12 (6%)	18	38
14	LH	169/171 (99%)	152 (90%)	17 (10%)	7	16
15	LI	172/181 (95%)	166 (96%)	6 (4%)	32	58
16	LJ	148/149 (99%)	139 (94%)	9 (6%)	17	37
17	LL	176/177 (99%)	166 (94%)	10 (6%)	18	40
18	LM	118/161 (73%)	114 (97%)	4 (3%)	32	59
19	LN	171/172 (99%)	165 (96%)	6 (4%)	32	58
20	LO	173/174 (99%)	168 (97%)	5 (3%)	37	64
21	LP	134/163 (82%)	130 (97%)	4 (3%)	36	63
22	LQ	164/165 (99%)	159 (97%)	5 (3%)	36	63
23	LR	166/175 (95%)	159 (96%)	7 (4%)	26	52
24	LS	156/157 (99%)	146 (94%)	10 (6%)	16	35
25	LT	139/140 (99%)	135 (97%)	4 (3%)	37	64
26	LU	91/115 (79%)	86 (94%)	5 (6%)	19	41
27	LV	101/107 (94%)	96 (95%)	5 (5%)	22	45
28	LW	97/126 (77%)	95 (98%)	2 (2%)	47	73
29	LX	108/133 (81%)	103 (95%)	5 (5%)	24	48
30	LY	124/135 (92%)	116 (94%)	8 (6%)	15	34
31	LZ	117/118 (99%)	113 (97%)	4 (3%)	32	59
32	La	120/121 (99%)	114 (95%)	6 (5%)	22	45
33	Lb	88/126 (70%)	85 (97%)	3 (3%)	32	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Lc	83/97 (86%)	77 (93%)	6 (7%)	13	29
35	Ld	98/110 (89%)	90 (92%)	8 (8%)	10	24
36	Le	114/121 (94%)	107 (94%)	7 (6%)	17	37
37	Lf	88/89 (99%)	85 (97%)	3 (3%)	32	59
38	Lg	98/100 (98%)	95 (97%)	3 (3%)	35	62
39	Lh	109/110 (99%)	107 (98%)	2 (2%)	51	76
40	Li	86/89 (97%)	85 (99%)	1 (1%)	63	82
41	Lj	73/80 (91%)	72 (99%)	1 (1%)	59	80
42	Lk	64/65 (98%)	64 (100%)	0	100	100
43	Ll	47/48 (98%)	45 (96%)	2 (4%)	26	51
44	Lm	48/116 (41%)	46 (96%)	2 (4%)	26	52
45	Ln	23/24 (96%)	23 (100%)	0	100	100
46	Lo	93/94 (99%)	87 (94%)	6 (6%)	15	34
47	Lp	74/75 (99%)	72 (97%)	2 (3%)	39	67
48	Lr	109/121 (90%)	105 (96%)	4 (4%)	30	56
49	Lz	195/196 (100%)	188 (96%)	7 (4%)	31	57
50	N4	194/204 (95%)	189 (97%)	5 (3%)	40	68
51	NA	92/183 (50%)	91 (99%)	1 (1%)	65	83
52	NB	88/165 (53%)	84 (96%)	4 (4%)	24	49
54	SA	183/243 (75%)	175 (96%)	8 (4%)	25	50
55	SB	195/231 (84%)	183 (94%)	12 (6%)	16	36
56	SC	188/225 (84%)	176 (94%)	12 (6%)	16	35
57	SD	190/202 (94%)	183 (96%)	7 (4%)	30	56
58	SE	224/225 (100%)	212 (95%)	12 (5%)	20	42
59	SF	159/170 (94%)	154 (97%)	5 (3%)	35	62
60	SG	207/218 (95%)	196 (95%)	11 (5%)	20	43
61	SH	166/174 (95%)	159 (96%)	7 (4%)	26	52
62	SI	178/180 (99%)	171 (96%)	7 (4%)	28	54
63	SJ	161/168 (96%)	158 (98%)	3 (2%)	50	75
64	SK	89/136 (65%)	88 (99%)	1 (1%)	65	83
65	SL	137/142 (96%)	130 (95%)	7 (5%)	21	44

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	SM	102/108 (94%)	98 (96%)	4 (4%)	28	54
67	SN	130/131 (99%)	129 (99%)	1 (1%)	73	87
68	SO	110/119 (92%)	108 (98%)	2 (2%)	51	76
69	SP	107/130 (82%)	98 (92%)	9 (8%)	10	23
70	SQ	119/121 (98%)	118 (99%)	1 (1%)	73	87
71	SR	122/122 (100%)	118 (97%)	4 (3%)	33	60
72	SS	126/132 (96%)	123 (98%)	3 (2%)	43	70
73	ST	113/115 (98%)	107 (95%)	6 (5%)	20	43
74	SU	94/107 (88%)	90 (96%)	4 (4%)	26	51
75	SV	67/67 (100%)	62 (92%)	5 (8%)	12	28
76	SW	112/113 (99%)	102 (91%)	10 (9%)	9	21
77	SX	113/115 (98%)	108 (96%)	5 (4%)	25	50
78	SY	113/115 (98%)	109 (96%)	4 (4%)	32	58
79	SZ	66/103 (64%)	61 (92%)	5 (8%)	12	27
80	Sa	89/98 (91%)	86 (97%)	3 (3%)	32	59
81	Sb	75/76 (99%)	71 (95%)	4 (5%)	20	43
82	Sc	57/62 (92%)	55 (96%)	2 (4%)	32	58
83	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	73
84	Se	47/104 (45%)	46 (98%)	1 (2%)	47	73
85	Sf	60/140 (43%)	57 (95%)	3 (5%)	22	45
86	Sg	272/275 (99%)	262 (96%)	10 (4%)	30	56
All	All	11191/12657 (88%)	10707 (96%)	484 (4%)	27	51

5 of 484 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
31	LZ	106	LEU
76	SW	74	VAL
48	Lr	80	THR
76	SW	33	VAL
85	Sf	146	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 130 such sidechains are listed below:

Mol	Chain	Res	Type
74	SU	85	HIS
78	SY	29	HIS
20	LO	63	ASN
19	LN	145	ASN
79	SZ	112	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CC	84/85 (98%)	20 (23%)	1 (1%)
4	L5	3704/5070 (73%)	884 (23%)	17 (0%)
5	L7	119/121 (98%)	16 (13%)	0
53	S2	1715/1869 (91%)	437 (25%)	4 (0%)
6	L8	155/157 (98%)	33 (21%)	0
All	All	5777/7302 (79%)	1390 (24%)	22 (0%)

5 of 1390 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	CC	7	G
2	CC	8	U
2	CC	9	G
2	CC	14	A
2	CC	16	U

5 of 22 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	L5	3673	C
4	L5	4913	G
4	L5	4699	U
53	S2	112	U
4	L5	1633	G

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

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.

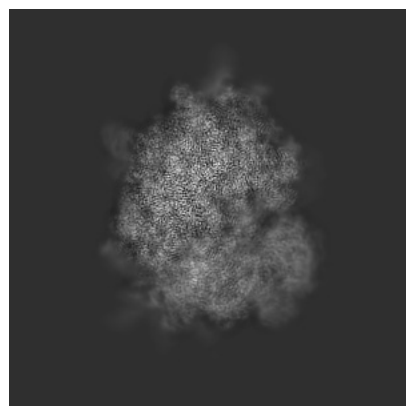
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-55613. These allow visual inspection of the internal detail of the map and identification of artifacts.

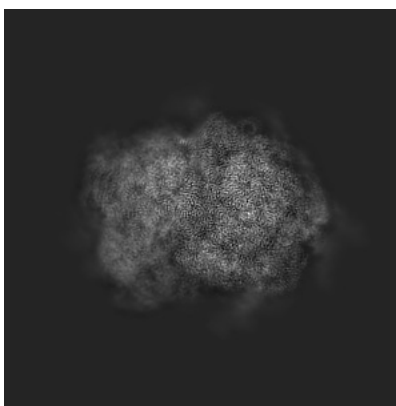
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

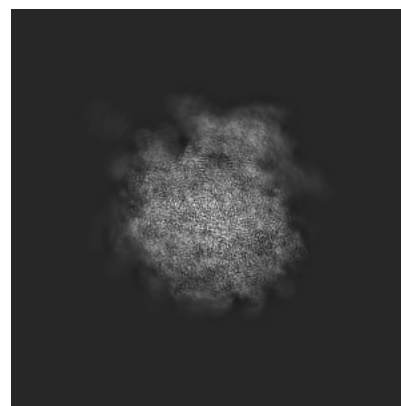
6.1.1 Primary map



X

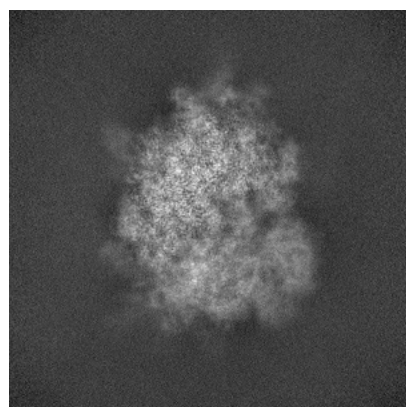


Y

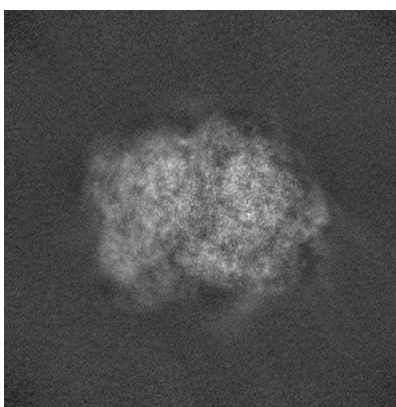


Z

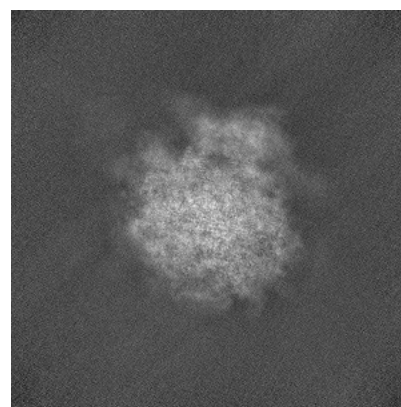
6.1.2 Raw map



X



Y

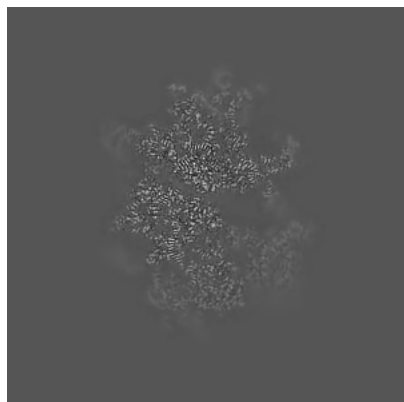


Z

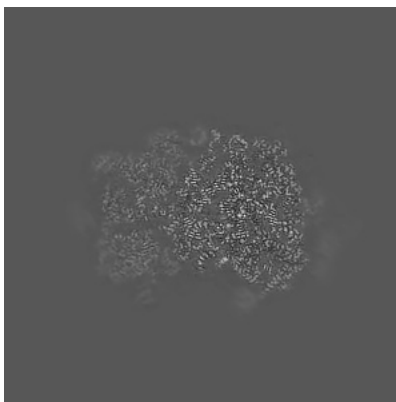
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

6.2.1 Primary map



X Index: 320

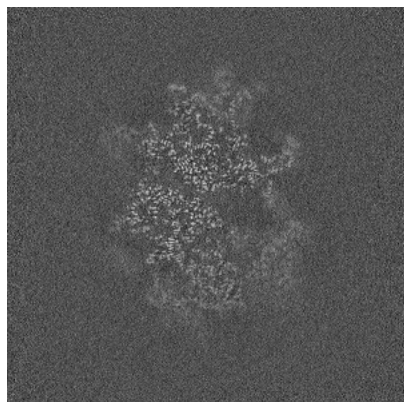


Y Index: 320

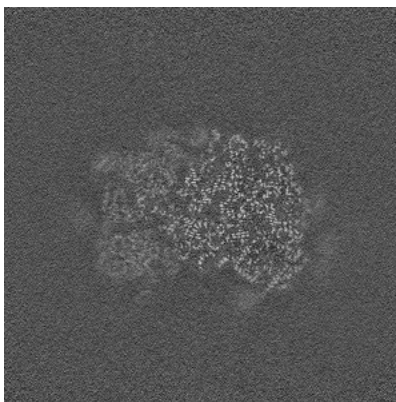


Z Index: 320

6.2.2 Raw map



X Index: 320



Y Index: 320

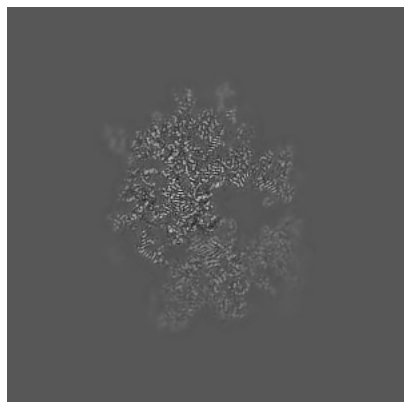


Z Index: 320

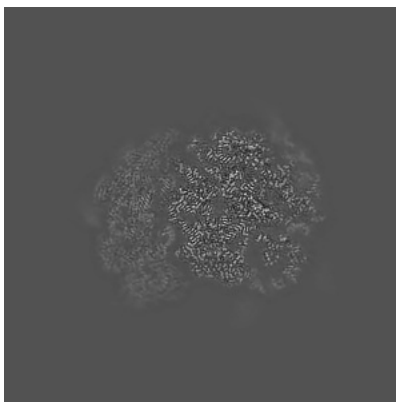
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

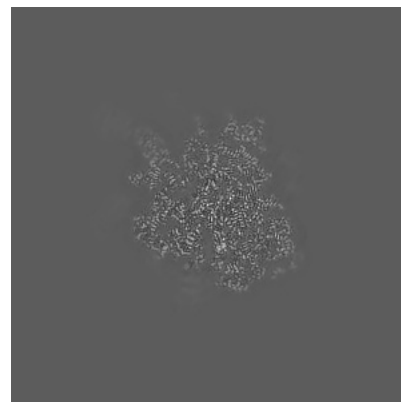
6.3.1 Primary map



X Index: 346

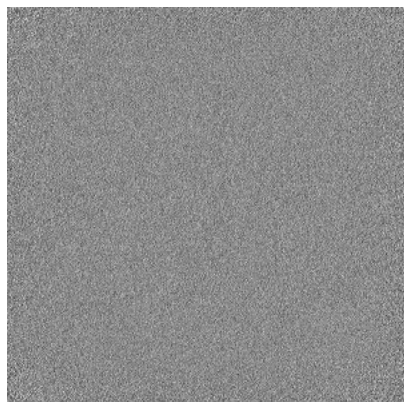


Y Index: 295

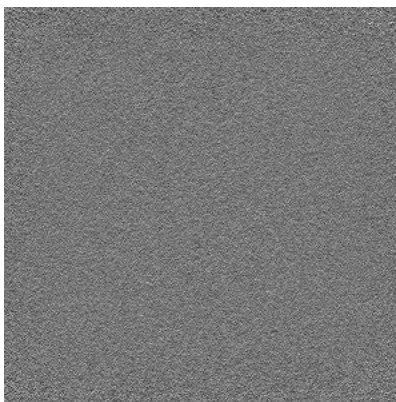


Z Index: 367

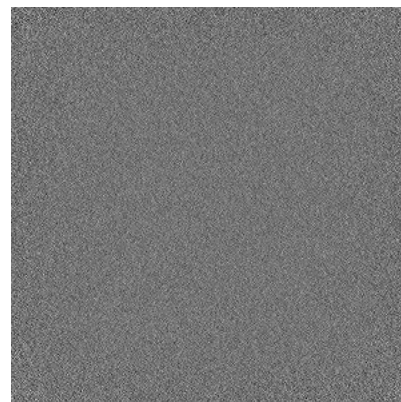
6.3.2 Raw map



X Index: 0



Y Index: 0

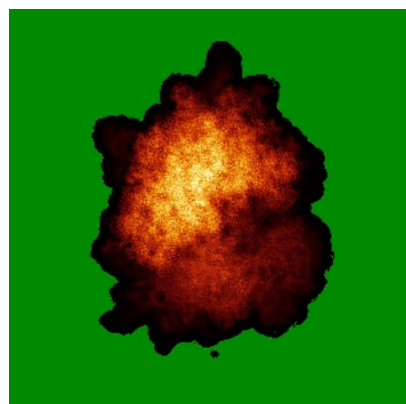


Z Index: 639

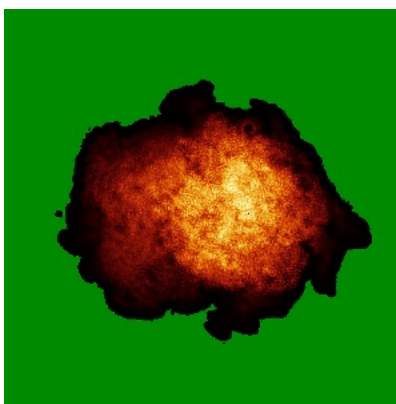
The images above show the largest variance slices of the map in three orthogonal directions.

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

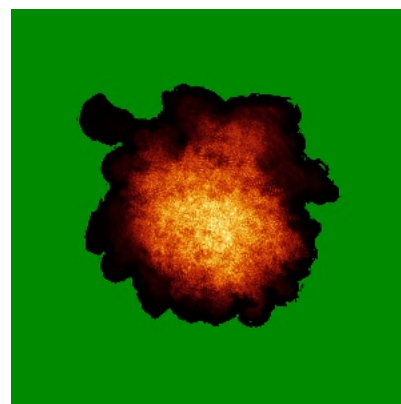
6.4.1 Primary map



X

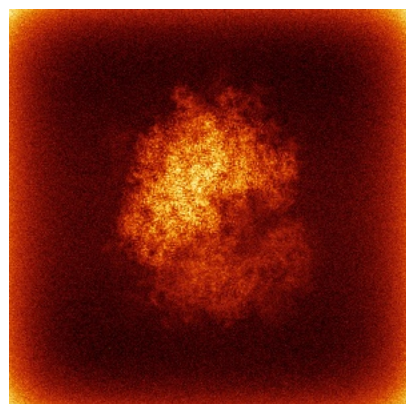


Y

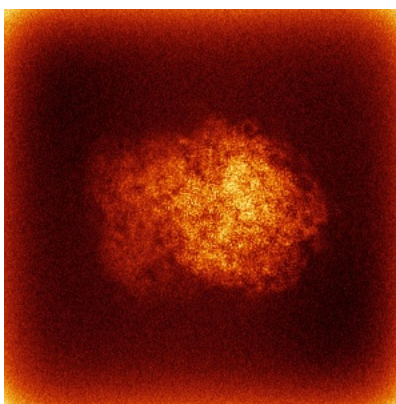


Z

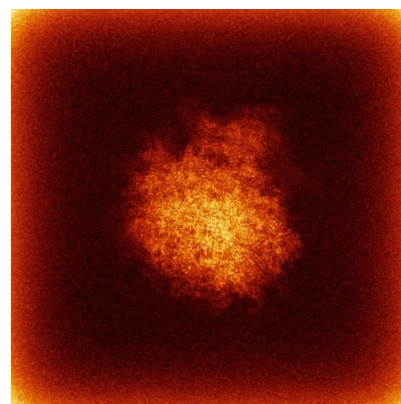
6.4.2 Raw map



X



Y

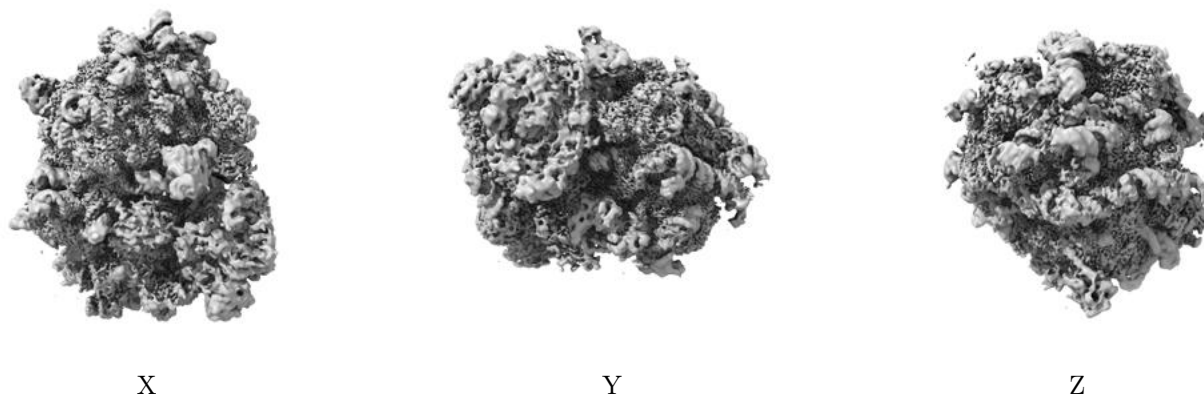


Z

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

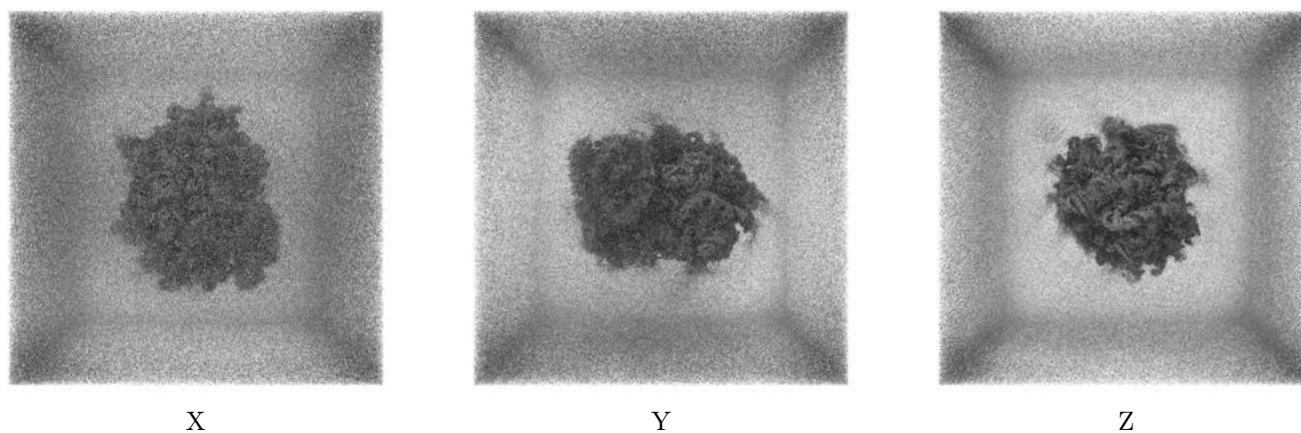
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.13. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

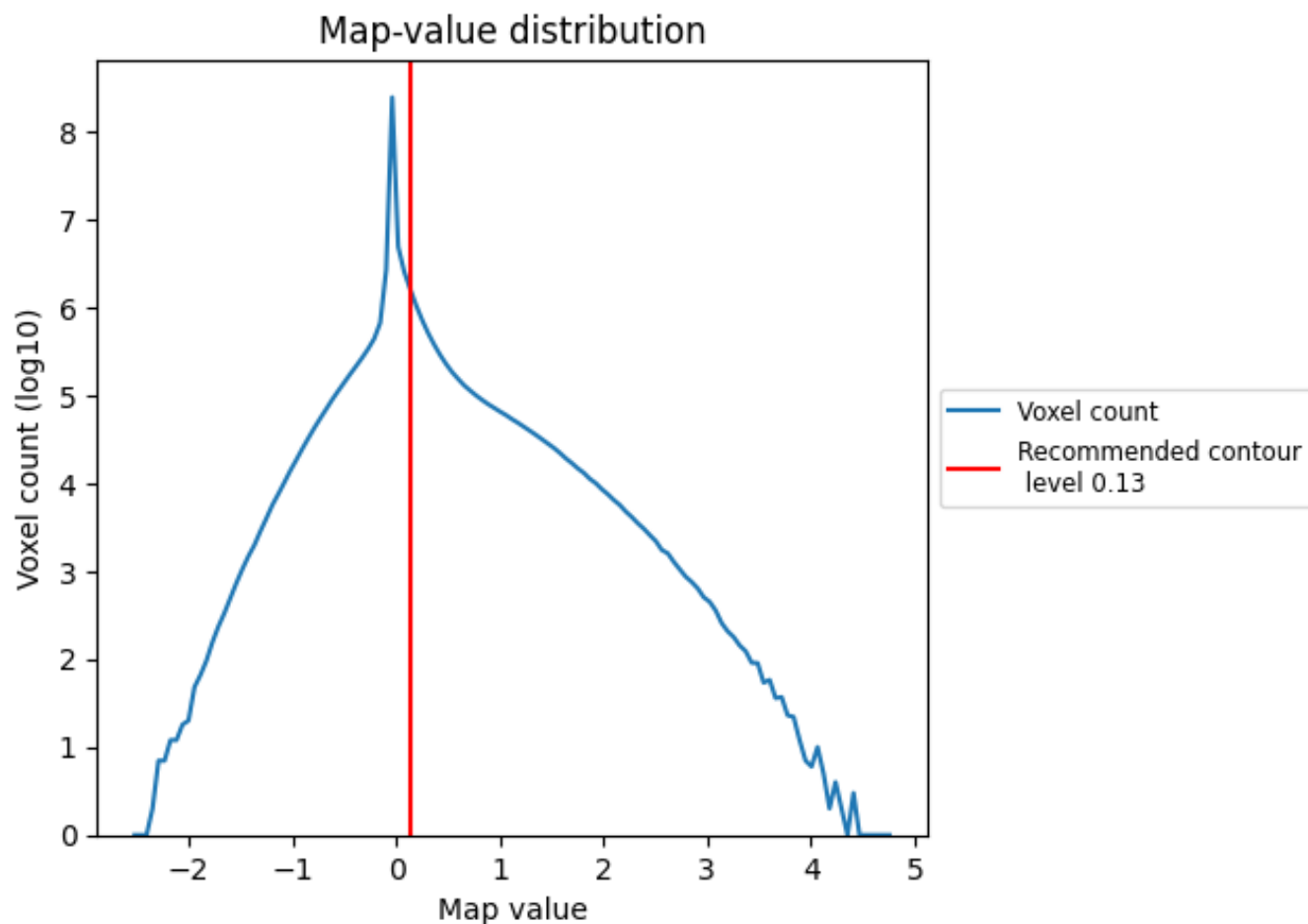
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

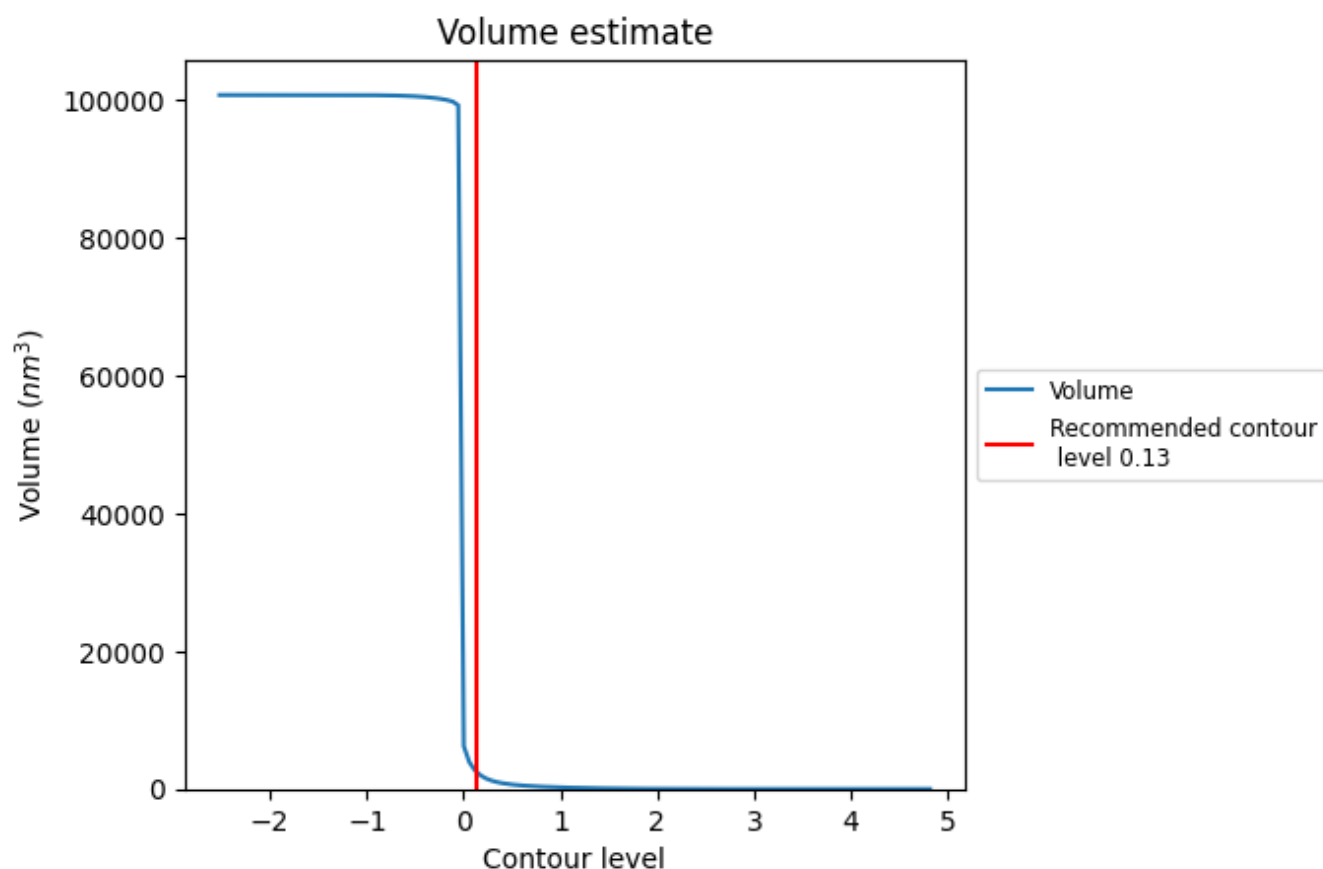
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

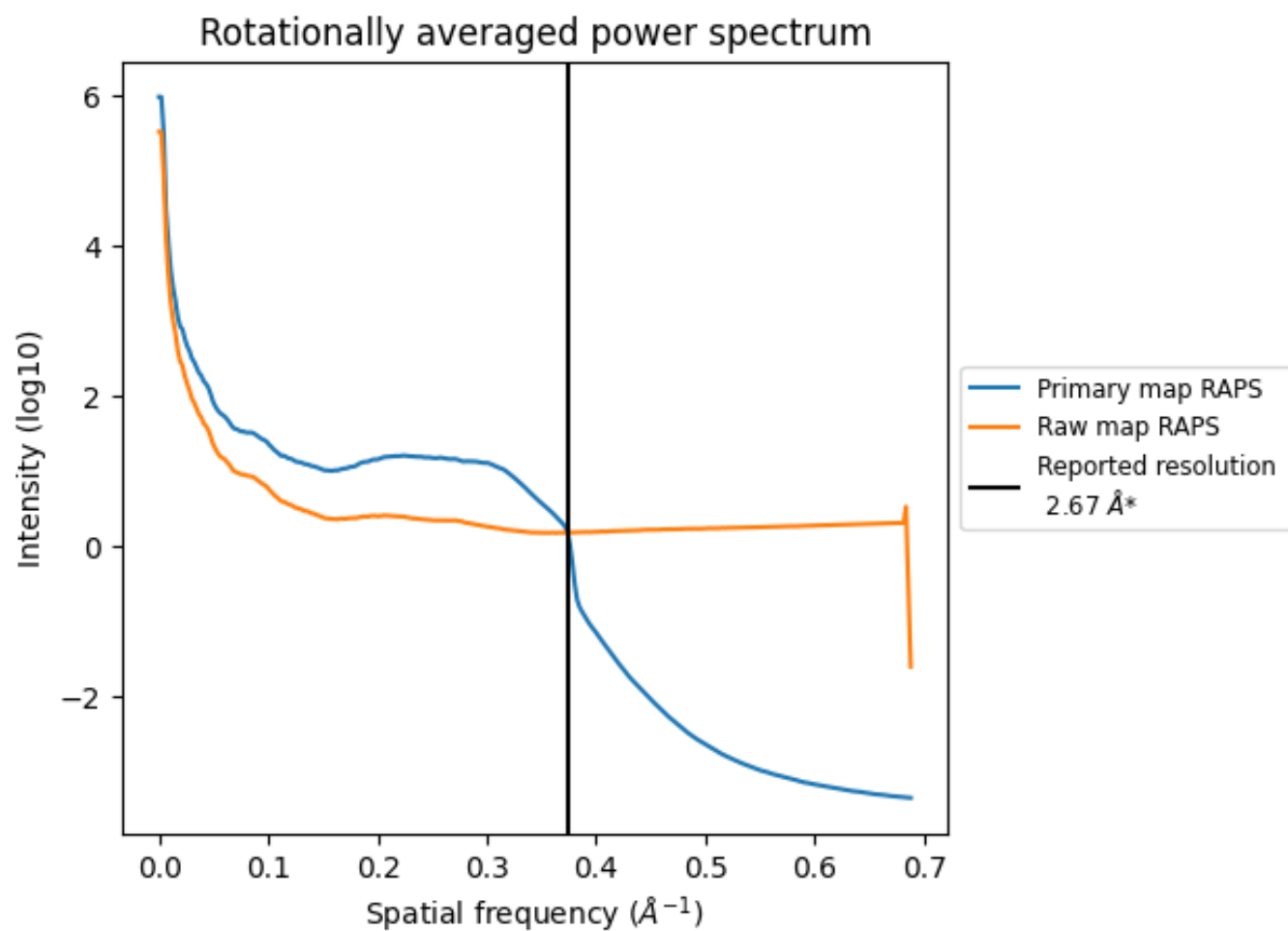
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2535 nm^3 ; this corresponds to an approximate mass of 2290 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 ⓘ

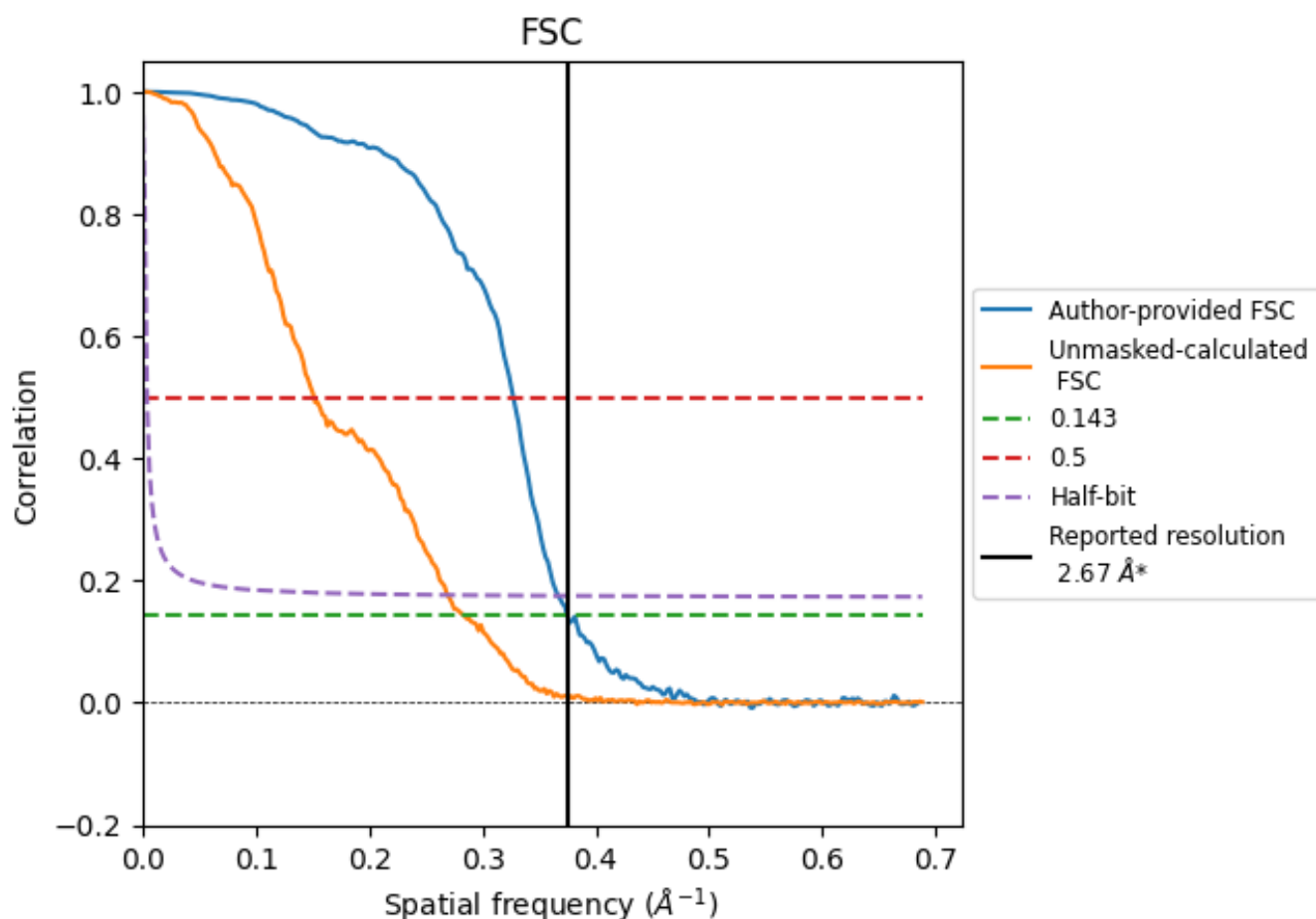


*Reported resolution corresponds to spatial frequency of 0.375 Å⁻¹

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 0.375 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

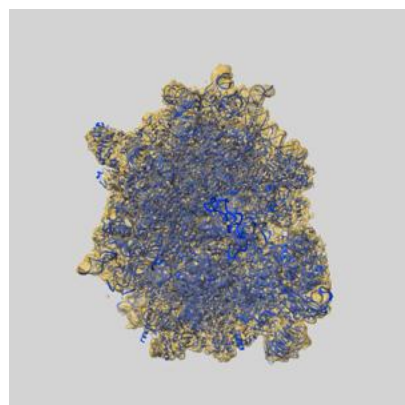
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.67	-	-
Author-provided FSC curve	2.67	3.06	2.73
Unmasked-calculated*	3.52	6.61	3.71

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.52 differs from the reported value 2.67 by more than 10 %

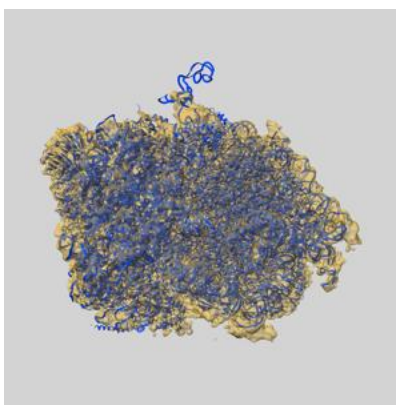
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-55613 and PDB model 9T6D. Per-residue inclusion information can be found in section [3](#) on page [21](#).

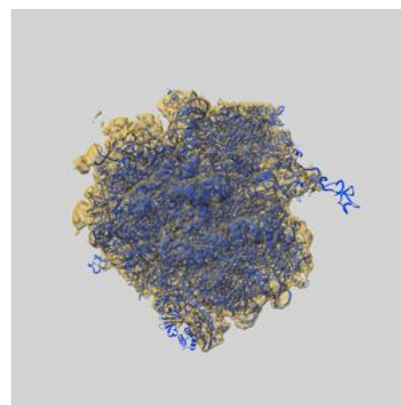
9.1 Map-model overlay [i](#)



X



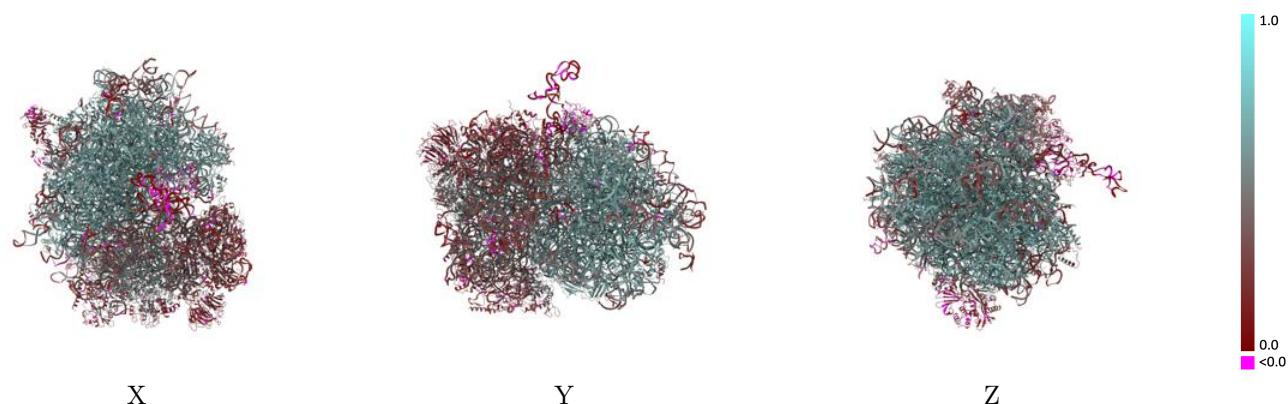
Y



Z

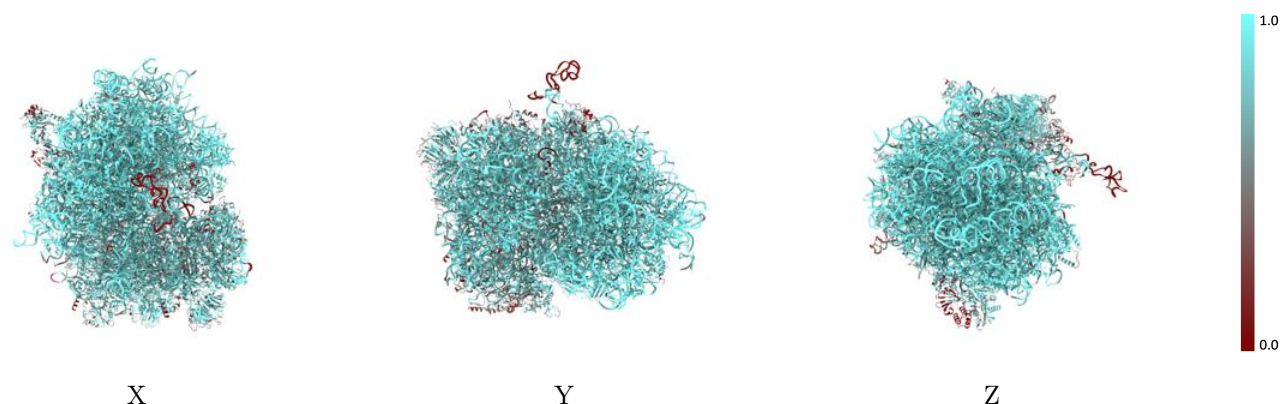
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



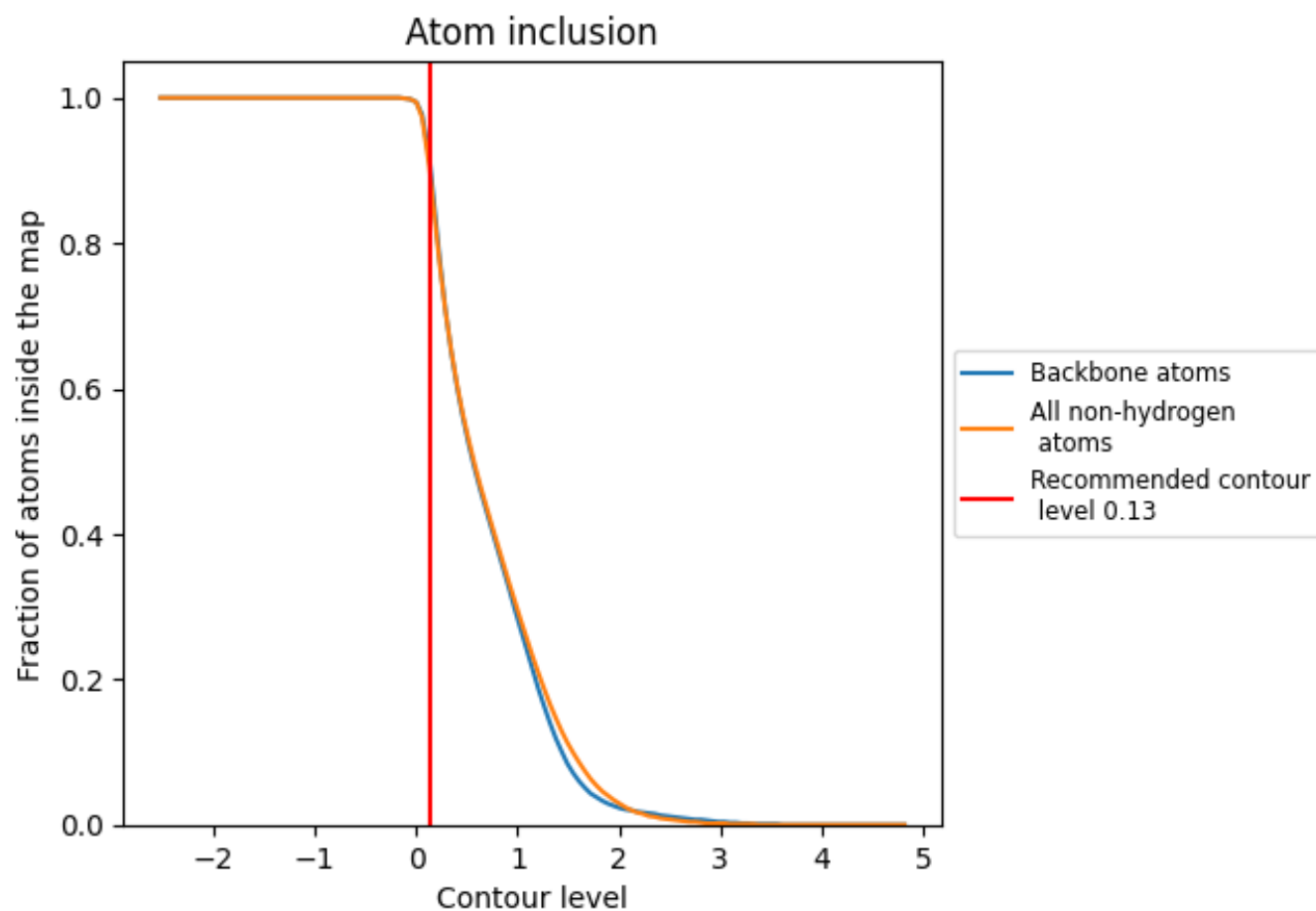
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 90% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9050	 0.4840
CB	 0.7380	 0.3860
CC	 0.7950	 0.2800
CD	 0.7240	 0.3610
L5	 0.9710	 0.5640
L7	 0.9950	 0.6300
L8	 0.9850	 0.6030
LA	 0.9840	 0.6430
LB	 0.9700	 0.6200
LC	 0.9720	 0.6250
LD	 0.9750	 0.5670
LE	 0.9400	 0.5510
LF	 0.9850	 0.6420
LG	 0.9260	 0.5420
LH	 0.9760	 0.6030
LI	 0.9830	 0.6210
LJ	 0.8980	 0.4940
LL	 0.9520	 0.5810
LM	 0.9830	 0.5990
LN	 0.9930	 0.6510
LO	 0.9820	 0.6370
LP	 0.9820	 0.6370
LQ	 0.9950	 0.6490
LR	 0.9210	 0.5640
LS	 0.9900	 0.6430
LT	 0.9620	 0.5930
LU	 0.9280	 0.5200
LV	 0.9820	 0.6390
LW	 0.7120	 0.4250
LX	 0.9660	 0.6060
LY	 0.9860	 0.6270
LZ	 0.9860	 0.5920
La	 0.9850	 0.6430
Lb	 0.9360	 0.5450
Lc	 0.9570	 0.5820



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Chain	Atom inclusion	Q-score
Ld	 0.9590	 0.5990
Le	 0.9910	 0.6470
Lf	 0.9910	 0.6470
Lg	 0.9640	 0.6130
Lh	 0.9610	 0.5930
Li	 0.9740	 0.5840
Lj	 0.9790	 0.6390
Lk	 0.9340	 0.5390
Ll	 0.9840	 0.6210
Lm	 0.9590	 0.6150
Ln	 0.9380	 0.5600
Lo	 0.9550	 0.6040
Lp	 0.9750	 0.6360
Lr	 0.9810	 0.6250
Lz	 0.3960	 0.0660
N4	 0.7160	 0.2150
NA	 0.1340	 0.0850
NB	 0.4280	 0.2060
S2	 0.8930	 0.3800
SA	 0.8590	 0.3850
SB	 0.7900	 0.3400
SC	 0.9130	 0.4610
SD	 0.8220	 0.3380
SE	 0.8430	 0.3370
SF	 0.6440	 0.2290
SG	 0.6150	 0.2170
SH	 0.7480	 0.2870
SI	 0.7190	 0.2760
SJ	 0.8720	 0.3820
SK	 0.8480	 0.2970
SL	 0.8010	 0.3660
SM	 0.7490	 0.1580
SN	 0.8390	 0.3960
SO	 0.7970	 0.3400
SP	 0.7950	 0.2500
SQ	 0.7320	 0.2570
SR	 0.7650	 0.2970
SS	 0.6960	 0.2290
ST	 0.7740	 0.2550
SU	 0.8770	 0.2930
SV	 0.8730	 0.4180
SW	 0.9080	 0.4820

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Chain	Atom inclusion	Q-score
SX	 0.8970	 0.4760
SY	 0.6570	 0.2350
SZ	 0.4750	 0.1730
Sa	 0.8470	 0.3910
Sb	 0.8420	 0.3250
Sc	 0.5330	 0.2460
Sd	 0.9410	 0.4030
Se	 0.7500	 0.3590
Sf	 0.6280	 0.1950
Sg	 0.7520	 0.2080