



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 01:07 AM UTC

PDB ID : 9G8M / pdb_00009g8m
EMDB ID : EMD-51132
Title : human 80S ribosome bound by a SKI2-exosome complex
Authors : Koegel, A.; Keidel, A.; Loukeri, M.J.; Kuhn, C.C.; Langer, L.M.; Schaefer, I.B.; Conti, E.
Deposited on : 2024-07-23
Resolution : 3.30 Å(reported)

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

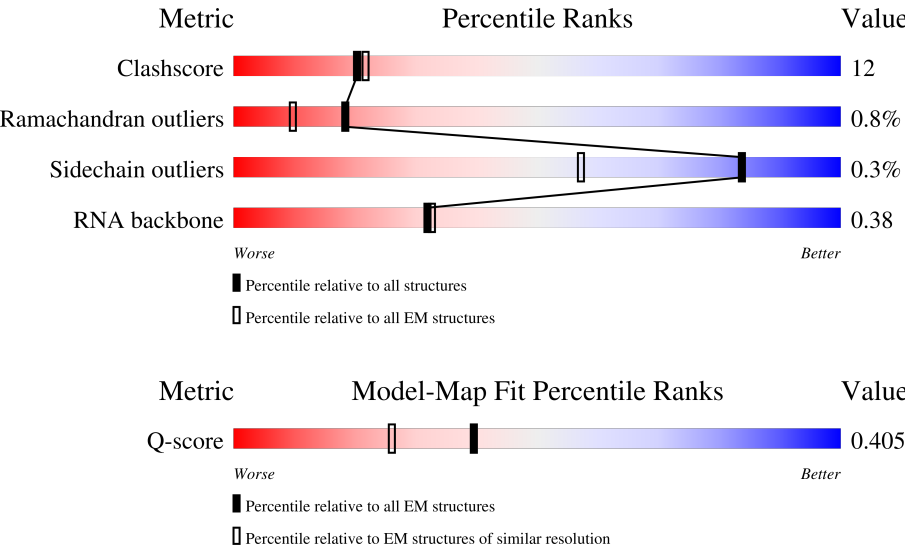
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.30 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	15087 (2.80 - 3.80)

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	A	1246	
2	L	245	
3	N	280	

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Mol	Chain	Length	Quality of chain
4	O	239	
5	F	295	
6	G	272	
7	H	371	
8	I	297	
9	J	199	
10	K	443	
11	E	274	
12	M	1096	
13	X	249	
14	S2	1869	
15	SA	295	
16	SB	264	
17	SD	243	
18	SE	263	
19	SF	204	
20	SH	194	
21	SI	208	
22	SK	165	
23	SL	158	
24	SP	145	
25	SQ	146	
26	SR	135	
27	SS	152	
28	ST	145	

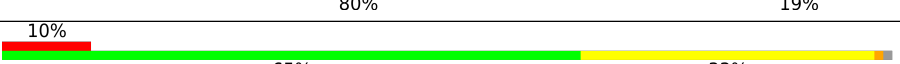
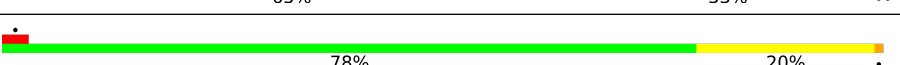
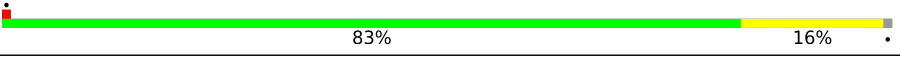
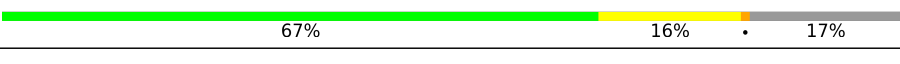
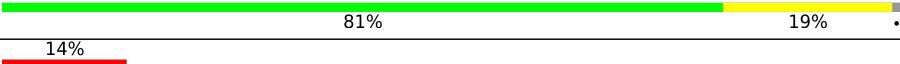
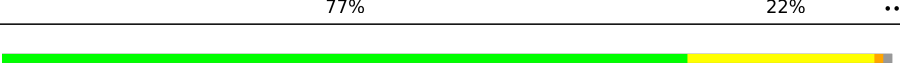
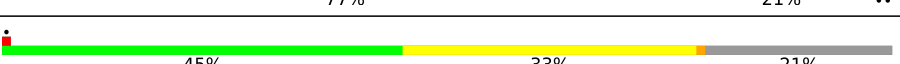
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Mol	Chain	Length	Quality of chain
29	SU	119	
30	SV	83	
31	SX	143	
32	Sa	115	
33	Sc	69	
34	Sd	56	
35	Sf	156	
36	Sg	317	
37	SC	293	
38	SG	249	
39	SJ	194	
40	SM	132	
41	SN	151	
42	SO	151	
43	SW	130	
44	SY	133	
45	SZ	125	
46	Sb	84	
47	Se	59	
48	L5	5066	
49	L7	121	
50	L8	157	
51	LA	257	
52	LB	403	
53	LC	427	

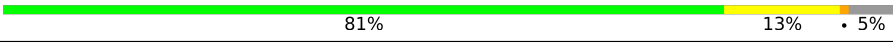
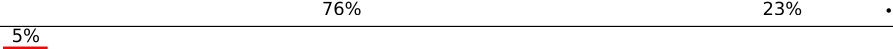
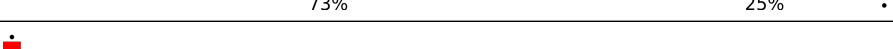
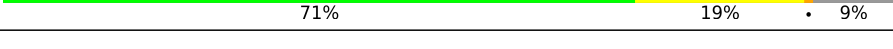
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Mol	Chain	Length	Quality of chain
54	LD	297	
55	LE	288	
56	LF	248	
57	LG	266	
58	LH	192	
59	LI	214	
60	LJ	178	
61	LL	211	
62	LM	215	
63	LN	204	
64	LO	203	
65	LP	184	
66	LQ	188	
67	LR	196	
68	LS	176	
69	LT	160	
70	LU	128	
71	LV	140	
72	LW	157	
73	LX	156	
74	LY	145	
75	LZ	136	
76	La	148	
77	Lb	159	
78	Lc	115	

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Mol	Chain	Length	Quality of chain
79	Ld	125	
80	Le	135	
81	Lf	110	
82	Lg	117	
83	Lh	123	
84	Li	105	
85	Lj	97	
86	Lk	70	
87	Ll	51	
88	Lm	128	
89	Ln	25	
90	Lo	106	
91	Lp	92	
92	Lr	137	

2 Entry composition

There are 94 unique types of molecules in this entry. The entry contains 251092 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 Helicase SKI2W.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	949	Total	C	N	O	S	0	0
			7438	4710	1316	1370	42		

- Molecule 2 is a protein called Exosome complex component RRP41.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	L	241	Total	C	N	O	S	0	0
			1819	1123	343	344	9		

- Molecule 3 is a protein called Exosome complex component RRP43.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	N	265	Total	C	N	O	S	0	0
			2020	1272	337	397	14		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
N	-3	GLY	-	expression tag	UNP Q96B26
N	-2	PRO	-	expression tag	UNP Q96B26
N	-1	ASP	-	expression tag	UNP Q96B26
N	0	SER	-	expression tag	UNP Q96B26

- Molecule 4 is a protein called Exosome complex component RRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	O	208	Total	C	N	O	S	0	0
			1566	979	278	297	12		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	-3	GLY	-	expression tag	UNP Q9NQT4

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Chain	Residue	Modelled	Actual	Comment	Reference
O	-2	PRO	-	expression tag	UNP Q9NQT4
O	-1	ASP	-	expression tag	UNP Q9NQT4
O	0	SER	-	expression tag	UNP Q9NQT4

- Molecule 5 is a protein called Exosome complex component RRP42.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	F	286	Total	C	N	O	S	0	0
			2194	1373	374	432	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	-3	GLY	-	expression tag	UNP Q15024
F	-2	PRO	-	expression tag	UNP Q15024
F	-1	ASP	-	expression tag	UNP Q15024
F	0	SER	-	expression tag	UNP Q15024

- Molecule 6 is a protein called Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	G	251	Total	C	N	O	S	0	0
			1852	1149	352	344	7		

- Molecule 7 is a protein called Exosome complex component RRP40,Exosome complex component MTR3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	H	237	Total	C	N	O	S	0	0
			1810	1139	331	328	12		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
H	-3	GLY	-	expression tag	UNP Q9NQT5
H	-2	PRO	-	expression tag	UNP Q9NQT5
H	-1	ASP	-	expression tag	UNP Q9NQT5
H	0	SER	-	expression tag	UNP Q9NQT5
H	61	HIS	SER	conflict	UNP Q9NQT5
H	225	HIS	TYR	variant	UNP Q9NQT5

- Molecule 8 is a protein called Exosome complex component RRP4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	I	289	Total	C	N	O	S	0	0
			2263	1424	405	419	15		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	-3	GLY	-	expression tag	UNP Q13868
I	-2	PRO	-	expression tag	UNP Q13868
I	-1	ASP	-	expression tag	UNP Q13868
I	0	SER	-	expression tag	UNP Q13868

- Molecule 9 is a protein called Exosome complex component CSL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	J	184	Total	C	N	O	S	0	0
			1414	889	248	267	10		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
J	-3	GLY	-	expression tag	UNP Q9Y3B2
J	-2	PRO	-	expression tag	UNP Q9Y3B2
J	-1	ASP	-	expression tag	UNP Q9Y3B2
J	0	SER	-	expression tag	UNP Q9Y3B2

- Molecule 10 is a protein called Exosome complex component RRP45.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	K	341	Total	C	N	O	S	0	0
			2673	1680	468	506	19		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	-3	GLY	-	expression tag	UNP Q06265
K	-2	PRO	-	expression tag	UNP Q06265
K	-1	ASP	-	expression tag	UNP Q06265
K	0	SER	-	expression tag	UNP Q06265

- Molecule 11 is a protein called Isoform 2 of HBS1-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	E	63	Total	C	N	O	S	0	0
			499	324	83	91	1		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	365	GLY	-	expression tag	UNP Q9Y450
E	366	PRO	-	expression tag	UNP Q9Y450
E	367	ASP	-	expression tag	UNP Q9Y450
E	368	SER	-	expression tag	UNP Q9Y450
E	633	LEU	-	expression tag	UNP Q9Y450
E	634	GLU	-	expression tag	UNP Q9Y450
E	635	VAL	-	expression tag	UNP Q9Y450
E	636	LEU	-	expression tag	UNP Q9Y450
E	637	PHE	-	expression tag	UNP Q9Y450
E	638	GLN	-	expression tag	UNP Q9Y450

- Molecule 12 is a protein called DIS3-like exonuclease 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	M	983	Total	C	N	O	S	0	0
			7967	5028	1412	1486	41		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	-41	MET	-	initiating methionine	UNP Q8TF46
M	-40	SER	-	expression tag	UNP Q8TF46
M	-39	ALA	-	expression tag	UNP Q8TF46
M	-38	TRP	-	expression tag	UNP Q8TF46
M	-37	SER	-	expression tag	UNP Q8TF46
M	-36	HIS	-	expression tag	UNP Q8TF46
M	-35	PRO	-	expression tag	UNP Q8TF46
M	-34	GLN	-	expression tag	UNP Q8TF46
M	-33	PHE	-	expression tag	UNP Q8TF46
M	-32	GLU	-	expression tag	UNP Q8TF46
M	-31	LYS	-	expression tag	UNP Q8TF46
M	-30	GLY	-	expression tag	UNP Q8TF46
M	-29	GLY	-	expression tag	UNP Q8TF46
M	-28	GLY	-	expression tag	UNP Q8TF46
M	-27	SER	-	expression tag	UNP Q8TF46
M	-26	GLY	-	expression tag	UNP Q8TF46
M	-25	GLY	-	expression tag	UNP Q8TF46

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Chain	Residue	Modelled	Actual	Comment	Reference
M	-24	GLY	-	expression tag	UNP Q8TF46
M	-23	SER	-	expression tag	UNP Q8TF46
M	-22	GLY	-	expression tag	UNP Q8TF46
M	-21	GLY	-	expression tag	UNP Q8TF46
M	-20	SER	-	expression tag	UNP Q8TF46
M	-19	ALA	-	expression tag	UNP Q8TF46
M	-18	TRP	-	expression tag	UNP Q8TF46
M	-17	SER	-	expression tag	UNP Q8TF46
M	-16	HIS	-	expression tag	UNP Q8TF46
M	-15	PRO	-	expression tag	UNP Q8TF46
M	-14	GLN	-	expression tag	UNP Q8TF46
M	-13	PHE	-	expression tag	UNP Q8TF46
M	-12	GLU	-	expression tag	UNP Q8TF46
M	-11	LYS	-	expression tag	UNP Q8TF46
M	-10	THR	-	expression tag	UNP Q8TF46
M	-9	ALA	-	expression tag	UNP Q8TF46
M	-8	GLY	-	expression tag	UNP Q8TF46
M	-7	LEU	-	expression tag	UNP Q8TF46
M	-6	GLU	-	expression tag	UNP Q8TF46
M	-5	VAL	-	expression tag	UNP Q8TF46
M	-4	LEU	-	expression tag	UNP Q8TF46
M	-3	PHE	-	expression tag	UNP Q8TF46
M	-2	GLN	-	expression tag	UNP Q8TF46
M	-1	GLY	-	expression tag	UNP Q8TF46
M	0	PRO	-	expression tag	UNP Q8TF46
M	486	ASN	ASP	conflict	UNP Q8TF46

- Molecule 13 is a RNA chain called CrPV-IRES RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	X	194	Total	C	N	O	P	0	0
			4020	1802	633	1391	194		

- Molecule 14 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S2	1742	Total	C	N	O	P	0	0
			36900	16458	6595	12106	1741		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	SA	222	Total	C	N	O	S	0	0
			1747	1109	306	324	8		

- Molecule 16 is a protein called 40S ribosomal protein S3a.

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

- Molecule 17 is a protein called 40S ribosomal protein S3.

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

- Molecule 18 is a protein called 40S ribosomal protein S4, X isoform.

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

- Molecule 19 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	SF	191	Total	C	N	O	S	0	0
			1509	943	286	273	7		

- Molecule 20 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	SH	189	Total	C	N	O	S	0	0
			1521	969	280	271	1		

- Molecule 21 is a protein called 40S ribosomal protein S8.

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

- Molecule 22 is a protein called 40S ribosomal protein S10.

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

- Molecule 23 is a protein called 40S ribosomal protein S11.

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

- Molecule 24 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	SP	97	Total	C	N	O	S	0	0
			804	505	155	138	6		

- Molecule 25 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	SQ	146	Total	C	N	O	S	0	0
			1158	736	218	200	4		

- Molecule 26 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	SR	132	Total	C	N	O	S	0	0
			1072	673	199	195	5		

- Molecule 27 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	SS	150	Total	C	N	O	S	0	0
			1235	776	250	208	1		

- Molecule 28 is a protein called 40S ribosomal protein S19.

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

- Molecule 29 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	SU	104	Total	C	N	O	S	0	0
			822	514	156	148	4		

- Molecule 30 is a protein called 40S ribosomal protein S21.

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

- Molecule 31 is a protein called 40S ribosomal protein S23.

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

- Molecule 32 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	Sa	107	Total	C	N	O	S	0	0
			847	528	176	138	5		

- Molecule 33 is a protein called 40S ribosomal protein S28.

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

- Molecule 34 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	Sd	53	Total	C	N	O	S	0	0
			445	278	90	72	5		

- Molecule 35 is a protein called Ubiquitin.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Sf	71	Total	C	N	O	S	0	0
			581	367	109	98	7		

- Molecule 36 is a protein called Receptor of activated protein C kinase 1.

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

- Molecule 37 is a protein called 40S ribosomal protein S2.

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

- Molecule 38 is a protein called 40S ribosomal protein S6.

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

- Molecule 39 is a protein called 40S ribosomal protein S9.

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
40	SM	122	Total	C	N	O	S	0	0
			952	596	169	179	8		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P25398
SM	69	LEU	CYS	conflict	UNP P25398
SM	99	ASN	LYS	conflict	UNP P25398

- Molecule 41 is a protein called 40S ribosomal protein S13.

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

- Molecule 42 is a protein called 40S ribosomal protein S14.

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

- Molecule 43 is a protein called 40S ribosomal protein S15a.

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

- Molecule 44 is a protein called 40S ribosomal protein S24.

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

- Molecule 45 is a protein called 40S ribosomal protein S25.

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

- Molecule 46 is a protein called 40S ribosomal protein S27.

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

- Molecule 47 is a protein called 40S ribosomal protein S30.

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

- Molecule 48 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	L5	3654	Total	C	N	O	P	0	0
			78316	34871	14334	25458	3653		

- Molecule 49 is a RNA chain called 5S ribosomal RNA.

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

- Molecule 50 is a RNA chain called 5.8S ribosomal RNA.

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

- Molecule 51 is a protein called 60S ribosomal protein L8.

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

- Molecule 52 is a protein called 60S ribosomal protein L3.

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

- Molecule 53 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	LC	367	Total	C	N	O	S	0	0
			2919	1835	582	488	14		

- Molecule 54 is a protein called 60S ribosomal protein L5.

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

- Molecule 55 is a protein called Large ribosomal subunit protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	LE	242	Total	C	N	O	S	0	0
			1958	1257	372	325	4		

- Molecule 56 is a protein called Large ribosomal subunit protein uL30.

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

- Molecule 57 is a protein called 60S ribosomal protein L7a.

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

- Molecule 58 is a protein called 60S ribosomal protein L9.

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

- Molecule 59 is a protein called Ribosomal protein uL16-like.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	LI	213	Total	C	N	O	S	0	0
			1711	1082	329	285	15		

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

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

- Molecule 61 is a protein called 60S ribosomal protein L13.

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

- Molecule 62 is a protein called 60S ribosomal protein L14.

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

- Molecule 63 is a protein called 60S ribosomal protein L15.

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

- Molecule 64 is a protein called 60S ribosomal protein L13a.

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

- Molecule 65 is a protein called 60S ribosomal protein L17.

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

- Molecule 66 is a protein called 60S ribosomal protein L18.

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

- Molecule 67 is a protein called 60S ribosomal protein L19.

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

- Molecule 68 is a protein called 60S ribosomal protein L18a.

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

- Molecule 69 is a protein called 60S ribosomal protein L21.

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

- Molecule 70 is a protein called 60S ribosomal protein L22.

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

- Molecule 71 is a protein called 60S ribosomal protein L23.

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

- Molecule 72 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	LW	124	Total	C	N	O	S	0	0
			1015	634	207	170	4		

- Molecule 73 is a protein called 60S ribosomal protein L23a.

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

- Molecule 74 is a protein called 60S ribosomal protein L26.

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

- Molecule 75 is a protein called 60S ribosomal protein L27.

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

- Molecule 76 is a protein called 60S ribosomal protein L27a.

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

- Molecule 77 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Lb	75	Total	C	N	O	S	0	0
			610	378	130	99	3		

- Molecule 78 is a protein called 60S ribosomal protein L30.

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

- Molecule 79 is a protein called 60S ribosomal protein L31.

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

- Molecule 80 is a protein called 60S ribosomal protein L32.

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

- Molecule 81 is a protein called 60S ribosomal protein L35a.

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

- Molecule 82 is a protein called 60S ribosomal protein L34.

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

- Molecule 83 is a protein called 60S ribosomal protein L35.

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

- Molecule 84 is a protein called 60S ribosomal protein L36.

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

- Molecule 85 is a protein called 60S ribosomal protein L37.

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

- Molecule 86 is a protein called 60S ribosomal protein L38.

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

- Molecule 87 is a protein called 60S ribosomal protein L39.

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

- Molecule 88 is a protein called Ubiquitin-60S ribosomal protein L40.

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

- Molecule 89 is a protein called 60S ribosomal protein L41.

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

- Molecule 90 is a protein called 60S ribosomal protein L36a.

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

- Molecule 91 is a protein called 60S ribosomal protein L37a.

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

- Molecule 92 is a protein called 60S ribosomal protein L28.

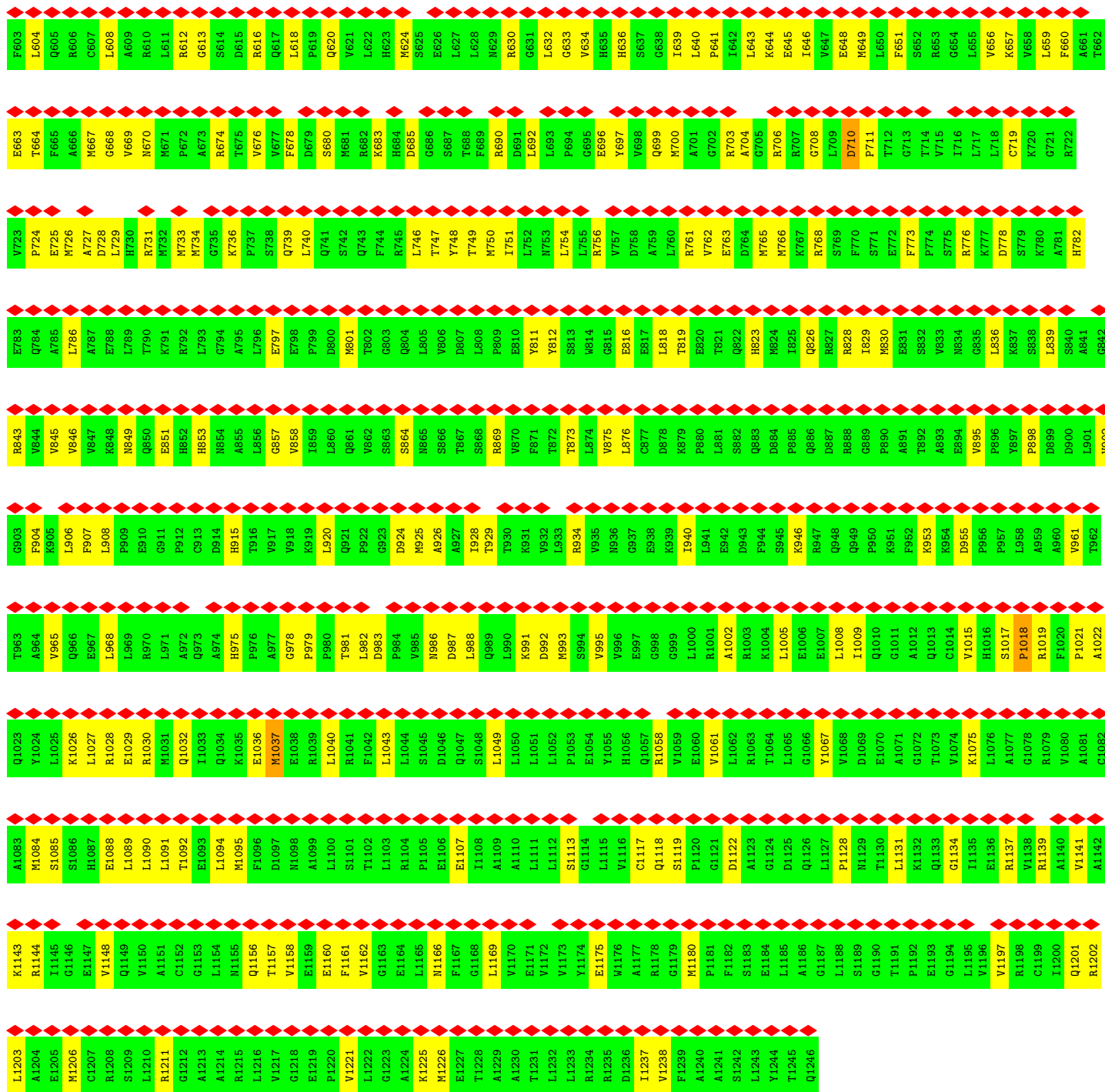
Mol	Chain	Residues	Atoms					AltConf	Trace
92	Lr	125	Total	C	N	O	S	0	0
			1002	622	207	168	5		

- Molecule 93 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

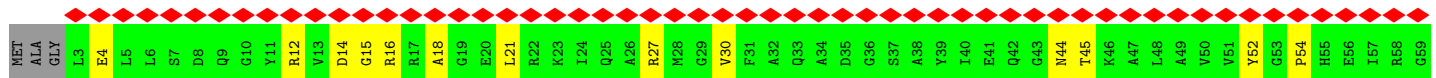
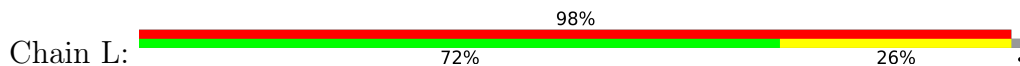
Mol	Chain	Residues	Atoms		AltConf
93	S2	65	Total	Mg	0
			65	65	
93	Sc	1	Total	Mg	0
			1	1	
93	L5	145	Total	Mg	0
			145	145	
93	L7	7	Total	Mg	0
			7	7	
93	L8	5	Total	Mg	0
			5	5	
93	LA	1	Total	Mg	0
			1	1	
93	LH	1	Total	Mg	0
			1	1	
93	LN	1	Total	Mg	0
			1	1	
93	LP	1	Total	Mg	0
			1	1	
93	LQ	1	Total	Mg	0
			1	1	
93	LV	2	Total	Mg	0
			2	2	
93	Ll	1	Total	Mg	0
			1	1	
93	Lr	1	Total	Mg	0
			1	1	

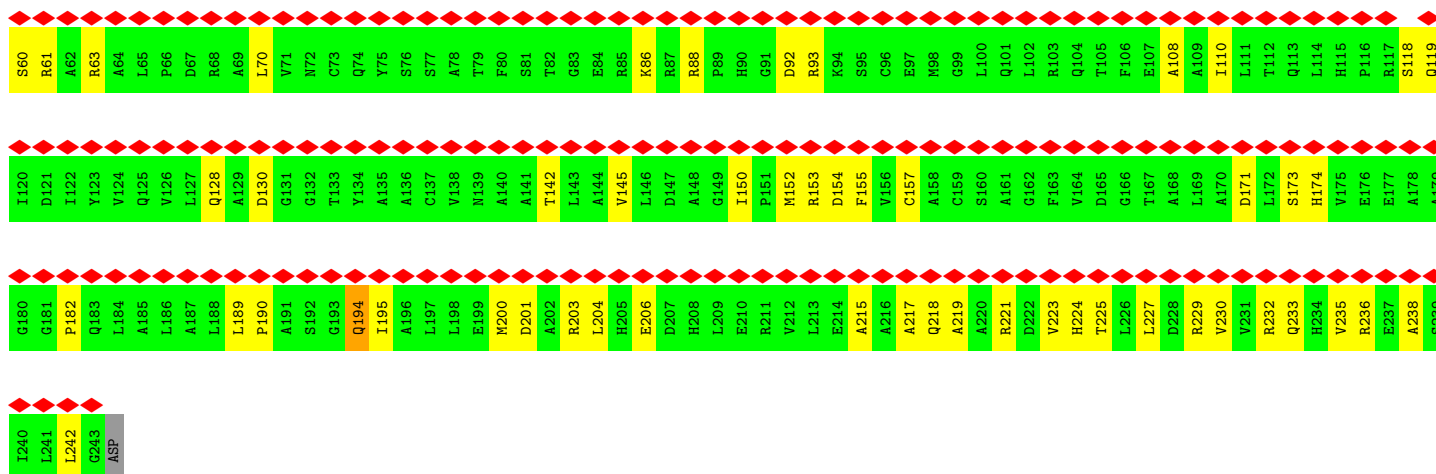
- Molecule 94 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

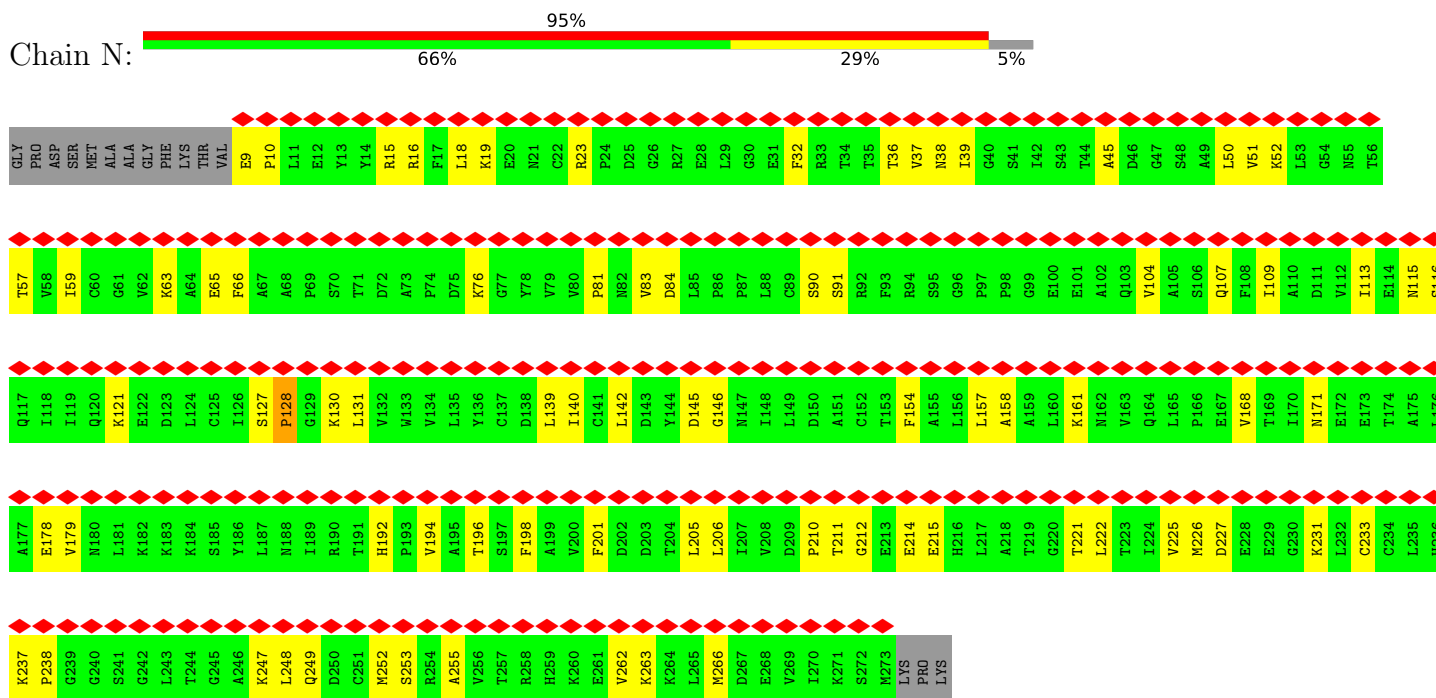


● Molecule 2: Exosome complex component RRP41

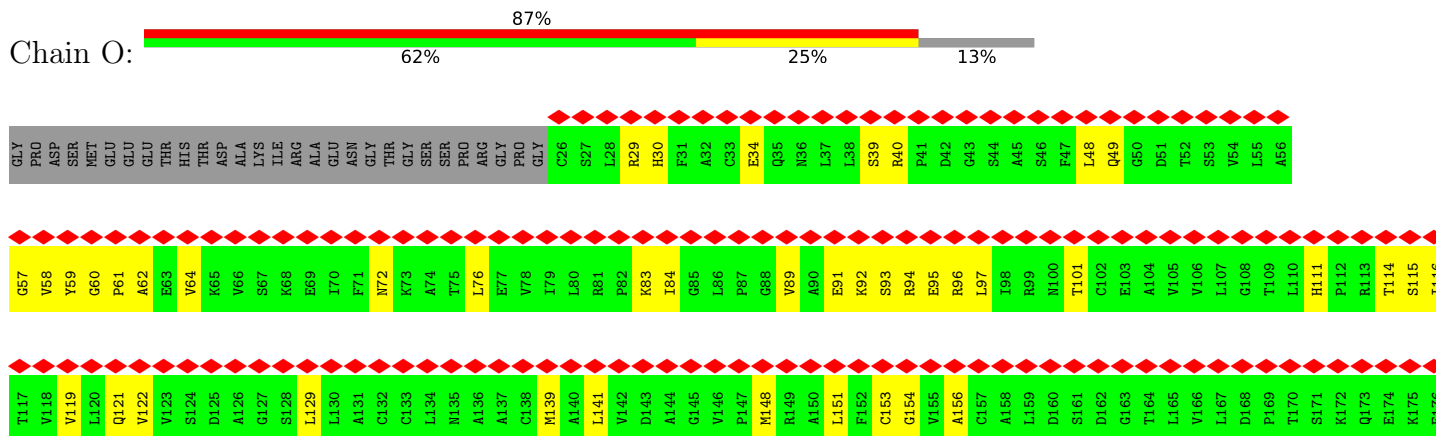




• Molecule 3: Exosome complex component RRP43

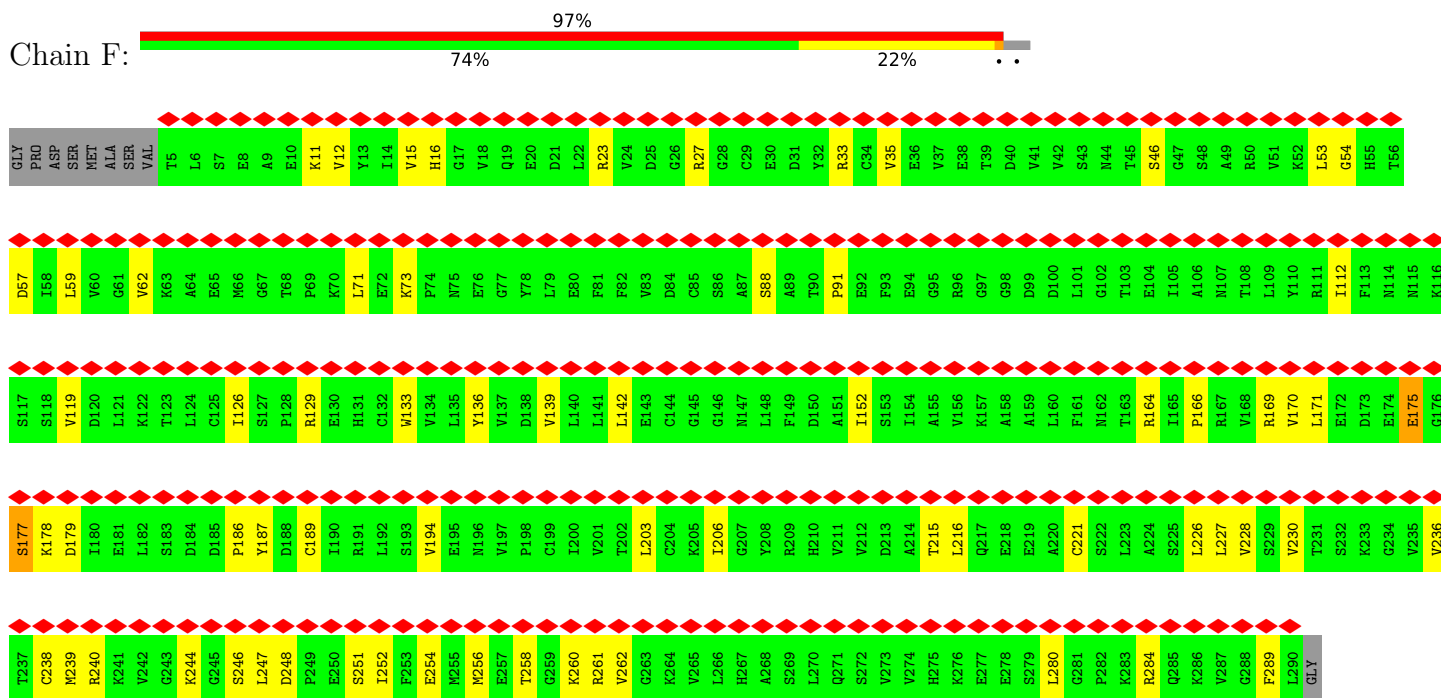


• Molecule 4: Exosome complex component RRP46

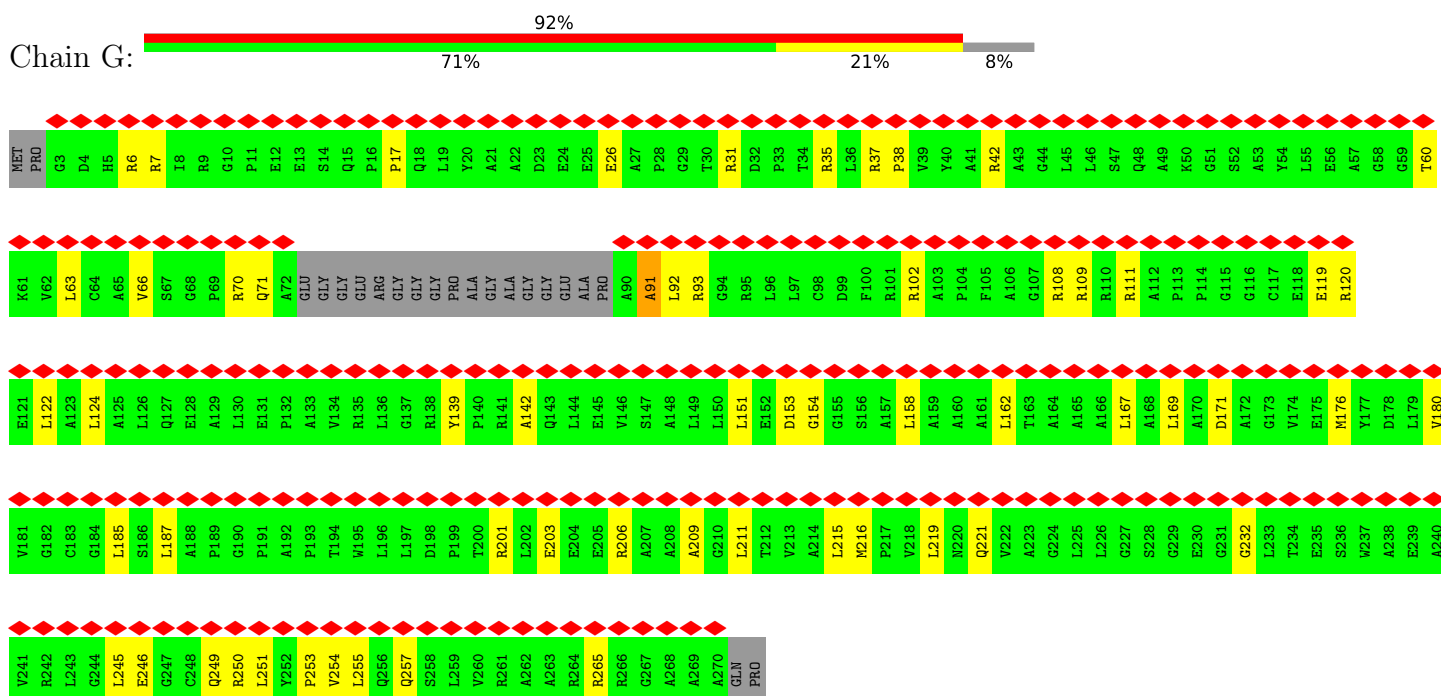




• Molecule 5: Exosome complex component RRP42

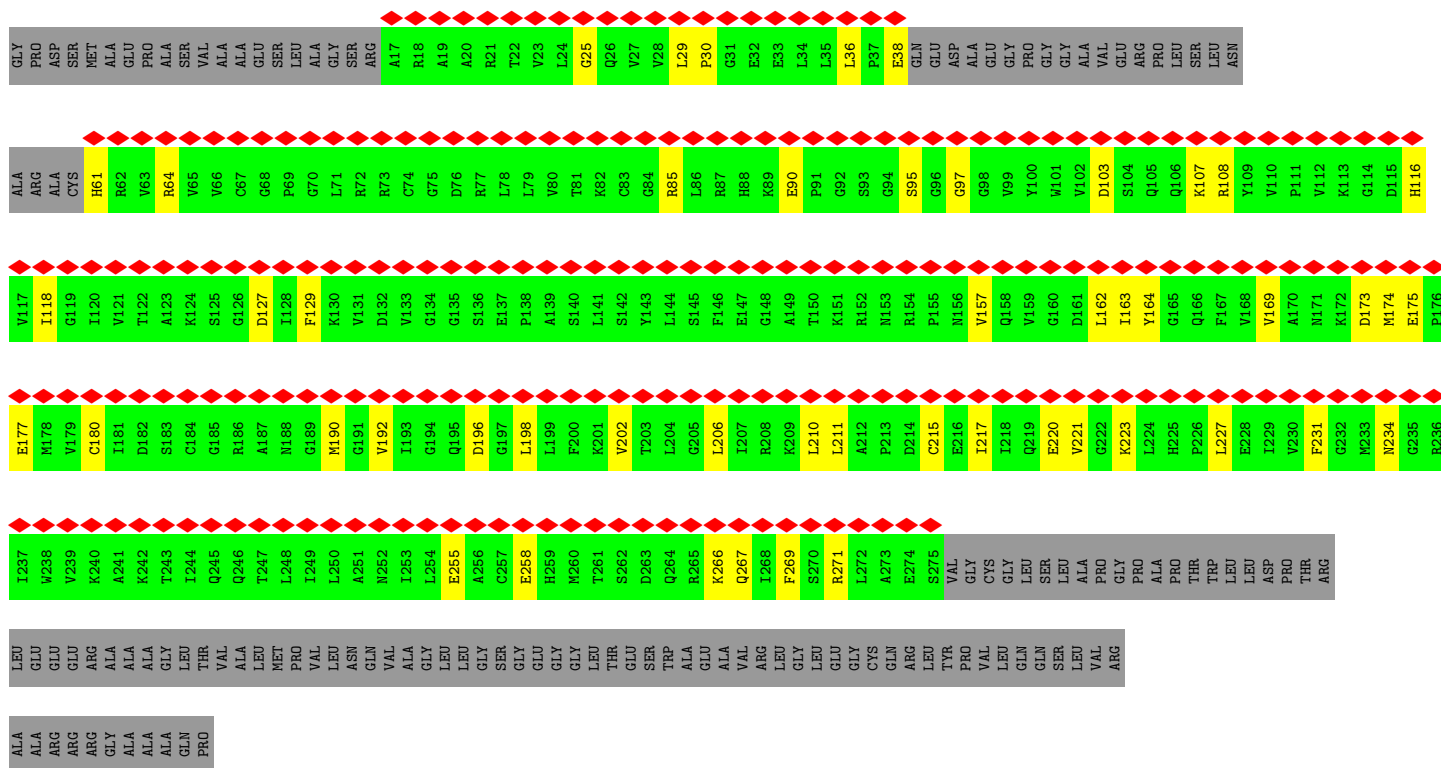


• Molecule 6: Exosome complex component MTR3

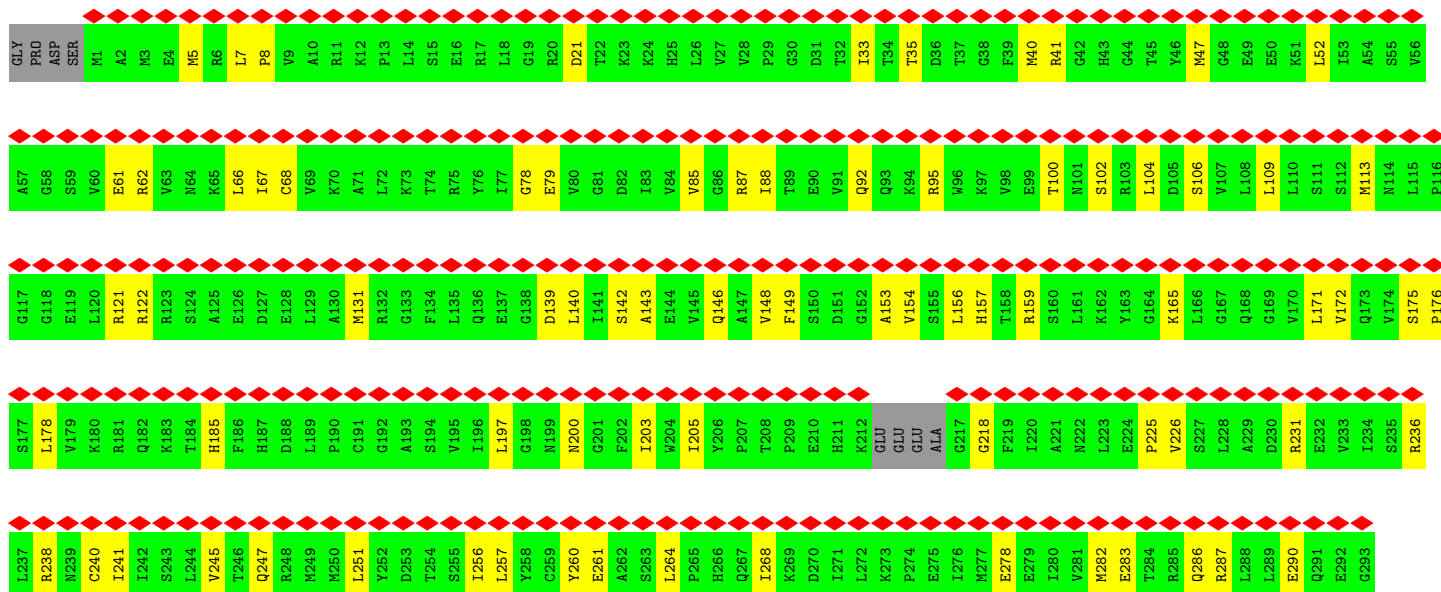


• Molecule 7: Exosome complex component RRP40, Exosome complex component MTR3

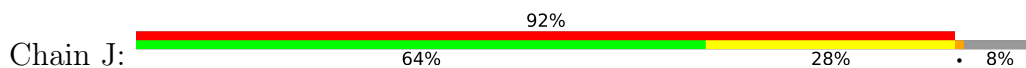


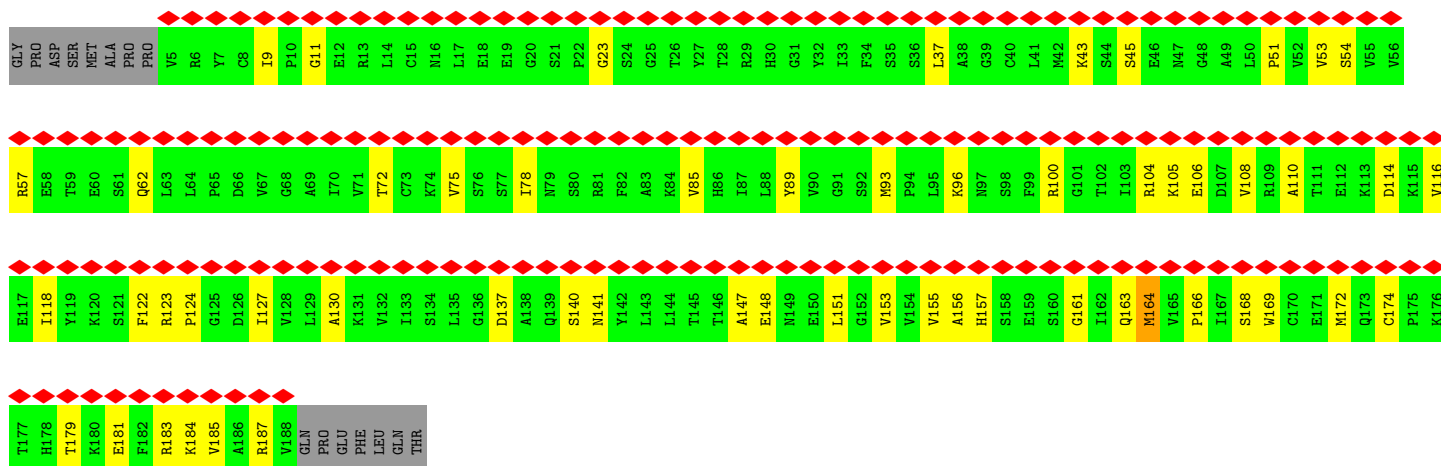


● Molecule 8: Exosome complex component RRP4

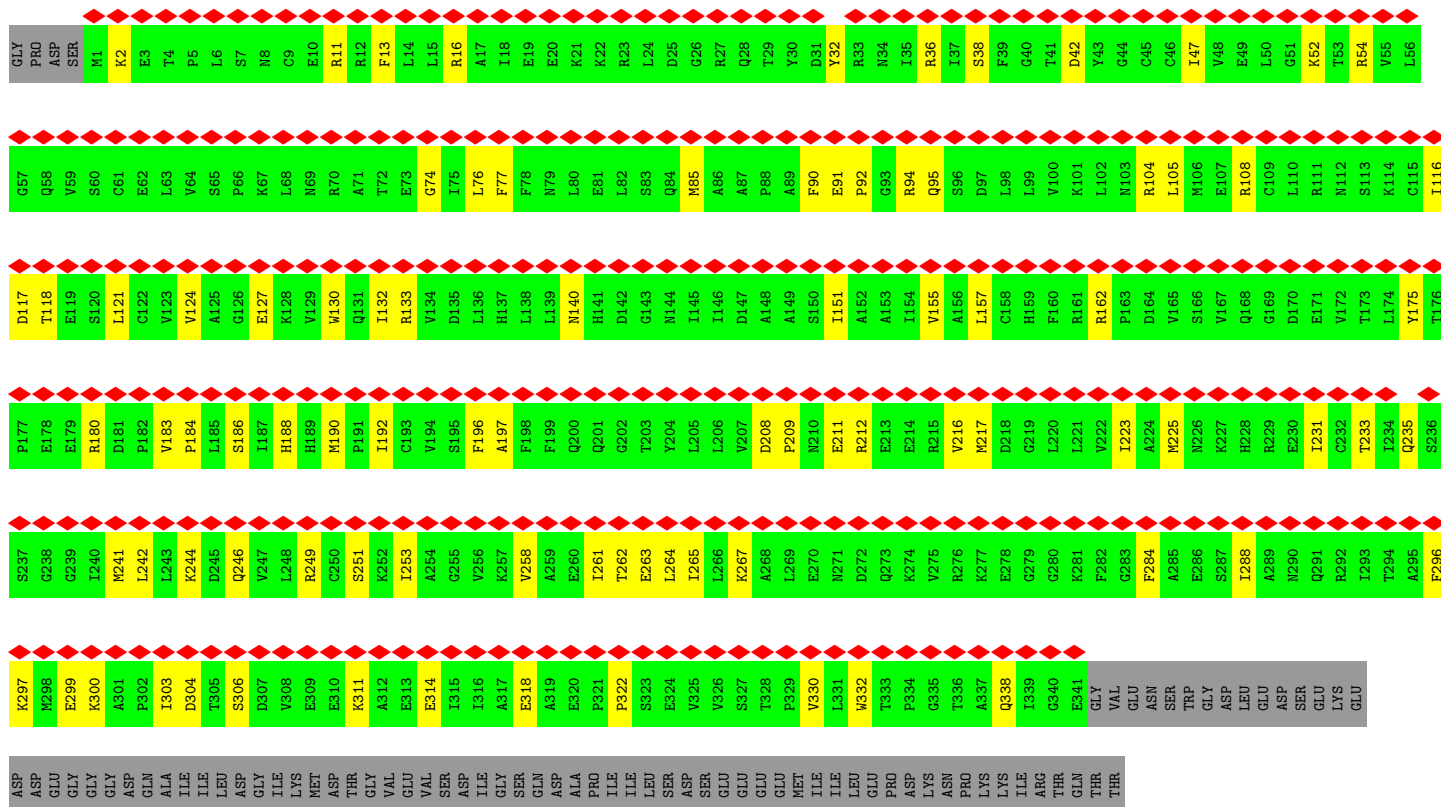
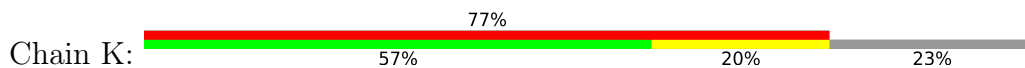


● Molecule 9: Exosome complex component CSL4

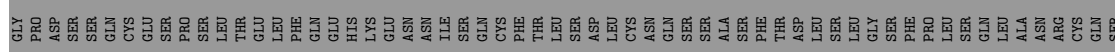


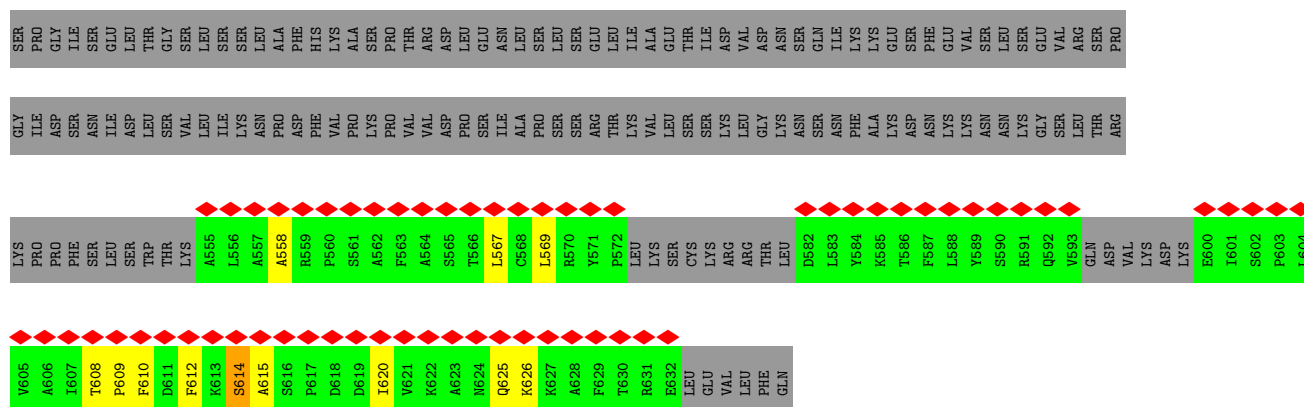


• Molecule 10: Exosome complex component RRP45

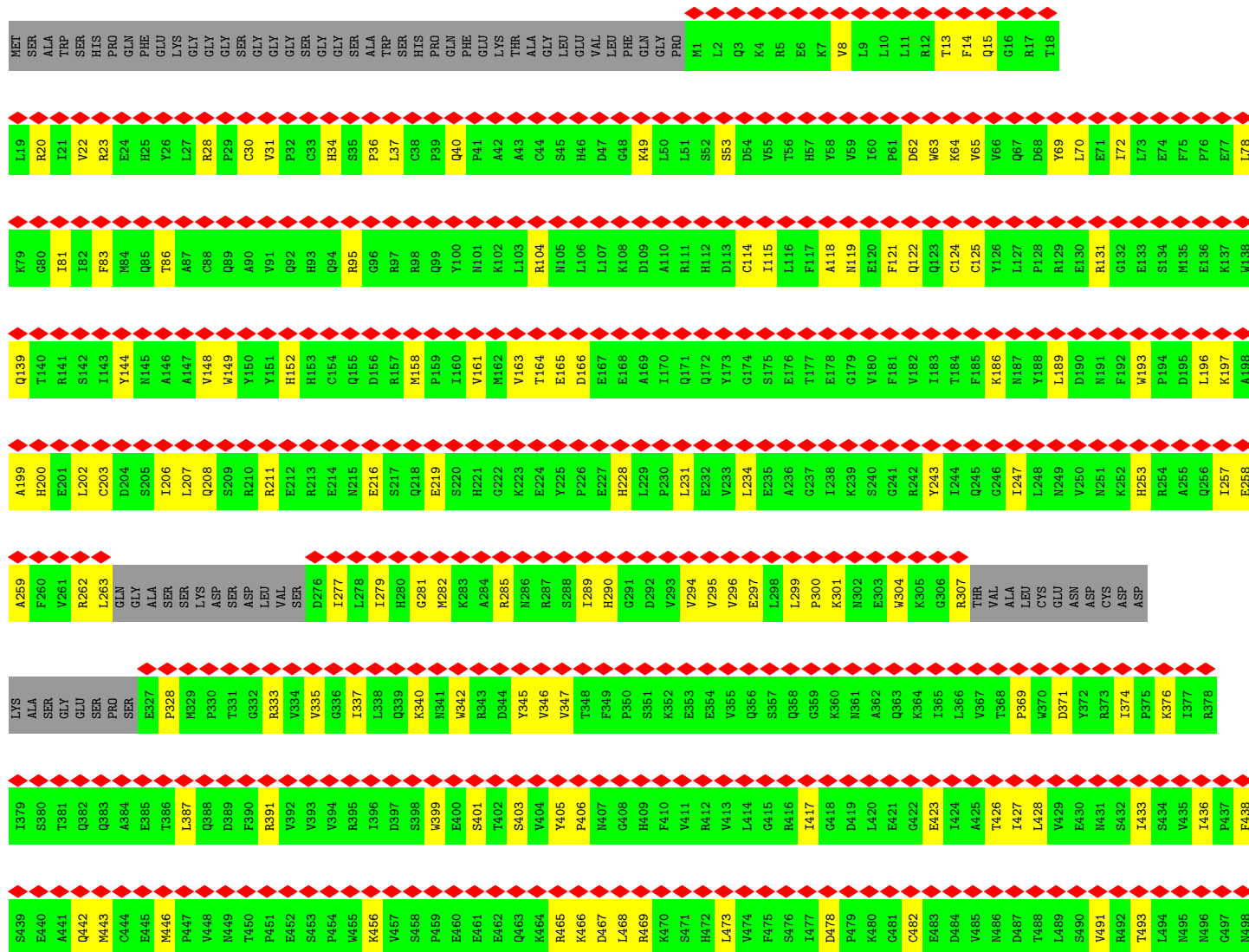


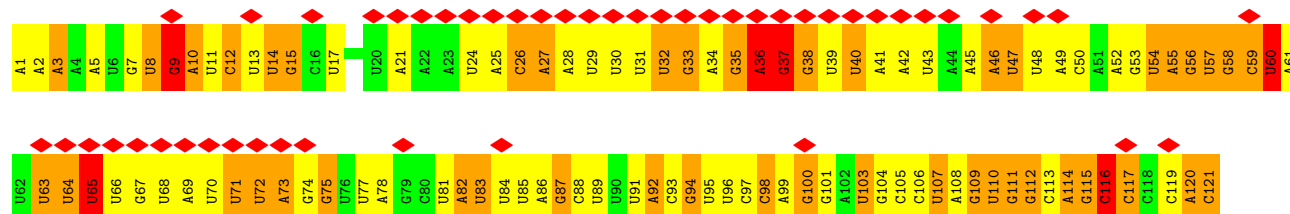
• Molecule 11: Isoform 2 of HBS1-like protein

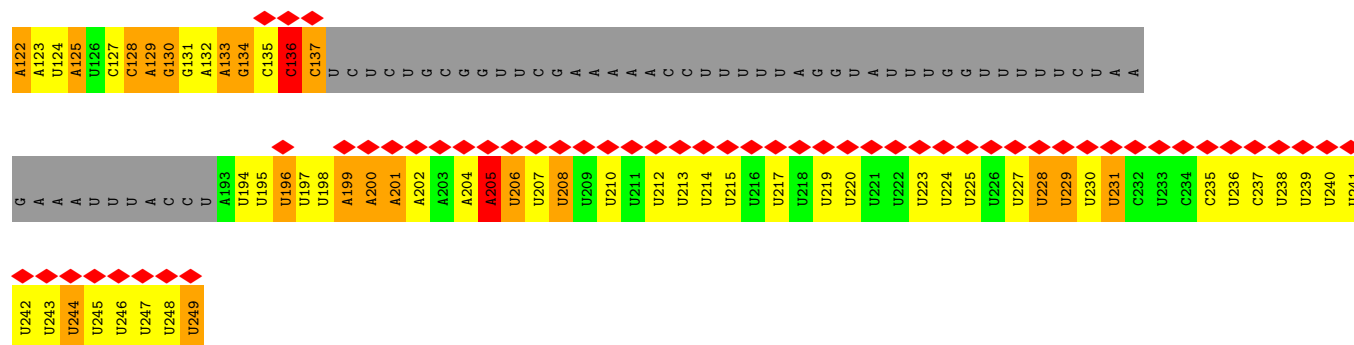




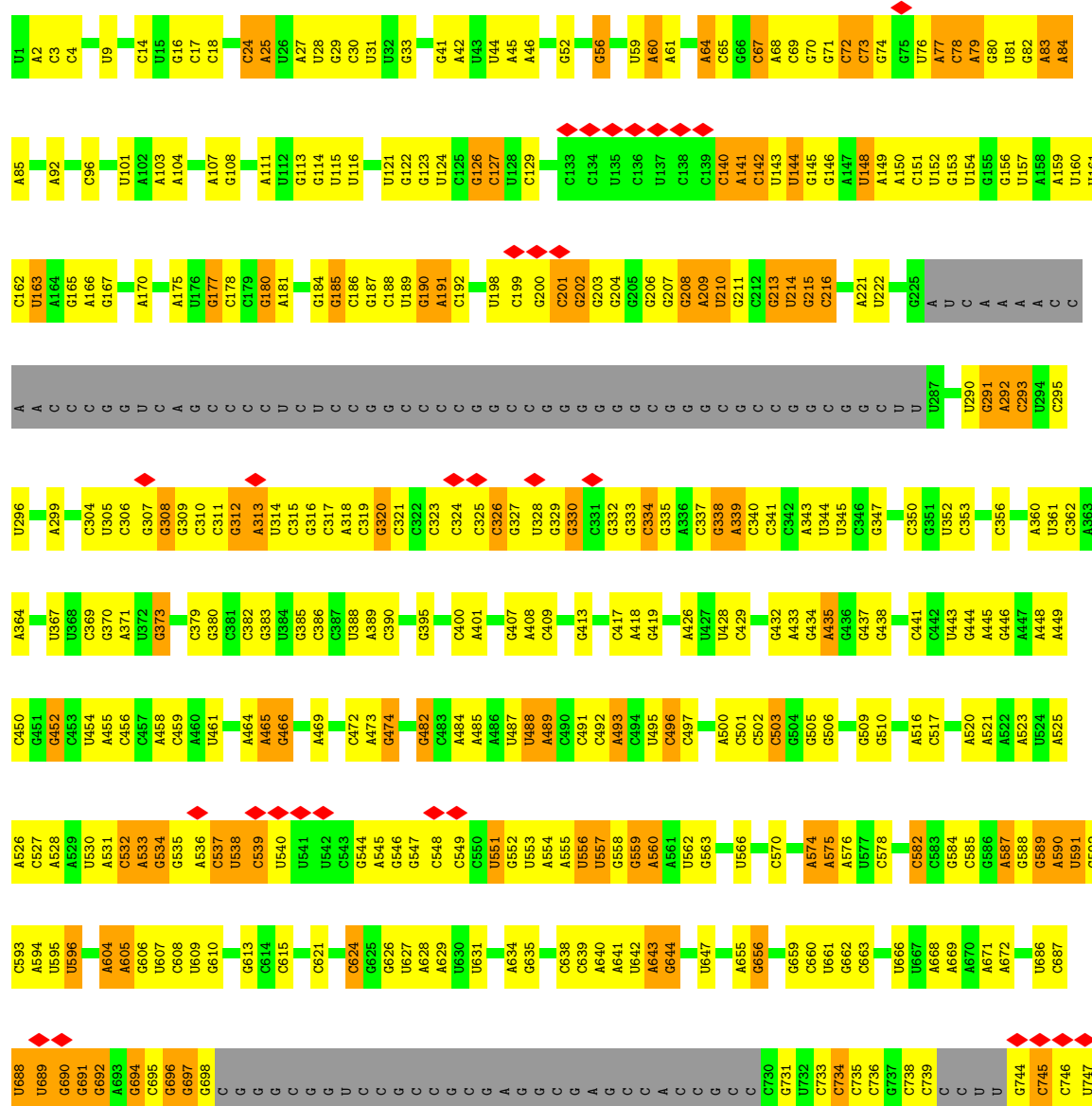
• Molecule 12: DIS3-like exonuclease 1



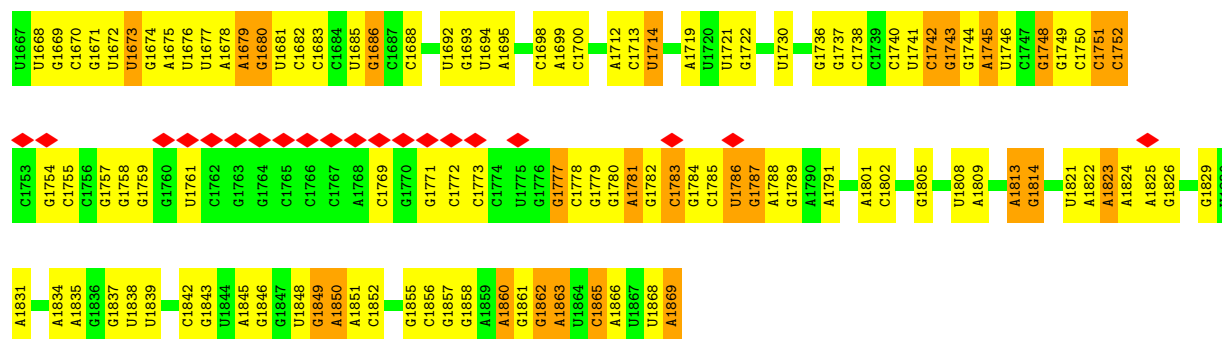




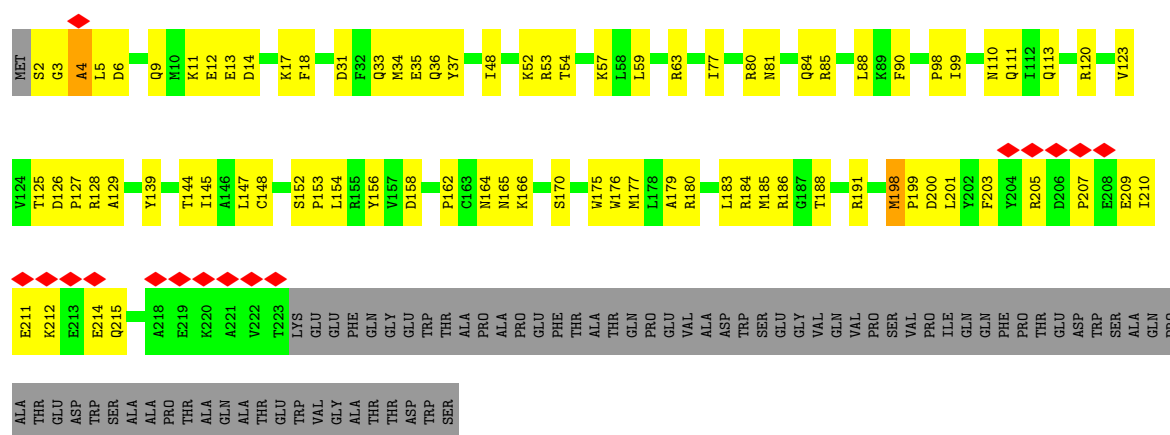
• Molecule 14: 18S ribosomal RNA



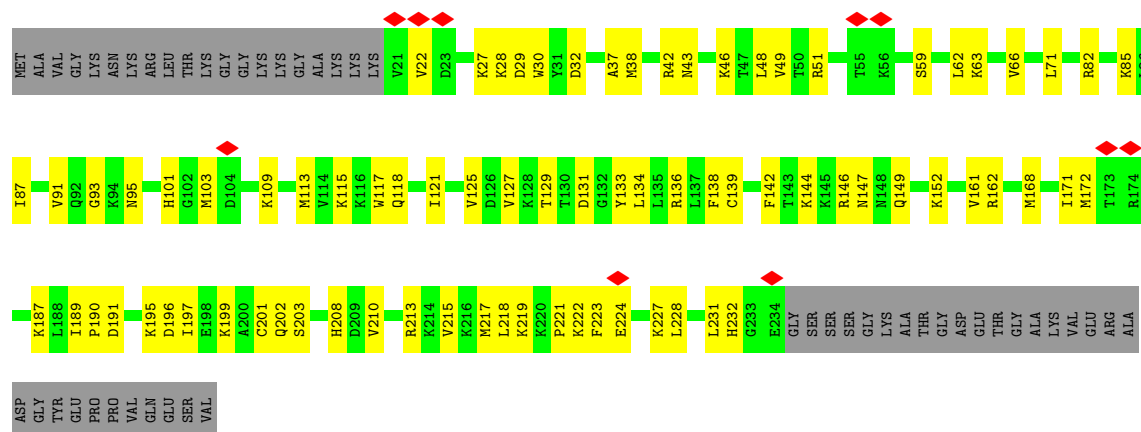




• Molecule 15: 40S ribosomal protein SA

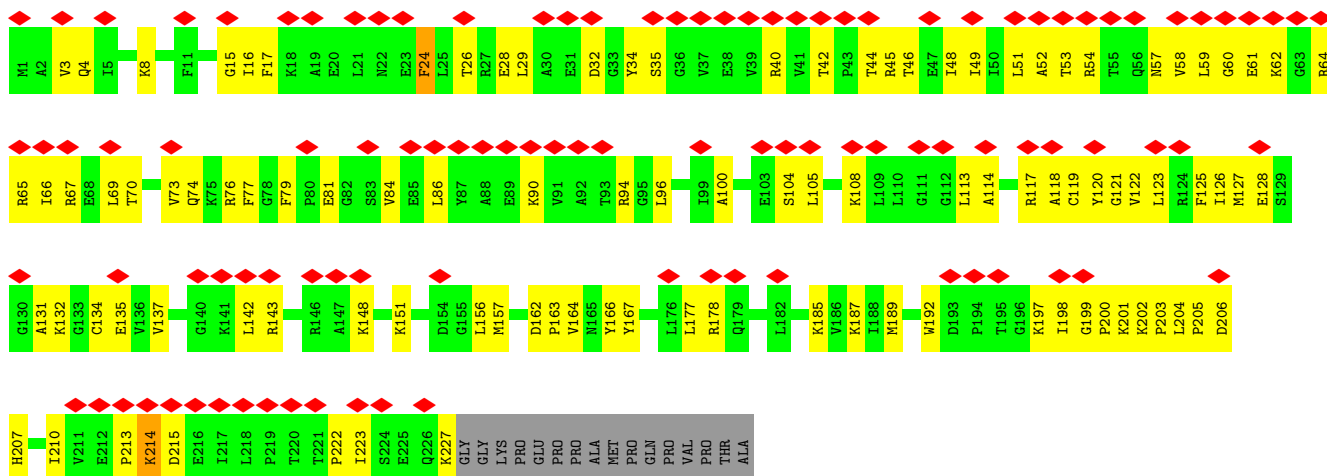


• Molecule 16: 40S ribosomal protein S3a

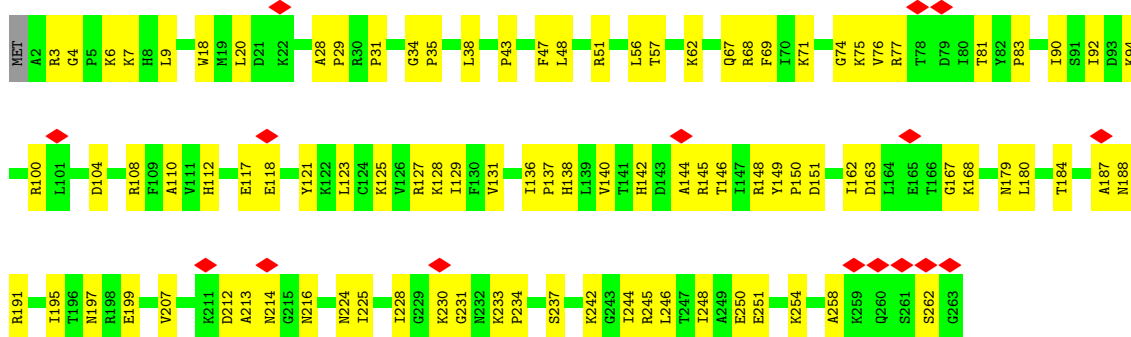


• Molecule 17: 40S ribosomal protein S3

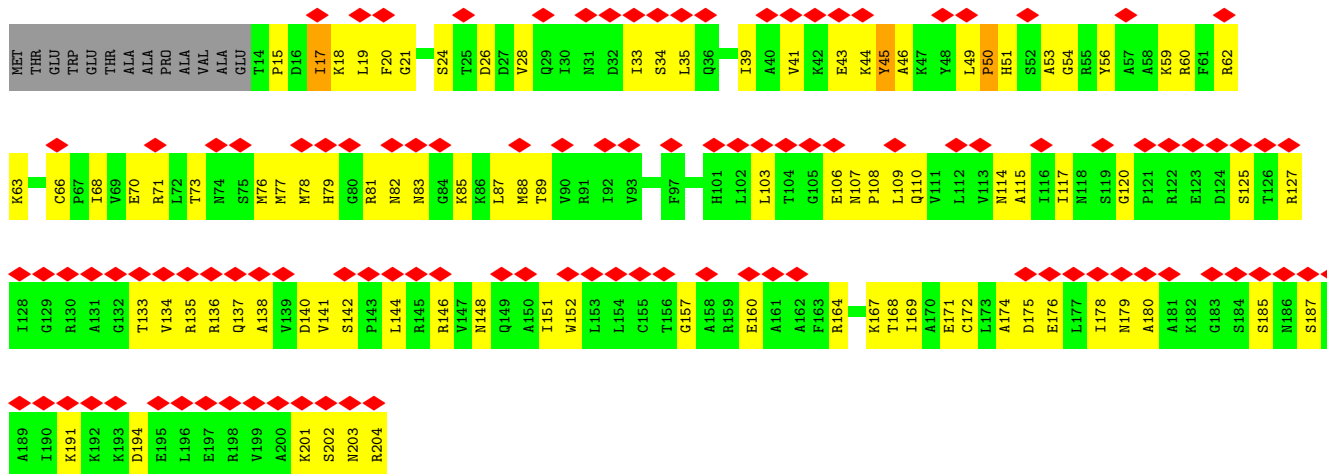




- Molecule 18: 40S ribosomal protein S4, X isoform

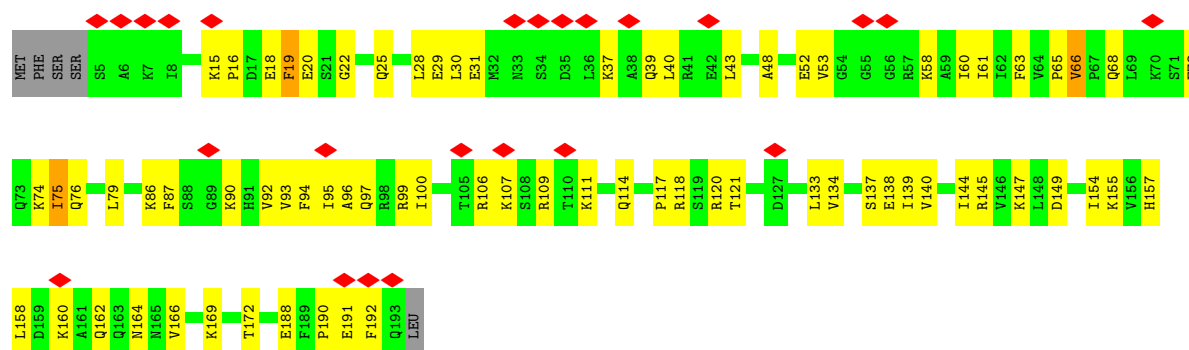


- Molecule 19: 40S ribosomal protein S5



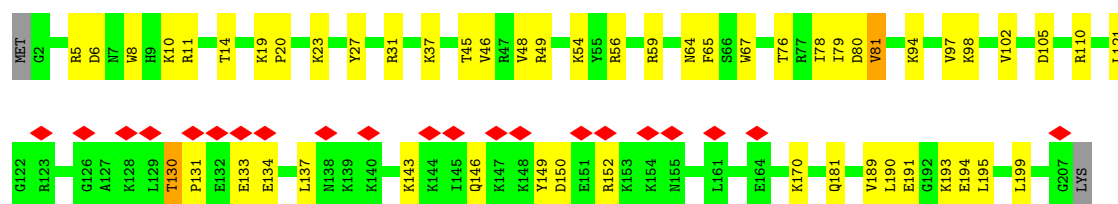
- Molecule 20: 40S ribosomal protein S7

Chain SH: 



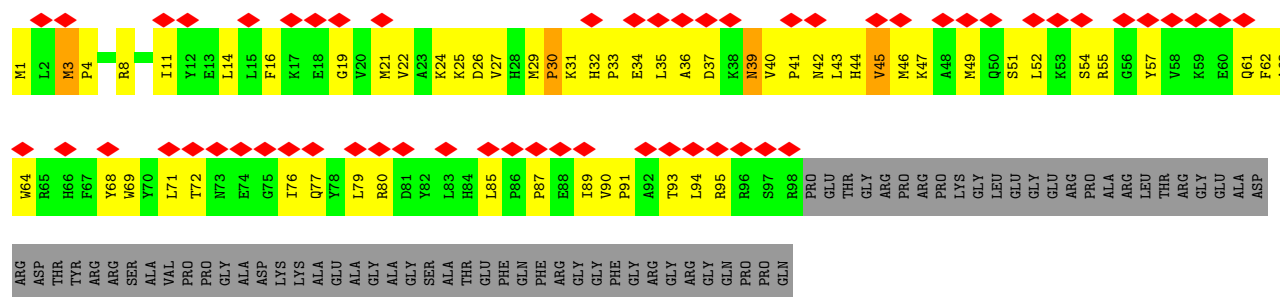
- Molecule 21: 40S ribosomal protein S8

Chain SI: 



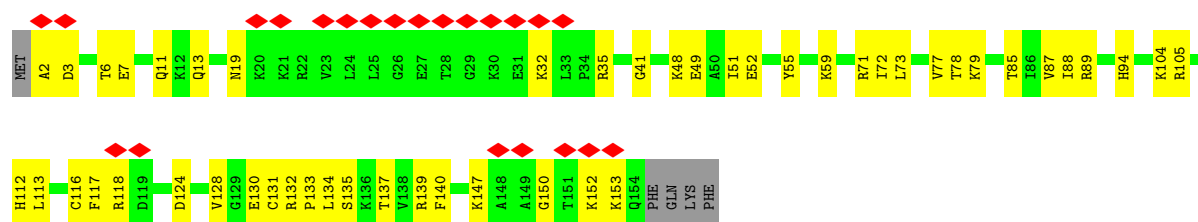
- Molecule 22: 40S ribosomal protein S10

Chain SK: 

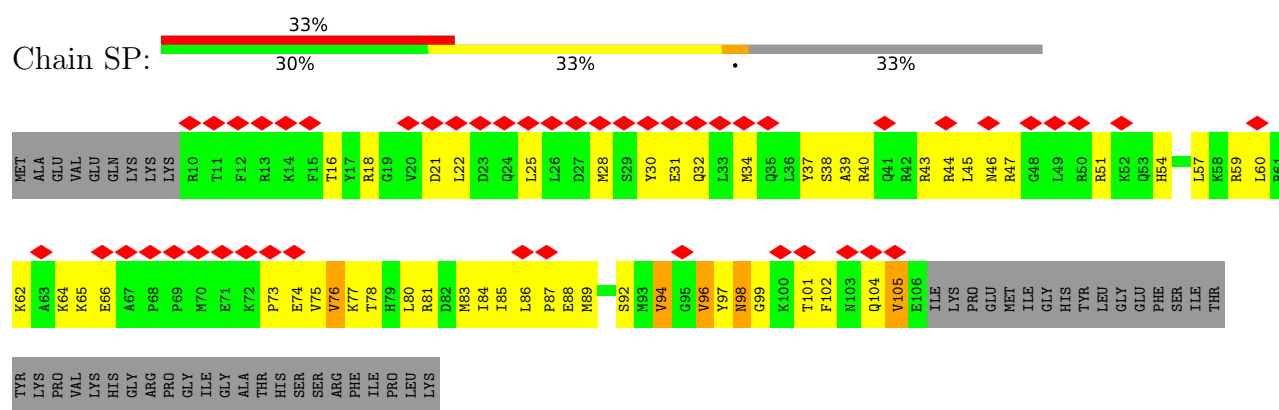


- Molecule 23: 40S ribosomal protein S11

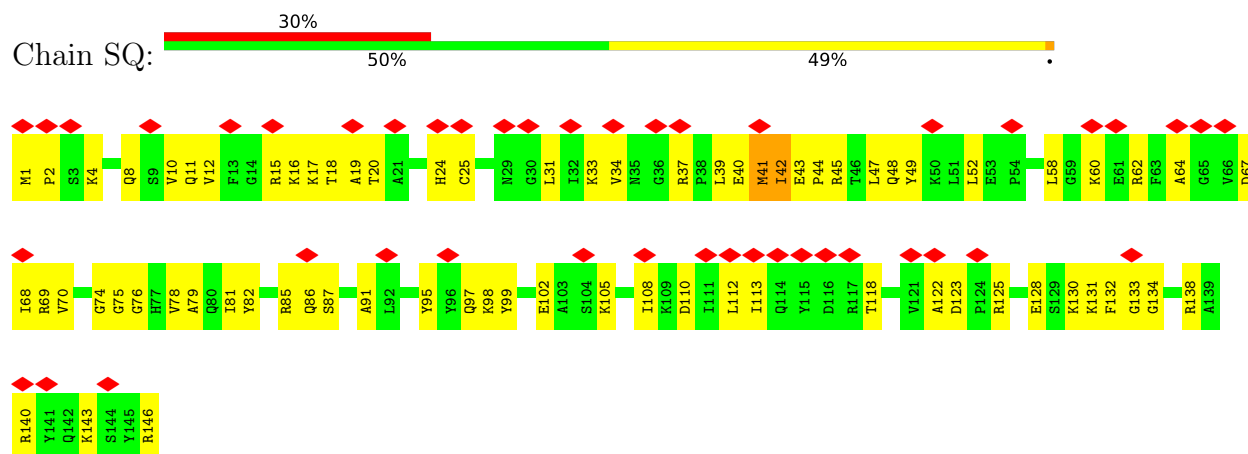
Chain SL: 



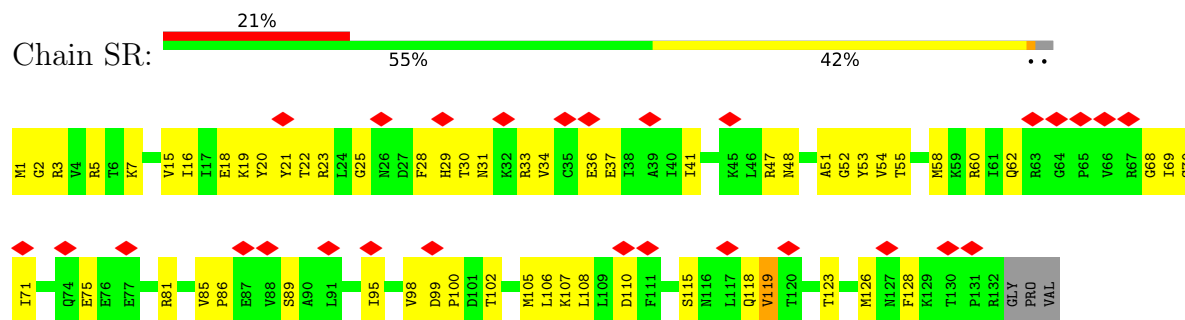
- Molecule 24: 40S ribosomal protein S15



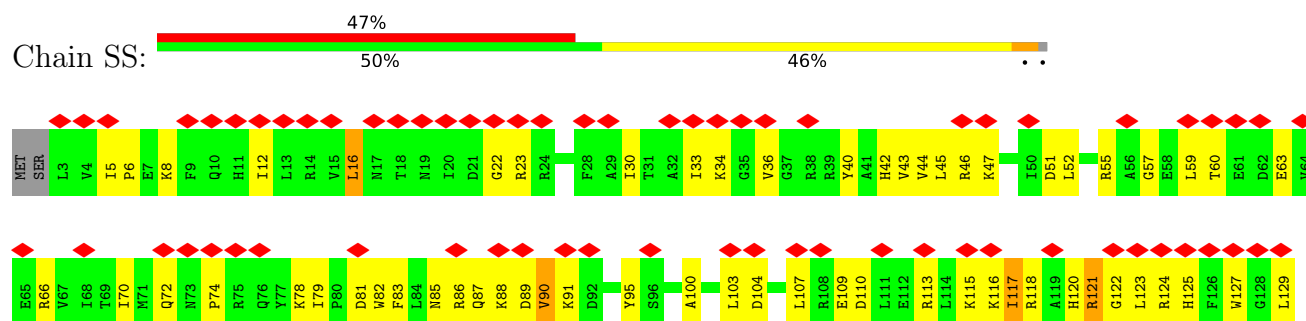
• Molecule 25: 40S ribosomal protein S16

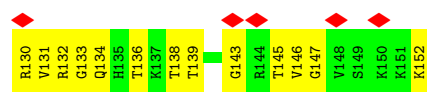


• Molecule 26: 40S ribosomal protein S17

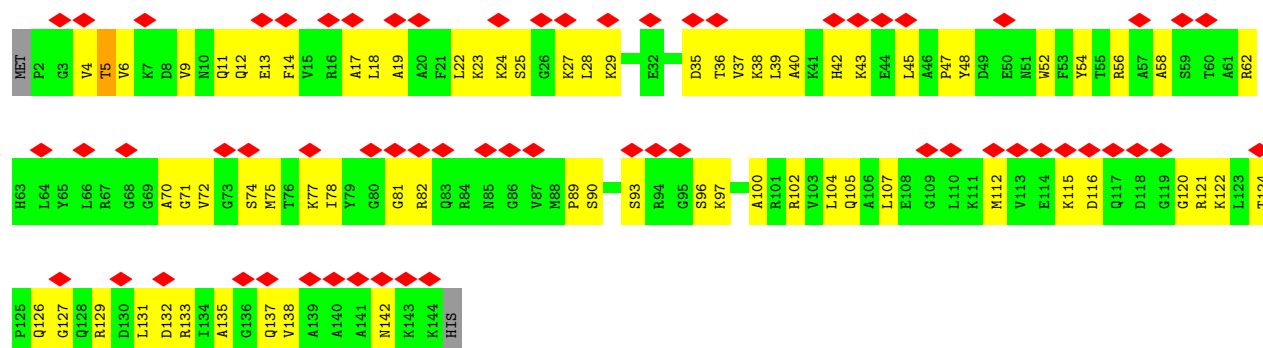
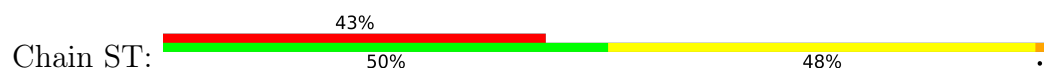


• Molecule 27: 40S ribosomal protein S18

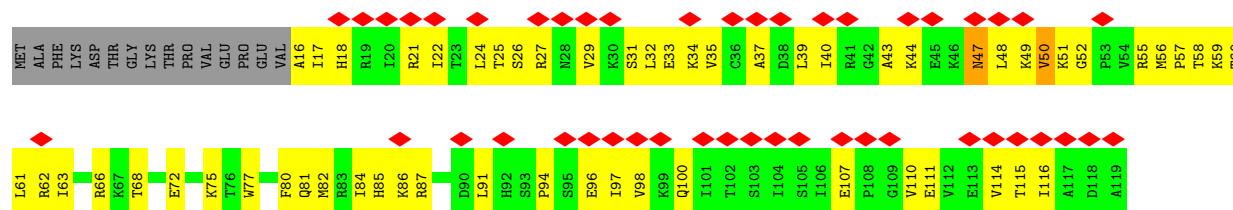




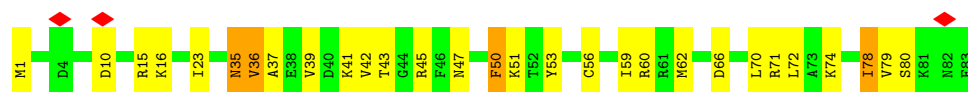
• Molecule 28: 40S ribosomal protein S19



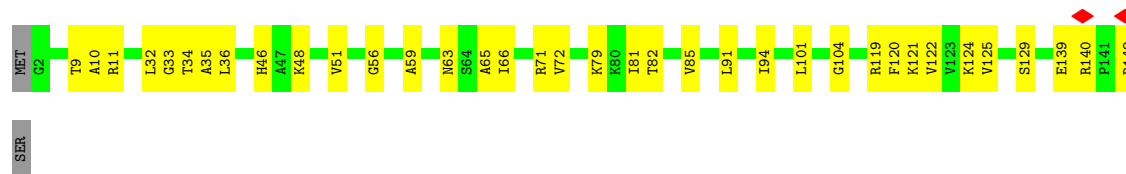
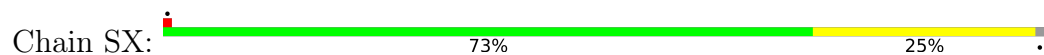
• Molecule 29: 40S ribosomal protein S20



• Molecule 30: 40S ribosomal protein S21



• Molecule 31: 40S ribosomal protein S23

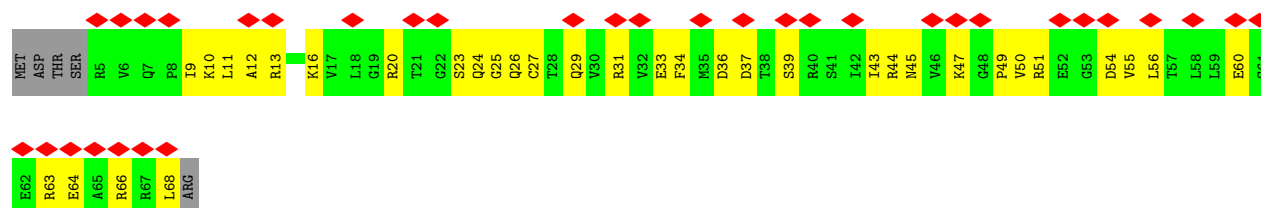
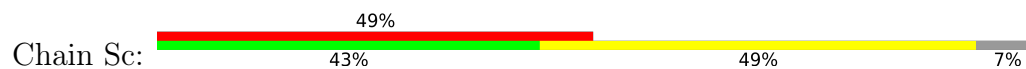


• Molecule 32: 40S ribosomal protein S26





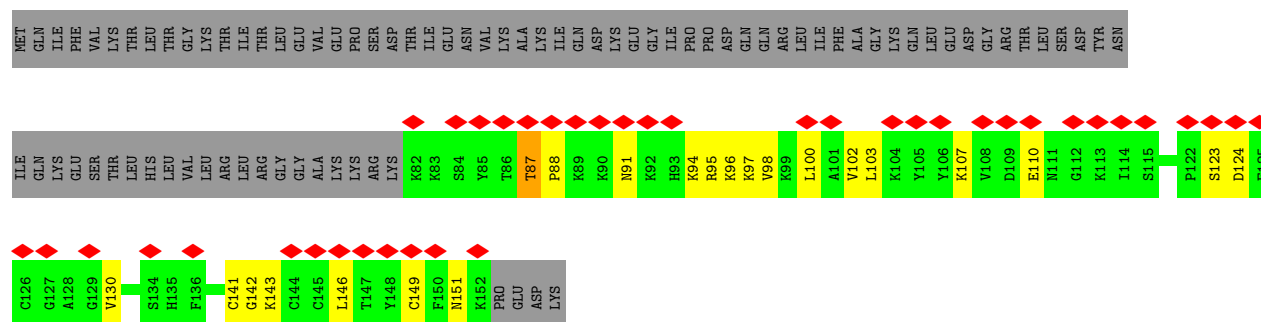
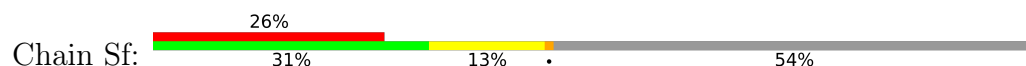
• Molecule 33: 40S ribosomal protein S28



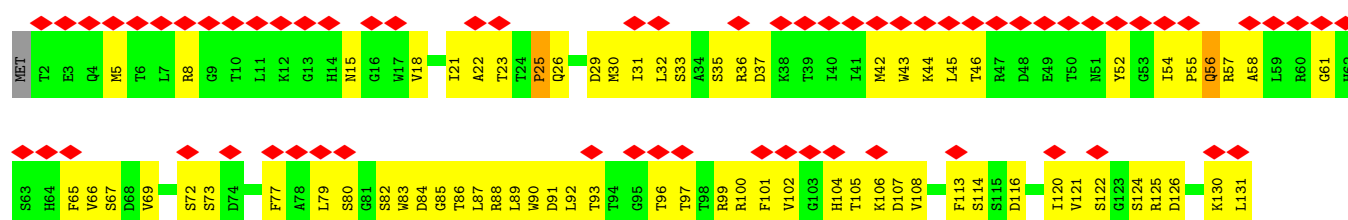
• Molecule 34: 40S ribosomal protein S29



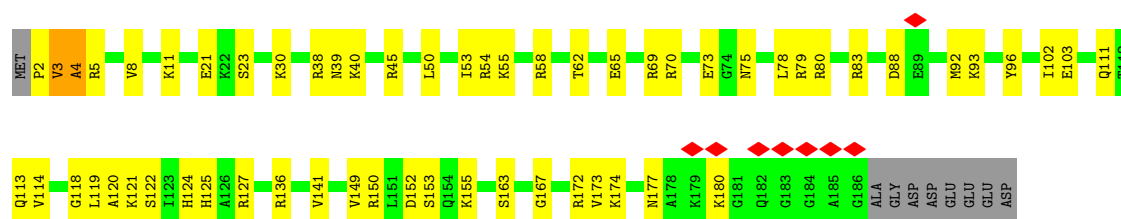
• Molecule 35: Ubiquitin



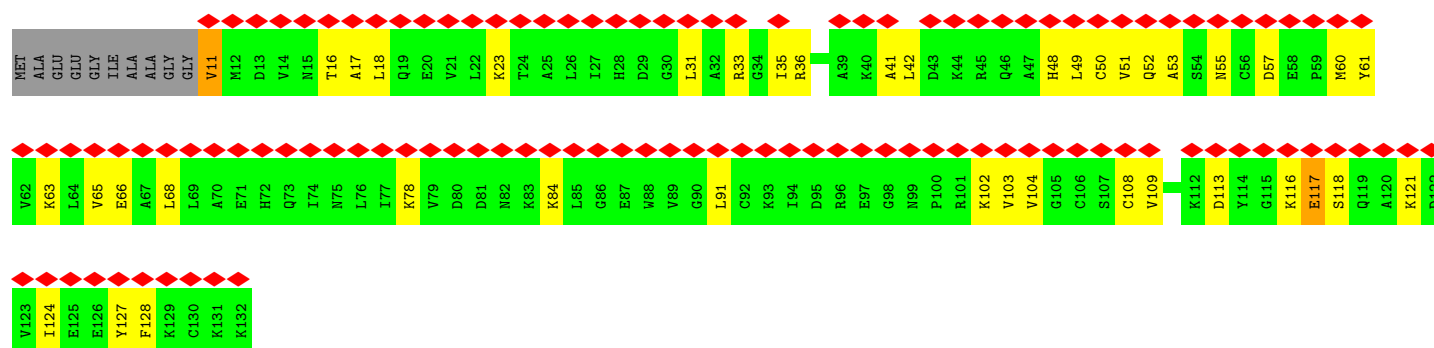
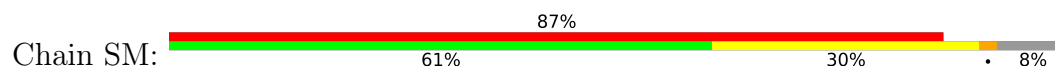
• Molecule 36: Receptor of activated protein C kinase 1



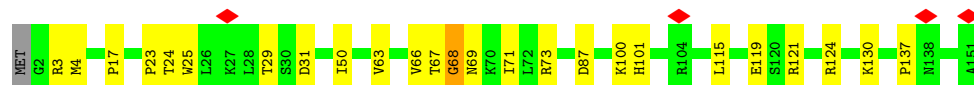
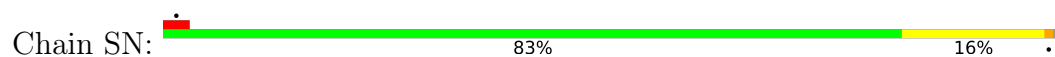




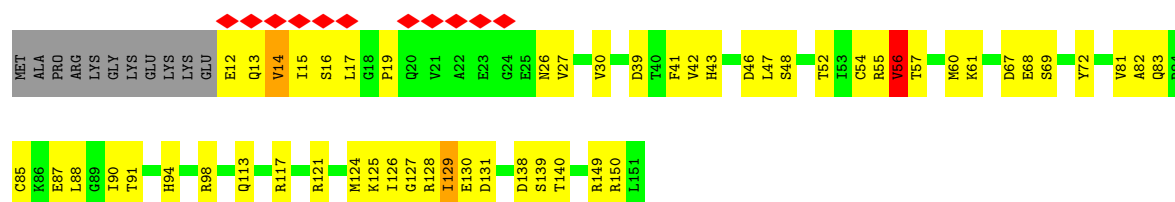
• Molecule 40: 40S ribosomal protein S12



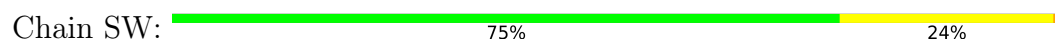
• Molecule 41: 40S ribosomal protein S13



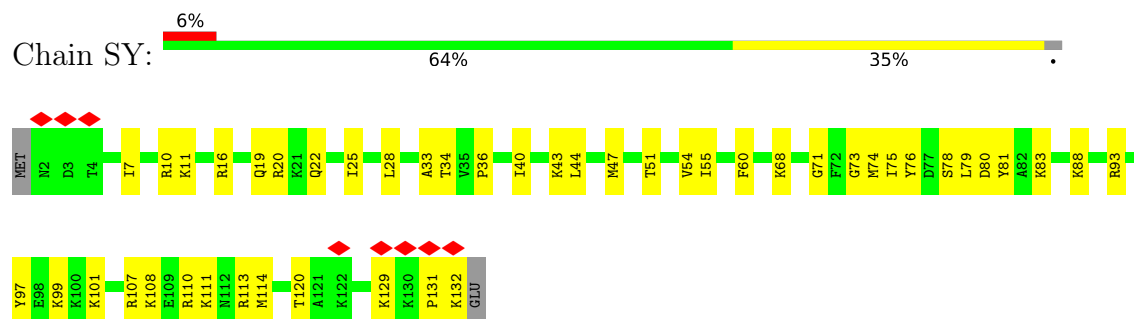
• Molecule 42: 40S ribosomal protein S14



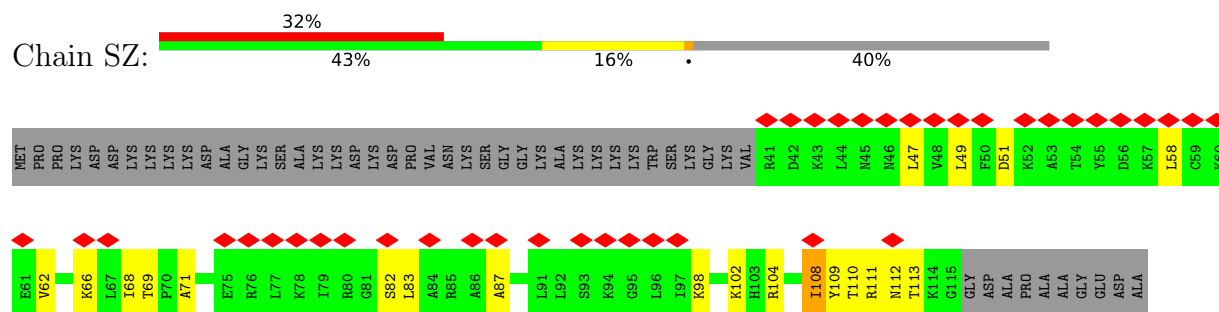
• Molecule 43: 40S ribosomal protein S15a



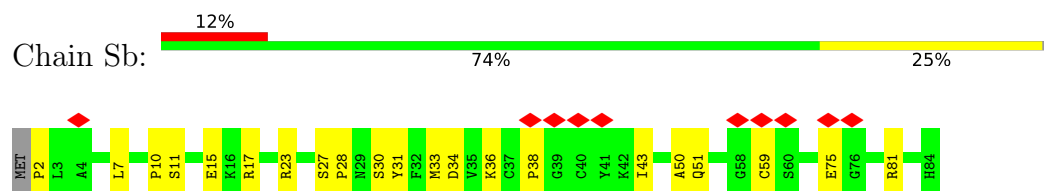
- Molecule 44: 40S ribosomal protein S24



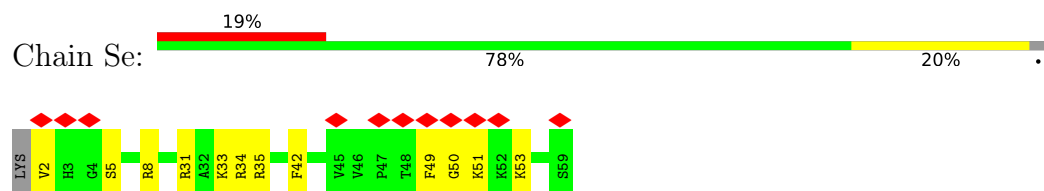
- Molecule 45: 40S ribosomal protein S25



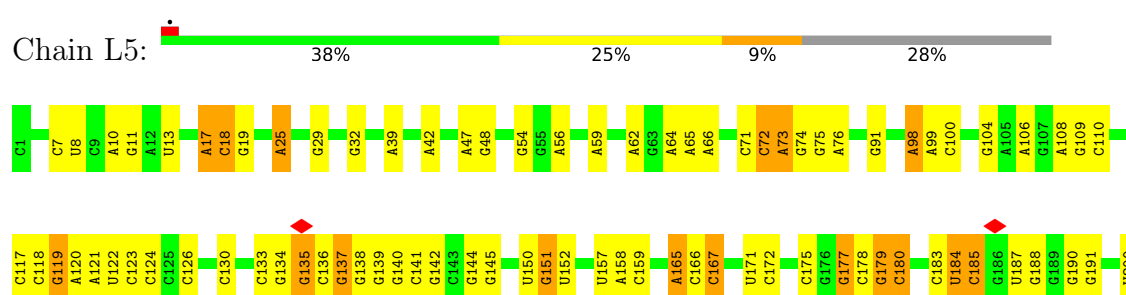
- Molecule 46: 40S ribosomal protein S27

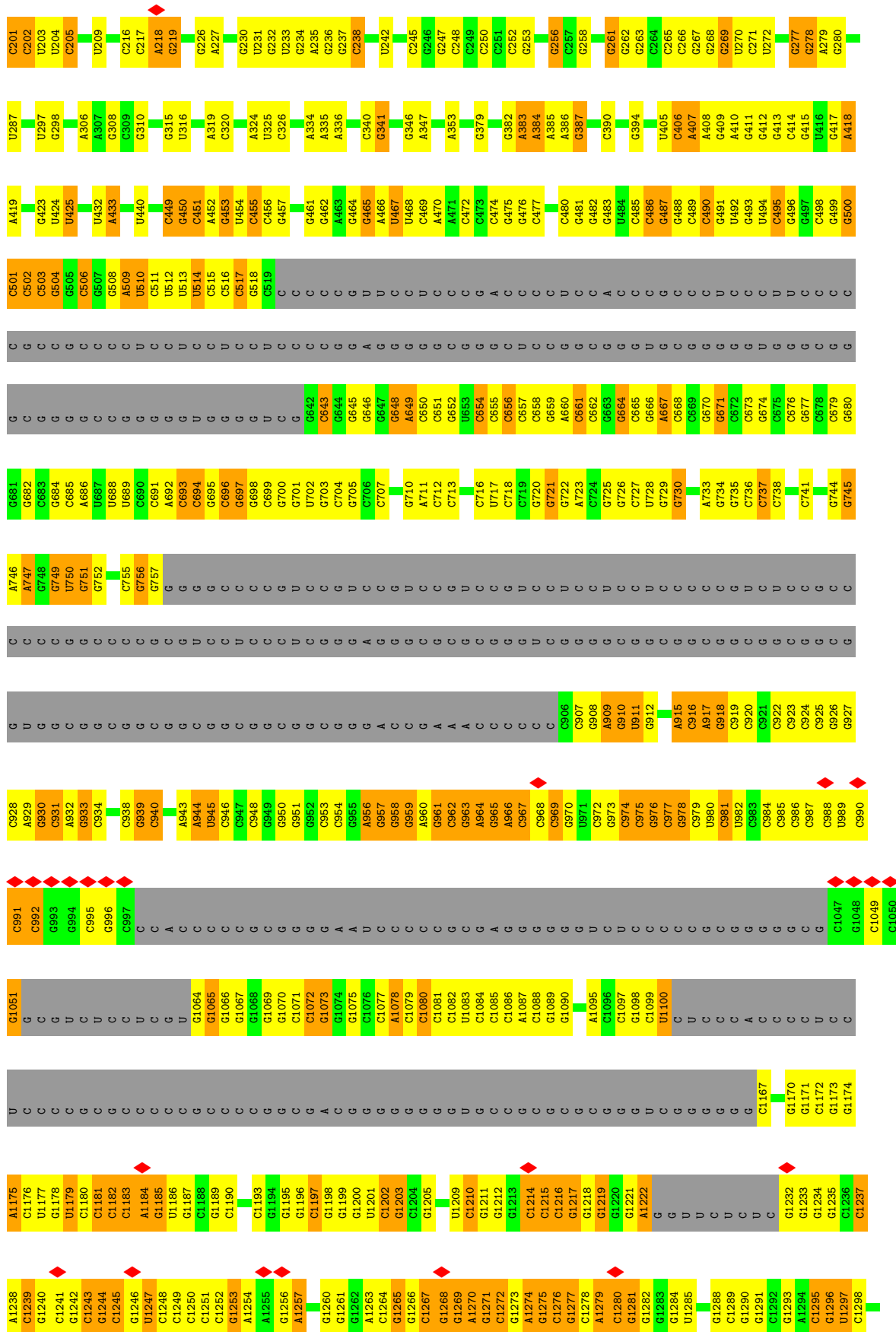


- Molecule 47: 40S ribosomal protein S30



- Molecule 48: 28S ribosomal RNA

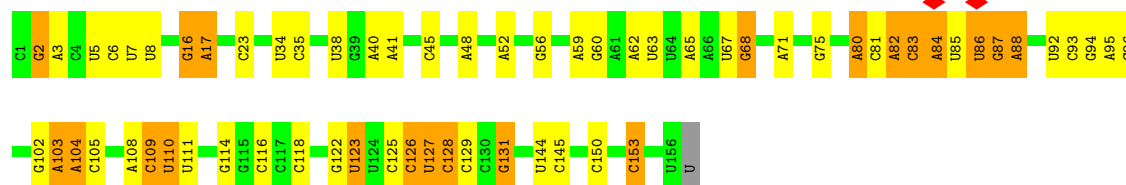




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A2525	C2435	G2276	G	C2089	G1931	G1803	◆	A1623	C1481	A1392	C1306
G2526	C2436	A2277	C	G2090	A1932	A1804	◆	G1624	C1482	G1393	A1307
A2527	C2439	C2287	C	A2091	C1933	A1805	◆	A1719	C1483	G1394	C1308
A2535	C2440	C2288	C	G2092	C1934	G1806	◆	G1720	C1486	U1395	C1309
U2536	U2445	C2289	C	A2093	G1938	C1812	◆	G1721	C1497	A1397	C1310
G2537	G2446	C2290	C	U2094	A1939	U1725	◆	A1631	A1497	A1396	U1317
C2538	A2447	G2291	C	G2095	A1940	G1820	◆	A1632	G1498	G1399	C1318
G2542	G2448	C2292	C	G2096	A1941	G1821	◆	A1634	C1501	G1401	C1401
C2543	C2462	A2093	C	U2097	U1945	U1822	◆	A1638	C1502	G1402	A1322
G2544	U2310	G2094	C	A2098	G1946	U1829	◆	A1641	G1503	G1403	A1323
G2545	G2316	U2095	C	C2009	G1949	G1831	◆	G1642	A1504	G1404	A1324
C2546	C2317	G2096	C	A2010	U1951	U1832	◆	A1646	C1505	G1405	A1325
G2548	G2319	G2097	C	A2011	U1952	U1833	◆	A1651	U1514	G1406	A1326
A2549	C2345	C2098	C	G2012	G1953	G1834	◆	G1654	A1515	G1407	C1327
G2550	G2346	U2099	C	C2013	A1954	G1835	◆	U1656	A1523	G1408	C1328
A2551	A2350	C2100	C	A2014	U1955	A1836	◆	G1655	U1410	G1409	G1329
U2552	G2331	G2101	C	C2015	A1956	A1837	◆	U1657	C1411	U1411	A1330
G2553	C2344	G2102	C	A2016	U1957	A1837	◆	G1658	C1412	C1332	A1332
G2554	G2347	C2103	C	C2017	A1958	U1837	◆	U1656	G1413	A1333	C1333
G2555	A2345	G2104	C	U2018	G1959	G1840	◆	A1681	C1414	G1414	A1334
C2556	G2346	C2105	C	G2021	A1960	U1842	◆	C1681	U1415	G1415	A1337
G2557	C2349	G2106	C	C2024	C1961	G1843	◆	U1754	G1416	G1416	G1338
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C2560	G2374	C2109	C	U2032	C1964	G1853	◆	U1759	A1547	A1419	A1420
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G2572	A2387	G2116	C	G2050	G1973	G1870	◆	C1692	C1566	U1438	U1364
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G2577	G2395	C2119	C	G2054	A1977	U1891	◆	C1698	G1576	A1442	C1367
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G2584	C2409	C2123	C	G2061	A1981	G1917	◆	C	U1591	C1446	G1371
A2585	A2410	C2124	C	C2062	A1982	G1918	◆	C	C1594	C1447	A1372
C2586	U2413	G2125	C	U2066	G1983	C1919	◆	G	U1591	C1448	A1373
G2588	A2415	C2126	C	A2067	U1984	G1920	◆	A	G1597	G1455	G1377
A2589	U2416	C2129	C	U2068	C1985	C1919	◆	C	C1597	C1378	C1379
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A2599		G	C	G2082	G1988	G1922	◆	C	U1606	C1469	
		G	C	C2083	A1989	G1923	◆	C			
		G	C	G2084	U1990	U1928	◆	C	G1612		
		A	C	C2085	C1991	C1929	◆	C	A1613		
			C	A2086	C1992		◆				
				G2087	U1995						
					A1996						

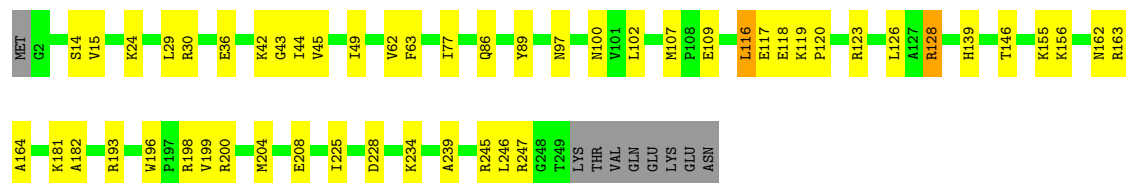


Chain L8:  59% 27% 13%



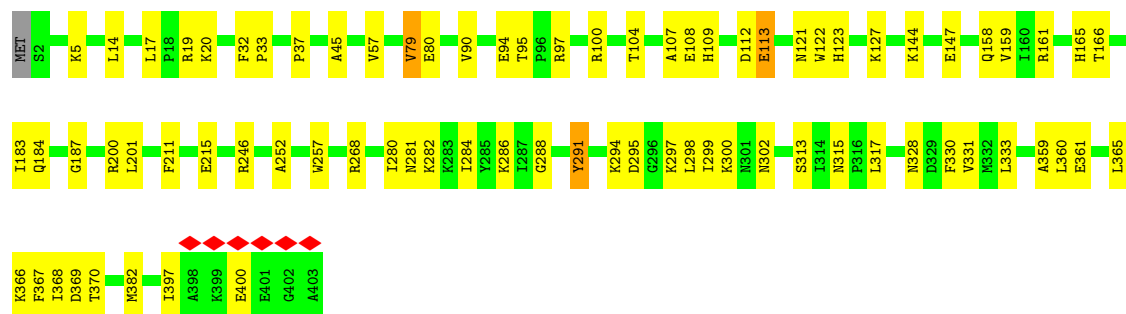
- Molecule 51: 60S ribosomal protein L8

Chain LA:  76% 19%



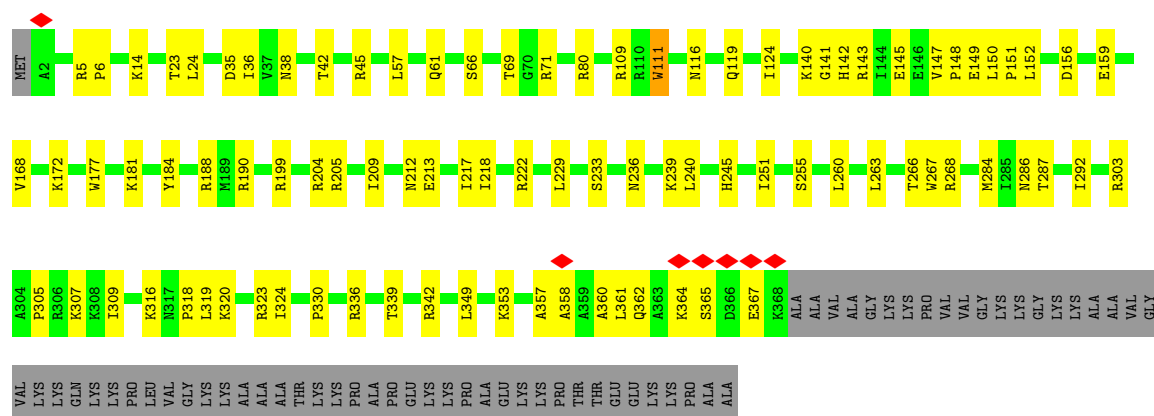
- Molecule 52: 60S ribosomal protein L3

Chain LB:  80% 19%



- Molecule 53: 60S ribosomal protein L4

Chain LC:  65% 21% 14%





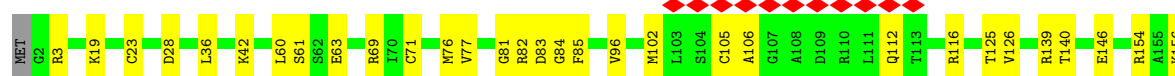
- Molecule 58: 60S ribosomal protein L9

Chain LH: 75% 24%



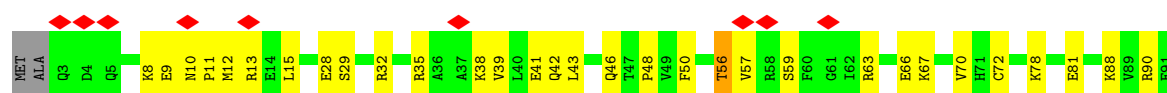
- Molecule 59: Ribosomal protein uL16-like

Chain LI: 5% 80% 19%



- Molecule 60: 60S ribosomal protein L11

Chain LJ: 10% 65% 33%



- Molecule 61: 60S ribosomal protein L13

Chain LL: 78% 20%



- Molecule 62: 60S ribosomal protein L14

LYS	ALA	SER	GLY	LYS	ALA	THR	MET
ALA	ALA	GLY	LYS	LYS	ALA	ALA	V2
							F6
							R11
							V12
							D29
							V30
							I31
							D32
							Q33
							N34
							R35
							D39
							T43
							R47
							F52
							T58
							D59
							H69
							Q70
							K71
							Y72
							W91
							I95
							E96
							E99
							T105
							D108
							R109
							F110
							K111
							V112
							N125
							E126
							S139
							P140
							LYS
							LYS
							ALA
							GLN
							PRO
							GLY
							THR
							LYS
							GLY

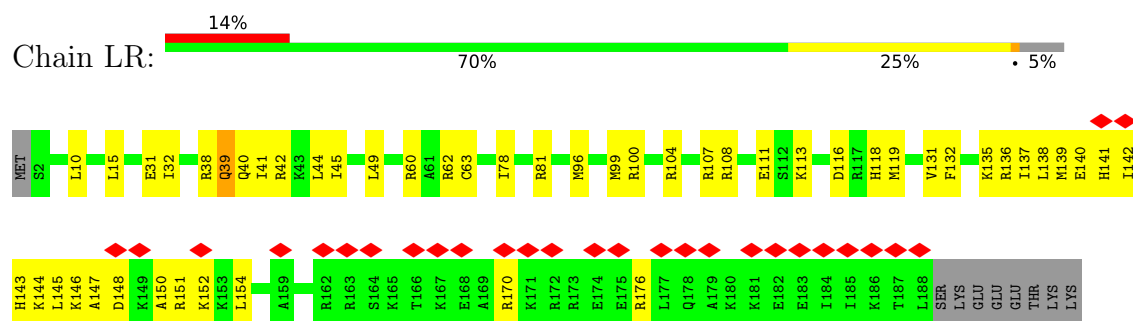
-
- | Amino Acid | Count |
|------------|-------|
| MET | 10 |
| G2 | 10 |
| A3 | 10 |
| Y4 | 10 |
| W11 | 10 |
| D17 | 10 |
| V18 | 10 |
| Q32 | 10 |
| L33 | 10 |
| V60 | 10 |
| I64 | 10 |
| R68 | 10 |
| K72 | 10 |
| R73 | 10 |
| V89 | 10 |
| K93 | 10 |
| L98 | 10 |
| A106 | 10 |
| R114 | 10 |
| D124 | 10 |
| S125 | 10 |
| K128 | 10 |
| L134 | 10 |
| P137 | 10 |
| F138 | 10 |
| P146 | 10 |
| D147 | 10 |
| T148 | 10 |
| H158 | 10 |
| E159 | 10 |
| E160 | 10 |
| M161 | 10 |
| R172 | 10 |
| G173 | 10 |
| L174 | 10 |
| K179 | 10 |
| I184 | 10 |
| P194 | 10 |

-
- Sequence logo for the 100bp window centered on the mutation site. The y-axis represents information content in bits, ranging from 0 to 0.4. The x-axis shows amino acid positions from E194 to Y192. The logo shows a strong preference for Glutamine (Q) at position 197, with a peak of approximately 0.35 bits. Other positions show lower information content, generally below 0.1 bits.

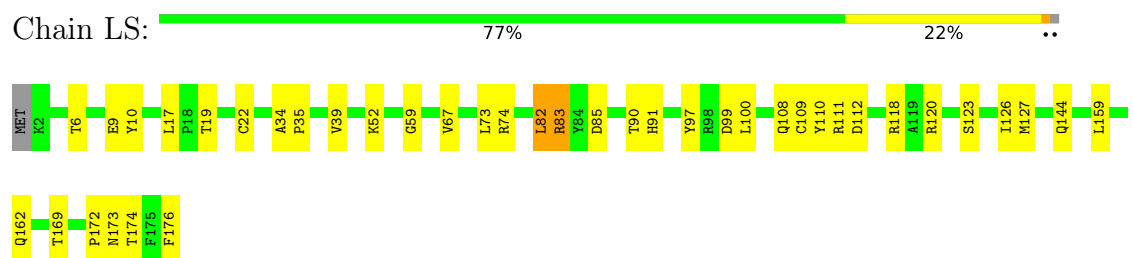
- | | | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|-----|-----|-----|-----|
| PRO | GLU | GLU | GLU | VAL | ALA | GLN | LYS | LYS | LYS | ILE | SER | GLN | LYS | LYS | LYS | LEU | LYS | LYS | GLN | LYS | LYS | LEU | MET | ALA | ARG | GLU | | | | | | | | | | | | | | |
| MET | V2 | E9 | R23 | F76 | K37 | D50 | Q54 | K55 | Q56 | C57 | V58 | R61 | R62 | Q72 | R82 | W83 | E89 | F90 | L91 | L92 | K96 | E103 | L112 | H116 | V119 | M125 | A132 | C144 | H145 | I146 | E147 | M148 | I149 | L150 | E154 | GLN | ILE | VAL | PRO | LYS |

-
- | Category | Count |
|----------|-------|
| MET | 1 |
| G2 | 1 |
| V3 | 1 |
| D4 | 1 |
| D10 | 1 |
| R11 | 1 |
| K19 | 1 |
| L35 | 1 |
| R38 | 1 |
| T39 | 1 |
| K49 | 1 |
| M53 | 1 |
| L61 | 1 |
| R65 | 1 |
| M66 | 1 |
| I67 | 1 |
| R68 | 1 |
| K69 | 1 |
| E76 | 1 |
| V81 | 1 |
| D88 | 1 |
| D89 | 1 |
| V90 | 1 |
| R91 | 1 |
| P96 | 1 |
| C101 | 1 |
| A109 | 1 |
| I113 | 1 |
| L114 | 1 |
| T122 | 1 |
| F123 | 1 |
| D124 | 1 |
| G125 | 1 |
| L126 | 1 |
| L138 | 1 |
| K154 | 1 |
| G167 | 1 |
| T168 | 1 |
| P159 | 1 |
| E170 | 1 |
| R178 | 1 |
| R181 | 1 |
| N188 | 1 |

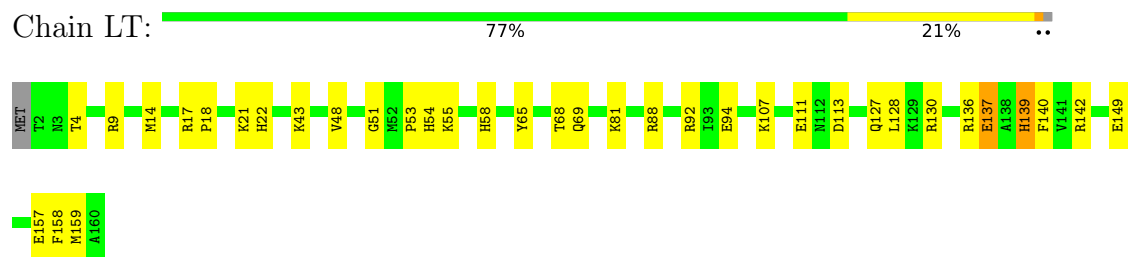
- Molecule 67: 60S ribosomal protein L19



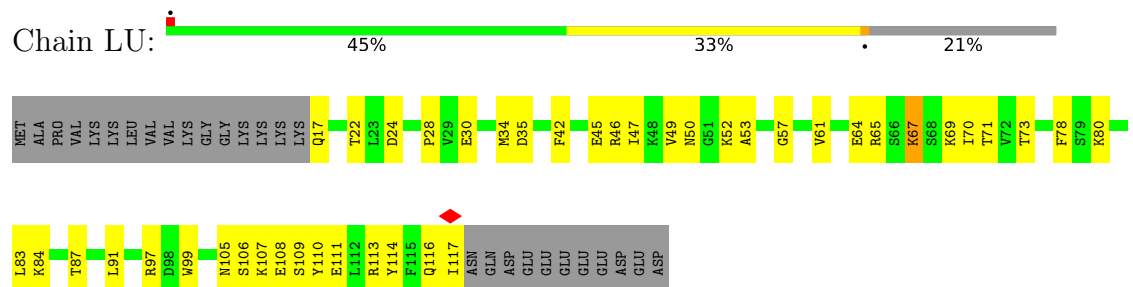
- Molecule 68: 60S ribosomal protein L18a



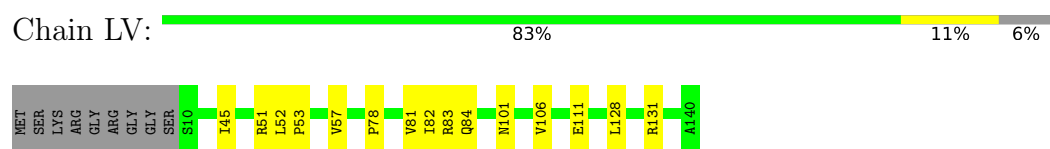
- Molecule 69: 60S ribosomal protein L21



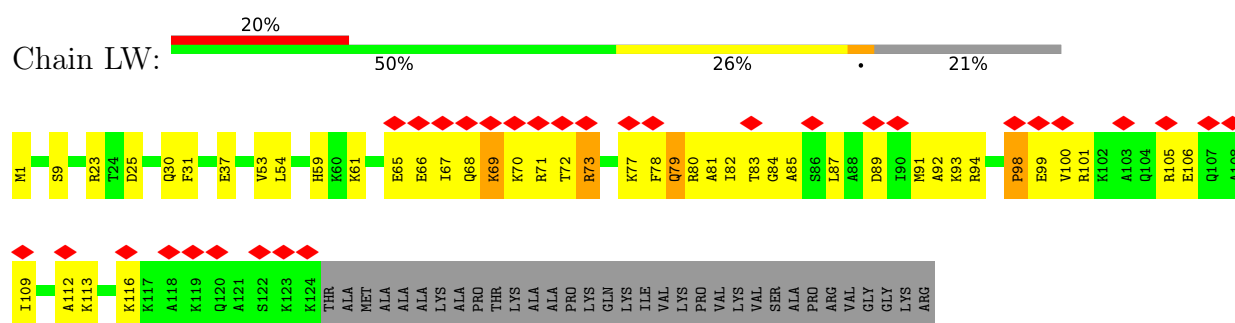
- Molecule 70: 60S ribosomal protein L22



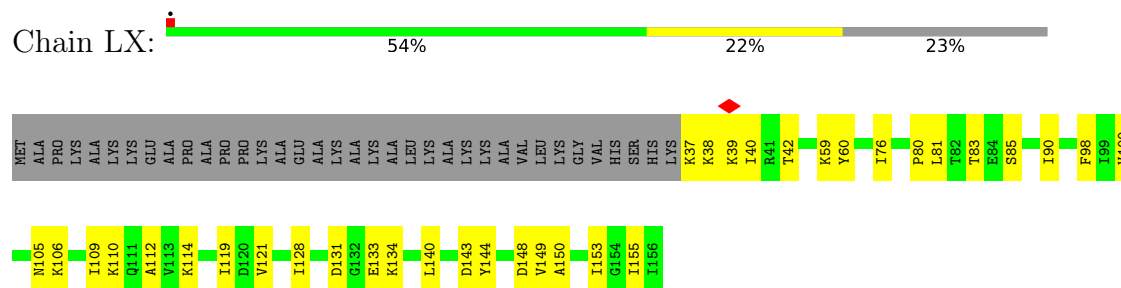
- Molecule 71: 60S ribosomal protein L23



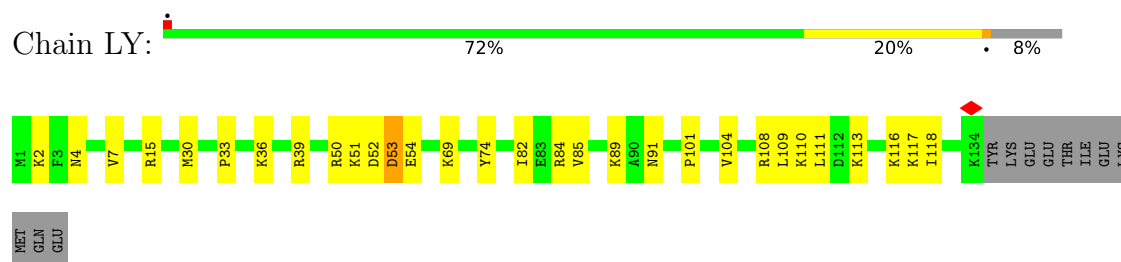
- Molecule 72: 60S ribosomal protein L24



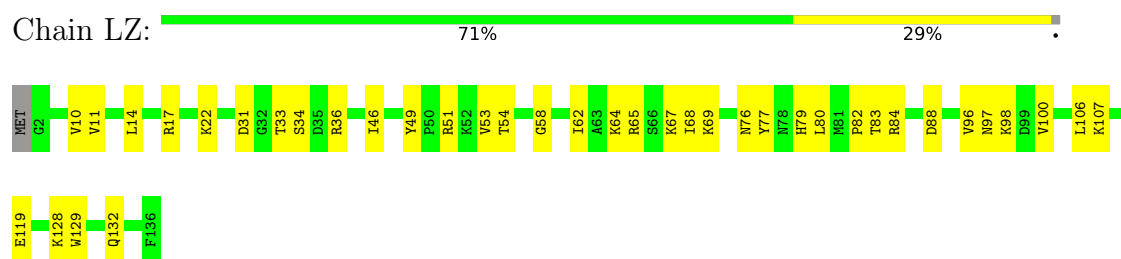
- Molecule 73: 60S ribosomal protein L23a



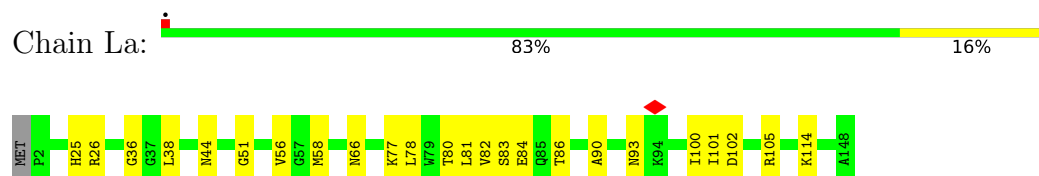
- Molecule 74: 60S ribosomal protein L26



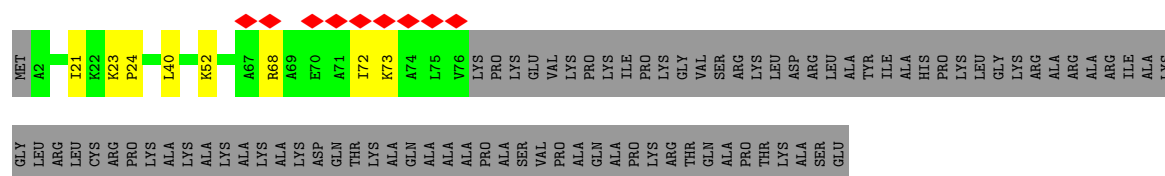
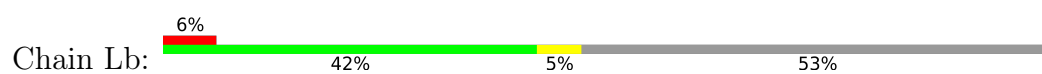
- Molecule 75: 60S ribosomal protein L27



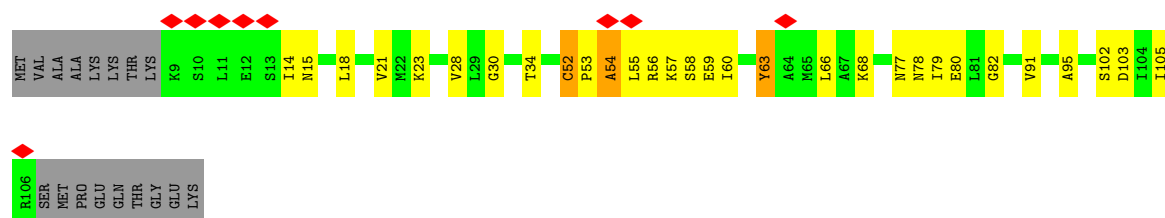
- Molecule 76: 60S ribosomal protein L27a



- Molecule 77: 60S ribosomal protein L29



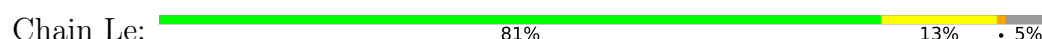
- Molecule 78: 60S ribosomal protein L30



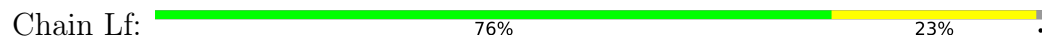
- Molecule 79: 60S ribosomal protein L31



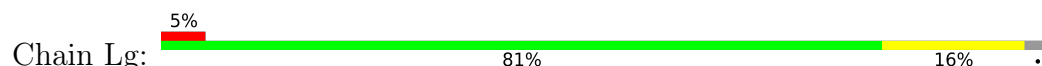
- Molecule 80: 60S ribosomal protein L32



- Molecule 81: 60S ribosomal protein L35a



- Molecule 82: 60S ribosomal protein L34



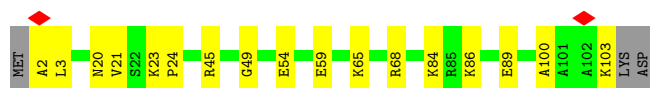
- Molecule 83: 60S ribosomal protein L35

Chain Lh:  74% 24% ..



- Molecule 84: 60S ribosomal protein L36

Chain Li:  81% 16% .



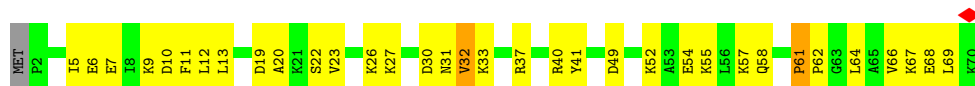
- Molecule 85: 60S ribosomal protein L37

Chain Lj:  66% 23% 11%



- Molecule 86: 60S ribosomal protein L38

Chain Lk:  50% 46% ..



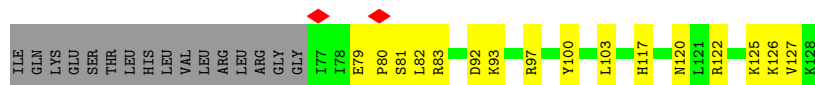
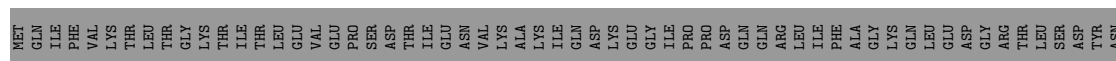
- Molecule 87: 60S ribosomal protein L39

Chain Ll:  73% 25% .



- Molecule 88: Ubiquitin-60S ribosomal protein L40

Chain Lm:  28% 12% 59%

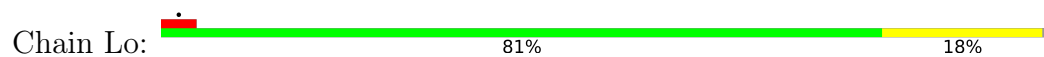


- Molecule 89: 60S ribosomal protein L41

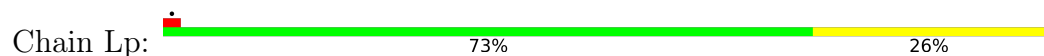
Chain Ln:  84% 12% .



- Molecule 90: 60S ribosomal protein L36a



- Molecule 91: 60S ribosomal protein L37a



- Molecule 92: 60S ribosomal protein L28



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	79353	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 ($e^-/\text{\AA}^2$)	64.2	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2400	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.070	Depositor
Minimum map value	-0.023	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.002	Depositor
Recommended contour level	0.01	Depositor
Map size (Å)	708.19836, 708.19836, 708.19836	wwPDB
Map dimensions	832, 832, 832	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8512, 0.8512, 0.8512	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	0.15	0/7577	0.38	1/10257 (0.0%)
2	L	0.22	1/1843 (0.1%)	0.33	0/2492
3	N	0.70	2/2053 (0.1%)	0.81	4/2786 (0.1%)
4	O	0.13	0/1586	0.35	0/2145
5	F	0.12	0/2225	0.36	0/3007
6	G	0.15	0/1881	0.42	2/2551 (0.1%)
7	H	0.14	0/1837	0.39	0/2474
8	I	0.12	0/2296	0.37	0/3092
9	J	0.16	0/1438	0.39	0/1942
10	K	0.14	0/2714	0.33	0/3665
11	E	0.13	0/509	0.32	0/687
12	M	0.26	4/8139 (0.0%)	0.46	8/11009 (0.1%)
13	X	0.45	1/4477 (0.0%)	0.82	24/6954 (0.3%)
14	S2	0.13	0/41243	0.31	0/64257
15	SA	0.18	0/1784	0.54	2/2424 (0.1%)
16	SB	0.22	0/1765	0.53	0/2362
17	SD	0.21	0/1793	0.54	1/2414 (0.0%)
18	SE	0.17	0/2118	0.47	0/2849
19	SF	0.21	0/1531	0.62	4/2059 (0.2%)
20	SH	0.21	0/1544	0.56	1/2068 (0.0%)
21	SI	0.22	0/1715	0.51	0/2287
22	SK	0.32	0/851	0.77	3/1147 (0.3%)
23	SL	0.18	0/1268	0.50	0/1696
24	SP	0.23	0/815	0.76	4/1087 (0.4%)
25	SQ	0.21	0/1177	0.55	1/1575 (0.1%)
26	SR	0.20	0/1086	0.78	4/1457 (0.3%)
27	SS	0.23	0/1253	0.47	0/1676
28	ST	0.18	0/1131	0.55	0/1515
29	SU	0.21	0/832	0.61	2/1117 (0.2%)
30	SV	0.18	0/643	0.47	0/860
31	SX	0.17	0/1116	0.46	0/1490
32	Sa	0.35	1/863 (0.1%)	0.69	5/1159 (0.4%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	Sc	0.22	0/508	0.58	0/680
34	Sd	1.44	3/455 (0.7%)	1.65	5/603 (0.8%)
35	Sf	0.18	0/593	0.49	0/786
36	Sg	0.28	1/2493 (0.0%)	0.62	4/3394 (0.1%)
37	SC	0.19	0/1762	0.50	0/2381
38	SG	0.17	0/1946	0.49	0/2590
39	SJ	0.17	0/1550	0.55	2/2069 (0.1%)
40	SM	0.27	1/962 (0.1%)	0.57	1/1290 (0.1%)
41	SN	0.16	0/1232	0.41	0/1656
42	SO	0.23	0/1062	0.63	3/1425 (0.2%)
43	SW	0.20	0/1051	0.46	0/1406
44	SY	0.16	0/1083	0.44	0/1438
45	SZ	0.13	0/604	0.47	0/810
46	Sb	0.21	0/665	0.51	0/891
47	Se	0.17	0/465	0.55	0/612
48	L5	0.17	0/87605	0.34	0/136661
49	L7	0.16	0/2858	0.28	0/4455
50	L8	0.15	0/3701	0.29	0/5766
51	LA	0.24	0/1936	0.56	2/2596 (0.1%)
52	LB	0.21	0/3306	0.49	0/4424
53	LC	0.22	0/2973	0.48	0/3992
54	LD	0.20	0/2428	0.46	0/3252
55	LE	0.23	0/1996	0.84	13/2673 (0.5%)
56	LF	0.22	0/1905	0.46	0/2539
57	LG	0.21	0/1960	0.51	0/2637
58	LH	0.25	0/1537	0.56	0/2066
59	LI	0.22	0/1751	0.53	0/2340
60	LJ	0.23	0/1433	0.58	2/1915 (0.1%)
61	LL	0.21	0/1732	0.70	4/2315 (0.2%)
62	LM	0.22	0/1161	0.50	0/1554
63	LN	0.24	0/1746	0.49	0/2338
64	LO	0.22	0/1682	0.45	0/2250
65	LP	0.23	0/1268	0.53	1/1701 (0.1%)
66	LQ	0.23	0/1537	0.50	0/2052
67	LR	0.22	0/1582	0.55	1/2091 (0.0%)
68	LS	0.26	0/1493	0.57	1/2003 (0.0%)
69	LT	0.23	0/1326	0.54	0/1770
70	LU	0.27	0/839	0.59	1/1126 (0.1%)
71	LV	0.24	0/993	0.55	0/1332
72	LW	0.21	0/1030	0.84	6/1364 (0.4%)
73	LX	0.22	0/1002	0.52	0/1345
74	LY	0.22	0/1132	0.52	0/1504
75	LZ	0.21	0/1130	0.53	1/1507 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	La	0.23	0/1191	0.49	0/1591
77	Lb	0.20	0/620	0.44	0/819
78	Lc	0.29	0/774	0.54	0/1038
79	Ld	0.23	0/903	0.53	1/1216 (0.1%)
80	Le	0.25	0/1071	0.54	0/1429
81	Lf	0.22	0/895	0.49	0/1198
82	Lg	0.23	0/916	0.50	0/1220
83	Lh	0.23	0/1023	0.50	0/1351
84	Li	0.20	0/843	0.52	0/1115
85	Lj	0.26	0/720	0.52	0/952
86	Lk	0.30	0/575	0.67	1/761 (0.1%)
87	Ll	0.22	0/454	0.45	0/599
88	Lm	0.21	0/435	0.51	0/575
89	Ln	0.25	0/231	0.49	0/294
90	Lo	0.22	0/876	0.47	0/1156
91	Lp	0.22	0/718	0.51	0/953
92	Lr	0.24	0/1017	0.59	1/1364 (0.1%)
All	All	0.21	14/267838 (0.0%)	0.44	116/389790 (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	A	0	1
32	Sa	0	3
70	LU	0	1
All	All	0	5

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	N	128	PRO	CB-CG	24.51	2.72	1.49
34	Sd	11	PRO	CB-CG	22.57	2.62	1.49
34	Sd	11	PRO	CG-CD	-18.51	0.87	1.50
3	N	128	PRO	CG-CD	-18.44	0.88	1.50
12	M	980	PRO	CG-CD	-16.13	0.95	1.50

The worst 5 of 116 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	N	128	PRO	CB-CG-CD	-33.15	0.01	106.10
34	Sd	11	PRO	CB-CG-CD	-31.42	5.56	106.10
12	M	980	PRO	N-CD-CG	-19.36	74.17	103.20
36	Sg	25	PRO	N-CD-CG	-18.20	75.91	103.20
61	LL	54	PRO	CA-C-N	14.34	147.51	121.70

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1017	SER	Peptide
70	LU	97	ARG	Peptide
32	Sa	100	ARG	Sidechain
32	Sa	99	PRO	Peptide,Mainchain

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	A	7438	0	7568	241	0
2	L	1819	0	1818	55	0
3	N	2020	0	2035	65	0
4	O	1566	0	1605	47	0
5	F	2194	0	2205	53	0
6	G	1852	0	1881	45	0
7	H	1810	0	1867	44	0
8	I	2263	0	2337	53	0
9	J	1414	0	1441	42	0
10	K	2673	0	2718	78	0
11	E	499	0	505	11	0
12	M	7967	0	7892	210	0
13	X	4020	0	2025	91	0
14	S2	36900	0	18591	862	0
15	SA	1747	0	1751	72	0
16	SB	1738	0	1809	63	0
17	SD	1765	0	1865	92	0
18	SE	2076	0	2177	64	0
19	SF	1509	0	1563	78	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
20	SH	1521	0	1616	62	0
21	SI	1686	0	1772	46	0
22	SK	827	0	854	65	0
23	SL	1247	0	1323	31	0
24	SP	804	0	841	56	0
25	SQ	1158	0	1232	73	0
26	SR	1072	0	1130	65	0
27	SS	1235	0	1309	89	0
28	ST	1112	0	1146	72	0
29	SU	822	0	887	66	0
30	SV	636	0	637	31	0
31	SX	1098	0	1167	23	0
32	Sa	847	0	895	30	0
33	Sc	506	0	535	34	0
34	Sd	445	0	442	34	0
35	Sf	581	0	597	20	0
36	Sg	2436	0	2393	130	0
37	SC	1725	0	1813	53	0
38	SG	1923	0	2089	117	0
39	SJ	1525	0	1640	44	0
40	SM	952	0	983	36	0
41	SN	1208	0	1294	17	0
42	SO	1049	0	1073	50	0
43	SW	1034	0	1080	25	0
44	SY	1065	0	1142	39	0
45	SZ	598	0	656	17	0
46	Sb	651	0	672	17	0
47	Se	459	0	503	12	0
48	L5	78316	0	39566	1147	0
49	L7	2558	0	1295	19	0
50	L8	3314	0	1683	41	0
51	LA	1898	0	1993	39	0
52	LB	3238	0	3376	58	0
53	LC	2919	0	3092	71	0
54	LD	2382	0	2410	52	0
55	LE	1958	0	2126	56	0
56	LF	1870	0	1996	32	0
57	LG	1927	0	2074	49	0
58	LH	1518	0	1601	35	0
59	LI	1711	0	1749	26	0
60	LJ	1410	0	1441	82	0
61	LL	1701	0	1818	34	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
62	LM	1138	0	1204	25	0
63	LN	1701	0	1749	28	0
64	LO	1650	0	1794	24	0
65	LP	1242	0	1269	20	0
66	LQ	1513	0	1628	29	0
67	LR	1566	0	1729	46	0
68	LS	1453	0	1490	33	0
69	LT	1298	0	1366	28	0
70	LU	825	0	850	36	0
71	LV	979	0	1038	10	0
72	LW	1015	0	1079	38	0
73	LX	985	0	1066	25	0
74	LY	1115	0	1205	25	0
75	LZ	1107	0	1182	26	0
76	La	1162	0	1213	23	0
77	Lb	610	0	650	6	0
78	Lc	764	0	804	25	0
79	Ld	888	0	930	17	0
80	Le	1053	0	1147	14	0
81	Lf	876	0	912	17	0
82	Lg	906	0	998	17	0
83	Lh	1015	0	1148	26	0
84	Li	832	0	917	11	0
85	Lj	705	0	738	19	0
86	Lk	569	0	637	29	0
87	Ll	444	0	483	10	0
88	Lm	429	0	466	13	0
89	Ln	230	0	276	4	0
90	Lo	862	0	932	29	0
91	Lp	708	0	756	18	0
92	Lr	1002	0	1067	25	0
93	L5	145	0	0	0	0
93	L7	7	0	0	0	0
93	L8	5	0	0	0	0
93	LA	1	0	0	0	0
93	LH	1	0	0	0	0
93	LN	1	0	0	0	0
93	LP	1	0	0	0	0
93	LQ	1	0	0	0	0
93	LV	2	0	0	0	0
93	Ll	1	0	0	0	0
93	Lr	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
93	S2	65	0	0	1	0
93	Sc	1	0	0	0	0
94	Lg	1	0	0	0	0
94	Lj	1	0	0	0	0
94	Lm	1	0	0	0	0
94	Lo	1	0	0	0	0
94	Lp	1	0	0	0	0
94	Sa	1	0	0	0	0
All	All	251092	0	194317	5320	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 12.

The worst 5 of 5320 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)
60:LJ:63:ARG:HD2	90:Lo:106:PHE:CB	1.43	1.47
34:Sd:11:PRO:N	34:Sd:11:PRO:CG	1.84	1.37
3:N:128:PRO:CG	3:N:128:PRO:N	1.81	1.36
48:L5:747:A:N6	48:L5:916:C:H42	1.39	1.20
48:L5:747:A:H62	48:L5:916:C:N4	1.37	1.19

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	A	945/1246 (76%)	874 (92%)	70 (7%)	1 (0%)	48	75
2	L	239/245 (98%)	227 (95%)	11 (5%)	1 (0%)	30	60
3	N	263/280 (94%)	251 (95%)	12 (5%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	O	206/239 (86%)	204 (99%)	2 (1%)	0	100	100
5	F	284/295 (96%)	257 (90%)	24 (8%)	3 (1%)	11	39
6	G	247/272 (91%)	238 (96%)	8 (3%)	1 (0%)	30	60
7	H	233/371 (63%)	210 (90%)	23 (10%)	0	100	100
8	I	285/297 (96%)	253 (89%)	31 (11%)	1 (0%)	30	60
9	J	182/199 (92%)	157 (86%)	25 (14%)	0	100	100
10	K	339/443 (76%)	313 (92%)	26 (8%)	0	100	100
11	E	57/274 (21%)	48 (84%)	8 (14%)	1 (2%)	6	29
12	M	975/1096 (89%)	914 (94%)	59 (6%)	2 (0%)	43	71
15	SA	220/295 (75%)	195 (89%)	24 (11%)	1 (0%)	24	55
16	SB	212/264 (80%)	192 (91%)	18 (8%)	2 (1%)	14	43
17	SD	225/243 (93%)	192 (85%)	30 (13%)	3 (1%)	9	35
18	SE	260/263 (99%)	232 (89%)	25 (10%)	3 (1%)	10	37
19	SF	189/204 (93%)	154 (82%)	32 (17%)	3 (2%)	7	31
20	SH	187/194 (96%)	152 (81%)	33 (18%)	2 (1%)	11	39
21	SI	204/208 (98%)	176 (86%)	26 (13%)	2 (1%)	12	40
22	SK	96/165 (58%)	81 (84%)	13 (14%)	2 (2%)	5	26
23	SL	151/158 (96%)	134 (89%)	16 (11%)	1 (1%)	18	49
24	SP	95/145 (66%)	70 (74%)	21 (22%)	4 (4%)	2	14
25	SQ	144/146 (99%)	124 (86%)	17 (12%)	3 (2%)	5	26
26	SR	130/135 (96%)	114 (88%)	15 (12%)	1 (1%)	16	45
27	SS	148/152 (97%)	124 (84%)	19 (13%)	5 (3%)	3	18
28	ST	141/145 (97%)	128 (91%)	11 (8%)	2 (1%)	9	33
29	SU	102/119 (86%)	93 (91%)	7 (7%)	2 (2%)	6	27
30	SV	81/83 (98%)	68 (84%)	11 (14%)	2 (2%)	4	23
31	SX	139/143 (97%)	122 (88%)	14 (10%)	3 (2%)	5	26
32	Sa	105/115 (91%)	85 (81%)	18 (17%)	2 (2%)	6	28
33	Sc	62/69 (90%)	49 (79%)	13 (21%)	0	100	100
34	Sd	51/56 (91%)	50 (98%)	1 (2%)	0	100	100
35	Sf	69/156 (44%)	51 (74%)	14 (20%)	4 (6%)	1	9
36	Sg	311/317 (98%)	256 (82%)	52 (17%)	3 (1%)	12	40

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	SC	220/293 (75%)	191 (87%)	26 (12%)	3 (1%)	9	33
38	SG	235/249 (94%)	204 (87%)	25 (11%)	6 (3%)	4	23
39	SJ	183/194 (94%)	163 (89%)	17 (9%)	3 (2%)	7	31
40	SM	120/132 (91%)	99 (82%)	18 (15%)	3 (2%)	4	23
41	SN	148/151 (98%)	142 (96%)	3 (2%)	3 (2%)	6	27
42	SO	138/151 (91%)	110 (80%)	23 (17%)	5 (4%)	2	17
43	SW	127/130 (98%)	117 (92%)	10 (8%)	0	100	100
44	SY	129/133 (97%)	114 (88%)	14 (11%)	1 (1%)	16	45
45	SZ	73/125 (58%)	63 (86%)	9 (12%)	1 (1%)	9	33
46	Sb	81/84 (96%)	70 (86%)	10 (12%)	1 (1%)	10	37
47	Se	56/59 (95%)	44 (79%)	12 (21%)	0	100	100
51	LA	246/257 (96%)	221 (90%)	24 (10%)	1 (0%)	30	60
52	LB	400/403 (99%)	359 (90%)	37 (9%)	4 (1%)	12	40
53	LC	365/427 (86%)	316 (87%)	47 (13%)	2 (0%)	24	55
54	LD	291/297 (98%)	270 (93%)	17 (6%)	4 (1%)	9	33
55	LE	238/288 (83%)	188 (79%)	44 (18%)	6 (2%)	4	23
56	LF	223/248 (90%)	212 (95%)	11 (5%)	0	100	100
57	LG	239/266 (90%)	213 (89%)	26 (11%)	0	100	100
58	LH	188/192 (98%)	175 (93%)	13 (7%)	0	100	100
59	LI	211/214 (99%)	202 (96%)	9 (4%)	0	100	100
60	LJ	174/178 (98%)	163 (94%)	9 (5%)	2 (1%)	11	39
61	LL	208/211 (99%)	185 (89%)	19 (9%)	4 (2%)	6	28
62	LM	137/215 (64%)	118 (86%)	17 (12%)	2 (2%)	8	32
63	LN	201/204 (98%)	190 (94%)	11 (6%)	0	100	100
64	LO	199/203 (98%)	191 (96%)	8 (4%)	0	100	100
65	LP	151/184 (82%)	139 (92%)	11 (7%)	1 (1%)	18	49
66	LQ	185/188 (98%)	172 (93%)	13 (7%)	0	100	100
67	LR	185/196 (94%)	180 (97%)	5 (3%)	0	100	100
68	LS	173/176 (98%)	153 (88%)	19 (11%)	1 (1%)	21	52
69	LT	157/160 (98%)	146 (93%)	8 (5%)	3 (2%)	6	28
70	LU	99/128 (77%)	91 (92%)	8 (8%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
71	LV	129/140 (92%)	119 (92%)	10 (8%)	0	100	100
72	LW	122/157 (78%)	104 (85%)	16 (13%)	2 (2%)	7	31
73	LX	118/156 (76%)	111 (94%)	7 (6%)	0	100	100
74	LY	132/145 (91%)	123 (93%)	8 (6%)	1 (1%)	16	45
75	LZ	133/136 (98%)	120 (90%)	13 (10%)	0	100	100
76	La	145/148 (98%)	127 (88%)	18 (12%)	0	100	100
77	Lb	73/159 (46%)	68 (93%)	4 (6%)	1 (1%)	9	33
78	Lc	96/115 (84%)	85 (88%)	9 (9%)	2 (2%)	5	26
79	Ld	105/125 (84%)	98 (93%)	7 (7%)	0	100	100
80	Le	126/135 (93%)	116 (92%)	9 (7%)	1 (1%)	16	45
81	Lf	107/110 (97%)	100 (94%)	6 (6%)	1 (1%)	14	43
82	Lg	112/117 (96%)	108 (96%)	4 (4%)	0	100	100
83	Lh	120/123 (98%)	112 (93%)	7 (6%)	1 (1%)	16	45
84	Li	100/105 (95%)	93 (93%)	7 (7%)	0	100	100
85	Lj	84/97 (87%)	76 (90%)	7 (8%)	1 (1%)	10	37
86	Lk	67/70 (96%)	58 (87%)	8 (12%)	1 (2%)	8	32
87	Ll	48/51 (94%)	45 (94%)	3 (6%)	0	100	100
88	Lm	50/128 (39%)	49 (98%)	0	1 (2%)	6	27
89	Ln	22/25 (88%)	20 (91%)	2 (9%)	0	100	100
90	Lo	103/106 (97%)	96 (93%)	6 (6%)	1 (1%)	12	40
91	Lp	89/92 (97%)	80 (90%)	8 (9%)	1 (1%)	11	39
92	Lr	123/137 (90%)	109 (89%)	13 (11%)	1 (1%)	16	45
All	All	15561/17945 (87%)	14006 (90%)	1424 (9%)	131 (1%)	18	45

5 of 131 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1018	PRO
12	M	14	PHE
16	SB	147	ASN
18	SE	76	VAL
19	SF	15	PRO

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	813/1062 (77%)	812 (100%)	1 (0%)	88	90
2	L	183/186 (98%)	183 (100%)	0	100	100
3	N	227/238 (95%)	227 (100%)	0	100	100
4	O	172/196 (88%)	172 (100%)	0	100	100
5	F	249/255 (98%)	249 (100%)	0	100	100
6	G	178/188 (95%)	178 (100%)	0	100	100
7	H	196/290 (68%)	196 (100%)	0	100	100
8	I	251/257 (98%)	251 (100%)	0	100	100
9	J	160/173 (92%)	159 (99%)	1 (1%)	78	81
10	K	297/384 (77%)	297 (100%)	0	100	100
11	E	54/251 (22%)	54 (100%)	0	100	100
12	M	881/973 (90%)	880 (100%)	1 (0%)	88	90
15	SA	184/243 (76%)	183 (100%)	1 (0%)	81	83
16	SB	195/231 (84%)	195 (100%)	0	100	100
17	SD	190/202 (94%)	189 (100%)	1 (0%)	81	83
18	SE	224/225 (100%)	224 (100%)	0	100	100
19	SF	161/170 (95%)	161 (100%)	0	100	100
20	SH	169/174 (97%)	168 (99%)	1 (1%)	78	81
21	SI	178/180 (99%)	176 (99%)	2 (1%)	65	76
22	SK	89/136 (65%)	89 (100%)	0	100	100
23	SL	137/142 (96%)	137 (100%)	0	100	100
24	SP	87/130 (67%)	87 (100%)	0	100	100
25	SQ	121/121 (100%)	121 (100%)	0	100	100
26	SR	120/122 (98%)	119 (99%)	1 (1%)	73	79
27	SS	130/132 (98%)	130 (100%)	0	100	100
28	ST	113/115 (98%)	113 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
29	SU	94/107 (88%)	94 (100%)	0	100	100
30	SV	67/67 (100%)	65 (97%)	2 (3%)	36	61
31	SX	113/115 (98%)	113 (100%)	0	100	100
32	Sa	90/98 (92%)	88 (98%)	2 (2%)	45	66
33	Sc	57/62 (92%)	57 (100%)	0	100	100
34	Sd	47/49 (96%)	47 (100%)	0	100	100
35	Sf	64/140 (46%)	63 (98%)	1 (2%)	55	72
36	Sg	272/275 (99%)	272 (100%)	0	100	100
37	SC	188/225 (84%)	188 (100%)	0	100	100
38	SG	207/218 (95%)	207 (100%)	0	100	100
39	SJ	161/168 (96%)	161 (100%)	0	100	100
40	SM	104/108 (96%)	104 (100%)	0	100	100
41	SN	130/131 (99%)	129 (99%)	1 (1%)	73	79
42	SO	110/119 (92%)	109 (99%)	1 (1%)	70	78
43	SW	112/113 (99%)	110 (98%)	2 (2%)	51	70
44	SY	113/115 (98%)	112 (99%)	1 (1%)	70	78
45	SZ	66/103 (64%)	66 (100%)	0	100	100
46	Sb	75/76 (99%)	75 (100%)	0	100	100
47	Se	47/48 (98%)	47 (100%)	0	100	100
51	LA	190/199 (96%)	189 (100%)	1 (0%)	81	83
52	LB	348/349 (100%)	346 (99%)	2 (1%)	78	81
53	LC	305/348 (88%)	305 (100%)	0	100	100
54	LD	246/250 (98%)	245 (100%)	1 (0%)	84	84
55	LE	215/252 (85%)	214 (100%)	1 (0%)	81	83
56	LF	194/215 (90%)	194 (100%)	0	100	100
57	LG	203/223 (91%)	203 (100%)	0	100	100
58	LH	169/171 (99%)	168 (99%)	1 (1%)	78	81
59	LI	180/181 (99%)	178 (99%)	2 (1%)	65	76
60	LJ	148/149 (99%)	147 (99%)	1 (1%)	76	80
61	LL	176/177 (99%)	176 (100%)	0	100	100
62	LM	118/161 (73%)	118 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
63	LN	171/172 (99%)	170 (99%)	1 (1%)	78	81
64	LO	173/174 (99%)	173 (100%)	0	100	100
65	LP	134/163 (82%)	133 (99%)	1 (1%)	76	80
66	LQ	164/165 (99%)	164 (100%)	0	100	100
67	LR	166/175 (95%)	165 (99%)	1 (1%)	78	81
68	LS	156/157 (99%)	155 (99%)	1 (1%)	78	81
69	LT	139/140 (99%)	138 (99%)	1 (1%)	76	80
70	LU	91/115 (79%)	91 (100%)	0	100	100
71	LV	101/107 (94%)	101 (100%)	0	100	100
72	LW	103/126 (82%)	103 (100%)	0	100	100
73	LX	108/133 (81%)	108 (100%)	0	100	100
74	LY	124/135 (92%)	124 (100%)	0	100	100
75	LZ	117/118 (99%)	117 (100%)	0	100	100
76	La	120/121 (99%)	120 (100%)	0	100	100
77	Lb	63/126 (50%)	63 (100%)	0	100	100
78	Lc	83/97 (86%)	82 (99%)	1 (1%)	63	75
79	Ld	98/110 (89%)	98 (100%)	0	100	100
80	Le	114/121 (94%)	113 (99%)	1 (1%)	70	78
81	Lf	88/89 (99%)	88 (100%)	0	100	100
82	Lg	98/100 (98%)	98 (100%)	0	100	100
83	Lh	109/110 (99%)	108 (99%)	1 (1%)	70	78
84	Li	86/89 (97%)	86 (100%)	0	100	100
85	Lj	73/80 (91%)	73 (100%)	0	100	100
86	Lk	64/65 (98%)	64 (100%)	0	100	100
87	Ll	47/48 (98%)	47 (100%)	0	100	100
88	Lm	48/116 (41%)	48 (100%)	0	100	100
89	Ln	23/24 (96%)	23 (100%)	0	100	100
90	Lo	93/94 (99%)	93 (100%)	0	100	100
91	Lp	74/75 (99%)	73 (99%)	1 (1%)	59	73
92	Lr	109/121 (90%)	108 (99%)	1 (1%)	70	78
All	All	13505/15254 (88%)	13467 (100%)	38 (0%)	84	86

5 of 38 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
63	LN	174	LEU
83	Lh	116	LEU
65	LP	149	ILE
69	LT	139	HIS
92	Lr	85	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 115 such sidechains are listed below:

Mol	Chain	Res	Type
37	SC	136	HIS
85	Lj	13	ASN
53	LC	119	GLN
83	Lh	98	HIS
69	LT	70	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
13	X	192/249 (77%)	128 (66%)	13 (6%)
14	S2	1714/1869 (91%)	623 (36%)	23 (1%)
48	L5	3640/5066 (71%)	1083 (29%)	52 (1%)
49	L7	119/121 (98%)	18 (15%)	0
50	L8	155/157 (98%)	39 (25%)	2 (1%)
All	All	5820/7462 (77%)	1891 (32%)	90 (1%)

5 of 1891 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
13	X	3	A
13	X	8	U
13	X	9	G
13	X	10	A
13	X	12	C

5 of 90 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
48	L5	2094	G
48	L5	3711	U

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Mol	Chain	Res	Type
48	L5	2117	C
48	L5	2693	A
48	L5	3886	G

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 238 ligands modelled in this entry, 238 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

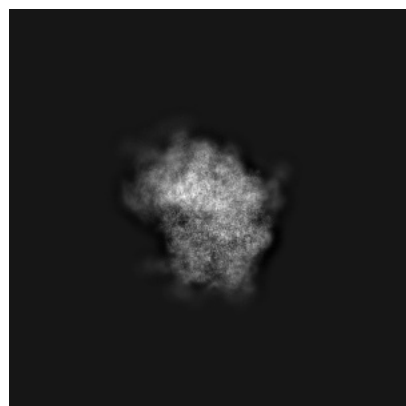
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51132. These allow visual inspection of the internal detail of the map and identification of artifacts.

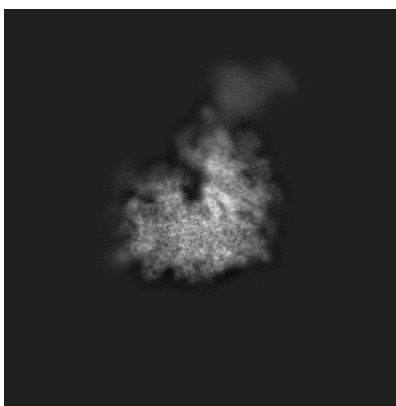
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

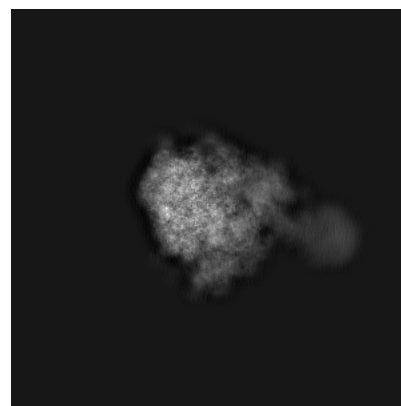
6.1.1 Primary map



X

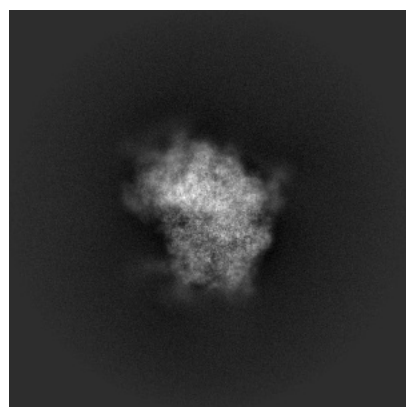


Y

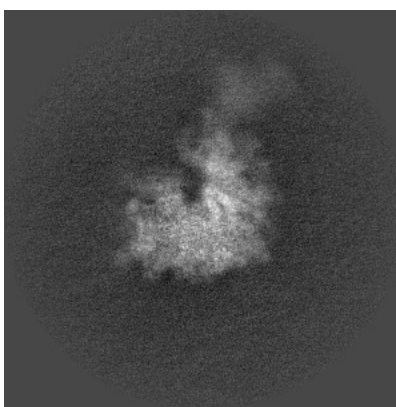


Z

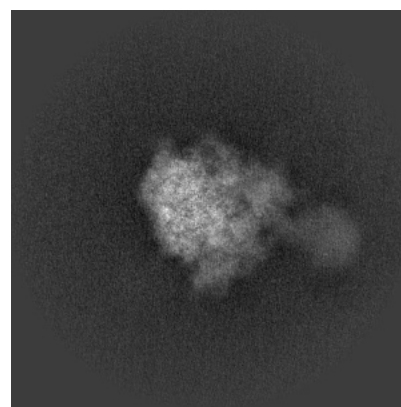
6.1.2 Raw map



X



Y

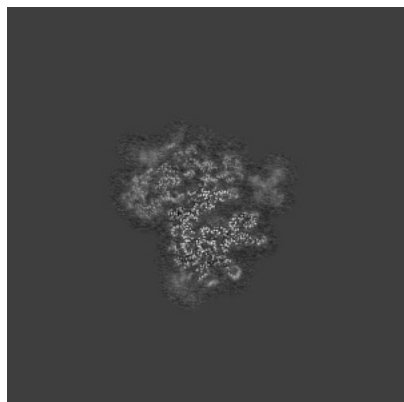


Z

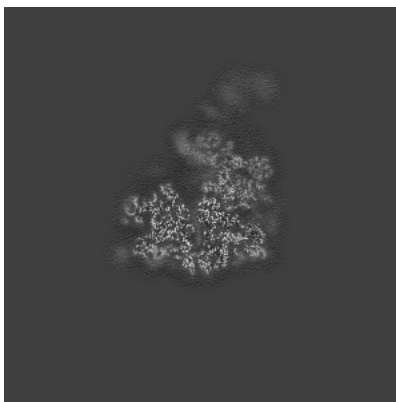
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

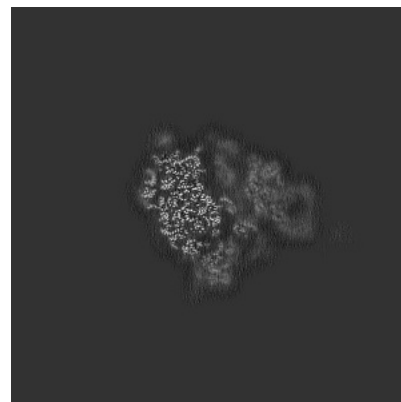
6.2.1 Primary map



X Index: 416

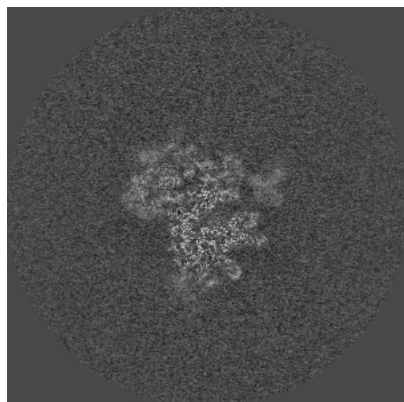


Y Index: 416

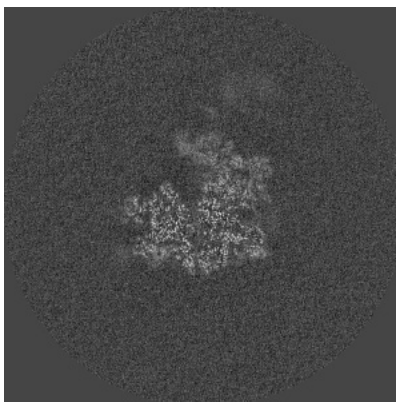


Z Index: 416

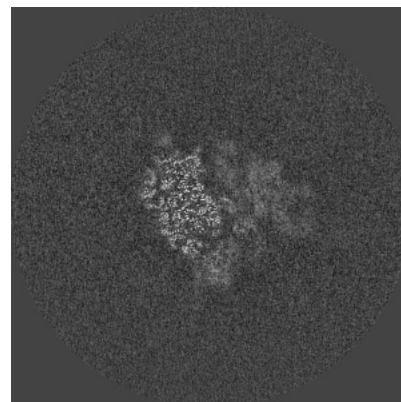
6.2.2 Raw map



X Index: 416



Y Index: 416

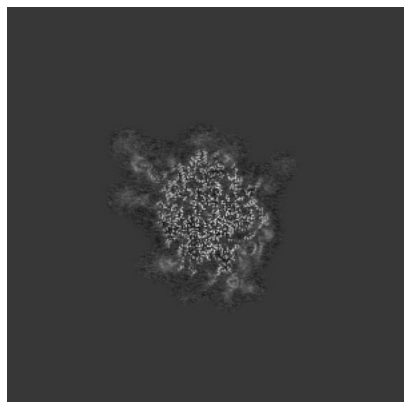


Z Index: 416

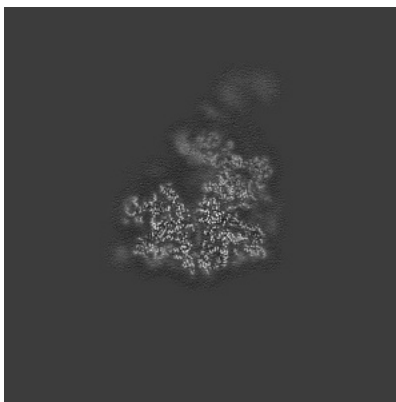
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

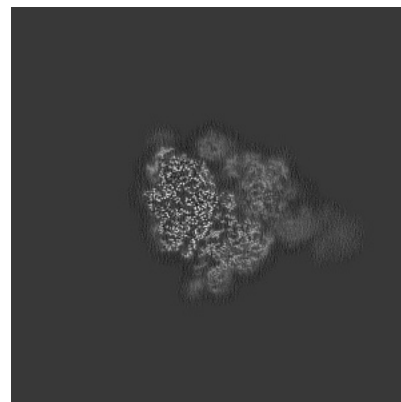
6.3.1 Primary map



X Index: 380

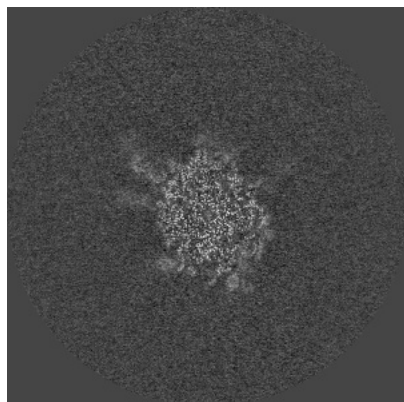


Y Index: 417

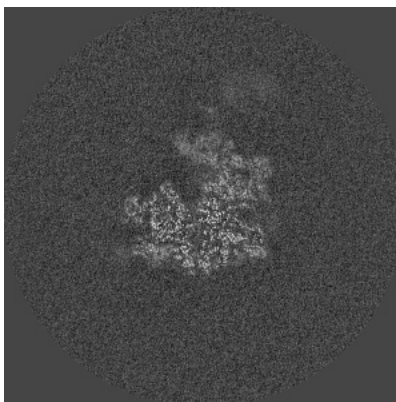


Z Index: 441

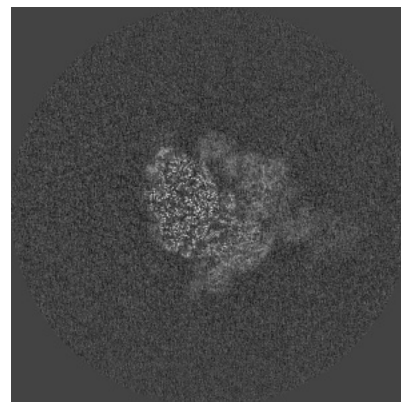
6.3.2 Raw map



X Index: 381



Y Index: 417

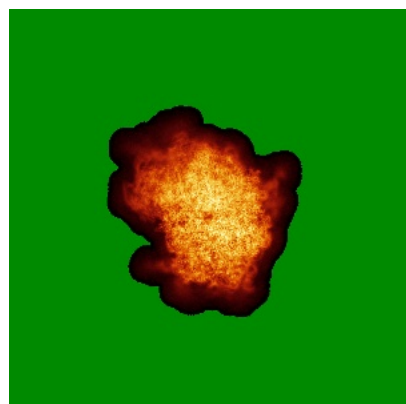


Z Index: 440

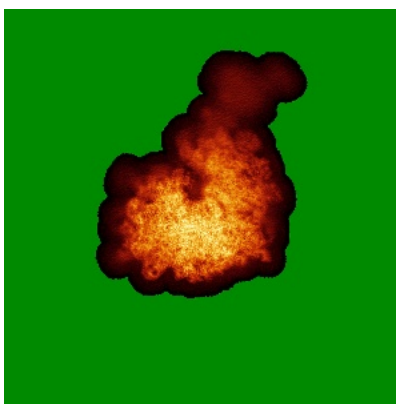
The images above show the largest variance slices of the map in three orthogonal directions.

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

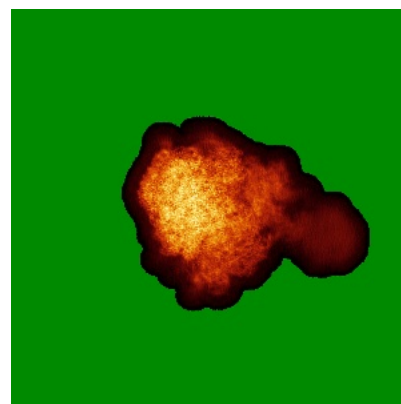
6.4.1 Primary map



X

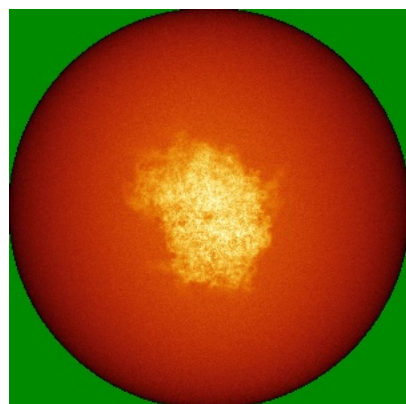


Y

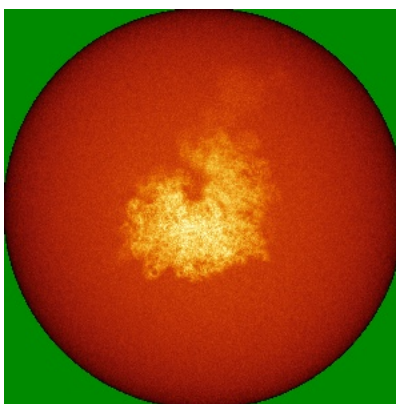


Z

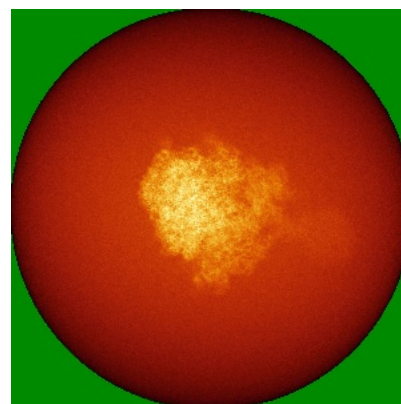
6.4.2 Raw map



X



Y

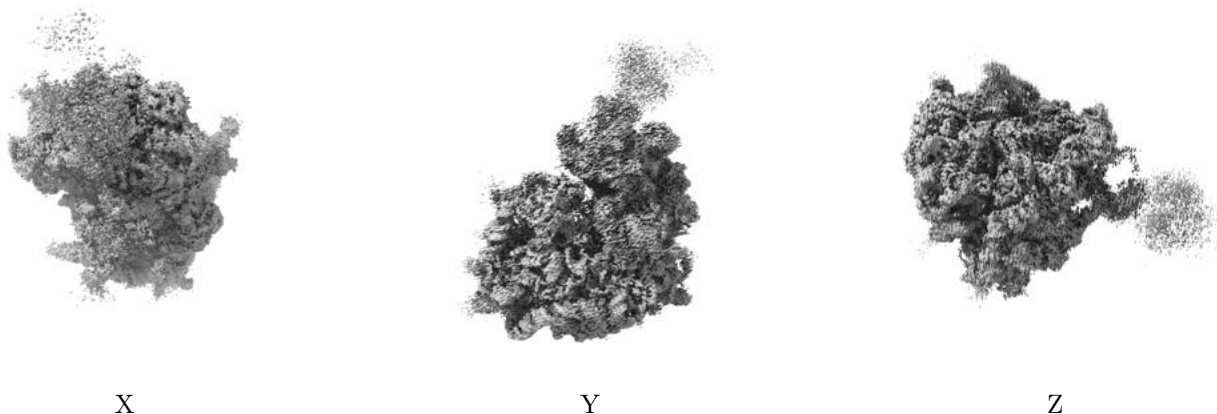


Z

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.

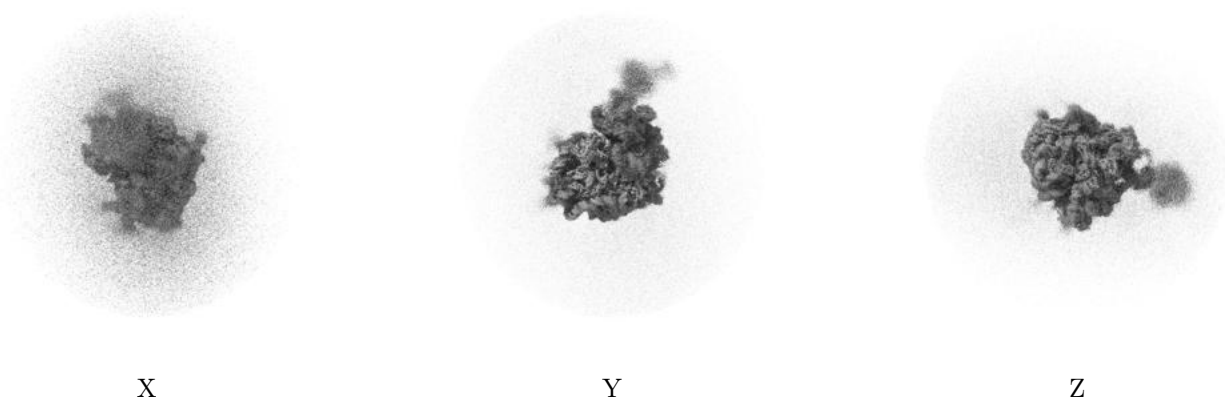
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.01. 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.

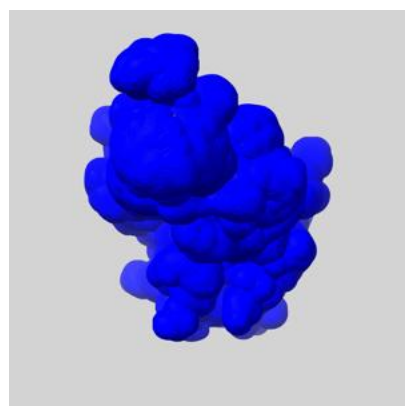
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

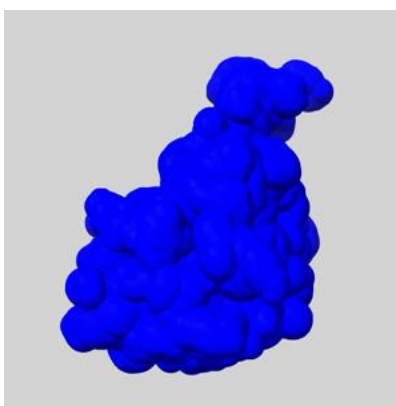
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

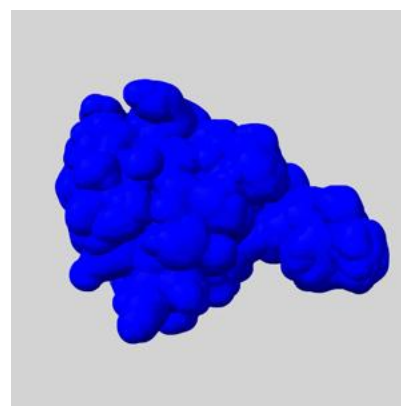
6.6.1 emd_51132_msk_1.map [i](#)



X



Y

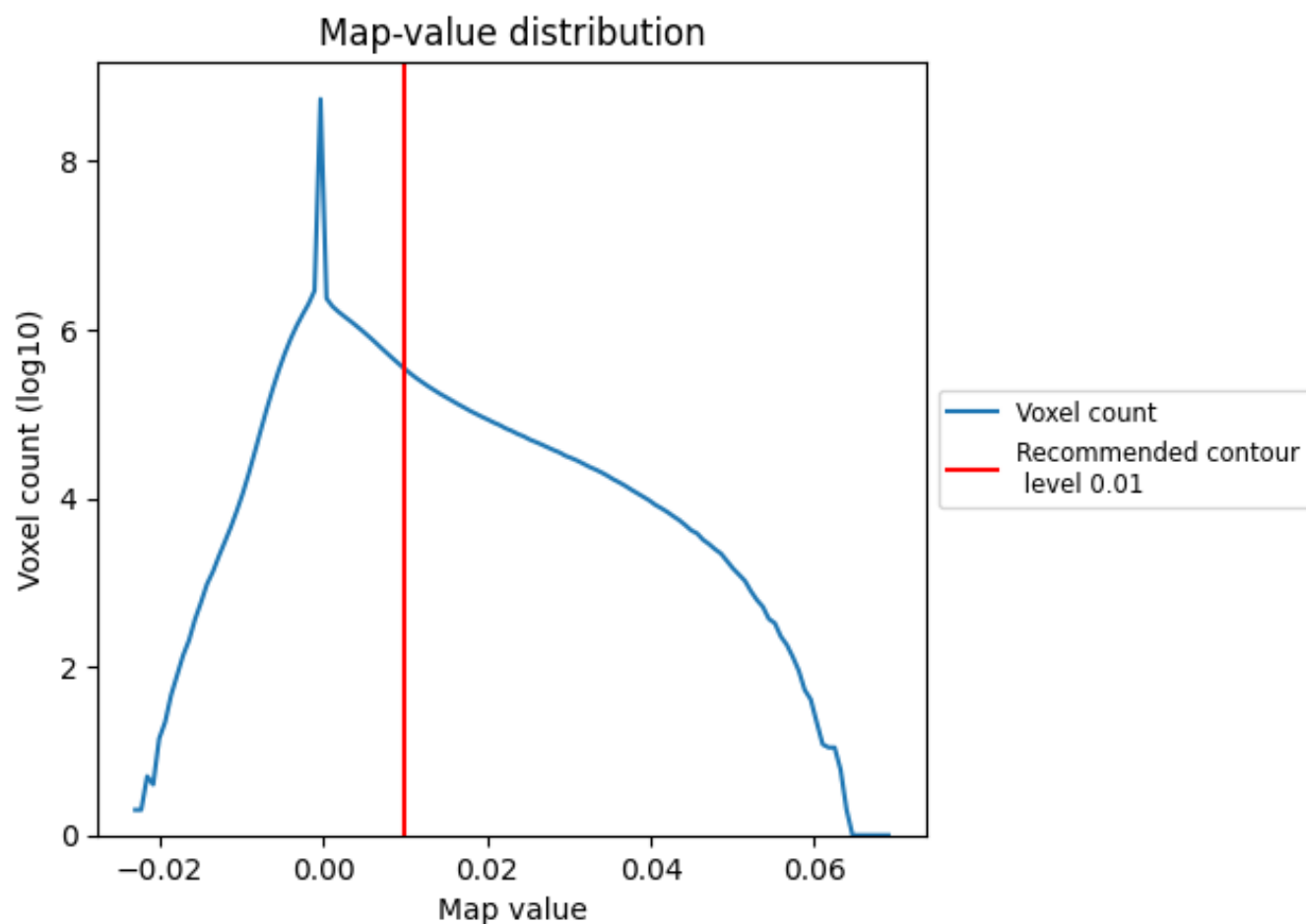


Z

7 Map analysis [i](#)

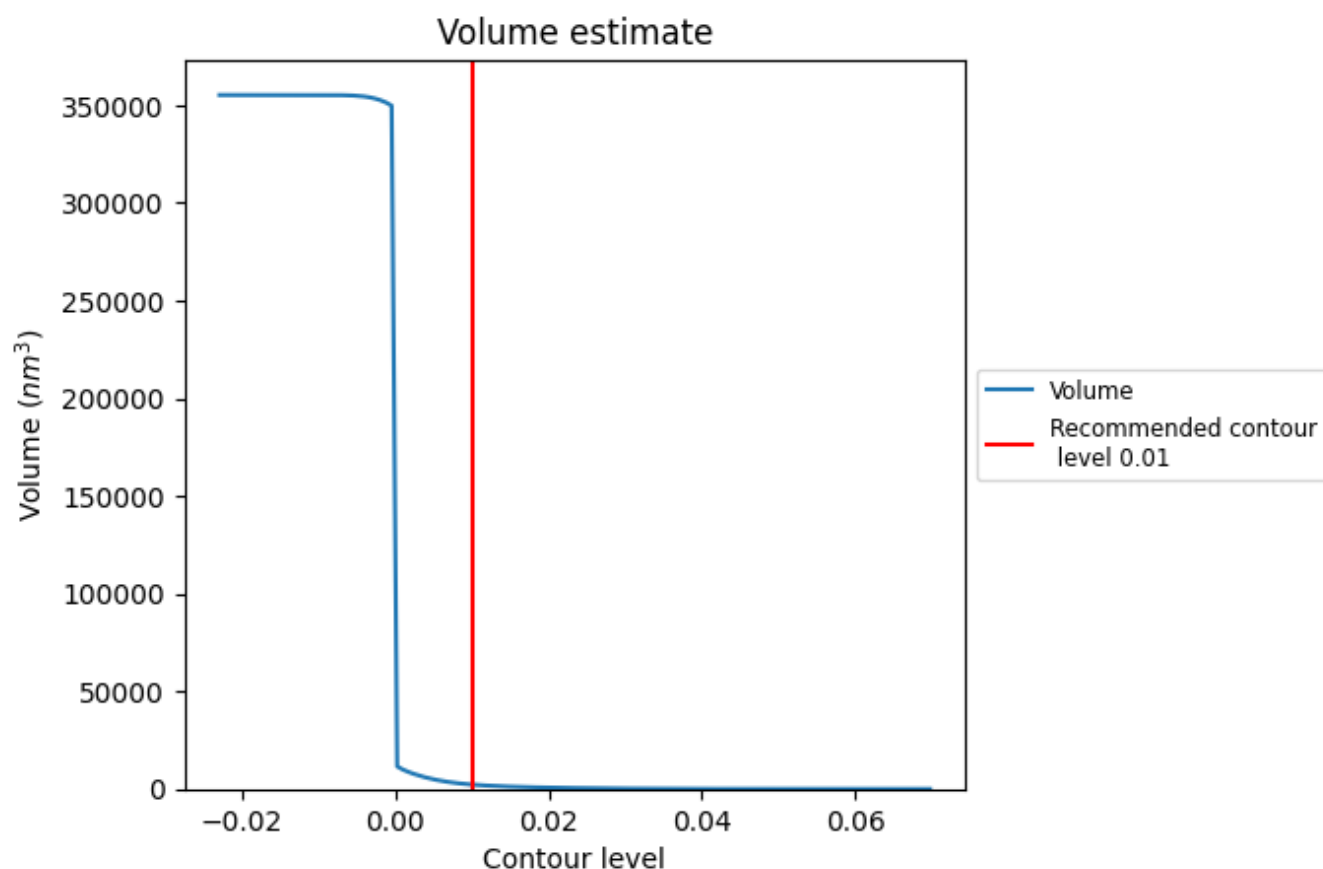
This section contains the results of statistical analysis of the map.

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.

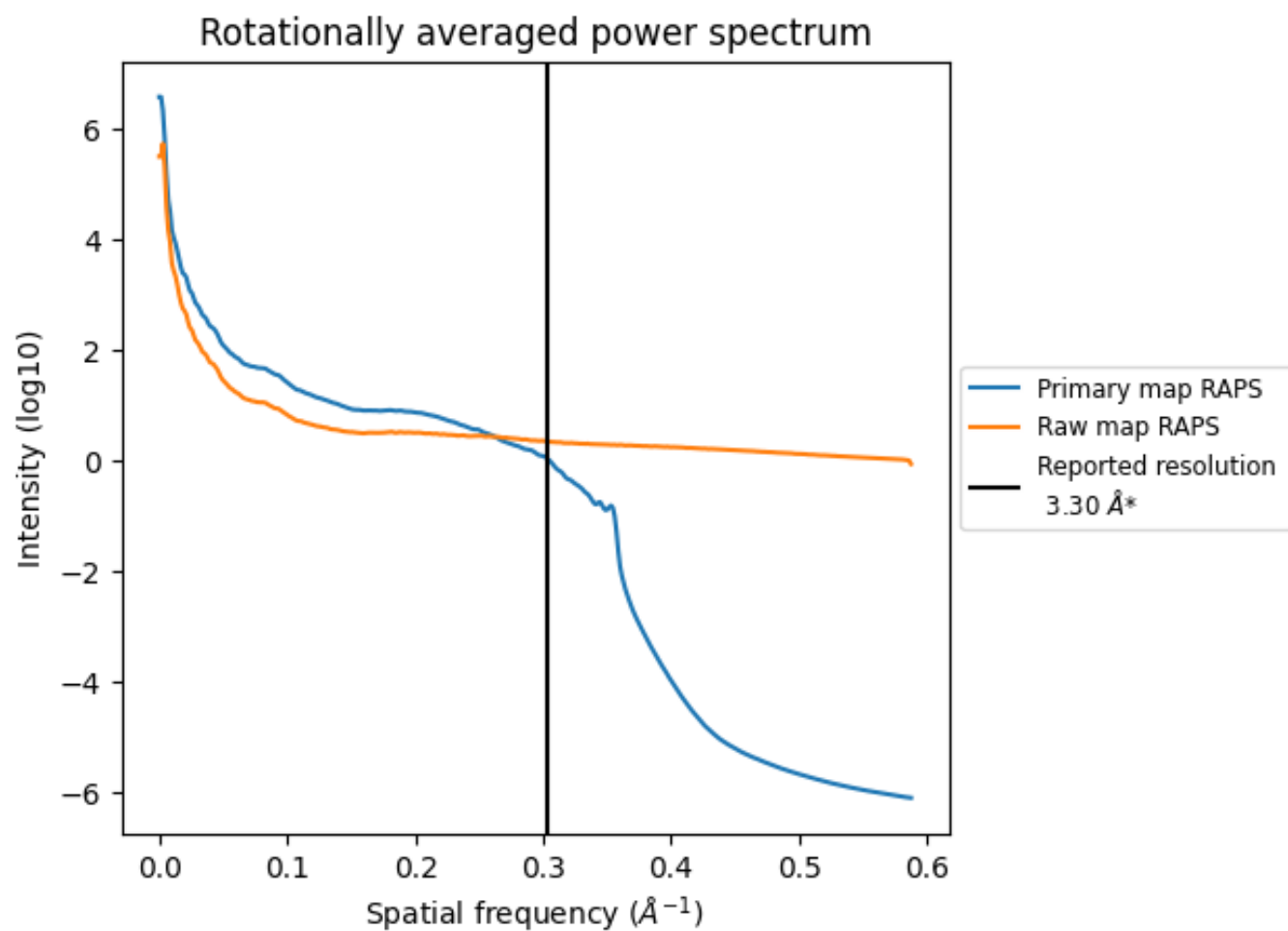
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2249 nm^3 ; this corresponds to an approximate mass of 2031 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 ⓘ

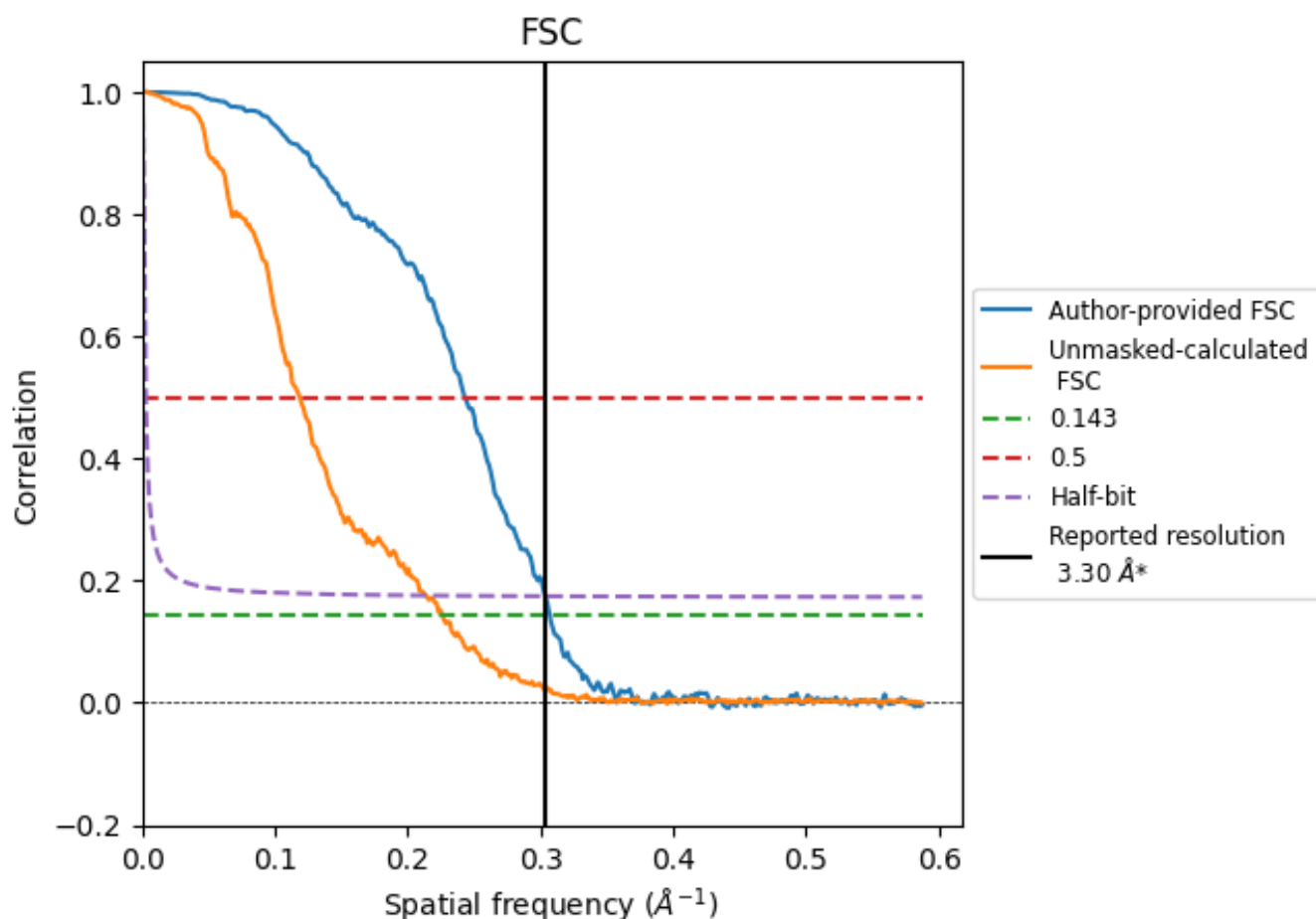


*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.303 Å⁻¹

8.2 Resolution estimates [i](#)

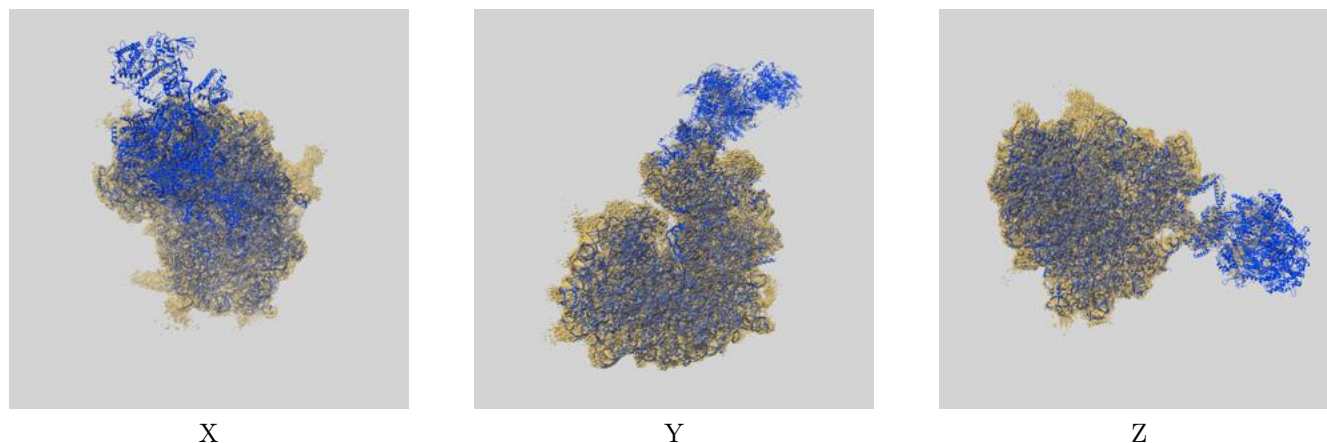
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	3.26	4.12	3.29
Unmasked-calculated*	4.42	8.42	4.68

*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 4.42 differs from the reported value 3.3 by more than 10 %

9 Map-model fit [i](#)

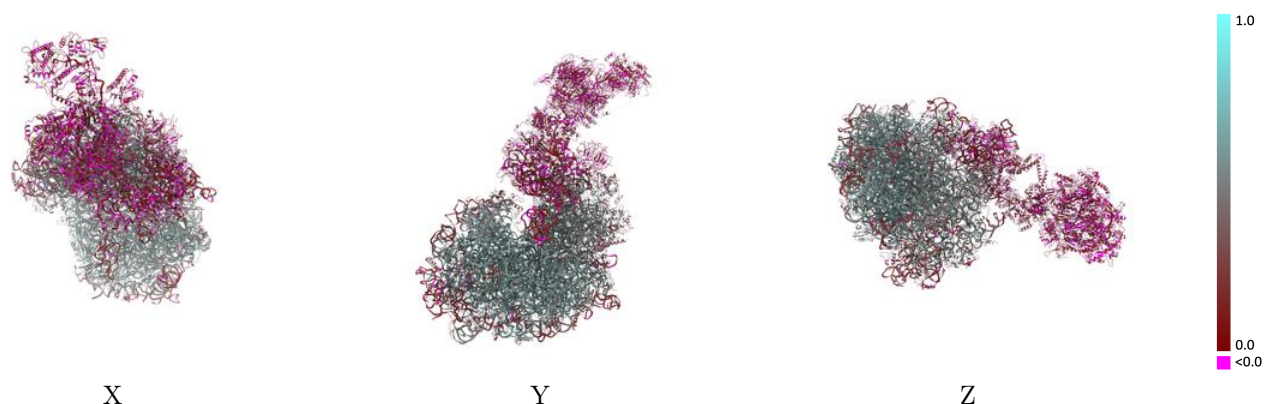
This section contains information regarding the fit between EMDB map EMD-51132 and PDB model 9G8M. Per-residue inclusion information can be found in section [3](#) on page [25](#).

9.1 Map-model overlay [i](#)



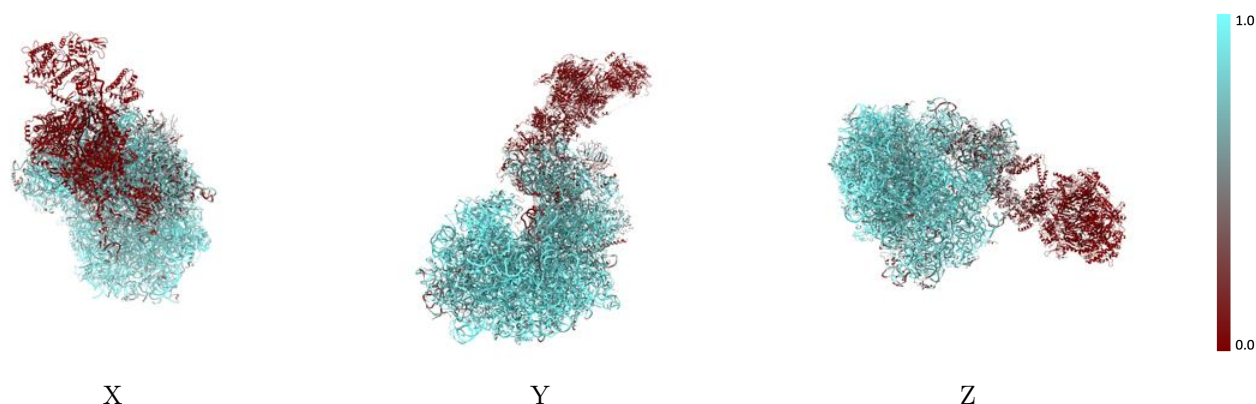
The images above show the 3D surface view of the map at the recommended contour level 0.01 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



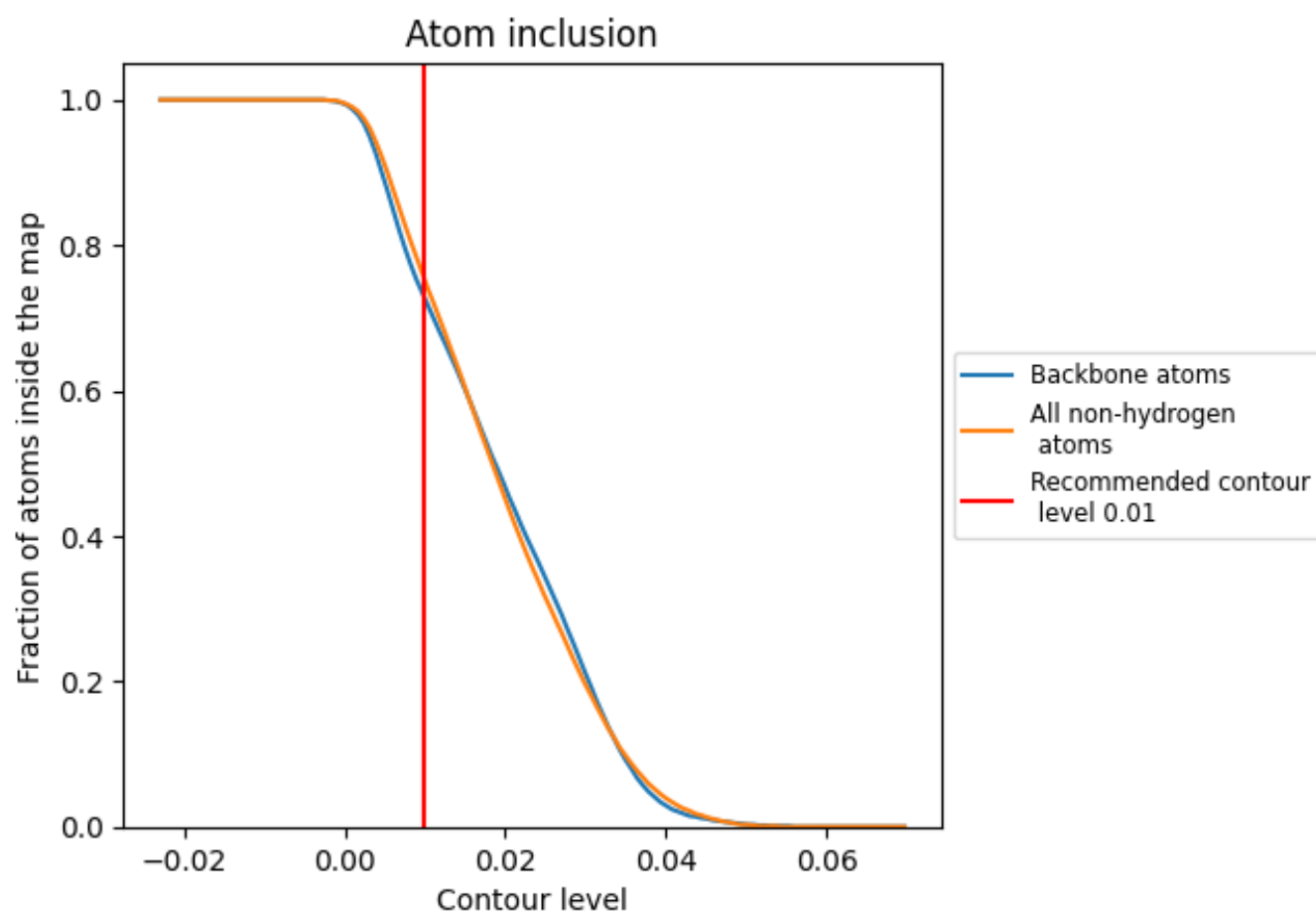
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.01).

9.4 Atom inclusion ⓘ



At the recommended contour level, 73% of all backbone atoms, 75% 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 (0.01) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7510	 0.4050
A	 0.0980	 0.1490
E	 0.0060	 0.1440
F	 0.0230	 0.1110
G	 0.0190	 0.1170
H	 0.0250	 0.1240
I	 0.0160	 0.1330
J	 0.0080	 0.0860
K	 0.0280	 0.1260
L	 0.0190	 0.1140
L5	 0.9430	 0.4950
L7	 0.9930	 0.5610
L8	 0.9720	 0.5360
LA	 0.9580	 0.5750
LB	 0.9280	 0.5520
LC	 0.9270	 0.5460
LD	 0.9160	 0.5030
LE	 0.8410	 0.4430
LF	 0.9290	 0.5550
LG	 0.8660	 0.4850
LH	 0.9320	 0.5380
LI	 0.8980	 0.5380
LJ	 0.8170	 0.4030
LL	 0.9080	 0.5290
LM	 0.9440	 0.5340
LN	 0.9680	 0.5860
LO	 0.9520	 0.5650
LP	 0.9510	 0.5670
LQ	 0.9550	 0.5700
LR	 0.8100	 0.4390
LS	 0.9620	 0.5650
LT	 0.9430	 0.5510
LU	 0.9030	 0.4580
LV	 0.9400	 0.5690
LW	 0.6880	 0.3800



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Chain	Atom inclusion	Q-score
LX	 0.9160	 0.5300
LY	 0.9370	 0.5410
LZ	 0.9420	 0.5350
La	 0.9660	 0.5740
Lb	 0.8400	 0.4950
Lc	 0.8550	 0.4550
Ld	 0.9240	 0.5330
Le	 0.9500	 0.5730
Lf	 0.9640	 0.5790
Lg	 0.9230	 0.5420
Lh	 0.9180	 0.5370
Li	 0.9110	 0.5300
Lj	 0.9600	 0.5720
Lk	 0.8670	 0.4610
Ll	 0.9410	 0.5580
Lm	 0.9250	 0.5440
Ln	 0.9280	 0.5520
Lo	 0.8960	 0.5310
Lp	 0.9170	 0.5620
Lr	 0.9530	 0.5590
M	 0.0050	 0.1180
N	 0.0150	 0.1180
O	 0.0170	 0.0910
S2	 0.8560	 0.3830
SA	 0.8160	 0.4250
SB	 0.8160	 0.4570
SC	 0.8570	 0.4820
SD	 0.4590	 0.2350
SE	 0.7990	 0.4430
SF	 0.3850	 0.1110
SG	 0.7030	 0.3060
SH	 0.7080	 0.3870
SI	 0.7660	 0.4450
SJ	 0.8250	 0.4580
SK	 0.3680	 0.1330
SL	 0.7560	 0.4790
SM	 0.0840	 0.1210
SN	 0.8530	 0.5020
SO	 0.8200	 0.4770
SP	 0.4290	 0.1480
SQ	 0.5610	 0.1250
SR	 0.5940	 0.2280

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Chain	Atom inclusion	Q-score
SS	 0.4700	 0.1180
ST	 0.5130	 0.1250
SU	 0.4620	 0.1900
SV	 0.8540	 0.4450
SW	 0.8820	 0.5120
SX	 0.8960	 0.5080
SY	 0.8220	 0.4120
SZ	 0.4240	 0.1120
Sa	 0.8490	 0.4650
Sb	 0.7570	 0.4320
Sc	 0.3780	 0.1100
Sd	 0.6390	 0.2680
Se	 0.6960	 0.3720
Sf	 0.3710	 0.1380
Sg	 0.4180	 0.1140
X	 0.4040	 0.1240