



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 02:50 PM UTC

PDB ID : 9M0P / pdb_00009m0p
EMDB ID : EMD-63560
Title : Cryo-EM structure of human 80S ribosome in complex with montanine
Authors : Sakai, R.; Tanaka, Y.; Sato, K.; Tsugita, A.; Matumoto, K.; Thaveepornkul, L.; Chimnaronk, S.; Takada, A.; Miyamoto, H.; Kurokawa, R.; Yoshida, M.; Yokoyama, T.; Evidente, A.; Tsuge, Y.; Watari, H.; Sumiya, T.
Deposited on : 2025-02-25
Resolution : 2.78 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
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

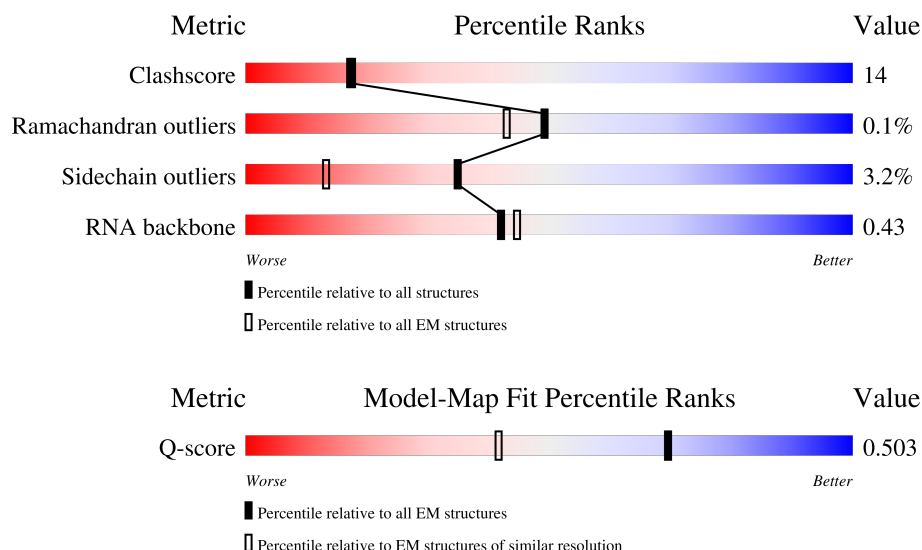
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.78 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	10754 (2.28 - 3.28)

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	SL	158	
2	SR	135	
3	SP	145	

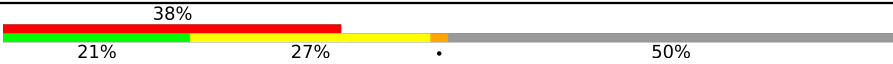
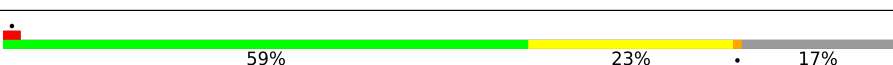
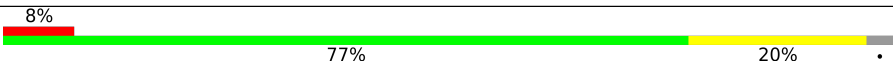
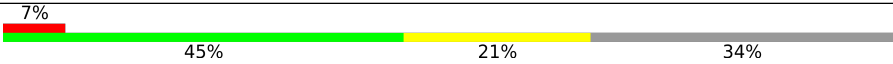
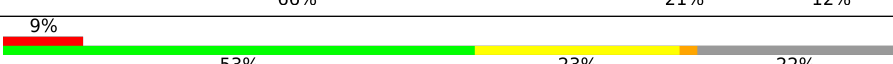
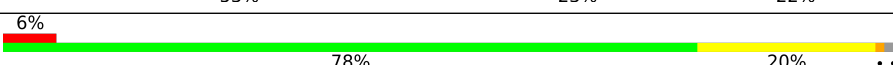
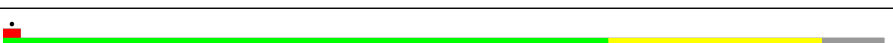
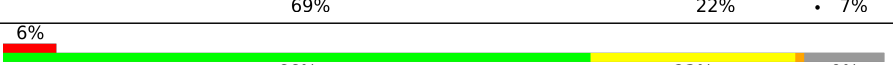
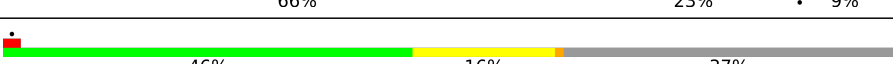
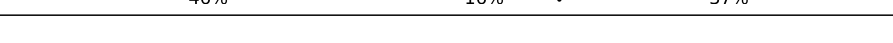
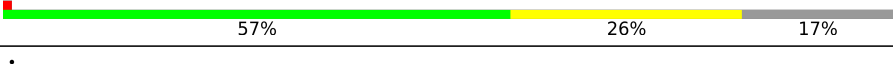
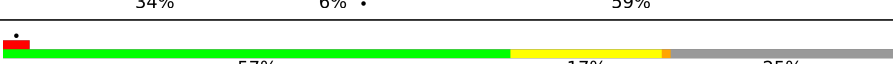
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Mol	Chain	Length	Quality of chain
4	SQ	146	
5	SV	83	
6	SX	143	
7	Sa	115	
8	SU	119	
9	Sc	69	
10	ST	145	
11	Sg	317	
12	SC	293	
13	Sd	56	
14	SJ	194	
15	SN	151	
16	SO	151	
17	SG	249	
18	SW	130	
19	SY	133	
20	Se	59	
21	Sb	84	
22	SZ	125	
23	SA	295	
24	SB	264	
25	SE	263	
26	SD	243	
27	SH	194	
28	SI	208	

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Mol	Chain	Length	Quality of chain
29	SK	165	
30	SF	204	
31	LA	257	
32	LB	403	
33	LC	427	
34	LD	297	
35	LE	288	
36	LF	248	
37	LG	266	
38	LH	192	
39	LI	214	
40	LJ	178	
41	LL	211	
42	LM	215	
43	LN	204	
44	LO	203	
45	LP	184	
46	LQ	188	
47	LR	196	
48	LS	176	
49	LT	160	
50	LU	128	
51	LV	140	
52	LW	157	
53	LX	156	

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Mol	Chain	Length	Quality of chain
54	LY	145	
55	LZ	136	
56	La	148	
57	Lb	159	
58	Lc	115	
59	Ld	125	
60	Le	135	
61	Lf	110	
62	Lg	117	
63	Lh	123	
64	Li	105	
65	Lj	97	
66	Lk	70	
67	Ll	51	
68	Lm	128	
69	Ln	25	
70	Lo	106	
71	Lp	92	
72	Lr	137	
73	L5	5070	
74	L7	121	
75	L8	157	
76	S2	1869	
77	S6	75	
78	CA	858	

2 Entry composition

There are 81 unique types of molecules in this entry. The entry contains 202018 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 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	SL	133	Total	C	N	O	S	0	0
			1099	700	206	187	6		

- Molecule 2 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	SR	108	Total	C	N	O	S	0	0
			883	556	161	163	3		

- Molecule 3 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	SP	58	Total	C	N	O	S	0	0
			494	306	102	83	3		

- Molecule 4 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	SQ	141	Total	C	N	O	S	0	0
			1124	715	212	194	3		

- Molecule 5 is a protein called 40S ribosomal protein S21.

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

- Molecule 6 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	SX	137	Total	C	N	O	S	0	0
			1060	671	209	177	3		

- Molecule 7 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	Sa	96	Total	C	N	O	S	0	0
			767	476	159	127	5		

- Molecule 8 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	SU	69	Total	C	N	O	S	0	0
			554	346	109	95	4		

- Molecule 9 is a protein called 40S ribosomal protein S28.

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

- Molecule 10 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	ST	138	Total	C	N	O	S	0	0
			1078	675	208	192	3		

- Molecule 11 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 12 is a protein called 40S ribosomal protein S2.

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

- Molecule 13 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	Sd	44	Total	C	N	O	S	0	0
			361	224	76	56	5		

- Molecule 14 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	SJ	179	Total	C	N	O	S	0	0
			1495	953	299	241	2		

- Molecule 15 is a protein called 40S ribosomal protein S13.

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

- Molecule 16 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	SO	128	Total	C	N	O	S	0	0
			961	587	190	178	6		

- Molecule 17 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	SG	230	Total	C	N	O	S	0	0
			1862	1164	371	320	7		

- Molecule 18 is a protein called 40S ribosomal protein S15a.

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

- Molecule 19 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SY	125	Total	C	N	O	S	0	0
			1015	642	199	169	5		

- Molecule 20 is a protein called 40S ribosomal protein S30.

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

- Molecule 21 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Sb	81	Total	C	N	O	S	0	0
			631	397	116	111	7		

- Molecule 22 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	SZ	66	Total	C	N	O	S	0	0
			523	338	93	91	1		

- Molecule 23 is a protein called Small ribosomal subunit protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	SA	180	Total	C	N	O	S	0	0
			1436	916	256	257	7		

- Molecule 24 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SB	211	Total	C	N	O	S	0	0
			1715	1088	307	306	14		

- Molecule 25 is a protein called 40S ribosomal protein S4, X isoform.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SE	258	Total	C	N	O	S	0	0
			2050	1311	381	350	8		

- Molecule 26 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SD	211	Total	C	N	O	S	0	0
			1641	1047	298	289	7		

- Molecule 27 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SH	184	Total	C	N	O	S	0	0
			1481	943	273	264	1		

- Molecule 28 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	SI	184	Total	C	N	O	S	0	0
			1510	949	297	259	5		

- Molecule 29 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SK	82	Total	C	N	O	S	0	0
			697	456	121	114	6		

- Molecule 30 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	SF	179	Total	C	N	O	S	0	0
			1419	890	265	257	7		

- Molecule 31 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	LA	245	Total	C	N	O	S	0	0
			1876	1177	383	310	6		

- Molecule 32 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	LB	395	Total	C	N	O	S	0	0
			3189	2030	600	545	14		

- Molecule 33 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	LC	354	Total	C	N	O	S	0	0
			2830	1782	566	469	13		

- Molecule 34 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	LD	287	Total	C	N	O	S	0	0
			2332	1476	423	419	14		

- Molecule 35 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	LE	190	Total	C	N	O	S	0	0
			1547	999	293	251	4		

- Molecule 36 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	LF	217	Total	C	N	O	S	0	0
			1803	1157	347	290	9		

- Molecule 37 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	LG	207	Total	C	N	O	S	0	0
			1673	1069	318	282	4		

- Molecule 38 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	LH	189	Total	C	N	O	S	0	0
			1513	953	283	271	6		

- Molecule 39 is a protein called 60S ribosomal protein L10-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	LI	199	Total	C	N	O	S	0	0
			1615	1027	311	264	13		

- Molecule 40 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	LJ	165	Total	C	N	O	S	0	0
			1324	837	248	233	6		

- Molecule 41 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	LL	191	Total	C	N	O	S	0	0
			1553	975	328	246	4		

- Molecule 42 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	LM	135	Total	C	N	O	S	0	0
			1111	713	213	178	7		

- Molecule 43 is a protein called 60S ribosomal protein L15.

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

- Molecule 44 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	LO	199	Total	C	N	O	S	0	0
			1634	1053	319	257	5		

- Molecule 45 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	LP	152	Total	C	N	O	S	0	0
			1233	771	240	213	9		

- Molecule 46 is a protein called 60S ribosomal protein L18.

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

- Molecule 47 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	LR	173	Total	C	N	O	S	0	0
			1448	896	315	228	9		

- Molecule 48 is a protein called 60S ribosomal protein L18a.

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

- Molecule 49 is a protein called 60S ribosomal protein L21.

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

- Molecule 50 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	LU	99	Total	C	N	O	S	0	0
			808	518	141	147	2		

- Molecule 51 is a protein called 60S ribosomal protein L23.

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

- Molecule 52 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	LW	64	Total	C	N	O	S	0	0
			534	340	104	87	3		

- Molecule 53 is a protein called 60S ribosomal protein L23a.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LX	117	Total	C	N	O	S	0	0
			958	612	180	165	1		

- Molecule 54 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	LY	131	Total	C	N	O	S	0	0
			1093	686	221	183	3		

- Molecule 55 is a protein called 60S ribosomal protein L27.

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

- Molecule 56 is a protein called 60S ribosomal protein L27a.

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

- Molecule 57 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	Lb	66	Total	C	N	O	S	0	0
			543	335	117	88	3		

- Molecule 58 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	Lc	93	Total	C	N	O	S	0	0
			721	459	126	130	6		

- Molecule 59 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	Ld	106	Total	C	N	O	S	0	0
			879	555	170	152	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Le	127	Total	C	N	O	S	0	0
			1048	664	215	164	5		

- Molecule 61 is a protein called 60S ribosomal protein L35a.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Lf	108	Total	C	N	O	S	0	0
			870	552	173	142	3		

- Molecule 62 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Lg	106	Total	C	N	O	S	0	0
			845	530	174	135	6		

- Molecule 63 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	Lh	120	Total	C	N	O	S	0	0
			1001	632	202	166	1		

- Molecule 64 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	Li	100	Total	C	N	O	S	0	0
			818	512	174	127	5		

- Molecule 65 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	Lj	85	Total	C	N	O	S	0	0
			696	428	153	110	5		

- Molecule 66 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Lk	68	Total	C	N	O	S	0	0
			559	360	101	97	1		

- Molecule 67 is a protein called 60S ribosomal protein L39.

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

- Molecule 68 is a protein called Ubiquitin-60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Lm	51	Total	C	N	O	S	0	0
			419	260	88	65	6		

- Molecule 69 is a protein called 60S ribosomal protein L41.

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

- Molecule 70 is a protein called 60S ribosomal protein L36a.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Lo	102	Total	C	N	O	S	0	0
			834	522	171	135	6		

- Molecule 71 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Lp	89	Total	C	N	O	S	0	0
			690	436	133	114	7		

- Molecule 72 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Lr	124	Total	C	N	O	S	0	0
			995	617	206	167	5		

- Molecule 73 is a RNA chain called 28S ribosomal RNA|HOMO SAPIENS.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	L5	3292	Total	C	N	O	P	0	0
			70611	31452	12942	22925	3292		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
L5	4942	G	C	conflict	GB 86475748
L5	4943	C	A	conflict	GB 86475748

- Molecule 74 is a RNA chain called 5S ribosomal RNA|HOMO SAPIENS.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	L7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 75 is a RNA chain called 5.8S ribosomal RNA|HOMO SAPIENS.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	L8	151	Total	C	N	O	P	0	0
			3214	1434	570	1059	151		

- Molecule 76 is a RNA chain called 18S ribosomal RNA|HOMO SAPIENS.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	S2	1625	Total	C	N	O	P	0	0
			34646	15464	6230	11328	1624		

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	582	C	U	conflict	GB 36162
S2	583	C	A	conflict	GB 36162
S2	584	G	A	conflict	GB 36162
S2	798	A	G	conflict	GB 36162
S2	1095	U	C	conflict	GB 36162

- Molecule 77 is a RNA chain called HUMAN INITIATOR MET-TRNA-I|HOMO SAPIENS.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	S6	75	Total	C	N	O	P	0	0
			1604	717	298	515	74		

- Molecule 78 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	CA	550	Total	C	N	O	S	0	0
			4327	2756	747	798	26		

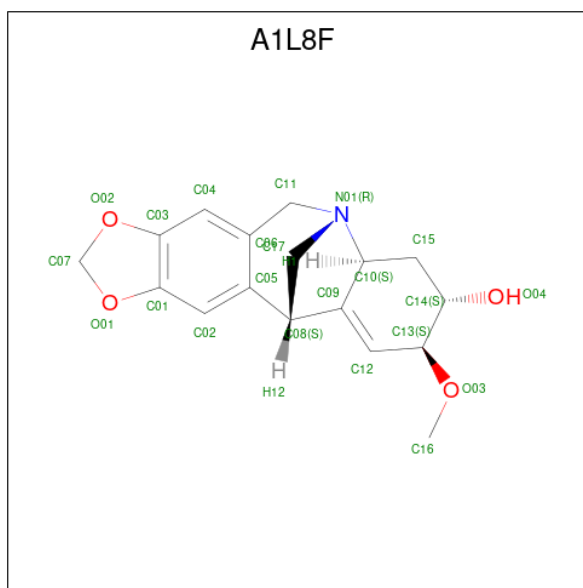
- Molecule 79 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
79	SX	1	Total	Mg	0
			1	1	
79	LA	3	Total	Mg	0
			3	3	
79	LN	1	Total	Mg	0
			1	1	
79	LO	1	Total	Mg	0
			1	1	
79	L5	234	Total	Mg	0
			234	234	
79	L7	10	Total	Mg	0
			10	10	
79	L8	6	Total	Mg	0
			6	6	
79	S2	35	Total	Mg	0
			35	35	

- Molecule 80 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 81 is (1S,13S,15S,16S)-16-methoxy-5,7-dioxa-12-azapentacyclo[10.6.1.0²,10.0⁴,8.0¹³,18]nonadeca-2,4(8),9,17-tetraen-15-ol (CCD ID: A1L8F) (formula: C₁₇H₁₉NO₄) (labeled as "Ligand of Interest" by depositor).

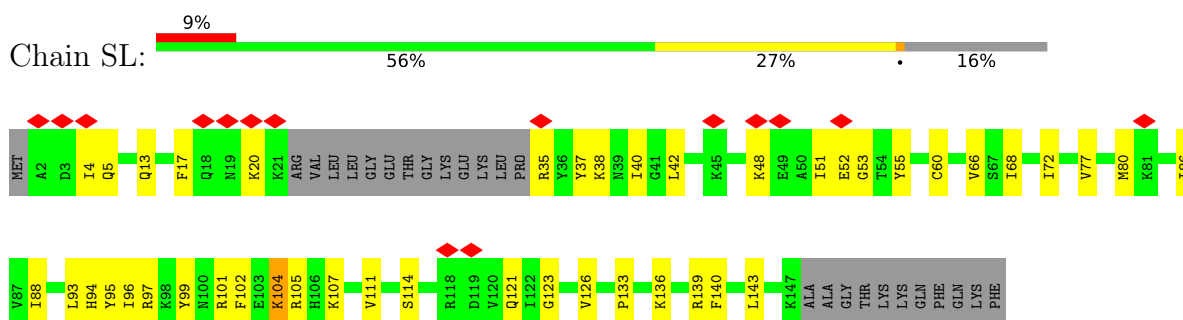


Mol	Chain	Residues	Atoms				AltConf
81	L5	1	Total	C	N	O	0
			22	17	1	4	

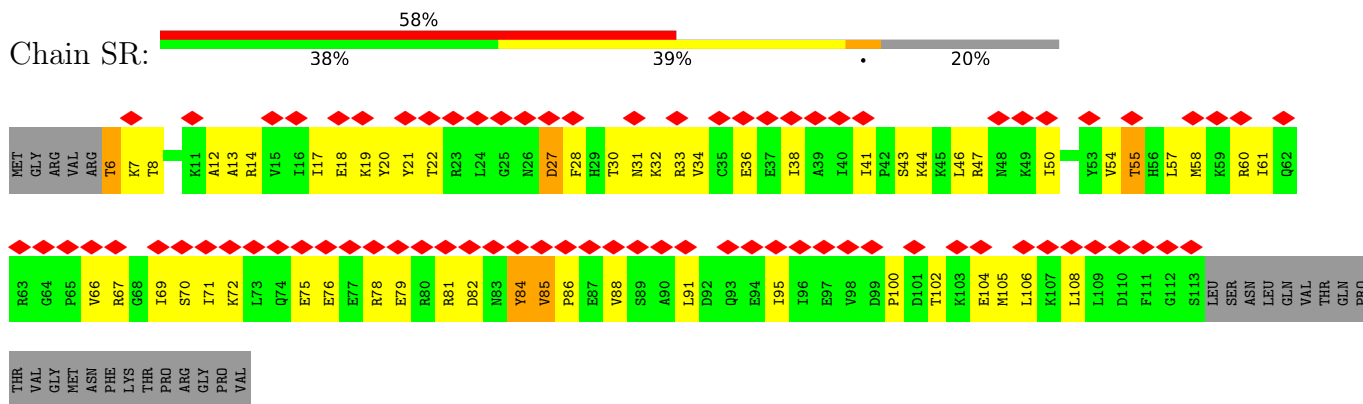
3 Residue-property plots [i](#)

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.

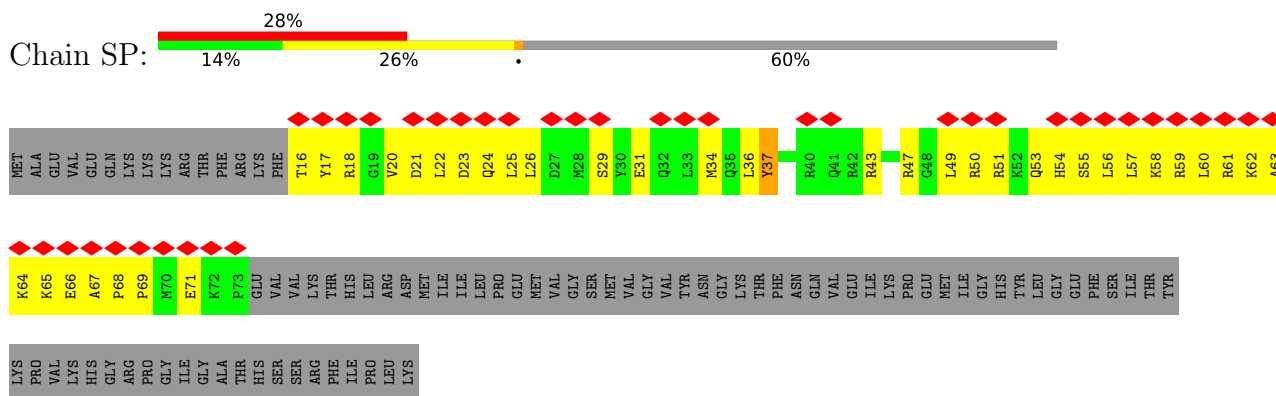
- Molecule 1: 40S ribosomal protein S11



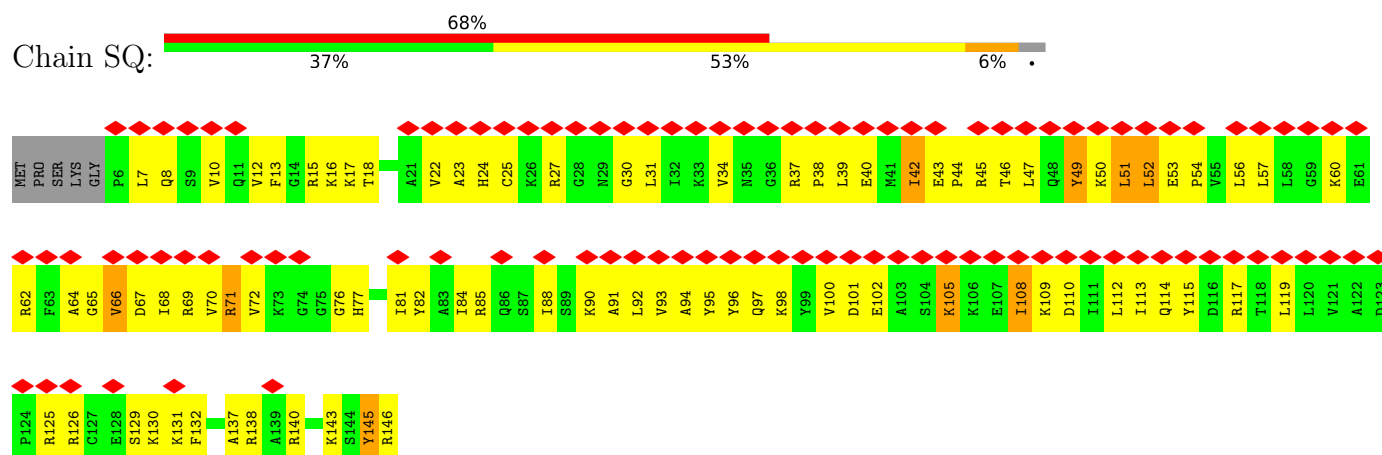
- Molecule 2: 40S ribosomal protein S17



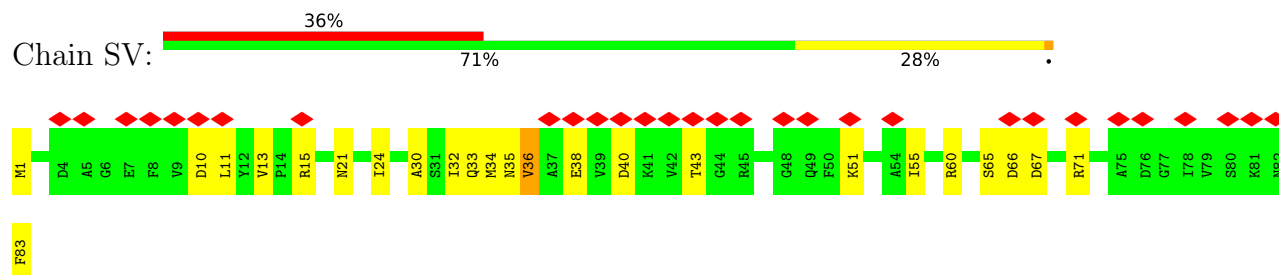
- Molecule 3: 40S ribosomal protein S15



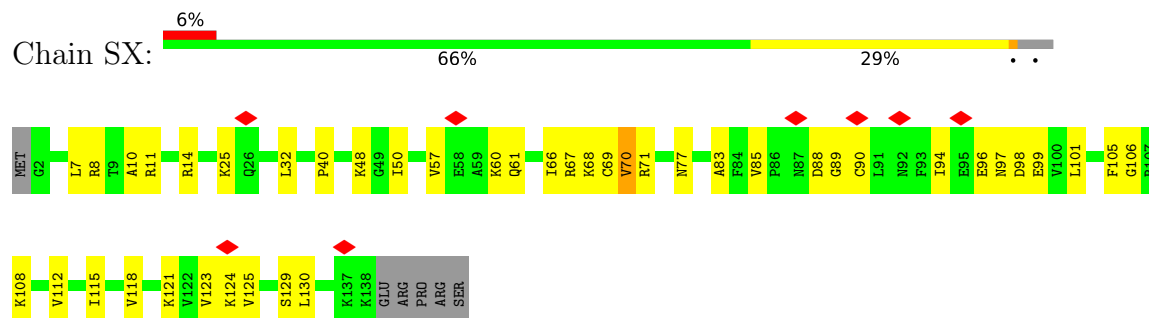
- Molecule 4: 40S ribosomal protein S16



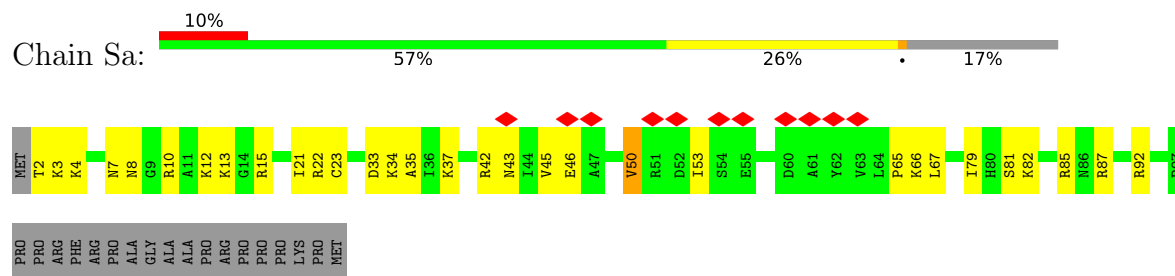
- Molecule 5: 40S ribosomal protein S21



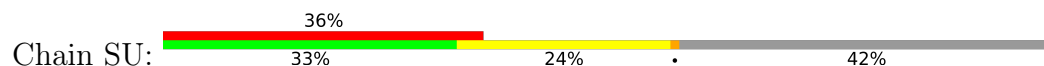
- Molecule 6: 40S ribosomal protein S23

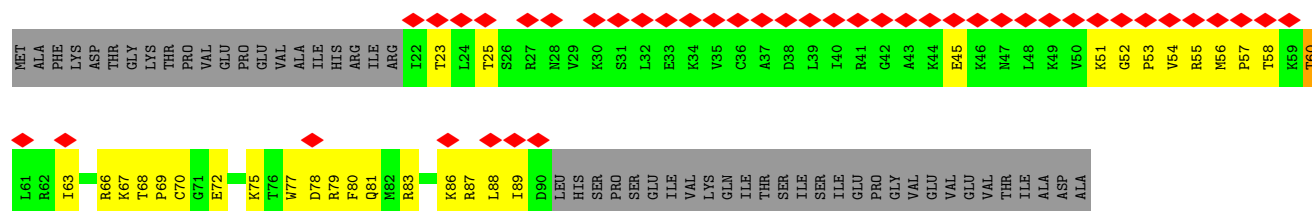


- Molecule 7: 40S ribosomal protein S26

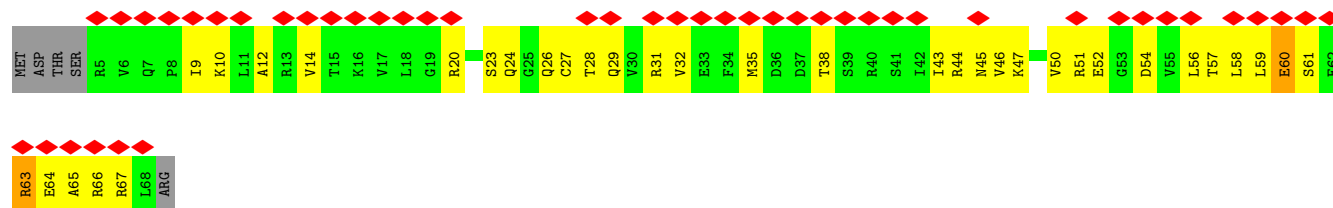
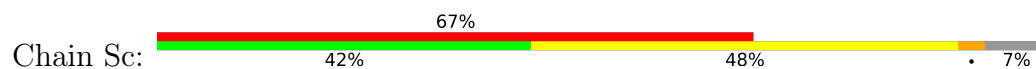


- Molecule 8: 40S ribosomal protein S20

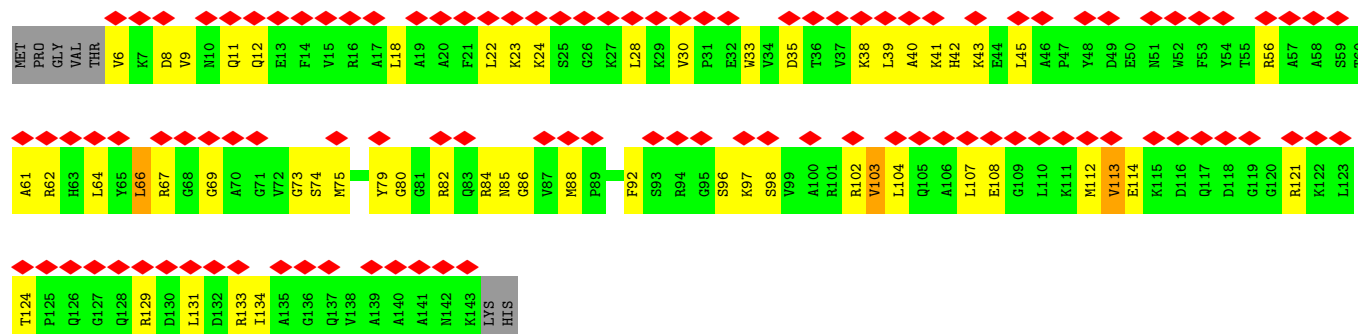
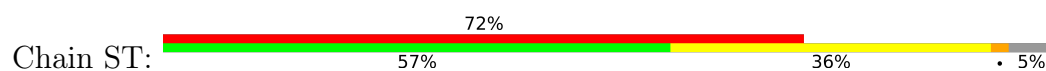




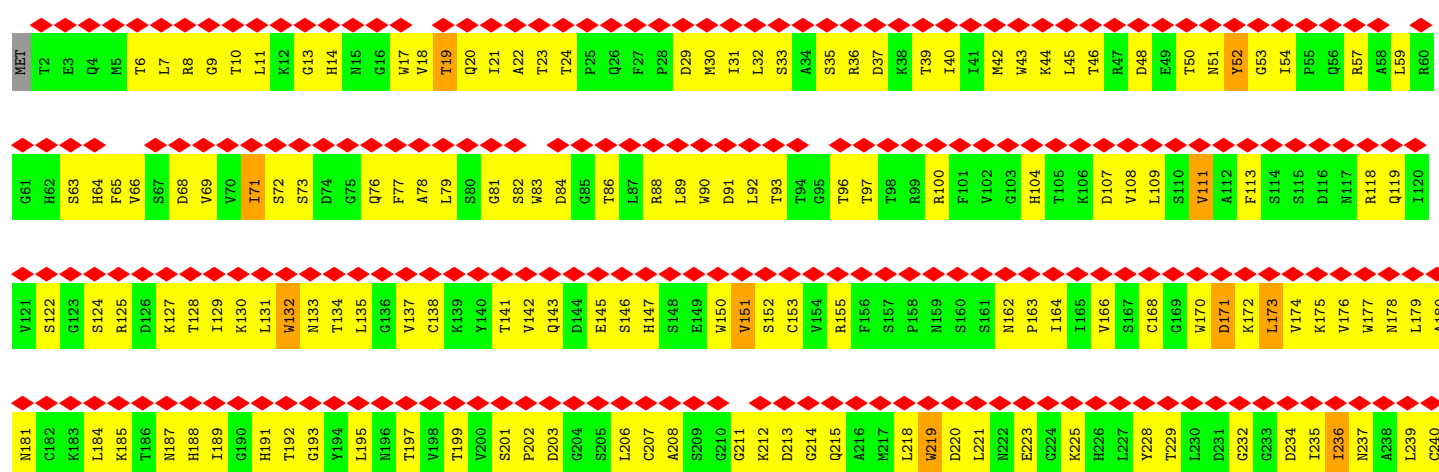
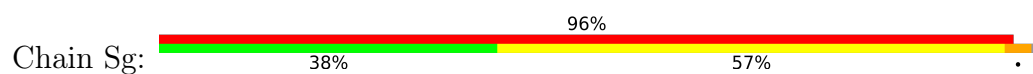
• Molecule 9: 40S ribosomal protein S28

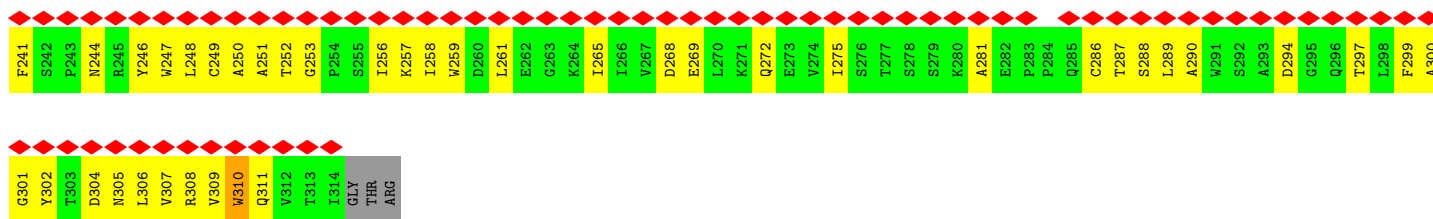


• Molecule 10: 40S ribosomal protein S19

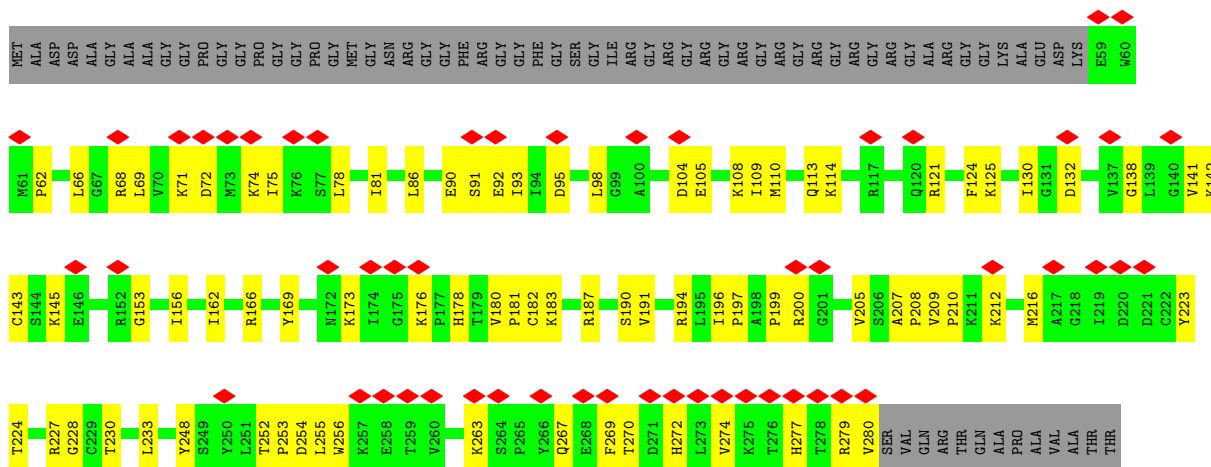


• Molecule 11: Receptor of activated protein C kinase 1

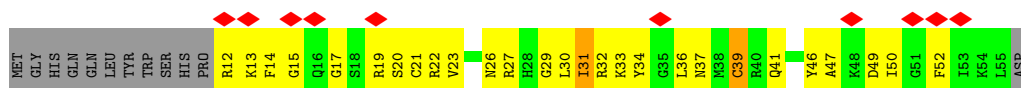




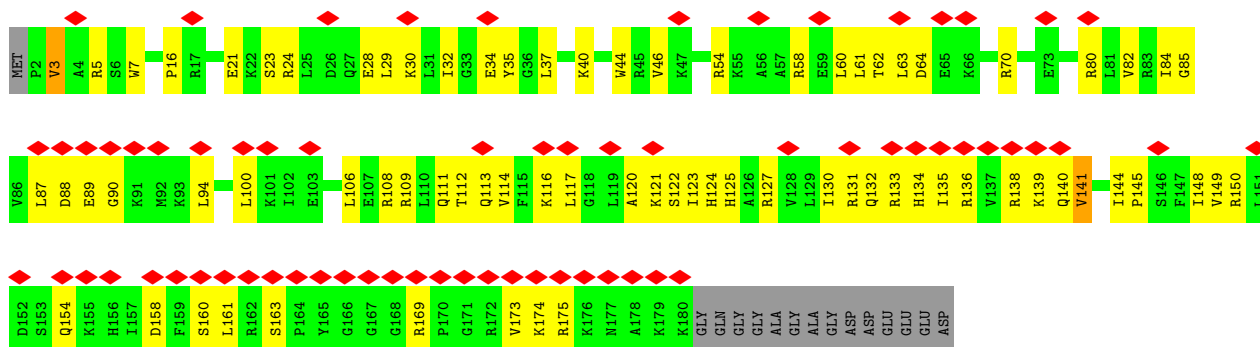
• Molecule 12: 40S ribosomal protein S2



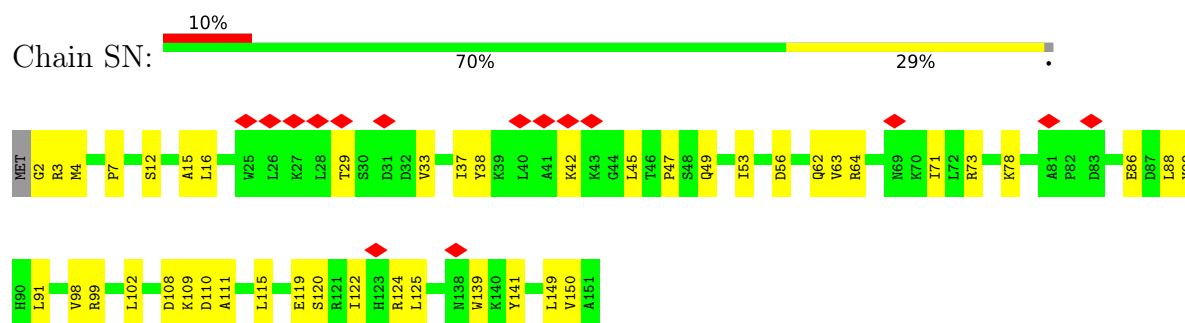
• Molecule 13: 40S ribosomal protein S29



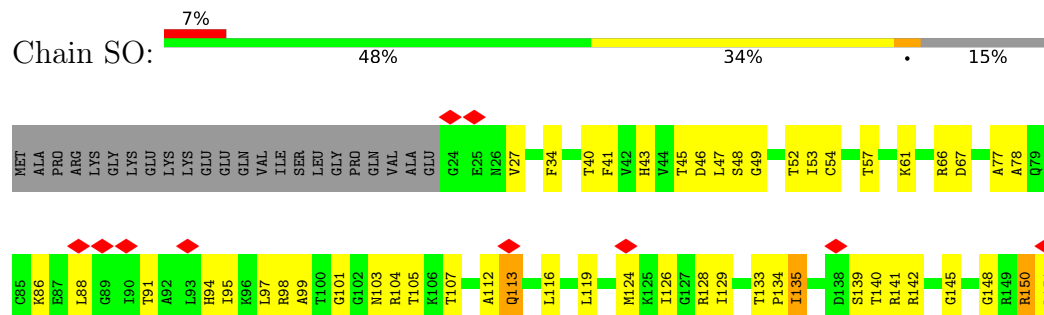
• Molecule 14: 40S ribosomal protein S9



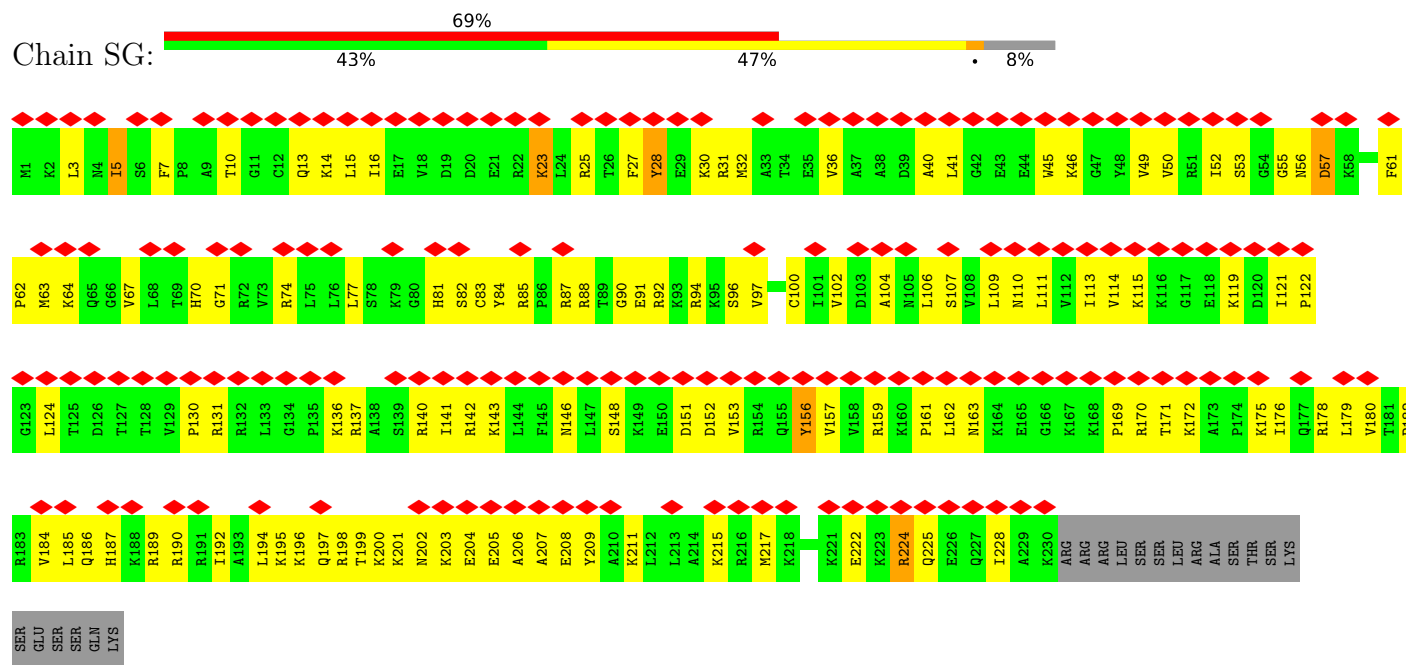
• Molecule 15: 40S ribosomal protein S13



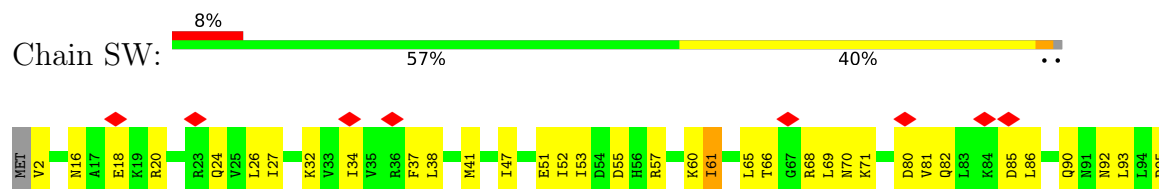
• Molecule 16: 40S ribosomal protein S14



• Molecule 17: 40S ribosomal protein S6

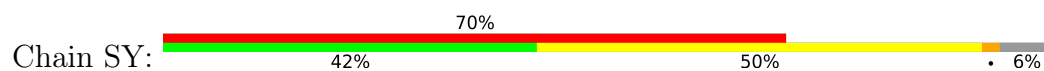


• Molecule 18: 40S ribosomal protein S15a





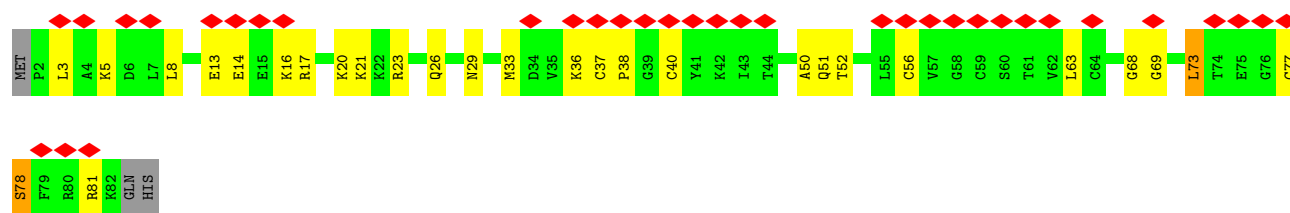
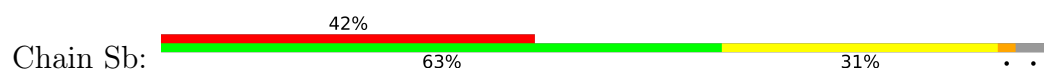
• Molecule 19: 40S ribosomal protein S24



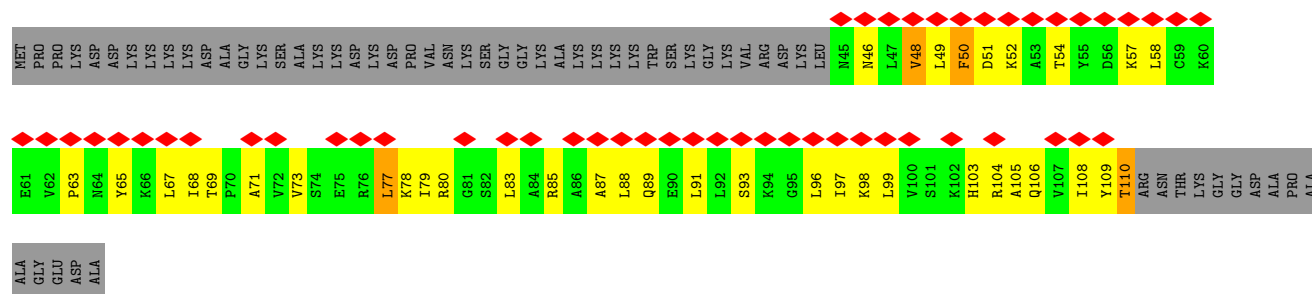
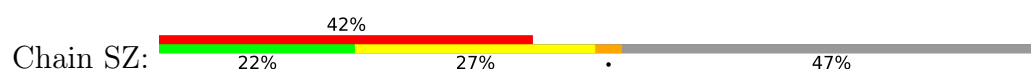
• Molecule 20: 40S ribosomal protein S30



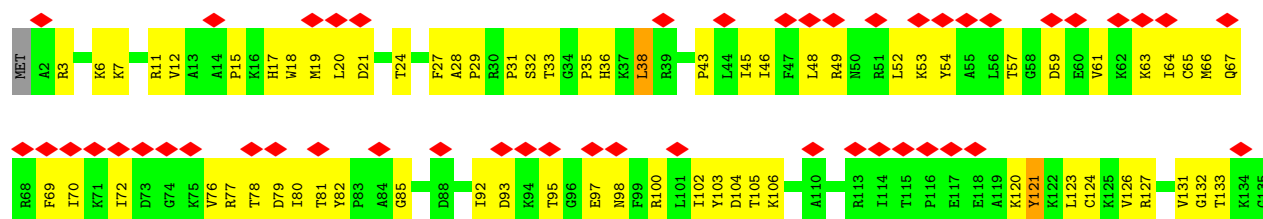
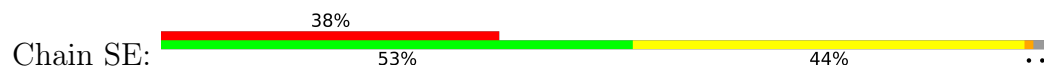
• Molecule 21: 40S ribosomal protein S27

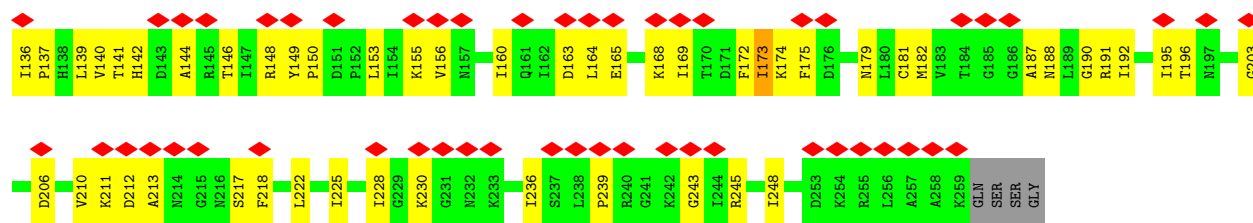


• Molecule 22: 40S ribosomal protein S25

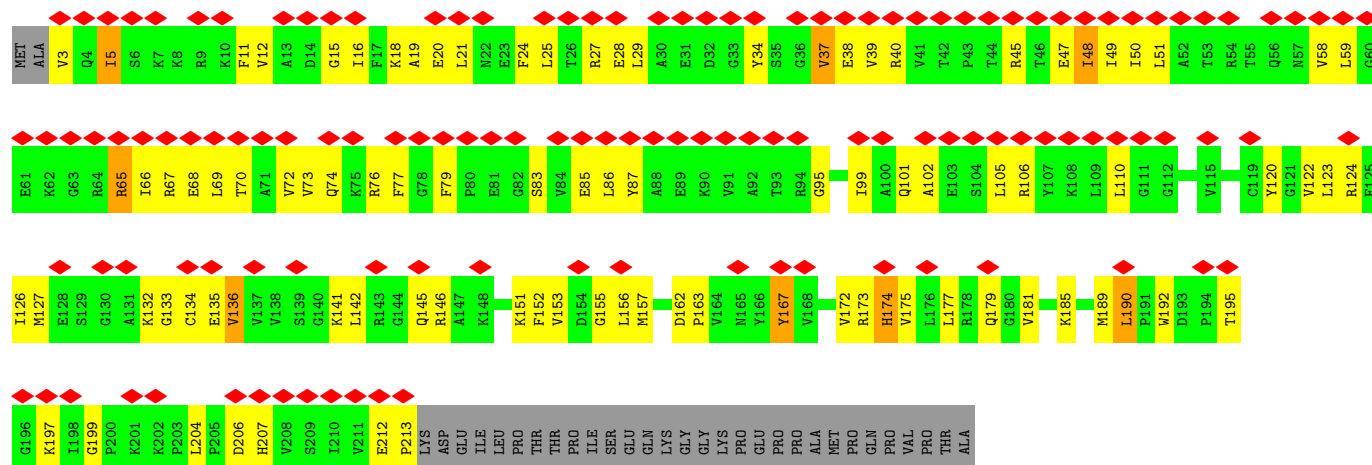


Chain SA:

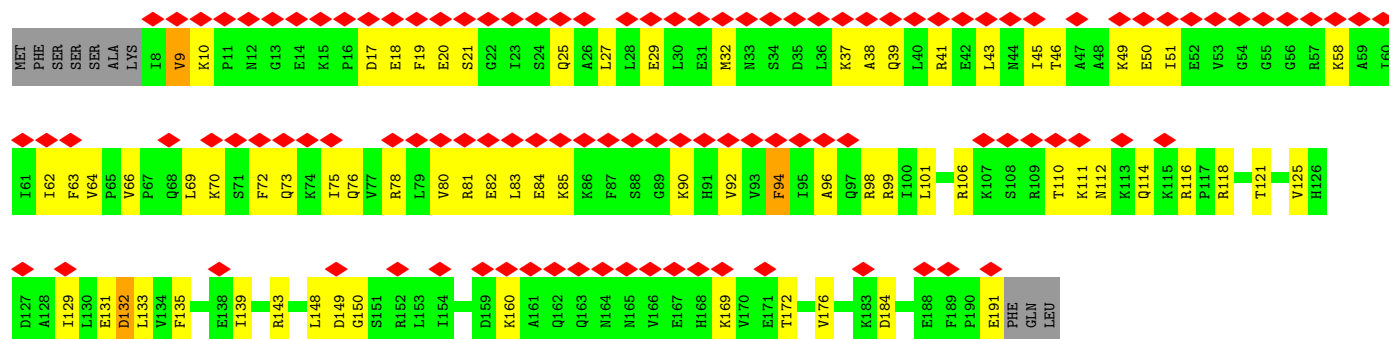




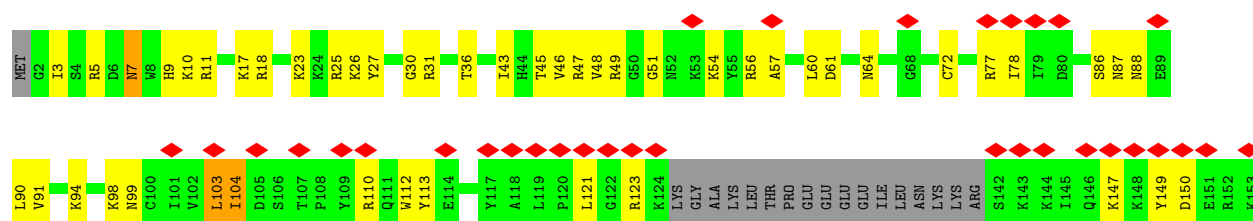
• Molecule 26: 40S ribosomal protein S3

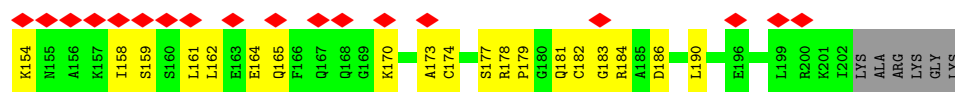


• Molecule 27: 40S ribosomal protein S7

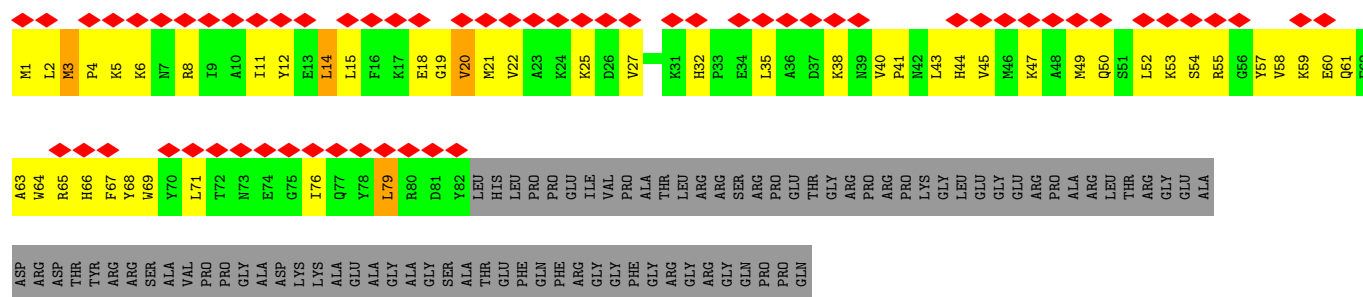
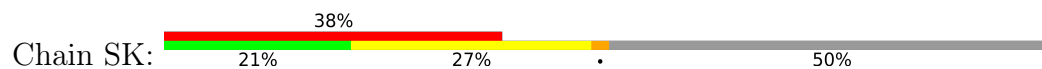


• Molecule 28: 40S ribosomal protein S8





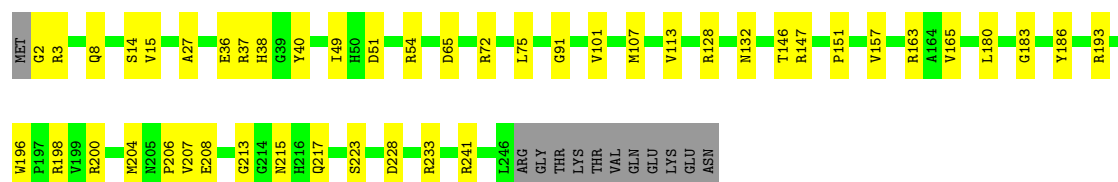
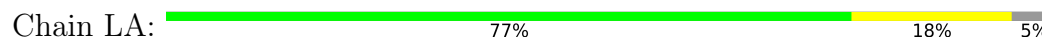
• Molecule 29: 40S ribosomal protein S10



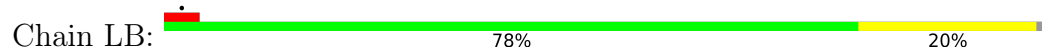
• Molecule 30: 40S ribosomal protein S5

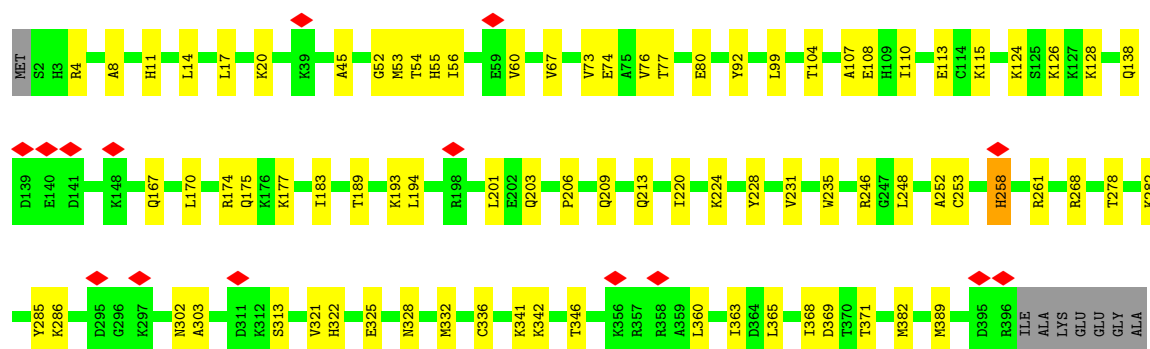


• Molecule 31: 60S ribosomal protein L8



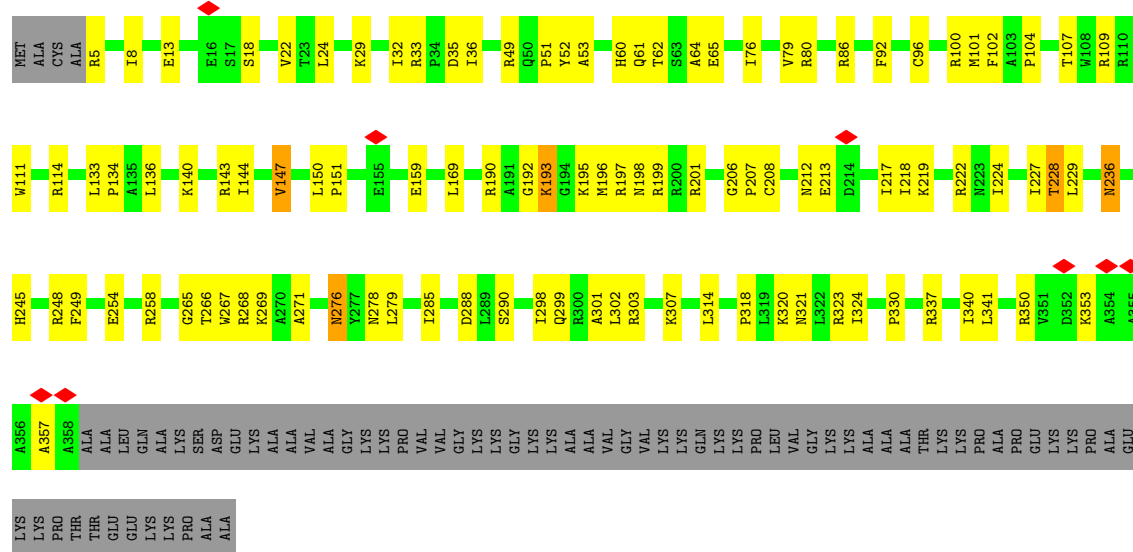
• Molecule 32: 60S ribosomal protein L3





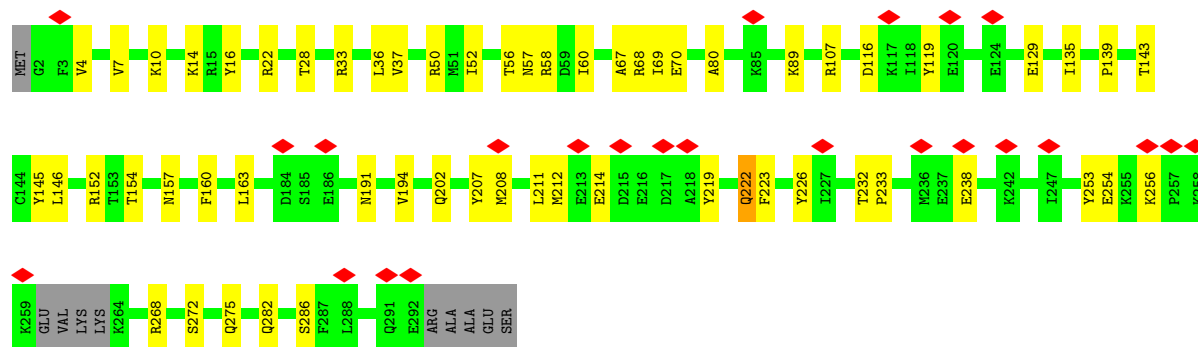
• Molecule 33: 60S ribosomal protein L4

Chain LC: 59% 23% 17%



• Molecule 34: 60S ribosomal protein L5

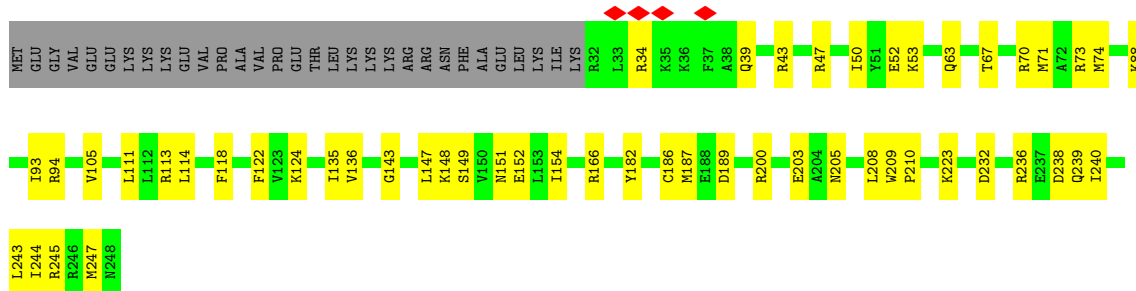
Chain LD: 8% 77% 20%



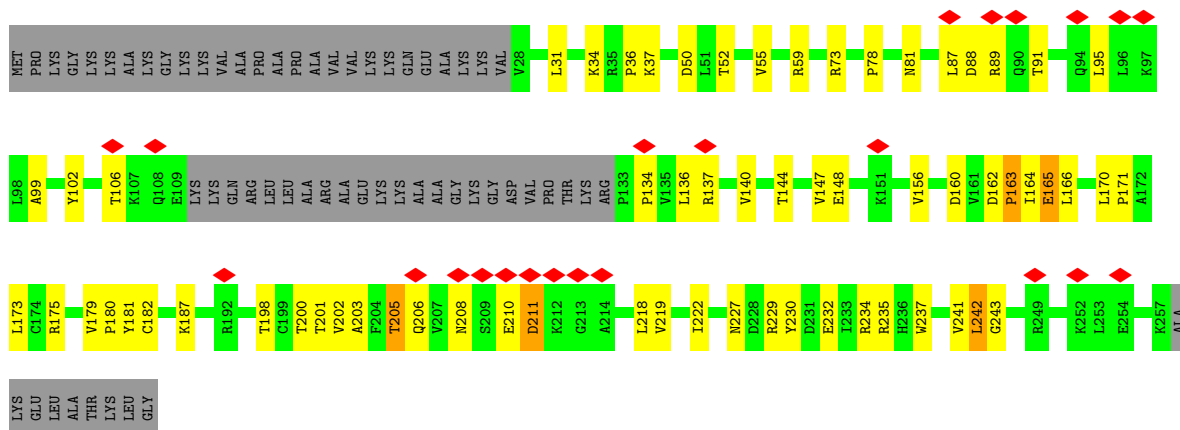
• Molecule 35: 60S ribosomal protein L6

Chain LE: 7% 45% 21% 34%

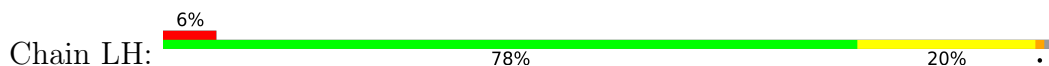
- Molecule 36: 60S ribosomal protein L7

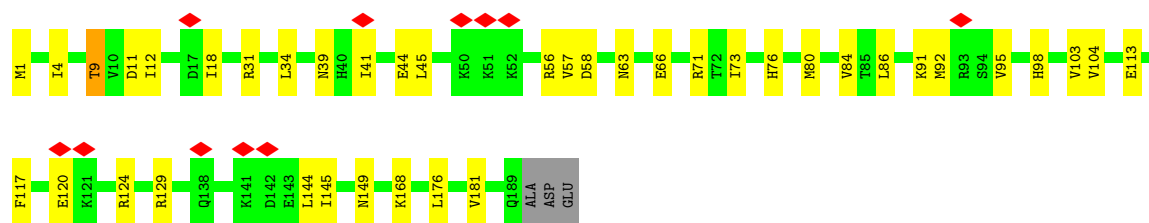


- Molecule 37: 60S ribosomal protein L7a



- Molecule 38: 60S ribosomal protein L9

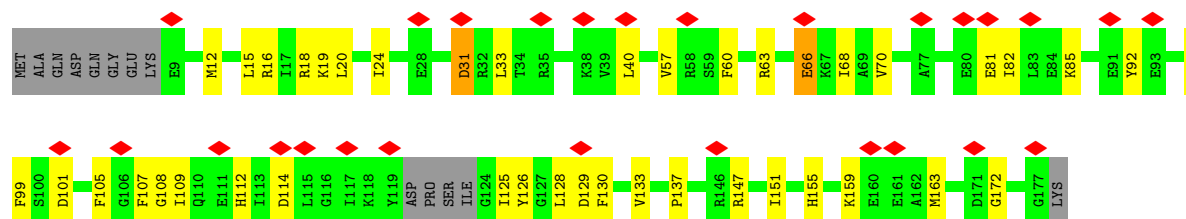
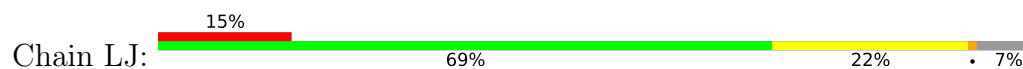




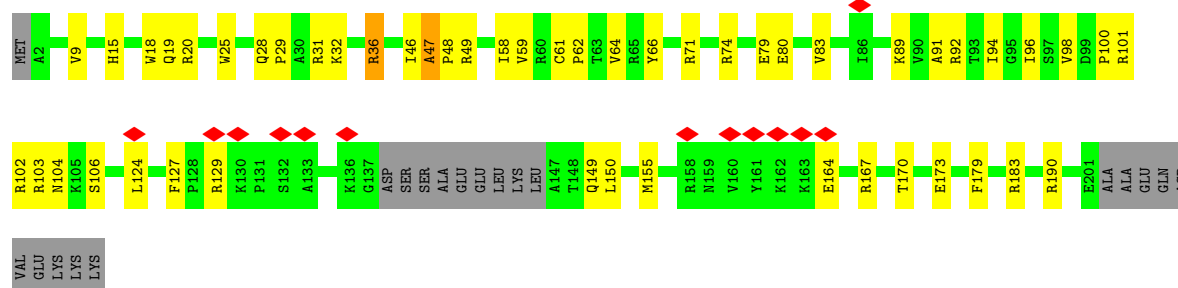
- Molecule 39: 60S ribosomal protein L10-like



- Molecule 40: 60S ribosomal protein L11

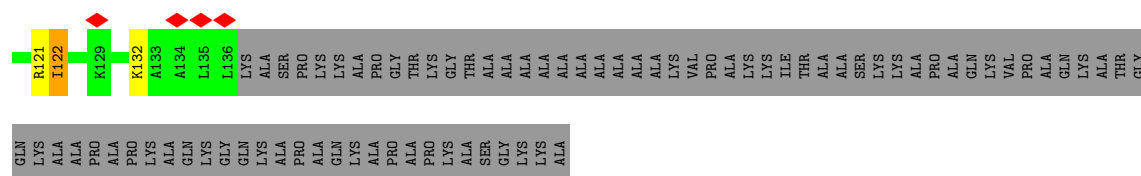


- Molecule 41: 60S ribosomal protein L13



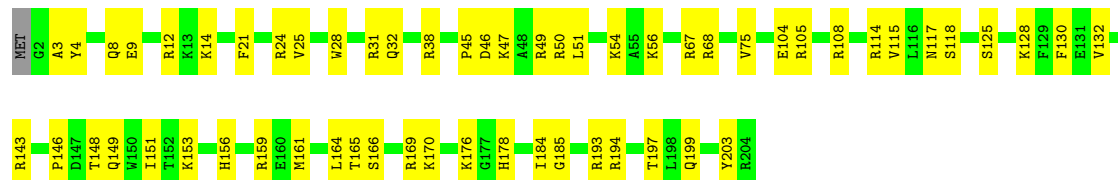
- Molecule 42: 60S ribosomal protein L14





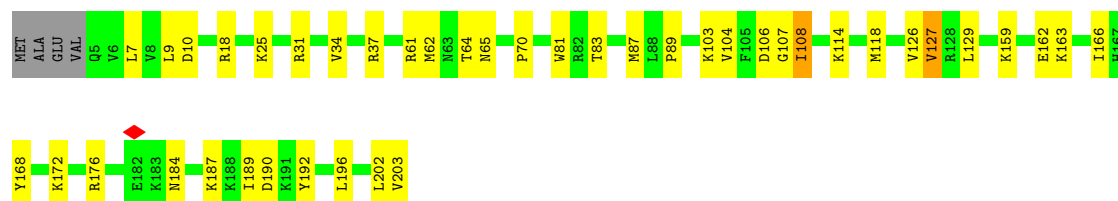
- Molecule 43: 60S ribosomal protein L15

Chain LN: 71% 28%



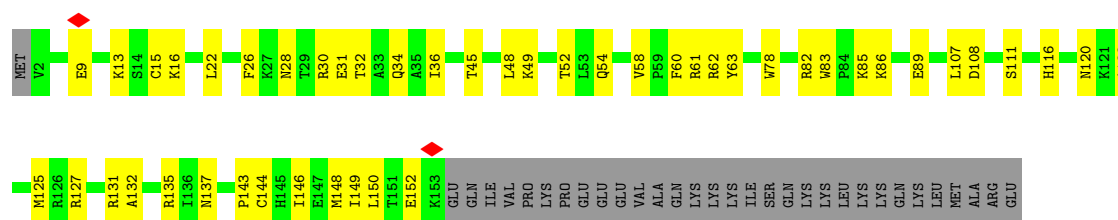
- Molecule 44: 60S ribosomal protein L13a

Chain LO: 77% 20%



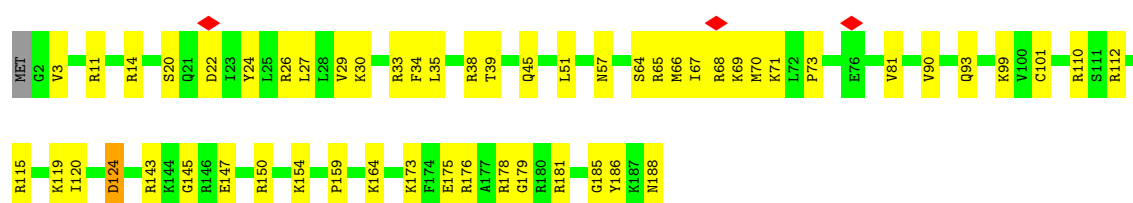
- Molecule 45: 60S ribosomal protein L17

Chain LP: 57% 26% 17%

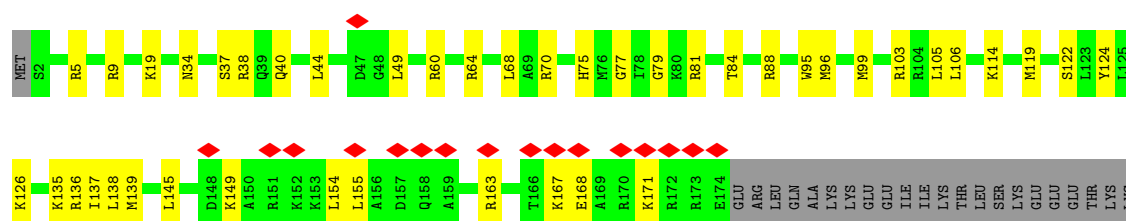


- Molecule 46: 60S ribosomal protein L18

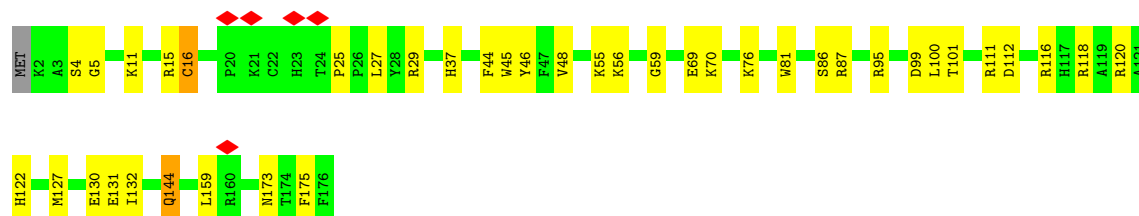
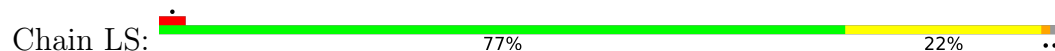
Chain LQ: 71% 28%



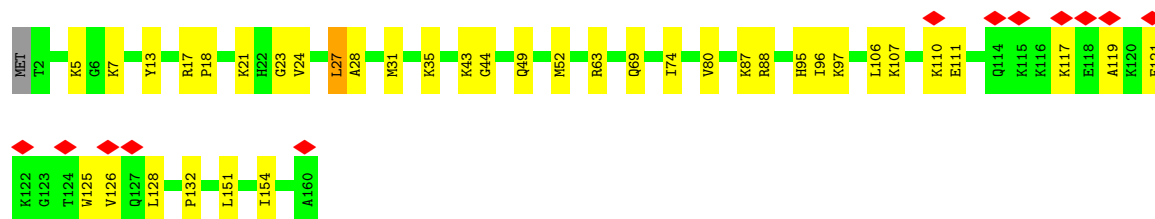
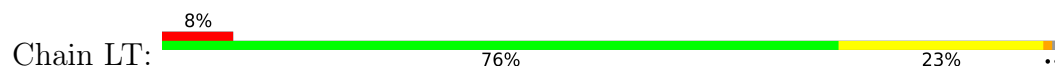
- Molecule 47: 60S ribosomal protein L19



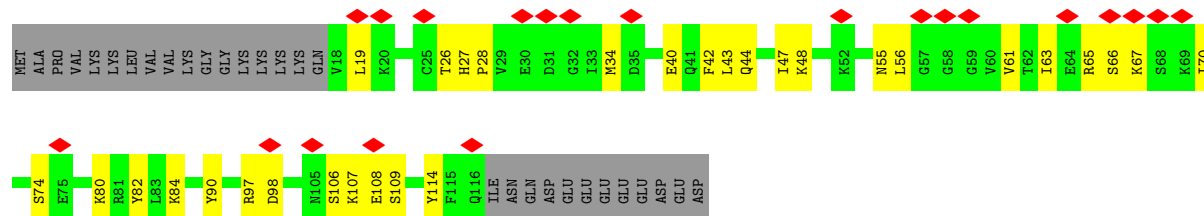
- Molecule 48: 60S ribosomal protein L18a



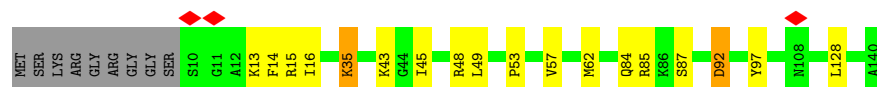
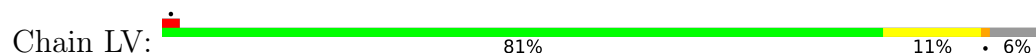
- Molecule 49: 60S ribosomal protein L21



- Molecule 50: 60S ribosomal protein L22



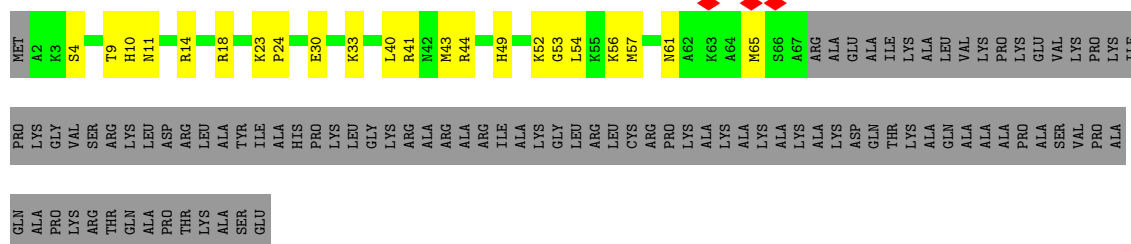
- Molecule 51: 60S ribosomal protein L23



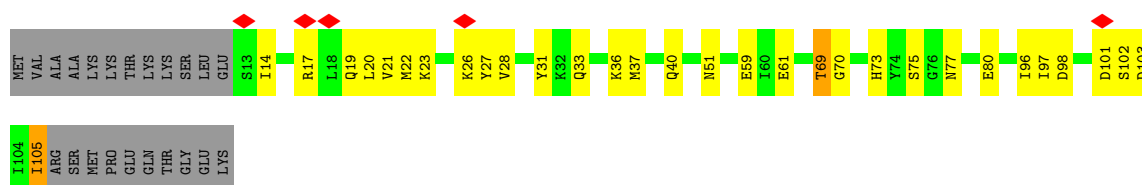
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|-----|
| P2 |
| S3 |
| R4 |
| L5 |
| R6 |
| K10 |
| G18 |
| H19 |
| G20 |
| R26 |
| P29 |
| R32 |
| A35 |
| G36 |
| G37 |
| L38 |
| H39 |
| H40 |
| H41 |
| R42 |
| D46 |
| H49 |
| P50 |
| G51 |
| K55 |
| V56 |
| H62 |
| Q67 |
| L75 |
| w79 |
| T80 |
| E84 |
| Q85 |
| T86 |
| R87 |
| H88 |
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| K92 |
| N93 |
| K94 |
| T95 |
| G96 |
| A97 |
| A98 |
| P99 |



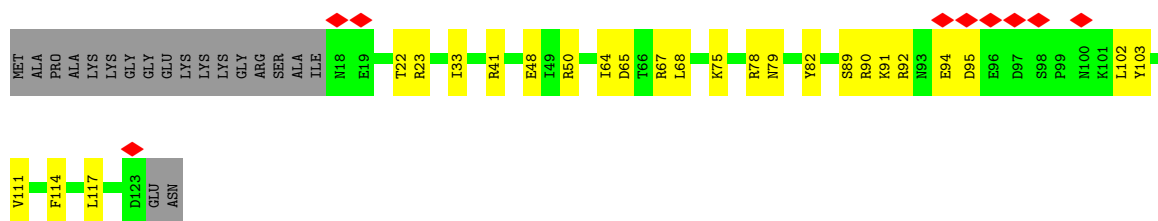
- Molecule 57: 60S ribosomal protein L29



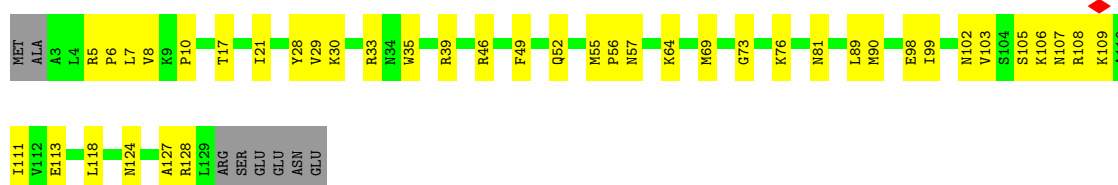
- Molecule 58: 60S ribosomal protein L30



- Molecule 59: 60S ribosomal protein L31



- Molecule 60: 60S ribosomal protein L32



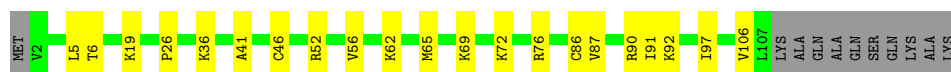
- Molecule 61: 60S ribosomal protein L35a

Chain Lf:  85% 14%



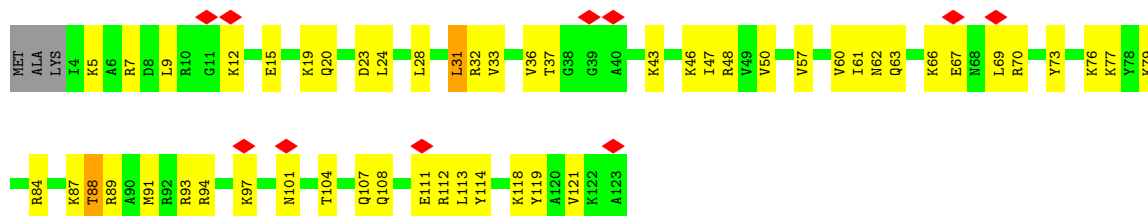
- Molecule 62: 60S ribosomal protein L34

Chain Lg:  73% 18% 9%



- Molecule 63: 60S ribosomal protein L35

Chain Lh:  8% 55% 41%



- Molecule 64: 60S ribosomal protein L36

Chain Li:  10% 70% 23% 5%



- Molecule 65: 60S ribosomal protein L37

Chain Lj:  59% 28% 12%



- Molecule 66: 60S ribosomal protein L38

Chain Lk:  24% 67% 30%

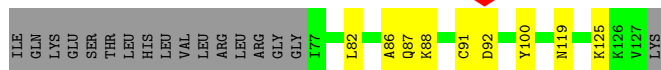
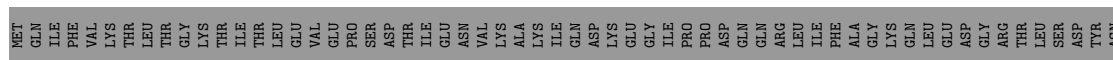
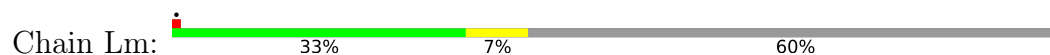


- Molecule 67: 60S ribosomal protein L39

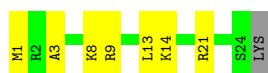
Chain Ll:  47% 47%



- Molecule 68: Ubiquitin-60S ribosomal protein L40



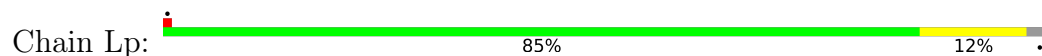
- Molecule 69: 60S ribosomal protein L41



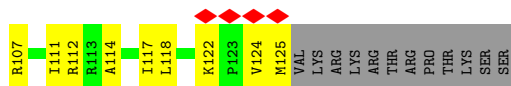
- Molecule 70: 60S ribosomal protein L36a



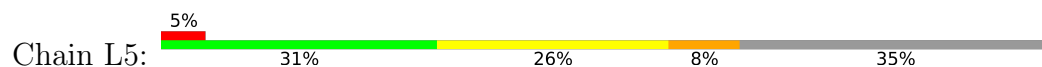
- Molecule 71: 60S ribosomal protein L37a

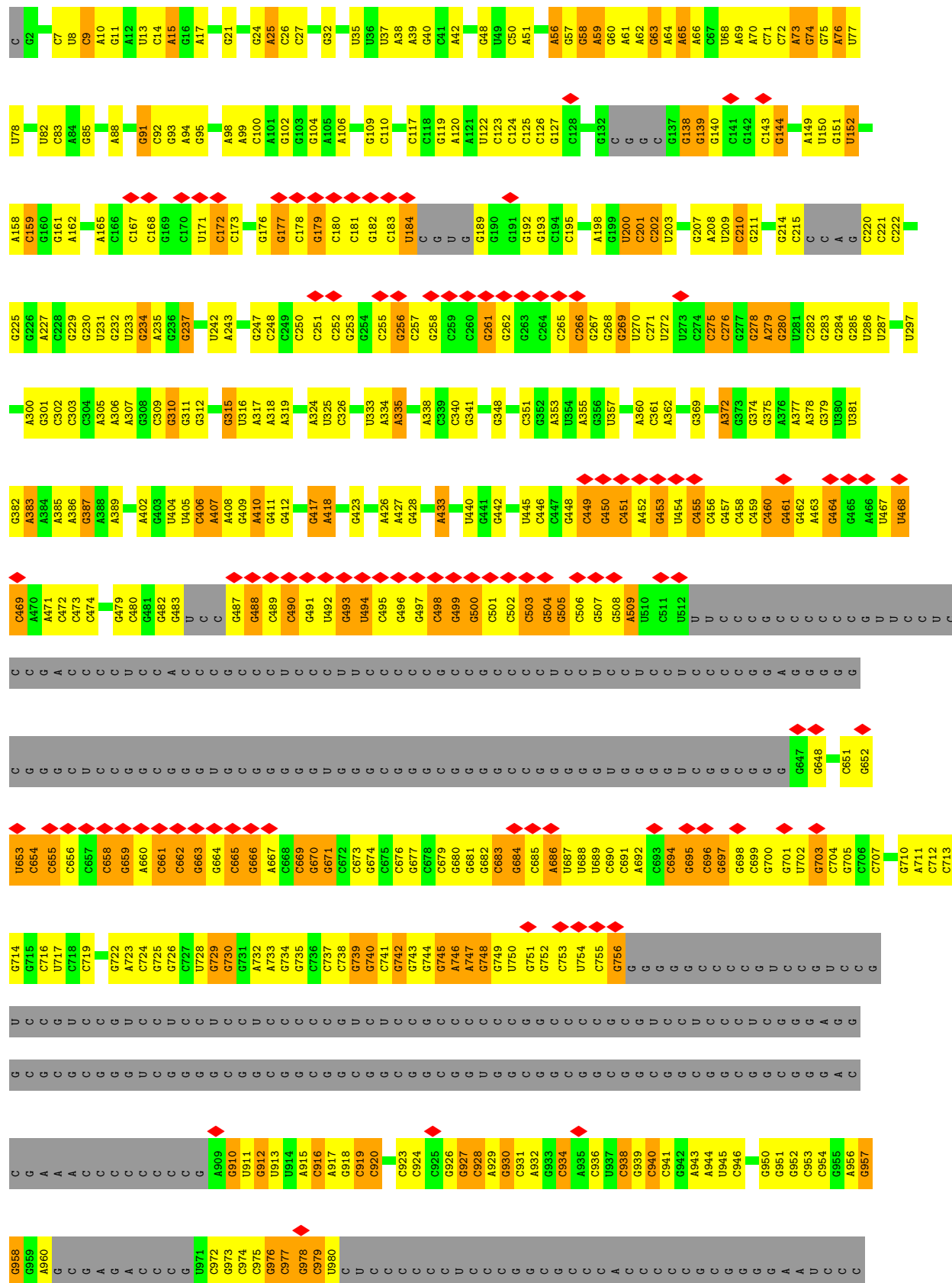


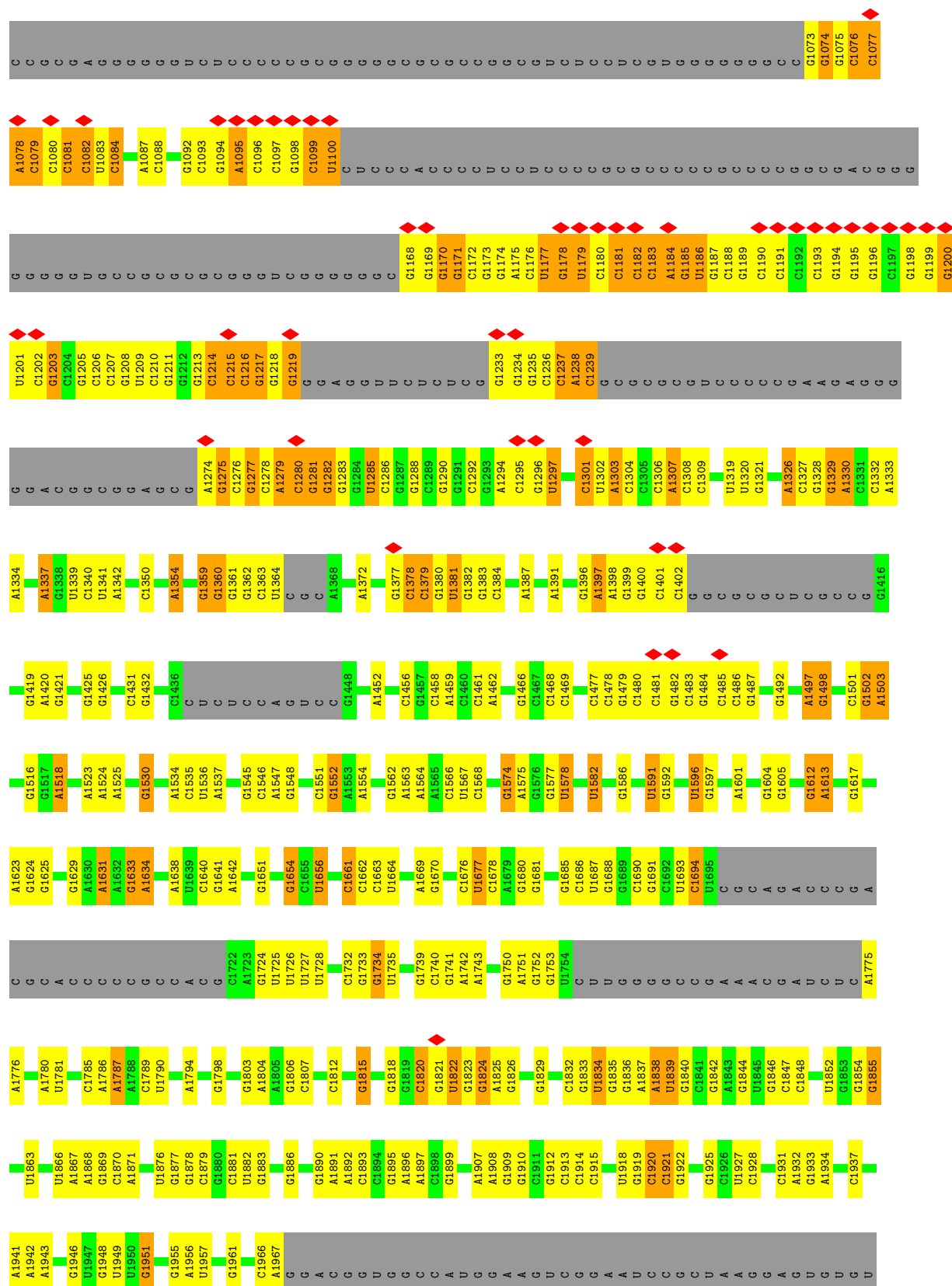
- Molecule 72: 60S ribosomal protein L28



- Molecule 73: 28S ribosomal RNA|HOMO SAPIENS

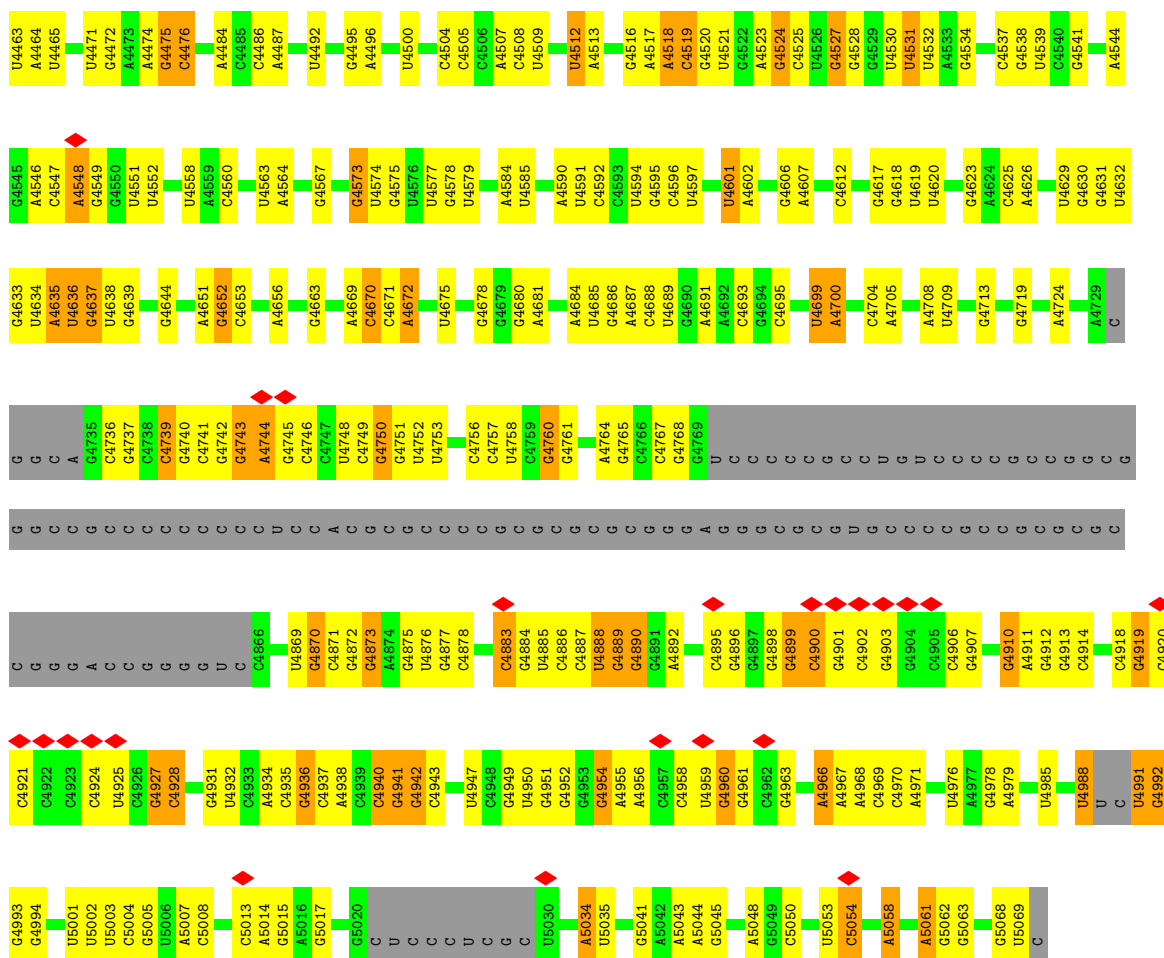




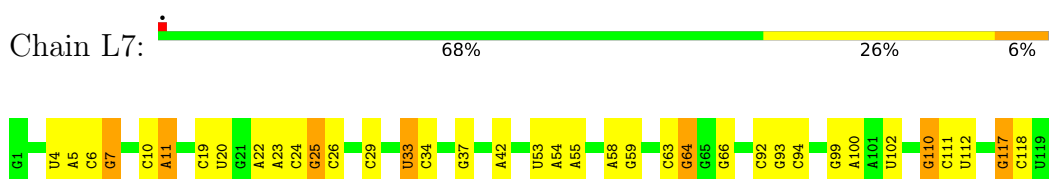




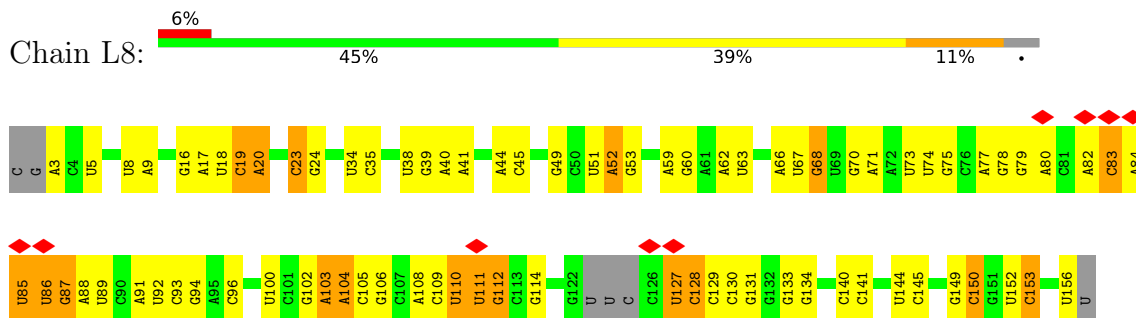




• Molecule 74: 5S ribosomal RNA|HOMO SAPIENS

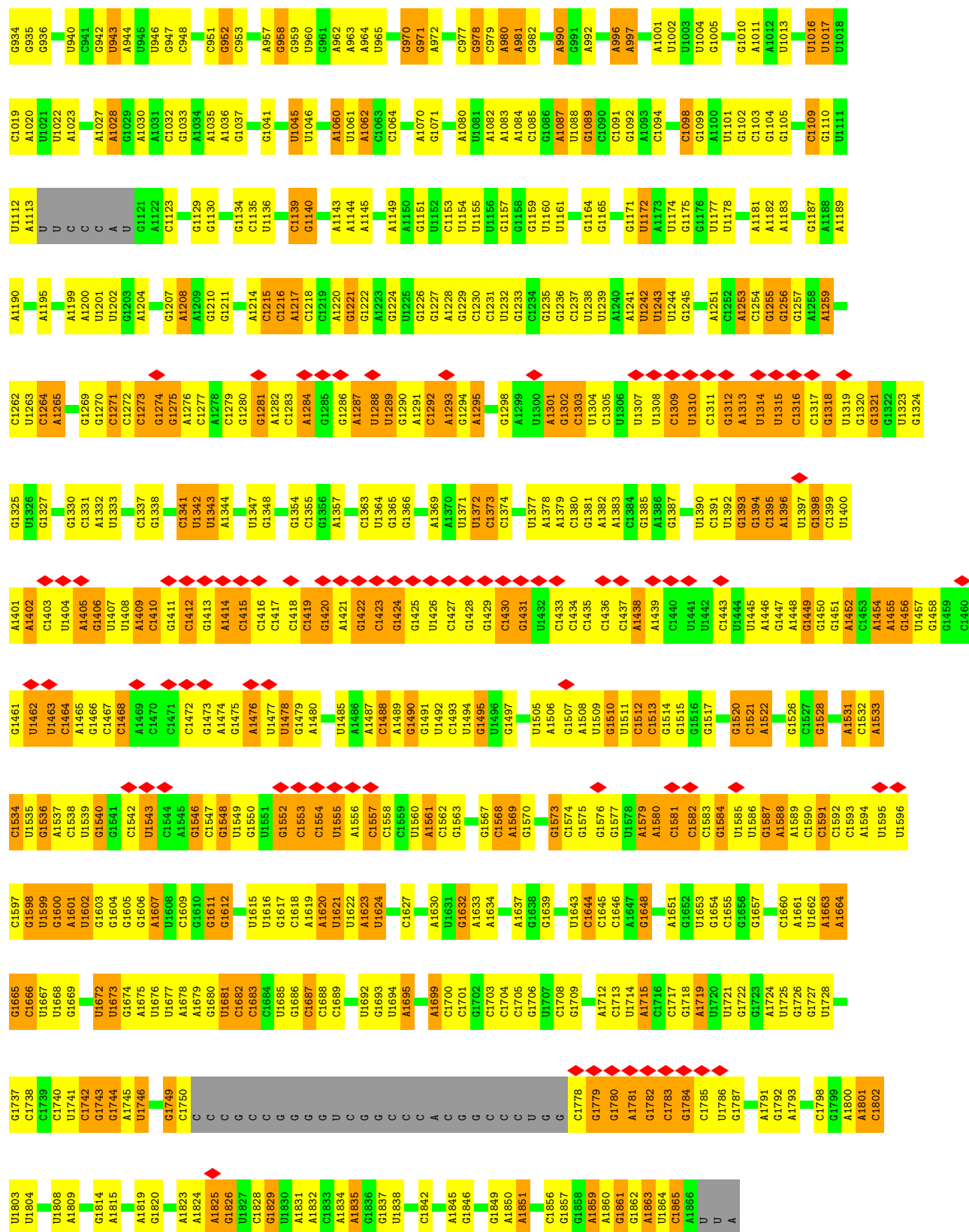


• Molecule 75: 5.8S ribosomal RNA|HOMO SAPIENS



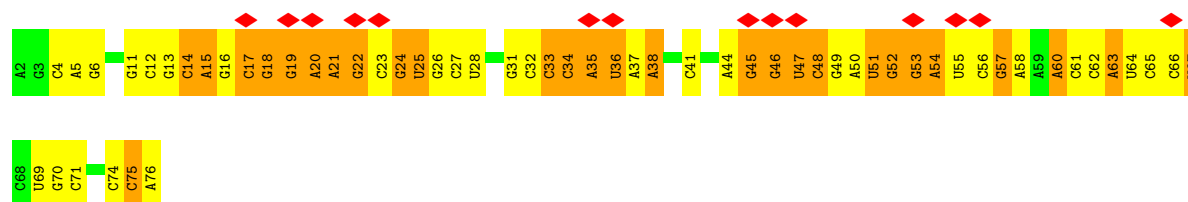
• Molecule 76: 18S ribosomal RNA|HOMO SAPIENS



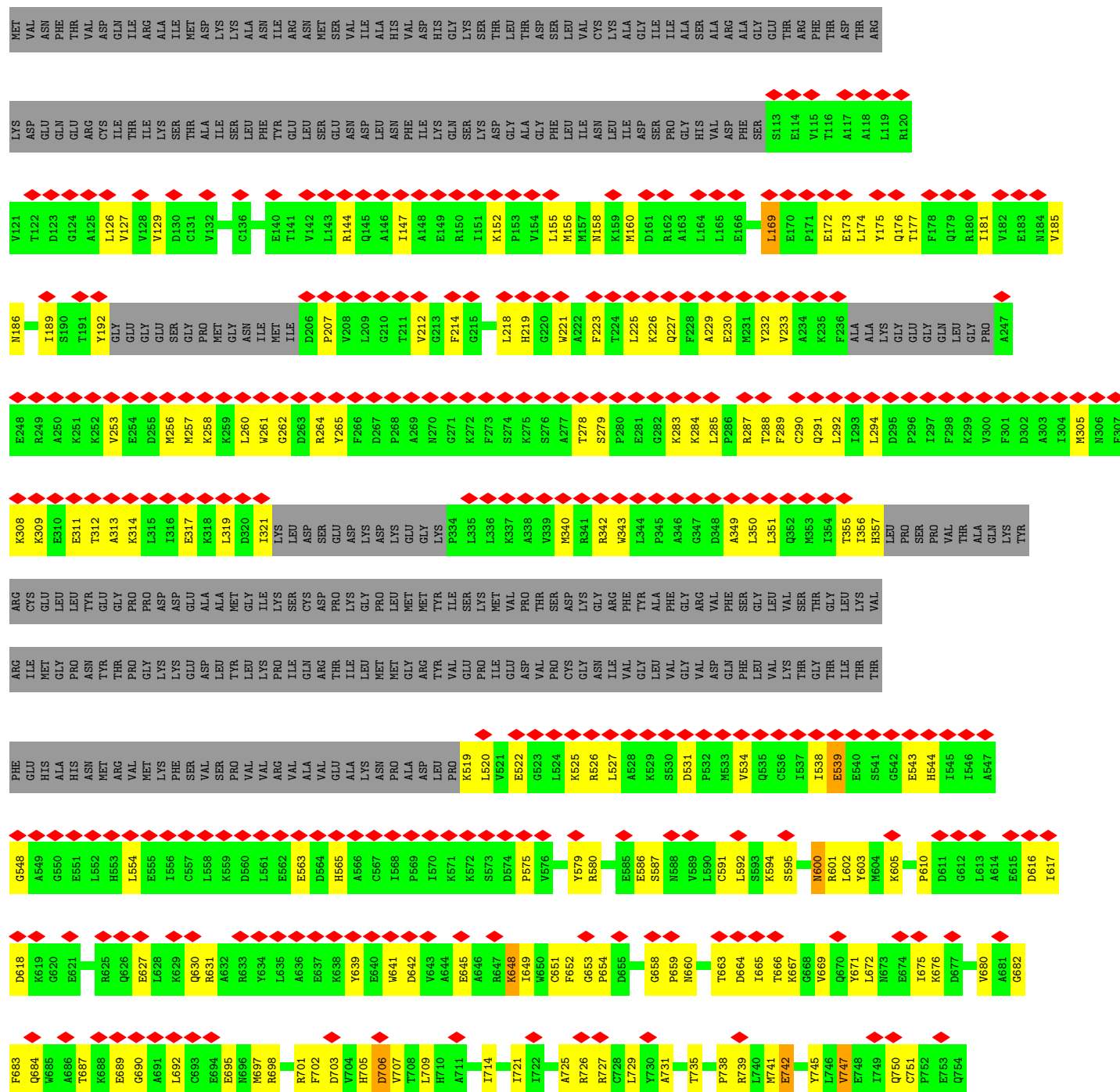
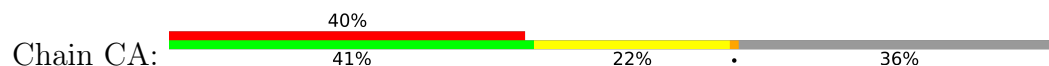


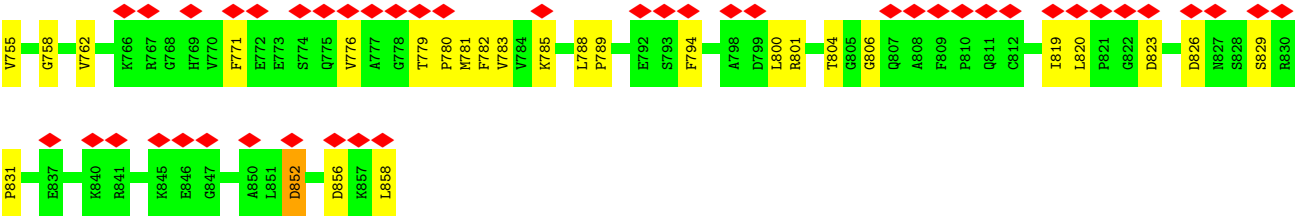
• Molecule 77: HUMAN INITIATOR MET-TRNA-I|HOMO SAPIENS

Chain S6: 19% 21% 41% 37%



• Molecule 78: Elongation factor 2





4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	Not provided	
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	JEOL CRYO ARM 300	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.721	Depositor
Minimum map value	-0.370	Depositor
Average map value	0.006	Depositor
Map value standard deviation	0.037	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	403.45596, 403.45596, 403.45596	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.7879999, 0.7879999, 0.7879999	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, A1L8F, MG

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	SL	0.17	0/1118	0.33	0/1495
2	SR	0.19	0/894	0.54	0/1198
3	SP	0.20	0/500	0.58	0/663
4	SQ	0.21	0/1142	0.50	0/1528
5	SV	0.14	0/643	0.36	0/860
6	SX	0.17	0/1077	0.38	0/1438
7	Sa	0.17	0/778	0.33	0/1041
8	SU	0.22	0/560	0.49	0/747
9	Sc	0.19	0/508	0.58	0/680
10	ST	0.16	0/1096	0.48	0/1468
11	Sg	0.19	0/2493	0.52	0/3394
12	SC	0.16	0/1762	0.37	0/2381
13	Sd	0.17	0/366	0.46	0/481
14	SJ	0.17	0/1520	0.39	0/2030
15	SN	0.16	0/1232	0.32	0/1656
16	SO	0.16	0/973	0.35	0/1303
17	SG	0.19	0/1885	0.52	0/2510
18	SW	0.19	0/1051	0.40	0/1406
19	SY	0.18	0/1032	0.42	0/1371
20	Se	0.16	0/465	0.42	0/612
21	Sb	0.16	0/644	0.45	0/864
22	SZ	0.19	0/529	0.52	0/712
23	SA	0.17	0/1471	0.37	0/2004
24	SB	0.15	0/1742	0.31	0/2330
25	SE	0.16	0/2092	0.44	0/2816
26	SD	0.17	0/1667	0.41	0/2243
27	SH	0.16	0/1503	0.37	0/2014
28	SI	0.16	0/1537	0.40	0/2052
29	SK	0.19	0/717	0.46	0/963
30	SF	0.19	0/1439	0.50	0/1933
31	LA	0.22	0/1914	0.36	0/2567
32	LB	0.20	0/3257	0.33	0/4359

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	LC	0.18	0/2884	0.36	0/3873
34	LD	0.16	0/2377	0.33	0/3184
35	LE	0.16	0/1577	0.36	0/2115
36	LF	0.18	0/1837	0.28	0/2449
37	LG	0.21	0/1704	0.38	1/2299 (0.0%)
38	LH	0.17	0/1532	0.29	0/2059
39	LI	0.18	0/1654	0.32	0/2210
40	LJ	0.16	0/1345	0.34	0/1796
41	LL	0.16	0/1583	0.32	0/2117
42	LM	0.15	0/1133	0.29	0/1516
43	LN	0.19	0/1746	0.35	0/2338
44	LO	0.18	0/1666	0.30	0/2228
45	LP	0.18	0/1259	0.31	0/1689
46	LQ	0.18	0/1537	0.37	0/2052
47	LR	0.16	0/1464	0.32	0/1935
48	LS	0.24	0/1493	0.34	0/2003
49	LT	0.17	0/1326	0.29	0/1770
50	LU	0.13	0/822	0.33	0/1103
51	LV	0.18	0/993	0.33	0/1332
52	LW	0.15	0/547	0.31	0/728
53	LX	0.17	0/975	0.36	0/1312
54	LY	0.16	0/1110	0.31	0/1477
55	LZ	0.16	0/1130	0.30	0/1507
56	La	0.22	0/1191	0.44	0/1591
57	Lb	0.16	0/553	0.31	0/729
58	Lc	0.18	0/731	0.37	0/982
59	Ld	0.19	0/894	0.33	0/1204
60	Le	0.20	0/1066	0.35	0/1422
61	Lf	0.20	0/889	0.35	0/1190
62	Lg	0.17	0/855	0.33	0/1140
63	Lh	0.16	0/1009	0.34	0/1333
64	Li	0.17	0/829	0.41	0/1097
65	Lj	0.19	0/711	0.42	0/941
66	Lk	0.16	0/565	0.27	0/750
67	Ll	0.21	0/454	0.40	0/599
68	Lm	0.17	0/425	0.42	0/564
69	Ln	0.18	0/231	0.28	0/294
70	Lo	0.25	0/847	0.40	0/1117
71	Lp	0.18	0/700	0.29	0/930
72	Lr	0.19	0/1010	0.39	0/1354
73	L5	0.23	0/78988	0.36	0/123170
74	L7	0.20	0/2858	0.26	0/4455
75	L8	0.20	0/3589	0.32	0/5589

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	S2	0.18	0/38744	0.36	0/60383
77	S6	0.18	0/1795	0.41	0/2798
78	CA	0.14	0/4411	0.36	0/5955
All	All	0.20	0/216646	0.36	1/317798 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	LG	163	PRO	N-CA-C	-5.40	101.35	112.47

There are no chirality outliers.

There are no planarity outliers.

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	SL	1099	0	1155	36	0
2	SR	883	0	925	56	0
3	SP	494	0	527	35	0
4	SQ	1124	0	1193	95	0
5	SV	636	0	637	21	0
6	SX	1060	0	1128	40	0
7	Sa	767	0	815	31	0
8	SU	554	0	608	36	0
9	Sc	506	0	536	37	0
10	ST	1078	0	1106	46	0
11	Sg	2436	0	2393	177	0
12	SC	1725	0	1813	66	0
13	Sd	361	0	369	32	0
14	SJ	1495	0	1615	74	0
15	SN	1208	0	1294	32	0
16	SO	961	0	985	41	0
17	SG	1862	0	2018	136	0
18	SW	1034	0	1080	45	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
19	SY	1015	0	1086	85	0
20	Se	459	0	503	29	0
21	Sb	631	0	655	22	0
22	SZ	523	0	573	42	0
23	SA	1436	0	1443	52	0
24	SB	1715	0	1785	48	0
25	SE	2050	0	2156	94	0
26	SD	1641	0	1732	78	0
27	SH	1481	0	1576	51	0
28	SI	1510	0	1574	59	0
29	SK	697	0	711	53	0
30	SF	1419	0	1467	100	0
31	LA	1876	0	1970	34	0
32	LB	3189	0	3327	52	0
33	LC	2830	0	3002	84	0
34	LD	2332	0	2350	42	0
35	LE	1547	0	1683	45	0
36	LF	1803	0	1922	39	0
37	LG	1673	0	1781	58	0
38	LH	1513	0	1596	28	0
39	LI	1615	0	1654	34	0
40	LJ	1324	0	1358	33	0
41	LL	1553	0	1669	44	0
42	LM	1111	0	1174	27	0
43	LN	1701	0	1749	46	0
44	LO	1634	0	1779	35	0
45	LP	1233	0	1263	36	0
46	LQ	1513	0	1628	49	0
47	LR	1448	0	1595	35	0
48	LS	1453	0	1490	27	0
49	LT	1298	0	1366	36	0
50	LU	808	0	831	24	0
51	LV	979	0	1039	13	0
52	LW	534	0	546	7	0
53	LX	958	0	1029	22	0
54	LY	1093	0	1176	45	0
55	LZ	1107	0	1182	27	0
56	La	1162	0	1213	43	0
57	Lb	543	0	572	19	0
58	Lc	721	0	756	21	0
59	Ld	879	0	924	16	0
60	Le	1048	0	1142	31	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
61	Lf	870	0	907	13	0
62	Lg	845	0	933	20	0
63	Lh	1001	0	1130	46	0
64	Li	818	0	899	23	0
65	Lj	696	0	724	30	0
66	Lk	559	0	624	18	0
67	Ll	444	0	483	26	0
68	Lm	419	0	452	9	0
69	Ln	230	0	276	8	0
70	Lo	834	0	901	23	0
71	Lp	690	0	744	8	0
72	Lr	995	0	1059	26	0
73	L5	70611	0	35657	1290	0
74	L7	2558	0	1296	29	0
75	L8	3214	0	1630	73	0
76	S2	34646	0	17488	983	0
77	S6	1604	0	816	50	0
78	CA	4327	0	4370	131	0
79	L5	234	0	0	0	0
79	L7	10	0	0	0	0
79	L8	6	0	0	0	0
79	LA	3	0	0	0	0
79	LN	1	0	0	0	0
79	LO	1	0	0	0	0
79	S2	35	0	0	0	0
79	SX	1	0	0	0	0
80	Lg	1	0	0	0	0
80	Lj	1	0	0	0	0
80	Lm	1	0	0	0	0
80	Lo	1	0	0	0	0
80	Lp	1	0	0	0	0
80	Sa	1	0	0	0	0
81	L5	22	0	0	0	0
All	All	202018	0	150613	4766	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 14.

The worst 5 of 4766 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)
73:L5:1173:G:H22	73:L5:1187:G:H22	1.04	1.01
73:L5:492:U:H3	73:L5:662:C:N4	1.60	0.99
10:ST:18:LEU:HD23	10:ST:134:ILE:HG21	1.47	0.96
22:SZ:79:ILE:HD12	22:SZ:83:LEU:HD22	1.46	0.96
76:S2:320:G:N2	76:S2:331:C:O2	1.98	0.96

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	SL	129/158 (82%)	125 (97%)	4 (3%)	0	100	100
2	SR	106/135 (78%)	95 (90%)	11 (10%)	0	100	100
3	SP	56/145 (39%)	45 (80%)	11 (20%)	0	100	100
4	SQ	139/146 (95%)	118 (85%)	21 (15%)	0	100	100
5	SV	81/83 (98%)	78 (96%)	3 (4%)	0	100	100
6	SX	135/143 (94%)	122 (90%)	13 (10%)	0	100	100
7	Sa	94/115 (82%)	91 (97%)	3 (3%)	0	100	100
8	SU	67/119 (56%)	63 (94%)	4 (6%)	0	100	100
9	Sc	62/69 (90%)	52 (84%)	8 (13%)	2 (3%)	3	10
10	ST	136/145 (94%)	122 (90%)	14 (10%)	0	100	100
11	Sg	311/317 (98%)	251 (81%)	59 (19%)	1 (0%)	36	63
12	SC	220/293 (75%)	207 (94%)	13 (6%)	0	100	100
13	Sd	42/56 (75%)	41 (98%)	1 (2%)	0	100	100
14	SJ	177/194 (91%)	164 (93%)	13 (7%)	0	100	100
15	SN	148/151 (98%)	146 (99%)	2 (1%)	0	100	100
16	SO	126/151 (83%)	116 (92%)	10 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
17	SG	228/249 (92%)	204 (90%)	24 (10%)	0	100	100
18	SW	127/130 (98%)	118 (93%)	9 (7%)	0	100	100
19	SY	123/133 (92%)	118 (96%)	4 (3%)	1 (1%)	16	40
20	Se	56/59 (95%)	53 (95%)	3 (5%)	0	100	100
21	Sb	79/84 (94%)	68 (86%)	11 (14%)	0	100	100
22	SZ	64/125 (51%)	55 (86%)	8 (12%)	1 (2%)	7	23
23	SA	178/295 (60%)	163 (92%)	15 (8%)	0	100	100
24	SB	209/264 (79%)	202 (97%)	7 (3%)	0	100	100
25	SE	256/263 (97%)	229 (90%)	27 (10%)	0	100	100
26	SD	209/243 (86%)	198 (95%)	11 (5%)	0	100	100
27	SH	182/194 (94%)	171 (94%)	11 (6%)	0	100	100
28	SI	180/208 (86%)	165 (92%)	15 (8%)	0	100	100
29	SK	80/165 (48%)	76 (95%)	4 (5%)	0	100	100
30	SF	175/204 (86%)	146 (83%)	28 (16%)	1 (1%)	21	47
31	LA	243/257 (95%)	234 (96%)	9 (4%)	0	100	100
32	LB	393/403 (98%)	384 (98%)	9 (2%)	0	100	100
33	LC	352/427 (82%)	332 (94%)	20 (6%)	0	100	100
34	LD	283/297 (95%)	272 (96%)	10 (4%)	1 (0%)	30	57
35	LE	184/288 (64%)	174 (95%)	10 (5%)	0	100	100
36	LF	215/248 (87%)	206 (96%)	9 (4%)	0	100	100
37	LG	203/266 (76%)	194 (96%)	9 (4%)	0	100	100
38	LH	187/192 (97%)	172 (92%)	15 (8%)	0	100	100
39	LI	195/214 (91%)	190 (97%)	5 (3%)	0	100	100
40	LJ	161/178 (90%)	155 (96%)	6 (4%)	0	100	100
41	LL	187/211 (89%)	181 (97%)	5 (3%)	1 (0%)	24	52
42	LM	133/215 (62%)	127 (96%)	6 (4%)	0	100	100
43	LN	201/204 (98%)	195 (97%)	6 (3%)	0	100	100
44	LO	197/203 (97%)	196 (100%)	1 (0%)	0	100	100
45	LP	150/184 (82%)	147 (98%)	3 (2%)	0	100	100
46	LQ	185/188 (98%)	172 (93%)	13 (7%)	0	100	100
47	LR	171/196 (87%)	169 (99%)	2 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
48	LS	173/176 (98%)	170 (98%)	3 (2%)	0	100	100
49	LT	157/160 (98%)	150 (96%)	6 (4%)	1 (1%)	21	47
50	LU	97/128 (76%)	93 (96%)	4 (4%)	0	100	100
51	LV	129/140 (92%)	125 (97%)	4 (3%)	0	100	100
52	LW	62/157 (40%)	60 (97%)	2 (3%)	0	100	100
53	LX	115/156 (74%)	108 (94%)	7 (6%)	0	100	100
54	LY	129/145 (89%)	123 (95%)	6 (5%)	0	100	100
55	LZ	133/136 (98%)	127 (96%)	6 (4%)	0	100	100
56	La	145/148 (98%)	129 (89%)	15 (10%)	1 (1%)	18	44
57	Lb	64/159 (40%)	64 (100%)	0	0	100	100
58	Lc	91/115 (79%)	90 (99%)	1 (1%)	0	100	100
59	Ld	104/125 (83%)	100 (96%)	4 (4%)	0	100	100
60	Le	125/135 (93%)	121 (97%)	4 (3%)	0	100	100
61	Lf	106/110 (96%)	101 (95%)	4 (4%)	1 (1%)	14	37
62	Lg	104/117 (89%)	104 (100%)	0	0	100	100
63	Lh	118/123 (96%)	115 (98%)	2 (2%)	1 (1%)	16	40
64	Li	98/105 (93%)	94 (96%)	2 (2%)	2 (2%)	6	18
65	Lj	83/97 (86%)	77 (93%)	6 (7%)	0	100	100
66	Lk	66/70 (94%)	64 (97%)	2 (3%)	0	100	100
67	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
68	Lm	49/128 (38%)	48 (98%)	1 (2%)	0	100	100
69	Ln	22/25 (88%)	22 (100%)	0	0	100	100
70	Lo	100/106 (94%)	96 (96%)	4 (4%)	0	100	100
71	Lp	87/92 (95%)	85 (98%)	2 (2%)	0	100	100
72	Lr	122/137 (89%)	115 (94%)	7 (6%)	0	100	100
78	CA	540/858 (63%)	517 (96%)	22 (4%)	1 (0%)	43	70
All	All	10882/13106 (83%)	10245 (94%)	622 (6%)	15 (0%)	49	75

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
22	SZ	50	PHE
30	SF	140	ASP

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Mol	Chain	Res	Type
56	La	122	VAL
9	Sc	35	MET
9	Sc	63	ARG

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	SL	122/142 (86%)	118 (97%)	4 (3%)	33	66
2	SR	98/122 (80%)	87 (89%)	11 (11%)	6	17
3	SP	53/130 (41%)	50 (94%)	3 (6%)	18	46
4	SQ	117/121 (97%)	107 (92%)	10 (8%)	10	28
5	SV	67/67 (100%)	65 (97%)	2 (3%)	36	69
6	SX	109/115 (95%)	105 (96%)	4 (4%)	30	62
7	Sa	83/98 (85%)	82 (99%)	1 (1%)	63	84
8	SU	63/107 (59%)	61 (97%)	2 (3%)	34	67
9	Sc	57/62 (92%)	55 (96%)	2 (4%)	32	64
10	ST	109/115 (95%)	104 (95%)	5 (5%)	24	55
11	Sg	272/275 (99%)	256 (94%)	16 (6%)	18	44
12	SC	188/225 (84%)	181 (96%)	7 (4%)	30	62
13	Sd	38/49 (78%)	36 (95%)	2 (5%)	20	49
14	SJ	160/168 (95%)	154 (96%)	6 (4%)	29	61
15	SN	130/131 (99%)	128 (98%)	2 (2%)	57	81
16	SO	100/119 (84%)	93 (93%)	7 (7%)	14	37
17	SG	200/218 (92%)	189 (94%)	11 (6%)	19	47
18	SW	112/113 (99%)	106 (95%)	6 (5%)	20	48
19	SY	107/115 (93%)	104 (97%)	3 (3%)	38	70
20	Se	47/48 (98%)	46 (98%)	1 (2%)	47	76
21	Sb	73/76 (96%)	70 (96%)	3 (4%)	27	59

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	SZ	58/103 (56%)	54 (93%)	4 (7%)	14	38
23	SA	153/243 (63%)	146 (95%)	7 (5%)	24	55
24	SB	192/231 (83%)	185 (96%)	7 (4%)	31	63
25	SE	221/225 (98%)	209 (95%)	12 (5%)	20	48
26	SD	175/202 (87%)	164 (94%)	11 (6%)	16	41
27	SH	165/174 (95%)	157 (95%)	8 (5%)	23	53
28	SI	160/180 (89%)	155 (97%)	5 (3%)	35	68
29	SK	74/136 (54%)	70 (95%)	4 (5%)	20	48
30	SF	152/170 (89%)	144 (95%)	8 (5%)	20	49
31	LA	188/199 (94%)	187 (100%)	1 (0%)	81	92
32	LB	344/349 (99%)	335 (97%)	9 (3%)	40	72
33	LC	297/348 (85%)	288 (97%)	9 (3%)	36	69
34	LD	241/250 (96%)	232 (96%)	9 (4%)	30	62
35	LE	171/252 (68%)	167 (98%)	4 (2%)	44	75
36	LF	187/215 (87%)	186 (100%)	1 (0%)	81	92
37	LG	180/223 (81%)	174 (97%)	6 (3%)	33	66
38	LH	169/171 (99%)	166 (98%)	3 (2%)	51	79
39	LI	170/181 (94%)	164 (96%)	6 (4%)	32	64
40	LJ	138/149 (93%)	133 (96%)	5 (4%)	31	63
41	LL	160/177 (90%)	155 (97%)	5 (3%)	35	68
42	LM	115/161 (71%)	112 (97%)	3 (3%)	40	72
43	LN	171/172 (99%)	170 (99%)	1 (1%)	78	91
44	LO	171/174 (98%)	168 (98%)	3 (2%)	51	79
45	LP	133/163 (82%)	131 (98%)	2 (2%)	57	81
46	LQ	164/165 (99%)	160 (98%)	4 (2%)	43	74
47	LR	153/175 (87%)	153 (100%)	0	100	100
48	LS	156/157 (99%)	151 (97%)	5 (3%)	34	67
49	LT	139/140 (99%)	136 (98%)	3 (2%)	45	75
50	LU	89/115 (77%)	88 (99%)	1 (1%)	65	85
51	LV	101/107 (94%)	98 (97%)	3 (3%)	36	69
52	LW	56/126 (44%)	55 (98%)	1 (2%)	51	79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	LX	105/133 (79%)	103 (98%)	2 (2%)	50	78
54	LY	122/135 (90%)	117 (96%)	5 (4%)	27	59
55	LZ	117/118 (99%)	116 (99%)	1 (1%)	70	87
56	La	120/121 (99%)	119 (99%)	1 (1%)	73	89
57	Lb	57/126 (45%)	56 (98%)	1 (2%)	51	79
58	Lc	78/97 (80%)	76 (97%)	2 (3%)	40	72
59	Ld	97/110 (88%)	94 (97%)	3 (3%)	35	68
60	Le	114/121 (94%)	114 (100%)	0	100	100
61	Lf	87/89 (98%)	87 (100%)	0	100	100
62	Lg	92/100 (92%)	90 (98%)	2 (2%)	45	75
63	Lh	108/110 (98%)	106 (98%)	2 (2%)	50	78
64	Li	85/89 (96%)	83 (98%)	2 (2%)	43	74
65	Lj	72/80 (90%)	70 (97%)	2 (3%)	38	70
66	Lk	63/65 (97%)	62 (98%)	1 (2%)	55	81
67	Ll	47/48 (98%)	44 (94%)	3 (6%)	16	41
68	Lm	47/116 (40%)	47 (100%)	0	100	100
69	Ln	23/24 (96%)	23 (100%)	0	100	100
70	Lo	90/94 (96%)	88 (98%)	2 (2%)	45	75
71	Lp	72/75 (96%)	72 (100%)	0	100	100
72	Lr	108/121 (89%)	104 (96%)	4 (4%)	30	62
78	CA	468/730 (64%)	452 (97%)	16 (3%)	32	65
All	All	9520/11151 (85%)	9213 (97%)	307 (3%)	35	67

5 of 307 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	LL	155	MET
70	Lo	14	LYS
44	LO	129	LEU
54	LY	24	HIS
78	CA	651	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
38	LH	98	HIS
46	LQ	125	GLN
38	LH	116	ASN
44	LO	184	ASN
54	LY	43	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
73	L5	3262/5070 (64%)	750 (22%)	35 (1%)
74	L7	119/121 (98%)	14 (11%)	0
75	L8	149/157 (94%)	36 (24%)	0
76	S2	1615/1869 (86%)	514 (31%)	21 (1%)
77	S6	74/75 (98%)	37 (50%)	2 (2%)
All	All	5219/7292 (71%)	1351 (25%)	58 (1%)

5 of 1351 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
73	L5	9	C
73	L5	13	U
73	L5	14	C
73	L5	15	A
73	L5	25	A

5 of 58 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
73	L5	3974	G
76	S2	1825	A
76	S2	1	U
76	S2	1780	G
76	S2	915	G

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 298 ligands modelled in this entry, 297 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
81	A1L8F	L5	5332	-	24,26,26	2.76	8 (33%)	26,40,40	1.94	4 (15%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
81	A1L8F	L5	5332	-	-	0/2/44/44	0/5/5/5

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
81	L5	5332	A1L8F	C10-C09	-7.22	1.43	1.51
81	L5	5332	A1L8F	O01-C01	6.64	1.49	1.38
81	L5	5332	A1L8F	O02-C07	-4.54	1.34	1.43
81	L5	5332	A1L8F	C05-C08	-3.92	1.47	1.52
81	L5	5332	A1L8F	C15-C10	-3.53	1.47	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
81	L5	5332	A1L8F	C06-C11-N01	-6.71	102.06	113.36
81	L5	5332	A1L8F	O01-C01-C02	3.30	132.24	127.86
81	L5	5332	A1L8F	C07-O01-C01	-2.60	101.83	105.32
81	L5	5332	A1L8F	O02-C07-O01	2.54	112.08	108.09

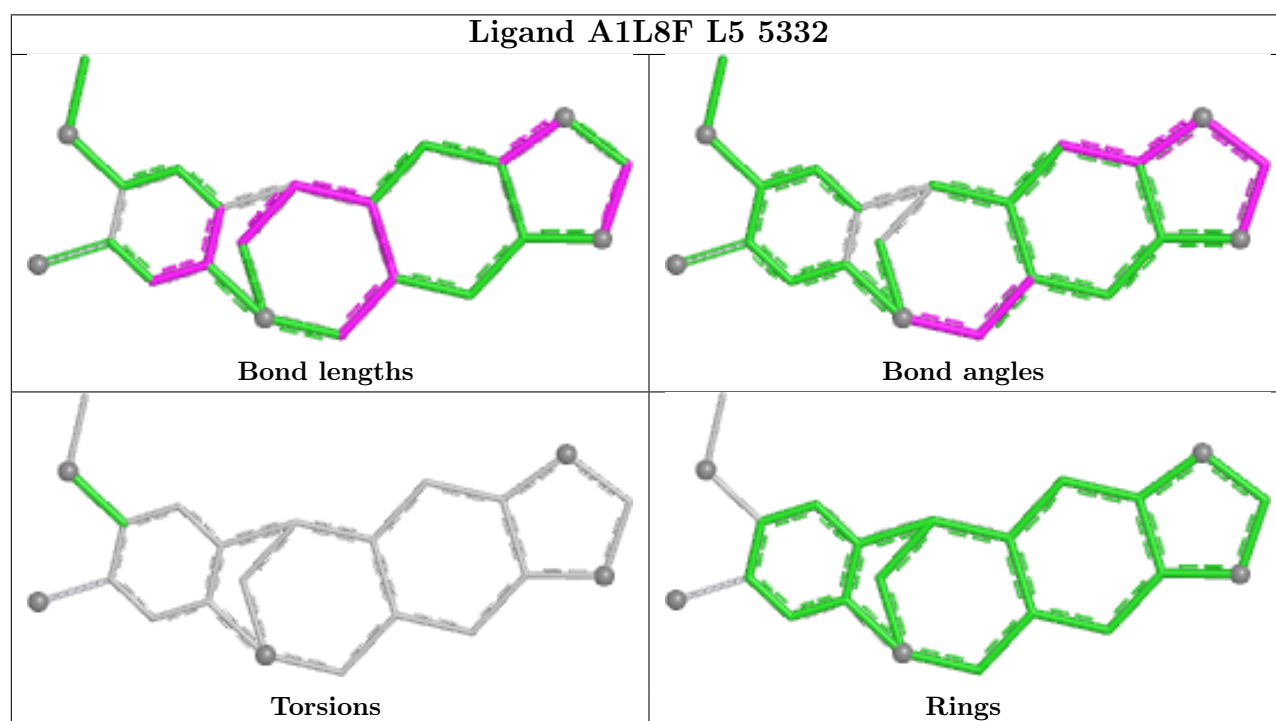
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

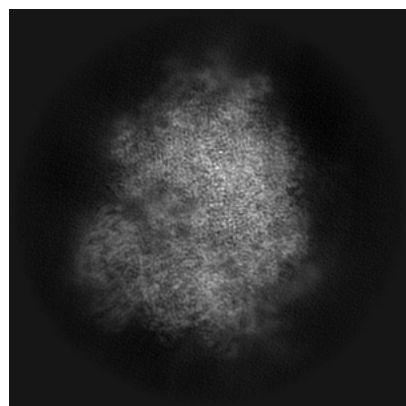
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-63560. These allow visual inspection of the internal detail of the map and identification of artifacts.

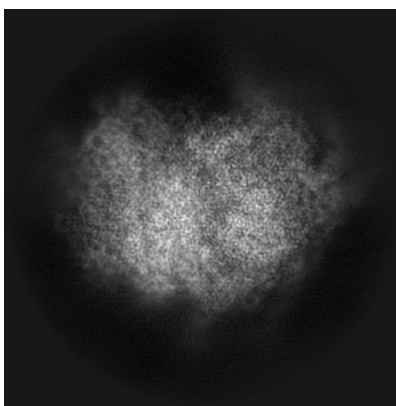
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

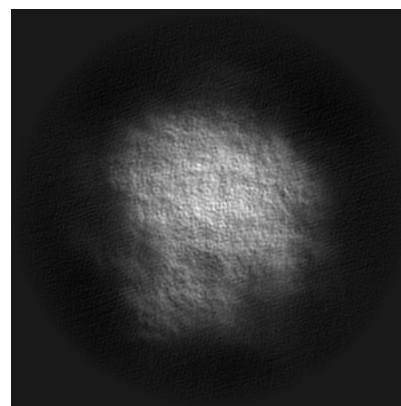
6.1.1 Primary map



X

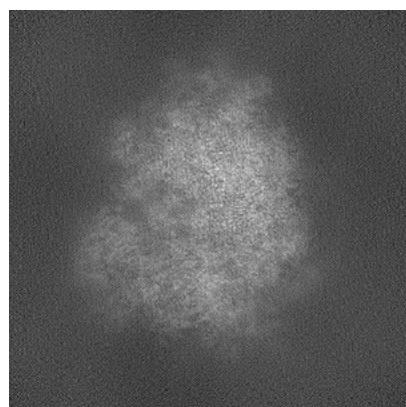


Y

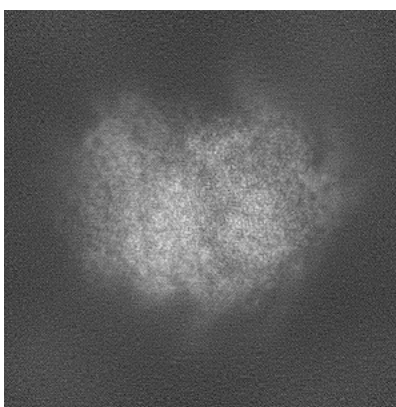


Z

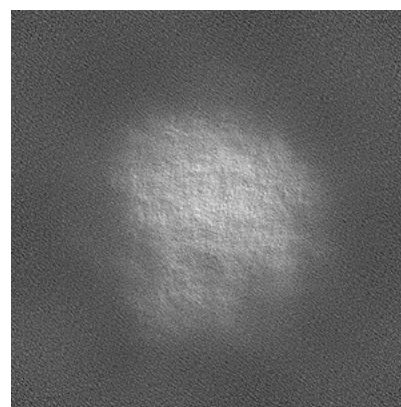
6.1.2 Raw map



X



Y

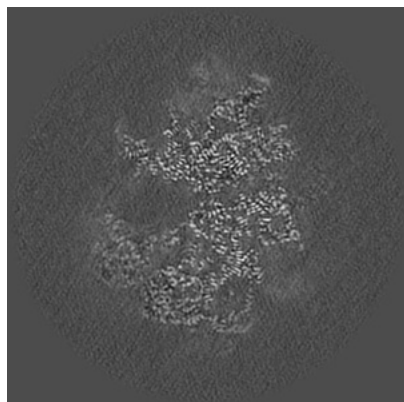


Z

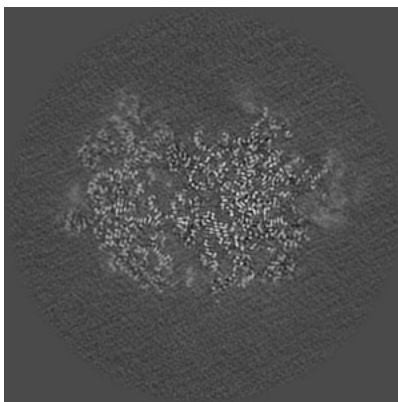
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

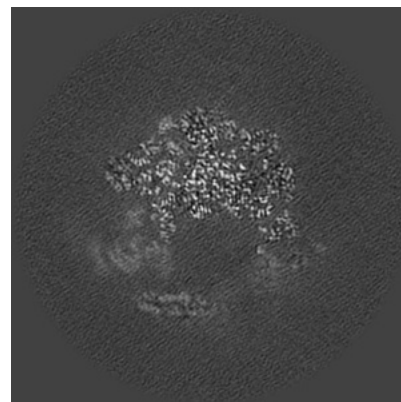
6.2.1 Primary map



X Index: 256

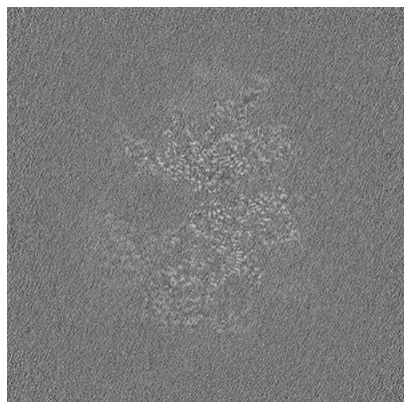


Y Index: 256

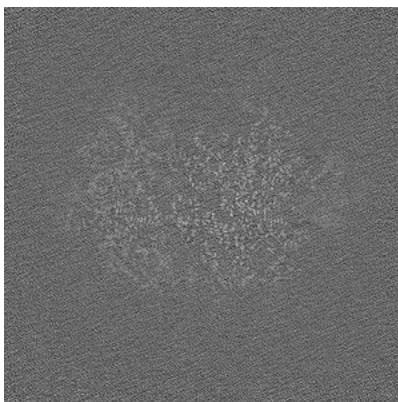


Z Index: 256

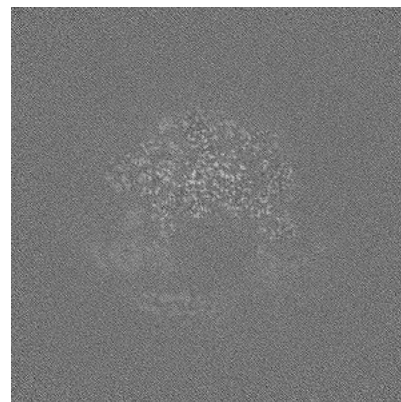
6.2.2 Raw map



X Index: 256



Y Index: 256

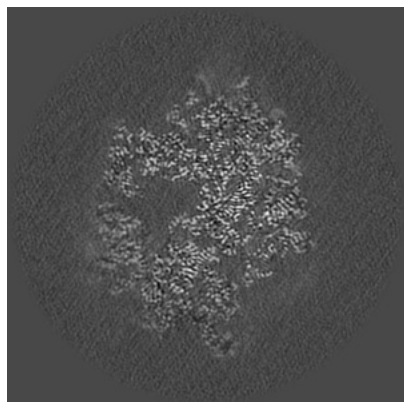


Z Index: 256

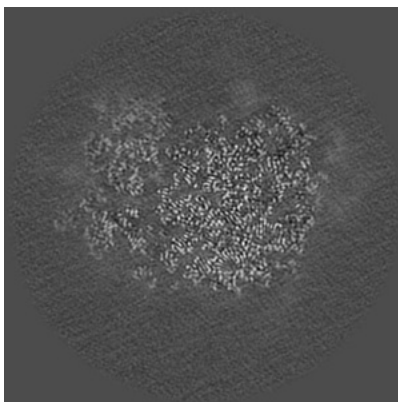
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

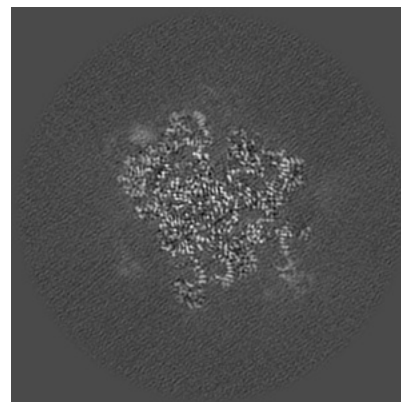
6.3.1 Primary map



X Index: 234

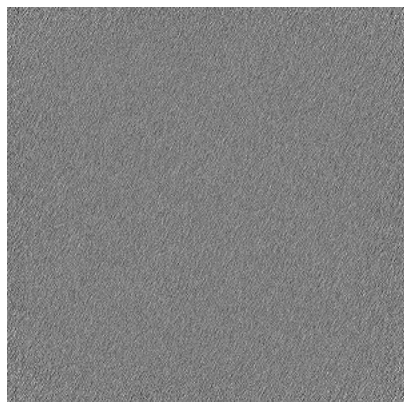


Y Index: 272

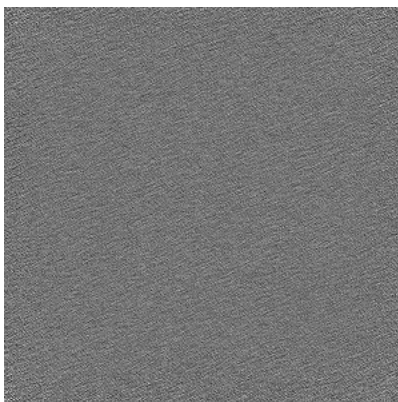


Z Index: 296

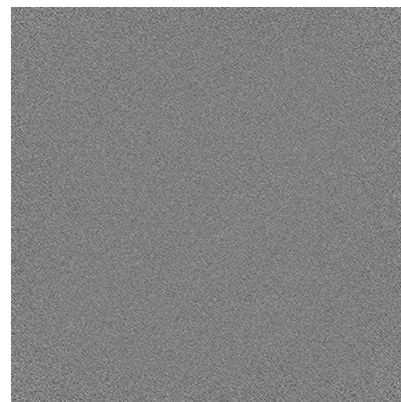
6.3.2 Raw map



X Index: 0



Y Index: 0

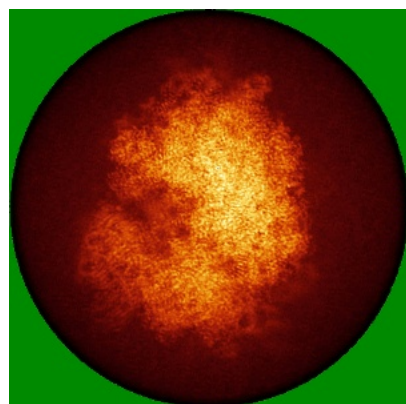


Z Index: 0

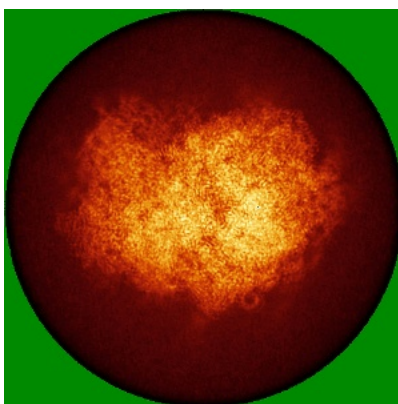
The images above show the largest variance slices of the map in three orthogonal directions.

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

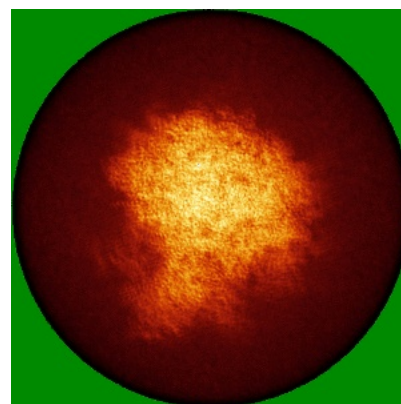
6.4.1 Primary map



X

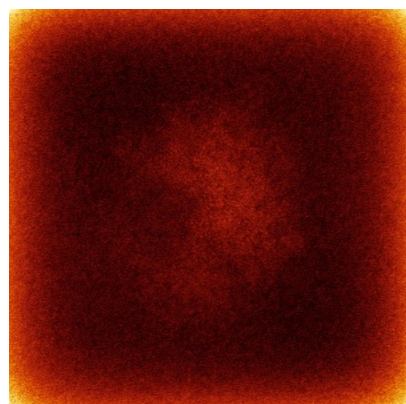


Y

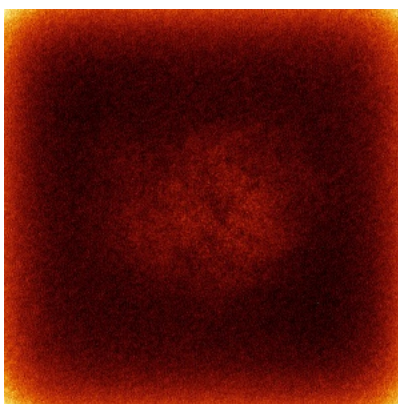


Z

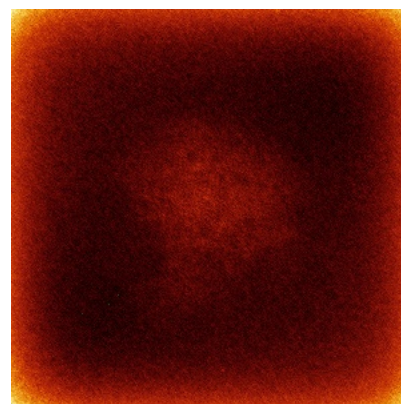
6.4.2 Raw map



X



Y



Z

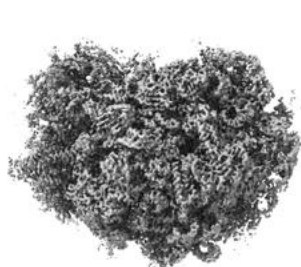
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



X



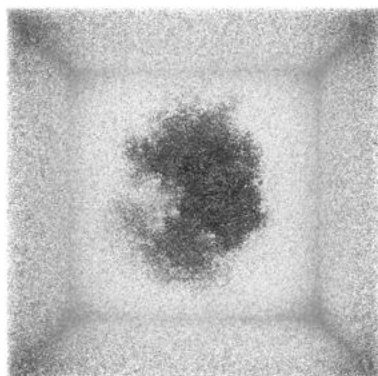
Y



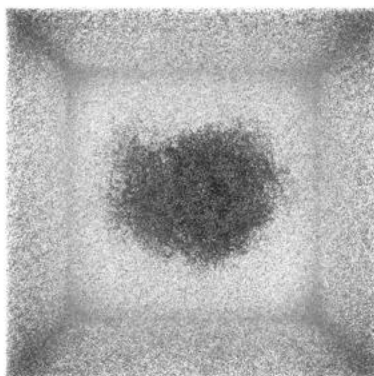
Z

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

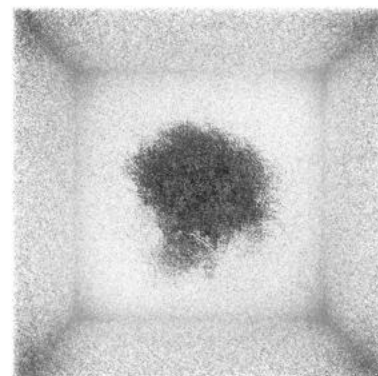
6.5.2 Raw map



X



Y



Z

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.

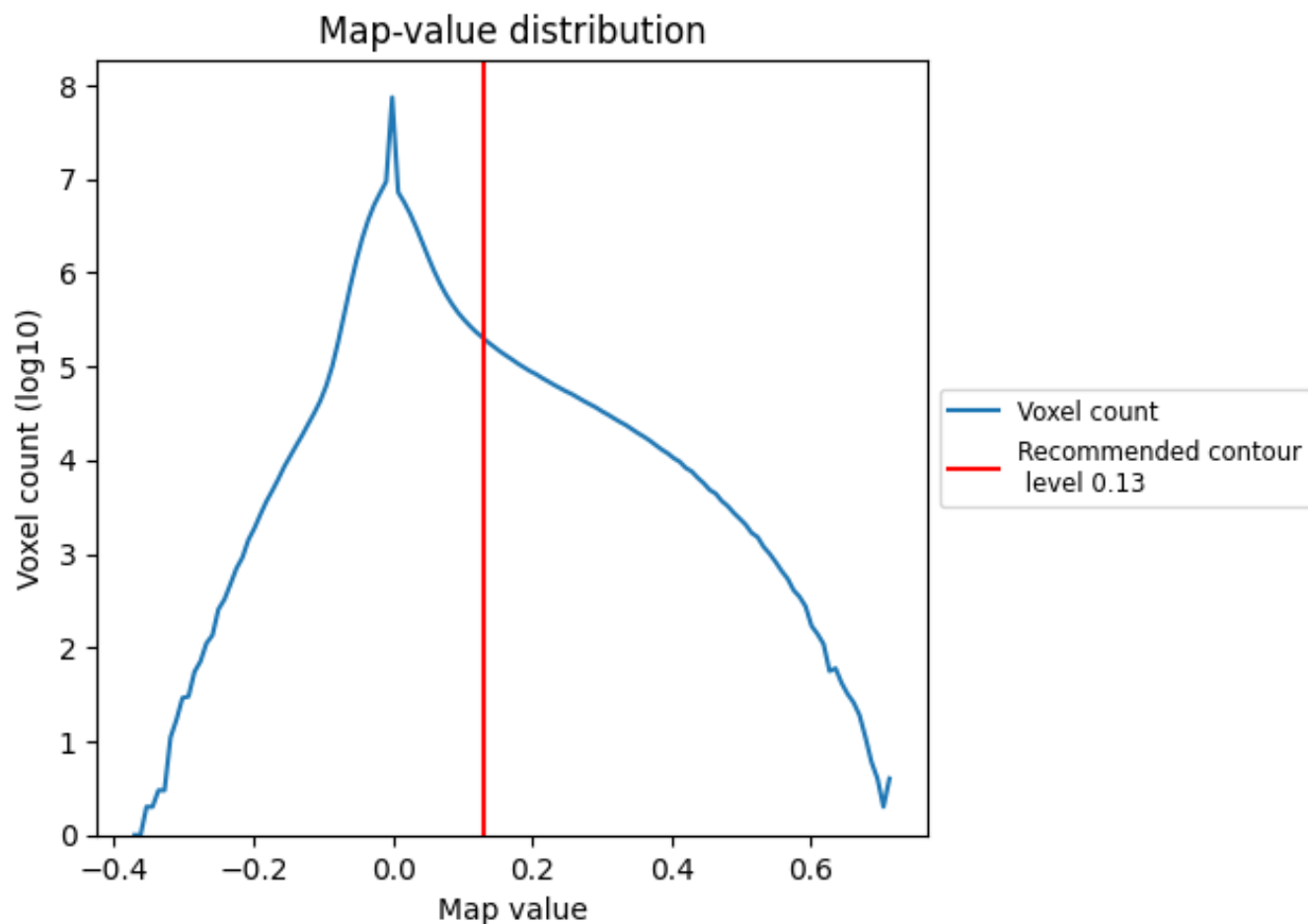
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

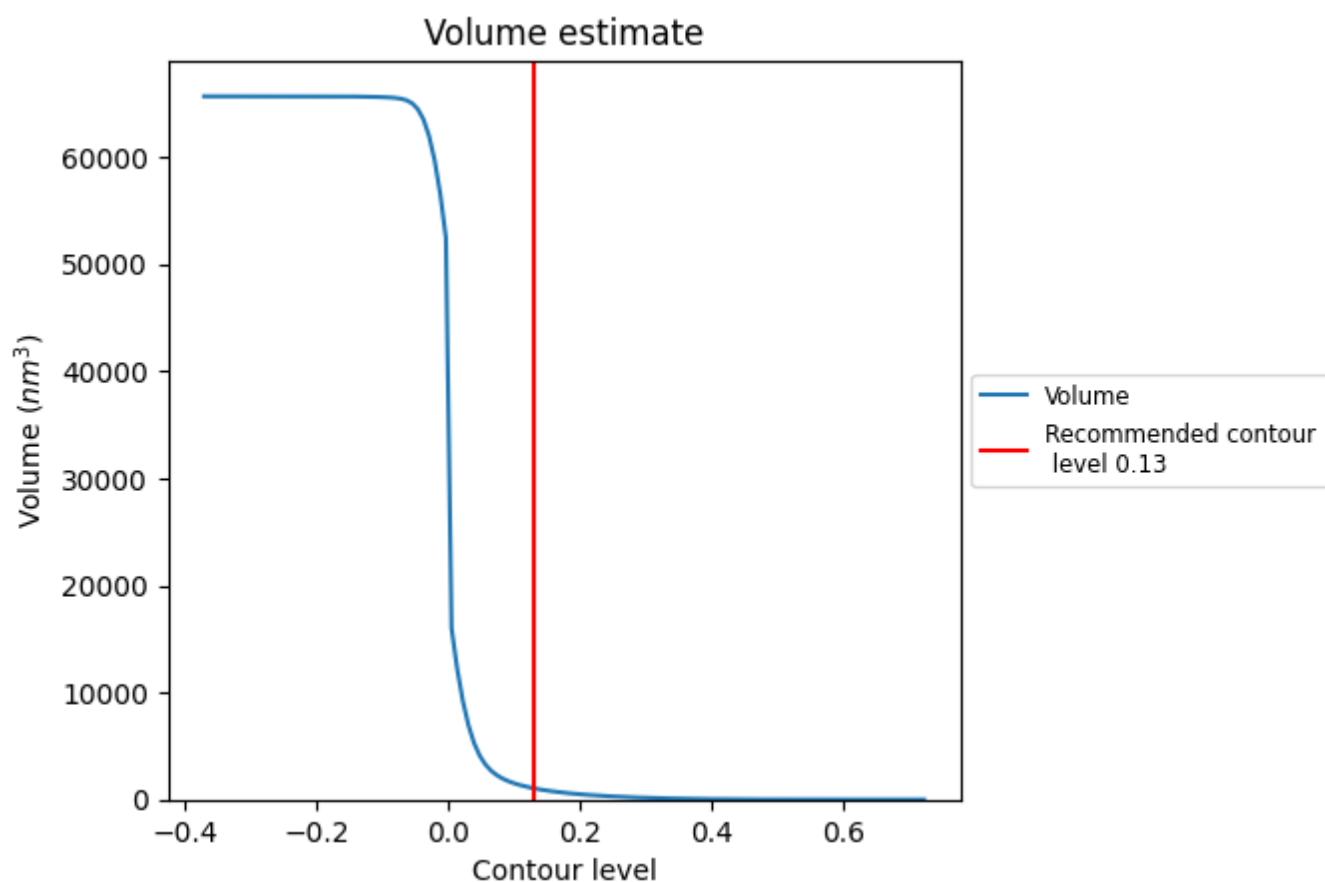
This section contains the results of statistical analysis of the map.

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.

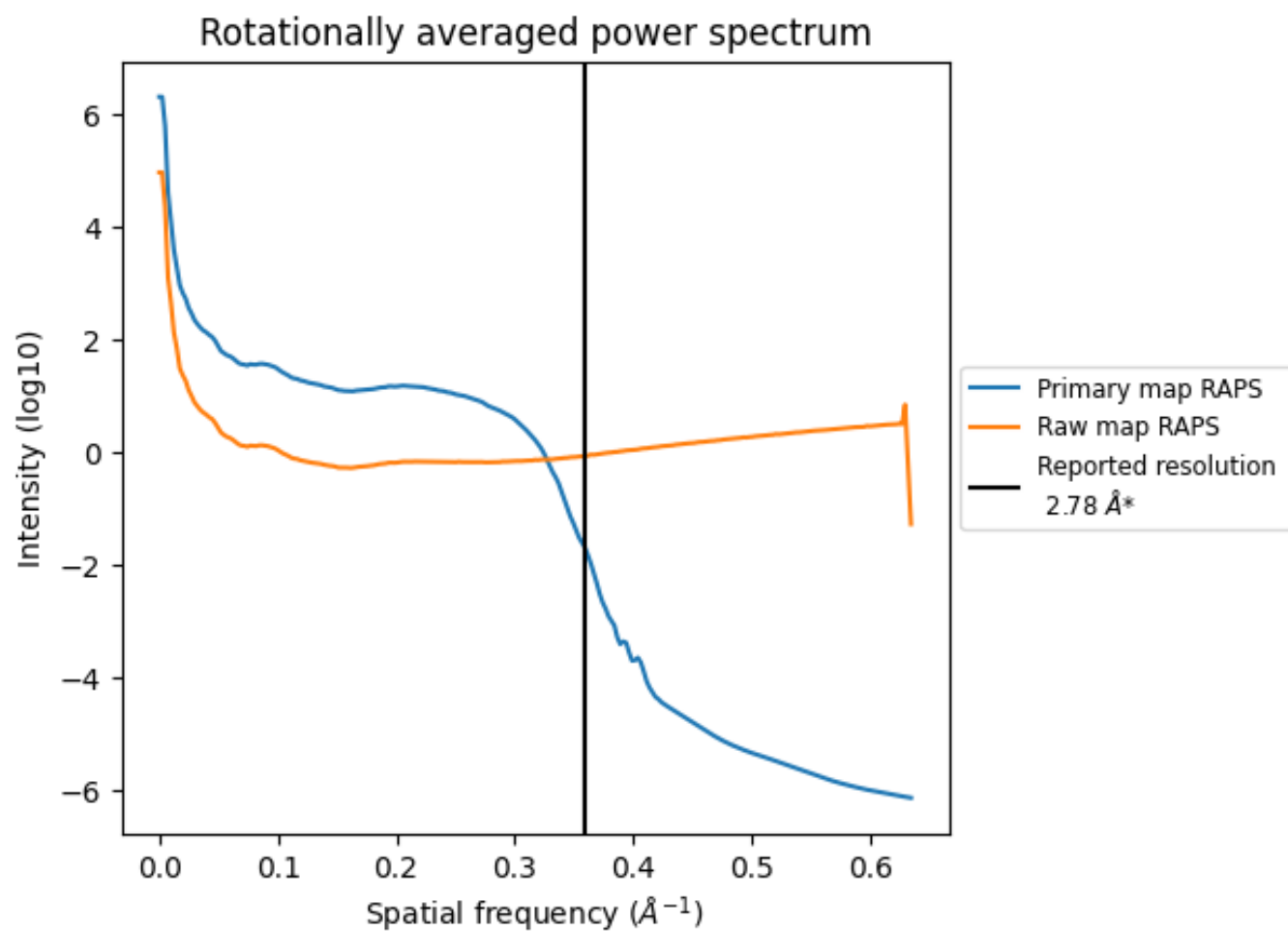
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1046 nm^3 ; this corresponds to an approximate mass of 945 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 [i](#)

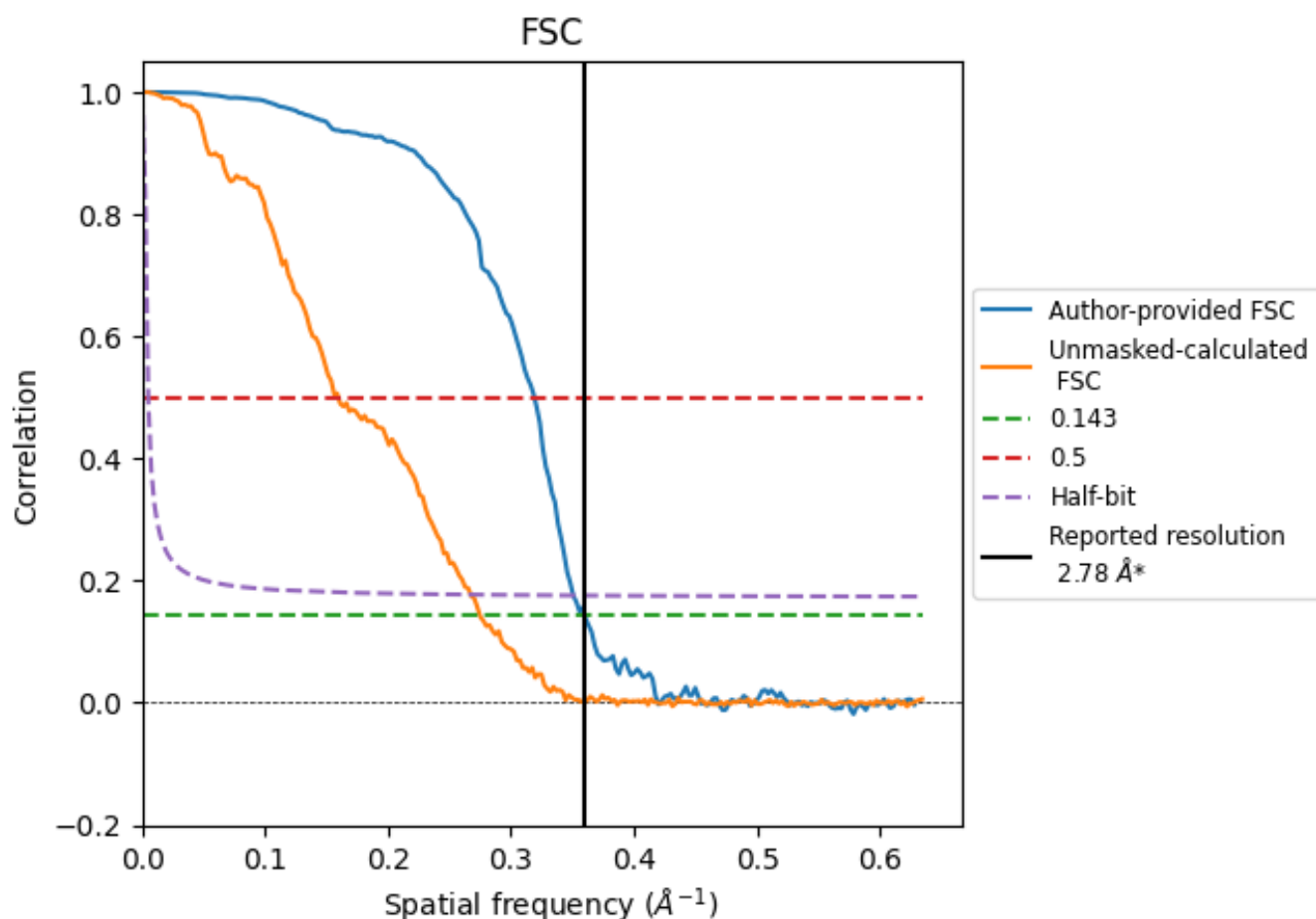


*Reported resolution corresponds to spatial frequency of 0.360 $\text{\AA}^{-1}$

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.360 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

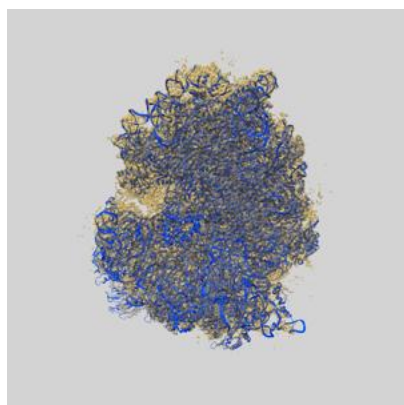
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.78	-	-
Author-provided FSC curve	2.78	3.13	2.85
Unmasked-calculated*	3.64	6.27	3.74

*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 3.64 differs from the reported value 2.78 by more than 10 %

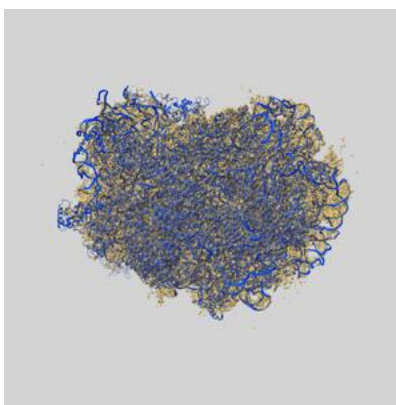
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-63560 and PDB model 9M0P. Per-residue inclusion information can be found in section 3 on page 19.

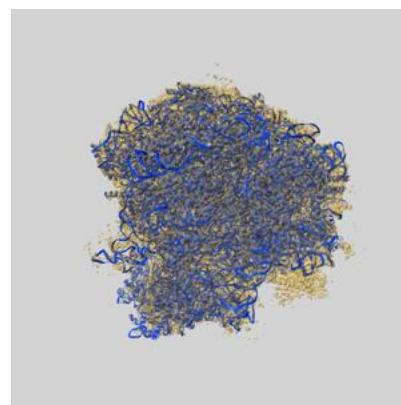
9.1 Map-model overlay [i](#)



X



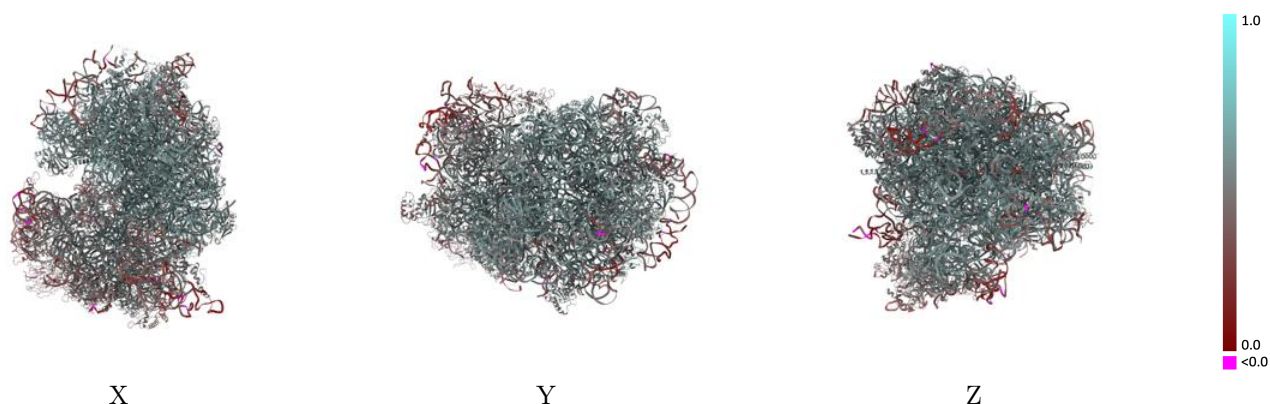
Y



Z

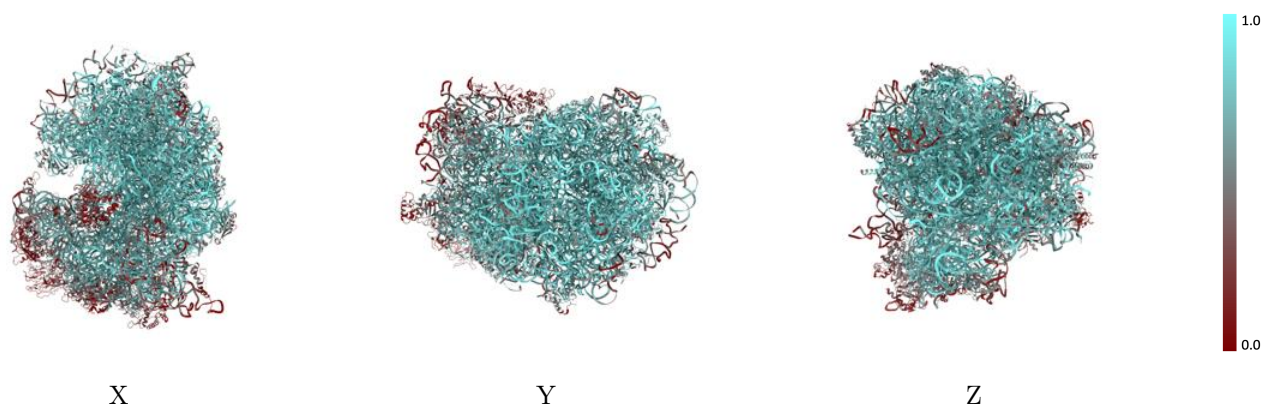
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



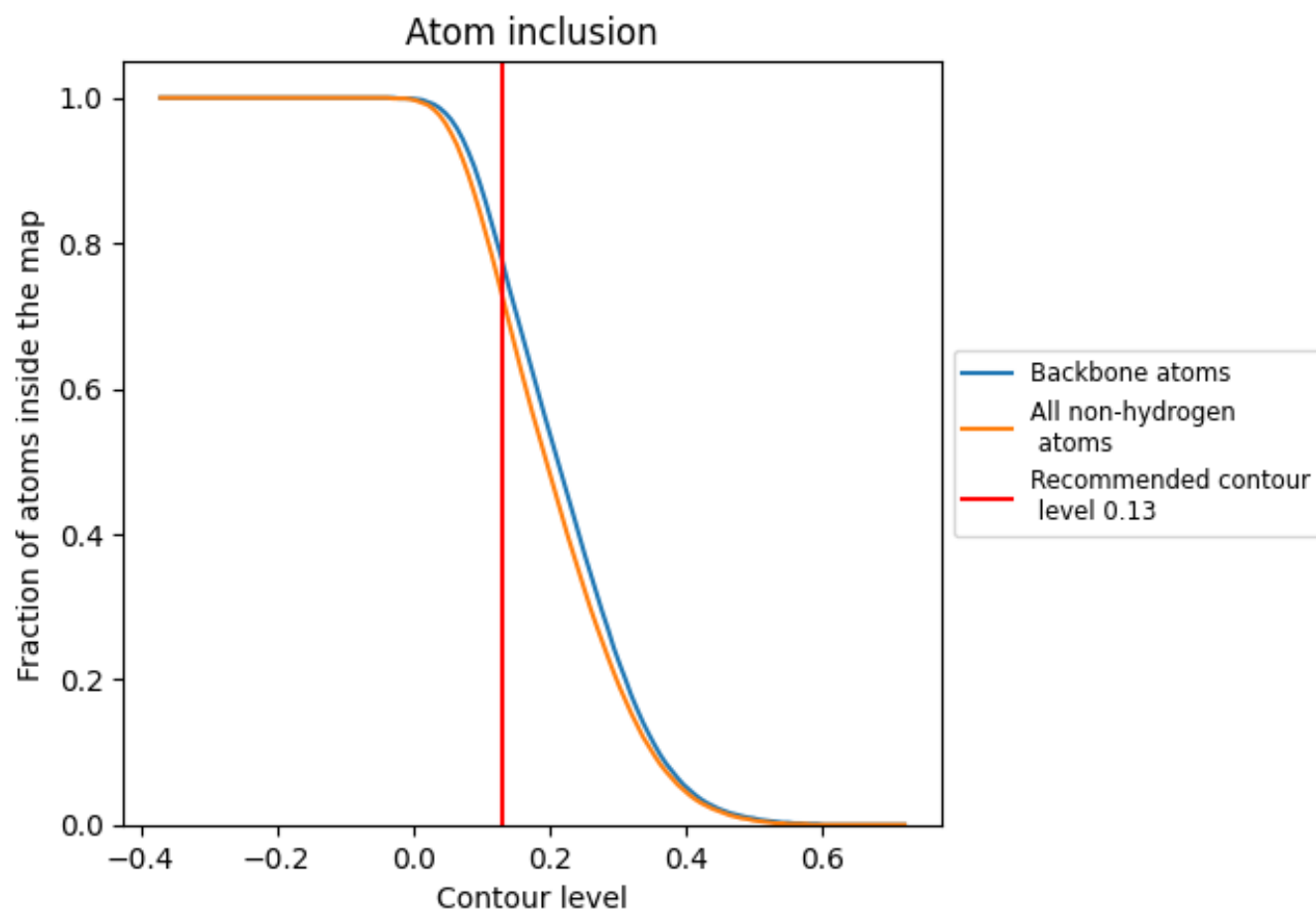
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



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

9.4 Atom inclusion [i](#)



At the recommended contour level, 78% of all backbone atoms, 73% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

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

Chain	Atom inclusion	Q-score
All	 0.7310	 0.5030
CA	 0.3250	 0.4630
L5	 0.8570	 0.5230
L7	 0.9160	 0.5680
L8	 0.8680	 0.5110
LA	 0.9000	 0.5980
LB	 0.7840	 0.5800
LC	 0.7960	 0.5510
LD	 0.7290	 0.5540
LE	 0.6740	 0.5400
LF	 0.8320	 0.5780
LG	 0.6790	 0.5280
LH	 0.7090	 0.5540
LI	 0.8170	 0.5770
LJ	 0.6240	 0.5350
LL	 0.7510	 0.5350
LM	 0.7580	 0.5580
LN	 0.9080	 0.5720
LO	 0.8170	 0.5790
LP	 0.8310	 0.5750
LQ	 0.8380	 0.5680
LR	 0.7740	 0.5500
LS	 0.8290	 0.5800
LT	 0.7720	 0.5670
LU	 0.5950	 0.5060
LV	 0.7880	 0.5780
LW	 0.7360	 0.5740
LX	 0.7370	 0.5460
LY	 0.6990	 0.5190
LZ	 0.7410	 0.5540
La	 0.8370	 0.5700
Lb	 0.7810	 0.5580
Lc	 0.7620	 0.5580
Ld	 0.7620	 0.5520
Le	 0.8170	 0.5730



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Chain	Atom inclusion	Q-score
Lf	 0.8520	 0.5820
Lg	 0.8520	 0.5730
Lh	 0.6890	 0.5200
Li	 0.7470	 0.5380
Lj	 0.9110	 0.5790
Lk	 0.6090	 0.5270
Ll	 0.8700	 0.5500
Lm	 0.8150	 0.5660
Ln	 0.8610	 0.5730
Lo	 0.8250	 0.5810
Lp	 0.8540	 0.5900
Lr	 0.7250	 0.5330
S2	 0.7220	 0.4440
S6	 0.6230	 0.4140
SA	 0.4960	 0.4870
SB	 0.6100	 0.5210
SC	 0.5540	 0.4810
SD	 0.3350	 0.4120
SE	 0.4810	 0.4600
SF	 0.3050	 0.4030
SG	 0.2540	 0.3680
SH	 0.3200	 0.4390
SI	 0.5370	 0.4860
SJ	 0.4920	 0.4530
SK	 0.2730	 0.3580
SL	 0.6830	 0.5320
SN	 0.6690	 0.5330
SO	 0.6890	 0.5300
SP	 0.2990	 0.3780
SQ	 0.2720	 0.3890
SR	 0.2830	 0.4190
ST	 0.2560	 0.3940
SU	 0.3220	 0.3610
SV	 0.4740	 0.4870
SW	 0.6730	 0.5190
SX	 0.7120	 0.5230
SY	 0.2700	 0.4010
SZ	 0.2110	 0.3510
Sa	 0.7210	 0.5340
Sb	 0.4590	 0.4710
Sc	 0.2370	 0.3980
Sd	 0.6320	 0.4930

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Chain	Atom inclusion	Q-score
Se	 0.4050	 0.4070
Sg	 0.0620	 0.3050