



wwPDB EM Validation Summary Report ⓘ

Mar 20, 2026 – 04:18 PM UTC

PDB ID : 9I2E / pdb_00009i2e
EMDB ID : EMD-52582
Title : NMT1-NAC bound human ribosome (combined translational states)
Authors : Denk, T.; Berninghausen, O.; Beckmann, R.
Deposited on : 2025-01-20
Resolution : 2.95 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:

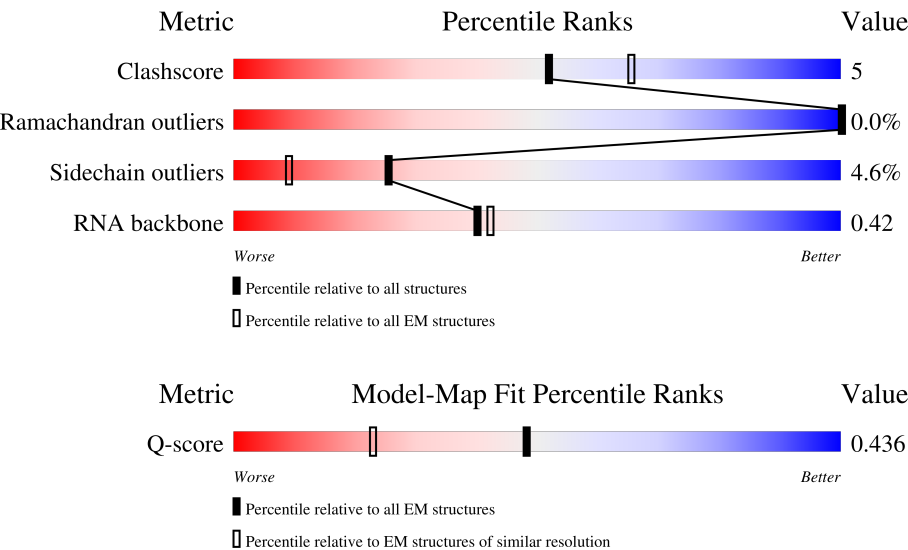
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDb archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 2.95 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.









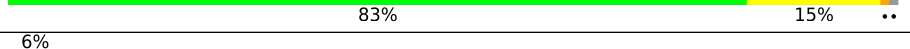
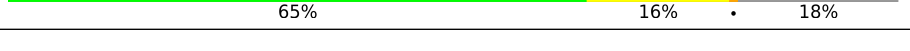
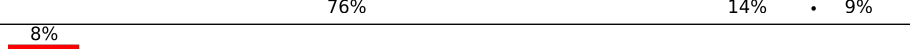
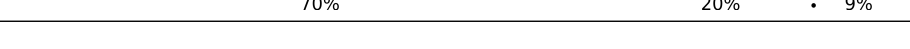
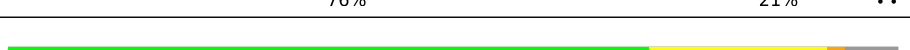

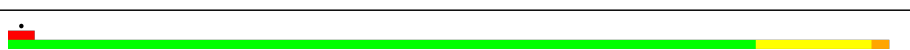

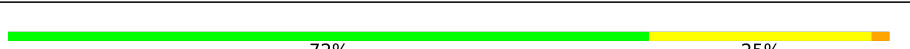





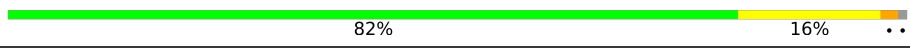
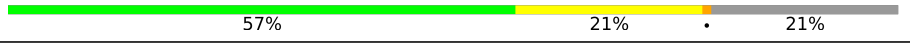



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13114 (2.45 - 3.45)

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	







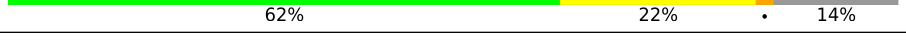
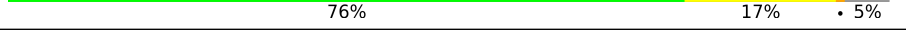
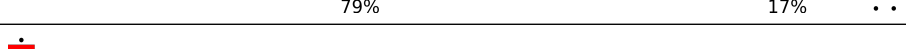
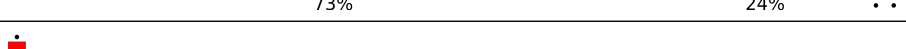
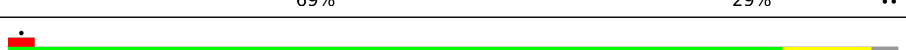

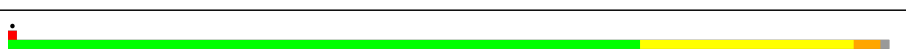








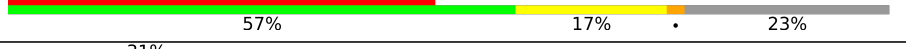



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Mol	Chain	Length	Quality of chain
4	L5	5070	
5	L7	121	
6	L8	157	
7	LA	257	
8	LB	403	
9	LC	427	
10	LD	297	
11	LE	288	
12	LF	248	
13	LG	266	
14	LH	192	
15	LI	214	
16	LJ	178	
17	LL	211	
18	LM	215	
19	LN	204	
20	LO	203	
21	LP	184	
22	LQ	188	
23	LR	196	
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	NA	215	
51	NB	162	
52	NM	496	
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 230824 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 60S ribosomal protein L13.

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 60S ribosomal protein L37.

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 Nascent polypeptide-associated complex subunit alpha.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	NA	67	Total	C	N	O	S	0	0
			531	335	97	98	1		

- Molecule 51 is a protein called Isoform 2 of Transcription factor BTF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	NB	124	Total	C	N	O	S	0	0
			963	597	175	188	3		

- Molecule 52 is a protein called Glycylpeptide N-tetradecanoyltransferase 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	NM	393	Total	C	N	O	S	3	0
			3209	2075	544	573	17		

- 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 40S ribosomal protein S4, 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
			822	514	156	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	211	Total	Mg	0
			211	211	
87	L7	3	Total	Mg	0
			3	3	
87	L8	5	Total	Mg	0
			5	5	
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	LT	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	

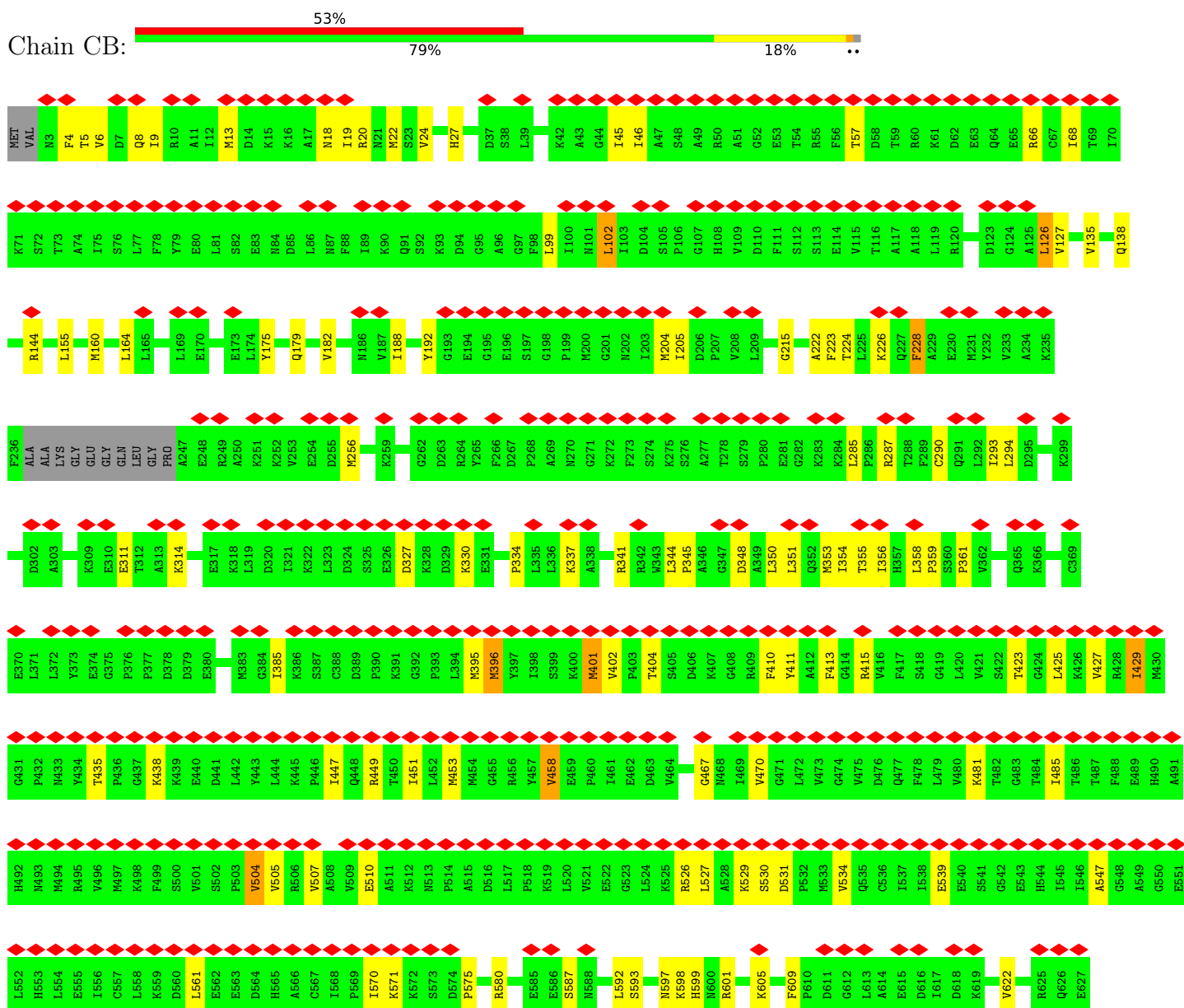
- Molecule 88 is ZINC ION (CCD ID: ZN) (formula: Zn).

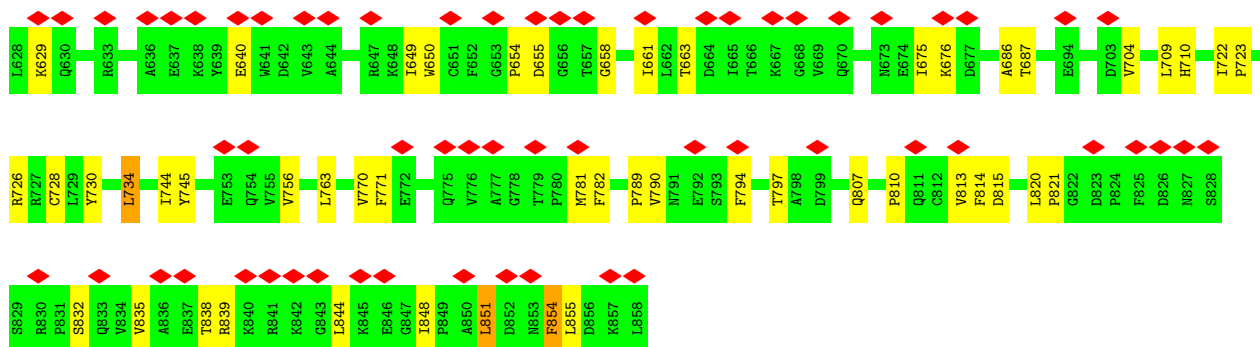
Mol	Chain	Residues	Atoms		AltConf
88	Lg	1	Total 1	Zn 1	0
88	Lj	1	Total 1	Zn 1	0
88	Lm	1	Total 1	Zn 1	0
88	Lo	1	Total 1	Zn 1	0
88	Lp	1	Total 1	Zn 1	0
88	SM	1	Total 1	Zn 1	0
88	Sa	1	Total 1	Zn 1	0
88	Sd	1	Total 1	Zn 1	0

3 Residue-property plots

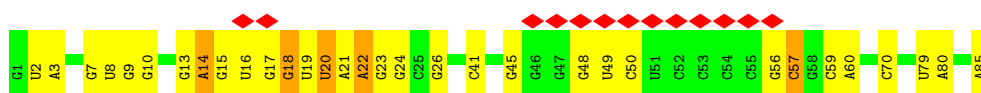
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

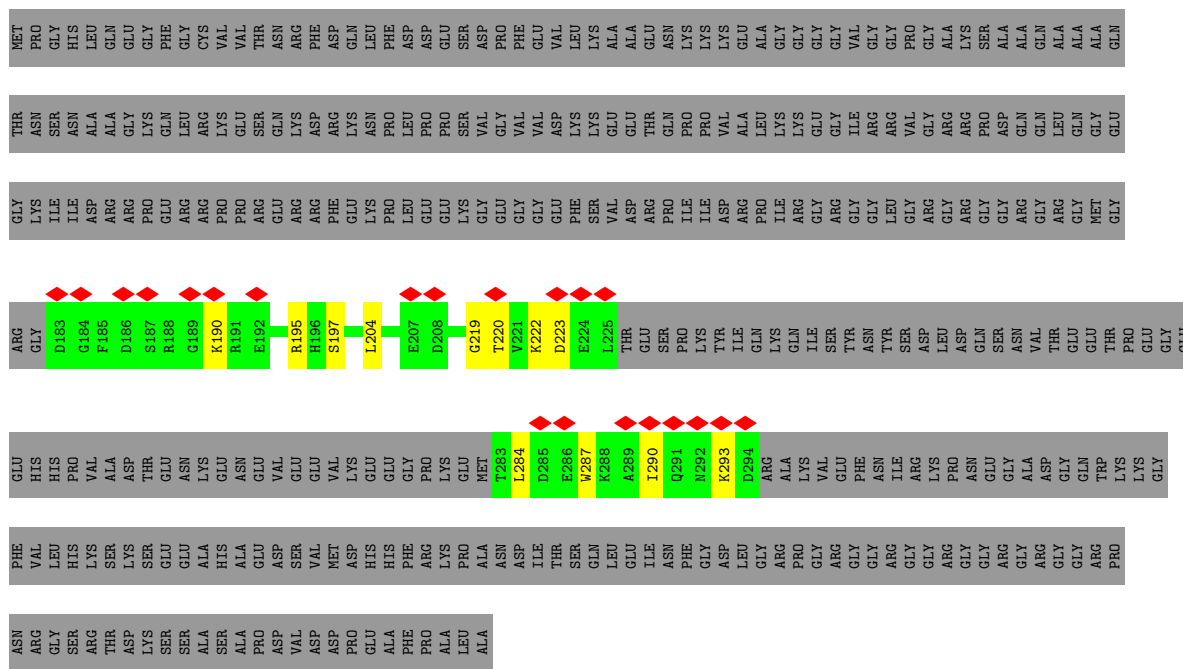




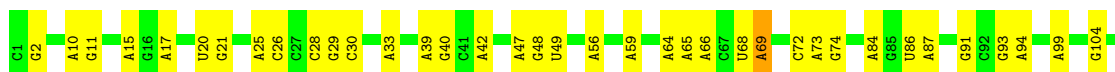
- Molecule 2: E-site tRNA



- Molecule 3: Isoform 2 of SERPINE1 mRNA-binding protein 1



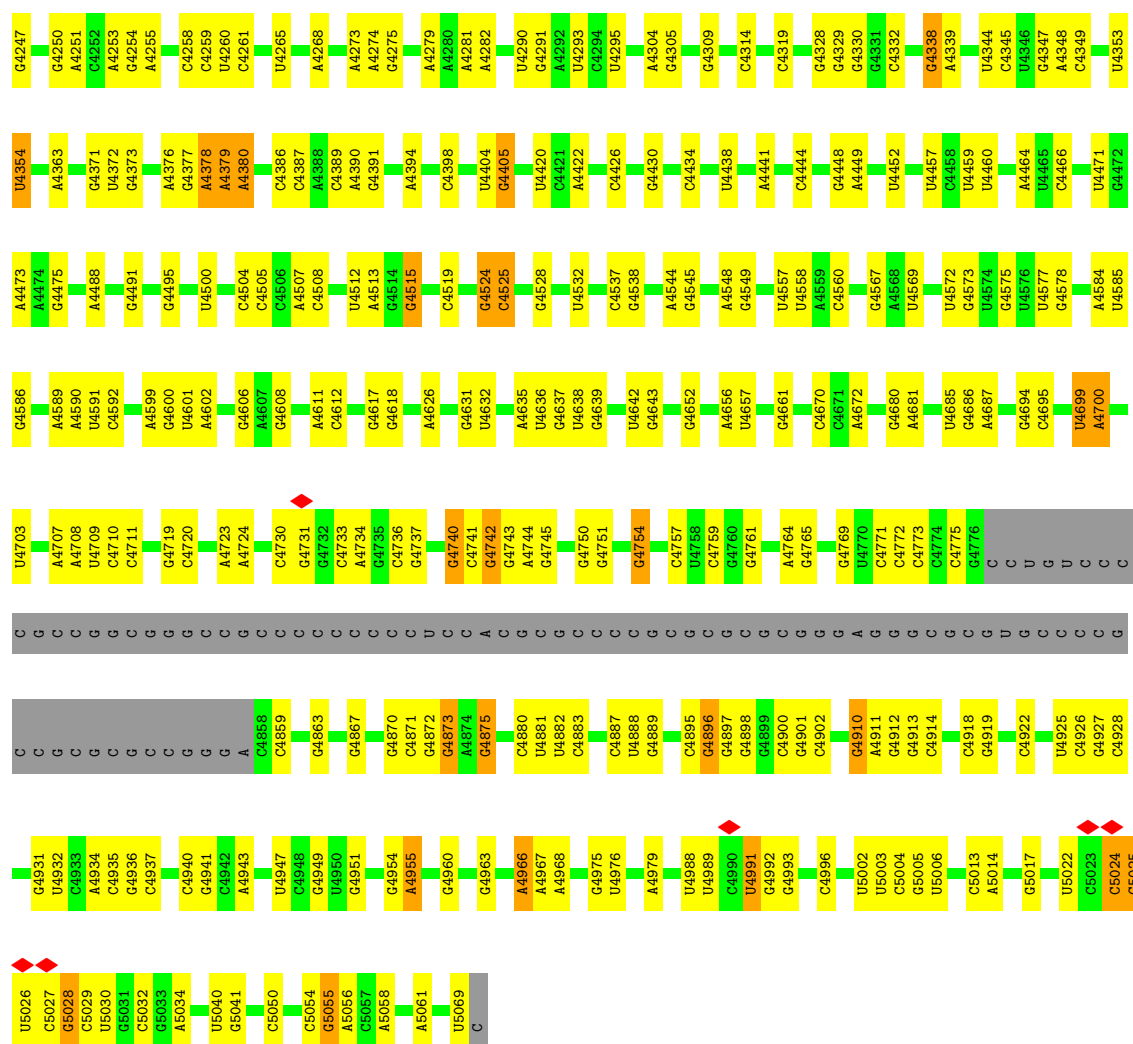
- Molecule 4: 28S rRNA



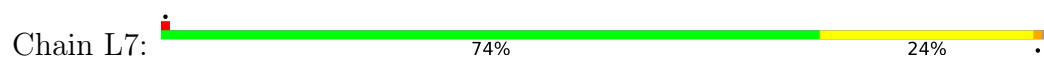


U2843	G2569	G2474	A2332	G	G	G1769	C1696	A1565	G1435	A1337
A2844	U2570	G2475	G2333	G	G	A1770	G1697	C1566	G1436	G1338
G2845	C2583	G2478	C2337	G	U	A1775	C1698	G1574	A1437	U1339
G2847	G2586	G2479	G2343	G	U	A1787	G1700	G1577	U1438	C1340
G2848	C2588	G2483	U2344	G	U	A1788	C1703	U1578	U1439	U1341
G2855	C2589	A2484	G2345	G	G	G1799	G1704	U1582	U1440	G1346
C2856	C2590	G2485	G2348	G	G	G1803	C1705	G1705	C1441	G1347
A2857	G2606	G2486	G2351	G	U	A1804	A1706	G1706	A1443	U1348
A2864	A2611	C2488	A2026	C	C	G1806	G1707	C1590	G1444	G1349
A2870	G2627	C2489	A2029	G	C	A	G1708	U1591	U1445	G1353
A2871	G2629	C2490	A2030	U	U	C	C1709	G1592	U1446	A1354
G2876	C2632	C2491	A2033	U	C	C	C	A1593	C1447	G1355
G2877	C2633	G2494	G2034	C	C	G1810	C	U1596	G1457	U1356
G2878	C2634	U2495	A2036	C	C	G1815	C1714	C1603	C1460	C1357
G2879	C2635	G2496	G2046	C	C	C1820	C1715	G1604	G1468	G1358
G2884	G2662	G2503	A2047	G	U	G1821	G1716	G1612	C1469	U1364
A2885	G2663	C2504	U2048	C	G	U1822	C1717	A1613	G1478	C1365
C2892	G2664	G2505	G2055	C	U	G1823	A1719	A1621	C1479	G1366
A2895	C2669	G2511	G2056	C	G	G1830	G1724	G1624	C1480	C1367
G2902	G2675	A2512	G2061	C	U	U1725	U1726	G1625	C1481	A1368
G2903	A2676	A2513	C2062	C	U	U1730	C	C1628	G1482	C1369
U2904	G2677	G2514	G2069	C	C	C1731	C	U1631	C1483	G1370
G2906	U2687	G2518	A2076	C	C	G1732	C1733	A1632	A1497	C1378
G2907	G2688	G2520	G2076	C	U	G1734	G1734	A1633	G1498	C1379
G2908	G2693	G2521	G2084	A	C	A1738	A1738	A1634	C1499	G1380
U2909	G2694	G2522	G2085	G	G	G1739	G1739	A1637	A1500	U1381
G2910	A2695	G2523	G2086	C	G	C1847	C1740	A1638	G1501	G1382
G	A2696	G2524	G2089	C	A	U1848	G1741	U1639	G1502	G1383
G	G2700	G2525	U2090	U	G	G1846	A1742	A1640	A1503	A1387
G	U2701	G2526	G2091	C	G	C1847	A1743	G1641	U1514	G1394
G	G2702	G2527	A2093	C	U	G1855	U1744	A1642	A1515	A1397
G	G2703	G2528	G2094	C	G	C1857	G1745	C1645	G1516	G1517
G	G2704	G2529	A2095	C	C	A1858	G1750	A1646	A1518	A1398
G	G2705	G2530	G2096	C	G	A1867	A1751	G1654	G1519	G1404
G	U2708	G2531	G2097	C	G	A1868	G1752	C1662	C1405	C1406
G	C2709	G2532	G2098	U	C	G1869	G1753	C1663	A1534	G1408
G	G2710	G2533	C2101	C	C	C1881	U1757	C1664	U1538	C1409
A	G2711	G2534	G2102	C	U	U1882	G1758	C1665	G1539	U1410
A	G2712	G2535	G2103	C	G	A1888	G1759	C1666	G1542	C1411
C	C2719	G2536	G2107	C	C	A1892	G1760	C1667	A1547	G1412
G	C2720	A2537	G2108	C	G	C1893	G1761	C1668	C1413	C1414
G	G2721	G2538	G2109	C	C	A1897	C1762	C1669	G1415	G1416
G	G2722	G2539	G2110	C	C	A1897	G1763	C1670	G1558	C1417
G	G2723	G2540	G2111	C	C	C1913	A1765	C1671	G1562	A1420
G	G2724	U2467	G2112	A	C	G	A1766	U1695	G1562	G1421
G	A2725	U2468	G2113	C	C	C1914	C1768			
G	G2726	C2469	G2114	C	C					
G	U2730	G2470	G2115	C	C					
U	G2731	G2471	G2116	C	C					
G		G2472	G2117	C	C					
G		G2473	G2118	C	C					
G		G2474	G2119	C	C					
G		G2475	G2120	C	C					
G		G2476	G2121	C	C					
G		G2477	G2122	C	C					
G		G2478	G2123	C	C					
G		G2479	G2124	C	C					
G		G2480	G2125	C	C					
G		G2481	G2126	C	C					
G		G2482	G2127	C	C					
G		G2483	G2128	C	C					
G		G2484	G2129	C	C					
G		G2485	G2130	C	C					
G		G2486	G2131	C	C					
G		G2487	G2132	C	C					
G		G2488	G2133	C	C					
G		G2489	G2134	C	C					
G		G2490	G2135	C	C					
G		G2491	G2136	C	C					
G		G2492	G2137	C	C					
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G		G2494	G2139	C	C					
G		G2495	G2140	C	C					
G		G2496	G2141	C	C					
G		G2497	G2142	C	C					
G		G2498	G2143	C	C					
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G		G2500	G2145	C	C					
G		G2501	G2146	C	C					
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G		G2505	G2150	C	C					
G		G2506	G2151	C	C					
G		G2507	G2152	C	C					
G		G2508	G2153	C	C					
G		G2509	G2154	C	C					
G		G2510	G2155	C	C					
G		G2511	G2156	C	C					
G		G2512	G2157	C	C					
G		G2513	G2158	C	C					
G		G2514	G2159	C	C					
G		G2515	G2160	C	C					
G		G2516	G2161	C	C					
G		G2517	G2162	C	C					
G		G2518	G2163	C	C					
G		G2519	G2164	C	C					
G		G2520	G2165	C	C					
G		G2521	G2166	C	C					
G		G2522	G2167	C	C					
G		G2523	G2168	C	C					
G		G2524	G2169	C	C					
G		G2525	G2170	C	C					
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G		G2529	G2174	C	C					
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G		G2531	G2176	C	C					
G		G2532	G2177	C	C					
G		G2533	G2178	C	C					
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G		G2535	G2180	C	C					
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G		G2537	G2182	C	C					
G		G2538	G2183	C	C					
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G		G2561	G2206	C	C					
G		G2562	G2207	C	C					
G		G2563	G2208	C	C					
G		G2564	G2209	C	C					
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G		G2569	G2214	C	C					
G		G2570	G2215	C	C					
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G		G2576	G2221	C	C					
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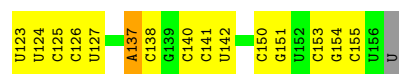




• Molecule 5: 5S rRNA




• Molecule 6: 5.8S rRNA



• Molecule 7: 60S ribosomal protein L8

V169	G173	D176	K177	Y186	W196	V199	M204	E208	G213	A229	K234	L246	T249	LYS	THR	VAL	GLN	GLU	LYS	GLU	ASN																					
RET	G2	R3	V4	G13	S14	V15	R28	V32	I44	V45	R54	G55	A56	L75	F76	I77	L96	V101	L102	P103	I112	V113	C114	G115	L116	K119	R123	L126	A127	R128	A129	S130	T135	K145	T146	R147	V148	K149	K155	R163	A164	V165

- Chain LB:  85% 13% 2%

Category	Item	Value	Color
MET	S2	1220	Blue
	H3	1223	Blue
	L14	1224	Blue
	L17	1225	Red
	K34	1226	Blue
	K35	1230	Blue
	L56	1234	Blue
	V57	1235	Blue
	V73	1247	Orange
	E74	1252	Blue
MET	M84	1253	Blue
	Y92	1254	Blue
	V93	1258	Green
	E94	1275	Green
	T95	1278	Orange
	L99	1285	Blue
	A107	1286	Orange
	R117	1287	Blue
	K120	1288	Blue
	K128	1292	Blue
MET	K144	1301	Red
	V159	1330	Orange
	Q167	1331	Blue
	M168	1334	Blue
	L171	1337	Blue
	K177	1345	Blue
	V185	1351	Blue
	K193	1364	Blue
	L194	1378	Blue
	L201	1384	Blue
MET	Q204	1399	Red
	V207	1400	Red
	V210	1401	Red
	M216	1403	Red

- Chain LC:  71% 14% 14%

Protein	Position	Residue	Score
PRO	1	M1	0.99
THR	2	A2	0.98
GLU	3	L7	0.97
GLU	4	V10	0.96
LYS	5	E13	0.95
PRO	6	K14	0.94
ALA	7	K20	0.93
ALA	8	N21	0.92
ALA	9	V22	0.91
ALA	10	T23	0.90
ALA	11	F28	0.89
ALA	12	P34	0.88
ALA	13	V37	0.87
ALA	14	V40	0.86
ALA	15	L44	0.85
ALA	16	V54	0.84
ALA	17	S55	0.83
ALA	18	E56	0.82
ALA	19	Q61	0.81
ALA	20	S66	0.80
ALA	21	V67	0.79
ALA	22	R71	0.78
ALA	23	P77	0.77
ALA	24	R80	0.76
ALA	25	N94	0.75
ALA	26	N95	0.74
ALA	27	M101	0.73
ALA	28	T105	0.72
ALA	29	R109	0.71
ALA	30	N116	0.70
ALA	31	Q119	0.69
ALA	32	A123	0.68
ALA	33	A129	0.67
ALA	34	M138	0.66
ALA	35	T144	0.65
ALA	36	E155	0.64
ALA	37	V158	0.63
ALA	38	K165	0.62
ALA	39	L169	0.61
ALA	40	L170	0.60
ALA	41	L171	0.59
ALA	42	A176	0.58
ALA	43	R205	0.57
ALA	44	I210	0.56
ALA	45	V211	0.55
ALA	46	N212	0.54
ALA	47	I227	0.53
ALA	48	L230	0.52
ALA	49	L235	0.51
ALA	50	N236	0.50
ALA	51	K239	0.49
ALA	52	V246	0.48
ALA	53	S255	0.47
ALA	54	R268	0.46
ALA	55	M284	0.45
ALA	56	T287	0.44
ALA	57	T298	0.43
ALA	58	R312	0.42
ALA	59	L319	0.41
ALA	60	K320	0.40
ALA	61	N321	0.39
ALA	62	L322	0.38
ALA	63	R323	0.37
ALA	64	L324	0.36
ALA	65	L328	0.35
ALA	66	K333	0.34
ALA	67	R336	0.33
ALA	68	R337	0.32
ALA	69	N338	0.31
ALA	70	T339	0.30
ALA	71	R345	0.29
ALA	72	L349	0.28
ALA	73	A360	0.27
ALA	74	L361	0.26
ALA	75	A363	0.25
ALA	76	K364	0.24
ALA	77	S365	0.23
ALA	78	D366	0.22
ALA	79	E367	0.21
ALA	80	K368	0.20
ALA	81	ALA	0.19
ALA	82	VAL	0.18
ALA	83	ALA	0.17
ALA	84	GLY	0.16
ALA	85	LYS	0.15
ALA	86	LYS	0.14
ALA	87	PRO	0.13
ALA	88	VAL	0.12
ALA	89	VAL	0.11
ALA	90	GLY	0.10
ALA	91	LYS	0.09
ALA	92	LYS	0.08
ALA	93	ALA	0.07
ALA	94	ALA	0.06
ALA	95	GLY	0.05
ALA	96	LYS	0.04
ALA	97	PRO	0.03
ALA	98	ALA	0.02
ALA	99	GLU	0.01
ALA	100	LYS	0.00

- Chain LD:  83% 15% .

V194	H195	V204	K208	K228	M235	E238	K241	K258	K259	E260	M271	S272	K283	E292	R293	A294	ALA GLU SER																			
G2	F3	V4	V7	A11	E25	G26	K27	R33	V37	M45	I52	V53	C52	Q53	I64	A65	I74	V75	C76	A80	V88	L92	L109	R112	L146	T155	G156	V159	L163	K164	I173	R179	F180	P181	G182	S185

- Chain LE: 

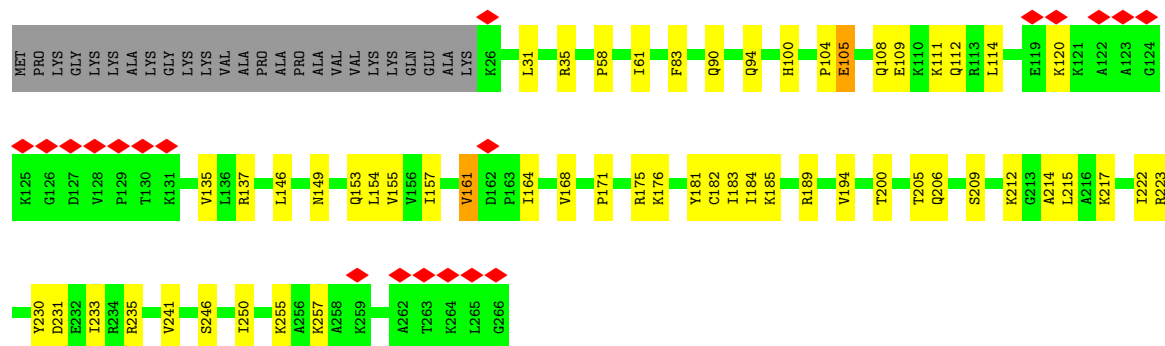
- Molecule 12: Large ribosomal subunit protein uL30

Chain LF: 76% 14% 9%




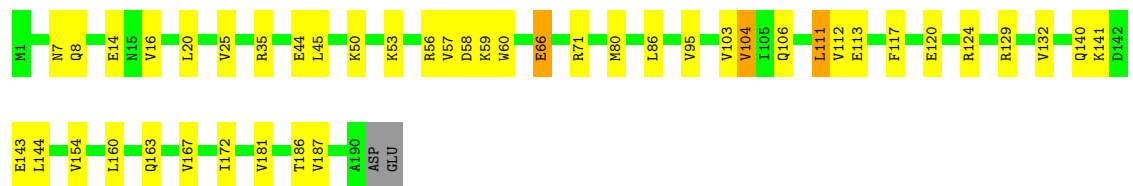
- Molecule 13: 60S ribosomal protein L7a

Chain LG: 



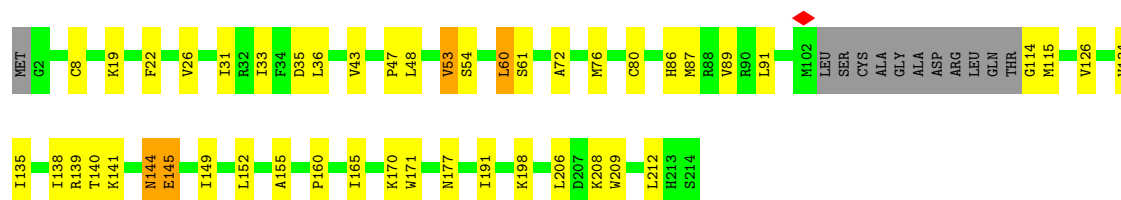
- Molecule 14: 60S ribosomal protein L9

Chain LH:  76% 21% 3%

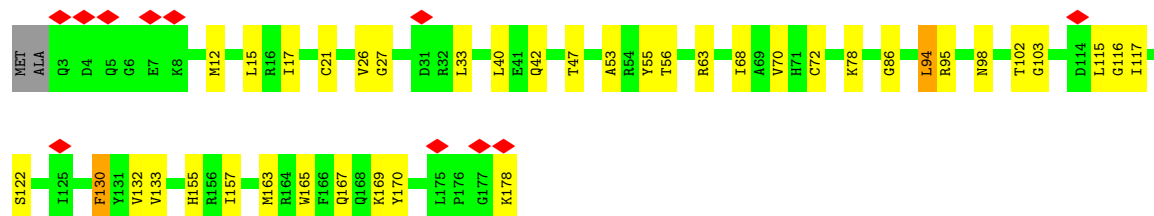
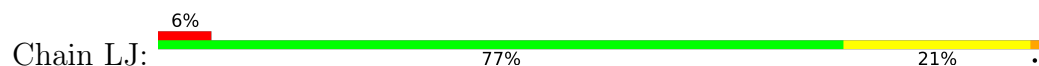


- Molecule 15: Ribosomal protein uL16-like

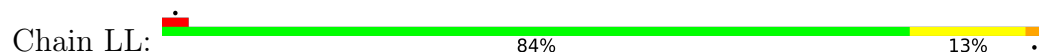
Chain LI:  72% 20% 6%



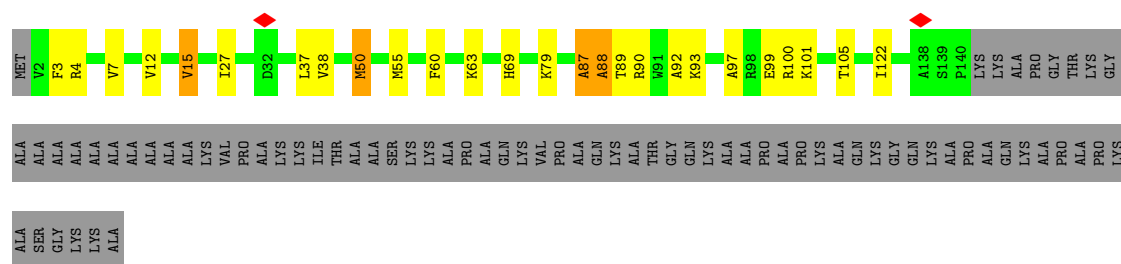
• Molecule 16: 60S ribosomal protein L11



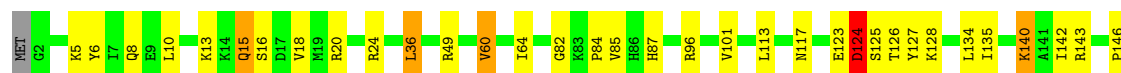
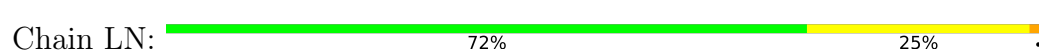
• Molecule 17: 60S ribosomal protein L13



• Molecule 18: 60S ribosomal protein L14



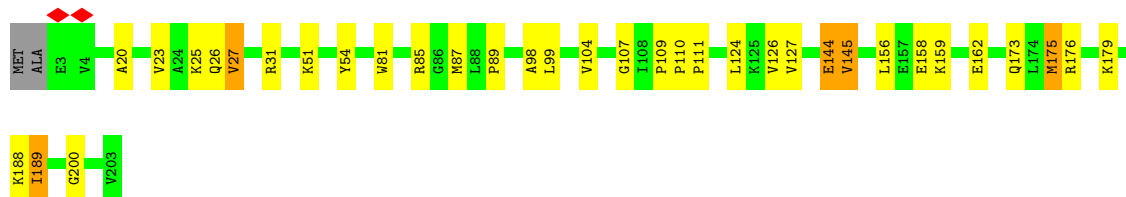
• Molecule 19: 60S ribosomal protein L15





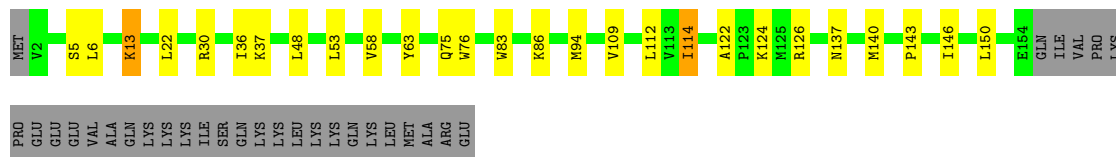
- Molecule 20: 60S ribosomal protein L13a

Chain LO: 82% 15% ..



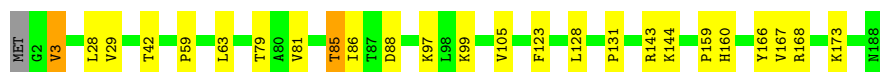
- Molecule 21: 60S ribosomal protein L17

Chain LP: 68% 14% 17%



- Molecule 22: 60S ribosomal protein L18

Chain LQ: 86% 12% ..



- Molecule 23: 60S ribosomal protein L19

Chain LR: 8% 78% 16% 5%



- Molecule 24: 60S ribosomal protein L18a

Chain LS: 85% 15%



- Molecule 25: 60S ribosomal protein L21

MET
T2
L27
M31
R32
I33
G46
F47
V48
M52
P53
T61
Q69
H70
A71
V72
I84
V91
R92
I96
K100
S101
S104
K115
E118
K122
A133
R136
L150
L151
E152
P153
M159
A160

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| Q116 | Q17 | Q18 | Q19 | Q20 | Q21 | Q22 | Q23 | Q24 | Q25 | Q26 | Q27 | Q28 | Q29 | Q30 | Q31 | Q32 | Q33 | Q34 | Q35 | Q36 | Q37 | Q38 | Q39 | Q40 | Q41 | Q42 | Q43 | Q44 | Q45 | Q46 | Q47 | Q48 | Q49 | Q50 | Q51 | Q52 | Q53 | Q54 | Q55 | Q56 | Q57 | Q58 | Q59 | Q60 | Q61 | Q62 | Q63 | Q64 | Q65 | Q66 | Q67 | Q68 | Q69 | Q70 | Q71 | Q72 | Q73 | Q74 | Q75 | Q76 | Q77 | Q78 | Q79 | Q80 | Q81 | Q82 | Q83 | Q84 | Q85 | Q86 | Q87 | Q88 | Q89 | Q90 | Q91 | Q92 | Q93 | Q94 | Q95 | Q96 | Q97 | Q98 | Q99 | Q100 | Q101 | Q102 | Q103 | Q104 | Q105 | Q106 | Q107 | Q108 | Q109 | Q110 | Q111 | Q112 | Q113 | Q114 | Q115 | Q116 | Q117 | Q118 | Q119 | Q120 | Q121 | Q122 | Q123 | Q124 | Q125 | Q126 | Q127 | Q128 | Q129 | Q130 | Q131 | Q132 | Q133 | Q134 | Q135 | Q136 | Q137 | Q138 | Q139 | Q140 | Q141 | Q142 | Q143 | Q144 | Q145 | Q146 | Q147 | Q148 | Q149 | Q150 | Q151 | Q152 | Q153 | Q154 | Q155 | Q156 | Q157 | Q158 | Q159 | Q160 | Q161 | Q162 | Q163 | Q164 | Q165 | Q166 | Q167 | Q168 | Q169 | Q170 | Q171 | Q172 | Q173 | Q174 | Q175 | Q176 | Q177 | Q178 | Q179 | Q180 | Q181 | Q182 | Q183 | Q184 | Q185 | Q186 | Q187 | Q188 | Q189 | Q190 | Q191 | Q192 | Q193 | Q194 | Q195 | Q196 | Q197 | Q198 | Q199 | Q200 | Q201 | Q202 | Q203 | Q204 | Q205 | Q206 | Q207 | Q208 | Q209 | Q210 | Q211 | Q212 | Q213 | Q214 | Q215 | Q216 | Q217 | Q218 | Q219 | Q220 | Q221 | Q222 | Q223 | Q224 | Q225 | Q226 | Q227 | Q228 | Q229 | Q230 | Q231 | Q232 | Q233 | Q234 | Q235 | Q236 | Q237 | Q238 | Q239 | Q240 | Q241 | Q242 | Q243 | Q244 | Q245 | Q246 | Q247 | Q248 | Q249 | Q250 | Q251 | Q252 | Q253 | Q254 | Q255 | Q256 | Q257 | Q258 | Q259 | Q260 | Q261 | Q262 | Q263 | Q264 | Q265 | Q266 | Q267 | Q268 | Q269 | Q270 | Q271 | Q272 | Q273 | Q274 | Q275 | Q276 | Q277 | Q278 | Q279 | Q280 | Q281 | Q282 | Q283 | Q284 | Q285 | Q286 | Q287 | Q288 | Q289 | Q290 | Q291 | Q292 | Q293 | Q294 | Q295 | Q296 | Q297 | Q298 | Q299 | Q300 | Q301 | Q302 | Q303 | Q304 | Q305 | Q306 | Q307 | Q308 | Q309 | Q310 | Q311 | Q312 | Q313 | Q314 | Q315 | Q316 | Q317 | Q318 | Q319 | Q320 | Q321 | Q322 | Q323 | Q324 | Q325 | Q326 | Q327 | Q328 | Q329 | Q330 | Q331 | Q332 | Q333 | Q334 | Q335 | Q336 | Q337 | Q338 | Q339 | Q340 | Q341 | Q342 | Q343 | Q344 | Q345 | Q346 | Q347 | Q348 | Q349 | Q350 | Q351 | Q352 | Q353 | Q354 | Q355 | Q356 | Q357 | Q358 | Q359 | Q360 | Q361 | Q362 | Q363 | Q364 | Q365 | Q366 | Q367 | Q368 | Q369 | Q370 | Q371 | Q372 | Q373 | Q374 | Q375 | Q376 | Q377 | Q378 | Q379 | Q380 | Q381 | Q382 | Q383 | Q384 | Q385 | Q386 | Q387 | Q388 | Q389 | Q390 | Q391 | Q392 | Q393 | Q394 | Q395 | Q396 | Q397 | Q398 | Q399 | Q400 | Q401 | Q402 | Q403 | Q404 | Q405 | Q406 | Q407 | Q408 | Q409 | Q410 | Q411 | Q412 | Q413 | Q414 | Q415 | Q416 | Q417 | Q418 | Q419 | Q420 | Q421 | Q422 | Q423 | Q424 | Q425 | Q426 | Q427 | Q428 | Q429 | Q430 | Q431 | Q432 | Q433 | Q434 | Q435 | Q436 | Q437 | Q438 | Q439 | Q440 | Q441 | Q442 | Q443 | Q444 | Q445 | Q446 | Q447 | Q448 | Q449 | Q450 | Q451 | Q452 | Q453 | Q454 | Q455 | Q456 | Q457 | Q458 | Q459 | Q460 | Q461 | Q462 | Q463 | Q464 | Q465 | Q466 | Q467 | Q468 | Q469 | Q470 | Q471 | Q472 | Q473 | Q474 | Q475 | Q476 | Q477 | Q478 | Q479 |
|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|

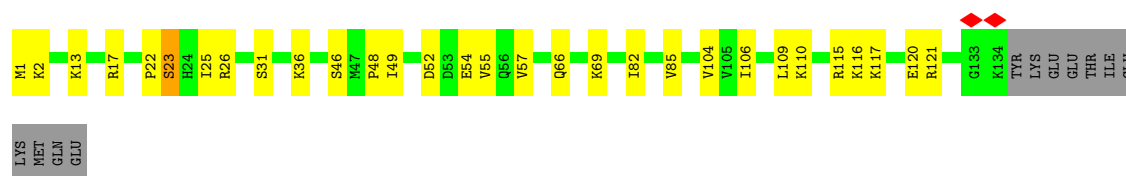
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|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|--|-----|-----|-----|--|-----|-----|--|-----|--|-----|--|-----|-----|--|-----|-----|-----|-----|--|-----|-----|-----|-----|-----|--|-----|-----|-----|--|------|------|------|------|------|------|--|--|--|------|--|------|------|
| MET | SR8 | LYS | ARG | GLY | ARG | GLY | GLY | GLY | SR8 | S10 | | R15 | | V22 | G23 | A24 | | I39 | I40 | | H60 | | V65 | | H77 | P78 | | Q84 | R85 | K86 | SR7 | | R90 | K91 | D92 | G93 | G94 | | P95 | L96 | Y97 | | N107 | N108 | K109 | G110 | E111 | M112 | | | | T118 | | I139 | A140 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|-----|--|-----|-----|-----|--|-----|-----|--|-----|--|-----|--|-----|-----|--|-----|-----|-----|-----|--|-----|-----|-----|-----|-----|--|-----|-----|-----|--|------|------|------|------|------|------|--|--|--|------|--|------|------|

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|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|------|------|------|------|------|------|------|
| I109 | R110 | A111 | A112 | K113 | E114 | A115 | K116 | K117 | A118 | K119 | Q120 | A121 | S122 | K123 | K124 | THR | ALA | GLU | ALA | MET | ILE | ALA | GLN | ALA | ALA | ALA | LYS | LYS | ALA | ALA | ALA | PRO | LYS | GLN | LYS | LYS | ILE | VAL | LYS | PRO | VAL | LYS | VAL | SER | ALA | ALA | PRO | ARG | VAL | GLY | GLY | LYS | ARG |
| M1 | E4 | F8 | R20 | Q30 | F31 | L32 | M45 | P46 | R47 | Q48 | I49 | G63 | SER | GLU | ALA | GLU | ILE | ALA | GLN | LYS | K70 | R71 | T72 | V76 | R80 | A81 | T82 | T83 | G84 | A85 | S86 | L87 | A88 | D89 | I90 | H91 | A92 | K93 | R94 | N95 | Q96 | K97 | P98 | E99 | V100 | R101 | K102 | A103 | Q104 | R105 | E106 | Q107 | A108 |

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| MET | ALA | PRO | LYS | ALA | LYS | LYS | GLU | ALA | PRO | ALA | PRO | PRO | LYS | ALA | ALA | LYS | LYS | LYS | ALA | ALA | VAL | LEU | LYS | ALA | LYS | LYS | LYS | LYS | GLY | VAL | HIS | SER | SER | HIS | LYS | LYS | K37 | K38 | S64 | A65 | D72 | H73 | I76 | L81 | T82 | T83 | E91 | L96 | V97 | K115 | L116 |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|------|

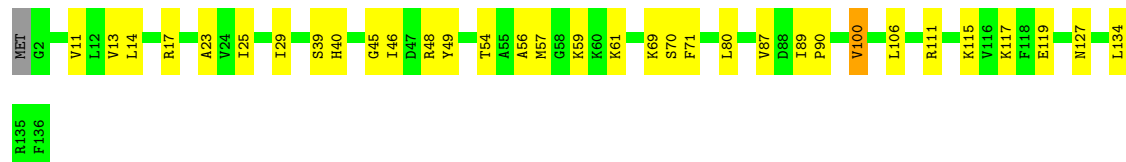
V138
R139
L140
L147
D148
V149
I156

- Chain LY: 72% 20% 8%



- Molecule 31: 60S ribosomal protein L27

Chain LZ: ..



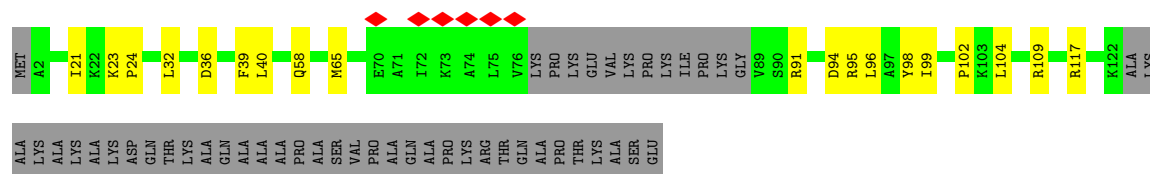
- Molecule 32: 60S ribosomal protein L27a

Chain La: .



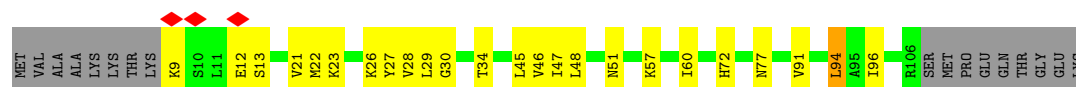
- Molecule 33: 60S ribosomal protein L29

Chain Lb:



- Molecule 34: 60S ribosomal protein L30

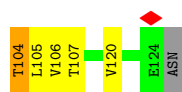
Chain Lc:



- Molecule 35: 60S ribosomal protein L31

Chain Ld:





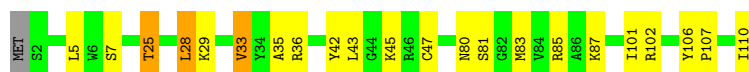
- Molecule 36: 60S ribosomal protein L32

Chain Le: 76% 17% 5%



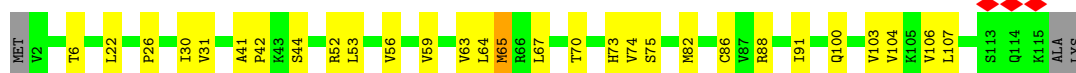
- Molecule 37: 60S ribosomal protein L35a

Chain Lf: 79% 17% ..



- Molecule 38: 60S ribosomal protein L34

Chain Lg: 73% 24% ..



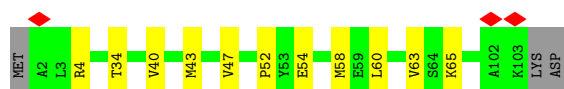
- Molecule 39: 60S ribosomal protein L35

Chain Lh: 69% 29% ..



- Molecule 40: 60S ribosomal protein L36

Chain Li: 87% 10% .

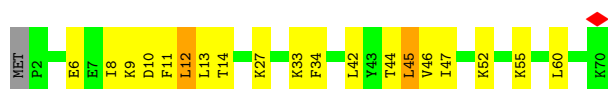


- Molecule 41: 60S ribosomal protein L37

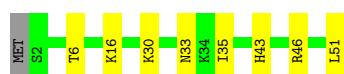
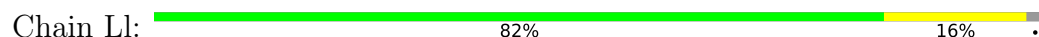
Chain Lj: 76% 11% . 11%



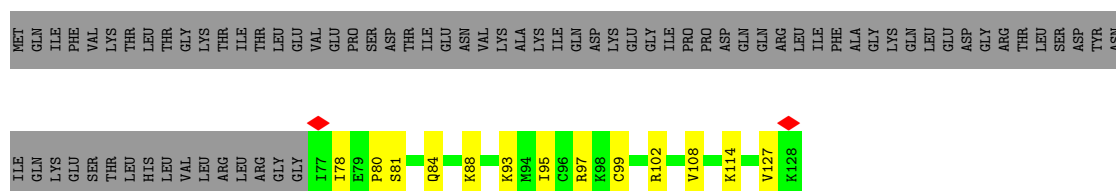
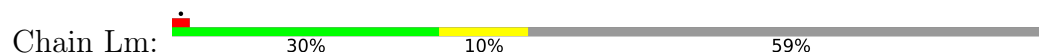
- Molecule 42: 60S ribosomal protein L38



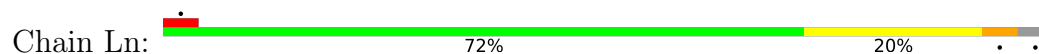
- Molecule 43: 60S ribosomal protein L39



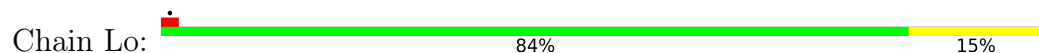
- Molecule 44: Ubiquitin-60S ribosomal protein L40



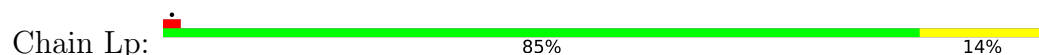
- Molecule 45: 60S ribosomal protein L41

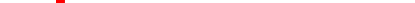


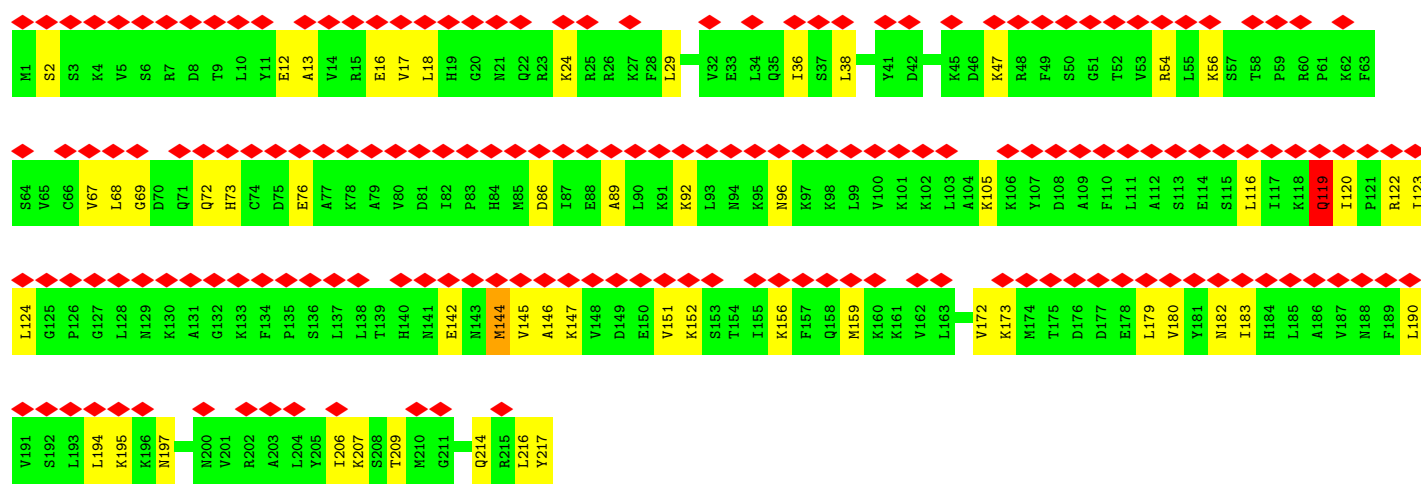
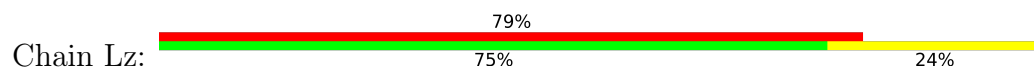
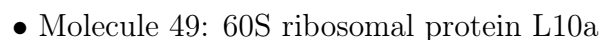
- Molecule 46: 60S ribosomal protein L36a



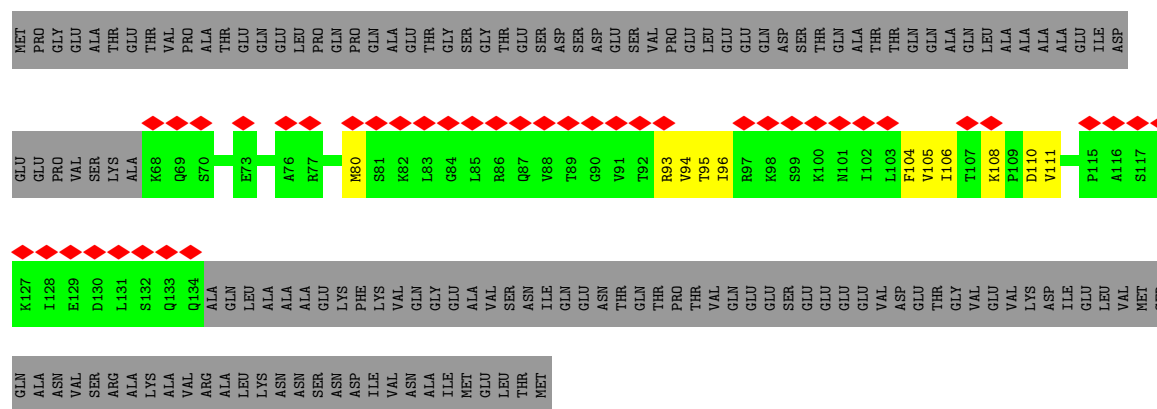
- Molecule 47: 60S ribosomal protein L37a



- Chain Lr:  74% 15% 9%

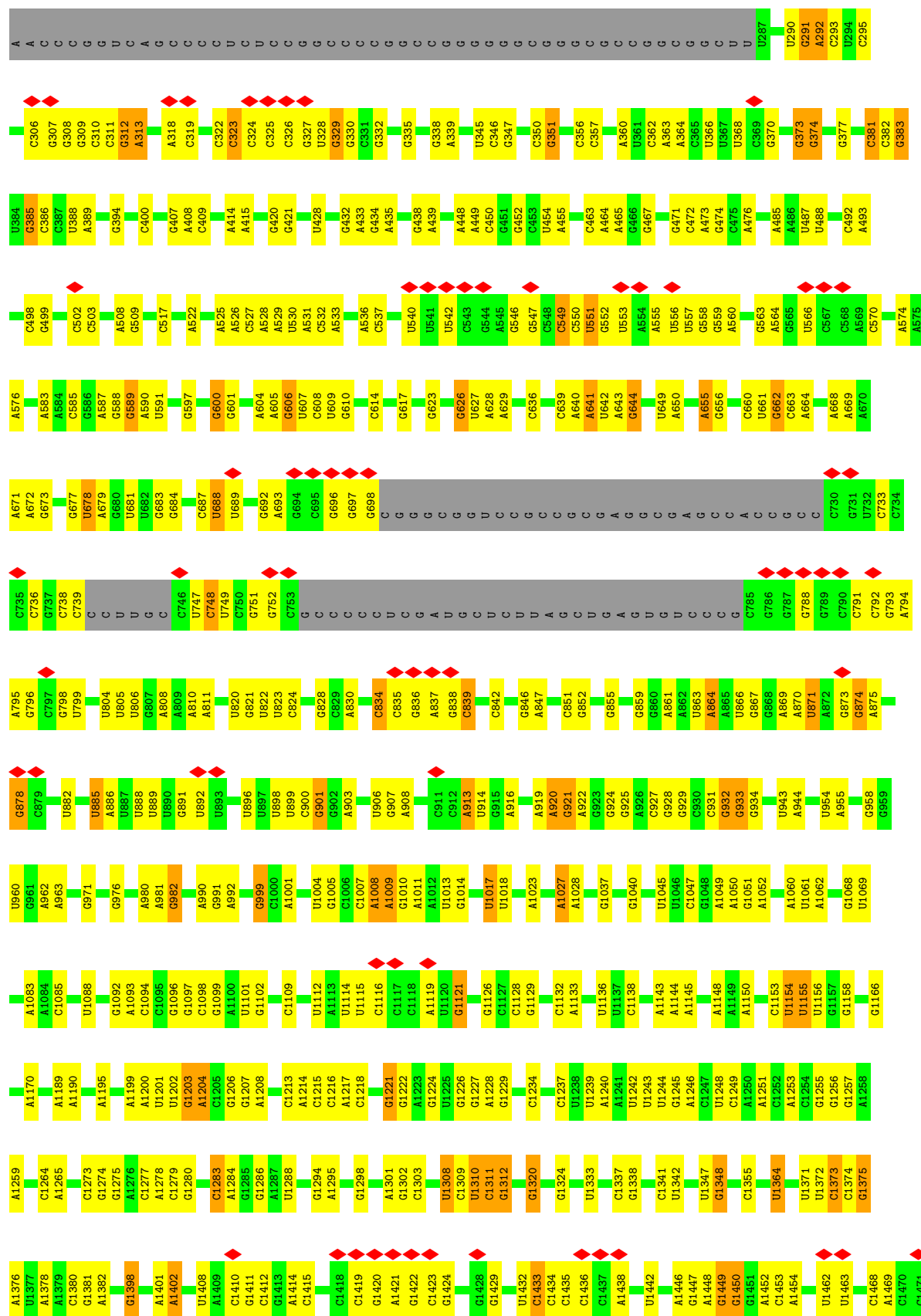


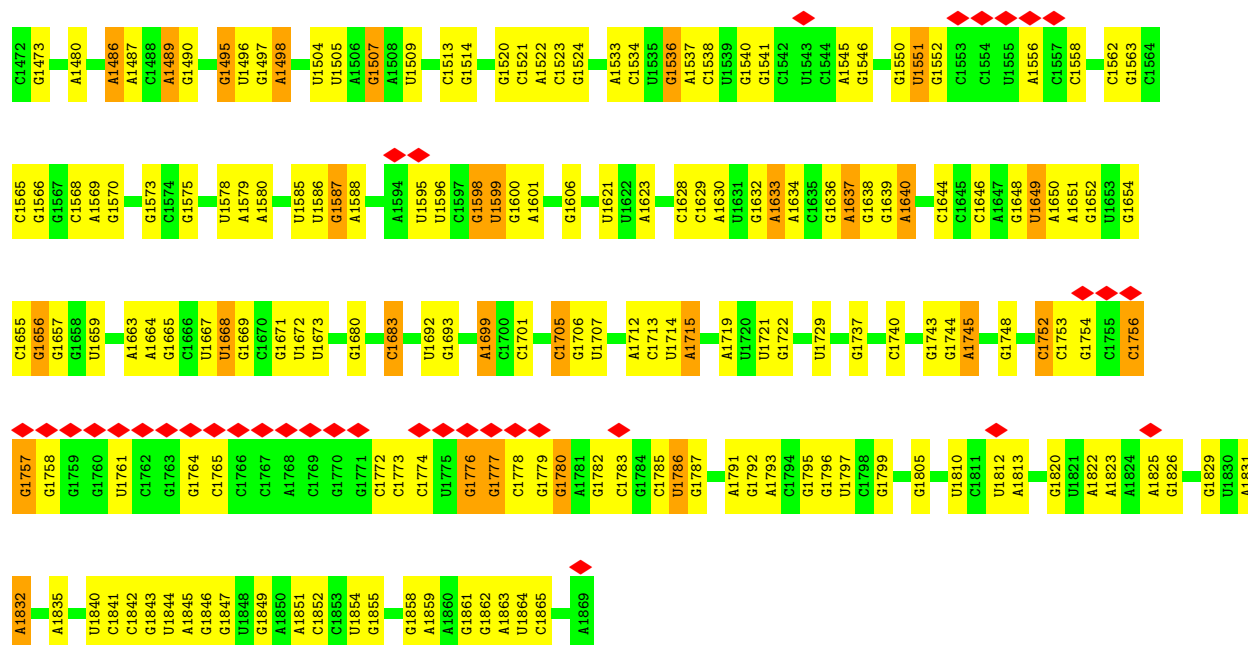
- Chain NA: 



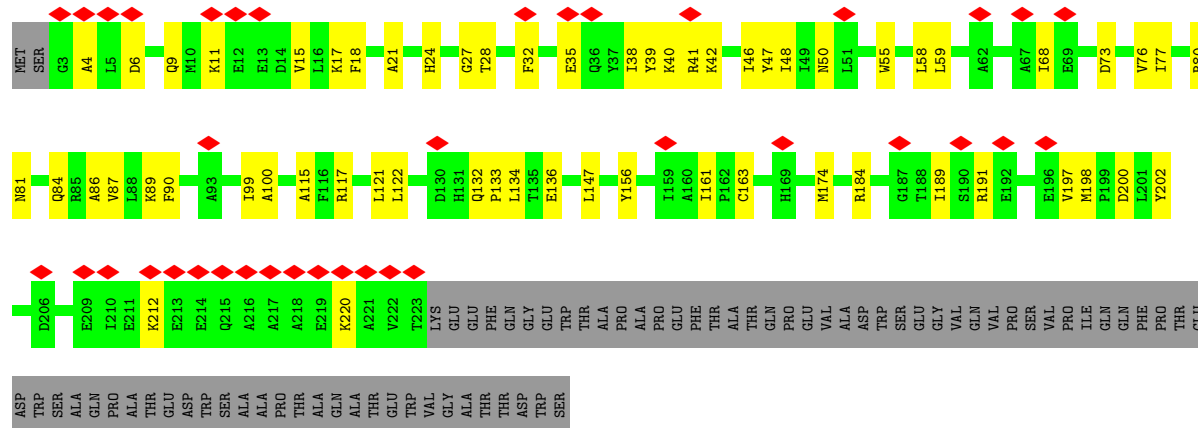
- Chain NB: 



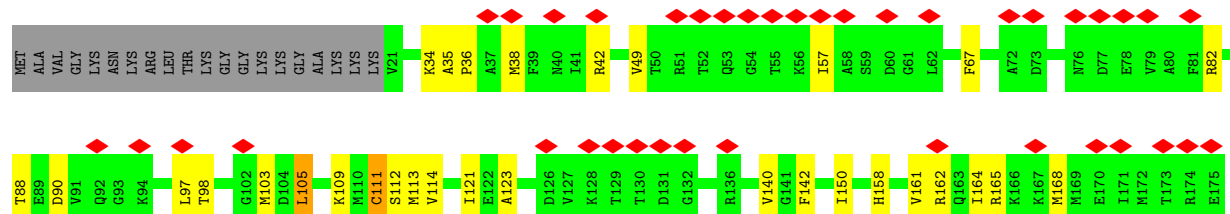


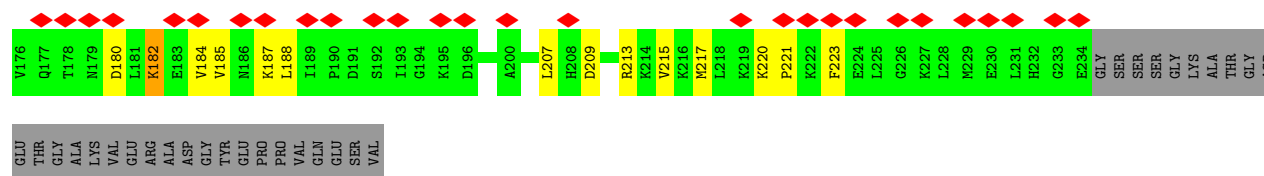


• Molecule 54: 40S ribosomal protein SA

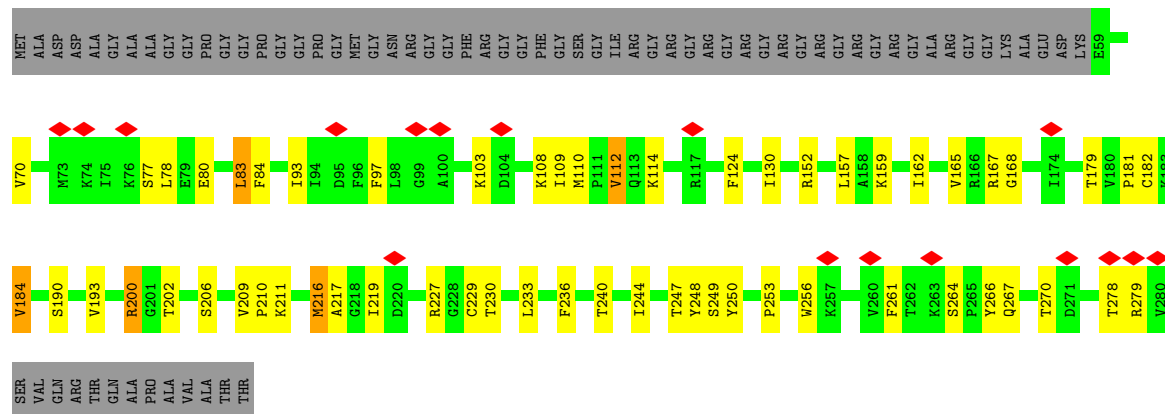


• Molecule 55: 40S ribosomal protein S3a

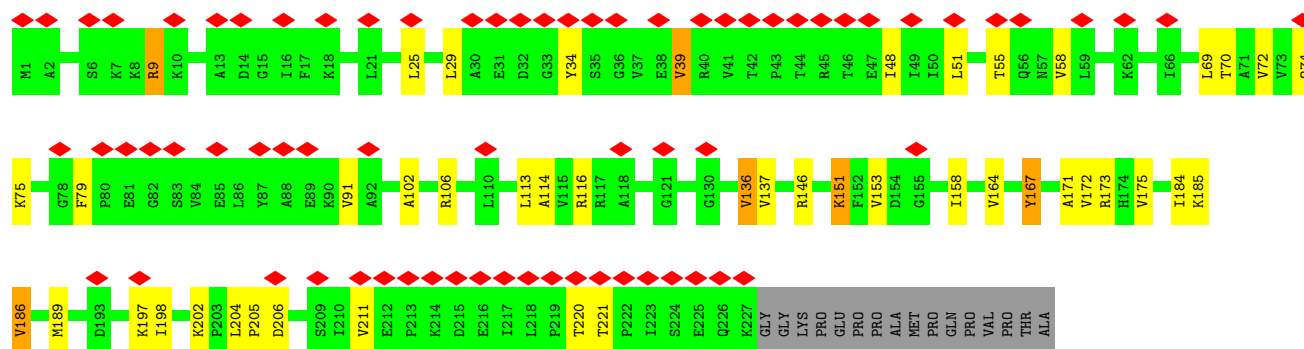
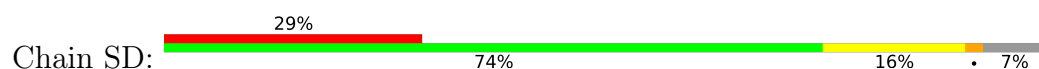




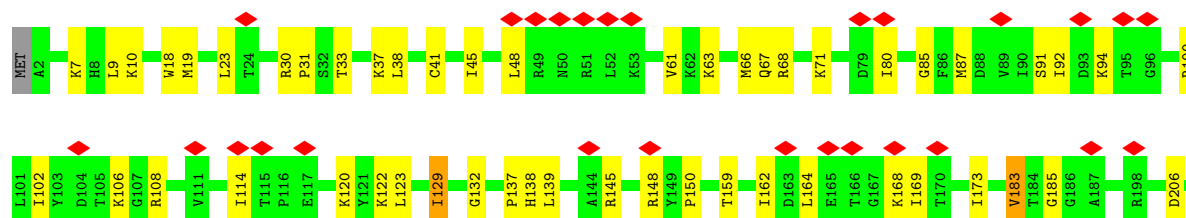
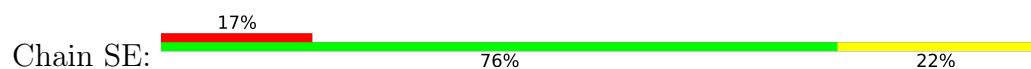
• Molecule 56: 40S ribosomal protein S2

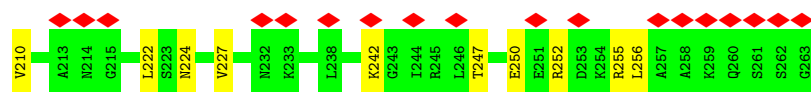


• Molecule 57: 40S ribosomal protein S3

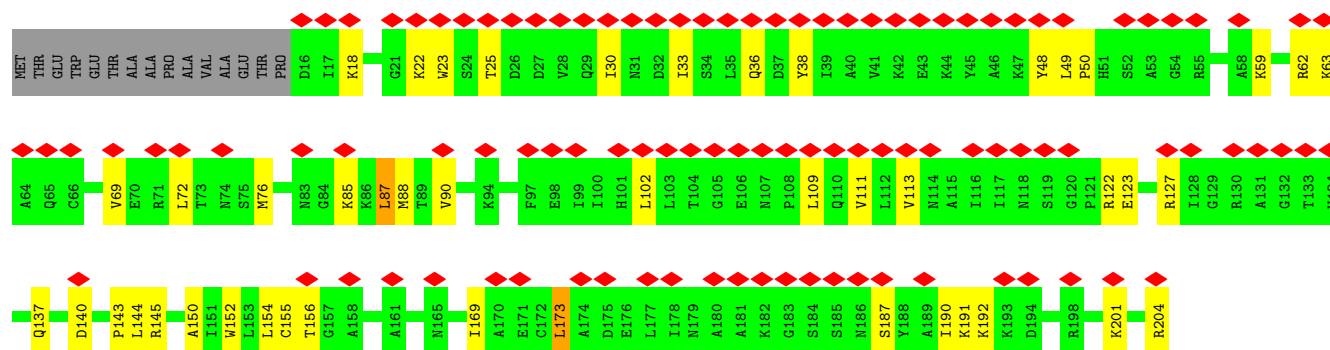
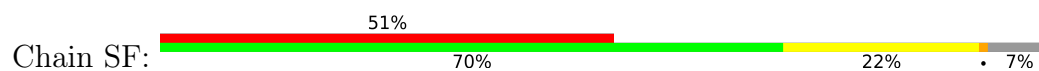


• Molecule 58: 40S ribosomal protein S4, X isoform

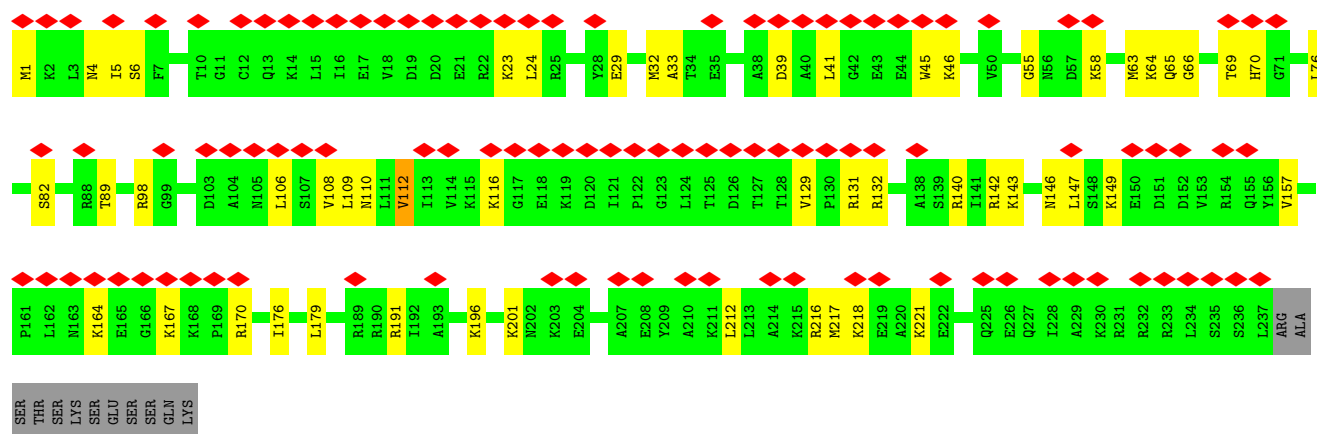
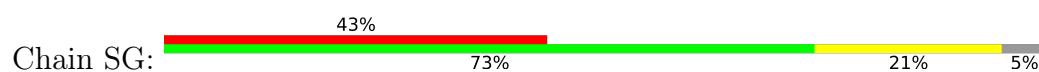




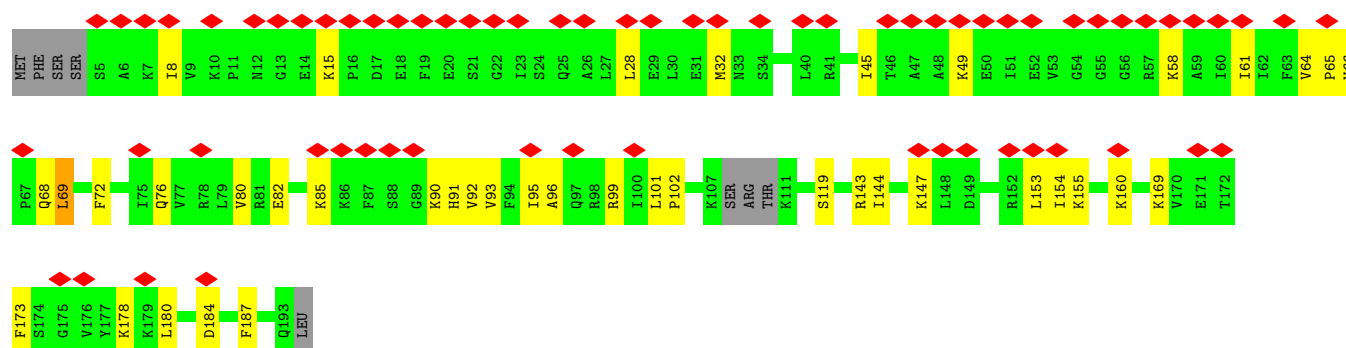
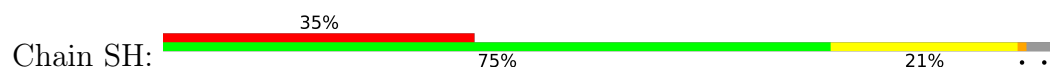
• Molecule 59: 40S ribosomal protein S5



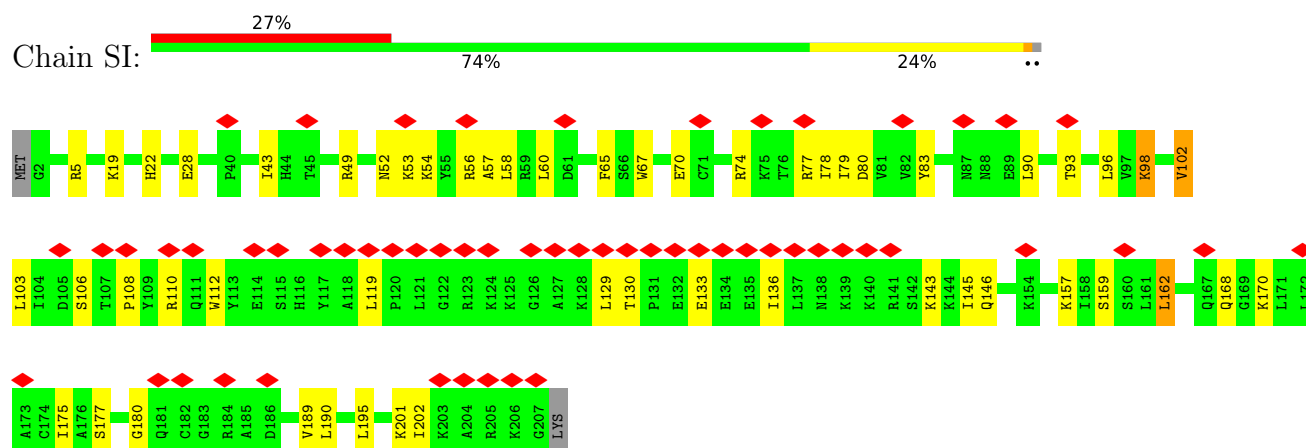
• Molecule 60: 40S ribosomal protein S6



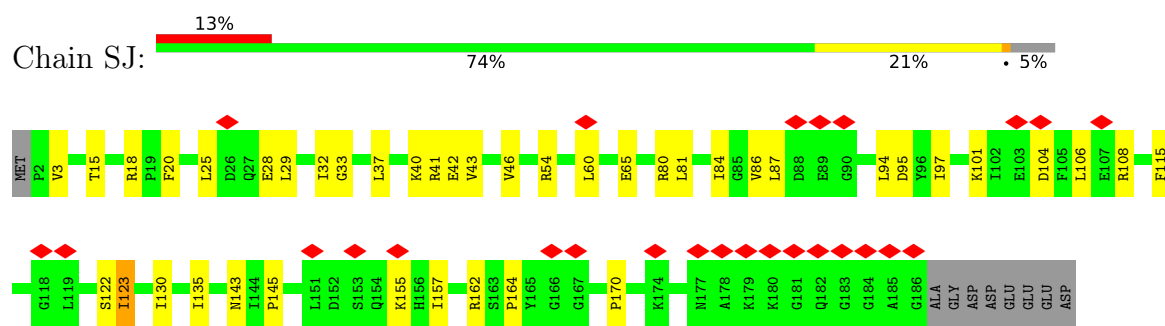
• Molecule 61: 40S ribosomal protein S7



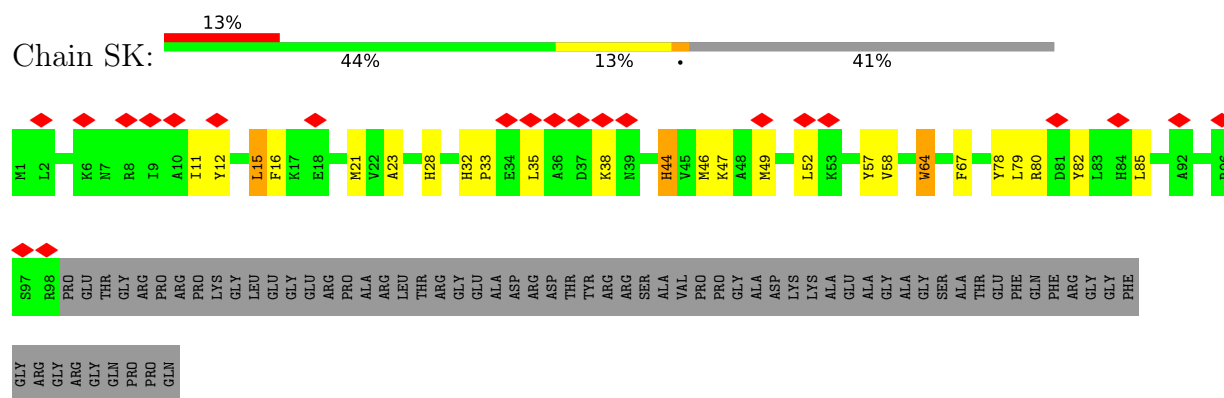
- Molecule 62: 40S ribosomal protein S8



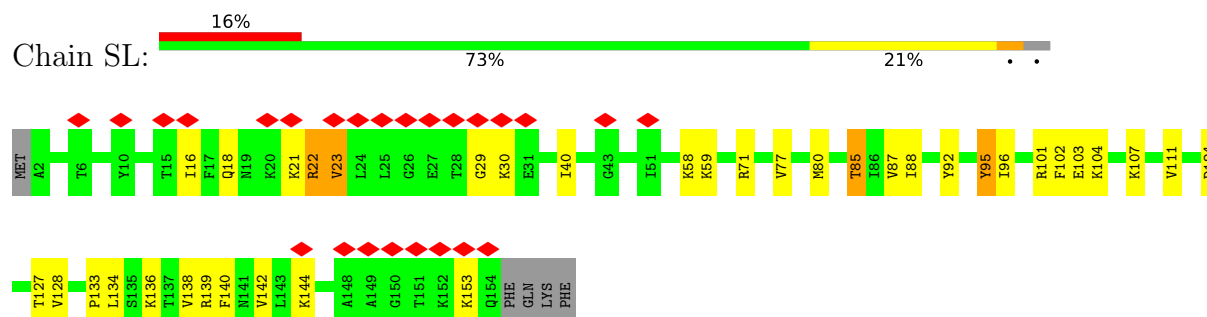
- Molecule 63: 40S ribosomal protein S9



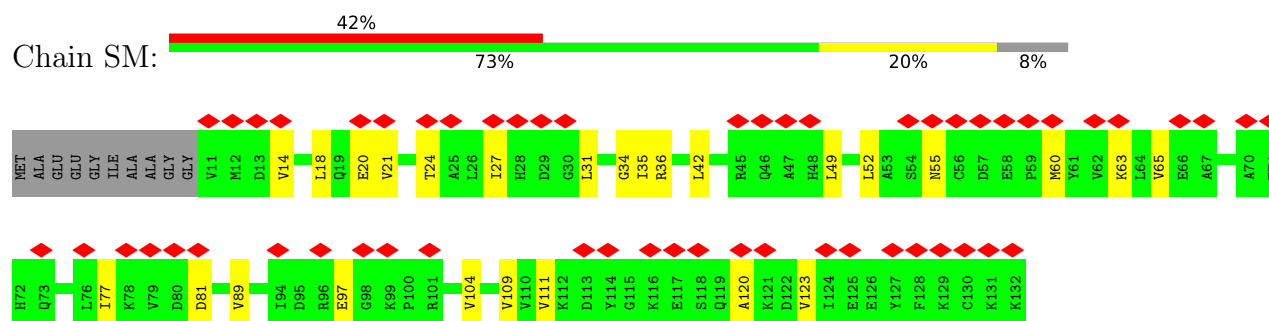
- Molecule 64: 40S ribosomal protein S10



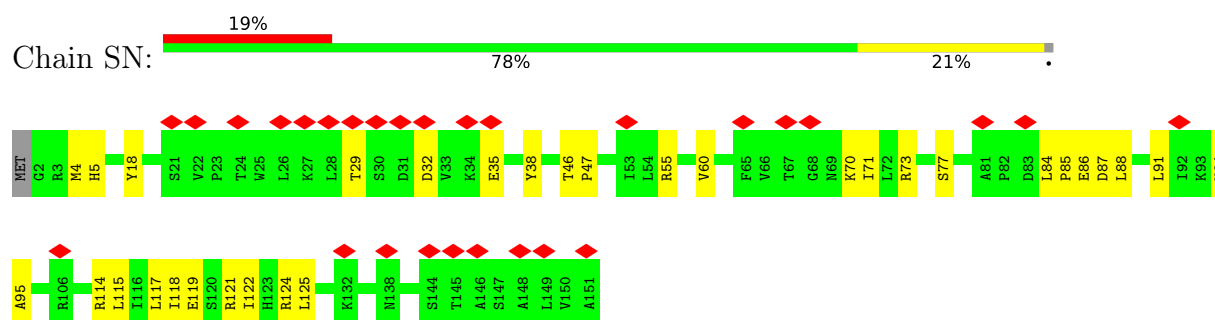
- Molecule 65: 40S ribosomal protein S11



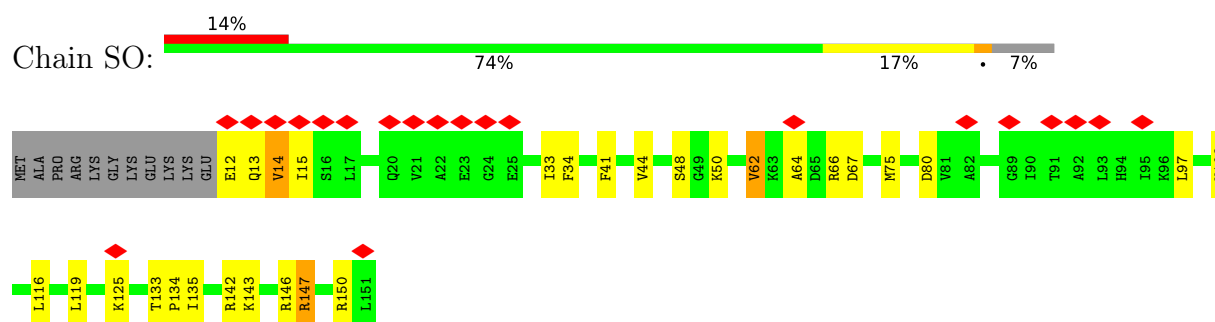
- Molecule 66: 40S ribosomal protein S12



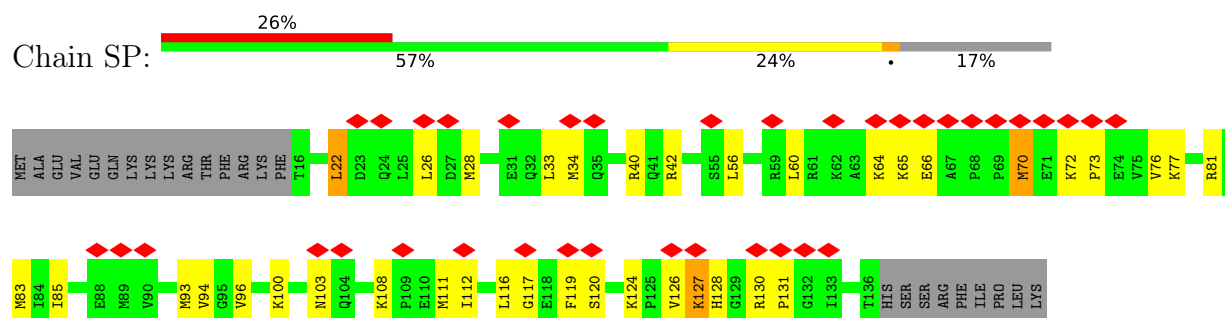
- Molecule 67: 40S ribosomal protein S13

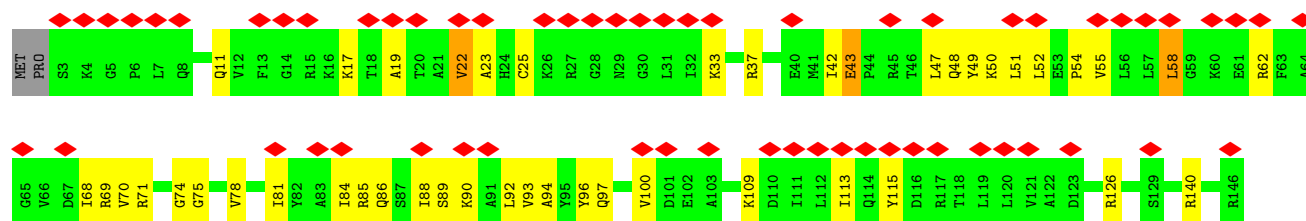


- Molecule 68: 40S ribosomal protein S14

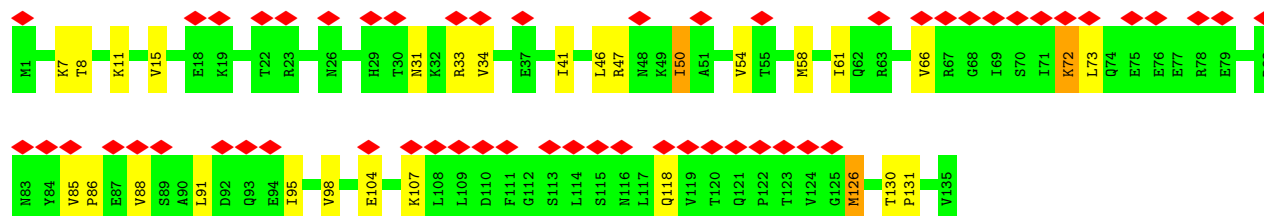
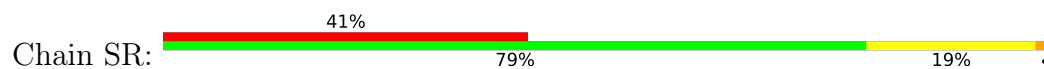


- Molecule 69: 40S ribosomal protein S15

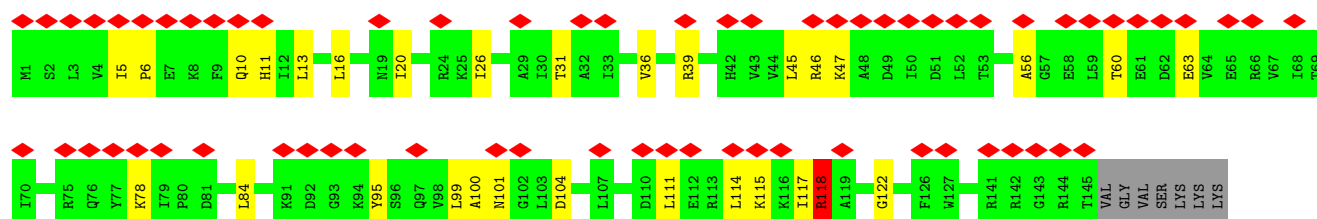
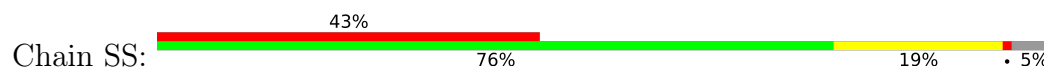




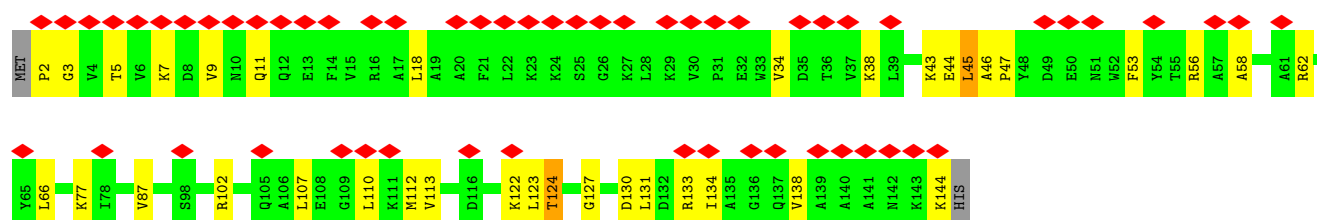
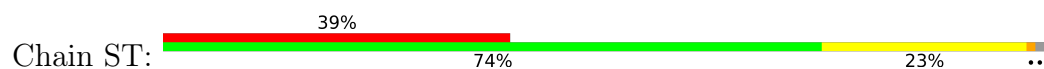
• Molecule 71: 40S ribosomal protein S17



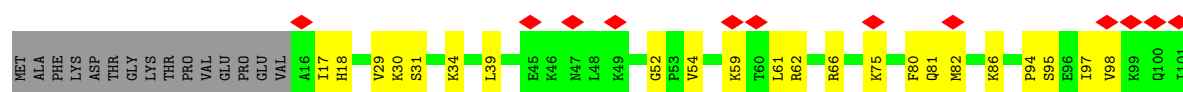
• Molecule 72: 40S ribosomal protein S18

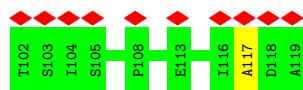


• Molecule 73: 40S ribosomal protein S19

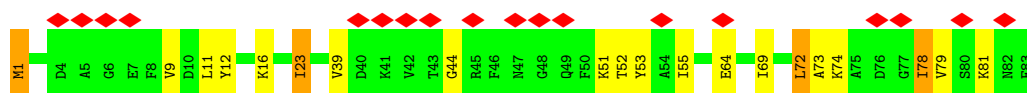
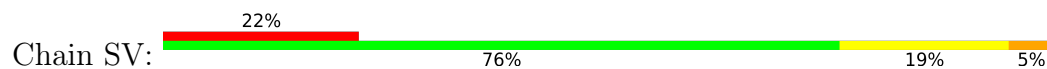


• Molecule 74: 40S ribosomal protein S20

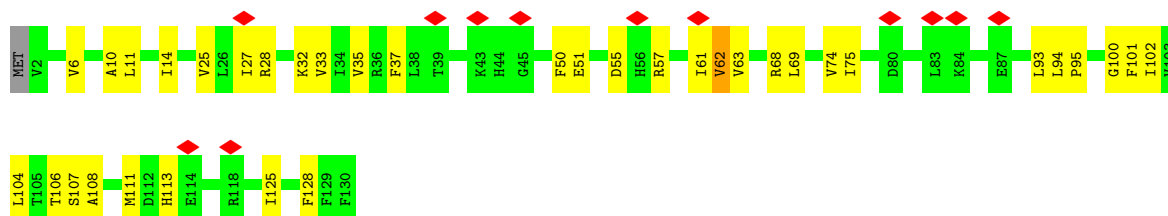




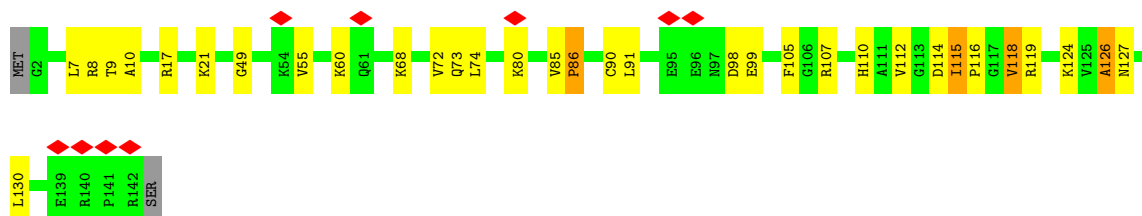
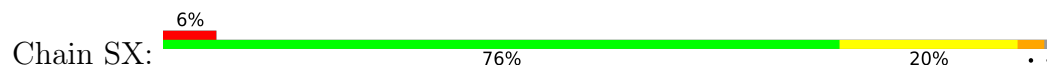
- Molecule 75: 40S ribosomal protein S21



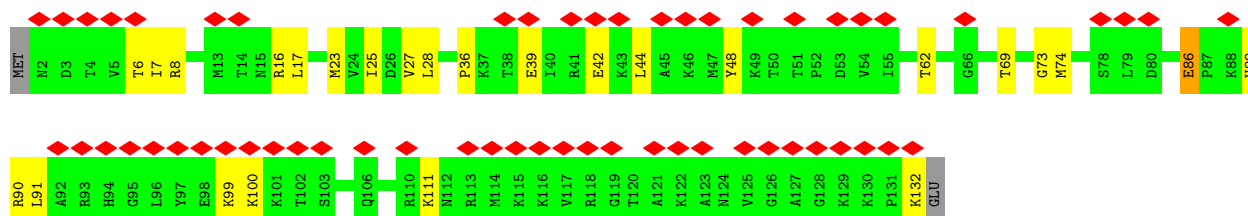
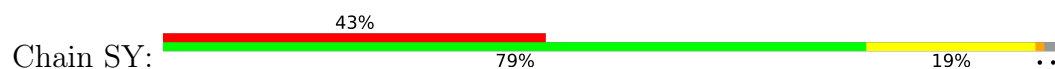
- Molecule 76: 40S ribosomal protein S15a



- Molecule 77: 40S ribosomal protein S23

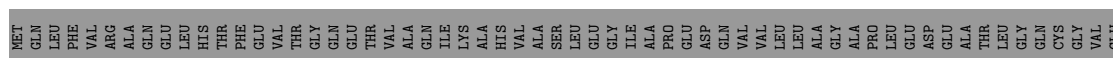


- Molecule 78: 40S ribosomal protein S24



- Molecule 79: 40S ribosomal protein S25





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	60808	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 ($e^-/\text{\AA}^2$)	45.6	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	6.289	Depositor
Minimum map value	-2.811	Depositor
Average map value	0.018	Depositor
Map value standard deviation	0.152	Depositor
Recommended contour level	0.35	Depositor
Map size (Å)	472.05002, 472.05002, 472.05002	wwPDB
Map dimensions	450, 450, 450	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.049, 1.049, 1.049	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	CB	0.24	0/6734	0.66	3/9094 (0.0%)
2	CC	0.15	0/2025	0.31	0/3155
3	CD	0.16	0/447	0.52	0/592
4	L5	0.29	0/89570	0.38	1/139647 (0.0%)
5	L7	0.26	0/2861	0.32	0/4459
6	L8	0.29	0/3701	0.34	0/5766
7	LA	0.34	0/1936	0.61	0/2596
8	LB	0.31	0/3306	0.59	1/4424 (0.0%)
9	LC	0.31	0/2981	0.60	4/4002 (0.1%)
10	LD	0.27	0/2428	0.62	1/3252 (0.0%)
11	LE	0.27	0/1942	0.64	1/2606 (0.0%)
12	LF	0.33	0/1905	0.61	0/2539
13	LG	0.30	0/1960	0.70	0/2637
14	LH	0.30	0/1537	0.68	1/2066 (0.0%)
15	LI	0.30	0/1673	0.60	1/2233 (0.0%)
16	LJ	0.26	0/1433	0.67	0/1915
17	LL	0.29	0/1732	0.56	0/2315
18	LM	0.29	0/1161	0.66	2/1554 (0.1%)
19	LN	0.33	0/1746	0.58	0/2338
20	LO	0.31	0/1682	0.55	0/2250
21	LP	0.32	0/1268	0.56	0/1701
22	LQ	0.31	0/1537	0.54	0/2052
23	LR	0.30	0/1582	0.69	3/2091 (0.1%)
24	LS	0.32	0/1493	0.53	0/2003
25	LT	0.33	0/1326	0.65	2/1770 (0.1%)
26	LU	0.30	0/839	0.79	1/1126 (0.1%)
27	LV	0.30	0/993	0.58	0/1332
28	LW	0.22	0/979	0.41	0/1295
29	LX	0.27	0/1002	0.56	0/1345
30	LY	0.25	0/1132	0.55	0/1504
31	LZ	0.27	0/1130	0.60	0/1507
32	La	0.31	0/1191	0.53	0/1591

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Lb	0.28	0/889	0.68	0/1175
34	Lc	0.29	0/774	0.64	0/1038
35	Ld	0.29	0/903	0.57	0/1216
36	Le	0.32	0/1071	0.57	0/1429
37	Lf	0.33	0/895	0.63	0/1198
38	Lg	0.30	0/916	0.57	0/1220
39	Lh	0.29	0/1023	0.61	1/1351 (0.1%)
40	Li	0.25	0/843	0.56	0/1115
41	Lj	0.33	0/720	0.58	0/952
42	Lk	0.36	0/575	0.81	2/761 (0.3%)
43	Ll	0.33	0/454	0.57	0/599
44	Lm	0.25	0/435	0.46	0/575
45	Ln	0.24	0/231	0.53	0/294
46	Lo	0.29	0/876	0.63	0/1156
47	Lp	0.27	0/718	0.52	0/953
48	Lr	0.29	0/1017	0.52	0/1364
49	Lz	0.23	0/1769	0.61	1/2371 (0.0%)
50	NA	0.22	0/536	0.62	2/715 (0.3%)
51	NB	0.24	0/972	0.58	1/1304 (0.1%)
52	NM	0.19	0/3299	0.56	3/4483 (0.1%)
53	S2	0.17	0/41244	0.34	1/64263 (0.0%)
54	SA	0.25	0/1778	0.70	1/2416 (0.0%)
55	SB	0.23	0/1765	0.60	1/2362 (0.0%)
56	SC	0.26	0/1762	0.71	1/2381 (0.0%)
57	SD	0.26	0/1793	0.68	0/2414
58	SE	0.20	0/2118	0.52	0/2849
59	SF	0.24	0/1516	0.71	1/2037 (0.0%)
60	SG	0.21	0/1946	0.60	2/2590 (0.1%)
61	SH	0.23	0/1519	0.66	2/2033 (0.1%)
62	SI	0.24	0/1715	0.61	2/2287 (0.1%)
63	SJ	0.25	0/1550	0.64	1/2069 (0.0%)
64	SK	0.24	0/851	0.75	0/1147
65	SL	0.24	0/1268	0.57	0/1696
66	SM	0.20	0/950	0.59	0/1275
67	SN	0.24	0/1232	0.62	0/1656
68	SO	0.25	0/1062	0.66	2/1425 (0.1%)
69	SP	0.28	0/1003	0.84	2/1342 (0.1%)
70	SQ	0.22	0/1160	0.69	0/1553
71	SR	0.27	0/1105	0.80	1/1484 (0.1%)
72	SS	0.22	0/1216	0.69	2/1628 (0.1%)
73	ST	0.23	0/1131	0.68	1/1515 (0.1%)
74	SU	0.29	0/832	0.68	1/1117 (0.1%)
75	SV	0.24	0/643	0.65	0/860

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
76	SW	0.27	0/1051	0.65	0/1406
77	SX	0.25	0/1116	0.71	2/1490 (0.1%)
78	SY	0.23	0/1083	0.64	0/1438
79	SZ	0.33	0/604	1.00	2/810 (0.2%)
80	Sa	0.25	0/836	0.65	1/1121 (0.1%)
81	Sb	0.23	0/665	0.67	1/891 (0.1%)
82	Sc	0.27	0/508	0.75	0/680
83	Sd	0.23	0/470	0.68	0/623
84	Se	0.21	0/465	0.62	1/612 (0.2%)
85	Sf	0.22	0/560	0.64	0/745
86	Sg	0.20	0/2493	0.57	1/3394 (0.0%)
All	All	0.27	0/247158	0.49	60/361635 (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
12	LF	0	1
13	LG	0	1
16	LJ	0	1
17	LL	0	1
18	LM	0	2
20	LO	0	1
25	LT	0	1
32	La	0	1
37	Lf	0	1
39	Lh	0	1
41	Lj	0	1
49	Lz	0	1
51	NB	0	1
55	SB	0	2
57	SD	0	1
59	SF	0	1
61	SH	0	1
63	SJ	0	1
69	SP	0	1
70	SQ	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
72	SS	0	1
73	ST	0	1
75	SV	0	1
77	SX	0	2
80	Sa	0	1
All	All	0	33

There are no bond length outliers.

The worst 5 of 60 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
51	NB	102	MET	CB-CG-SD	8.22	137.38	112.70
26	LU	18	VAL	N-CA-C	-7.70	103.76	111.77
23	LR	78	ILE	N-CA-C	-7.10	105.86	112.96
77	SX	127	ASN	N-CA-C	6.93	121.18	112.87
9	LC	67	TRP	CA-CB-CG	6.41	125.77	113.60

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	13	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	86	0
2	CC	1813	0	917	13	0
3	CD	440	0	402	10	0
4	L5	80116	0	40368	422	0
5	L7	2561	0	1295	12	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	L8	3314	0	1683	18	0
7	LA	1898	0	1993	19	0
8	LB	3238	0	3376	35	0
9	LC	2927	0	3104	32	0
10	LD	2382	0	2410	27	0
11	LE	1904	0	2055	29	0
12	LF	1870	0	1996	20	0
13	LG	1927	0	2074	33	0
14	LH	1518	0	1601	19	0
15	LI	1634	0	1671	26	0
16	LJ	1410	0	1441	25	0
17	LL	1701	0	1818	25	0
18	LM	1138	0	1204	12	0
19	LN	1701	0	1749	33	0
20	LO	1650	0	1794	20	0
21	LP	1242	0	1269	17	0
22	LQ	1513	0	1628	15	0
23	LR	1566	0	1729	20	0
24	LS	1453	0	1490	14	0
25	LT	1298	0	1366	16	0
26	LU	825	0	850	18	0
27	LV	979	0	1039	12	0
28	LW	965	0	1029	8	0
29	LX	985	0	1066	12	0
30	LY	1115	0	1205	14	0
31	LZ	1107	0	1182	16	0
32	La	1162	0	1213	14	0
33	Lb	876	0	948	12	0
34	Lc	764	0	804	11	0
35	Ld	888	0	930	17	0
36	Le	1053	0	1147	14	0
37	Lf	876	0	912	10	0
38	Lg	906	0	998	14	0
39	Lh	1015	0	1148	24	0
40	Li	832	0	917	9	0
41	Lj	705	0	737	8	0
42	Lk	569	0	637	8	0
43	Ll	444	0	483	4	0
44	Lm	429	0	465	4	0
45	Ln	230	0	276	3	0
46	Lo	862	0	930	11	0
47	Lp	708	0	756	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
48	Lr	1002	0	1068	10	0
49	Lz	1741	0	1854	32	0
50	NA	531	0	573	6	0
51	NB	963	0	982	20	0
52	NM	3209	0	3185	34	0
53	S2	36898	0	18602	325	0
54	SA	1741	0	1746	39	0
55	SB	1738	0	1809	31	0
56	SC	1725	0	1813	41	0
57	SD	1765	0	1865	32	0
58	SE	2076	0	2177	35	0
59	SF	1495	0	1549	35	0
60	SG	1923	0	2089	30	0
61	SH	1497	0	1590	26	0
62	SI	1686	0	1772	33	0
63	SJ	1525	0	1640	26	0
64	SK	827	0	854	17	0
65	SL	1247	0	1323	25	0
66	SM	940	0	965	17	0
67	SN	1208	0	1294	23	0
68	SO	1049	0	1073	18	0
69	SP	985	0	1031	28	0
70	SQ	1142	0	1213	27	0
71	SR	1090	0	1149	18	0
72	SS	1198	0	1261	20	0
73	ST	1112	0	1146	23	0
74	SU	822	0	887	16	0
75	SV	636	0	637	21	0
76	SW	1034	0	1080	19	0
77	SX	1098	0	1167	18	0
78	SY	1065	0	1142	17	0
79	SZ	598	0	656	15	0
80	Sa	821	0	870	16	0
81	Sb	651	0	672	14	0
82	Sc	506	0	536	20	0
83	Sd	459	0	452	19	0
84	Se	459	0	503	11	0
85	Sf	548	0	555	11	0
86	Sg	2436	0	2393	29	0
87	CC	1	0	0	0	0
87	L5	211	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	5	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	LT	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	230824	0	173959	2166	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 2166 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)
63:SJ:143:ASN:CA	63:SJ:143:ASN:CB	1.75	1.60
53:S2:886:A:N6	53:S2:901:G:C4	2.19	1.10
55:SB:109:LYS:O	55:SB:113:MET:HB2	1.53	1.06
4:L5:1762:C:N4	4:L5:1770:A:C2	2.25	1.04
4:L5:1269:G:N2	4:L5:1441:C:C2	2.24	1.04

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%)	791 (94%)	51 (6%)	0	100	100
3	CD	51/402 (13%)	50 (98%)	1 (2%)	0	100	100
7	LA	246/257 (96%)	223 (91%)	22 (9%)	1 (0%)	30	53
8	LB	400/403 (99%)	375 (94%)	25 (6%)	0	100	100
9	LC	366/427 (86%)	343 (94%)	23 (6%)	0	100	100
10	LD	291/297 (98%)	274 (94%)	17 (6%)	0	100	100
11	LE	232/288 (81%)	210 (90%)	22 (10%)	0	100	100
12	LF	223/248 (90%)	215 (96%)	8 (4%)	0	100	100
13	LG	239/266 (90%)	224 (94%)	15 (6%)	0	100	100
14	LH	188/192 (98%)	173 (92%)	15 (8%)	0	100	100
15	LI	198/214 (92%)	184 (93%)	14 (7%)	0	100	100
16	LJ	174/178 (98%)	153 (88%)	21 (12%)	0	100	100
17	LL	208/211 (99%)	195 (94%)	13 (6%)	0	100	100
18	LM	137/215 (64%)	125 (91%)	11 (8%)	1 (1%)	18	40
19	LN	201/204 (98%)	193 (96%)	7 (4%)	1 (0%)	24	49
20	LO	199/203 (98%)	191 (96%)	8 (4%)	0	100	100
21	LP	151/184 (82%)	143 (95%)	8 (5%)	0	100	100
22	LQ	185/188 (98%)	178 (96%)	7 (4%)	0	100	100
23	LR	185/196 (94%)	181 (98%)	3 (2%)	1 (0%)	24	49
24	LS	173/176 (98%)	163 (94%)	10 (6%)	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%)	111 (97%)	3 (3%)	0	100	100
29	LX	118/156 (76%)	113 (96%)	5 (4%)	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%)	135 (93%)	10 (7%)	0	100	100
33	Lb	105/159 (66%)	99 (94%)	6 (6%)	0	100	100
34	Lc	96/115 (84%)	92 (96%)	4 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	Ld	105/125 (84%)	102 (97%)	3 (3%)	0	100	100
36	Le	126/135 (93%)	121 (96%)	5 (4%)	0	100	100
37	Lf	107/110 (97%)	99 (92%)	7 (6%)	1 (1%)	14	34
38	Lg	112/117 (96%)	111 (99%)	1 (1%)	0	100	100
39	Lh	120/123 (98%)	118 (98%)	2 (2%)	0	100	100
40	Li	100/105 (95%)	97 (97%)	3 (3%)	0	100	100
41	Lj	84/97 (87%)	79 (94%)	5 (6%)	0	100	100
42	Lk	67/70 (96%)	66 (98%)	1 (2%)	0	100	100
43	Ll	48/51 (94%)	44 (92%)	4 (8%)	0	100	100
44	Lm	50/128 (39%)	48 (96%)	2 (4%)	0	100	100
45	Ln	22/25 (88%)	22 (100%)	0	0	100	100
46	Lo	103/106 (97%)	99 (96%)	4 (4%)	0	100	100
47	Lp	89/92 (97%)	87 (98%)	2 (2%)	0	100	100
48	Lr	123/137 (90%)	117 (95%)	6 (5%)	0	100	100
49	Lz	215/217 (99%)	161 (75%)	54 (25%)	0	100	100
50	NA	65/215 (30%)	59 (91%)	6 (9%)	0	100	100
51	NB	120/162 (74%)	113 (94%)	7 (6%)	0	100	100
52	NM	394/496 (79%)	382 (97%)	12 (3%)	0	100	100
54	SA	219/295 (74%)	198 (90%)	21 (10%)	0	100	100
55	SB	212/264 (80%)	204 (96%)	8 (4%)	0	100	100
56	SC	220/293 (75%)	207 (94%)	13 (6%)	0	100	100
57	SD	225/243 (93%)	200 (89%)	25 (11%)	0	100	100
58	SE	260/263 (99%)	238 (92%)	22 (8%)	0	100	100
59	SF	187/204 (92%)	167 (89%)	20 (11%)	0	100	100
60	SG	235/249 (94%)	221 (94%)	14 (6%)	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%)	170 (93%)	13 (7%)	0	100	100
64	SK	96/165 (58%)	80 (83%)	16 (17%)	0	100	100
65	SL	151/158 (96%)	137 (91%)	14 (9%)	0	100	100
66	SM	120/132 (91%)	115 (96%)	5 (4%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
67	SN	148/151 (98%)	144 (97%)	4 (3%)	0	100	100
68	SO	138/151 (91%)	128 (93%)	10 (7%)	0	100	100
69	SP	119/145 (82%)	110 (92%)	9 (8%)	0	100	100
70	SQ	142/146 (97%)	129 (91%)	13 (9%)	0	100	100
71	SR	133/135 (98%)	121 (91%)	12 (9%)	0	100	100
72	SS	143/152 (94%)	131 (92%)	12 (8%)	0	100	100
73	ST	141/145 (97%)	128 (91%)	13 (9%)	0	100	100
74	SU	102/119 (86%)	95 (93%)	7 (7%)	0	100	100
75	SV	81/83 (98%)	75 (93%)	6 (7%)	0	100	100
76	SW	127/130 (98%)	121 (95%)	6 (5%)	0	100	100
77	SX	139/143 (97%)	128 (92%)	11 (8%)	0	100	100
78	SY	129/133 (97%)	121 (94%)	8 (6%)	0	100	100
79	SZ	73/125 (58%)	56 (77%)	17 (23%)	0	100	100
80	Sa	100/115 (87%)	90 (90%)	10 (10%)	0	100	100
81	Sb	81/84 (96%)	72 (89%)	9 (11%)	0	100	100
82	Sc	62/69 (90%)	53 (86%)	9 (14%)	0	100	100
83	Sd	53/56 (95%)	49 (92%)	4 (8%)	0	100	100
84	Se	56/133 (42%)	48 (86%)	8 (14%)	0	100	100
85	Sf	65/156 (42%)	55 (85%)	10 (15%)	0	100	100
86	Sg	311/317 (98%)	273 (88%)	38 (12%)	0	100	100
All	All	13004/15112 (86%)	12084 (93%)	915 (7%)	5 (0%)	100	100

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
23	LR	39	GLN
19	LN	124	ASP
18	LM	88	ALA
37	Lf	107	PRO
7	LA	55	GLY

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%)	688 (95%)	34 (5%)	23	49
3	CD	46/322 (14%)	45 (98%)	1 (2%)	45	69
7	LA	190/199 (96%)	176 (93%)	14 (7%)	13	32
8	LB	348/349 (100%)	334 (96%)	14 (4%)	28	53
9	LC	306/348 (88%)	290 (95%)	16 (5%)	21	46
10	LD	246/250 (98%)	238 (97%)	8 (3%)	33	58
11	LE	209/252 (83%)	195 (93%)	14 (7%)	15	36
12	LF	194/215 (90%)	186 (96%)	8 (4%)	27	53
13	LG	203/223 (91%)	194 (96%)	9 (4%)	25	51
14	LH	169/171 (99%)	155 (92%)	14 (8%)	10	27
15	LI	172/181 (95%)	163 (95%)	9 (5%)	21	46
16	LJ	148/149 (99%)	138 (93%)	10 (7%)	14	35
17	LL	176/177 (99%)	165 (94%)	11 (6%)	16	38
18	LM	118/161 (73%)	110 (93%)	8 (7%)	14	35
19	LN	171/172 (99%)	157 (92%)	14 (8%)	10	27
20	LO	173/174 (99%)	165 (95%)	8 (5%)	24	50
21	LP	134/163 (82%)	127 (95%)	7 (5%)	21	46
22	LQ	164/165 (99%)	158 (96%)	6 (4%)	30	55
23	LR	166/175 (95%)	158 (95%)	8 (5%)	23	48
24	LS	156/157 (99%)	148 (95%)	8 (5%)	21	47
25	LT	139/140 (99%)	131 (94%)	8 (6%)	18	41
26	LU	91/115 (79%)	84 (92%)	7 (8%)	12	30
27	LV	101/107 (94%)	94 (93%)	7 (7%)	14	35
28	LW	97/126 (77%)	94 (97%)	3 (3%)	35	59
29	LX	108/133 (81%)	105 (97%)	3 (3%)	38	62
30	LY	124/135 (92%)	118 (95%)	6 (5%)	23	48
31	LZ	117/118 (99%)	109 (93%)	8 (7%)	14	35
32	La	120/121 (99%)	116 (97%)	4 (3%)	33	58
33	Lb	88/126 (70%)	87 (99%)	1 (1%)	65	80

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
34	Lc	83/97 (86%)	77 (93%)	6 (7%)	13	33
35	Ld	98/110 (89%)	89 (91%)	9 (9%)	8	23
36	Le	114/121 (94%)	106 (93%)	8 (7%)	14	34
37	Lf	88/89 (99%)	81 (92%)	7 (8%)	11	28
38	Lg	98/100 (98%)	89 (91%)	9 (9%)	8	23
39	Lh	109/110 (99%)	104 (95%)	5 (5%)	24	50
40	Li	86/89 (97%)	85 (99%)	1 (1%)	63	79
41	Lj	73/80 (91%)	71 (97%)	2 (3%)	39	64
42	Lk	64/65 (98%)	58 (91%)	6 (9%)	8	22
43	Ll	47/48 (98%)	44 (94%)	3 (6%)	16	38
44	Lm	48/116 (41%)	42 (88%)	6 (12%)	4	13
45	Ln	23/24 (96%)	21 (91%)	2 (9%)	9	25
46	Lo	93/94 (99%)	89 (96%)	4 (4%)	26	52
47	Lp	74/75 (99%)	71 (96%)	3 (4%)	27	53
48	Lr	109/121 (90%)	99 (91%)	10 (9%)	8	23
49	Lz	195/196 (100%)	190 (97%)	5 (3%)	40	65
50	NA	60/183 (33%)	60 (100%)	0	100	100
51	NB	106/136 (78%)	98 (92%)	8 (8%)	12	31
52	NM	353/443 (80%)	349 (99%)	4 (1%)	65	80
54	SA	183/243 (75%)	177 (97%)	6 (3%)	33	58
55	SB	195/231 (84%)	191 (98%)	4 (2%)	47	69
56	SC	188/225 (84%)	178 (95%)	10 (5%)	20	45
57	SD	190/202 (94%)	178 (94%)	12 (6%)	16	38
58	SE	224/225 (100%)	212 (95%)	12 (5%)	20	44
59	SF	159/170 (94%)	156 (98%)	3 (2%)	50	71
60	SG	207/218 (95%)	197 (95%)	10 (5%)	23	48
61	SH	166/174 (95%)	164 (99%)	2 (1%)	63	79
62	SI	178/180 (99%)	172 (97%)	6 (3%)	32	58
63	SJ	161/168 (96%)	155 (96%)	6 (4%)	30	55
64	SK	89/136 (65%)	84 (94%)	5 (6%)	19	43
65	SL	137/142 (96%)	127 (93%)	10 (7%)	13	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
66	SM	102/108 (94%)	100 (98%)	2 (2%)	48	71
67	SN	130/131 (99%)	129 (99%)	1 (1%)	73	85
68	SO	110/119 (92%)	104 (94%)	6 (6%)	19	43
69	SP	107/130 (82%)	105 (98%)	2 (2%)	50	71
70	SQ	119/121 (98%)	112 (94%)	7 (6%)	18	41
71	SR	122/122 (100%)	115 (94%)	7 (6%)	18	42
72	SS	126/132 (96%)	125 (99%)	1 (1%)	73	85
73	ST	113/115 (98%)	109 (96%)	4 (4%)	32	57
74	SU	94/107 (88%)	93 (99%)	1 (1%)	65	80
75	SV	67/67 (100%)	63 (94%)	4 (6%)	17	40
76	SW	112/113 (99%)	103 (92%)	9 (8%)	11	28
77	SX	113/115 (98%)	104 (92%)	9 (8%)	11	28
78	SY	113/115 (98%)	111 (98%)	2 (2%)	51	72
79	SZ	66/103 (64%)	64 (97%)	2 (3%)	36	60
80	Sa	89/98 (91%)	86 (97%)	3 (3%)	32	58
81	Sb	75/76 (99%)	73 (97%)	2 (3%)	39	64
82	Sc	57/62 (92%)	57 (100%)	0	100	100
83	Sd	48/49 (98%)	47 (98%)	1 (2%)	47	69
84	Se	47/104 (45%)	46 (98%)	1 (2%)	47	69
85	Sf	60/140 (43%)	58 (97%)	2 (3%)	33	58
86	Sg	272/275 (99%)	264 (97%)	8 (3%)	37	61
All	All	11336/12867 (88%)	10810 (95%)	526 (5%)	25	50

5 of 526 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
70	SQ	22	VAL
71	SR	130	THR
69	SP	126	VAL
86	Sg	26	GLN
21	LP	53	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 119 such sidechains are listed below:

Mol	Chain	Res	Type
36	Le	101	HIS
77	SX	127	ASN
50	NA	69	GLN
77	SX	92	ASN
86	Sg	181	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	CC	84/85 (98%)	22 (26%)	1 (1%)
4	L5	3704/5070 (73%)	977 (26%)	15 (0%)
5	L7	119/121 (98%)	17 (14%)	0
53	S2	1715/1869 (91%)	474 (27%)	4 (0%)
6	L8	155/157 (98%)	38 (24%)	0
All	All	5777/7302 (79%)	1528 (26%)	20 (0%)

5 of 1528 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	CC	7	G
2	CC	8	U
2	CC	9	G
2	CC	10	G
2	CC	14	A

5 of 20 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
4	L5	4699	U
53	S2	291	G
53	S2	1434	C
53	S2	688	U
4	L5	1977	C

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.

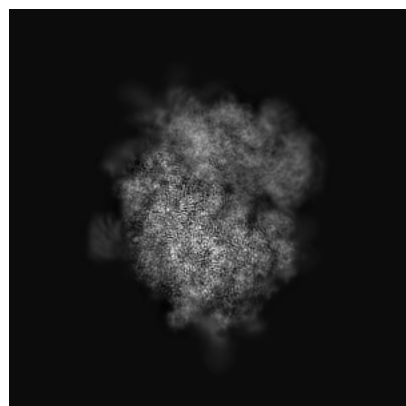
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-52582. These allow visual inspection of the internal detail of the map and identification of artifacts.

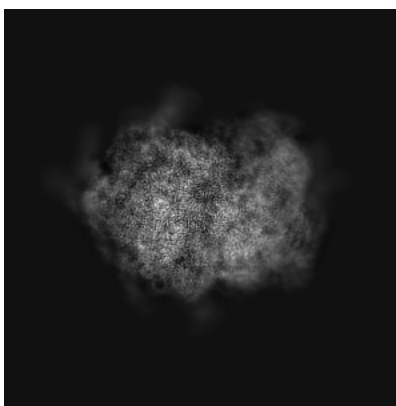
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

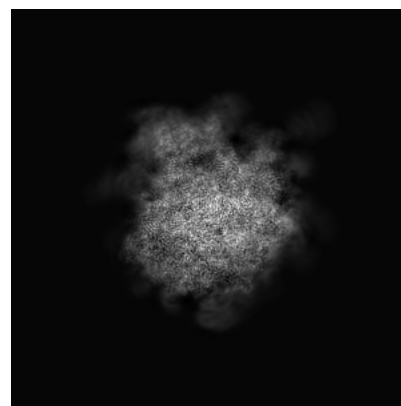
6.1.1 Primary map



X

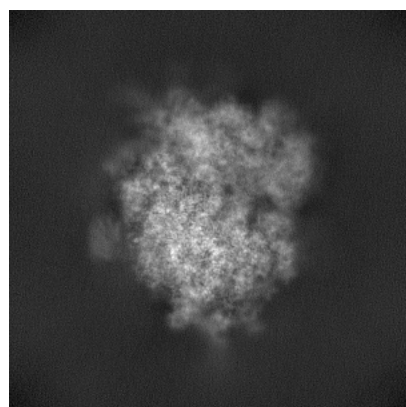


Y

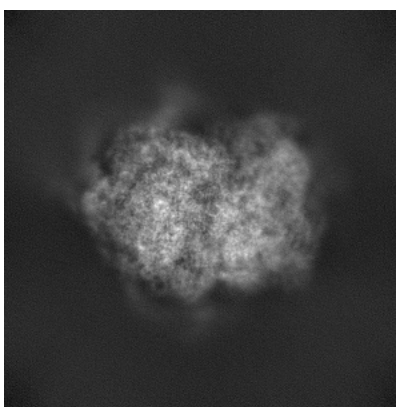


Z

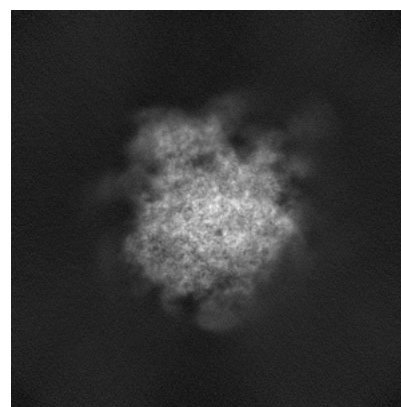
6.1.2 Raw map



X



Y

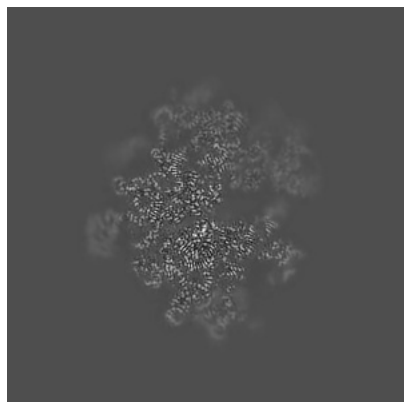


Z

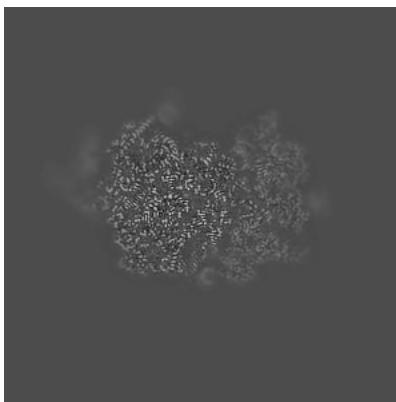
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

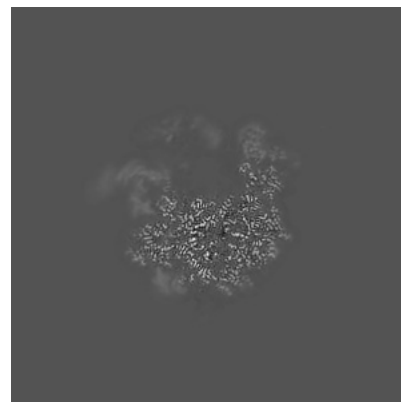
6.2.1 Primary map



X Index: 225

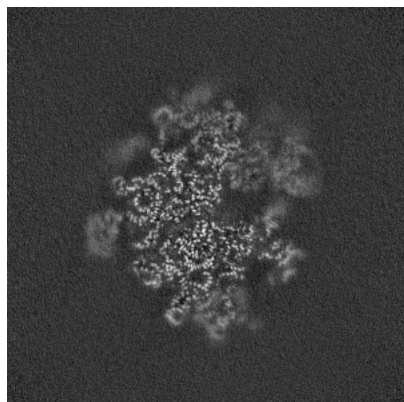


Y Index: 225

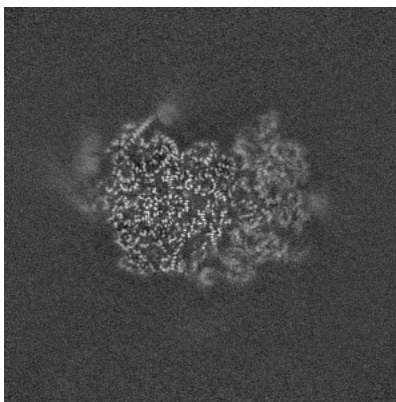


Z Index: 225

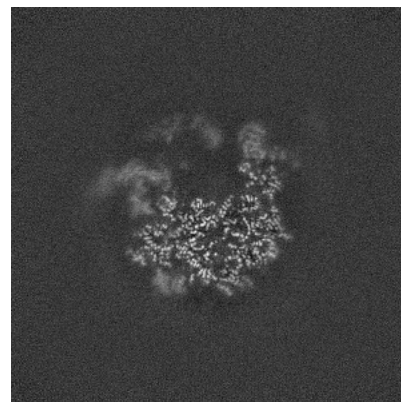
6.2.2 Raw map



X Index: 225



Y Index: 225

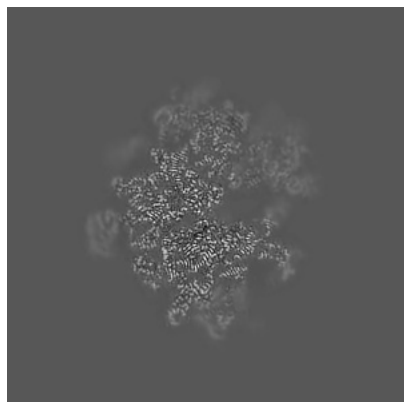


Z Index: 225

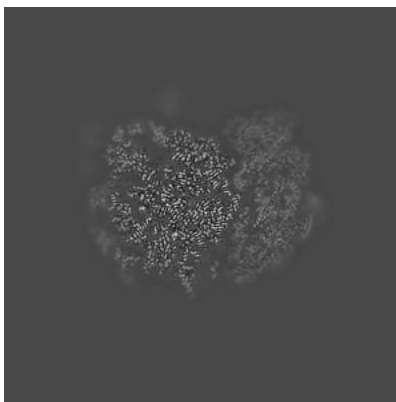
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

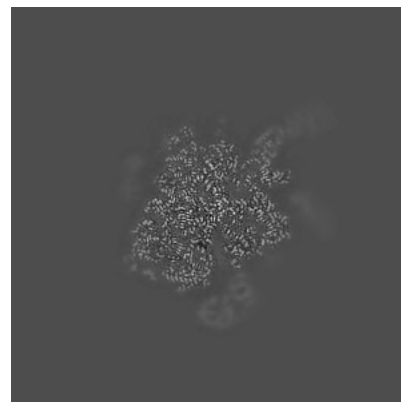
6.3.1 Primary map



X Index: 223

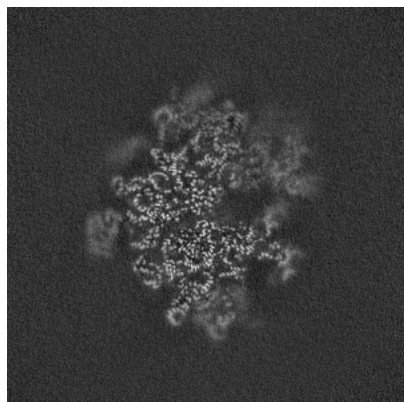


Y Index: 212

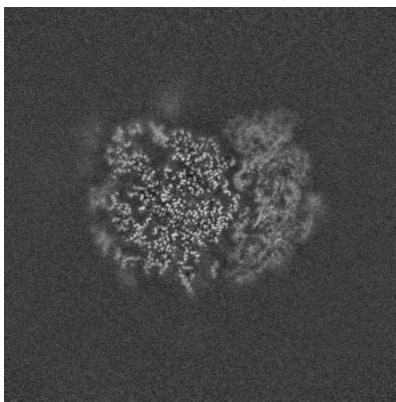


Z Index: 192

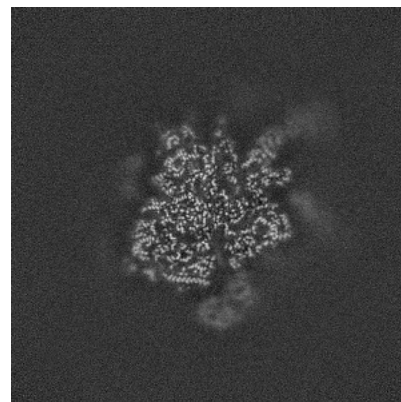
6.3.2 Raw map



X Index: 224



Y Index: 212

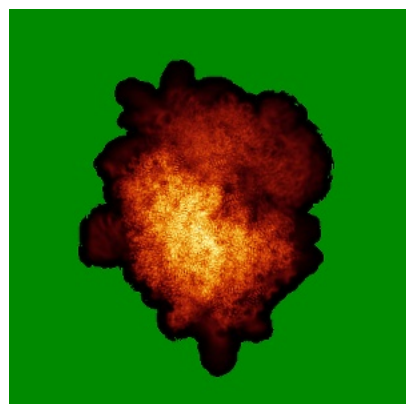


Z Index: 190

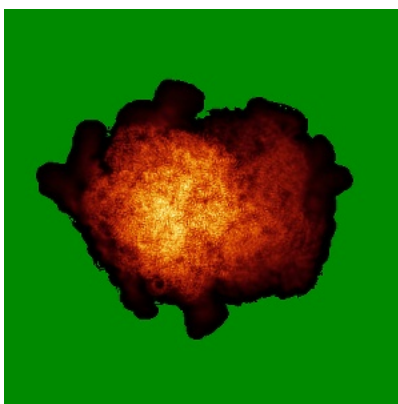
The images above show the largest variance slices of the map in three orthogonal directions.

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

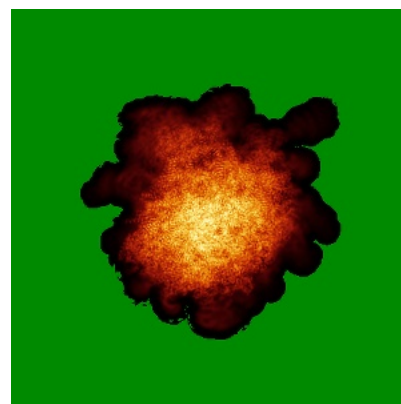
6.4.1 Primary map



X

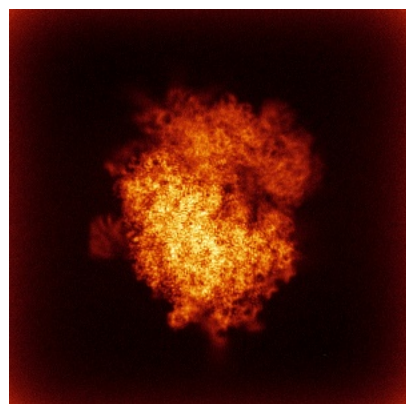


Y

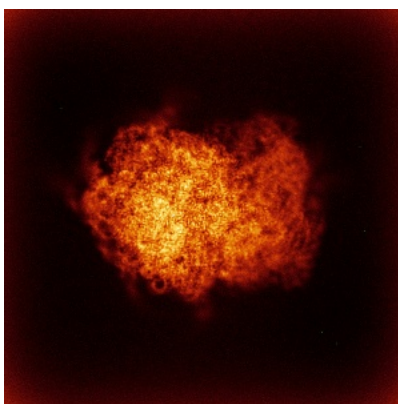


Z

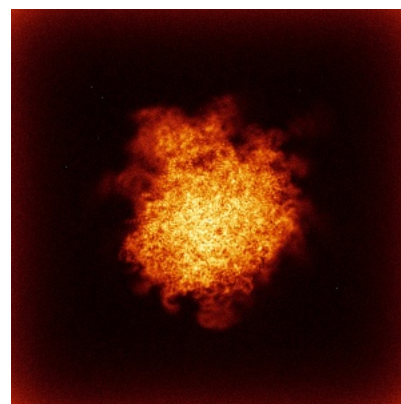
6.4.2 Raw map



X



Y

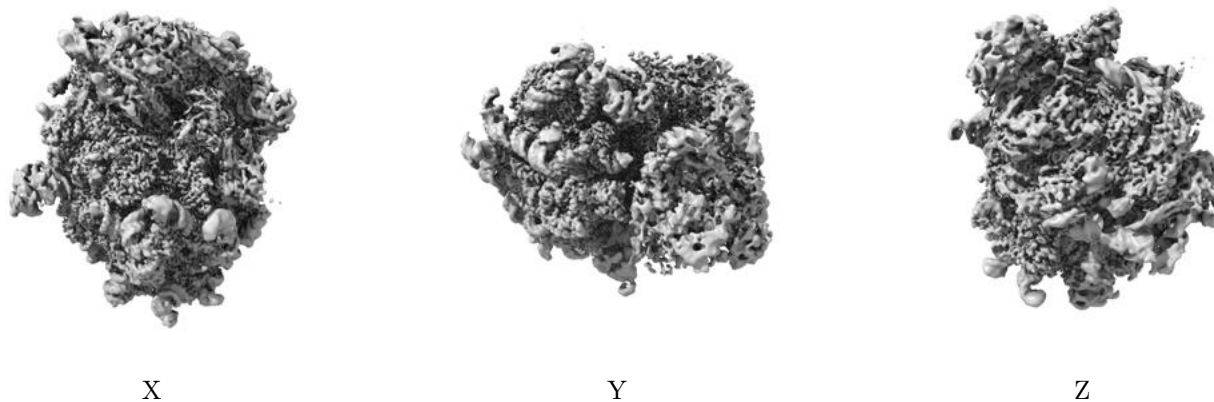


Z

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.

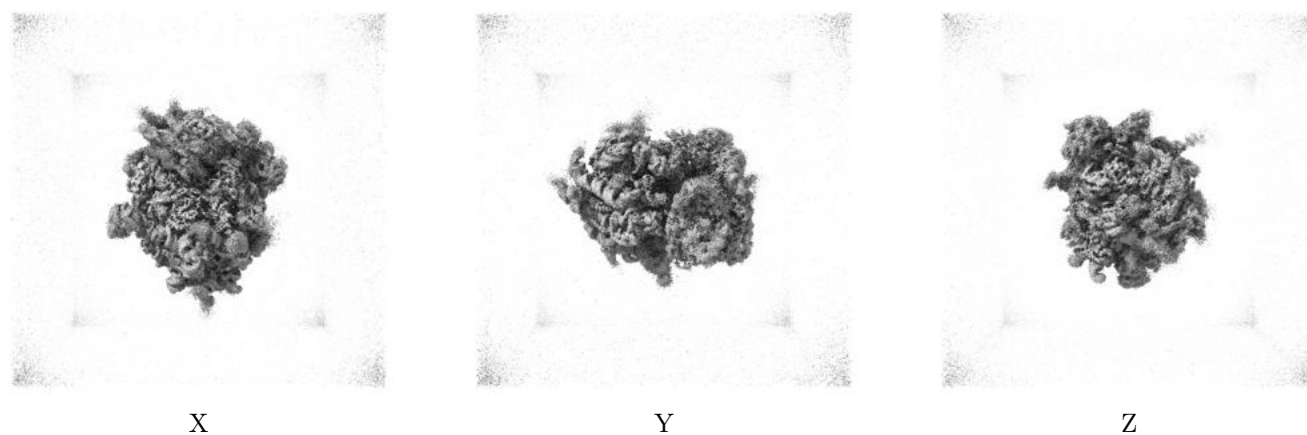
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.35. 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.

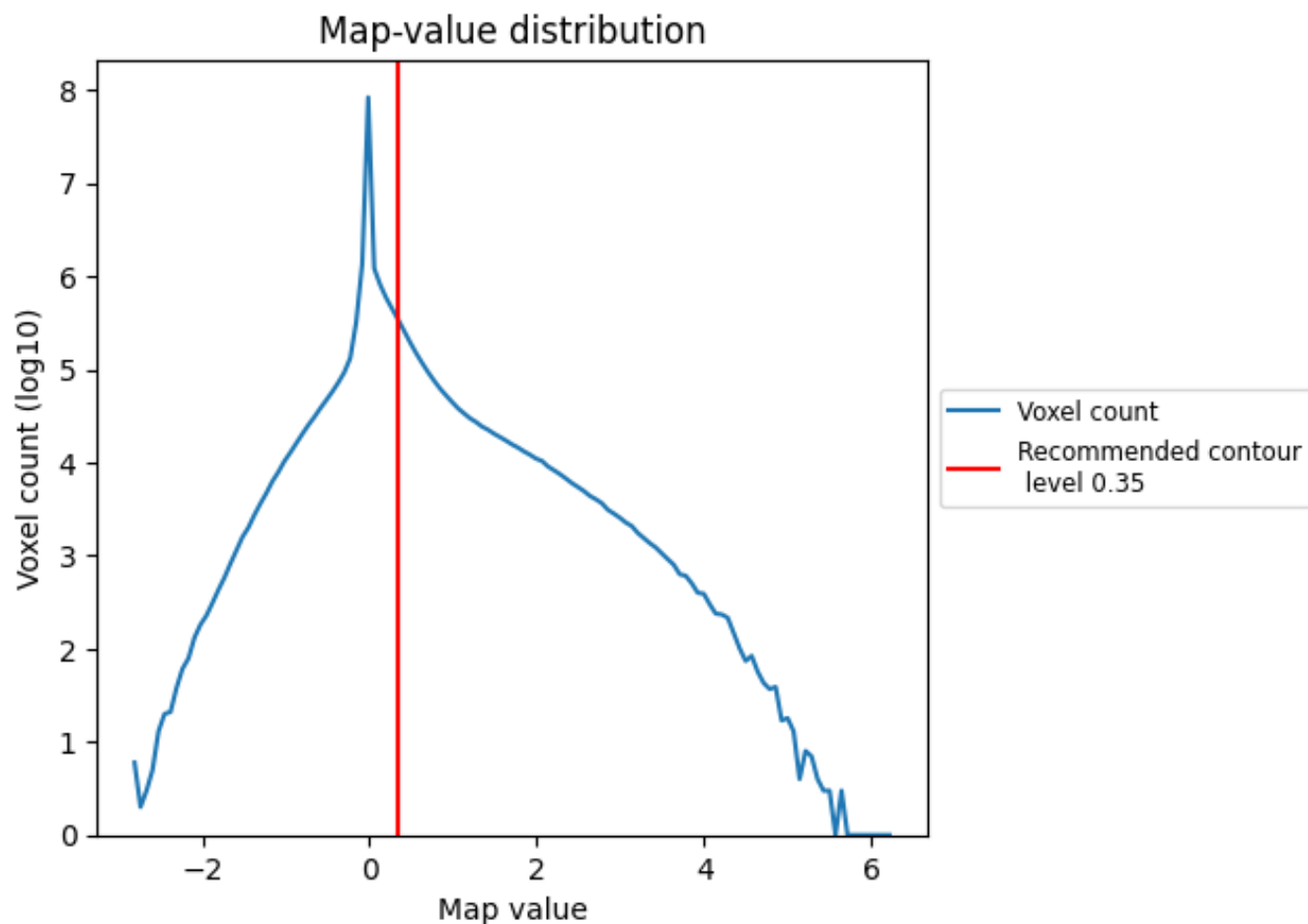
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

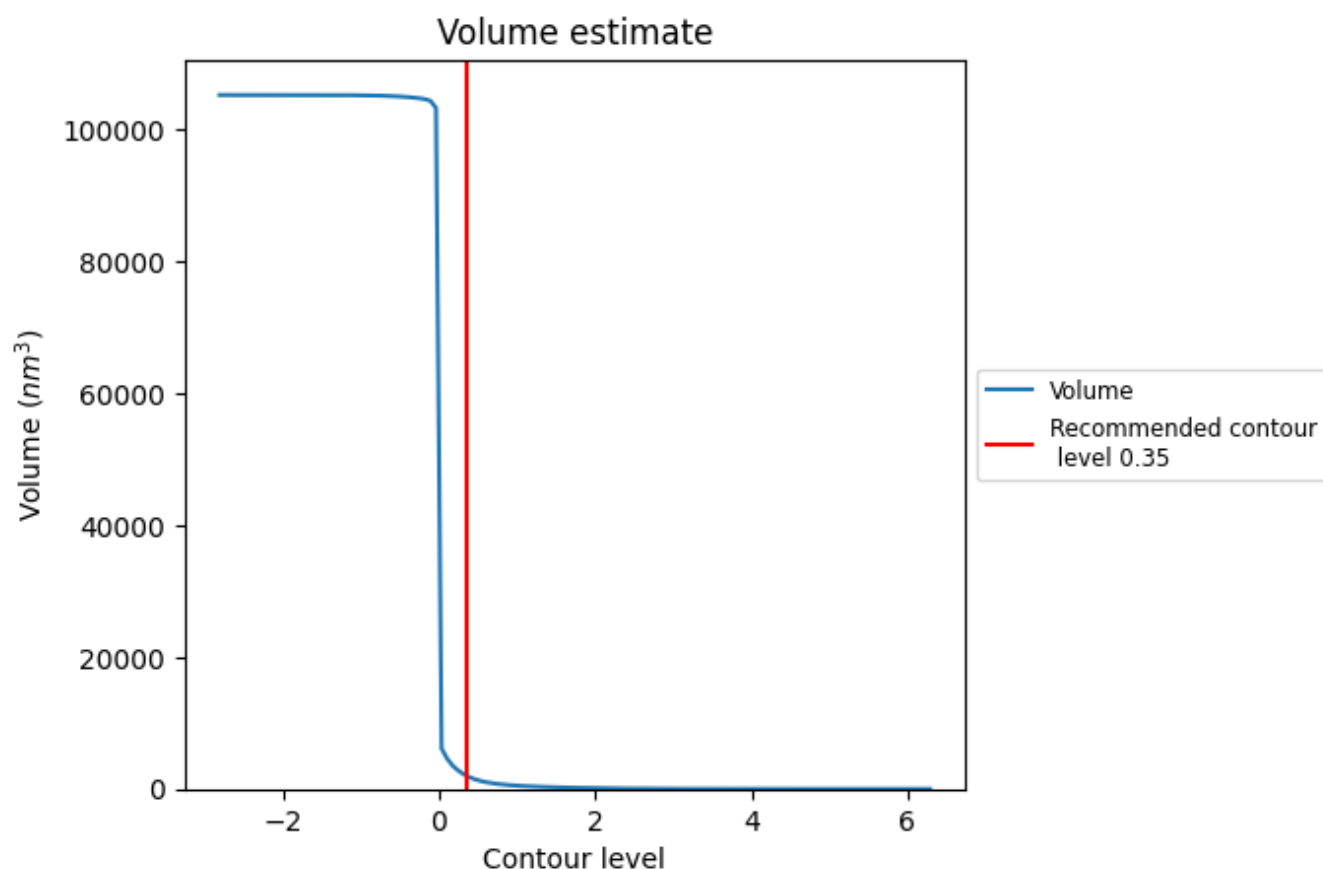
This section contains the results of statistical analysis of the map.

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.

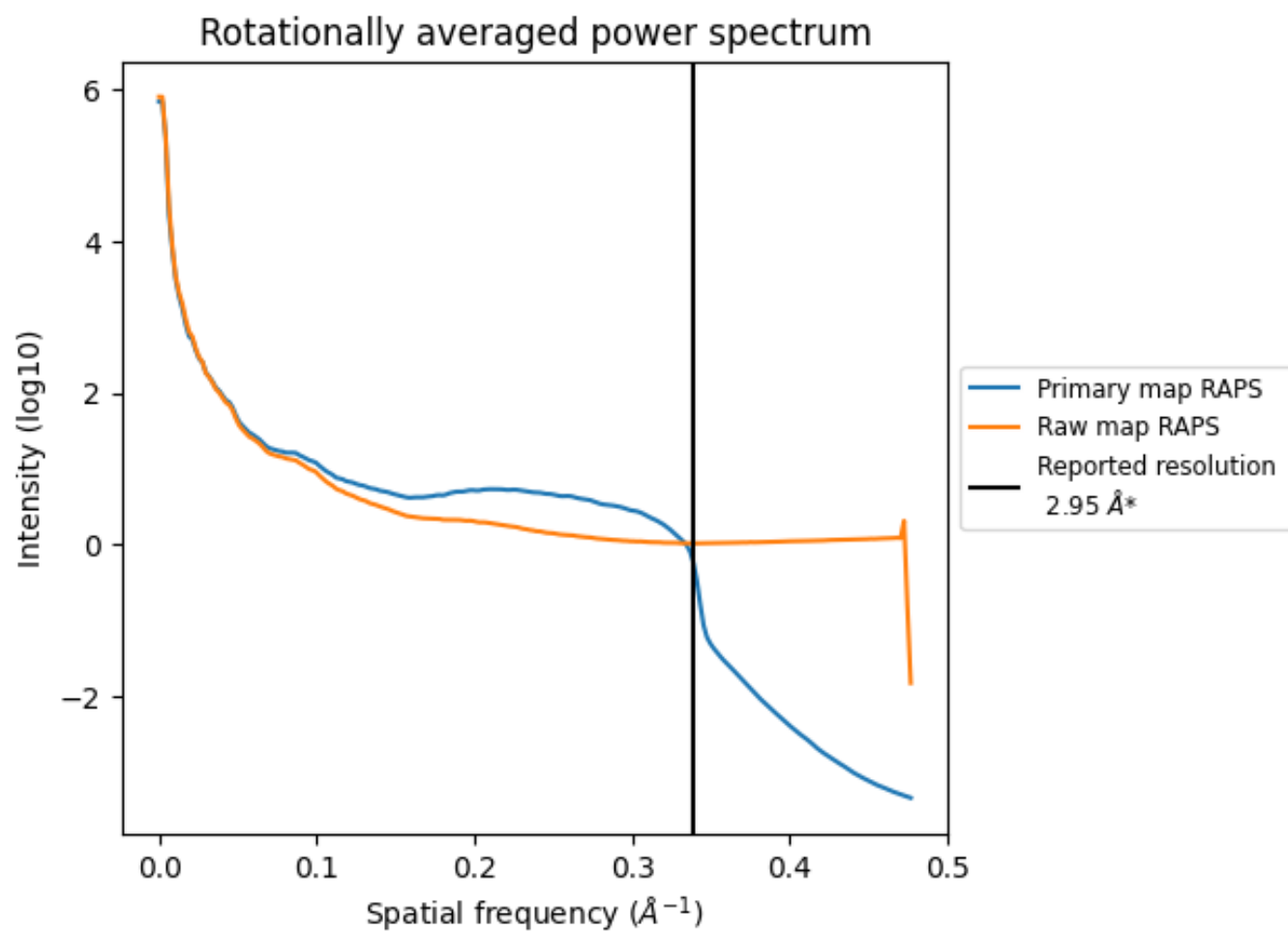
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2031 nm³; this corresponds to an approximate mass of 1834 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 ⓘ

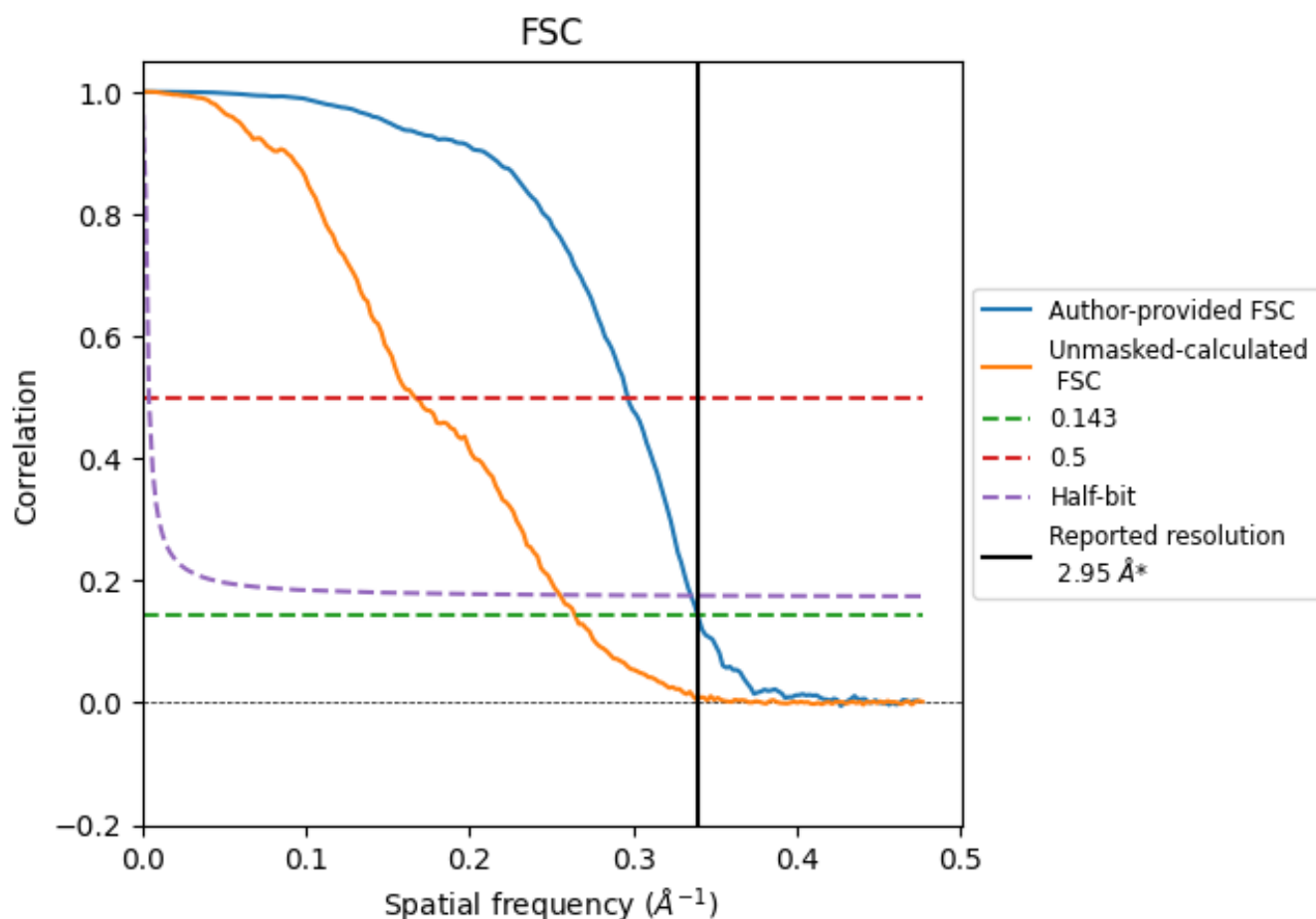


*Reported resolution corresponds to spatial frequency of 0.339 \AA^{-1}

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.339 Å⁻¹

8.2 Resolution estimates [i](#)

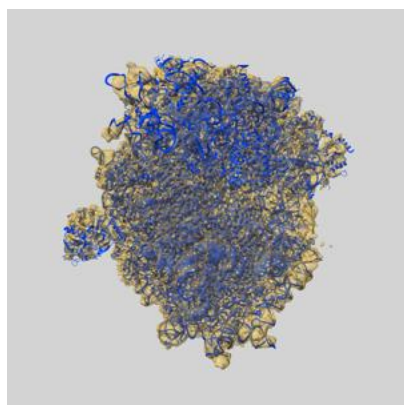
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.95	-	-
Author-provided FSC curve	2.95	3.37	2.98
Unmasked-calculated*	3.78	6.00	3.92

*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 3.78 differs from the reported value 2.95 by more than 10 %

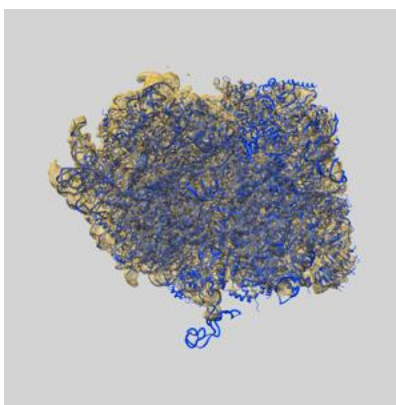
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-52582 and PDB model 9I2E. Per-residue inclusion information can be found in section 3 on page 21.

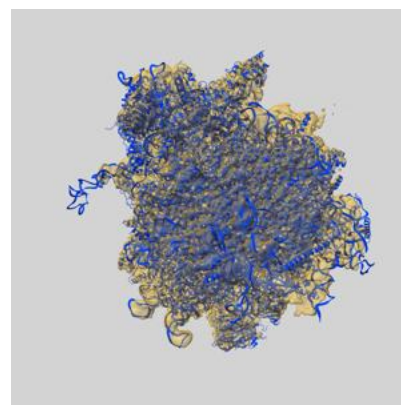
9.1 Map-model overlay [i](#)



X



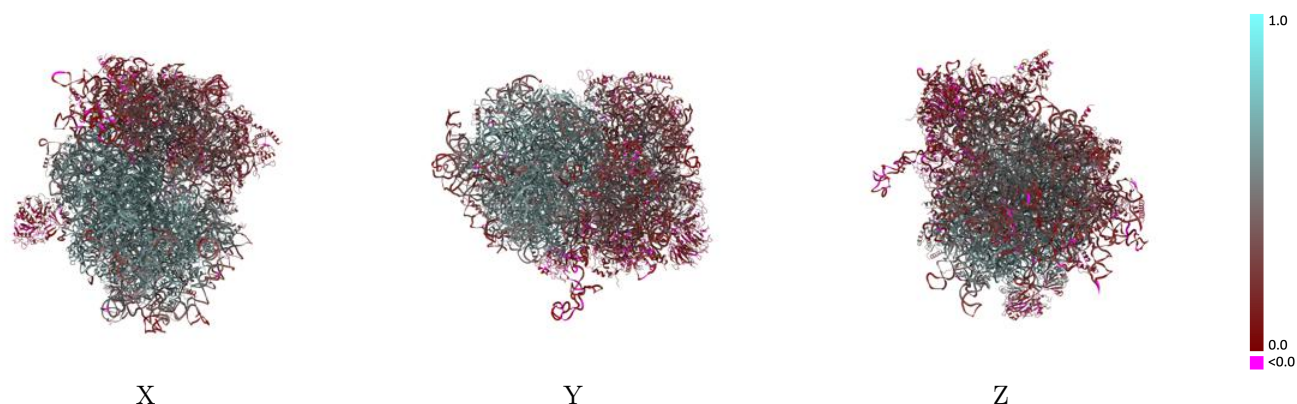
Y



Z

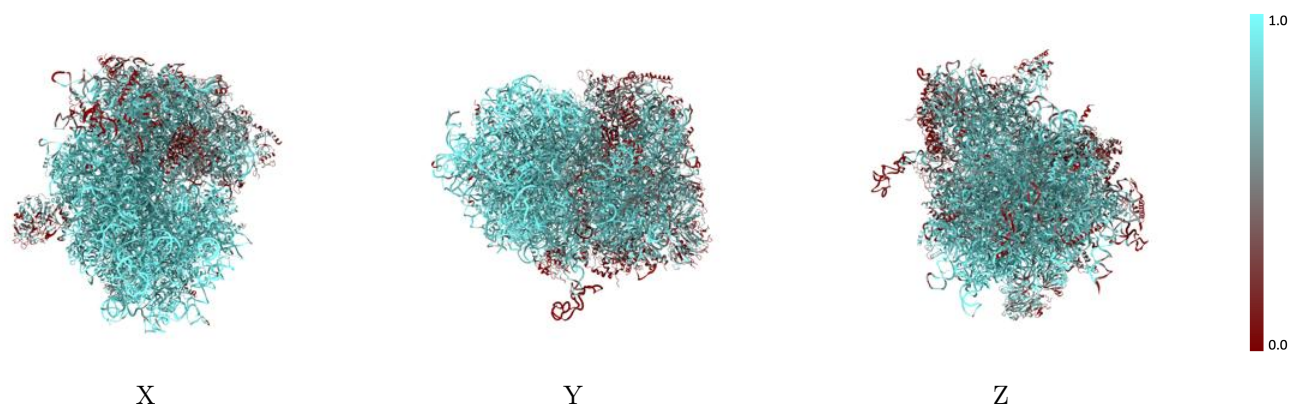
The images above show the 3D surface view of the map at the recommended contour level 0.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



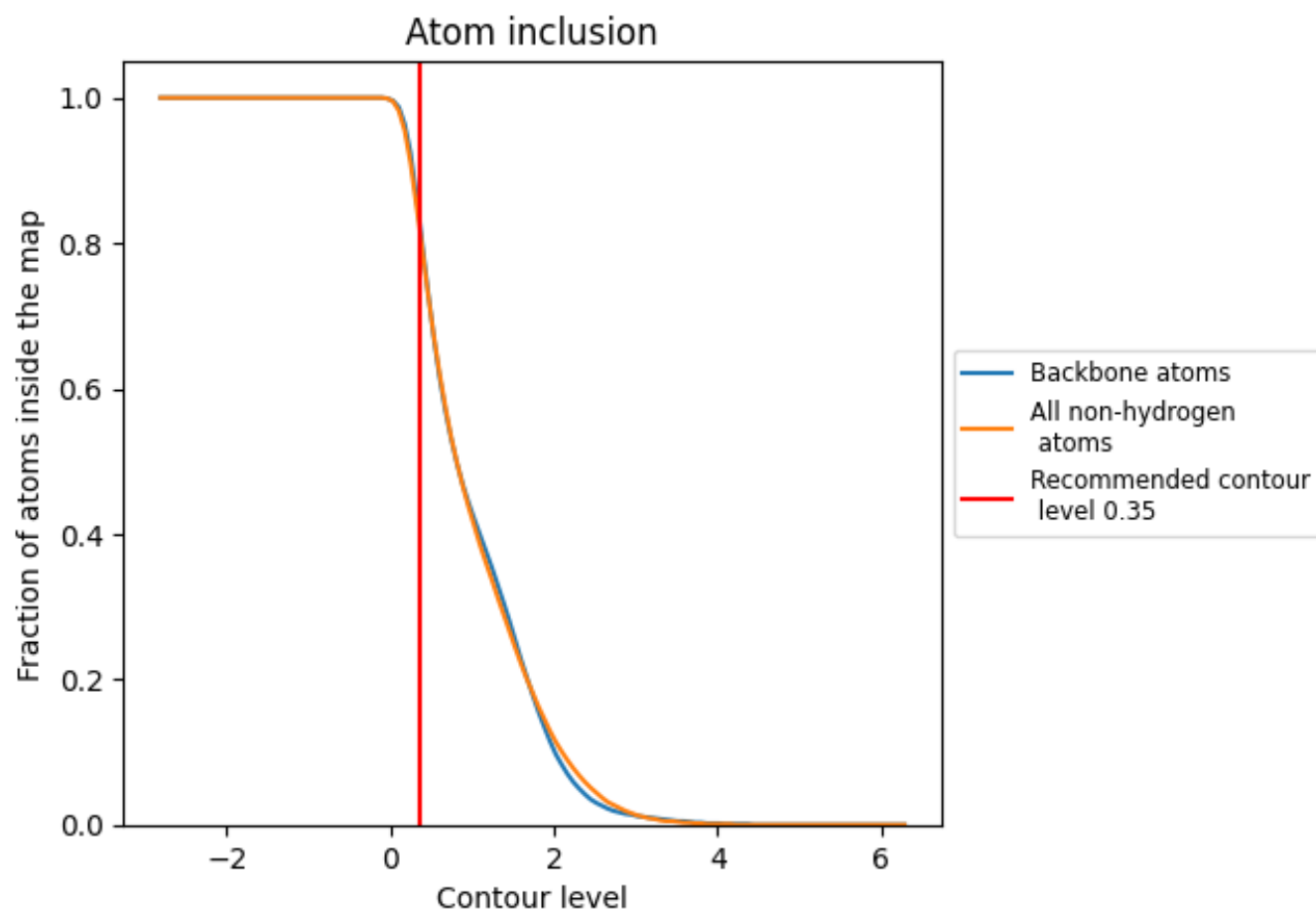
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.35).







































































9.4 Atom inclusion ⓘ



At the recommended contour level, 84% of all backbone atoms, 83% 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 (0.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8270	 0.4360
CB	 0.3630	 0.3030
CC	 0.7040	 0.2800
CD	 0.4860	 0.3230
L5	 0.9510	 0.5240
L7	 0.9910	 0.5690
L8	 0.9680	 0.5590
LA	 0.9670	 0.6040
LB	 0.9370	 0.5740
LC	 0.9410	 0.5700
LD	 0.9260	 0.5050
LE	 0.8620	 0.4850
LF	 0.9640	 0.5850
LG	 0.8600	 0.4920
LH	 0.9430	 0.5540
LI	 0.9490	 0.5780
LJ	 0.8210	 0.4300
LL	 0.9030	 0.5380
LM	 0.9530	 0.5440
LN	 0.9840	 0.6140
LO	 0.9420	 0.5810
LP	 0.9680	 0.6000
LQ	 0.9700	 0.6030
LR	 0.8770	 0.5160
LS	 0.9730	 0.5970
LT	 0.9450	 0.5650
LU	 0.8900	 0.4930
LV	 0.9440	 0.5950
LW	 0.5970	 0.3920
LX	 0.9340	 0.5630
LY	 0.9300	 0.5540
LZ	 0.9400	 0.5320
La	 0.9650	 0.5970
Lb	 0.8910	 0.4970
Lc	 0.9260	 0.5300























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Chain	Atom inclusion	Q-score
Ld	 0.9250	 0.5530
Le	 0.9760	 0.6080
Lf	 0.9760	 0.6060
Lg	 0.9390	 0.5720
Lh	 0.9340	 0.5550
Li	 0.9340	 0.5530
Lj	 0.9750	 0.6070
Lk	 0.8800	 0.4860
Ll	 0.9600	 0.5920
Lm	 0.9470	 0.5820
Ln	 0.8660	 0.5090
Lo	 0.9230	 0.5710
Lp	 0.9230	 0.5790
Lr	 0.9600	 0.5740
Lz	 0.2010	 0.0730
NA	 0.2990	 0.1220
NB	 0.3500	 0.2070
NM	 0.5060	 0.1400
S2	 0.8210	 0.3350
SA	 0.7050	 0.2790
SB	 0.5830	 0.2990
SC	 0.7610	 0.3620
SD	 0.5540	 0.2410
SE	 0.6790	 0.2770
SF	 0.3580	 0.1960
SG	 0.4640	 0.2010
SH	 0.5170	 0.2060
SI	 0.6040	 0.2710
SJ	 0.7350	 0.2970
SK	 0.6210	 0.2160
SL	 0.6900	 0.3400
SM	 0.4810	 0.1290
SN	 0.6770	 0.3500
SO	 0.7100	 0.3240
SP	 0.5510	 0.2110
SQ	 0.4640	 0.1790
SR	 0.5020	 0.2070
SS	 0.4620	 0.1920
ST	 0.4880	 0.1900
SU	 0.5970	 0.2190
SV	 0.6430	 0.2760
SW	 0.7420	 0.3660

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Chain	Atom inclusion	Q-score
SX	 0.7720	 0.4400
SY	 0.4800	 0.2280
SZ	 0.1820	 0.1900
Sa	 0.7200	 0.3820
Sb	 0.6090	 0.2530
Sc	 0.1830	 0.1860
Sd	 0.8100	 0.3140
Se	 0.5450	 0.3280
Sf	 0.3150	 0.1520
Sg	 0.4630	 0.1450