



## wwPDB EM Validation Summary Report ⓘ

Nov 20, 2022 – 08:57 PM EST

PDB ID : 4V6W  
EMDB ID : EMD-5591  
Title : Structure of the D. melanogaster 80S ribosome  
Authors : Anger, A.M.; Armache, J.-P.; Berninghausen, O.; Habeck, M.; Subklewe, M.;  
Wilson, D.N.; Beckmann, R.  
Deposited on : 2013-02-27  
Resolution : 6.00 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](mailto: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>.

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

EMDB validation analysis : 0.0.1.dev43  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.3

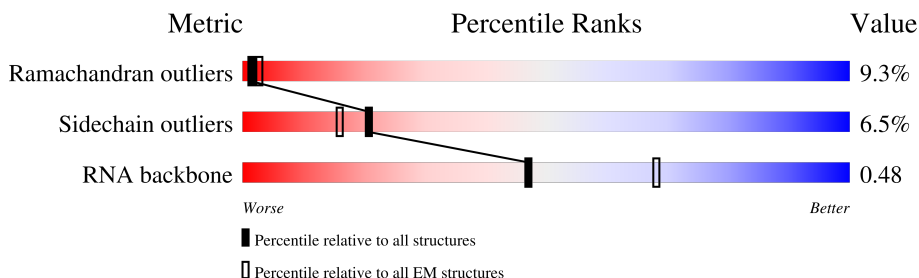
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 6.00 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)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	Az	844	<div> <div>43%</div> <div>70%</div> <div>22%</div> <div>5%</div> <div>..</div> </div>
2	Ag	318	<div> <div>29%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
3	AU	120	<div> <div>24%</div> <div>68%</div> <div>15%</div> <div>.</div> <div>15%</div> </div>
4	AK	163	<div> <div>42%</div> <div>12%</div> <div>..</div> <div>42%</div> </div>
5	AO	151	<div> <div>28%</div> <div>69%</div> <div>16%</div> <div>..</div> <div>11%</div> </div>
6	AX	143	<div> <div>24%</div> <div>83%</div> <div>14%</div> <div>.</div> </div>
7	AM	139	<div> <div>14%</div> <div>66%</div> <div>13%</div> <div>5%</div> <div>.</div> <div>14%</div> </div>
8	AS	152	<div> <div>22%</div> <div>72%</div> <div>14%</div> <div>..</div> <div>10%</div> </div>

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Mol	Chain	Length	Quality of chain
9	Ad	56	
10	AN	151	
11	AL	155	
12	AR	131	
13	AP	148	
14	AT	156	
15	AB	268	
16	AA	313	
17	AV	83	
18	AY	131	
19	AZ	117	
20	Aa	114	
21	Ab	84	
22	Ac	65	
23	AD	246	
24	Ae	132	
25	Af	80	
26	AJ	195	
27	AE	261	
28	AC	267	
29	AG	248	
30	AF	228	
31	AH	194	
32	AW	130	
33	AI	208	

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Mol	Chain	Length	Quality of chain
34	AQ	148	
35	Ah	121	
36	B2	1995	
37	BC	75	
38	Cz	218	
39	Cq	223	
40	CK	165	
41	CO	205	
42	CL	218	
43	CV	140	
44	CM	166	
45	Ca	149	
46	CN	204	
47	CI	218	
48	CD	299	
49	CQ	188	
50	CR	203	
51	CA	256	
52	CS	177	
53	CT	159	
54	CP	186	
55	CU	299	
56	CX	277	
57	CY	149	
58	CW	155	



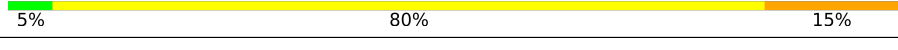
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Mol	Chain	Length	Quality of chain
59	CZ	135	
60	Cr	144	
61	Ch	123	
62	Cb	76	
63	CB	416	
64	CF	252	
65	Cc	111	
66	Cd	124	
67	Ce	134	
68	Cf	157	
69	Cg	162	
70	Ci	115	
71	Cj	93	
72	Ck	70	
73	Cl	51	
74	CC	401	
75	Cm	52	
76	Cn	25	
77	Cp	92	
78	Co	104	
79	CJ	184	
80	CH	190	
81	CE	243	
82	CG	271	
83	A5	3970	

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Mol	Chain	Length	Quality of chain
84	A9	30	 77% 23%
85	A7	120	 5% 74% 21%
86	A8	123	 5% 80% 15%

## 2 Entry composition

There are 86 unique types of molecules in this entry. The entry contains 230721 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called Elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	Az	837	Total	C	N	O	S	0	0
			6574	4170	1123	1235	46		

- Molecule 2 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	Ag	318	Total	C	N	O	S	0	0
			2511	1577	444	480	10		

- Molecule 3 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	AU	102	Total	C	N	O	S	0	0
			815	505	161	145	4		

- Molecule 4 is a protein called 40S ribosomal protein S10a.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	AK	95	Total	C	N	O	S	0	0
			797	522	136	137	2		

- Molecule 5 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	AO	134	Total	C	N	O	S	0	0
			1003	616	196	187	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
6	AX	143	Total	C	N	O	S	0	0
			1131	712	226	191	2		

- Molecule 7 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	AM	119	Total	C	N	O	S	0	0
			924	582	165	171	6		

- Molecule 8 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AS	137	Total	C	N	O	S	0	0
			1128	707	220	198	3		

- Molecule 9 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	Ad	52	Total	C	N	O	S	0	0
			433	269	87	72	5		

- Molecule 10 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	AN	150	Total	C	N	O	S	0	0
			1202	767	229	203	3		

- Molecule 11 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	AL	155	Total	C	N	O	S	0	0
			1274	803	254	211	6		

- Molecule 12 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	AR	120	Total	C	N	O	S	0	0
			981	618	183	176	4		

- Molecule 13 is a protein called 40S ribosomal protein S15, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	AP	124	Total	C	N	O	S	0	0
			1016	652	189	169	6		

- Molecule 14 is a protein called 40S ribosomal protein S19a.



Mol	Chain	Residues	Atoms					AltConf	Trace
14	AT	154	Total	C	N	O	S	0	0
			1203	762	230	207	4		

- Molecule 15 is a protein called 40S ribosomal protein S3a.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	AB	220	Total	C	N	O	S	0	0
			1798	1138	328	324	8		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	AA	218	Total	C	N	O	S	0	0
			1737	1113	298	321	5		

- Molecule 17 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	AV	82	Total	C	N	O	S	0	0
			617	373	114	125	5		

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AV	2	GLN	GLU	conflict	UNP O76927
AV	8	PHE	ASN	conflict	UNP O76927
AV	25	GLY	HIS	conflict	UNP O76927
AV	32	ILE	VAL	conflict	UNP O76927
AV	34	MET	LEU	conflict	UNP O76927
AV	35	ASN	SER	conflict	UNP O76927
AV	36	VAL	ILE	conflict	UNP O76927
AV	58	ALA	GLU	conflict	UNP O76927
AV	68	SER	CYS	conflict	UNP O76927
AV	70	LEU	VAL	conflict	UNP O76927
AV	75	ALA	LYS	conflict	UNP O76927
AV	79	VAL	ILE	conflict	UNP O76927
AV	80	SER	THR	conflict	UNP O76927

- Molecule 18 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	AY	126	Total	C	N	O	S	0	0
			1016	644	196	171	5		

- Molecule 19 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	AZ	74	Total	C	N	O		0	0
			608	390	112	106			

- Molecule 20 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Aa	107	Total	C	N	O	S	0	0
			867	539	182	140	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Ab	84	Total	C	N	O	S	0	0
			653	412	123	110	8		

- Molecule 22 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	Ac	62	Total	C	N	O	S	0	0
			498	307	100	89	2		

- Molecule 23 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	AD	227	Total	C	N	O	S	0	0
			1782	1127	319	326	10		

- Molecule 24 is a protein called 40S ribosomal protein S30, isoform A.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Ae	58	Total	C	N	O	0	0
			469	289	105	75		

- Molecule 25 is a protein called 40S ribosomal protein S27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Af	80	Total	C	N	O	S	0	0
			659	417	128	109	5		

- Molecule 26 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	AJ	181	Total	C	N	O	S	0	0
			1503	957	298	247	1		

- Molecule 27 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	AE	261	Total	C	N	O	S	0	0
			2054	1314	380	353	7		

- Molecule 28 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	AC	227	Total	C	N	O	S	0	0
			1746	1126	302	311	7		

- Molecule 29 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	AG	231	Total	C	N	O	S	0	0
			1866	1172	372	315	7		

- Molecule 30 is a protein called 40S ribosomal protein S5a.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	AF	190	Total	C	N	O	S	0	0
			1497	934	285	269	9		

- Molecule 31 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	AH	194	Total	C	N	O	S	0	0
			1566	1006	278	281	1		

- Molecule 32 is a protein called 40S ribosomal protein S15Aa.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	AW	129	Total	C	N	O	S	0	0
			1028	656	189	176	7		

- Molecule 33 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	AI	207	Total	C	N	O	S	0	0
			1665	1037	329	296	3		

- Molecule 34 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	AQ	148	Total	C	N	O	S	0	0
			1183	753	223	204	3		

- Molecule 35 is a protein called Vig2, isoform B.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	Ah	58	Total	C	N	O	S	0	0
			486	298	93	94	1		

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Ah	212	LYS	GLU	conflict	UNP Q9VBX3
Ah	213	GLU	ASP	conflict	UNP Q9VBX3
Ah	215	PRO	SER	conflict	UNP Q9VBX3
Ah	217	GLU	GLN	conflict	UNP Q9VBX3
Ah	226	ILE	LEU	conflict	UNP Q9VBX3
Ah	227	GLN	ARG	conflict	UNP Q9VBX3
Ah	228	ASN	ASP	conflict	UNP Q9VBX3

- Molecule 36 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	B2	1957	Total	C	N	O	P	0	0
			39523	17589	6780	13198	1956		

- Molecule 37 is a RNA chain called E-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	BC	75	Total	C	N	O	P	0	0
			1605	717	296	518	74		

- Molecule 38 is a protein called 60S ribosomal protein L10a-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	Cz	217	Total	C	N	O	S	0	0
			1702	1084	303	305	10		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Cz	72A	SER	-	expression tag	UNP Q9VTP4

- Molecule 39 is a protein called 60S acidic ribosomal protein P0.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	Cq	223	Total	C	N	O	S	0	0
			1710	1089	297	314	10		

- Molecule 40 is a protein called 60S ribosomal protein L12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	CK	158	Total	C	N	O	S	0	0
			1180	739	213	222	6		

- Molecule 41 is a protein called 60S ribosomal protein L13a.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	CO	205	Total	C	N	O	S	0	0
			1668	1063	331	268	6		

- Molecule 42 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	CL	210	Total	C	N	O	S	0	0
			1695	1066	342	284	3		

- Molecule 43 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	CV	134	Total	C	N	O	S	0	0
			998	629	190	173	6		

- Molecule 44 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	CM	159	Total	C	N	O	S	0	0
			1302	826	256	218	2		

- Molecule 45 is a protein called 60S ribosomal protein L27a.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	Ca	149	Total	C	N	O	S	0	0
			1204	769	242	189	4		

- Molecule 46 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	CN	203	Total	C	N	O	S	0	0
			1710	1072	362	271	5		

- Molecule 47 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	CI	217	Total	C	N	O	S	0	0
			1785	1125	343	304	13		

- Molecule 48 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	CD	290	Total	C	N	O	S	0	0
			2334	1471	434	423	6		

- Molecule 49 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	CQ	187	Total	C	N	O	S	0	0
			1518	957	306	251	4		

- Molecule 50 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	CR	203	Total	C	N	O	S	0	0
			1683	1047	350	277	9		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
51	CA	253	Total	C	N	O	S	0	0
			1935	1206	395	326	8		

- Molecule 52 is a protein called 60S ribosomal protein L18a.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	CS	173	Total	C	N	O	S	0	0
			1454	935	275	240	4		

- Molecule 53 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	CT	158	Total	C	N	O	S	0	0
			1297	829	253	212	3		

- Molecule 54 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	CP	185	Total	C	N	O	S	0	0
			1505	928	305	263	9		

- Molecule 55 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	CU	116	Total	C	N	O	S	0	0
			961	607	167	185	2		

- Molecule 56 is a protein called 60S ribosomal protein L23A.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	CX	120	Total	C	N	O	S	0	0
			984	625	192	165	2		

- Molecule 57 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	CY	131	Total	C	N	O	S	0	0
			1078	676	224	176	2		

- Molecule 58 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	CW	130	Total	C	N	O	S	0	0
			1047	662	207	172	6		

- Molecule 59 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	CZ	134	Total	C	N	O	S	0	0
			1115	723	209	180	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
60	Cr	134	Total	C	N	O	S	0	0
			1051	670	205	176			

- Molecule 61 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	Ch	123	Total	C	N	O	S	0	0
			1015	646	202	164	3		

- Molecule 62 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	Cb	75	Total	C	N	O	S	0	0
			619	378	133	107	1		

- Molecule 63 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
63	CB	414	Total	C	N	O	S	0	0
			3287	2083	621	565	18		

- Molecule 64 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	CF	229	Total	C	N	O	S	0	0
			1921	1234	372	312	3		

- Molecule 65 is a protein called 60S ribosomal protein L30.



Mol	Chain	Residues	Atoms					AltConf	Trace
65	Cc	100	Total	C	N	O	S	0	0
			770	486	132	147	5		

- Molecule 66 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	Cd	111	Total	C	N	O	S	0	0
			924	573	180	169	2		

- Molecule 67 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	Ce	132	Total	C	N	O	S	0	0
			1110	698	230	177	5		

- Molecule 68 is a protein called 60S ribosomal protein L35A.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	Cf	157	Total	C	N	O	S	0	0
			1244	781	255	203	5		

- Molecule 69 is a protein called 60S ribosomal protein L34a.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	Cg	113	Total	C	N	O	S	0	0
			926	575	193	152	6		

- Molecule 70 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	Ci	113	Total	C	N	O	S	0	0
			934	585	193	153	3		

- Molecule 71 is a protein called 60S ribosomal protein L37-A.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	Cj	92	Total	C	N	O	S	0	0
			737	450	160	122	5		

- Molecule 72 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	Ck	70	Total	C	N	O	S	0	0
			576	366	108	100	2		

- Molecule 73 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms				AltConf	Trace
73	Cl	50	Total	C	N	O	0	0
			437	276	98	63		

- Molecule 74 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	CC	392	Total	C	N	O	S	0	0
			3109	1959	622	522	6		

- Molecule 75 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	Cm	52	Total	C	N	O	S	0	0
			429	267	89	67	6		

- Molecule 76 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Cn	25	Total	C	N	O	S	0	0
			236	143	63	27	3		

- Molecule 77 is a protein called 60S ribosomal protein L37a.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	Cp	91	Total	C	N	O	S	0	0
			710	441	140	122	7		

- Molecule 78 is a protein called 60S ribosomal protein L36A.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	Co	104	Total	C	N	O	S	0	0
			874	548	180	138	8		

- Molecule 79 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	CJ	182	Total	C	N	O	S	0	0
			1468	926	278	258	6		

- Molecule 80 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	CH	190	Total	C	N	O	S	0	0
			1499	947	265	278	9		

- Molecule 81 is a protein called 60S ribosomal protein L6, isoform A.

Mol	Chain	Residues	Atoms					AltConf	Trace
81	CE	228	Total	C	N	O	S	0	0
			1845	1185	351	305	4		

- Molecule 82 is a protein called 60S ribosomal protein L7a.

Mol	Chain	Residues	Atoms					AltConf	Trace
82	CG	241	Total	C	N	O	S	0	0
			1936	1237	368	327	4		

- Molecule 83 is a RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
83	A5	3806	Total	C	N	O	P	0	0
			77967	34770	13566	25827	3804		

- Molecule 84 is a RNA chain called 2S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	A9	30	Total	C	N	O	P	0	0
			639	286	111	213	29		

- Molecule 85 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	A7	120	Total	C	N	O	P	0	0
			2554	1141	456	838	119		

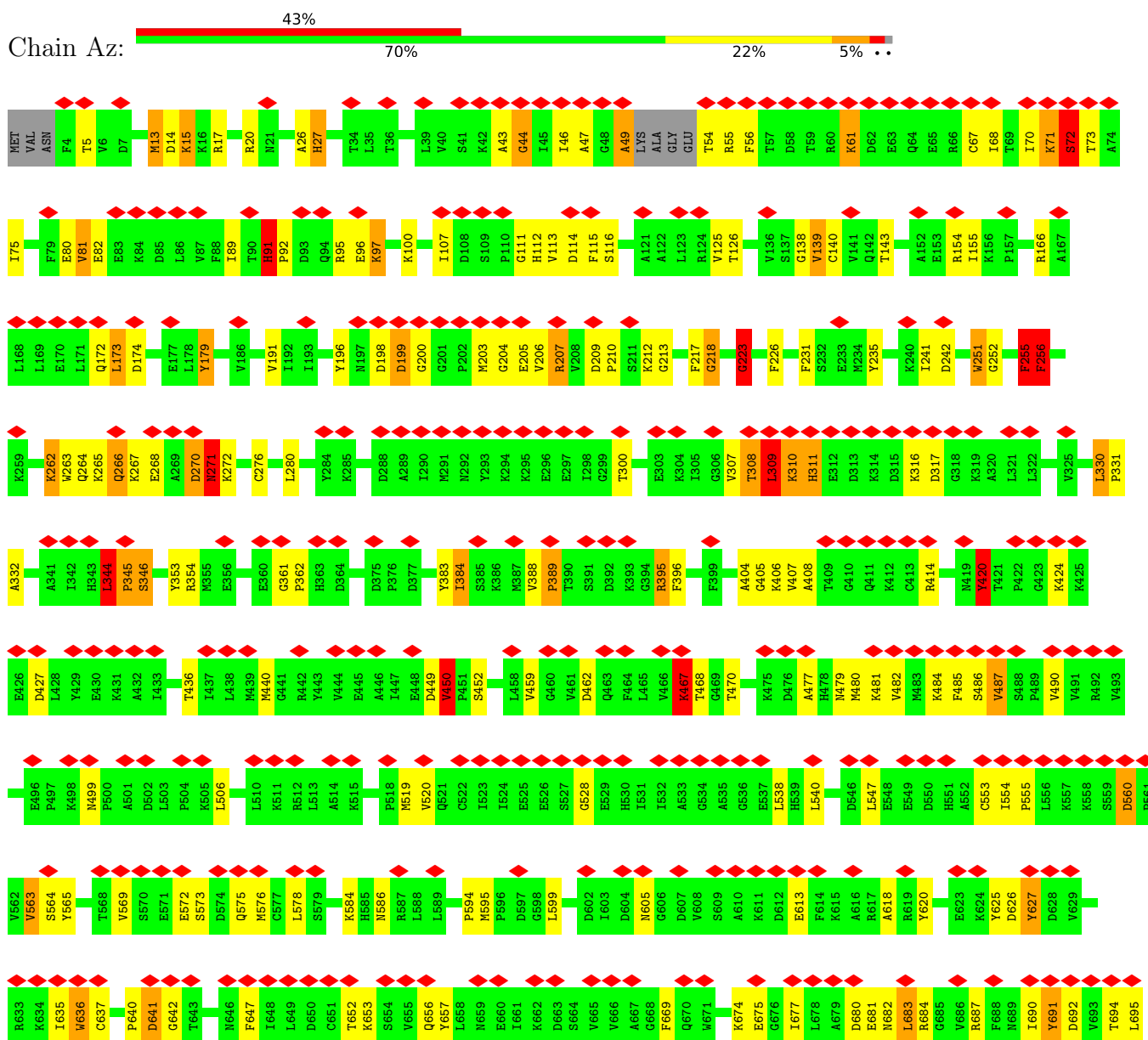
- Molecule 86 is a RNA chain called 5.8S ribosomal RNA.

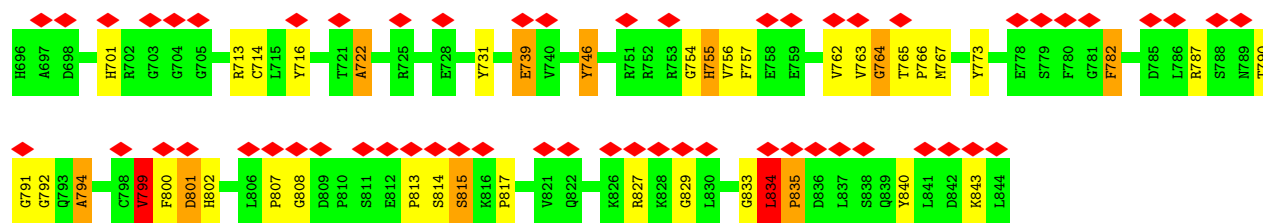
Mol	Chain	Residues	Atoms					AltConf	Trace
86	A8	123	Total	C	N	O	P	0	0
			2621	1173	474	852	122		

### 3 Residue-property plots [i](#)

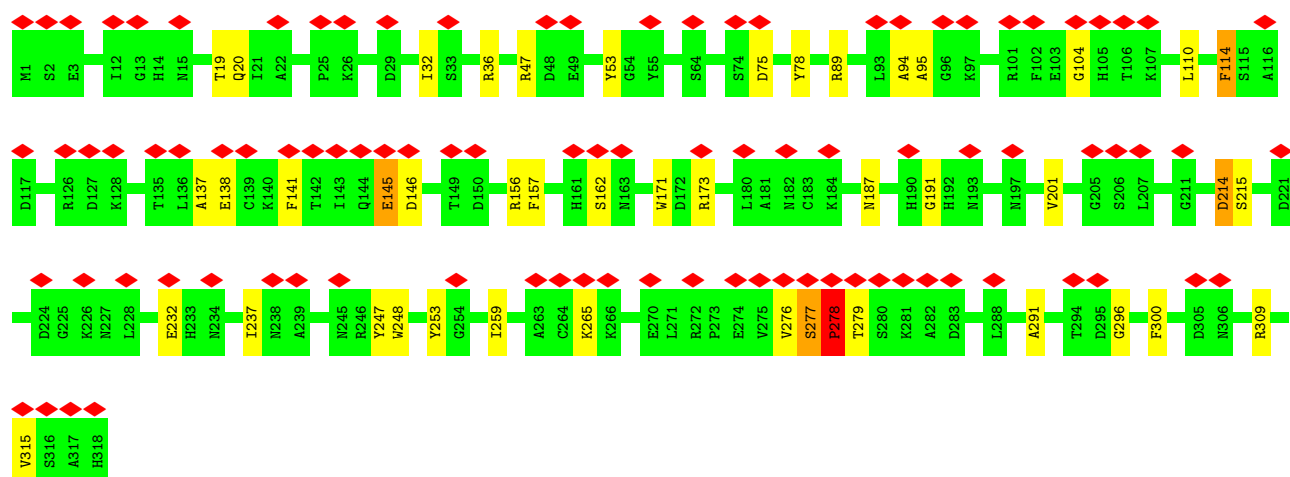
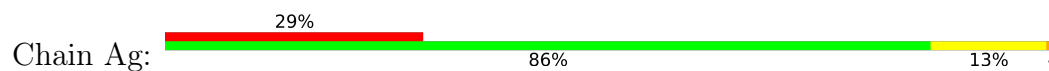
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Elongation factor 2

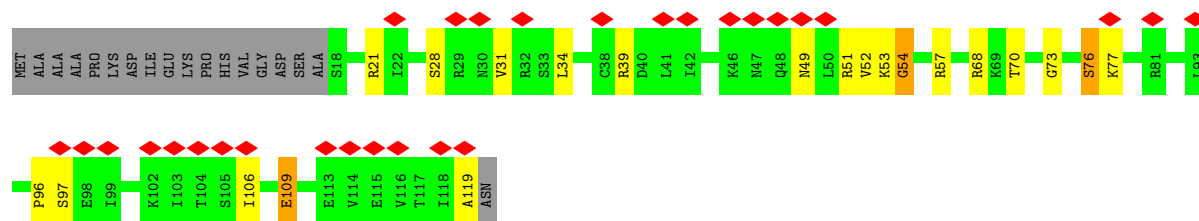




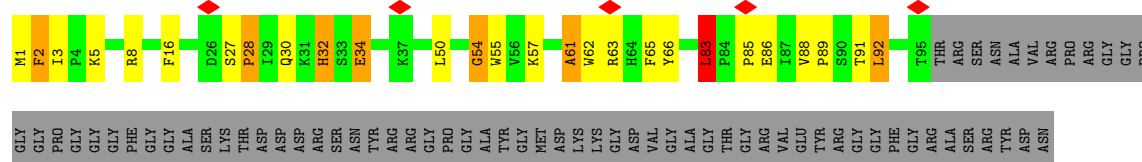
• Molecule 2: Guanine nucleotide-binding protein subunit beta-like protein



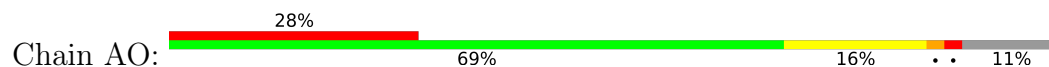
• Molecule 3: 40S ribosomal protein S20

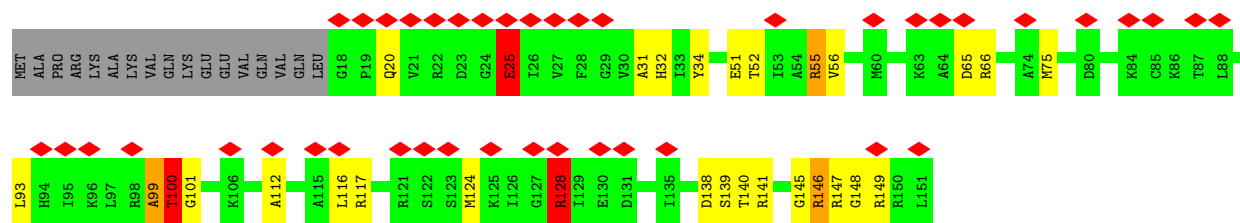


• Molecule 4: 40S ribosomal protein S10a

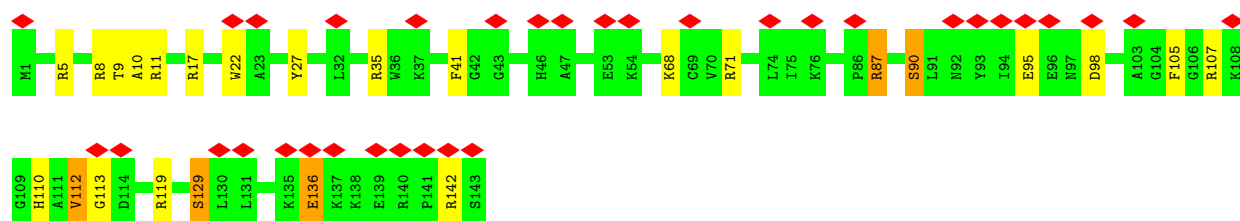
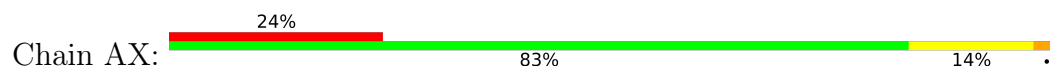


• Molecule 5: 40S ribosomal protein S14

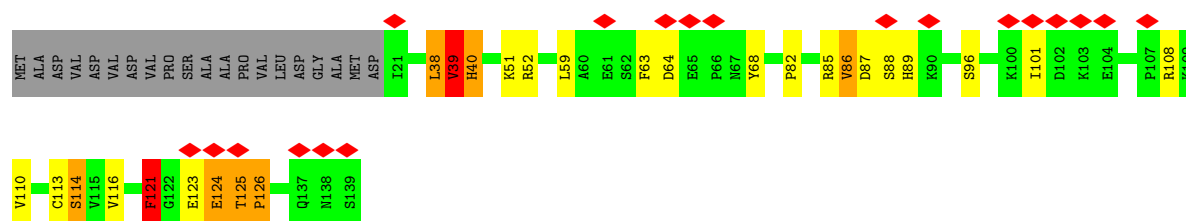




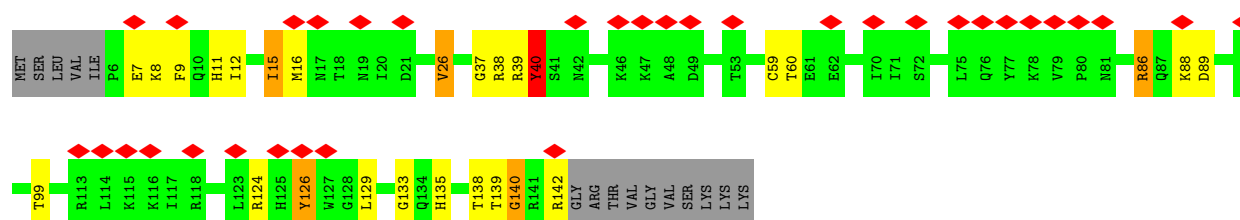
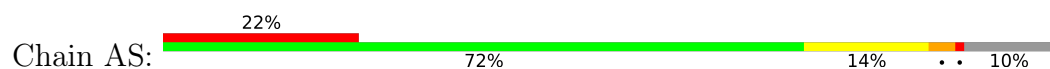
- Molecule 6: 40S ribosomal protein S23



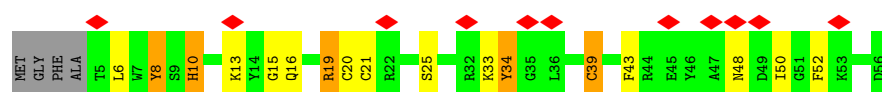
- Molecule 7: 40S ribosomal protein S12




- Molecule 8: 40S ribosomal protein S18

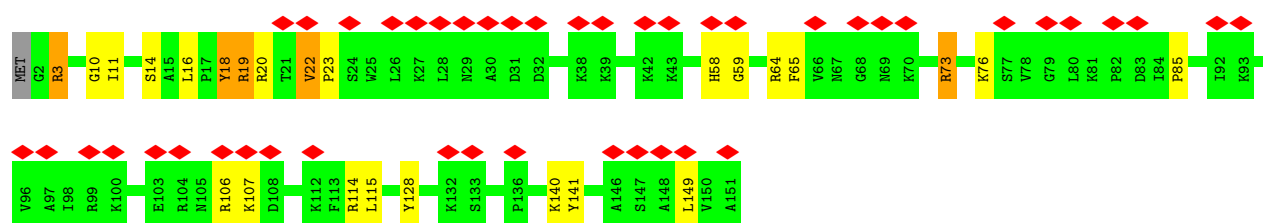


- Molecule 9: 40S ribosomal protein S29




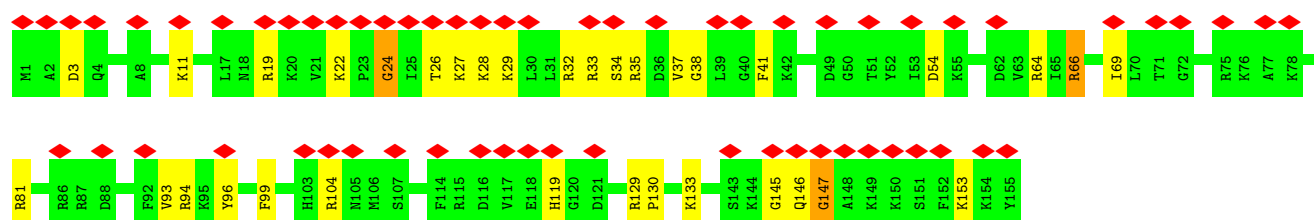
- Molecule 10: 40S ribosomal protein S13

Chain AN: 




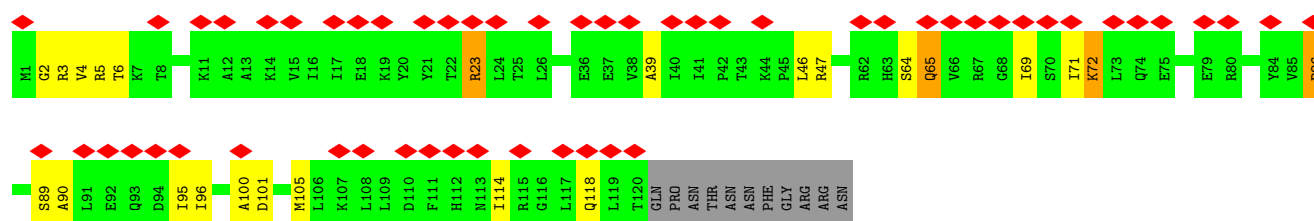
- Molecule 11: 40S ribosomal protein S11

Chain AL: 



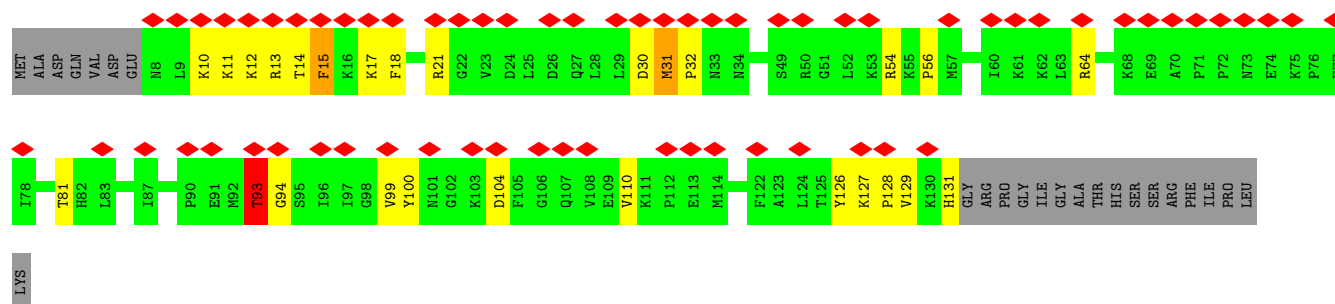
- Molecule 12: 40S ribosomal protein S17

Chain AR: 




- Molecule 13: 40S ribosomal protein S15, isoform A

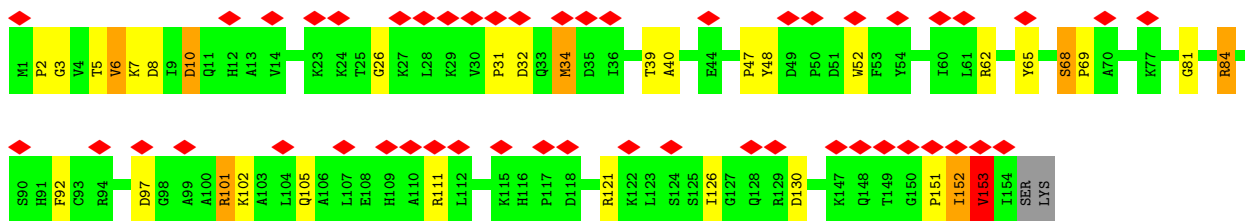
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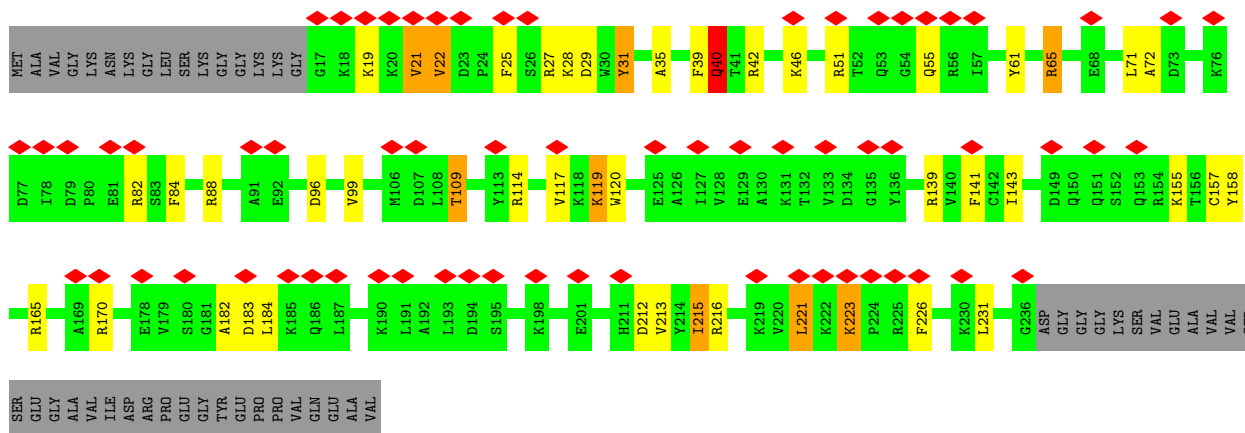
- Molecule 14: 40S ribosomal protein S19a

Chain AT: 

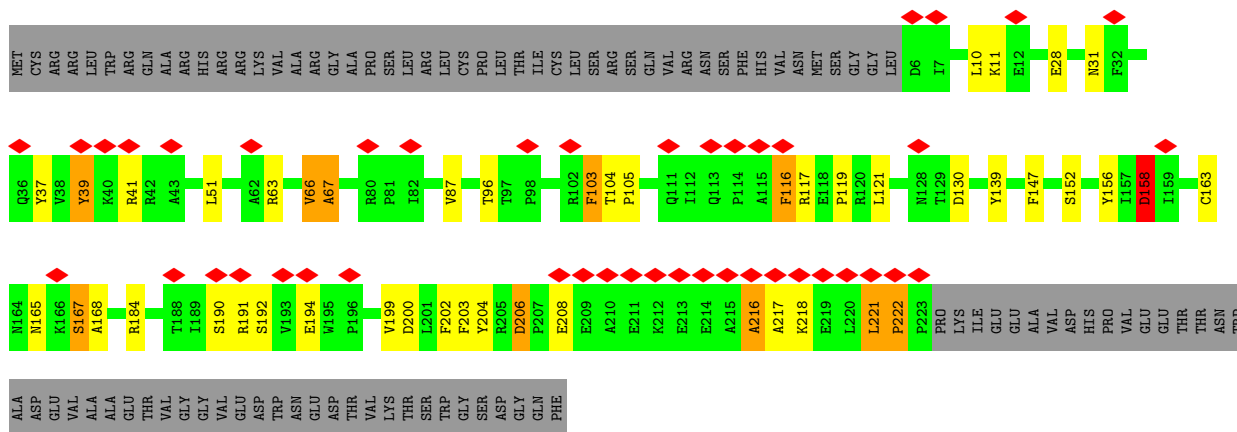




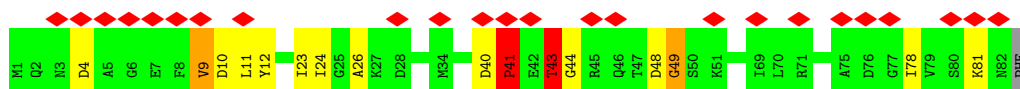
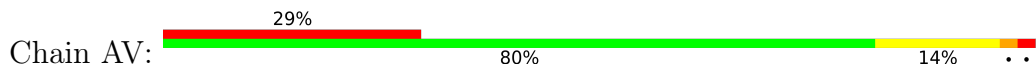
• Molecule 15: 40S ribosomal protein S3a



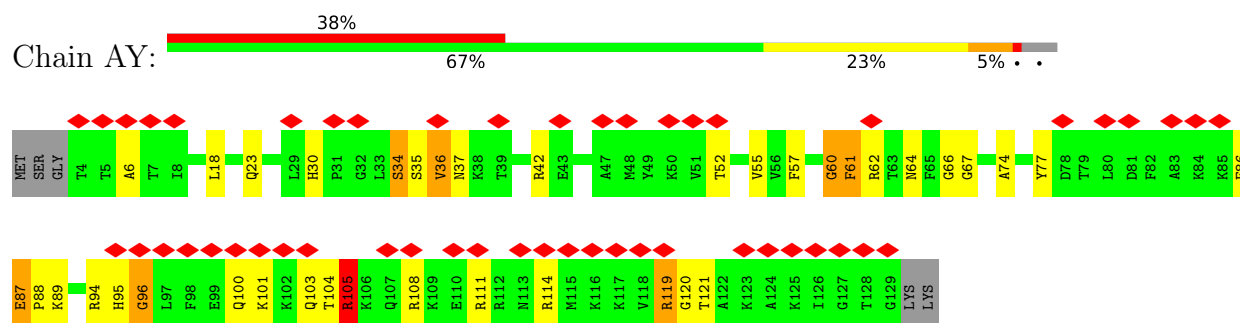
• Molecule 16: 40S ribosomal protein SA



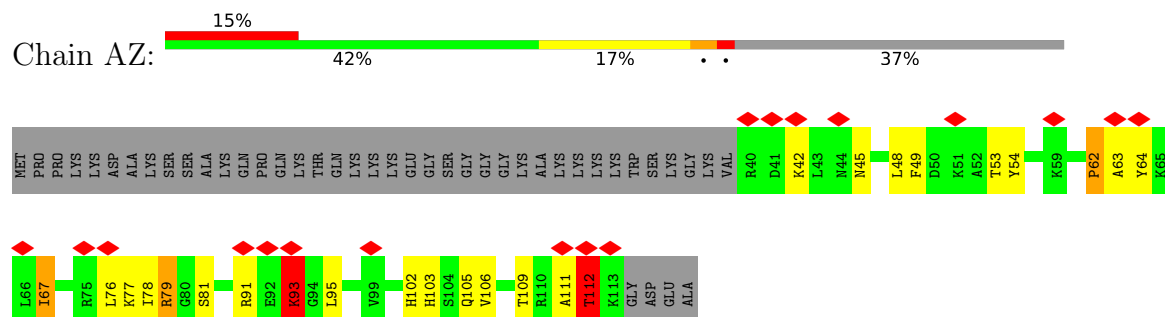
• Molecule 17: 40S ribosomal protein S21



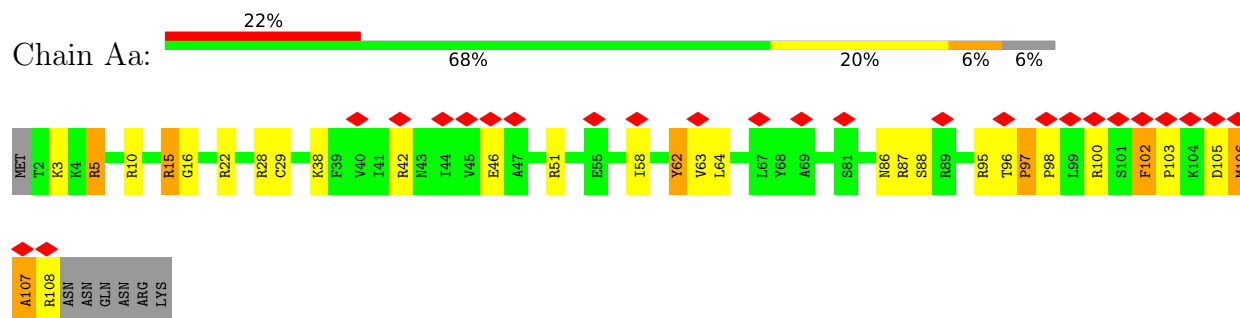
• Molecule 18: 40S ribosomal protein S24



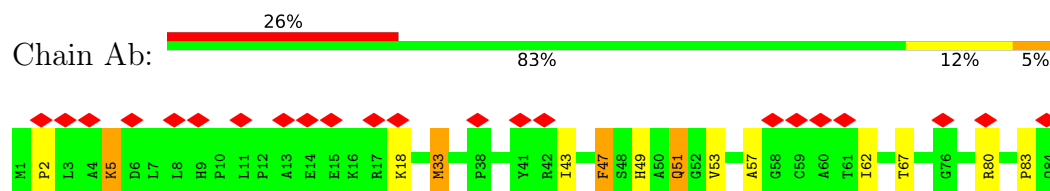
- Molecule 19: 40S ribosomal protein S25



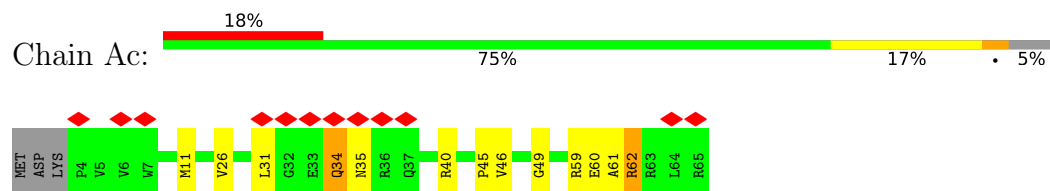
- Molecule 20: 40S ribosomal protein S26



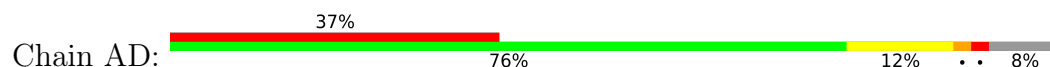
- Molecule 21: 40S ribosomal protein S27

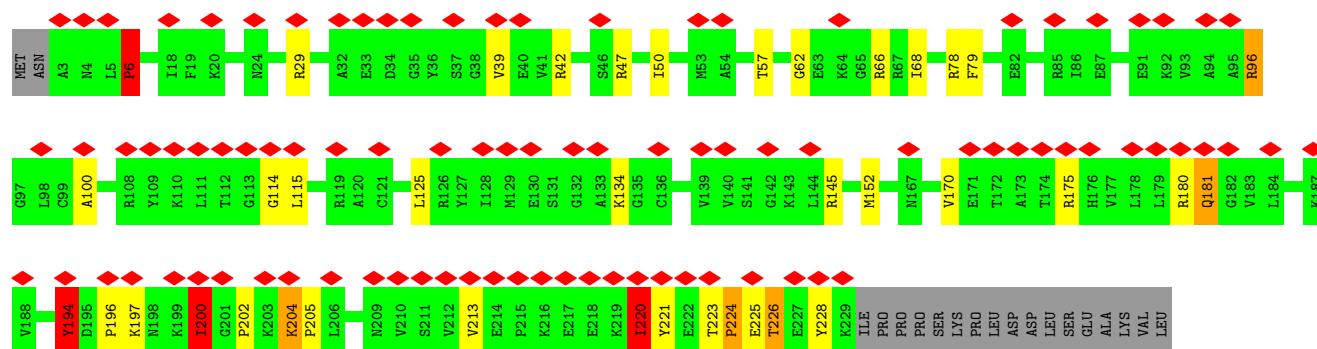


- Molecule 22: 40S ribosomal protein S28

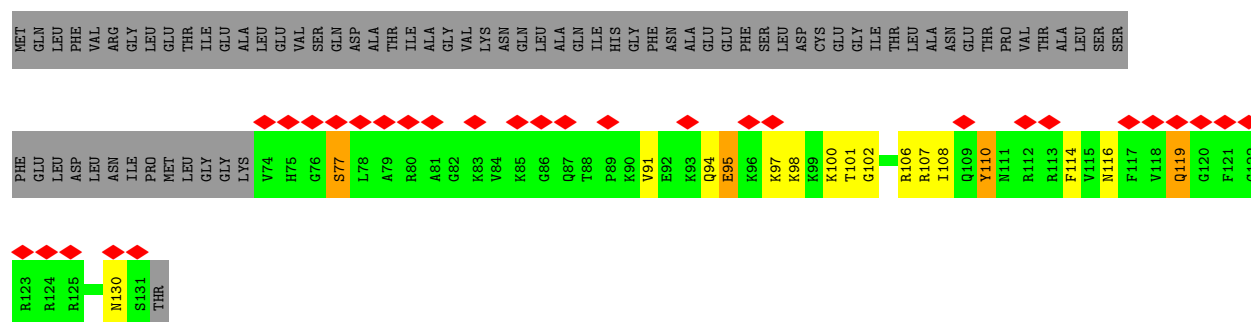
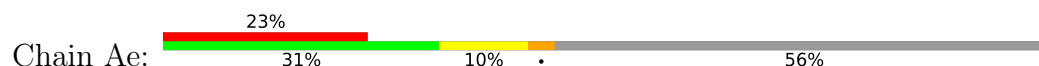


- Molecule 23: 40S ribosomal protein S3

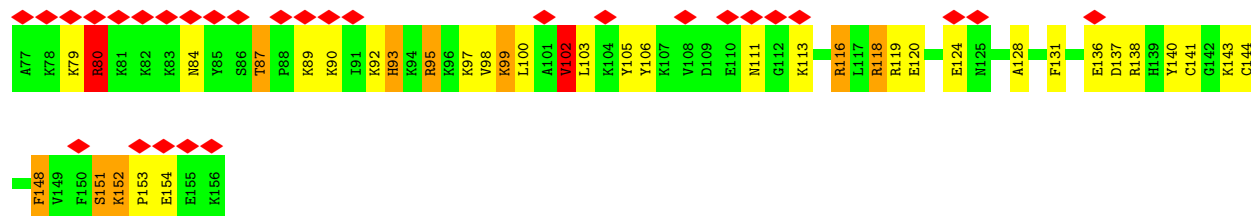




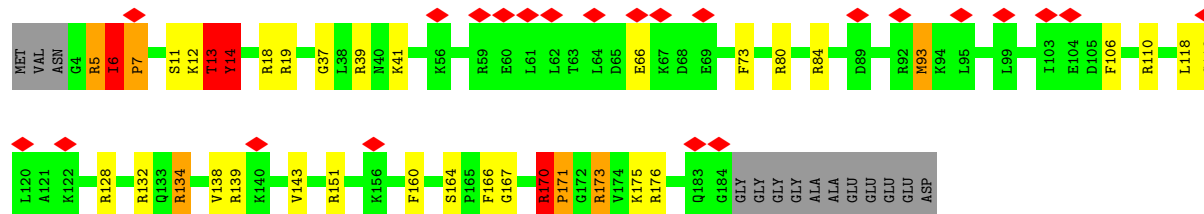
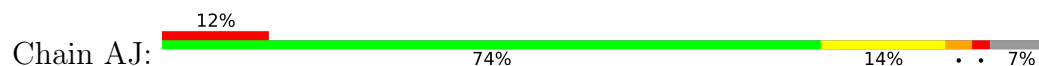
- Molecule 24: 40S ribosomal protein S30, isoform A



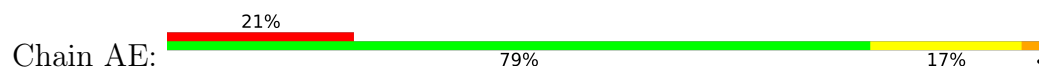
- Molecule 25: 40S ribosomal protein S27a

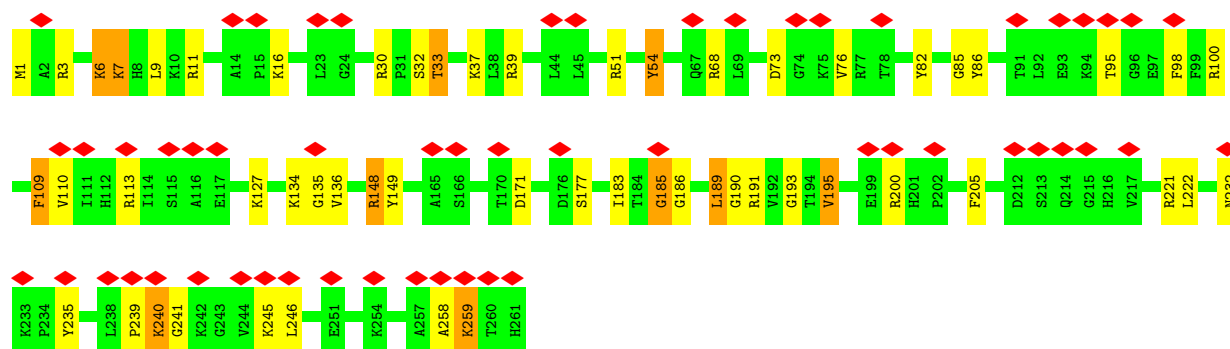


- Molecule 26: 40S ribosomal protein S9

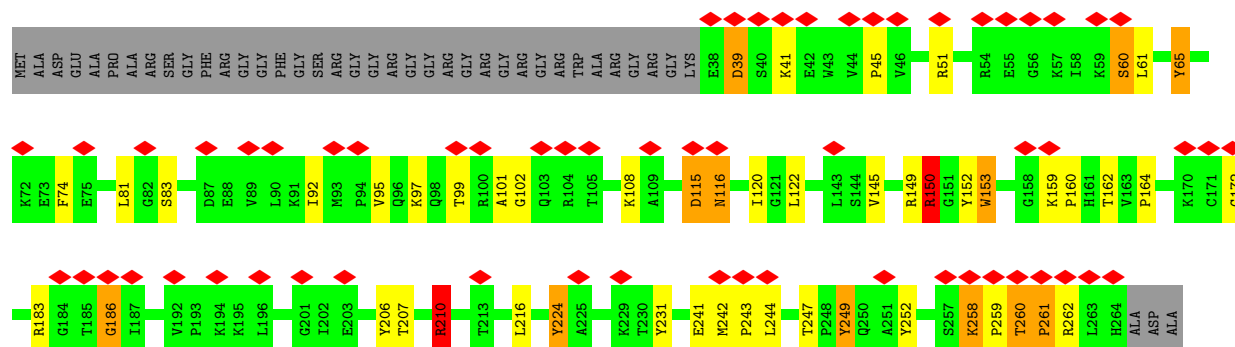


- Molecule 27: 40S ribosomal protein S4

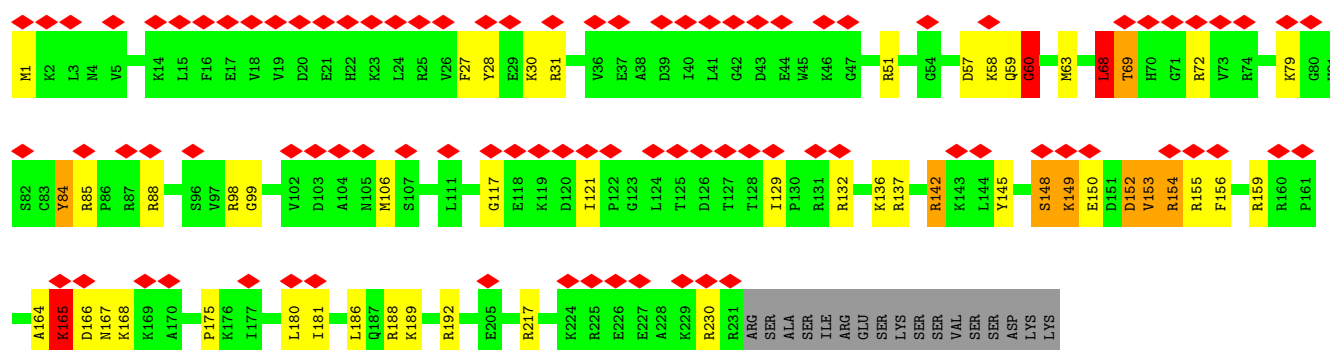
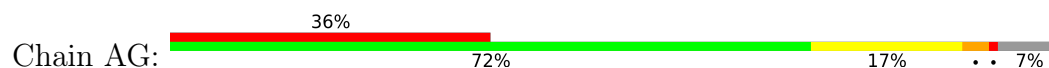




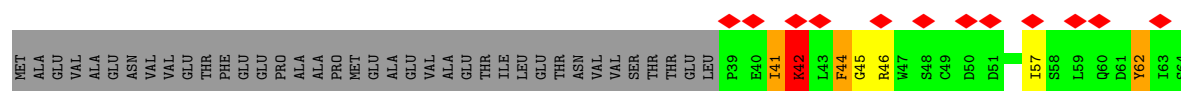
• Molecule 28: 40S ribosomal protein S2

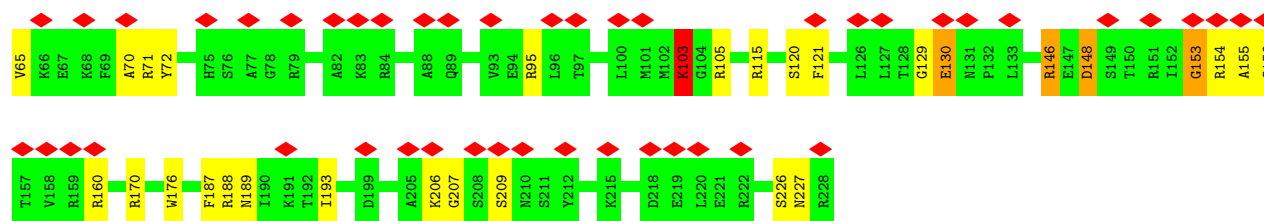


• Molecule 29: 40S ribosomal protein S6

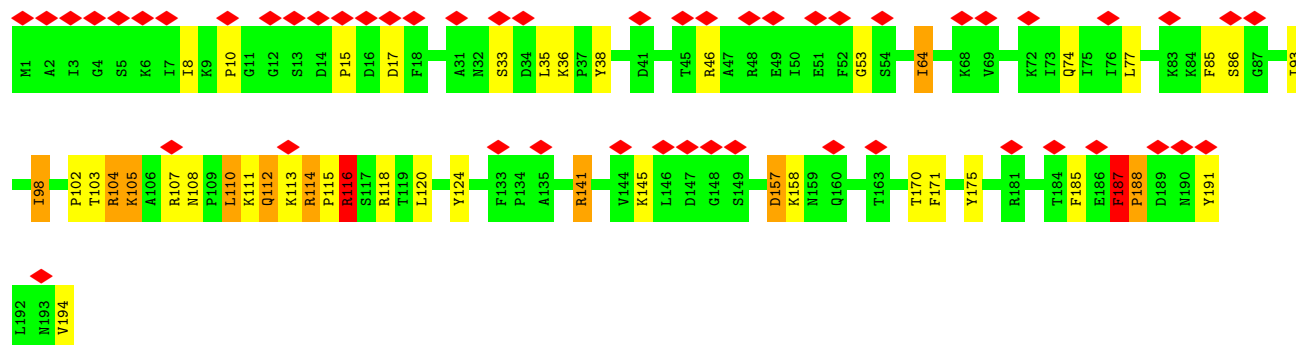
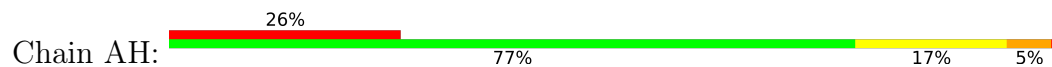


• Molecule 30: 40S ribosomal protein S5a

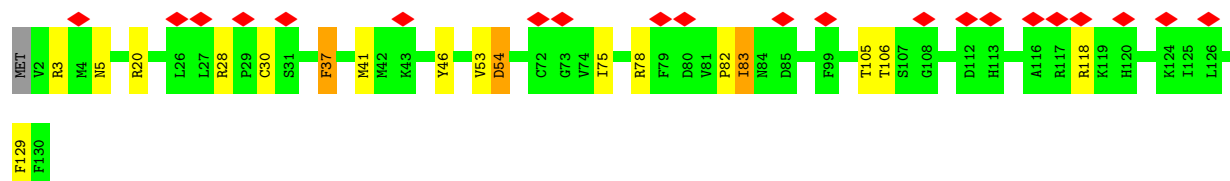
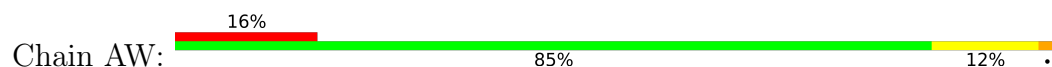




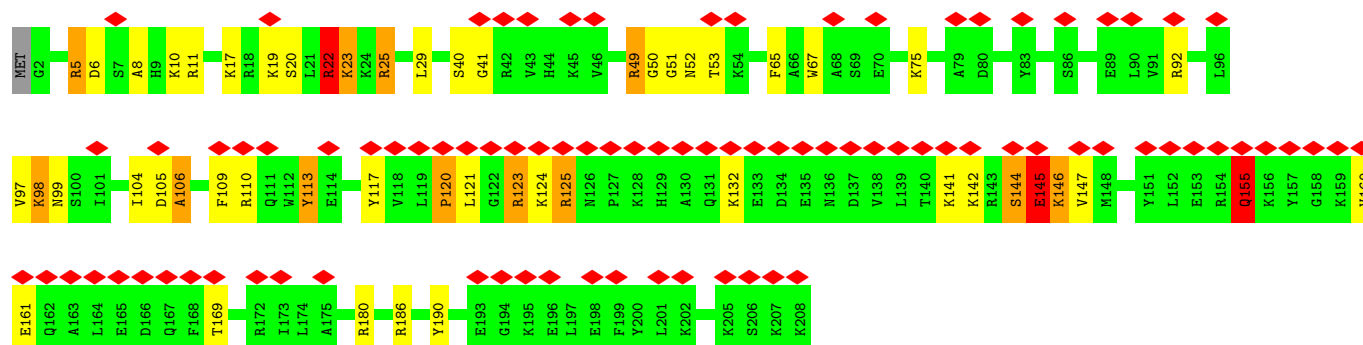
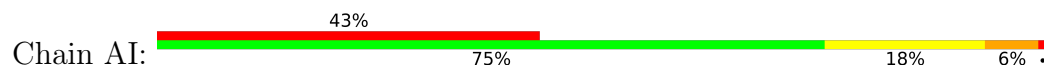
• Molecule 31: 40S ribosomal protein S7



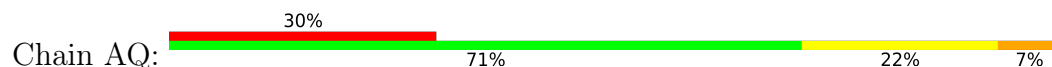
• Molecule 32: 40S ribosomal protein S15Aa

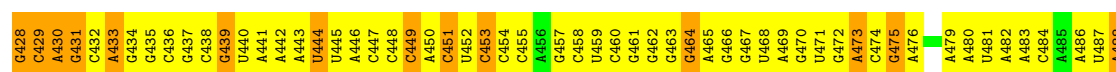


• Molecule 33: 40S ribosomal protein S8

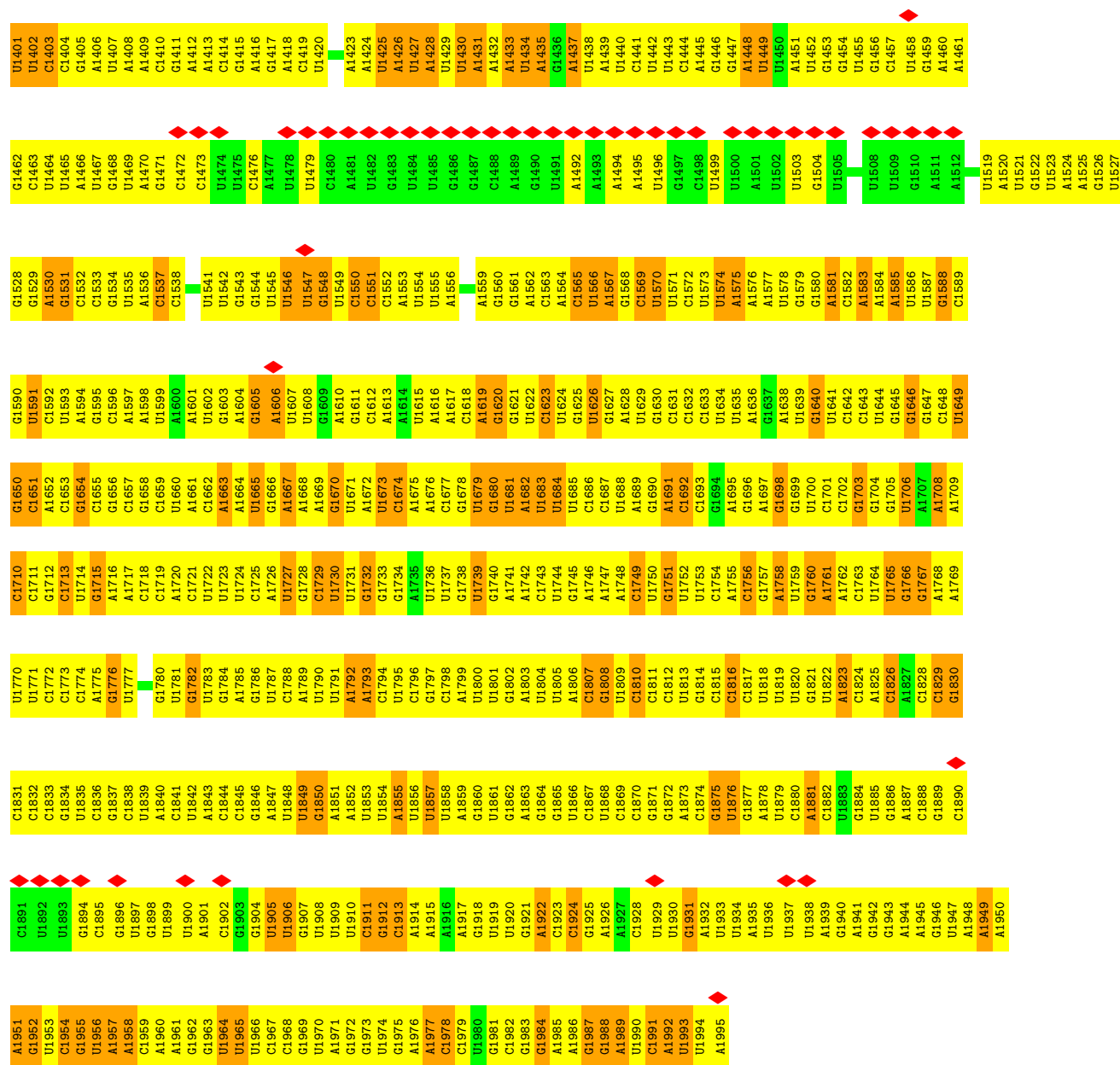


• Molecule 34: 40S ribosomal protein S16

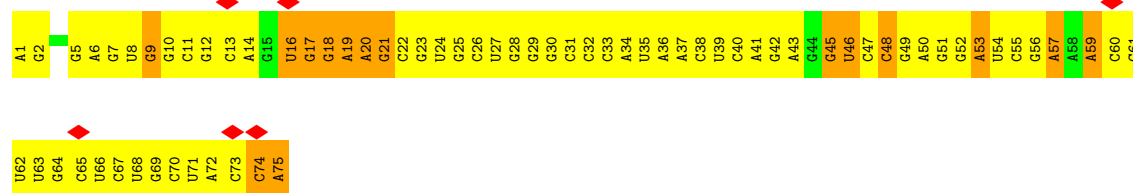
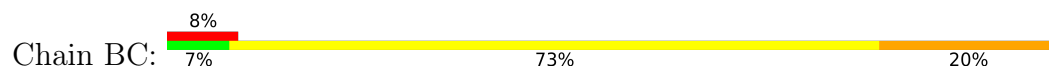




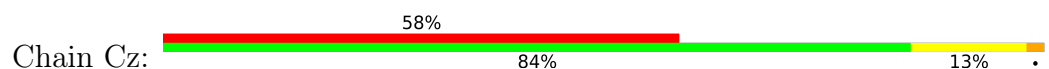
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A1344	C1283	U1162	U1162	G1101	G1041	C981	U920	C858	C795	U735	A	G615	U554	C494
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C1346	C1285	A1225	G1164	U1103	U1043	C983	G922	C860	C797	U737	U	U617	G556	C496
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G1360	A1299	A1239	A1178	A1117	A1057	C997	A937	U876	U810	U751	U	A631	U570	C509
C1361	G1300	A1240	U1118	U1118	A1058	U998	G938	U877	U811	U752	U	A632	U571	U510
A1362	U1301	G1241	A1180	G1119	U1059	U999	G939	U878	U812	U753	U	A633	U572	G511
U1363	U1302	G1242	G1181	C1120	A1060	G1000	U940	U879	U813	U754	U	A634	C573	U512
G1364	C1303	G1243	C1182	C1121	A1061	G1001	A941	U880	U814	U755	U	A635	C574	G513
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U1370	U1309	C1249	G1188	G1127	A1067	C1007	U947	A884	U817	U761	U	A641	U580	A519
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A1374	G1314	G1253	U1192	G1131	G1071	A1011	U951	G888	A822	U765	U	A645	G885	A523
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C1377	U1317	U1256	G1195	G1134	G1074	C1014	A954	A891	U825	U768	U	A648	A588	A526
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U1380	A1319	G1258	G1197	U1136	U1076	A1016	A956	A896	U827	U770	U	A650	U589	A528
G1381	G1320	A1259	G1198	G1137	G1077	A1017	C956	A897	U828	U771	U	A651	U590	A529
G1382	C1321	G1260	G1199	U1138	G1078	C1018	A957	U898	U829	U772	U	A652	C591	C529
A1383	C1322	C1261	U1200	U1139	G1079	U1019	G958	U899	U830	U773	U	A653	C592	U530
G1384	A1323	G1262	A1201	G1140	A1080	U1020	U959	A900	U831	U774	U	A654	U593	U531
U1385	G1324	U1263	G1202	C1141	G1081	A1021	U960	A901	U832	U775	U	A655	C594	U532
G1386	A1325	G1264	U1203	C1144	C1082	A1022	U961	G902	U833	U776	U	A656	A533	A533
A1387	U1326	C1265	A1204	U1145	C1083	G1023	G962	A903	A834	U777	U	A657	U534	A535
U1388	U1327	G1266	U1205	U1146	A1084	C1024	G963	C904	C835	U778	U	A658	U535	U536
U1389	G1328	G1267	G1206	U1147	U1085	A1025	G964	U905	C836	U779	U	A659	C537	C537
U1390	U1329	C1268	G1207	U1148	U1086	A1027	G965	C906	C837	U780	U	A660	U538	C538
G1391	U1330	U1269	U1208	U1149	C1087	A1028	A966	U907	A838	U781	U	A661	U539	U539
U1392	A1331	U1270	U1209	A1150	G1088	G1029	U969	G908	A839	U782	U	A662	U540	U540
C1393	G1332	A1271	G1210	U1151	A1089	C1030	U970	U909	U840	U783	U	A663	U541	U541
U1394	C1333	G1272	C1211	G1152	U1091	A1031	A971	U910	A841	U784	U	A664	G604	A542
G1395	U1334	U1273	A1212	G1153	A1092	U1032	U972	C911	A842	U785	U	A665	G605	A543
C1396	C1335	U1274	U1292	U1154	C1093	U1033	G973	C912	A843	U786	U	A666	C544	C544
U1397	U1336	U1275	G1215	U1155	G1094	U1034	U974	C913	A844	U787	U	A667	U606	U606
U1398	C1337	G1276	U1216	U1156	C1095	G1035	A975	C914	G845	U788	U	A668	A607	A607
A1399	U1338	A1277	U1217	U1157	G1096	C1036	U976	U915	A846	U789	U	A669	U608	U608
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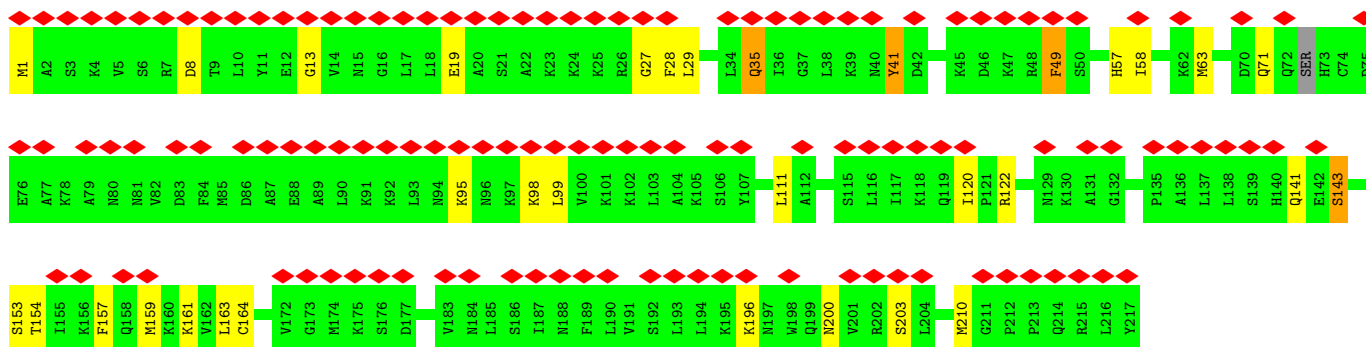
### • Molecule 37: E-tRNA



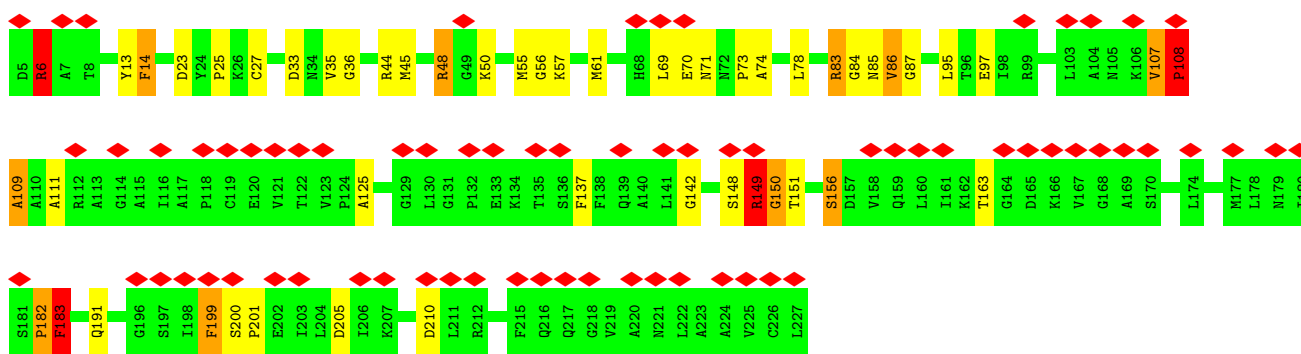
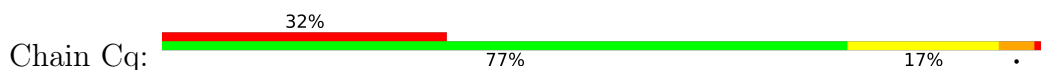
### • Molecule 38: 60S ribosomal protein L10a-2



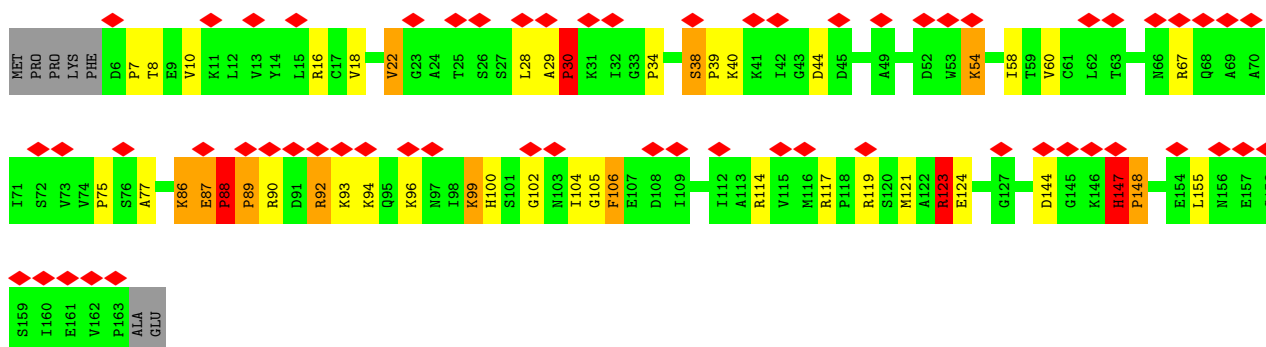




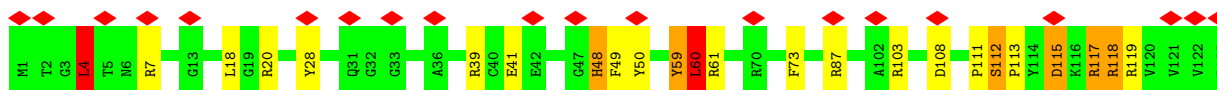
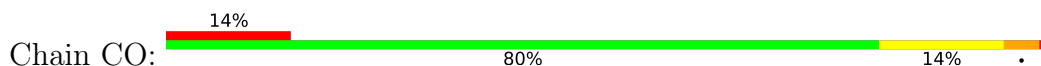
• Molecule 39: 60S acidic ribosomal protein P0

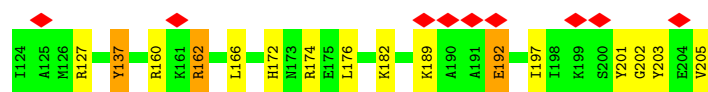


• Molecule 40: 60S ribosomal protein L12

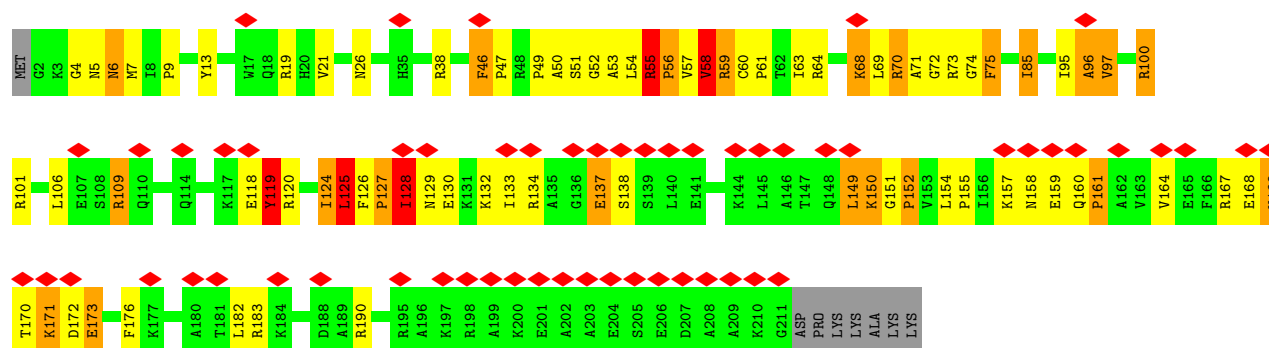


• Molecule 41: 60S ribosomal protein L13a

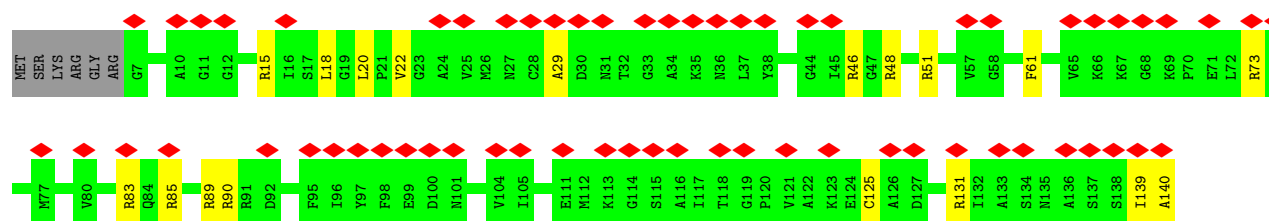
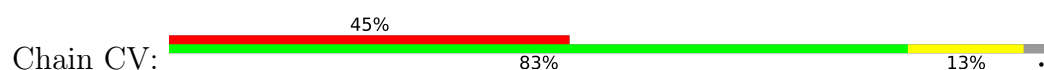




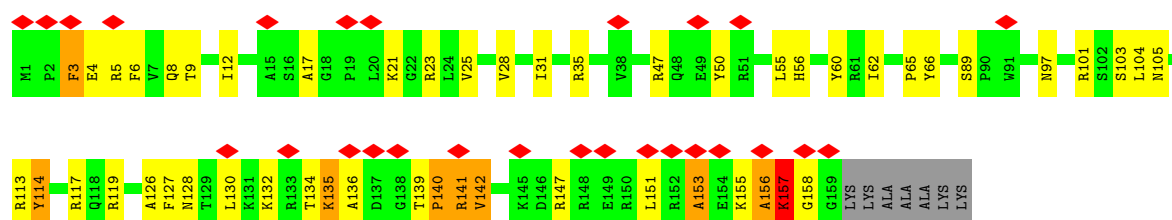
- Molecule 42: 60S ribosomal protein L13



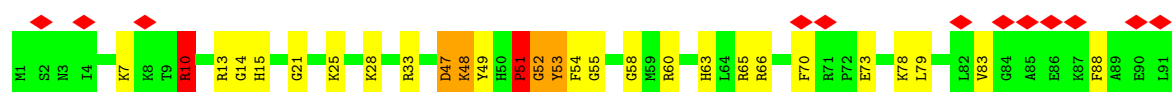
- Molecule 43: 60S ribosomal protein L23



- Molecule 44: 60S ribosomal protein L14



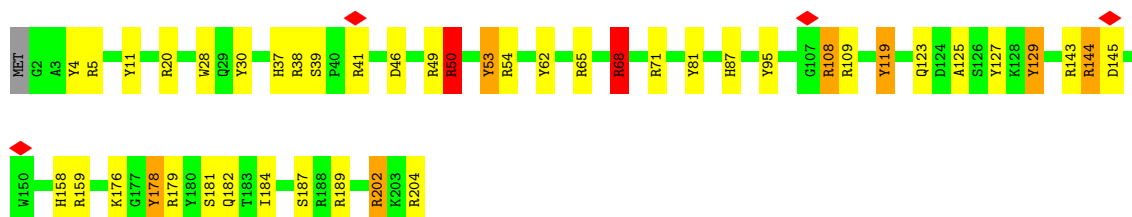
- Molecule 45: 60S ribosomal protein L27a





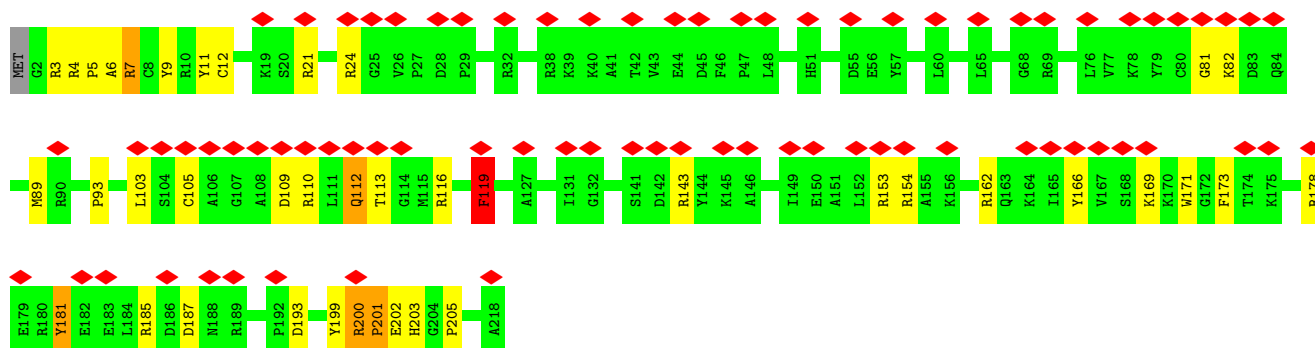
- Molecule 46: 60S ribosomal protein L15

Chain CN: 78% 17% ..



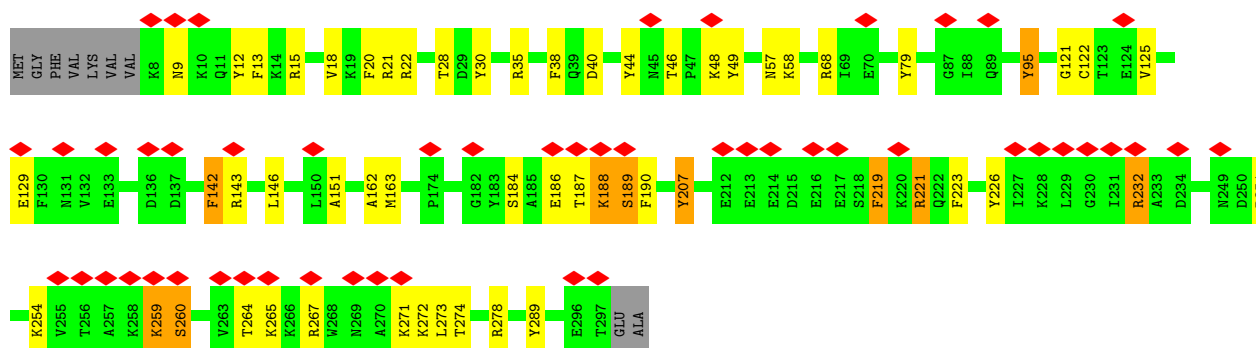
- Molecule 47: 60S ribosomal protein L10

Chain CI: 35% 81% 16% .



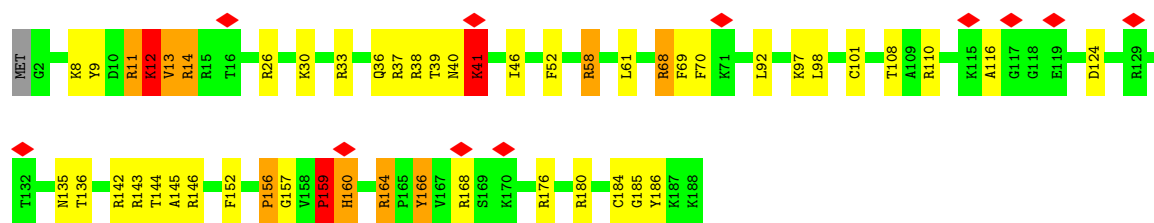
- Molecule 48: 60S ribosomal protein L5

Chain CD: 17% 78% 16% ..

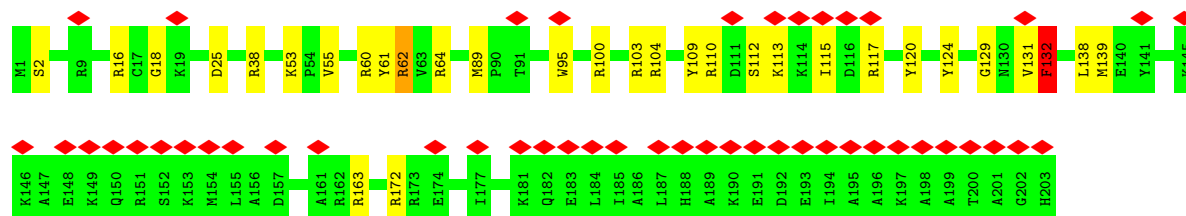
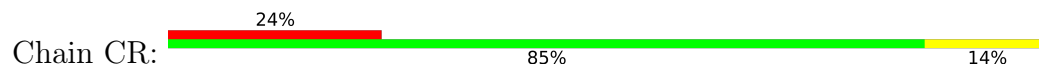


- Molecule 49: 60S ribosomal protein L18

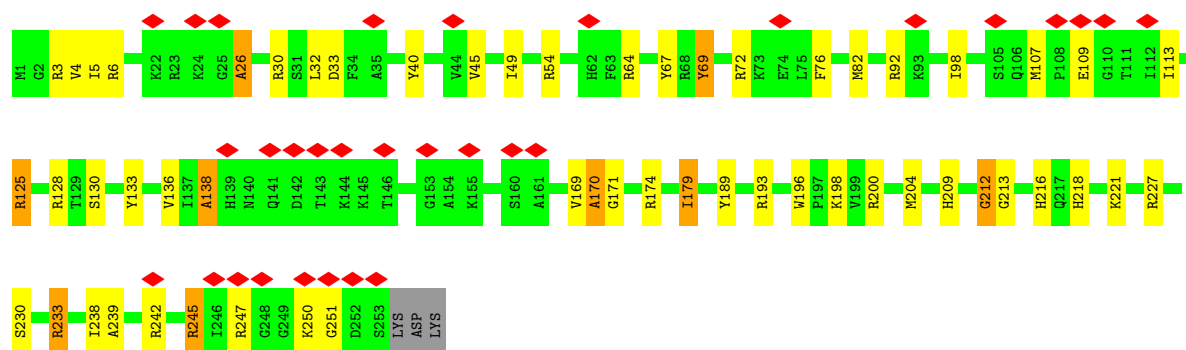
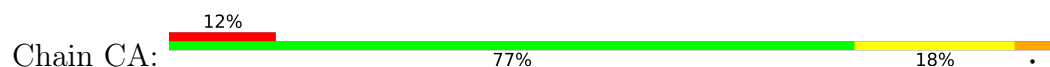
Chain CQ: 6% 73% 20% 5% ..



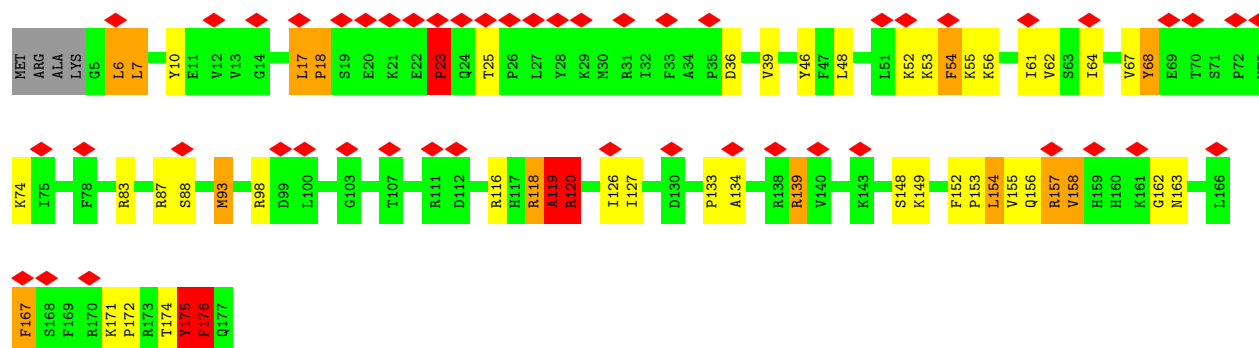
- Molecule 50: 60S ribosomal protein L19



- Molecule 51: 60S ribosomal protein L8

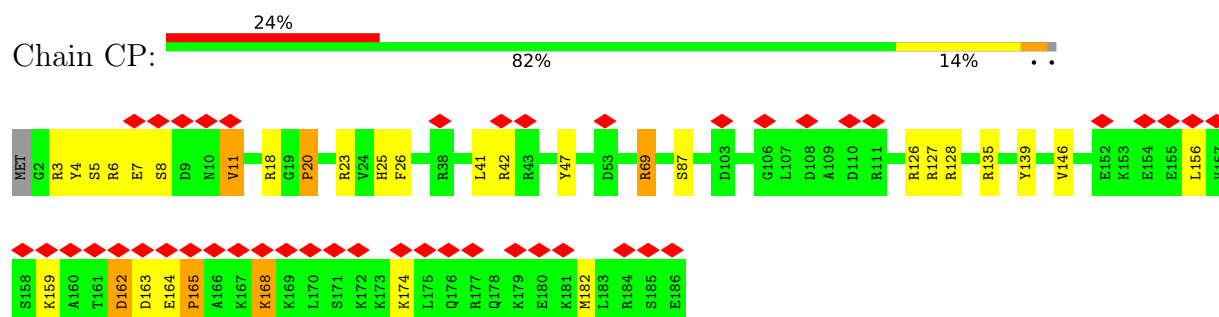


- Molecule 52: 60S ribosomal protein L18a

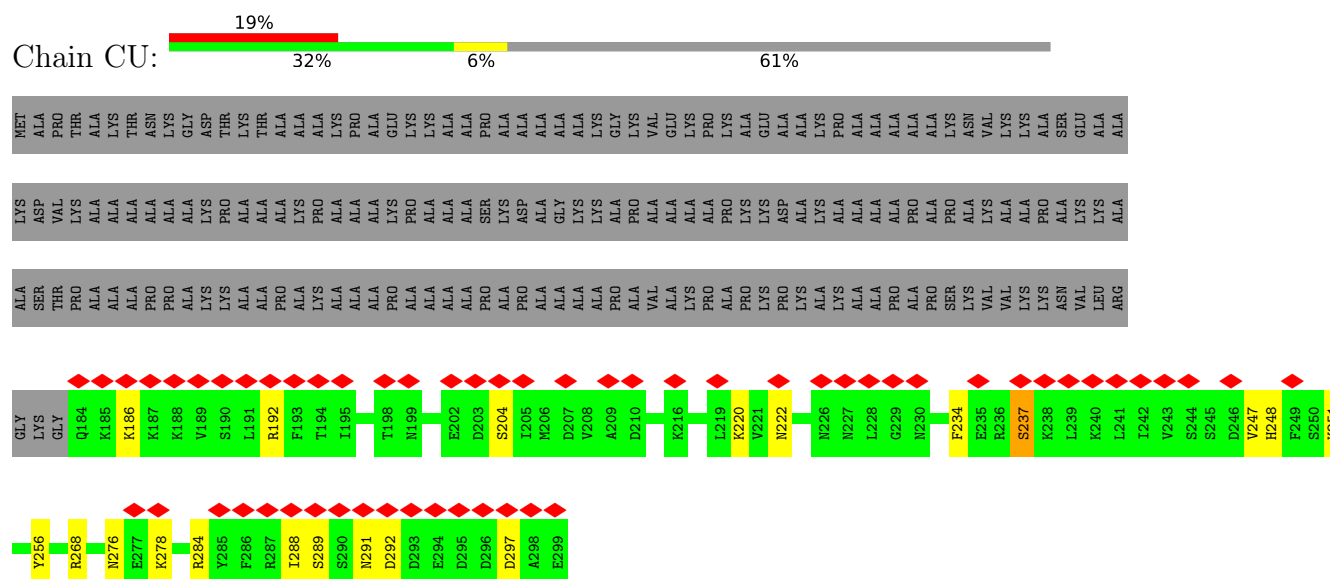


- Molecule 53: 60S ribosomal protein L21

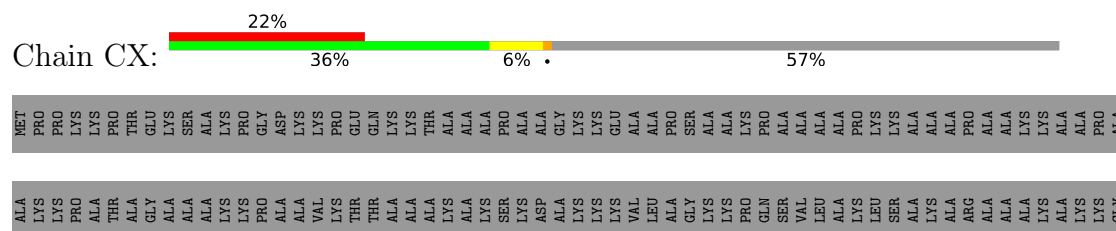
- Molecule 54: 60S ribosomal protein L17

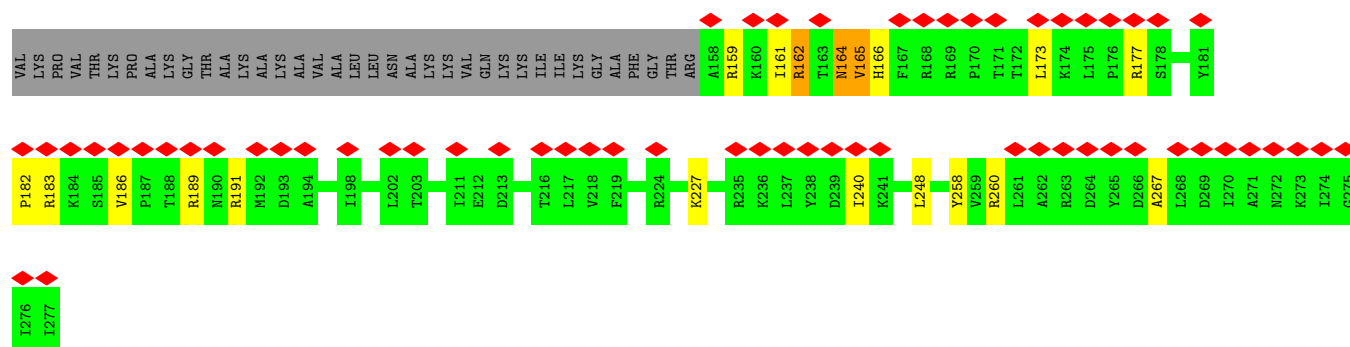


- Molecule 55: 60S ribosomal protein L22

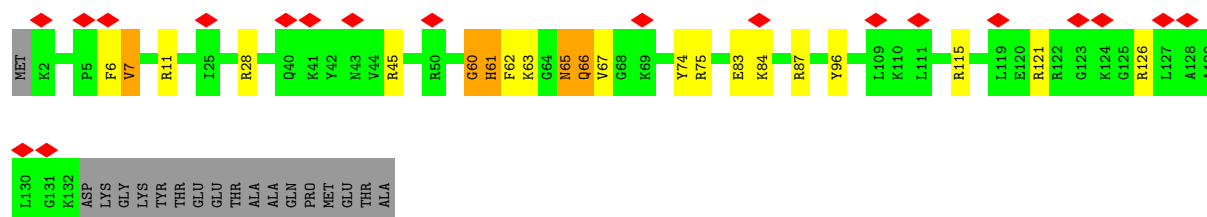
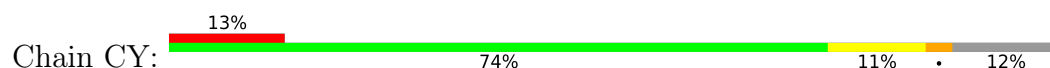


- Molecule 56: 60S ribosomal protein L23A

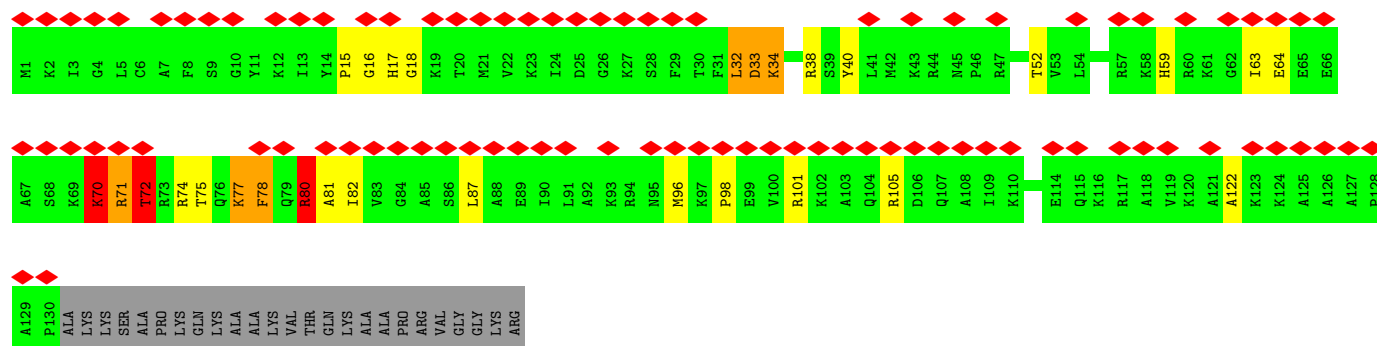




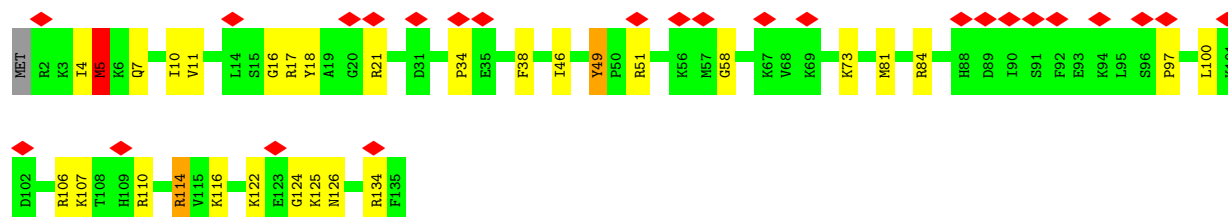
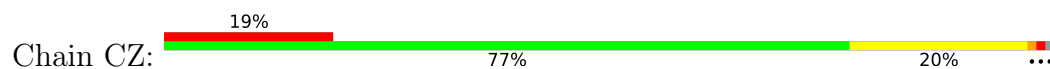
- Molecule 57: 60S ribosomal protein L26



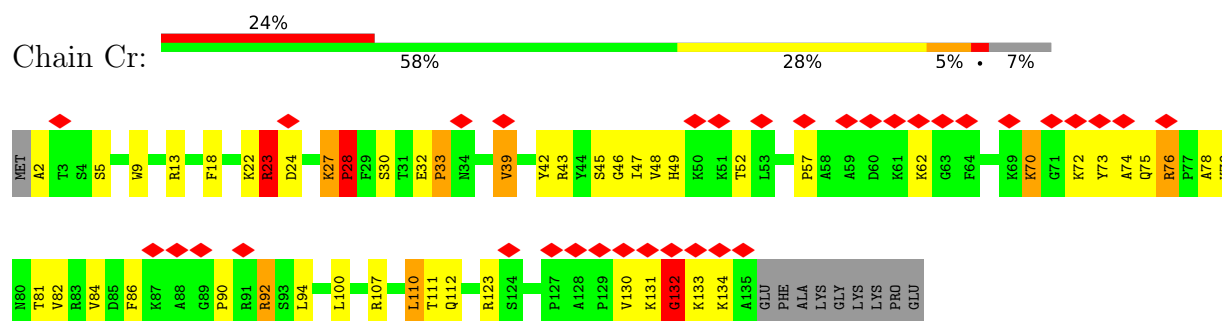
- Molecule 58: 60S ribosomal protein L24



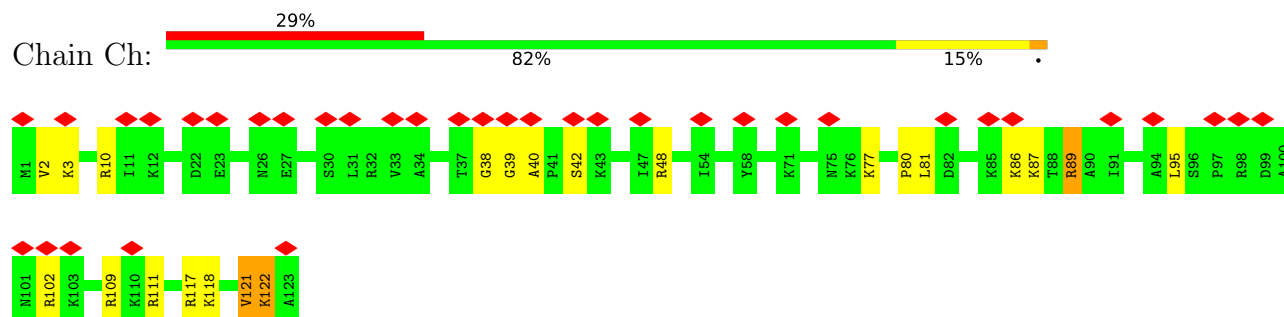
- Molecule 59: 60S ribosomal protein L27



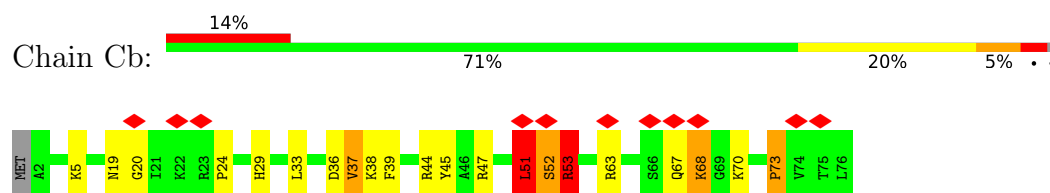
- Molecule 60: 60S ribosomal protein L28



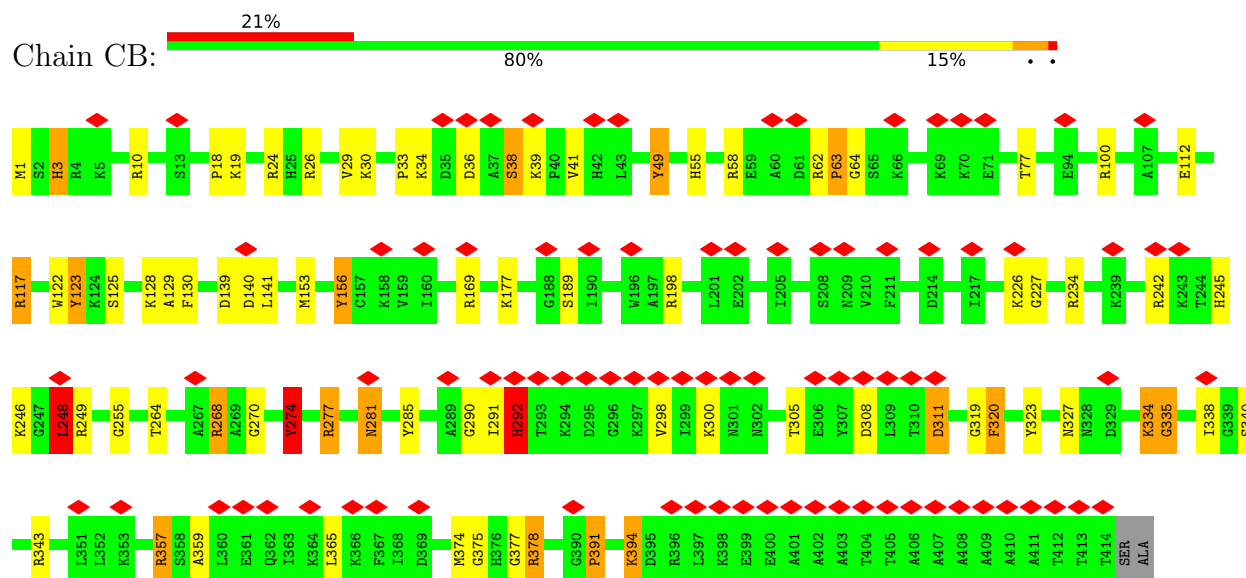
• Molecule 61: 60S ribosomal protein L35



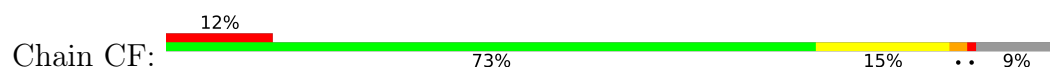
• Molecule 62: 60S ribosomal protein L29

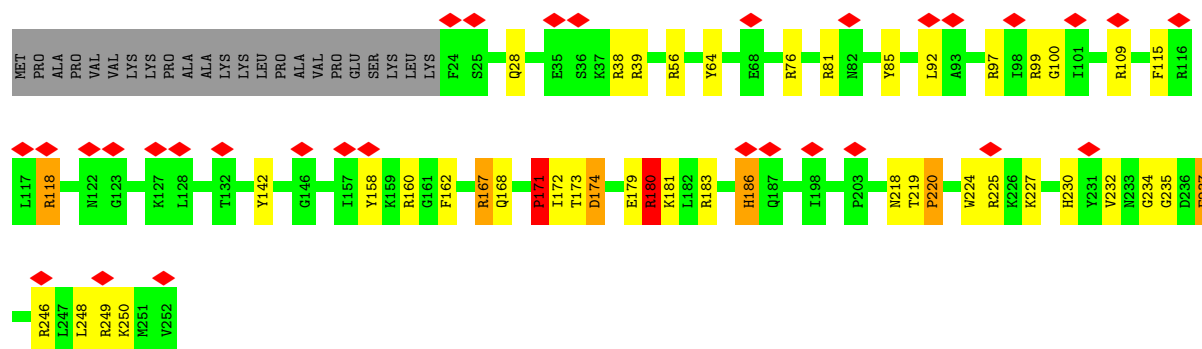


• Molecule 63: 60S ribosomal protein L3

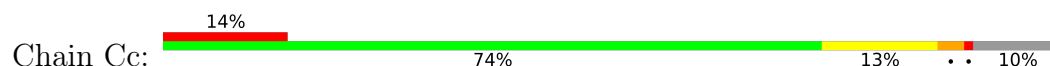


• Molecule 64: 60S ribosomal protein L7

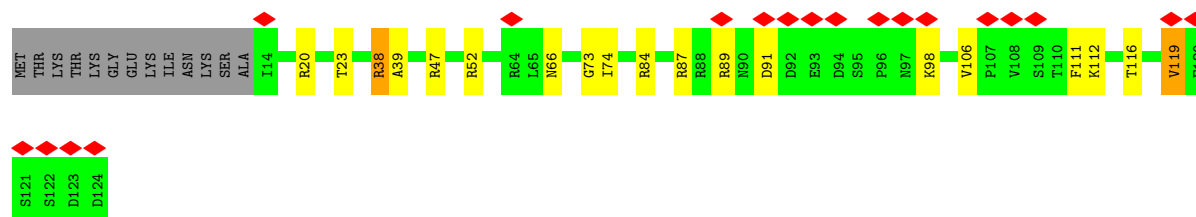
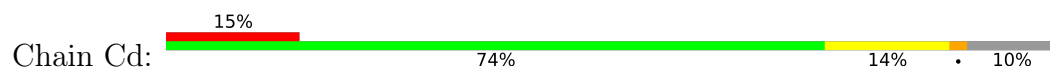




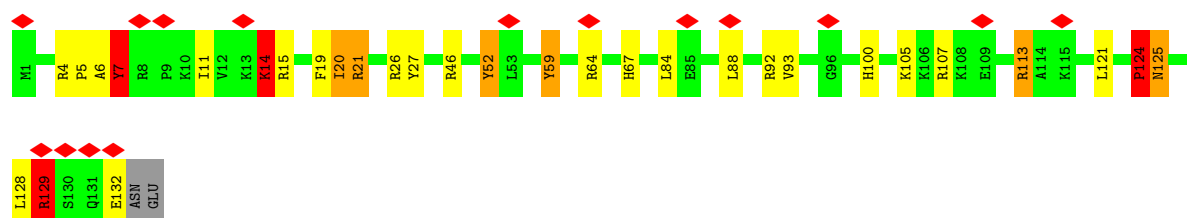
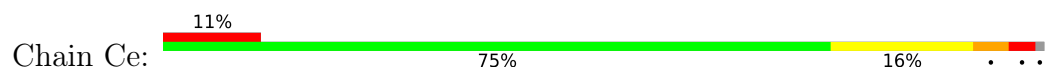
• Molecule 65: 60S ribosomal protein L30



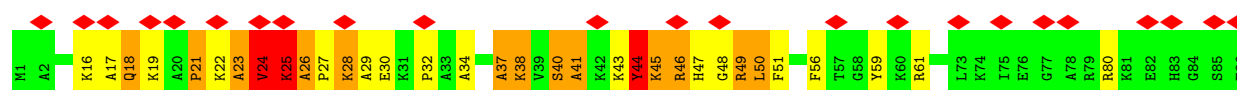
• Molecule 66: 60S ribosomal protein L31



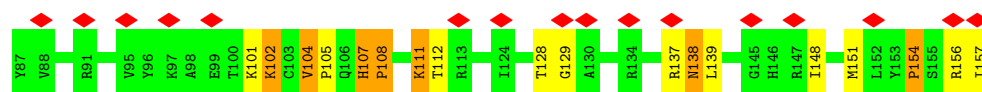
• Molecule 67: 60S ribosomal protein L32



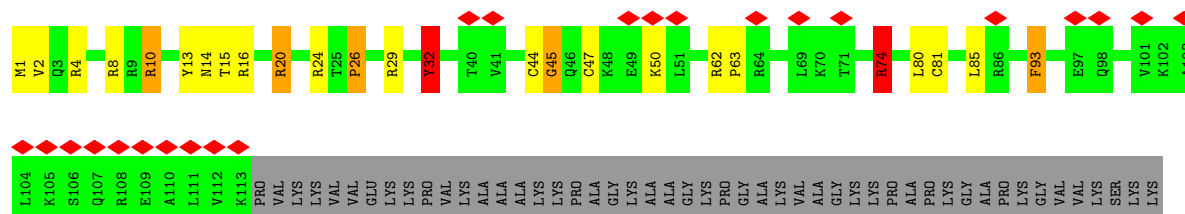
• Molecule 68: 60S ribosomal protein L35A



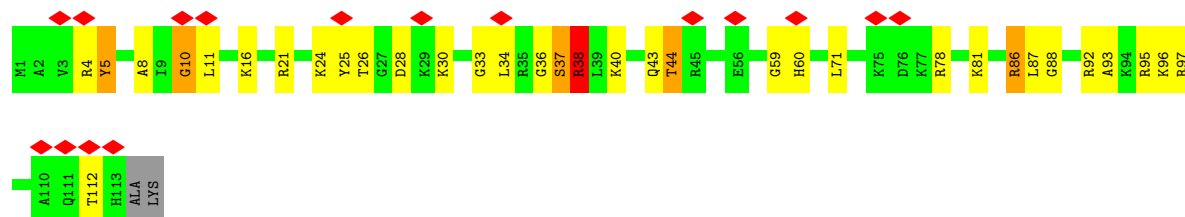




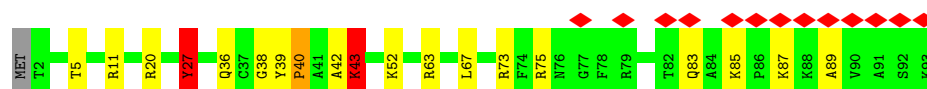
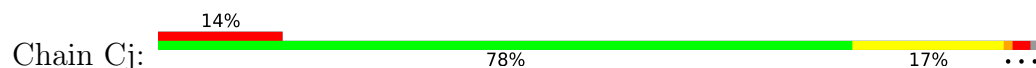
- Molecule 69: 60S ribosomal protein L34a



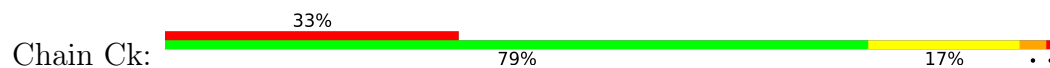
- Molecule 70: 60S ribosomal protein L36



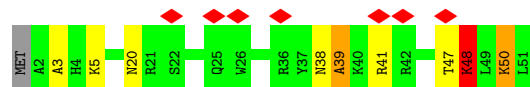
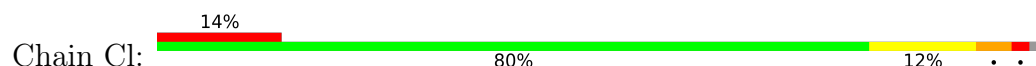
- Molecule 71: 60S ribosomal protein L37-A



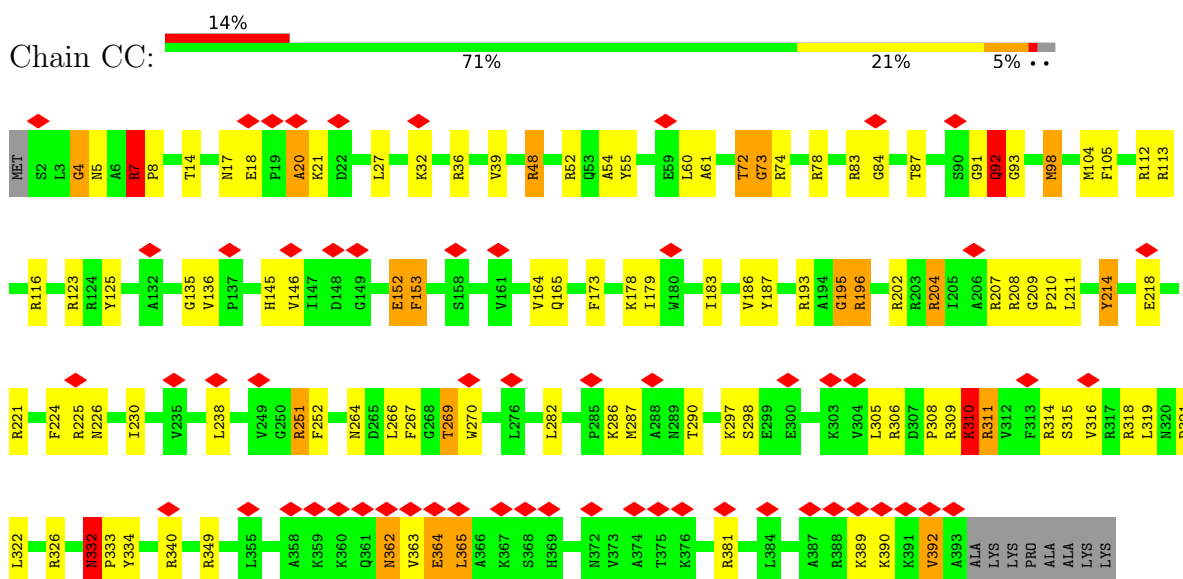
- Molecule 72: 60S ribosomal protein L38



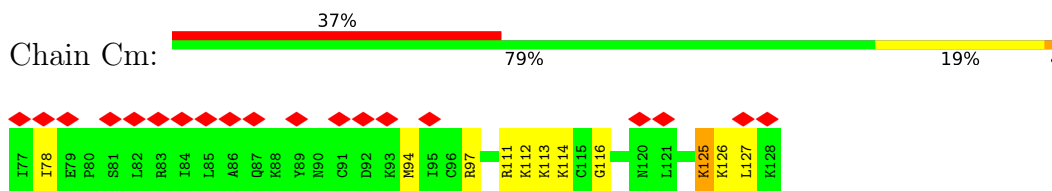
- Molecule 73: 60S ribosomal protein L39



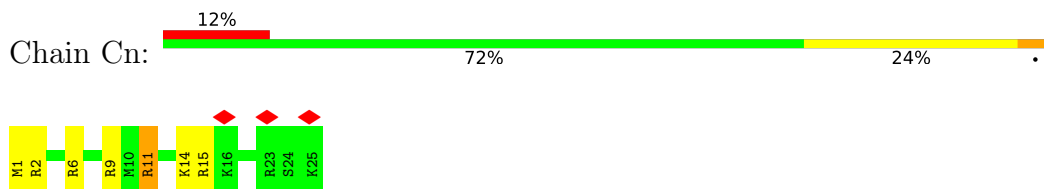
- Molecule 74: 60S ribosomal protein L4



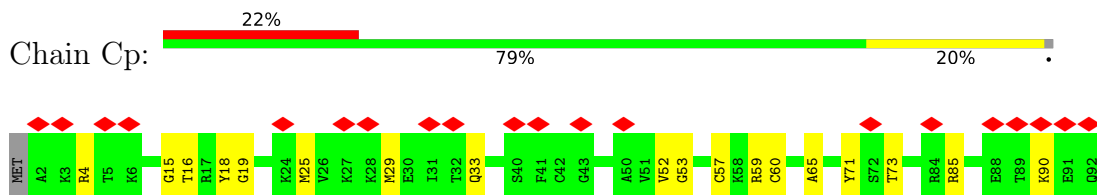
• Molecule 75: 60S ribosomal protein L40



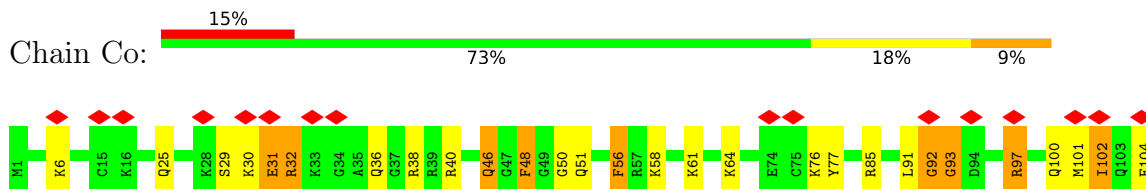
• Molecule 76: 60S ribosomal protein L41



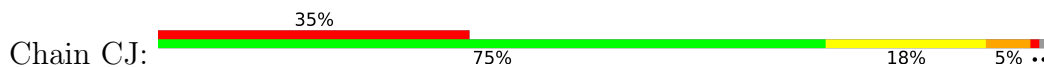
• Molecule 77: 60S ribosomal protein L37a

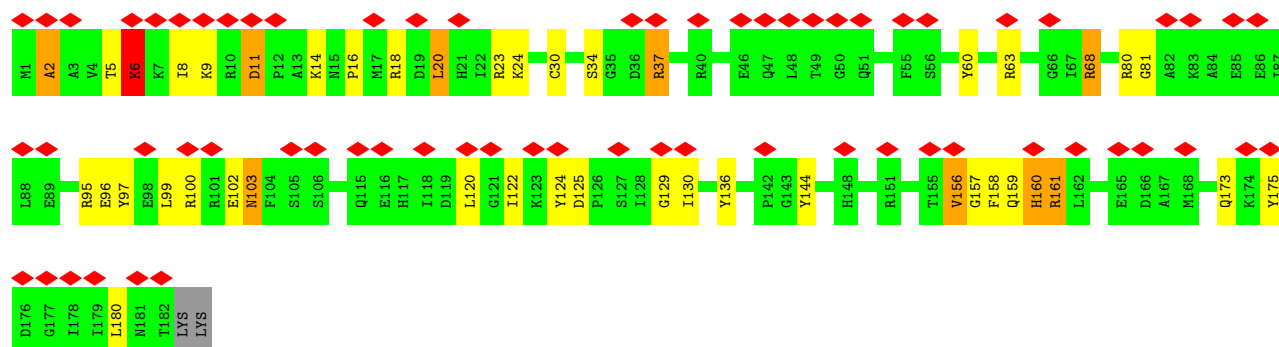


• Molecule 78: 60S ribosomal protein L36A



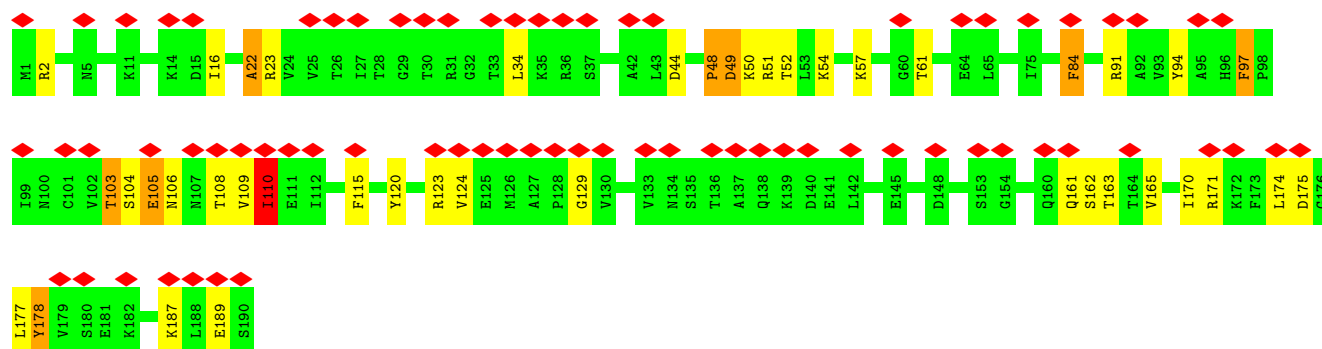
• Molecule 79: 60S ribosomal protein L11





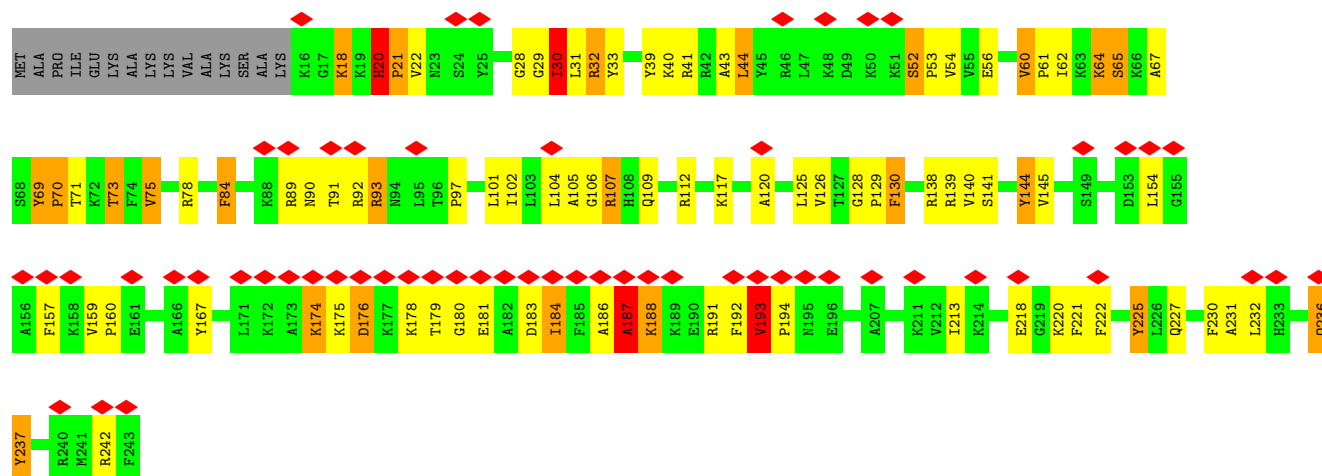
- Molecule 80: 60S ribosomal protein L9

Chain CH: 38% 78% 17%



- Molecule 81: 60S ribosomal protein L6, isoform A

Chain CE: 24% 56% 27% 10% 6%



- Molecule 82: 60S ribosomal protein L7a

Chain CG: 29% 70% 15% 11%



A1397	A1398	A1399	A1400	C1401	A1402	C1403	A1404	A1405	A1406	A1407	A1408	A1409	A1410	A1411	A1412	A1413	A1414	A1415	A1416	G1417	A1420	G1421	A1422	C1423	A1424	A1425	A1426	G1427	G1428	A1429	A1430	C1431	C1432	A1433	A1434	A1435	A1436	A1437	A1438	A1439	A1440	G1441	C1442	A1443	G1444	G1445	A1446	C1447	G1448	G1449	A1450	A1451	A1452	A1453	C1454	A1455	A1456	A1457					
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G1091	G1095	A1096	A1097	U1098	U1099	U1100	A1101	A1102	U1103	U1104	U1105	A1106	G1107	G1108	G1109	C1110	C1111	G1112	A1113	A1114	A1115	G1116	A1117	C1118	C1119	A1120	A1121	U1122	C1123	G1124	A1125	U1129	U1130	C1131	U1132	A1133	G1134	U1135	U1136	G1137	C1138	U1139	G1140	U1141	U1142	U1143	C1144	C1145	U1146	U1147	C1148	C1149	G1150	A1151	A1152								
A1030	G1031	C1032	U1033	U1034	G1035	A1036	A1037	G1038	U1039	C1040	A1041	G1042	G1043	G1044	G1045	A1046	A1047	A1048	C1049	C1050	C1051	G1052	G1053	A1054	U1055	G1056	A1059	G1060	A1061	C1062	C1063	G1064	A1065	A1066	A1067	C1068	A1069	G1070	U1071	A1072	C1073	U1074	G1075	A1076	C1077	G1078	U1079	G1080	C1081	A1082	A1083	U1084	U1085	C1086	G1087	U1088	U1089	U1090					
A970	C971	U972	U973	C974	A975	A976	C977	G978	U979	A980	C981	C982	U983	U984	G985	A986	G987	C988	A989	U990	A991	U992	A993	U994	G995	A996	A1059	G1060	A1061	C1062	C1063	C1003	C1004	G1005	A1006	A1007	A1008	G1009	A1010	U1011	U1012	C1013	U1014	G1015	A1016	A1017	C1018	U1019	A1020	U1021	U1022	C1023	U1024	U1025	G1026	U1027	C1028	C1029					
C910	A911	A912	U913	C914	C915	C916	G917	G918	U919	A920	C921	G922	U923	U924	C925	U926	A927	U928	A929	U930	A931	G932	U933	U934	A935	A936	G937	G937	U938	A939	U940	A941	A942	U943	U944	U945	A946	U947	U948	U949	U950	U951	U952	U953	A954	U955	U956	A957	U958	U959	U960	A961	U962	G963	C964	C965	U966	C967	U968	A969			
A850	G851	C852	U853	U854	A855	A856	U857	U858	A859	C860	G861	U862	U863	G864	C865	C866	U867	A868	A869	U870	A871	U872	U873	G874	C875	G876	A877	U878	U879	A880	G881	U882	U883	U884	U885	U886	U887	A888	G889	C890	U891	A892	U893	U894	U895	A896	U897	A898	G899	C900	U901	A902	U903	U904	U905	G906	A907	C908	A909				
U790	C791	U792	U793	G794	A795	A796	U797	C798	U799	C800	G801	C741	G802	A803	C804	C805	A806	A807	G808	U809	A810	G811	U812	C813	U814	A815	A816	C817	A818	U819	A820	U821	G822	U823	G824	C825	A826	A827	G828	U829	A830	A831	U832	U833	G834	U835	G836	A837	U838	U839	U840	A841	U842	G843	U844	A845	A846	U847	U848	U849			
U669	G670	A671	U672	U673	A674	C675	U676	G677	U678	C679	G680	C741	G681	U682	U683	A684	A685	U686	U687	U688	U689	U690	C691	G692	G693	A694	U695	U696	U697	A698	U699	A700	G701	A702	A703	U704	G705	G706	C707	U708	U709	A710	A711	U712	U713	A714	C715	C716	U717	U718	U719	G720	U721	U722	U723	U724	U725	U726	C727	U728	G729		
U609	G610	C611	U612	U613	G614	C615	A616	U617	U618	U619	A559	U620	A621	A622	C623	A624	C625	A626	G627	A628	A629	U630	C631	A632	A633	U634	G635	U636	U637	A638	U639	U640	A641	A642	U643	U644	U645	U646	U647	U648	A649	A650	A651	G652	U653	U654	U655	U656	G657	U658	U659	A660	G661	A662	U663	U664	U665	A666	U667	A668			
A548	A549	U550	C551	U552	A553	U554	U555	U556	C557	G558	U559	U560	A561	U562	A563	C564	C565	A566	A567	A568	U569	U570	U571	A572	U573	C574	A575	U576	A577	A578	A579	A580	U581	A582	U583	A584	A585	U586	U587	U588	A589	U590	A591	G592	U593	U594	U595	U596	U597	U598	A601	A602	U603	U604	A605	A606	A607	U608					

[illegible]



G3946	U3886	U3825	U3641	G3580	U3520	C3460	U3400	A3340	G3275	A3215
C3947	U3887	A3826	G3642	G3581	A3521	C3461	U3401	C3341	C3276	C3216
U3948	U3888	G3827	C3643	G3582	A3522	A3462	C3402	C3342		A3217
U3949	U3889	G3828	C3644	C3583	U3523	A3463	G3403	C3343	C3282	C3218
A3950	G3890	U3829	G3767	C3584	G3524	C3464	A3404	U3344	U3283	A3219
U3951	U3891	A3830	U3645	A3585	A3525	C3465	U3405	A3345	U3284	U3220
C3952	A3892	C3831	A3647	A3586	C3526	A3466	G3406	C3346	G3285	A3221
C3953	C3893	A3832	A3648	A3587	A3527	A3467	U3407	C3347	G3286	G3222
U3954	U3894	U3833	C3649	U3588	A3528	C3468	C3408	G3348	C3287	G3223
A3955	A3895	A3834	G3650	G3589	A3529	C3469	G3409	A3349	A3290	G3224
U3956	G3896	U3835	C3651	C3590	C3530	G3470	G3410	U3350	C3291	C3225
U3957	G3897	A3836	C3652	A3591	C3531	A3471	C3411	A3351	C3292	A3226
G3958	C3898	U3837	U3663	C3592	G3532	C3472	U3412	A3352	C3293	A3227
U3959	A3899	A3838	C3654	A3593	U3533	C3473	C3413	C3353	A3294	A3228
A3960	U3899	A3839	U3655	A3594	U3534	A3474	U3414	U3354	A3295	A3229
G3961	G3901	G3840	U3656	U3595	U3535	U3475	U3415	U3355	G3296	G3230
U3962	U3902	A3841	A3596	A3596	U3536	G3476	C3416	C3356	G3297	G3231
U3963	U3903	A3842	A3597	C3597	U3537	A3477	G3417	C3357	U3298	G3232
G3964	G3904	U3843	U3598	U3598	G3538	A3478	U3418	U3358	U3299	C3233
A3965	U3905	U3844	C3661	U3599	C3539	C3479	A3419	U3359	A3234	
U3966	G3907	A3845	G3662	G3600	G3540	U3480	U3420	U3360	U3240	
U3967	U3908	U3846	U3663	U3601	C3541	C3481	C3421	U3361	G3241	
G3968	A3909	U3847	U3784	U3602	C3542	C3482	A3422	G3362	A3242	
G3969	A3910	U3848	U3785	C3603	A3543	C3483	U3423	C3363	A3307	
A3970	A3911	A3849	C3666	G3604	G3544	U3484	U3424	C3364	A3308	
	G3912	A3850	C3667	A3605	C3545	U3485	G3425	G3365	A3309	
	U3913	U3851	G3668	G3606	A3546	U3486	U3426	G3366	U3310	
	G3914	A3852	U3669	C3607	U3547	A3487	C3427	G3367	U3311	
	U3915	G3907	C3670	A3610	C3548	G3488	A3428	C3368	A3312	
	U3916	A3853	G3671	C3611	U3549	A3489	A3429	A3369	U3313	
	G3917	U3854	U3672	C3612	C3550	C3490	G3430	C3370	U3314	
	A3918	U3855	G3673	A3613	U3551	C3491	C3431	A3371	U3315	
	G3919	U3856	G3674	G3614	G3552	C3492	A3432	C3372	U3316	
	C3920	A3860	A3675	U3614	G3553	U3493	A3433	U3373	U3317	
	A3921	A3861	C3676	C3615	G3554	C3494	A3434	U3374	U3250	
	G3922	A3862	U3677	U3616	U3555	C3495	A3435	U3375	G3251	
	C3923	A3863	G3678	U3617	A3556	U3496	U3436	C3376	G3252	
	U3924	C3864	C3679	A3618	G3557	G3497	U3437	A3377	G3253	
	G3925	U3865	A3680	U3619	U3558	A3498	C3438	A3318	U3254	
	C3926	U3866	U3681	C3620	C3559	C3499	A3439	A3319	G3255	
	C3927	A3867	G3682	A3621	G3560	A3500	C3440	C3320	U3256	
	A3928	G3868	C3683	C3622	G3561	C3501	C3441	A3321	U3257	
	U3929	U3869	A3684	G3623	A3562	A3502	A3442	A3322	G3258	
	C3930	A3870	U3685	C3624	G3563	G3503	A3443	G3323	A3259	
	G3931	U3871	A3686	U3625	A3564	G3504	G3444	A3324	U3261	
	U3932	C3872	A3687	A3626	G3565	G3505	G3445	A3325	A3262	
	G3933	A3873	U3688	C3627	G3566	U3506	G3446	G3326	C3263	
	C3934	U3874	A3690	C3628	A3567	A3507	U3447	U3327		
	A3935	U3875	A3691	U3629	A3568	U3508	U3448	G3328		
	U3936	G3876	G3692	C3630	C3569	G3509	G3449	A3329		
	G3937	U3877	C3693	C3631	C3570	U3510	G3450	A3330		
	C3938	U3878	G3694	G3632	C3571	U3511	A3451	A3331		
	U3939	A3879	G3695	U3633	G3572	U3512	G3452	A3332		
	A3940	U3879	G3696	U3634	C3573	A3513	U3453	A3333		
	G3941	A3880	C3697	G3635	A3574	C3514	G3454	A3334		
	U3942	A3881	A3698	A3636	G3575	C3515	U3455	A3335		
	G3943	C3882	C3820	A3637	G3576	C3516	U3456	A3336		
	A3944	G3883	U3761	U3638	U3577	U3517	C3457	A3337		
	C3945	A3884	U3700	U3639	A3578	C3518	A3458	U3338		
		G3885	U3701	A3640	C3579	C3519	C3459	A3339		

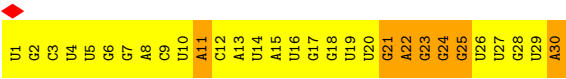
• Molecule 84: 2S ribosomal RNA

Chain A9:

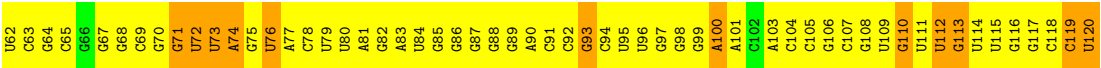
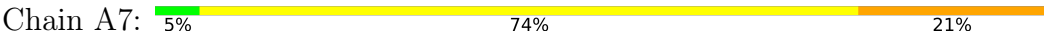
77%

23%

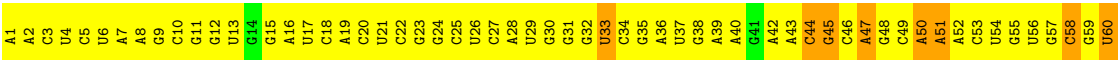
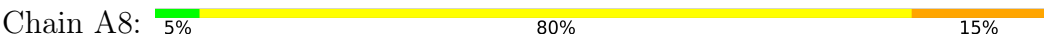




● Molecule 85: 5S ribosomal RNA



● Molecule 86: 5.8S ribosomal RNA



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	134500	Depositor
Resolution determination method	FSC 0.5 CUT-OFF	Depositor
CTF correction method	each subvolume	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	20	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	90000	Depositor
Image detector	FEI EAGLE (4k x 4k)	Depositor
Maximum map value	1.943	Depositor
Minimum map value	-0.877	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.168	Depositor
Recommended contour level	0.49	Depositor
Map size ( $\text{\AA}$ )	455.4, 455.4, 455.4	wwPDB
Map dimensions	368, 368, 368	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.2375, 1.2375, 1.2375	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

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	Az	1.21	2/6704 (0.0%)	1.68	114/9051 (1.3%)
2	Ag	1.19	0/2574	1.46	21/3506 (0.6%)
3	AU	1.26	1/825 (0.1%)	1.52	9/1111 (0.8%)
4	AK	1.20	0/819	1.52	10/1110 (0.9%)
5	AO	1.27	1/1016 (0.1%)	1.59	17/1364 (1.2%)
6	AX	1.30	1/1152 (0.1%)	1.50	11/1540 (0.7%)
7	AM	1.15	0/937	1.59	15/1260 (1.2%)
8	AS	1.25	1/1146 (0.1%)	1.64	19/1535 (1.2%)
9	Ad	1.38	0/443	1.61	7/589 (1.2%)
10	AN	1.26	1/1225 (0.1%)	1.45	13/1641 (0.8%)
11	AL	1.35	2/1296 (0.2%)	1.53	12/1725 (0.7%)
12	AR	1.26	1/993 (0.1%)	1.41	6/1333 (0.5%)
13	AP	1.22	0/1036	1.44	8/1383 (0.6%)
14	AT	1.23	0/1228	1.51	12/1653 (0.7%)
15	AB	1.24	2/1825 (0.1%)	1.49	22/2448 (0.9%)
16	AA	1.25	3/1777 (0.2%)	1.63	29/2422 (1.2%)
17	AV	1.29	0/622	1.47	4/835 (0.5%)
18	AY	2.40	7/1032 (0.7%)	1.64	17/1373 (1.2%)
19	AZ	1.27	1/616 (0.2%)	1.61	10/826 (1.2%)
20	Aa	1.34	2/883 (0.2%)	1.65	18/1184 (1.5%)
21	Ab	1.28	1/668 (0.1%)	1.48	4/898 (0.4%)
22	Ac	1.41	0/502	1.46	2/670 (0.3%)
23	AD	1.28	4/1808 (0.2%)	1.50	13/2427 (0.5%)
24	Ae	1.33	1/475 (0.2%)	1.53	7/625 (1.1%)
25	Af	1.30	3/672 (0.4%)	1.69	11/887 (1.2%)
26	AJ	1.34	6/1526 (0.4%)	1.65	23/2037 (1.1%)
27	AE	1.27	6/2096 (0.3%)	1.54	27/2819 (1.0%)
28	AC	1.24	3/1785 (0.2%)	1.57	26/2415 (1.1%)
29	AG	1.31	0/1891	1.61	34/2519 (1.3%)
30	AF	1.28	2/1518 (0.1%)	1.53	21/2037 (1.0%)
31	AH	1.25	2/1593 (0.1%)	1.63	19/2145 (0.9%)
32	AW	1.26	3/1046 (0.3%)	1.51	14/1402 (1.0%)
33	AI	1.31	2/1689 (0.1%)	1.62	29/2250 (1.3%)
34	AQ	1.30	1/1202 (0.1%)	1.70	25/1608 (1.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	Ah	1.37	1/495 (0.2%)	1.76	13/658 (2.0%)
36	B2	2.32	1859/44058 (4.2%)	2.09	2463/68404 (3.6%)
37	BC	2.25	72/1796 (4.0%)	1.89	84/2800 (3.0%)
38	Cz	1.18	0/1727	1.43	7/2308 (0.3%)
39	Cq	1.20	2/1736 (0.1%)	1.56	24/2342 (1.0%)
40	CK	1.19	1/1196 (0.1%)	1.57	13/1614 (0.8%)
41	CO	1.33	4/1700 (0.2%)	1.51	22/2277 (1.0%)
42	CL	1.35	4/1726 (0.2%)	1.76	47/2308 (2.0%)
43	CV	1.28	1/1014 (0.1%)	1.52	14/1362 (1.0%)
44	CM	1.37	1/1326 (0.1%)	1.65	20/1780 (1.1%)
45	Ca	1.28	2/1235 (0.2%)	1.66	29/1640 (1.8%)
46	CN	1.43	8/1750 (0.5%)	1.62	26/2335 (1.1%)
47	CI	1.33	2/1827 (0.1%)	1.54	14/2447 (0.6%)
48	CD	1.32	2/2379 (0.1%)	1.55	31/3196 (1.0%)
49	CQ	1.34	3/1544 (0.2%)	1.64	40/2069 (1.9%)
50	CR	1.27	3/1703 (0.2%)	1.46	19/2255 (0.8%)
51	CA	1.33	4/1970 (0.2%)	1.61	29/2635 (1.1%)
52	CS	1.29	1/1491 (0.1%)	1.66	26/1998 (1.3%)
53	CT	1.28	3/1326 (0.2%)	1.53	13/1773 (0.7%)
54	CP	1.31	2/1529 (0.1%)	1.50	16/2042 (0.8%)
55	CU	1.21	1/974 (0.1%)	1.46	6/1302 (0.5%)
56	CX	1.27	1/1001 (0.1%)	1.58	7/1348 (0.5%)
57	CY	1.36	3/1094 (0.3%)	1.51	14/1456 (1.0%)
58	CW	1.29	1/1063 (0.1%)	1.55	9/1410 (0.6%)
59	CZ	1.28	1/1141 (0.1%)	1.56	10/1517 (0.7%)
60	Cr	1.29	0/1069	1.70	20/1432 (1.4%)
61	Ch	1.30	0/1024	1.45	8/1353 (0.6%)
62	Cb	1.29	2/628 (0.3%)	1.67	12/832 (1.4%)
63	CB	1.24	3/3356 (0.1%)	1.61	41/4494 (0.9%)
64	CF	1.31	2/1958 (0.1%)	1.56	29/2622 (1.1%)
65	Cc	1.20	1/779 (0.1%)	1.55	9/1048 (0.9%)
66	Cd	1.28	0/939	1.54	10/1262 (0.8%)
67	Ce	1.36	1/1132 (0.1%)	1.54	13/1508 (0.9%)
68	Cf	1.33	0/1270	1.74	22/1696 (1.3%)
69	Cg	1.44	2/938 (0.2%)	1.65	19/1252 (1.5%)
70	Ci	1.30	1/944 (0.1%)	1.62	16/1250 (1.3%)
71	Cj	1.41	1/750 (0.1%)	1.47	5/993 (0.5%)
72	Ck	1.26	0/583	1.72	10/774 (1.3%)
73	Cl	1.39	0/445	1.46	3/589 (0.5%)
74	CC	1.32	5/3163 (0.2%)	1.57	43/4253 (1.0%)
75	Cm	1.24	0/435	1.51	4/575 (0.7%)
76	Cn	1.55	0/237	1.43	3/300 (1.0%)
77	Cp	1.30	0/719	1.49	9/954 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
78	Co	1.30	2/887 (0.2%)	1.63	15/1162 (1.3%)
79	CJ	1.30	3/1494 (0.2%)	1.53	15/2001 (0.7%)
80	CH	1.21	0/1519	1.54	23/2042 (1.1%)
81	CE	1.29	3/1883 (0.2%)	1.75	45/2514 (1.8%)
82	CG	1.26	7/1968 (0.4%)	1.47	21/2637 (0.8%)
83	A5	2.33	3665/87035 (4.2%)	2.12	5062/135254 (3.7%)
84	A9	2.28	39/714 (5.5%)	2.32	45/1112 (4.0%)
85	A7	2.35	134/2854 (4.7%)	2.03	160/4447 (3.6%)
86	A8	2.29	115/2932 (3.9%)	2.05	138/4568 (3.0%)
All	All	1.95	6027/247076 (2.4%)	1.91	9425/360828 (2.6%)

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	Az	105	86
2	Ag	0	4
3	AU	0	3
4	AK	0	8
5	AO	2	1
6	AX	0	3
7	AM	1	7
8	AS	0	6
9	Ad	0	4
10	AN	0	6
11	AL	0	9
12	AR	0	5
13	AP	1	4
14	AT	2	11
15	AB	0	4
16	AA	0	6
17	AV	0	2
18	AY	0	11
19	AZ	1	2
20	Aa	1	6
21	Ab	0	4
22	Ac	0	3
23	AD	1	10
24	Ae	0	2
25	Af	0	10

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Mol	Chain	#Chirality outliers	#Planarity outliers
26	AJ	0	7
27	AE	0	13
28	AC	0	14
29	AG	0	11
30	AF	0	7
31	AH	2	8
32	AW	0	2
33	AI	0	12
34	AQ	0	12
35	Ah	0	6
36	B2	1	0
38	Cz	1	2
39	Cq	1	16
40	CK	0	13
41	CO	0	9
42	CL	29	21
43	CV	0	4
44	CM	2	15
45	Ca	1	12
46	CN	1	13
47	CI	0	11
48	CD	1	8
49	CQ	0	7
50	CR	0	5
51	CA	0	8
52	CS	28	22
53	CT	1	12
54	CP	1	4
55	CU	0	4
56	CX	1	4
57	CY	0	4
58	CW	0	10
59	CZ	0	6
60	Cr	0	14
61	Ch	0	3
62	Cb	0	4
63	CB	1	24
64	CF	1	7
65	Cc	0	5
66	Cd	1	3
67	Ce	0	8
68	Cf	7	22

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Mol	Chain	#Chirality outliers	#Planarity outliers
69	Cg	0	7
70	Ci	0	5
71	Cj	0	3
72	Ck	0	2
73	Cl	0	4
74	CC	1	21
75	Cm	0	2
76	Cn	0	2
77	Cp	0	2
78	Co	0	5
79	CJ	1	10
80	CH	1	11
81	CE	3	26
82	CG	1	7
83	A5	7	0
All	All	208	716

The worst 5 of 6027 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
83	A5	1668	U	C2'-C1'	-31.14	1.19	1.53
36	B2	1320	G	C2'-C1'	-30.14	1.20	1.53
18	AY	77	TYR	CE1-CZ	30.11	1.77	1.38
18	AY	77	TYR	CE2-CZ	28.88	1.76	1.38
18	AY	77	TYR	CG-CD1	27.53	1.75	1.39

The worst 5 of 9425 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
83	A5	3514	C	O4'-C1'-N1	37.72	138.37	108.20
83	A5	3368	C	O4'-C1'-N1	35.09	136.28	108.20
36	B2	1087	C	O4'-C1'-N1	32.98	134.59	108.20
83	A5	3676	C	O4'-C1'-N1	31.58	133.46	108.20
83	A5	2491	C	O4'-C1'-N1	31.03	133.03	108.20

5 of 208 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	Az	4	PHE	CA
1	Az	15	LYS	CA
1	Az	49	ALA	CA
1	Az	55	ARG	CA

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Mol	Chain	Res	Type	Atom
1	Az	68	ILE	CA

5 of 716 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	Az	14	ASP	Peptide
1	Az	20	ARG	Sidechain
1	Az	27	HIS	Peptide
1	Az	47	ALA	Peptide
1	Az	49	ALA	Peptide

## 5.2 Too-close contacts [i](#)

Due to software issues we are unable to calculate clashes - this section is therefore empty.

## 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	Az	835/844 (99%)	647 (78%)	96 (12%)	92 (11%)	0	7
2	Ag	316/318 (99%)	274 (87%)	25 (8%)	17 (5%)	2	19
3	AU	100/120 (83%)	84 (84%)	6 (6%)	10 (10%)	0	9
4	AK	93/163 (57%)	75 (81%)	7 (8%)	11 (12%)	0	6
5	AO	132/151 (87%)	104 (79%)	13 (10%)	15 (11%)	0	7
6	AX	141/143 (99%)	118 (84%)	15 (11%)	8 (6%)	1	18
7	AM	117/139 (84%)	85 (73%)	16 (14%)	16 (14%)	0	4
8	AS	135/152 (89%)	107 (79%)	16 (12%)	12 (9%)	1	11
9	Ad	50/56 (89%)	30 (60%)	10 (20%)	10 (20%)	0	2
10	AN	148/151 (98%)	136 (92%)	7 (5%)	5 (3%)	3	26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	AL	153/155 (99%)	128 (84%)	16 (10%)	9 (6%)	1	17
12	AR	118/131 (90%)	99 (84%)	12 (10%)	7 (6%)	1	17
13	AP	122/148 (82%)	95 (78%)	13 (11%)	14 (12%)	0	6
14	AT	152/156 (97%)	125 (82%)	17 (11%)	10 (7%)	1	15
15	AB	218/268 (81%)	179 (82%)	23 (11%)	16 (7%)	1	13
16	AA	216/313 (69%)	174 (81%)	22 (10%)	20 (9%)	0	10
17	AV	80/83 (96%)	64 (80%)	6 (8%)	10 (12%)	0	5
18	AY	124/131 (95%)	96 (77%)	10 (8%)	18 (14%)	0	4
19	AZ	72/117 (62%)	49 (68%)	11 (15%)	12 (17%)	0	3
20	Aa	105/114 (92%)	75 (71%)	14 (13%)	16 (15%)	0	3
21	Ab	82/84 (98%)	64 (78%)	12 (15%)	6 (7%)	1	13
22	Ac	60/65 (92%)	53 (88%)	1 (2%)	6 (10%)	0	9
23	AD	225/246 (92%)	183 (81%)	29 (13%)	13 (6%)	1	17
24	Ae	56/132 (42%)	37 (66%)	10 (18%)	9 (16%)	0	3
25	Af	78/80 (98%)	46 (59%)	15 (19%)	17 (22%)	0	2
26	AJ	179/195 (92%)	148 (83%)	17 (10%)	14 (8%)	1	12
27	AE	259/261 (99%)	204 (79%)	37 (14%)	18 (7%)	1	14
28	AC	225/267 (84%)	186 (83%)	17 (8%)	22 (10%)	0	9
29	AG	229/248 (92%)	196 (86%)	20 (9%)	13 (6%)	1	18
30	AF	188/228 (82%)	152 (81%)	20 (11%)	16 (8%)	1	11
31	AH	192/194 (99%)	147 (77%)	28 (15%)	17 (9%)	1	11
32	AW	127/130 (98%)	114 (90%)	10 (8%)	3 (2%)	6	33
33	AI	205/208 (99%)	164 (80%)	12 (6%)	29 (14%)	0	4
34	AQ	146/148 (99%)	114 (78%)	14 (10%)	18 (12%)	0	5
35	Ah	54/121 (45%)	31 (57%)	6 (11%)	17 (32%)	0	0
38	Cz	215/218 (99%)	186 (86%)	17 (8%)	12 (6%)	2	18
39	Cq	221/223 (99%)	183 (83%)	21 (10%)	17 (8%)	1	13
40	CK	156/165 (94%)	95 (61%)	29 (19%)	32 (20%)	0	2
41	CO	203/205 (99%)	183 (90%)	12 (6%)	8 (4%)	3	23
42	CL	208/218 (95%)	141 (68%)	28 (14%)	39 (19%)	0	2
43	CV	132/140 (94%)	116 (88%)	13 (10%)	3 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
44	CM	157/166 (95%)	123 (78%)	20 (13%)	14 (9%)	1	11
45	Ca	147/149 (99%)	116 (79%)	17 (12%)	14 (10%)	0	10
46	CN	201/204 (98%)	175 (87%)	20 (10%)	6 (3%)	4	28
47	CI	215/218 (99%)	176 (82%)	19 (9%)	20 (9%)	0	10
48	CD	288/299 (96%)	242 (84%)	20 (7%)	26 (9%)	1	11
49	CQ	185/188 (98%)	153 (83%)	18 (10%)	14 (8%)	1	13
50	CR	201/203 (99%)	187 (93%)	7 (4%)	7 (4%)	3	25
51	CA	251/256 (98%)	205 (82%)	27 (11%)	19 (8%)	1	13
52	CS	171/177 (97%)	131 (77%)	18 (10%)	22 (13%)	0	5
53	CT	156/159 (98%)	122 (78%)	17 (11%)	17 (11%)	0	7
54	CP	183/186 (98%)	154 (84%)	16 (9%)	13 (7%)	1	14
55	CU	114/299 (38%)	88 (77%)	18 (16%)	8 (7%)	1	14
56	CX	118/277 (43%)	96 (81%)	15 (13%)	7 (6%)	1	17
57	CY	129/149 (87%)	113 (88%)	9 (7%)	7 (5%)	2	19
58	CW	128/155 (83%)	102 (80%)	12 (9%)	14 (11%)	0	7
59	CZ	132/135 (98%)	111 (84%)	15 (11%)	6 (4%)	2	22
60	Cr	132/144 (92%)	88 (67%)	22 (17%)	22 (17%)	0	3
61	Ch	121/123 (98%)	99 (82%)	10 (8%)	12 (10%)	0	9
62	Cb	73/76 (96%)	53 (73%)	11 (15%)	9 (12%)	0	5
63	CB	412/416 (99%)	325 (79%)	56 (14%)	31 (8%)	1	13
64	CF	227/252 (90%)	195 (86%)	17 (8%)	15 (7%)	1	15
65	Cc	98/111 (88%)	91 (93%)	3 (3%)	4 (4%)	3	22
66	Cd	109/124 (88%)	91 (84%)	14 (13%)	4 (4%)	3	25
67	Ce	130/134 (97%)	101 (78%)	16 (12%)	13 (10%)	0	9
68	Cf	155/157 (99%)	115 (74%)	14 (9%)	26 (17%)	0	3
69	Cg	111/162 (68%)	92 (83%)	12 (11%)	7 (6%)	1	16
70	Ci	111/115 (96%)	82 (74%)	16 (14%)	13 (12%)	0	6
71	Cj	90/93 (97%)	75 (83%)	9 (10%)	6 (7%)	1	15
72	Ck	68/70 (97%)	61 (90%)	4 (6%)	3 (4%)	2	22
73	Cl	48/51 (94%)	40 (83%)	4 (8%)	4 (8%)	1	12
74	CC	390/401 (97%)	309 (79%)	36 (9%)	45 (12%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
75	Cm	50/52 (96%)	38 (76%)	6 (12%)	6 (12%)	0	6
76	Cn	23/25 (92%)	22 (96%)	0	1 (4%)	2	22
77	Cp	89/92 (97%)	77 (86%)	8 (9%)	4 (4%)	2	22
78	Co	102/104 (98%)	79 (78%)	10 (10%)	13 (13%)	0	5
79	CJ	180/184 (98%)	139 (77%)	17 (9%)	24 (13%)	0	4
80	CH	188/190 (99%)	160 (85%)	16 (8%)	12 (6%)	1	16
81	CE	226/243 (93%)	149 (66%)	34 (15%)	43 (19%)	0	2
82	CG	239/271 (88%)	197 (82%)	22 (9%)	20 (8%)	1	11
All	All	13015/14439 (90%)	10459 (80%)	1348 (10%)	1208 (9%)	1	10

5 of 1208 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	Az	5	THR
1	Az	15	LYS
1	Az	44	GLY
1	Az	54	THR
1	Az	82	GLU

### 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	Az	721/726 (99%)	667 (92%)	54 (8%)	13	38
2	Ag	280/280 (100%)	268 (96%)	12 (4%)	29	54
3	AU	95/108 (88%)	93 (98%)	2 (2%)	53	72
4	AK	88/132 (67%)	80 (91%)	8 (9%)	9	30
5	AO	103/118 (87%)	92 (89%)	11 (11%)	6	24
6	AX	116/116 (100%)	109 (94%)	7 (6%)	19	44
7	AM	104/119 (87%)	98 (94%)	6 (6%)	20	45
8	AS	123/136 (90%)	120 (98%)	3 (2%)	49	69

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	Ad	45/47 (96%)	43 (96%)	2 (4%)	28	53
10	AN	130/131 (99%)	122 (94%)	8 (6%)	18	43
11	AL	138/138 (100%)	130 (94%)	8 (6%)	20	45
12	AR	108/118 (92%)	98 (91%)	10 (9%)	9	29
13	AP	111/130 (85%)	105 (95%)	6 (5%)	22	47
14	AT	125/127 (98%)	113 (90%)	12 (10%)	8	27
15	AB	199/233 (85%)	182 (92%)	17 (8%)	10	33
16	AA	190/271 (70%)	178 (94%)	12 (6%)	18	43
17	AV	67/68 (98%)	61 (91%)	6 (9%)	9	30
18	AY	105/110 (96%)	103 (98%)	2 (2%)	57	75
19	AZ	67/100 (67%)	57 (85%)	10 (15%)	3	15
20	Aa	94/101 (93%)	92 (98%)	2 (2%)	53	72
21	Ab	72/72 (100%)	69 (96%)	3 (4%)	30	54
22	Ac	54/57 (95%)	50 (93%)	4 (7%)	13	38
23	AD	192/210 (91%)	179 (93%)	13 (7%)	16	41
24	Ae	47/108 (44%)	45 (96%)	2 (4%)	29	54
25	Af	70/70 (100%)	58 (83%)	12 (17%)	2	11
26	AJ	161/169 (95%)	152 (94%)	9 (6%)	21	46
27	AE	220/220 (100%)	209 (95%)	11 (5%)	24	49
28	AC	188/209 (90%)	178 (95%)	10 (5%)	22	48
29	AG	200/216 (93%)	185 (92%)	15 (8%)	13	38
30	AF	161/193 (83%)	156 (97%)	5 (3%)	40	62
31	AH	175/175 (100%)	157 (90%)	18 (10%)	7	25
32	AW	113/114 (99%)	107 (95%)	6 (5%)	22	48
33	AI	175/176 (99%)	167 (95%)	8 (5%)	27	52
34	AQ	122/122 (100%)	115 (94%)	7 (6%)	20	46
35	Ah	51/100 (51%)	47 (92%)	4 (8%)	12	36
38	Cz	190/191 (100%)	173 (91%)	17 (9%)	9	31
39	Cq	186/186 (100%)	170 (91%)	16 (9%)	10	33
40	CK	131/137 (96%)	126 (96%)	5 (4%)	33	57
41	CO	175/175 (100%)	158 (90%)	17 (10%)	8	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
42	CL	173/180 (96%)	157 (91%)	16 (9%)	9	29
43	CV	101/106 (95%)	100 (99%)	1 (1%)	76	86
44	CM	138/142 (97%)	124 (90%)	14 (10%)	7	25
45	Ca	122/122 (100%)	112 (92%)	10 (8%)	11	34
46	CN	174/175 (99%)	165 (95%)	9 (5%)	23	48
47	CI	187/188 (100%)	181 (97%)	6 (3%)	39	62
48	CD	241/248 (97%)	234 (97%)	7 (3%)	42	64
49	CQ	164/165 (99%)	151 (92%)	13 (8%)	12	36
50	CR	176/176 (100%)	171 (97%)	5 (3%)	43	65
51	CA	195/198 (98%)	180 (92%)	15 (8%)	13	37
52	CS	156/159 (98%)	142 (91%)	14 (9%)	9	30
53	CT	137/138 (99%)	129 (94%)	8 (6%)	20	45
54	CP	160/161 (99%)	153 (96%)	7 (4%)	28	53
55	CU	108/203 (53%)	104 (96%)	4 (4%)	34	58
56	CX	106/205 (52%)	102 (96%)	4 (4%)	33	57
57	CY	116/130 (89%)	114 (98%)	2 (2%)	60	78
58	CW	107/124 (86%)	100 (94%)	7 (6%)	17	42
59	CZ	121/122 (99%)	108 (89%)	13 (11%)	6	24
60	Cr	112/120 (93%)	102 (91%)	10 (9%)	9	31
61	Ch	112/112 (100%)	110 (98%)	2 (2%)	59	77
62	Cb	67/68 (98%)	62 (92%)	5 (8%)	13	38
63	CB	349/350 (100%)	335 (96%)	14 (4%)	31	55
64	CF	203/222 (91%)	194 (96%)	9 (4%)	28	53
65	Cc	84/93 (90%)	78 (93%)	6 (7%)	14	39
66	Cd	103/114 (90%)	96 (93%)	7 (7%)	16	41
67	Ce	120/122 (98%)	108 (90%)	12 (10%)	7	26
68	Cf	123/123 (100%)	111 (90%)	12 (10%)	8	27
69	Cg	104/137 (76%)	97 (93%)	7 (7%)	16	41
70	Ci	100/101 (99%)	89 (89%)	11 (11%)	6	23
71	Cj	77/78 (99%)	67 (87%)	10 (13%)	4	18
72	Ck	65/65 (100%)	59 (91%)	6 (9%)	9	29

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	Cl	45/46 (98%)	43 (96%)	2 (4%)	28	53
74	CC	323/329 (98%)	294 (91%)	29 (9%)	9	30
75	Cm	48/48 (100%)	47 (98%)	1 (2%)	53	72
76	Cn	23/23 (100%)	21 (91%)	2 (9%)	10	31
77	Cp	74/75 (99%)	71 (96%)	3 (4%)	30	55
78	Co	94/94 (100%)	89 (95%)	5 (5%)	22	48
79	CJ	155/157 (99%)	148 (96%)	7 (4%)	27	52
80	CH	169/169 (100%)	156 (92%)	13 (8%)	13	37
81	CE	197/208 (95%)	177 (90%)	20 (10%)	7	25
82	CG	210/237 (89%)	196 (93%)	14 (7%)	16	41
All	All	11331/12242 (93%)	10589 (94%)	742 (6%)	21	42

5 of 742 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
51	CA	69	TYR
64	CF	248	LEU
52	CS	7	LEU
51	CA	49	ILE
58	CW	77	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 147 such sidechains are listed below:

Mol	Chain	Res	Type
64	CF	62	ASN
81	CE	236	GLN
65	Cc	51	ASN
74	CC	234	ASN
26	AJ	133	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
36	B2	1794/1995 (89%)	501 (27%)	117 (6%)
37	BC	74/75 (98%)	12 (16%)	3 (4%)
83	A5	3568/3970 (89%)	947 (26%)	263 (7%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
84	A9	29/30 (96%)	7 (24%)	2 (6%)
85	A7	119/120 (99%)	23 (19%)	5 (4%)
86	A8	122/123 (99%)	18 (14%)	4 (3%)
All	All	5706/6313 (90%)	1508 (26%)	394 (6%)

5 of 1508 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
36	B2	2	U
36	B2	3	U
36	B2	4	C
36	B2	8	U
36	B2	16	G

5 of 394 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
83	A5	1407	C
83	A5	2200	A
83	A5	1522	G
83	A5	1793	C
83	A5	2750	A

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.



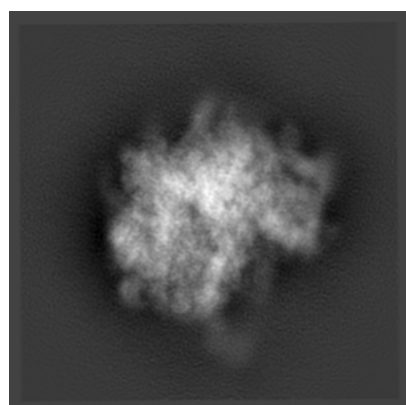
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5591. These allow visual inspection of the internal detail of the map and identification of artifacts.

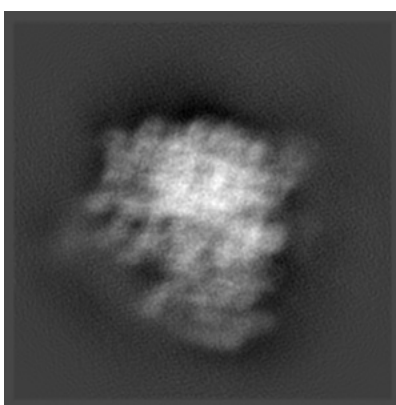
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

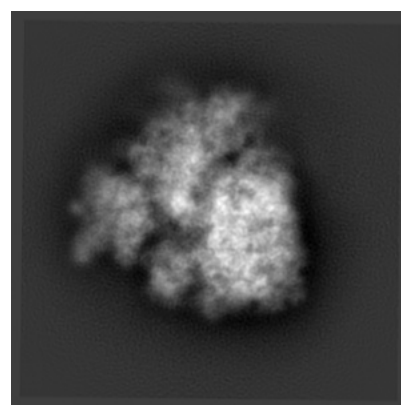
#### 6.1.1 Primary map



X



Y

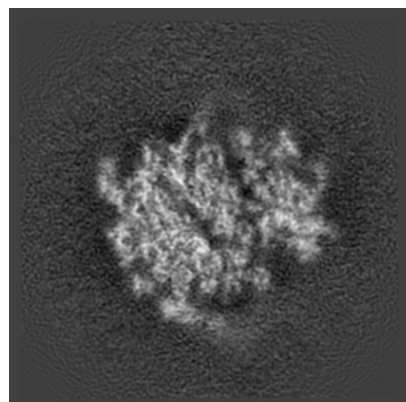


Z

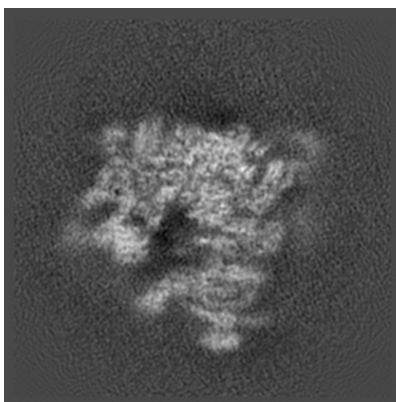
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

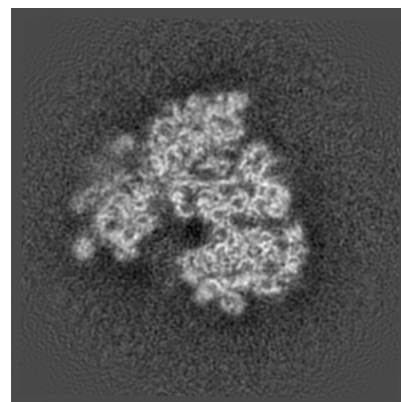
#### 6.2.1 Primary map



X Index: 184



Y Index: 184

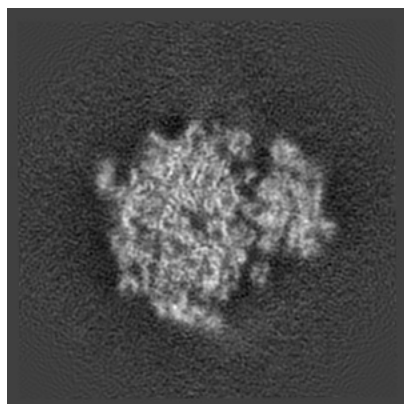


Z Index: 184

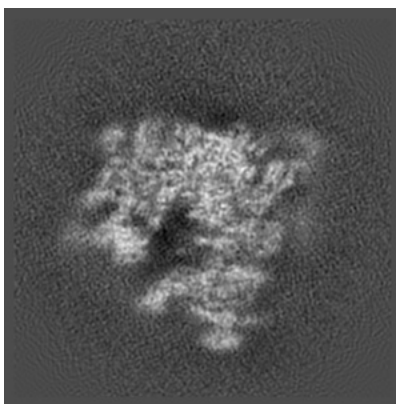
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

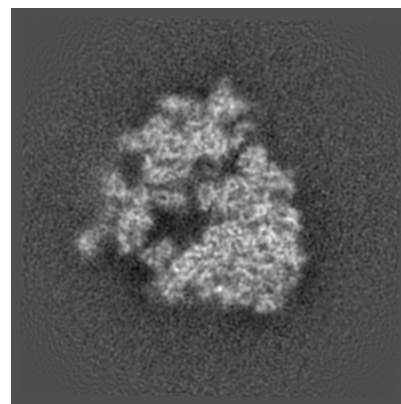
### 6.3.1 Primary map



X Index: 190



Y Index: 183



Z Index: 172

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

## 6.4 Orthogonal surface views [i](#)

### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.49. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

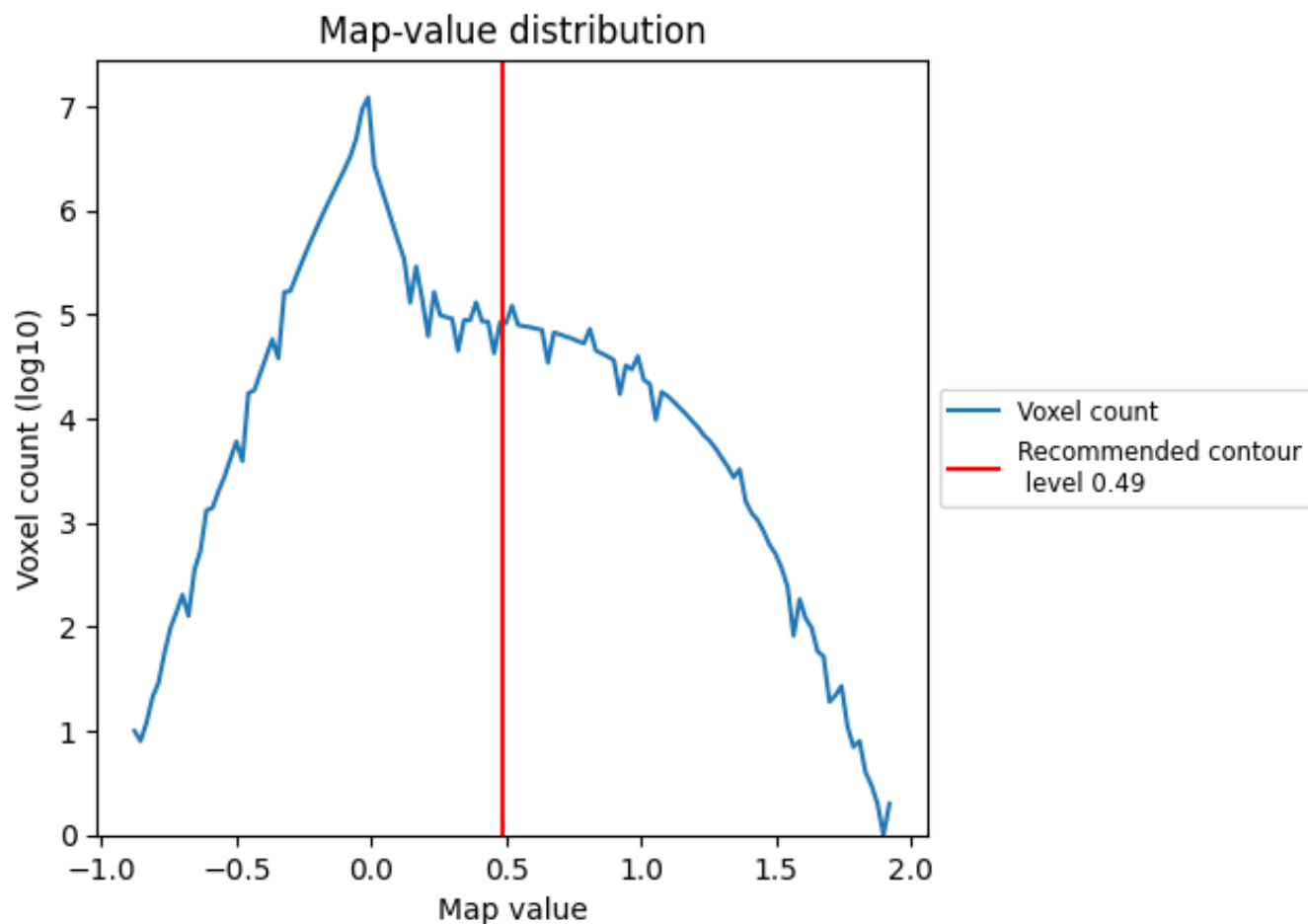
## 6.5 Mask visualisation

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

## 7 Map analysis [i](#)

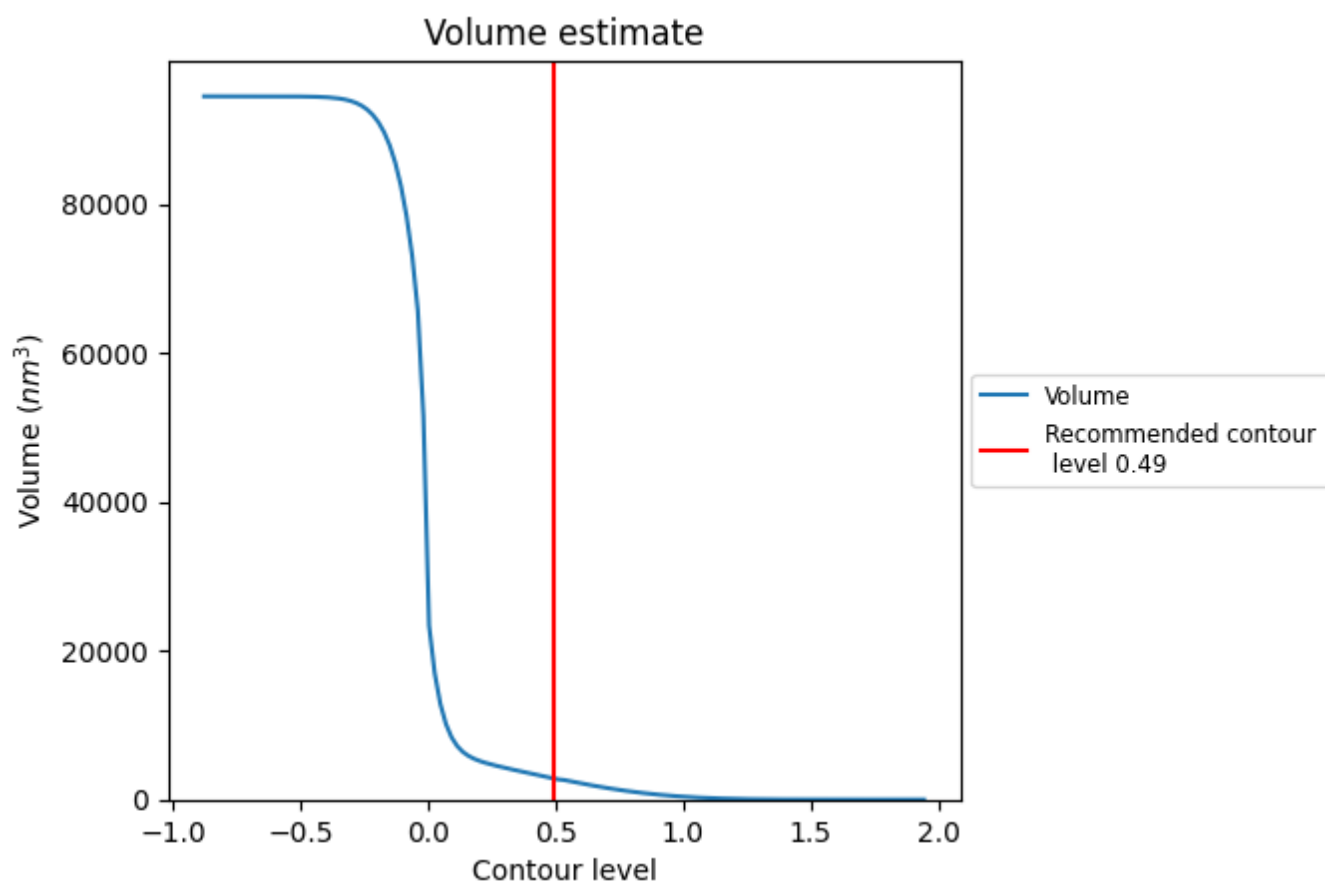
This section contains the results of statistical analysis of the map.

### 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.

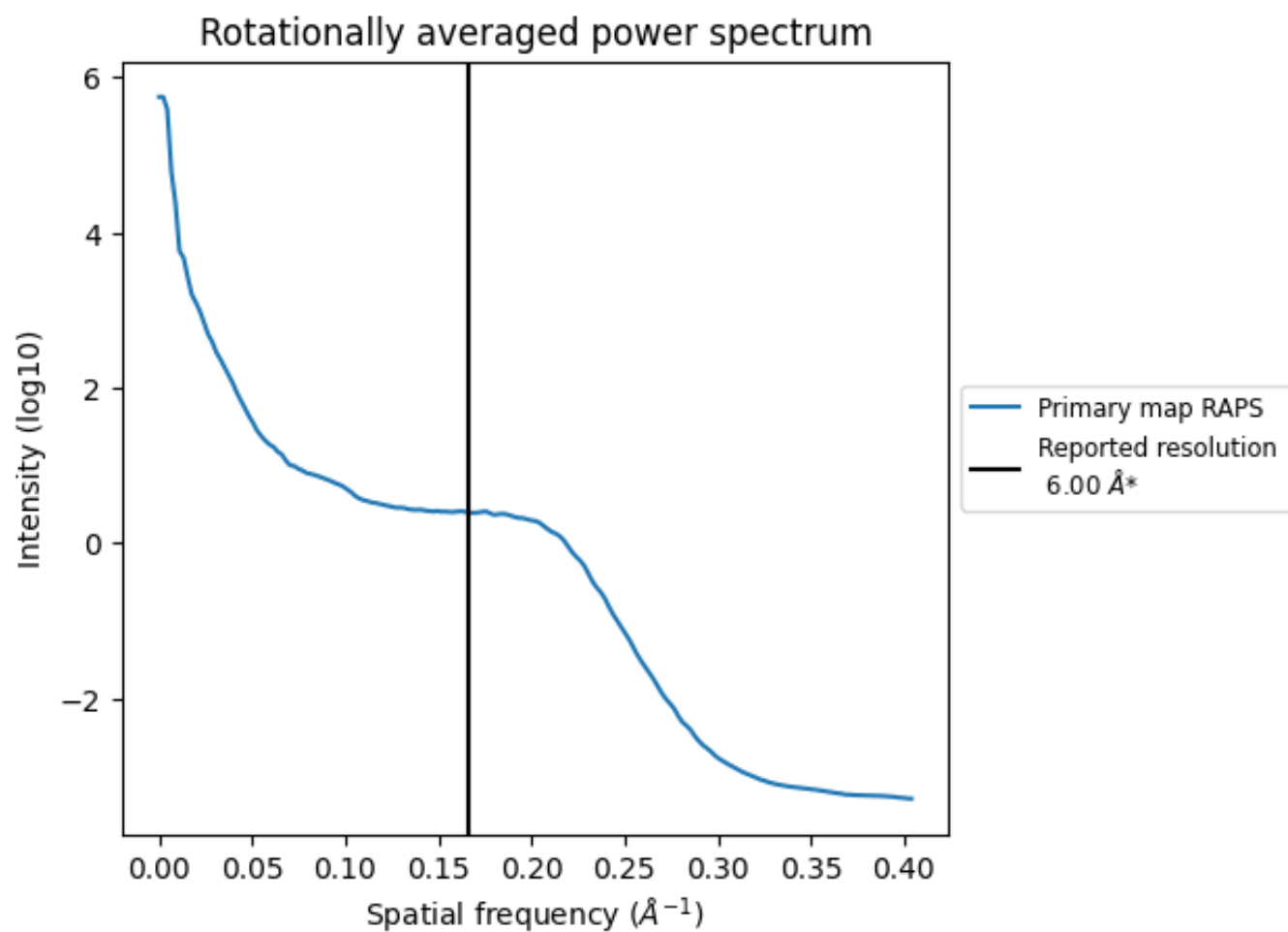
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2852 nm<sup>3</sup>; this corresponds to an approximate mass of 2576 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 0.167 Å<sup>-1</sup>

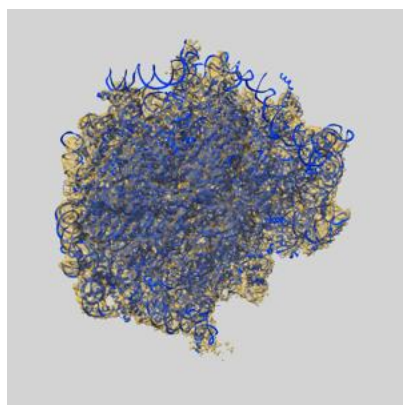
## 8 Fourier-Shell correlation

This section was not generated. No FSC curve or half-maps provided.

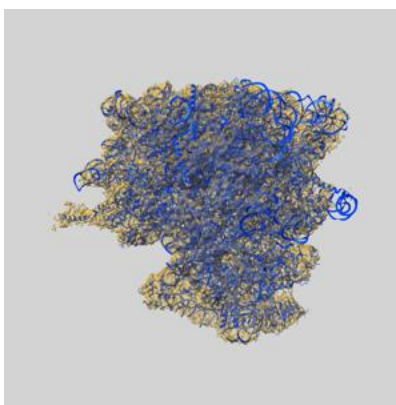
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5591 and PDB model 4V6W. Per-residue inclusion information can be found in section [3](#) on page [21](#).

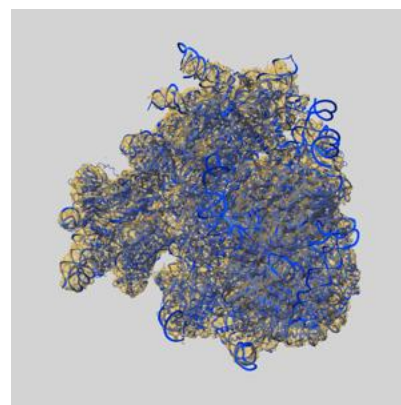
### 9.1 Map-model overlay [i](#)



X



Y

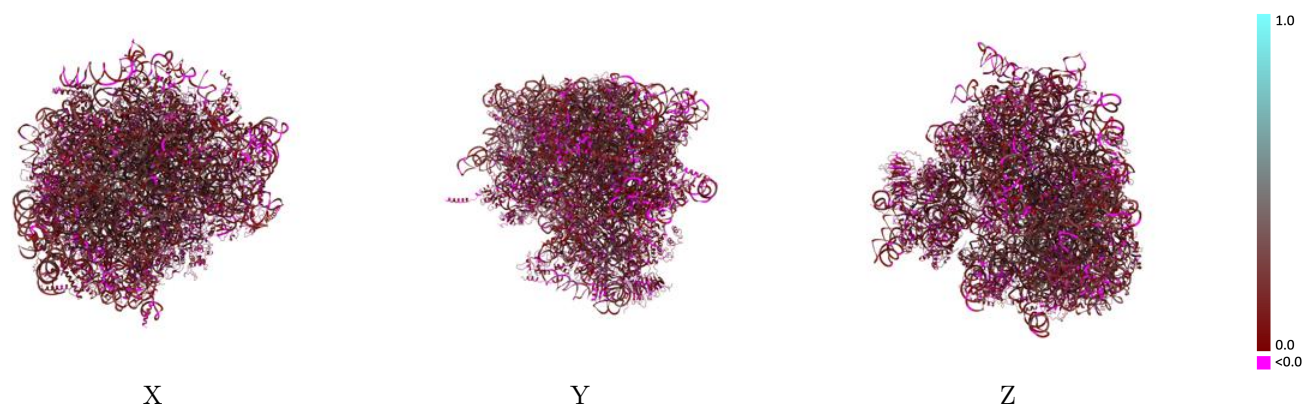


Z

The images above show the 3D surface view of the map at the recommended contour level 0.49 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.

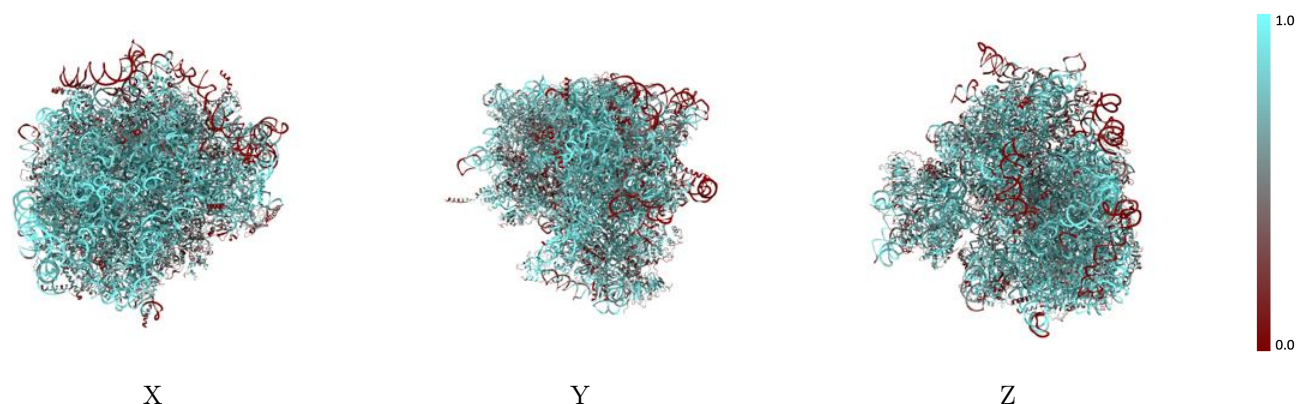


## 9.2 Q-score mapped to coordinate model [i](#)



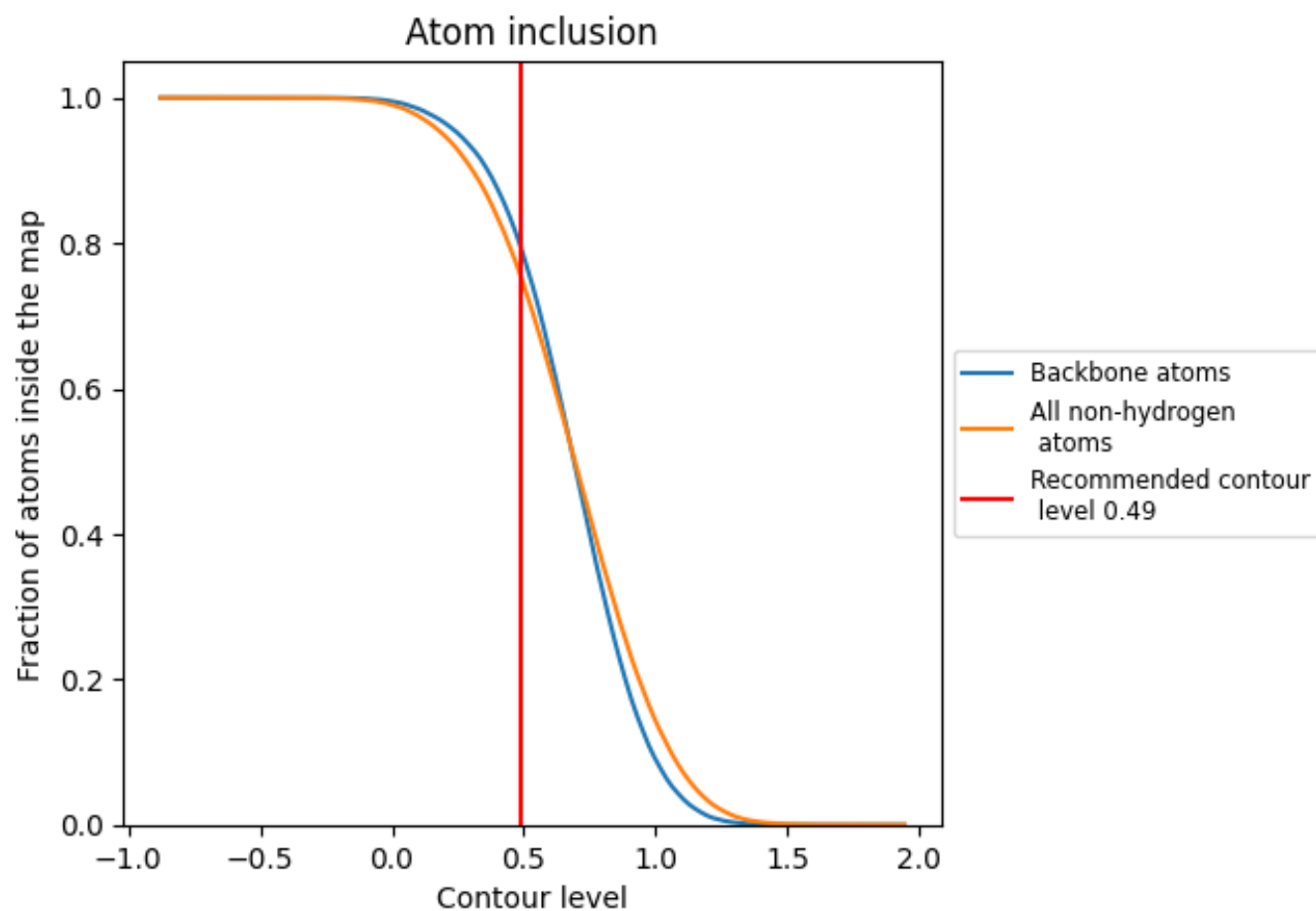
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.49).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 79% 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 (0.49) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7528	 0.1570
A5	 0.8875	 0.2040
A7	 0.9448	 0.2030
A8	 0.9252	 0.2330
A9	 0.8216	 0.2100
AA	 0.6569	 0.1060
AB	 0.5773	 0.0940
AC	 0.5684	 0.1340
AD	 0.4870	 0.1230
AE	 0.6539	 0.1060
AF	 0.5939	 0.0880
AG	 0.5125	 0.0690
AH	 0.6117	 0.1000
AI	 0.4733	 0.0910
AJ	 0.7222	 0.1220
AK	 0.8141	 0.1170
AL	 0.5216	 0.0890
AM	 0.7374	 0.0940
AN	 0.5954	 0.1050
AO	 0.5889	 0.0500
AP	 0.4214	 0.0960
AQ	 0.5711	 0.0960
AR	 0.4407	 0.1060
AS	 0.5940	 0.1060
AT	 0.5528	 0.0950
AU	 0.6190	 0.1120
AV	 0.5738	 0.1020
AW	 0.6498	 0.1020
AX	 0.6129	 0.1020
AY	 0.5320	 0.0900
AZ	 0.6267	 0.1060
Aa	 0.6378	 0.1240
Ab	 0.6448	 0.1240
Ac	 0.6660	 0.0940
Ad	 0.7101	 0.0920























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Chain	Atom inclusion	Q-score
Ae	 0.4378	 0.1370
Af	 0.5770	 0.0610
Ag	 0.5916	 0.1010
Ah	 0.4280	 0.0890
Az	 0.4648	 0.1100
B2	 0.8706	 0.1770
BC	 0.7146	 0.1770
CA	 0.7250	 0.1370
CB	 0.6331	 0.1340
CC	 0.6905	 0.1210
CD	 0.6853	 0.1110
CE	 0.6224	 0.1160
CF	 0.6430	 0.1340
CG	 0.5217	 0.1280
CH	 0.4969	 0.1400
CI	 0.5550	 0.1330
CJ	 0.5232	 0.1410
CK	 0.5293	 0.1020
CL	 0.6260	 0.1150
CM	 0.6614	 0.1170
CN	 0.8286	 0.1090
CO	 0.6451	 0.1390
CP	 0.6660	 0.1160
CQ	 0.7570	 0.1090
CR	 0.6424	 0.1390
CS	 0.5928	 0.1190
CT	 0.6330	 0.1250
CU	 0.4223	 0.1090
CV	 0.4173	 0.1400
CW	 0.3245	 0.1040
CX	 0.4053	 0.1310
CY	 0.6927	 0.1370
CZ	 0.5868	 0.1250
Ca	 0.7406	 0.1160
Cb	 0.7362	 0.1450
Cc	 0.6724	 0.1420
Cd	 0.7281	 0.1300
Ce	 0.7176	 0.1490
Cf	 0.5727	 0.0630
Cg	 0.6799	 0.1540
Ch	 0.5371	 0.1190
Ci	 0.7092	 0.1360

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Chain	Atom inclusion	Q-score
Cj	 0.7397	 0.1370
Ck	 0.5595	 0.0880
Cl	 0.7212	 0.1180
Cm	 0.5205	 0.1570
Cn	 0.6744	 0.1080
Co	 0.6706	 0.0950
Cp	 0.6272	 0.1340
Cq	 0.6165	 0.0900
Cr	 0.6143	 0.1170
Cz	 0.3547	 0.0350