



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 06:49 PM UTC

PDB ID : 3J7P / pdb_00003j7p
EMDB ID : EMD-2646
Title : Structure of the 80S mammalian ribosome bound to eEF2
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.
Deposited on : 2014-08-01
Resolution : 3.50 Å (reported)
Based on initial models : 3J3A, 3J3B, 3J3D, 3J3F

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

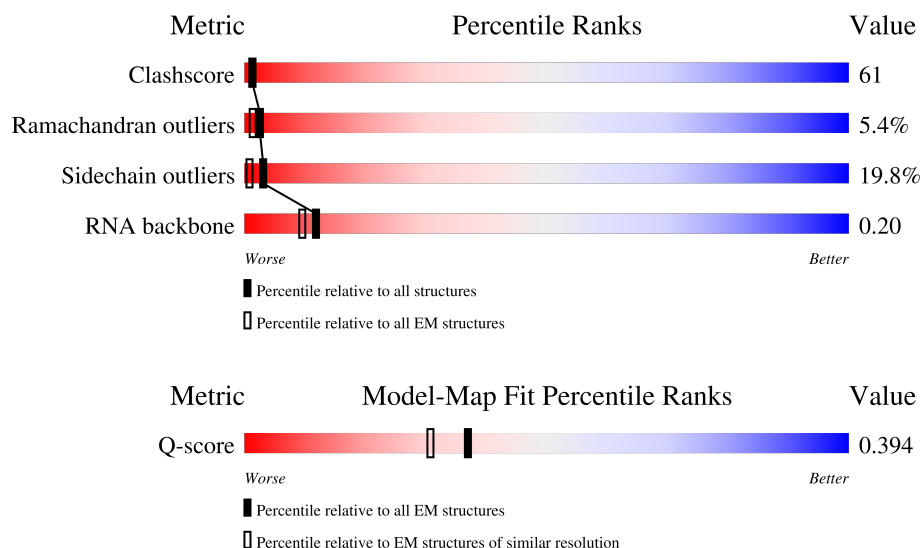
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.50 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.



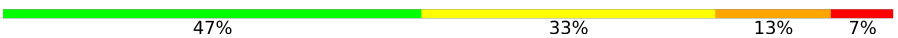
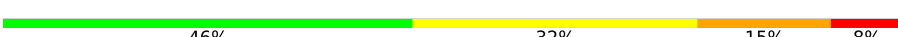
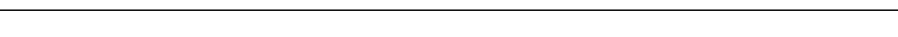
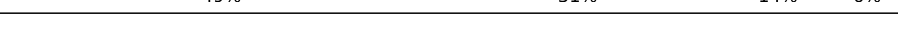
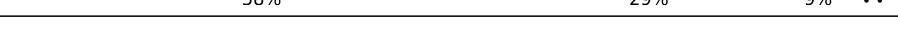
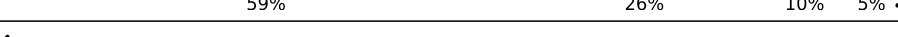
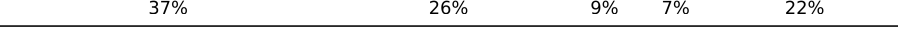
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	5	3664	
2	7	120	
3	8	156	

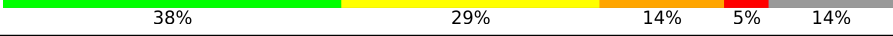
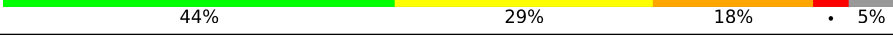
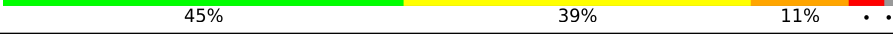
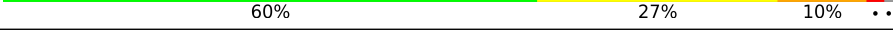
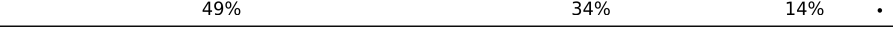
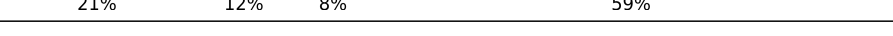
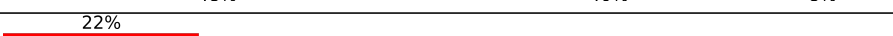
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Mol	Chain	Length	Quality of chain
4	A	257	
5	B	394	
6	C	367	
7	D	297	
8	E	236	
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	K	163	
15	L	211	
16	M	213	
17	N	204	
18	O	204	
19	P	153	
20	Q	188	
21	R	196	
22	S	224	
23	T	160	
24	U	128	
25	V	140	
26	W	157	
27	X	156	
28	Y	145	

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Mol	Chain	Length	Quality of chain
29	Z	136	
30	a	148	
31	b	160	
32	c	115	
33	d	125	
34	e	135	
35	f	110	
36	g	117	
37	h	123	
38	i	105	
39	j	86	
40	k	70	
41	l	51	
42	m	128	
43	n	25	
44	o	106	
45	p	91	
46	q	202	
47	r	125	
48	4	856	
49	S2	1742	
50	SA	295	
51	SB	264	
52	SC	218	
53	SD	243	

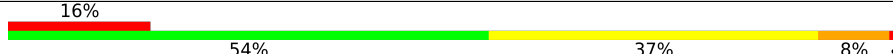
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Mol	Chain	Length	Quality of chain
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	
58	SI	208	
59	SJ	194	
60	SK	165	
61	SL	158	
62	SM	124	
63	SN	151	
64	SO	151	
65	SP	145	
66	SQ	146	
67	SR	135	
68	SS	152	
69	ST	145	
70	SU	119	
71	SV	83	
72	SW	130	
73	SX	143	
74	SY	132	
75	SZ	125	
76	Sa	115	
77	Sb	84	
78	Sc	69	

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Mol	Chain	Length	Quality of chain
79	Sd	56	
80	Se	133	
81	Sf	156	
82	Sg	317	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
84	ZN	Sa	201	-	-	X	-
84	ZN	m	201	-	-	X	-

2 Entry composition

There are 84 unique types of molecules in this entry. The entry contains 221686 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 RNA chain called 28S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	5	3662	Total	C	N	O	P	0	0
			78486	34947	14363	25515	3661		

- Molecule 2 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	7	120	Total	C	N	O	P	0	0
			2558	1141	456	842	119		

- Molecule 3 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	8	156	Total	C	N	O	P	0	0
			3314	1480	585	1094	155		

- Molecule 4 is a protein called Ribosomal protein uL2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	A	244	Total	C	N	O	S	0	0
			1868	1171	382	309	6		

- Molecule 5 is a protein called Ribosomal protein uL3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	B	394	Total	C	N	O	S	0	0
			3147	2005	591	538	13		

- Molecule 6 is a protein called Ribosomal protein uL4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	C	367	Total	C	N	O	S	0	0
			2919	1836	582	486	15		

- Molecule 7 is a protein called Ribosomal protein uL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	D	292	Total	C	N	O	S	0	0
			2380	1508	434	426	12		

- Molecule 8 is a protein called Ribosomal protein eL6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	E	236	Total	C	N	O	S	0	0
			1904	1219	364	316	5		

- Molecule 9 is a protein called Ribosomal protein uL30.

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

- Molecule 10 is a protein called Ribosomal protein eL8.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	G	241	Total	C	N	O	S	0	0
			1934	1232	372	326	4		

- Molecule 11 is a protein called Ribosomal protein uL6.

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

- Molecule 12 is a protein called Ribosomal protein uL16.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	I	213	Total	C	N	O	S	0	0
			1713	1083	331	284	15		

- Molecule 13 is a protein called Ribosomal protein uL5.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	J	170	Total	C	N	O	S	0	0
			1359	856	256	241	6		

- Molecule 14 is a protein called Ribosomal protein uL11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	K	151	Total	C	N	O	S	0	0
			1140	708	215	213	4		

- Molecule 15 is a protein called Ribosomal protein eL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	L	210	Total	C	N	O	S	0	0
			1703	1064	354	280	5		

- Molecule 16 is a protein called Ribosomal protein eL14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	M	138	Total	C	N	O	S	0	0
			1131	727	216	181	7		

- Molecule 17 is a protein called Ribosomal protein eL15.

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

- Molecule 18 is a protein called Ribosomal protein uL13.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	O	201	Total	C	N	O	S	0	0
			1651	1063	323	260	5		

- Molecule 19 is a protein called Ribosomal protein uL22.

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

- Molecule 20 is a protein called Ribosomal protein eL18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	Q	187	Total	C	N	O	S	0	0
			1506	941	311	249	5		

- Molecule 21 is a protein called Ribosomal protein eL19.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	R	180	Total	C	N	O	S	0	0
			1508	933	328	238	9		

- Molecule 22 is a protein called Ribosomal protein eL20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	S	175	Total	C	N	O	S	0	0
			1454	925	284	235	10		

- Molecule 23 is a protein called Ribosomal protein eL21.

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

- Molecule 24 is a protein called Ribosomal protein eL22.

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

- Molecule 25 is a protein called Ribosomal protein uL14.

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

- Molecule 26 is a protein called Ribosomal protein eL24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	W	63	Total	C	N	O	S	0	0
			528	337	103	85	3		

- Molecule 27 is a protein called Ribosomal protein uL23.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	X	119	Total	C	N	O	S	0	0
			976	624	183	168	1		

- Molecule 28 is a protein called Ribosomal protein uL24.

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

- Molecule 29 is a protein called Ribosomal protein eL27.

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

- Molecule 30 is a protein called Ribosomal protein uL15.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	147	Total	C	N	O	S	0	0
			1163	735	239	185	4		

- Molecule 31 is a protein called Ribosomal protein eL29.

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

- Molecule 32 is a protein called Ribosomal protein eL30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	c	94	Total	C	N	O	S	0	0
			732	465	130	131	6		

- Molecule 33 is a protein called Ribosomal protein eL31.

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

- Molecule 34 is a protein called Ribosomal protein eL32.

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

- Molecule 35 is a protein called Ribosomal protein eL33.

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

- Molecule 36 is a protein called Ribosomal protein eL34.

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

- Molecule 37 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	122	Total	C	N	O	S	0	0
			1015	642	205	167	1		

- Molecule 38 is a protein called Ribosomal protein eL36.

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

- Molecule 39 is a protein called Ribosomal protein eL37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	86	Total	C	N	O	S	0	0
			706	436	155	110	5		

- Molecule 40 is a protein called Ribosomal protein eL38.

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

- Molecule 41 is a protein called Ribosomal protein eL39.

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

- Molecule 42 is a protein called Ribosomal protein eL40.

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

- Molecule 43 is a protein called Ribosomal protein eL41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	n	23	Total	C	N	O	S	0	0
			222	134	61	25	2		

- Molecule 44 is a protein called Ribosomal protein eL42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	o	104	Total	C	N	O	S	0	0
			851	533	174	138	6		

- Molecule 45 is a protein called Ribosomal protein eL43.

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

- Molecule 46 is a protein called Ribosomal protein uL10.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	q	202	Total	C	N	O	S	0	0
			1556	989	272	286	9		

- Molecule 47 is a protein called Ribosomal protein eL28.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	125	Total	C	N	O	S	0	0
			1001	622	206	168	5		

- Molecule 48 is a protein called Eukaryotic elongation factor 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	4	856	Total	C	N	O	S	0	0
			6673	4234	1148	1247	44		

- Molecule 49 is a RNA chain called 18S ribosomal RNA.

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

- Molecule 50 is a protein called Ribosomal protein uS2.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	SA	208	Total	C	N	O	S	0	0
			1642	1045	289	300	8		

- Molecule 51 is a protein called Ribosomal protein eS1.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	SB	213	Total	C	N	O	S	0	0
			1725	1093	311	308	13		

- Molecule 52 is a protein called Ribosomal protein uS5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	SC	218	Total	C	N	O	S	0	0
			1690	1094	289	297	10		

- Molecule 53 is a protein called Ribosomal protein uS3.

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

- Molecule 54 is a protein called Ribosomal protein eS4.

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

- Molecule 55 is a protein called Ribosomal protein uS7.

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

- Molecule 56 is a protein called Ribosomal protein eS6.

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

- Molecule 57 is a protein called Ribosomal protein eS7.

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

- Molecule 58 is a protein called Ribosomal protein eS8.

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

- Molecule 59 is a protein called Ribosomal protein uS4.

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

- Molecule 60 is a protein called Ribosomal protein eS10.

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

- Molecule 61 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	SL	152	Total	C	N	O	S	0	0
			1238	788	232	212	6		

- Molecule 62 is a protein called Ribosomal protein eS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SM	124	Total	C	N	O	S	0	0
			960	600	171	181	8		

- Molecule 63 is a protein called Ribosomal protein uS15.

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

- Molecule 64 is a protein called Ribosomal protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	SO	136	Total	C	N	O	S	0	0
			1016	621	199	190	6		

- Molecule 65 is a protein called Ribosomal protein uS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	SP	96	Total	C	N	O	S	0	0
			805	506	158	135	6		

- Molecule 66 is a protein called Ribosomal protein uS9.

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

- Molecule 67 is a protein called Ribosomal protein eS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	SR	129	Total	C	N	O	S	0	0
			1047	658	193	191	5		

- Molecule 68 is a protein called Ribosomal protein uS13.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	SS	137	Total	C	N	O	S	0	0
			1139	714	231	193	1		

- Molecule 69 is a protein called Ribosomal protein eS19.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	ST	141	Total	C	N	O	S	0	0
			1101	690	212	196	3		

- Molecule 70 is a protein called Ribosomal protein uS10.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	SU	104	Total	C	N	O	S	0	0
			818	513	153	148	4		

- Molecule 71 is a protein called Ribosomal protein eS21.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	SV	82	Total	C	N	O	S	0	0
			625	384	116	120	5		

- Molecule 72 is a protein called Ribosomal protein uS8.

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

- Molecule 73 is a protein called Ribosomal protein uS12.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	SX	141	Total	C	N	O	S	0	0
			1099	694	220	182	3		

- Molecule 74 is a protein called Ribosomal protein eS24.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	SY	126	Total	C	N	O	S	0	0
			1023	646	200	172	5		

- Molecule 75 is a protein called Ribosomal protein es25.

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

- Molecule 76 is a protein called Ribosomal protein eS26.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	Sa	98	Total	C	N	O	S	0	0
			781	486	161	129	5		

- Molecule 77 is a protein called Ribosomal protein eS27.

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

- Molecule 78 is a protein called Ribosomal protein eS28.

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

- Molecule 79 is a protein called Ribosomal protein uS14.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	Sd	52	Total	C	N	O	S	0	0
			434	273	87	69	5		

- Molecule 80 is a protein called Ribosomal protein eS30.

Mol	Chain	Residues	Atoms					AltConf	Trace
80	Se	57	Total	C	N	O	S	0	0
			452	279	99	73	1		

- Molecule 81 is a protein called Ribosomal protein eS31.

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

- Molecule 82 is a protein called Ribosomal protein RACK1.

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

- Molecule 83 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
83	5	118	Total	Mg	0
			118	118	
83	7	5	Total	Mg	0
			5	5	
83	8	4	Total	Mg	0
			4	4	

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Mol	Chain	Residues	Atoms		AltConf
83	P	1	Total 1	Mg 1	0
83	V	1	Total 1	Mg 1	0
83	4	1	Total 1	Mg 1	0
83	S2	36	Total 36	Mg 36	0

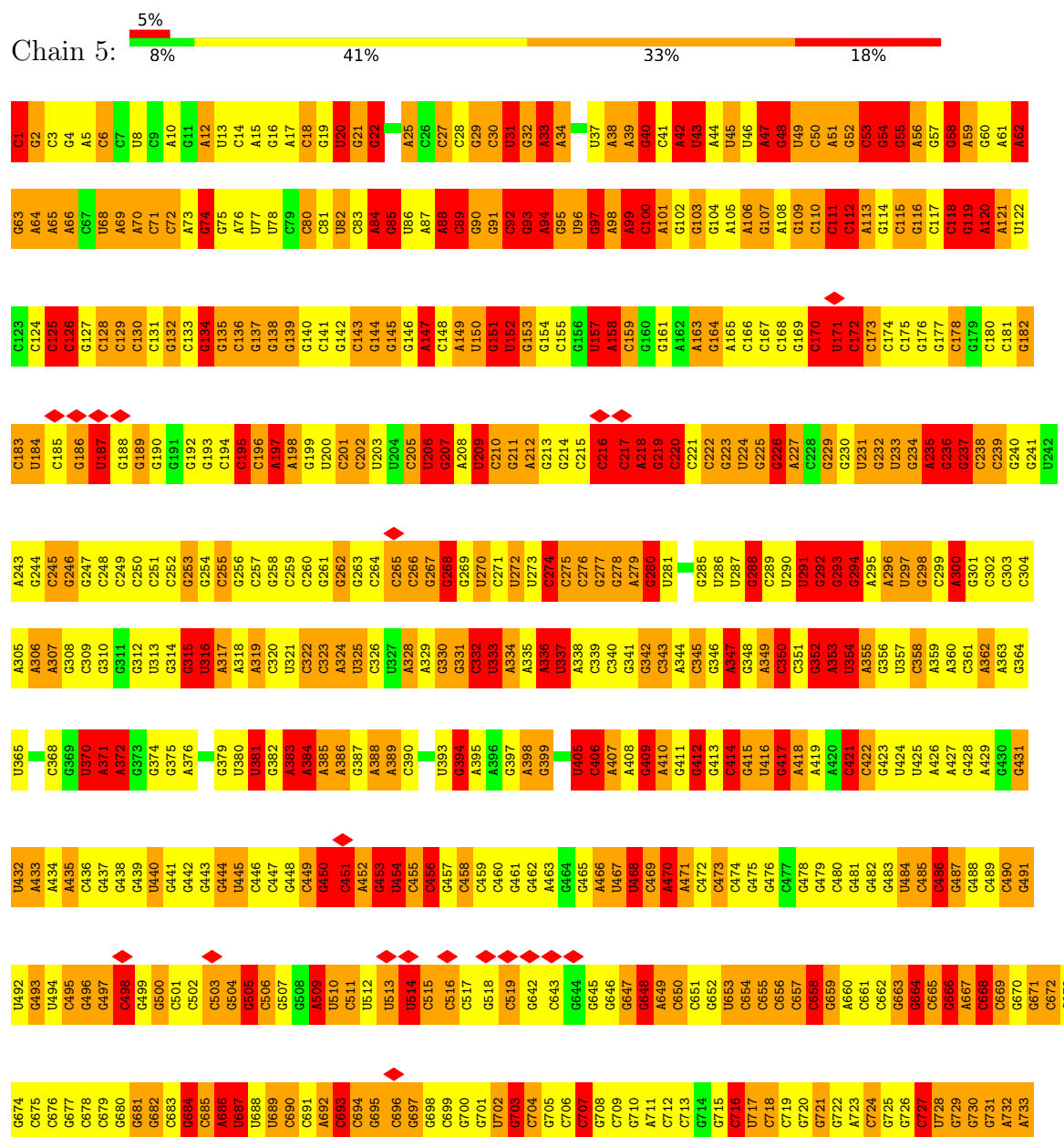
- Molecule 84 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
84	j	1	Total 1	Zn 1	0
84	m	1	Total 1	Zn 1	0
84	o	1	Total 1	Zn 1	0
84	Sa	1	Total 1	Zn 1	0

3 Residue-property plots

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

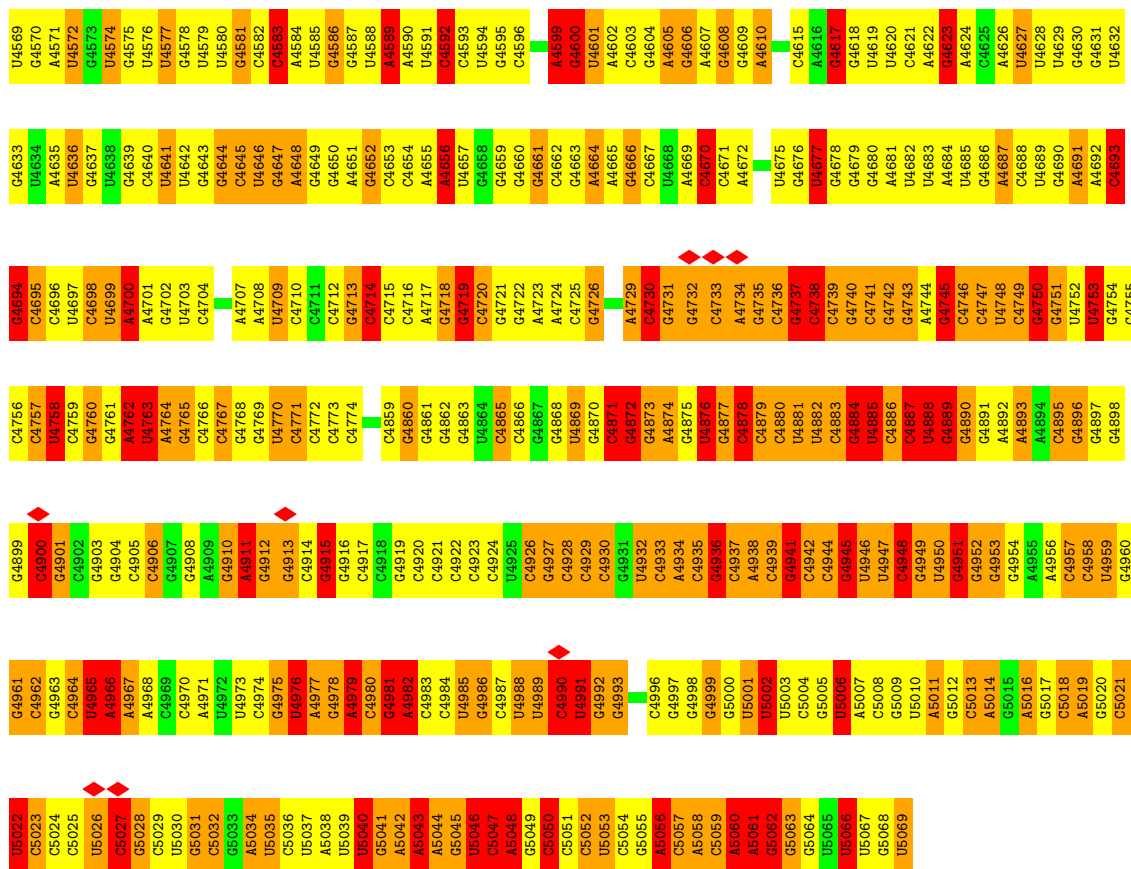
• Molecule 1: 28S ribosomal RNA



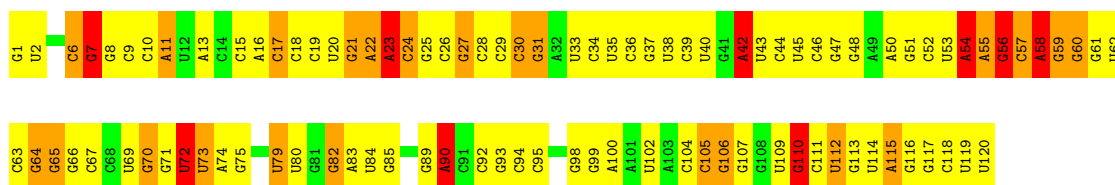
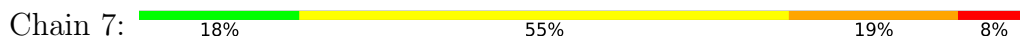




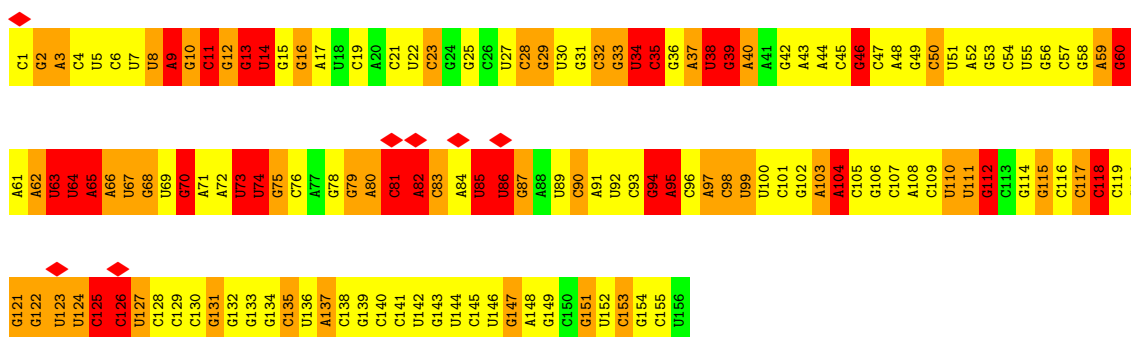
U4509	G4448	C4386	G4198	C4137	A4077	C3841	G3780	G3720	C3660	A2857
A4510	A4449	C4387	C4199	C4138	C4078	C3842	C3781	U3721	C3601	A2858
A4511	U4450	U4265	G4200	C4139	C4079	U3843	G3782	G3722	C3602	C2859
U4512	C4389	G4266	G4201	C4140	C4080	U3844	A3783	A3723	C3603	C2860
A4513	U4452	C4267	U4202	C4141	G4081	A3845	A3784	G3724	A3604	C2861
C4453	C4391	C4268	U4203	C4142	G4082	C3846	A3785	G3725	C3605	C2862
C4329	C4392	U4269	C4204	C4143	U4083	C3847	U3786	A3726	U3606	C2863
G4330	A4205	G4270	A4206	C4144	G4084	U3848	C3789	A3727	U3607	C2864
G4331	A4271	A4271	G4207	C4145	G4085	A3849	C3790	A3728	A3608	C2867
C4332	C4272	C4145	U4208	C4146	G4086	C3850	U3791	U3729	A3609	A2871
C4333	A4273	C4147	U4209	C4148	C4087	U3851	C3792	U3730	A3610	C2872
C4334	A4274	C4149	U4210	C4150	G4088	U3852	G3792	C3731	A3611	U2872
C4335	C4275	C4151	U4211	C4152	G4089	U3853	U3793	A3732	C3612	U2873
C4336	C4276	C4153	C4212	C4154	G4090	C3854	C3794	A3733	U3613	U2874
C4337	C4277	C4155	A4212	C4156	G4091	C3855	G3795	U3734	G3614	C2875
C4338	G4278	C4157	A4213	C4158	G4092	C3856	U3796	G3735	G3615	C2876
C4339	A4279	C4159	A4214	C4160	G4093	C3857	U3797	A3736	U3616	C2877
C4340	A4280	C4161	C4215	C4162	G4094	C3858	U3798	A3737	G3617	U2878
C4341	A4281	C4163	G4216	C4164	G4095	C3859	A3799	G3738	C3618	U2879
C4342	A4282	C4165	G4217	C4166	G4096	A3860	A3800	C3739	C3619	U2880
C4343	G4283	C4167	U4218	C4168	C4097	A3861	U3801	U3740	G3620	C2884
C4344	A4284	C4169	A4219	C4170	A4098	C3862	U3802	C3741	A3621	C2888
C4345	U4285	C4171	A4220	C4172	G4099	C3863	A3803	G3742	C3622	C2889
C4346	U4286	C4173	A4221	C4174	C4100	C3864	G3804	G3743	C3623	C2892
G4347	G4287	C4175	G4222	C4176	C4101	C3865	G3805	G3744	A3624	C2889
A4348	C4288	C4177	C4223	C4178	C4102	C3866	G3806	U3745	G3625	C2890
C4349	U4289	C4179	A4224	C4179	C4103	A3867	A3807	A3746	G3626	C2891
C4350	U4290	C4180	G4225	C4181	C4104	C3868	U3808	A3747	G3627	C2892
U4351	G4291	C4182	A4226	C4183	G4105	C3869	G3809	A3748	G3628	A2895
C4352	A4292	C4184	U4227	C4184	A4106	C3870	C3810	C3749	A3629	C2896
U4353	U4293	C4185	U4228	C4185	C4107	C3871	G3811	G3750	A3630	C2897
U4354	C4294	C4186	U4229	C4186	C4108	A3872	C3812	C3751	U3631	C2898
G4355	U4295	C4187	U4230	C4187	G4109	G3873	C3813	C3752	C3632	C2899
G4356	U4296	C4188	C4231	C4188	C4110	C3874	U3814	G3753	C3633	C2899
U4360	U4297	C4189	U4232	C4189	C4111	C3875	G3815	G3754	A3634	U2904
U4361	U4298	C4190	A4233	C4190	U4112	A3876	A3816	C3755	A3635	C2905
A4362	U4300	C4191	A4234	C4191	C4113	C3877	A3817	A3756	C3636	G2906
A4363	U4301	C4192	G4235	C4192	U4114	C3878	U3818	G3757	U3637	C2907
G4367	U4302	C4193	G4236	C4193	C4115	C3879	G3819	U3758	U3638	U2908
A4368	A4303	C4194	A4237	C4194	G4116	C3880	G3820	A3759	U3639	C2909
A4369	G4305	C4195	G4238	C4195	U4117	C3881	A3821	C3760	U3640	U2909
U4370	U4306	C4196	G4239	C4196	U4118	C3882	U3822	C3761	U3641	C2909
A4371	A4307	C4197	U4240	C4197	C4119	U3883	G3823	U3762	A3642	C2909
C4372	C4308	C4198	U4241	C4198	U4120	C3884	A3824	A3763	A3643	G2910
C4373	C4309	C4199	U4242	C4199	G4121	C3885	A3825	U3764	U3644	C3583
C4374	A4310	C4200	C4243	C4200	C4122	C3886	G3826	A3765	U3645	A3647
U4375	A4311	C4201	A4244	C4201	G4123	C3887	A3827	C3766	A3646	C3584
C4376	U4312	C4202	G4245	C4202	C4124	C3888	G3828	C3767	A3647	C3585
A4377	A4313	C4203	A4246	C4203	G4125	C3889	A3829	U3768	A3648	C3586
G4377	C4314	C4204	U4247	C4204	C4126	A3890	A3830	C3769	A3649	C3587
A4378	U4315	C4205	G4248	C4205	U4127	A3891	U3831	U3770	C3650	C3588
A4379	A4316	C4206	G4249	C4206	A4128	C3892	U3832	C3771	A3651	C3589
C4440	C4317	C4207	A4250	C4207	U4129	C3893	C3833	U3772	A3652	C3590
A4380	A4318	C4208	G4251	C4208	A4130	C3894	C3834	U3773	C3653	G3591
A4381	C4319	C4209	A4252	C4209	U4131	C3895	C3835	A3774	G3654	C3591
U4442	C4320	C4210	U4253	C4210	C4132	C3896	A3836	A3775	A3655	C3592
C4443	U4321	C4211	A4254	C4211	G4133	C3897	C3837	C3776	A3656	C3593
C4444	C4322	C4212	G4255	C4212	C4134	C3898	U3838	U3777	U3657	C3594
C4447	U4260	C4213	U4256	C4213	G4135	C3899	U3839	A3778	C3658	U3595
A4385		C4214	U4257	C4214	C4136	G3900	U3840	A3779	C3659	A3596
		C4215	C4258	C4215						C3597
		C4216	U4259	C4216						A3599



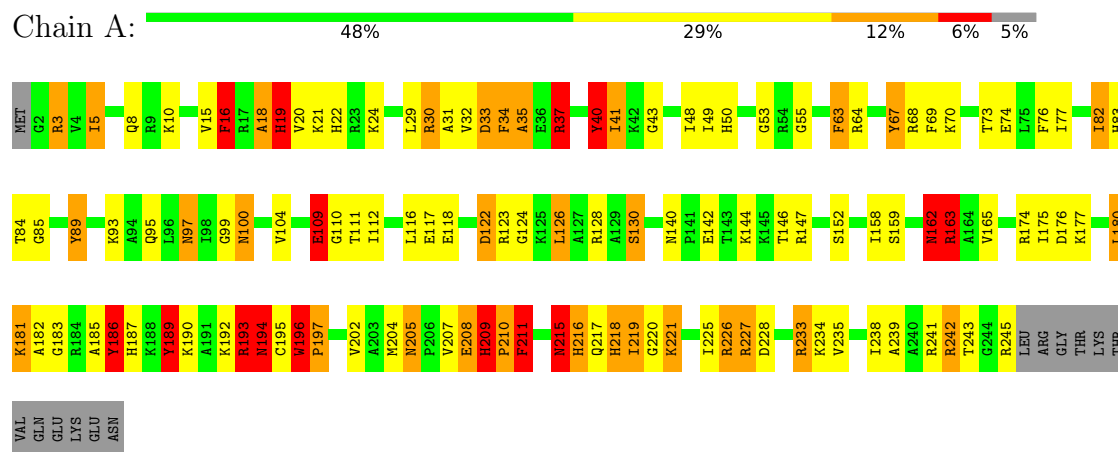
• Molecule 2: 5S ribosomal RNA



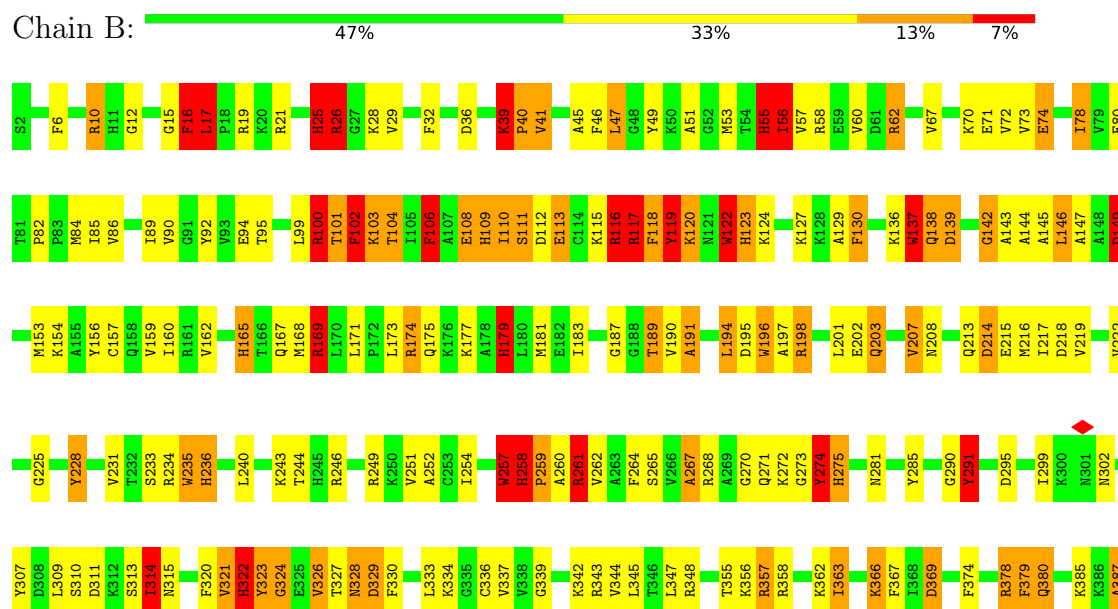
• Molecule 3: 5.8S ribosomal RNA



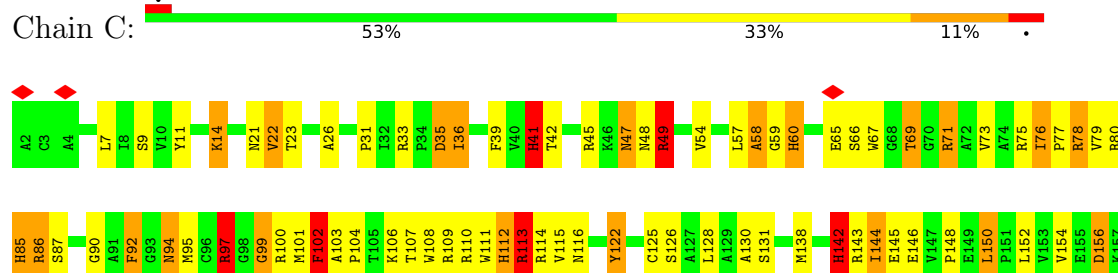
- Molecule 4: Ribosomal protein uL2

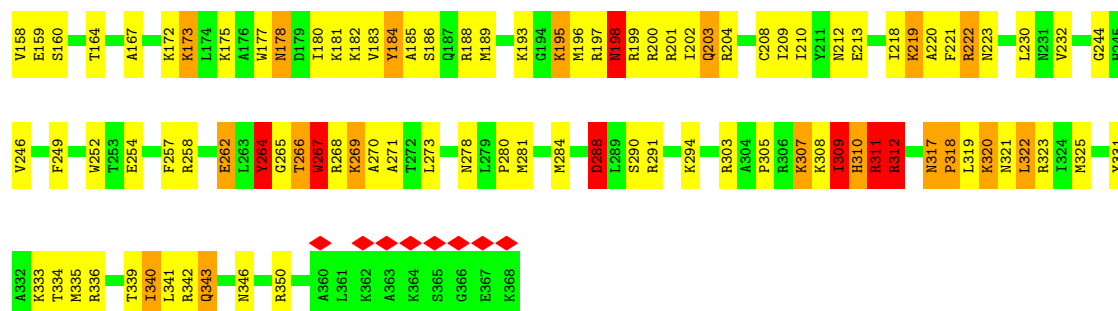


- Molecule 5: Ribosomal protein uL3

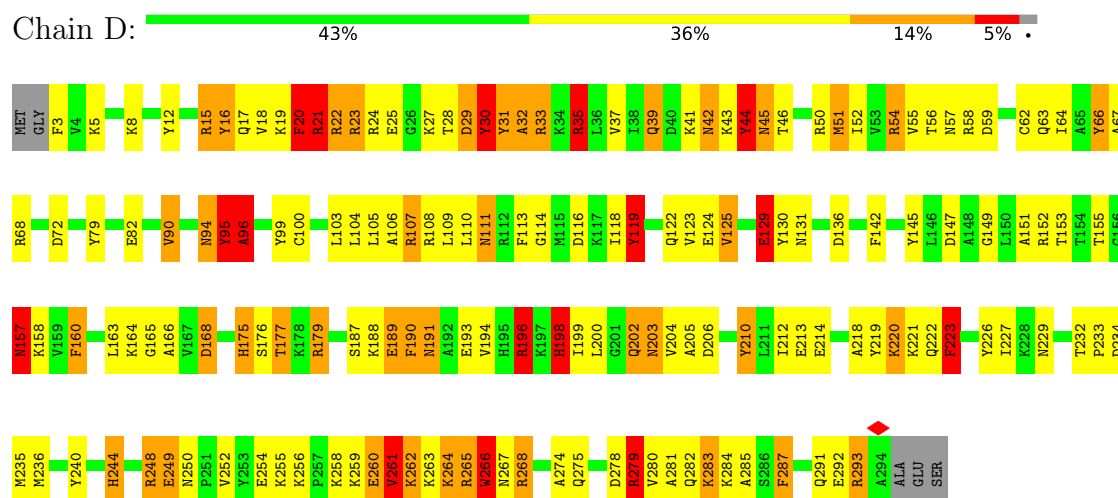


- Molecule 6: Ribosomal protein uL4

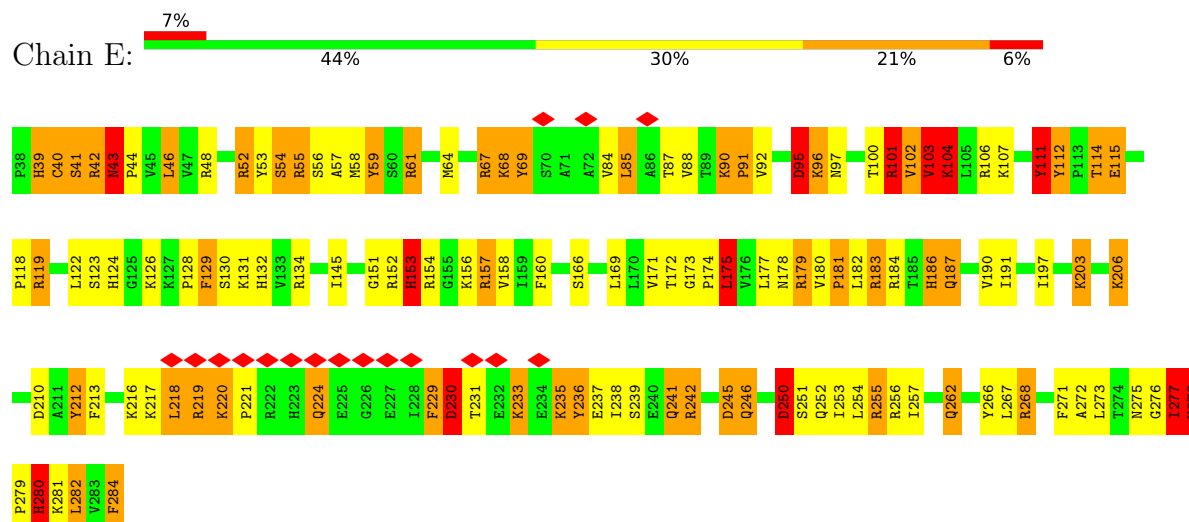




• Molecule 7: Ribosomal protein uL18

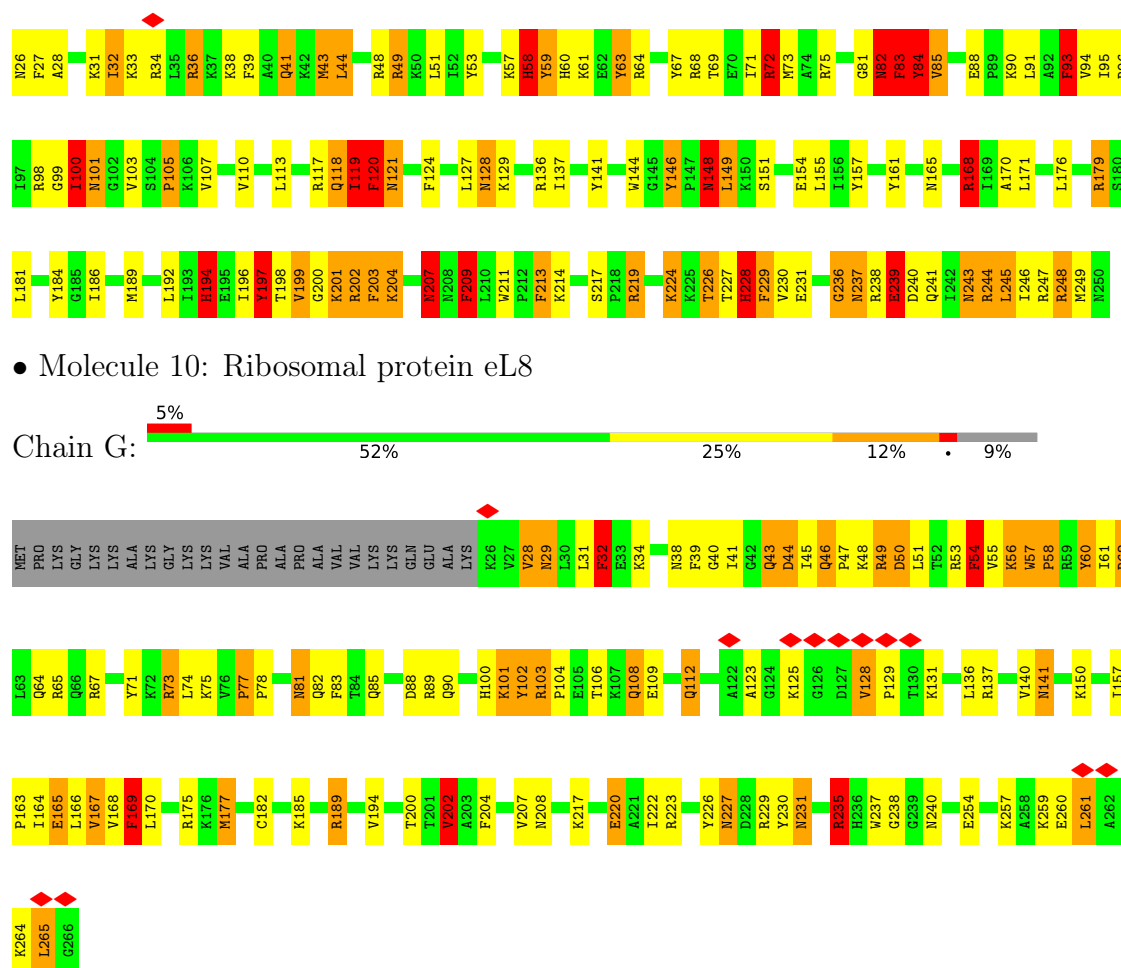


• Molecule 8: Ribosomal protein eL6

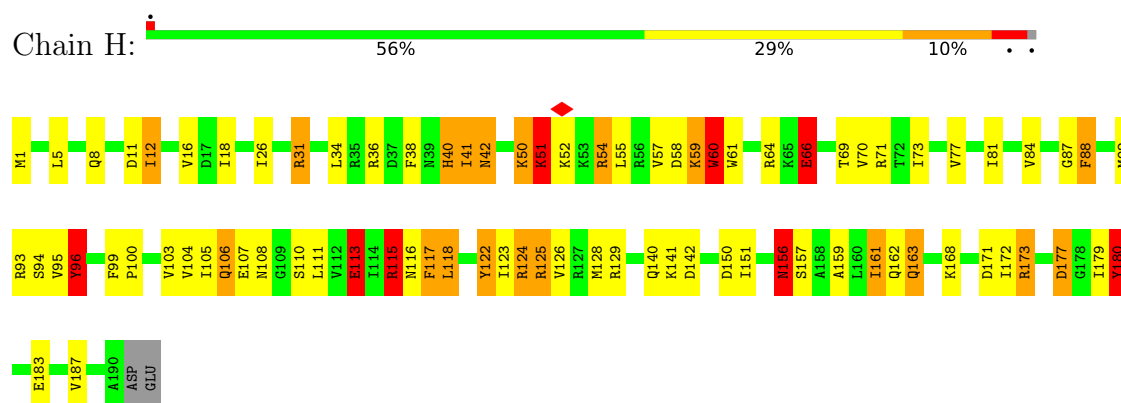


• Molecule 9: Ribosomal protein uL30

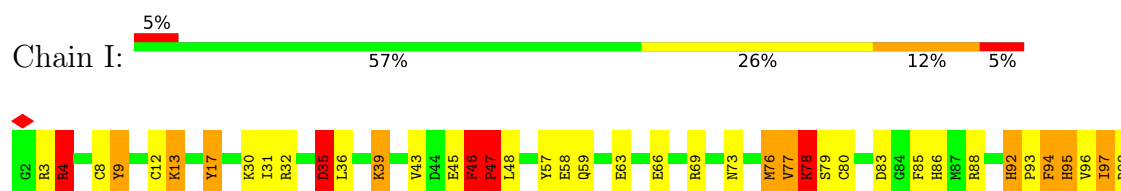


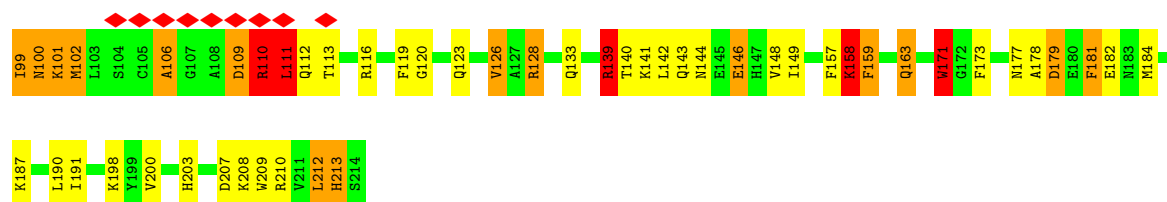


• Molecule 11: Ribosomal protein uL6

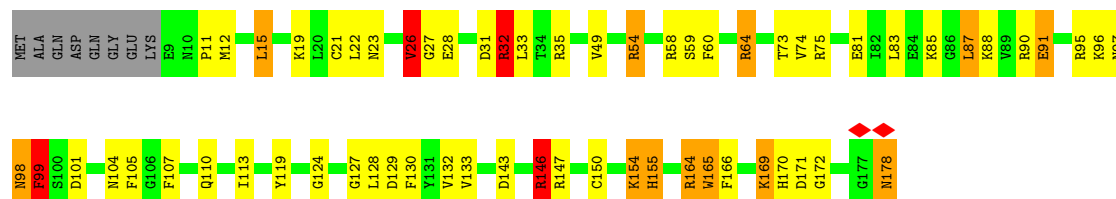


• Molecule 12: Ribosomal protein uL16

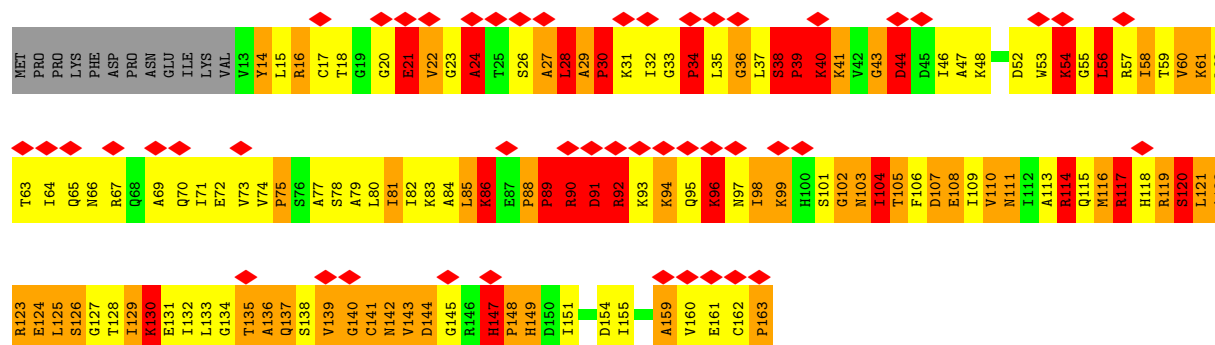




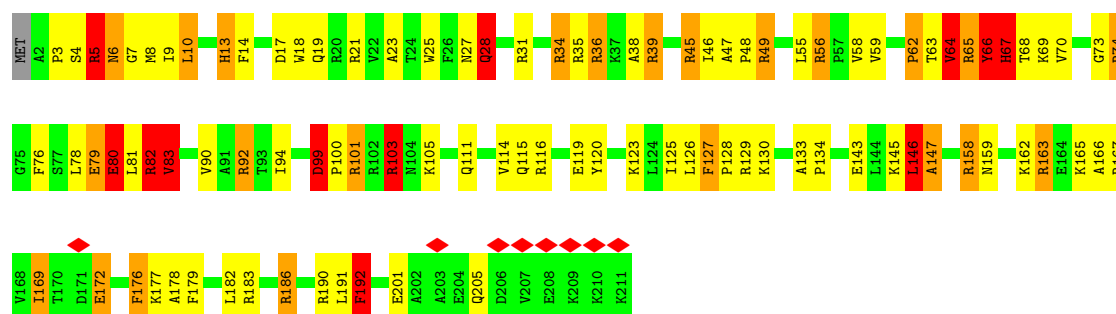
• Molecule 13: Ribosomal protein uL5



• Molecule 14: Ribosomal protein uL11

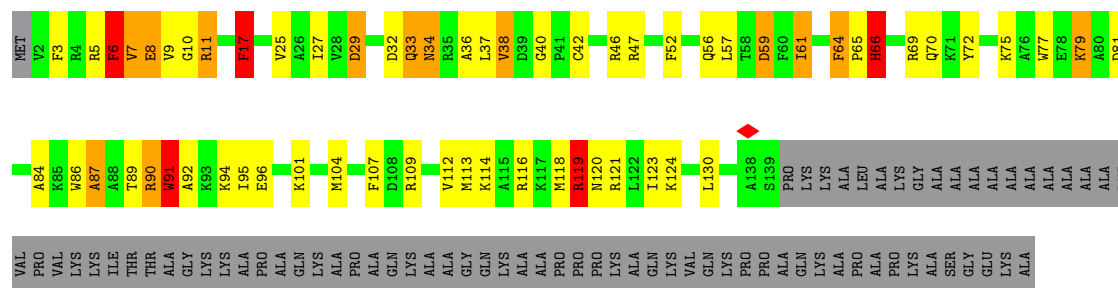


• Molecule 15: Ribosomal protein eL13

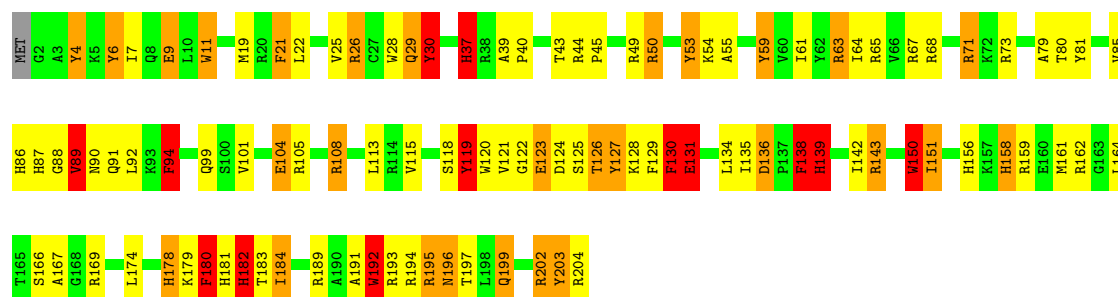


• Molecule 16: Ribosomal protein eL14

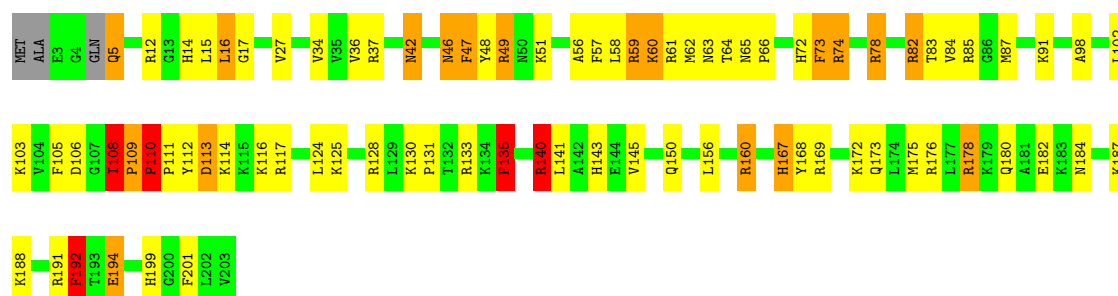




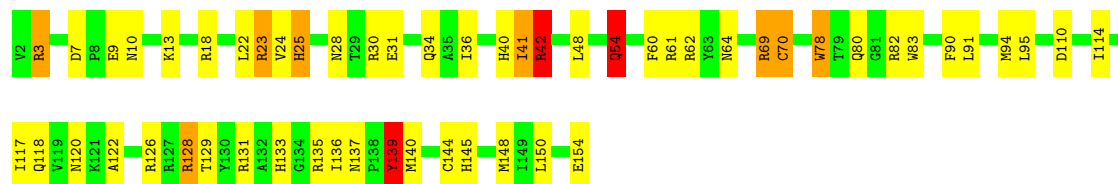
• Molecule 17: Ribosomal protein eL15



• Molecule 18: Ribosomal protein uL13

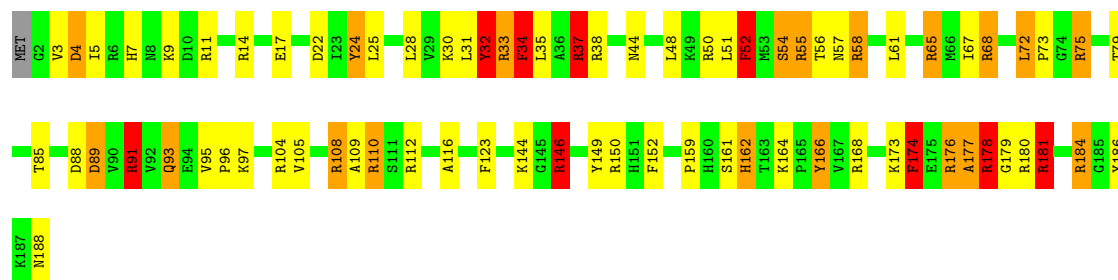


• Molecule 19: Ribosomal protein uL22

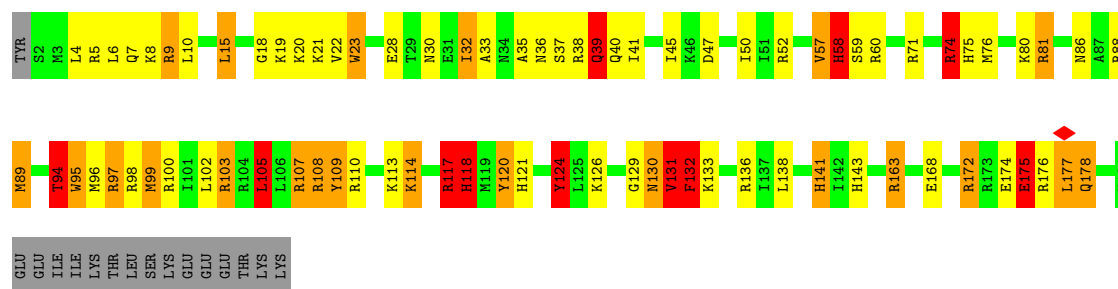


• Molecule 20: Ribosomal protein eL18

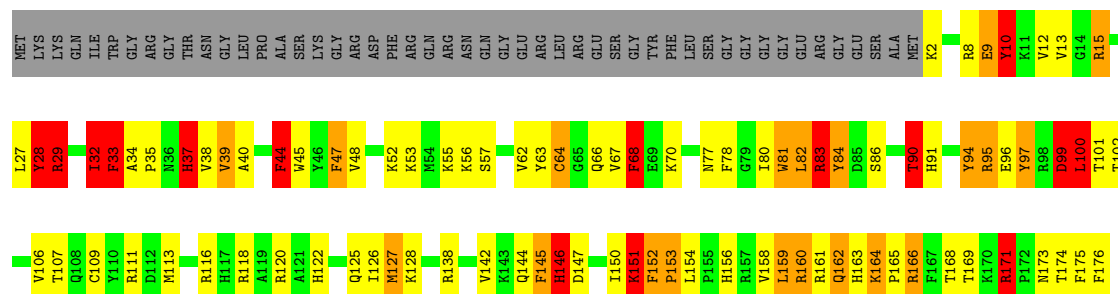




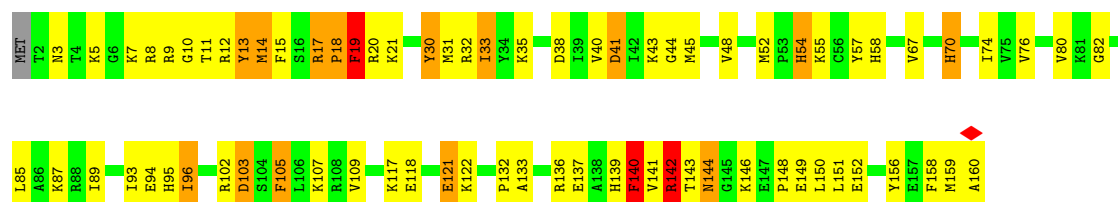
• Molecule 21: Ribosomal protein eL19



• Molecule 22: Ribosomal protein eL20

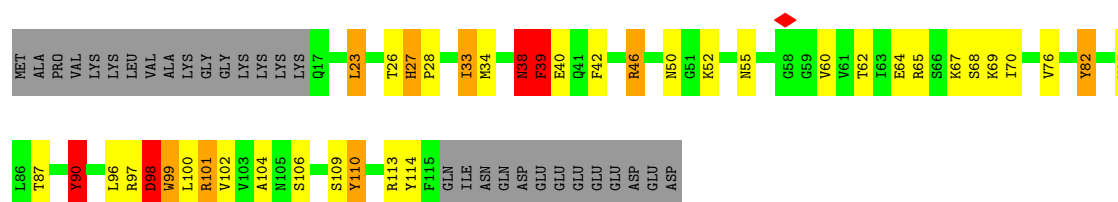


• Molecule 23: Ribosomal protein eL21



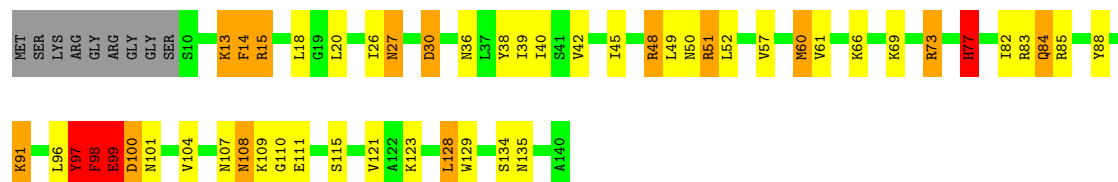
• Molecule 24: Ribosomal protein eL22





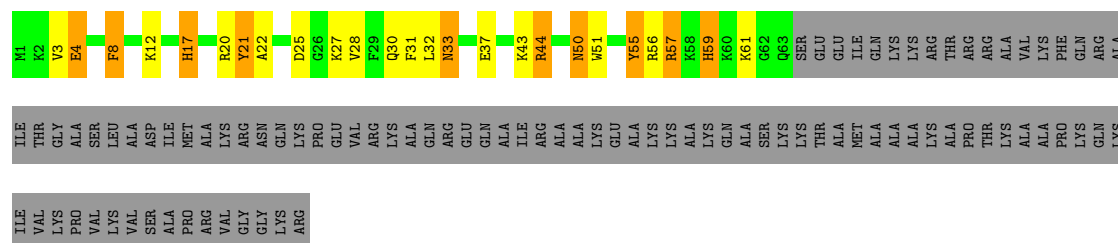
• Molecule 25: Ribosomal protein uL14

Chain V: 57% 24% 10% 6%



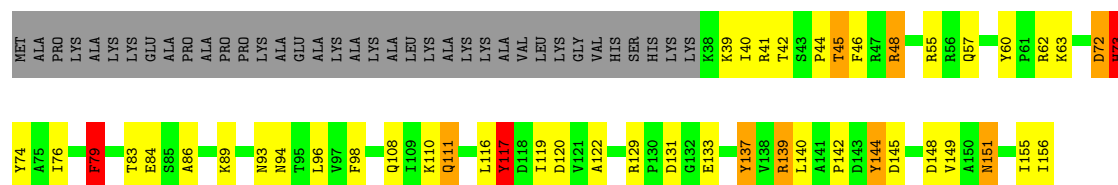
• Molecule 26: Ribosomal protein eL24

Chain W: 24% 10% 6% 60%



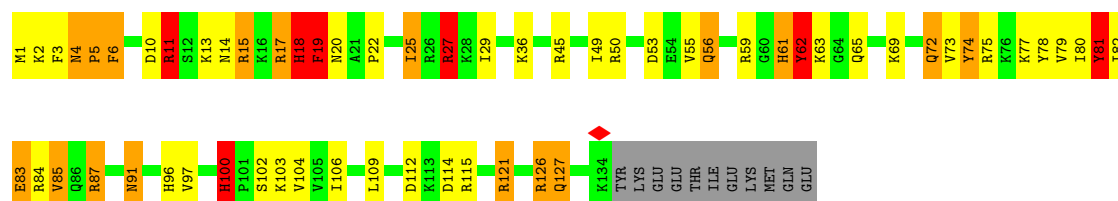
• Molecule 27: Ribosomal protein uL23

Chain X: 46% 24% 5% 24%

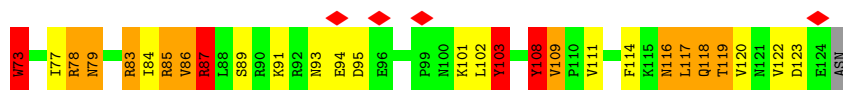


• Molecule 28: Ribosomal protein uL24

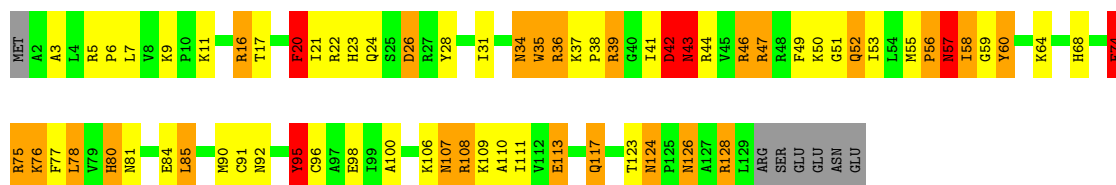
Chain Y: 50% 26% 12% 5% 8%



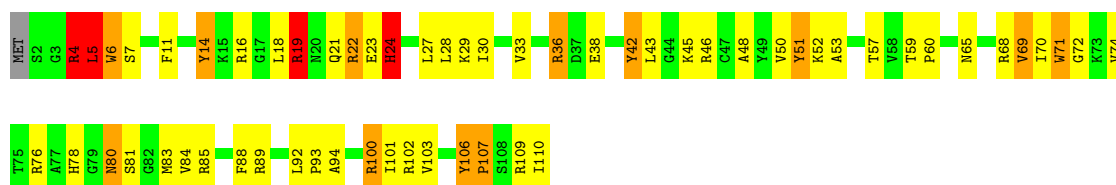
[illegible]



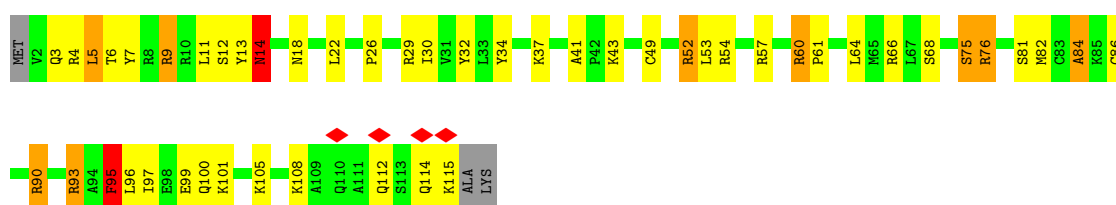
• Molecule 34: Ribosomal protein eL32



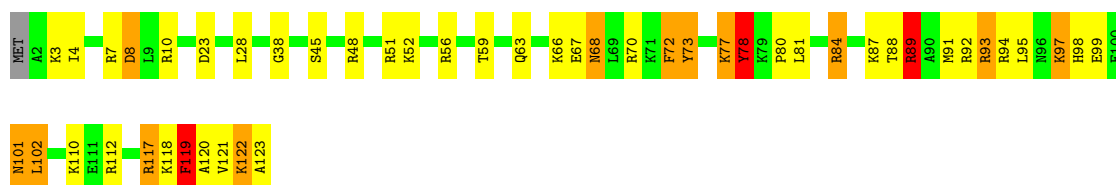
• Molecule 35: Ribosomal protein eL33



• Molecule 36: Ribosomal protein eL34

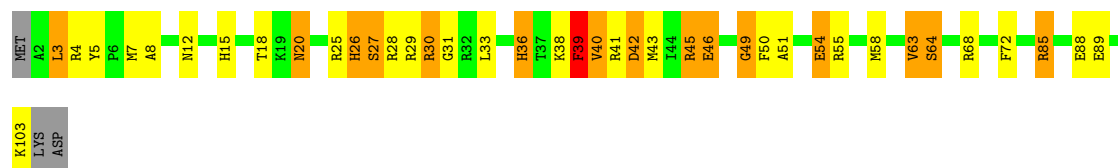


• Molecule 37: Ribosomal protein uL29



• Molecule 38: Ribosomal protein eL36





• Molecule 39: Ribosomal protein eL37



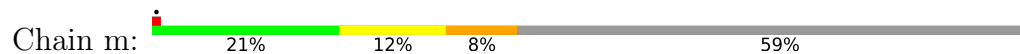
• Molecule 40: Ribosomal protein eL38



• Molecule 41: Ribosomal protein eL39



• Molecule 42: Ribosomal protein eL40



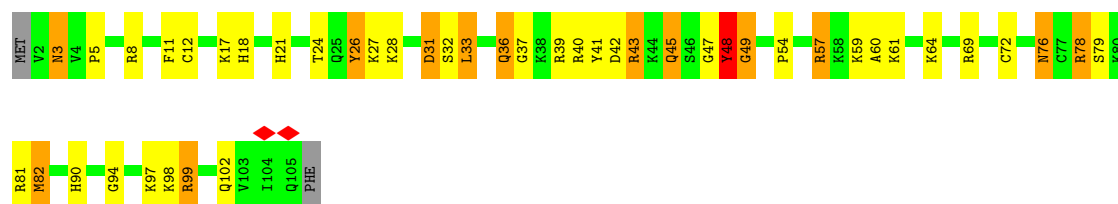
• Molecule 43: Ribosomal protein eL41



• Molecule 44: Ribosomal protein eL42



Chain o: 



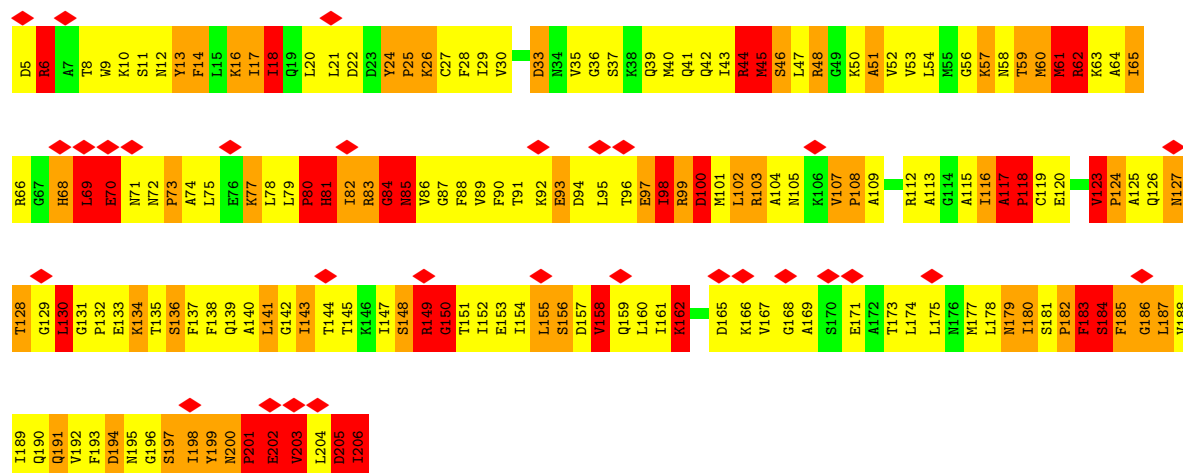
- Molecule 45: Ribosomal protein eL43

Chain p: 



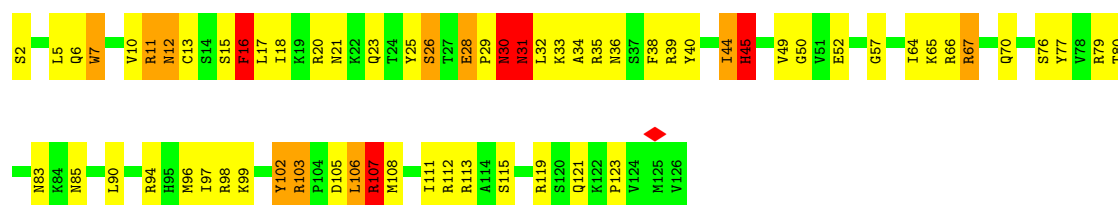
- Molecule 46: Ribosomal protein uL10

Chain q: 

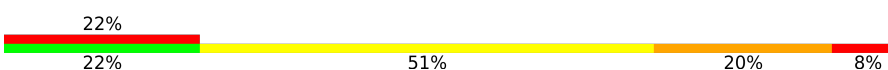


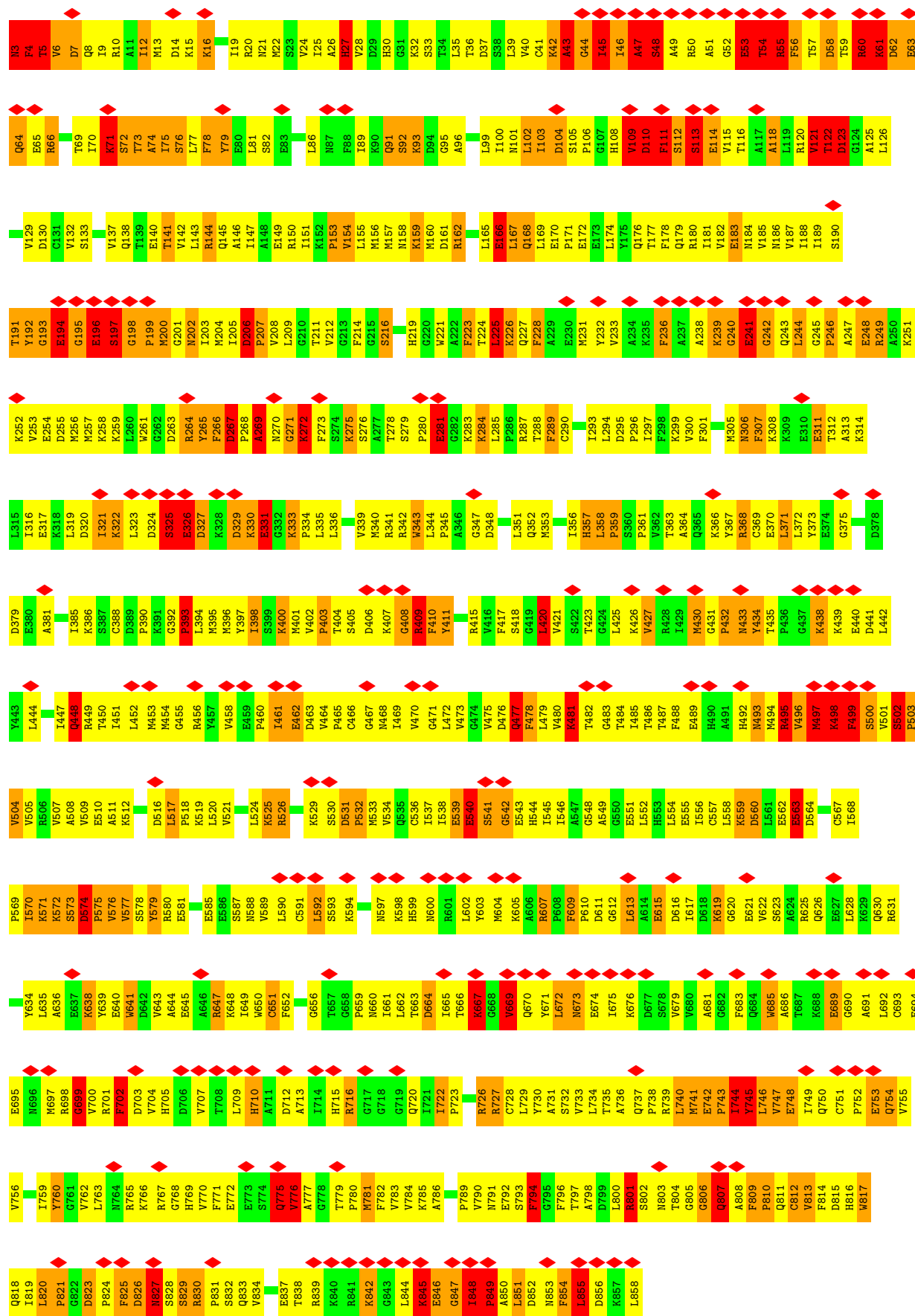
- Molecule 47: Ribosomal protein eL28

Chain r: 

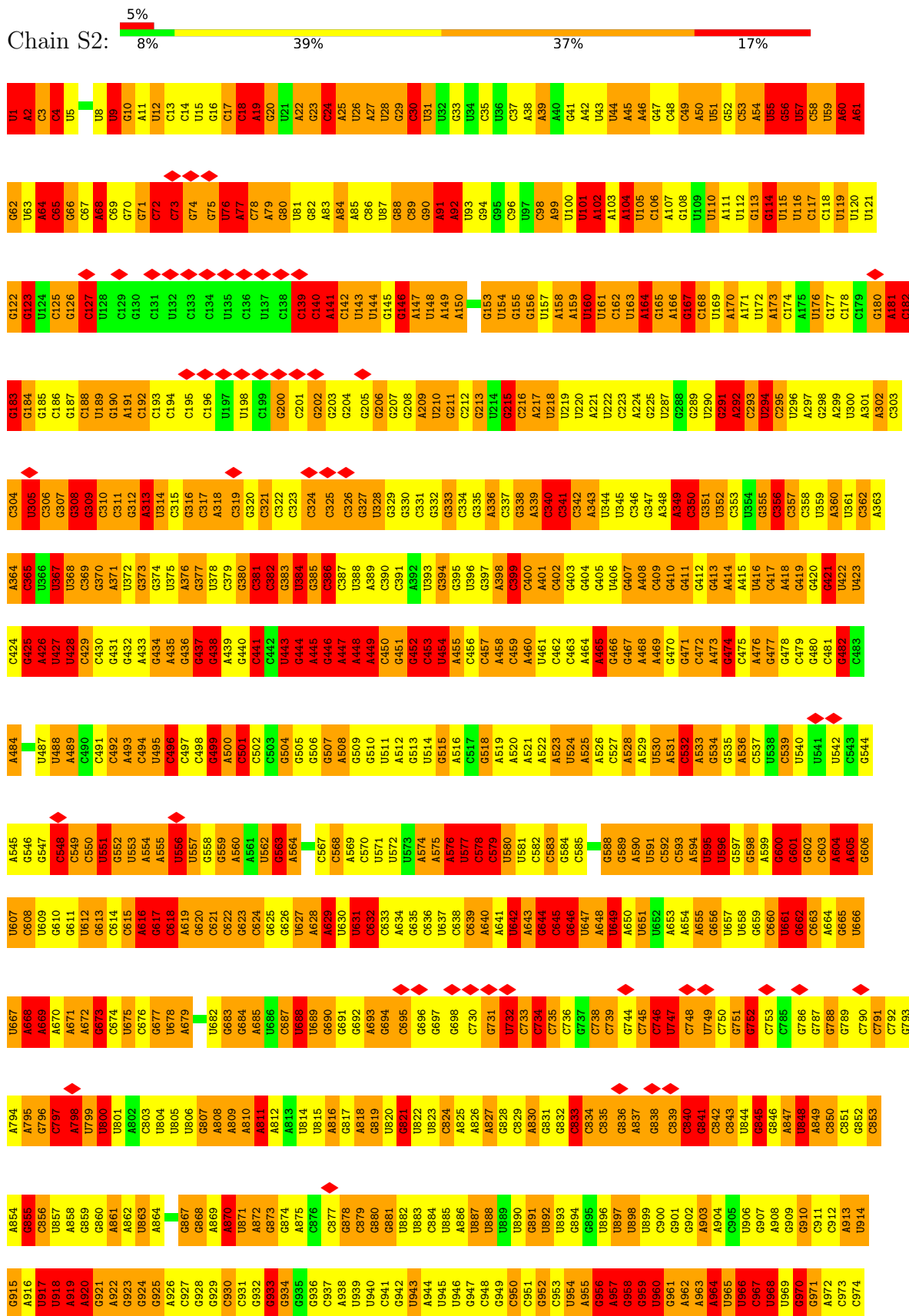


- Molecule 48: Eukaryotic elongation factor 2

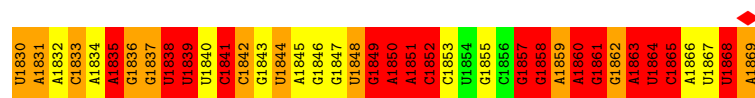
Chain 4: 



● Molecule 49: 18S ribosomal RNA

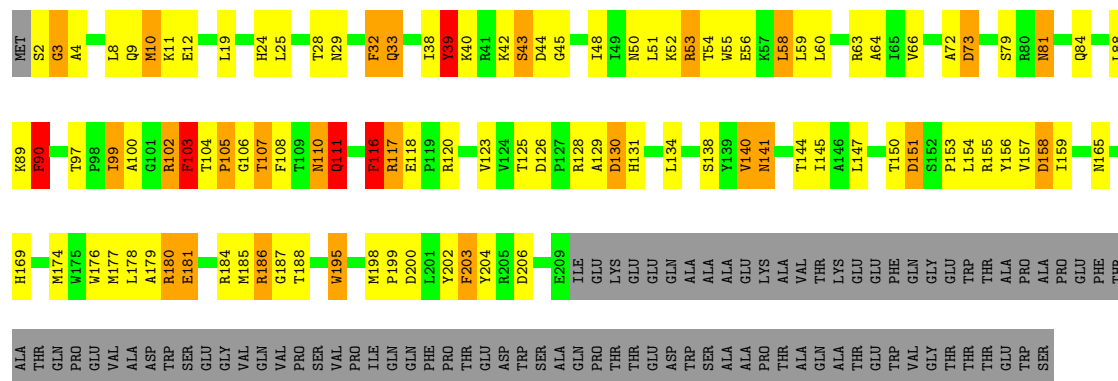


A1768	G1708	G1584	G1463	C1403	U1339	A1278	C1218	G1157	G1037	G975
G1769	G1709	U1585	C1464	U1404	U1340	C1279	C1219	G1158	U1038	G976
G1770	C1710	A1686	A1465	A1405	C1341	G1280	G1220	G1159	G1039	G977
G1771	C1711	G1466	G1406	G1406	U1342	G1281	A1221	U1160	G1040	G978
G1772	A1712	A1588	C1467	U1407	U1343	A1282	G1222	U1161	G1041	C979
G1773	C1713	A1589	C1468	U1408	A1344	C1283	A1223	U1162	A1042	A980
U1714	U1714	C1590	U1409	A1409	G1345	A1284	G1224	C1163	G1043	A981
A1651	A1715	A1531	C1471	C1410	U1346	G1285	U1225	G1164	G1044	G982
G1716	C1716	A1532	C1472	C1411	U1347	G1286	G1226	G1165	U1045	A983
G1775	C1717	A1533	A1473	C1412	G1348	A1287	G1227	G1166	U1046	A984
G1776	G1718	A1534	A1474	C1413	G1349	U1288	A1228	G1167	C1047	G985
G1777	C1719	U1535	G1475	A1414	U1350	U1289	G1229	G1168	C1048	G986
G1778	U1720	G1536	A1476	C1415	G1351	U1290	C1230	G1169	A1049	A987
G1779	U1721	A1537	U1477	C1416	G1352	A1291	C1231	A1170	A1050	C988
G1780	U1722	U1538	U1478	C1417	A1353	C1292	U1232	G1171	G1051	C989
A1781	G1723	C1539	U1479	C1418	G1354	A1293	G1233	U1172	A1052	A990
G1782	A1724	G1540	A1480	C1419	C1355	G1294	C1234	A1173	C1053	G991
C1783	U1725	G1541	G1481	G1420	G1356	A1295	G1235	U1174	G1054	A992
G1784	G1726	C1542	C1482	A1421	A1357	U1296	G1236	G1175	A1055	G993
C1785	A1663	U1543	A1483	C1423	U1358	U1297	C1237	G1176	U1056	G994
A1664	G1727	U1544	A1484	G1424	U1362	G1298	U1238	U1177	C1057	A996
G1665	U1728	A1545	A1485	G1425	C1363	U1299	U1239	U1178	A1058	A997
C1666	U1729	G1546	A1486	G1426	U1364	U1300	A1240	G1179	G1059	A998
U1667	U1730	C1547	A1487	U1426	G1365	A1301	U1241	C1180	A1060	A999
G1668	A1731	G1548	C1488	C1427	G1366	G1302	U1242	A1181	U1061	G999
A1669	G1732	U1549	A1489	G1428	U1367	U1303	U1243	A1182	A1062	C1000
C1670	U1733	G1550	G1490	G1429	U1368	U1304	U1244	A1183	C1063	A1001
A1791	G1734	U1551	G1491	C1430	A1369	U1305	G1245	A1184	G1064	U1002
G1792	A1735	G1552	U1492	G1431	A1370	U1306	A1246	C1185	G1065	U1003
A1793	C1736	C1553	C1493	U1432	A1371	U1307	G1247	U1186	U1066	U1004
G1794	G1737	C1554	U1494	U1433	U1372	U1308	U1248	G1187	G1067	G1005
C1795	U1674	U1555	G1495	C1434	U1373	C1309	G1249	C1127	U1068	G1006
G1796	A1675	U1556	U1496	C1435	C1374	U1310	A1250	U1069	G1007	C1007
U1676	U1677	A1497	G1497	C1436	G1375	C1311	U1251	A1070	A1008	U1008
A1678	A1678	U1499	U1499	C1437	U1376	G1312	A1253	U1072	U1012	A1012
G1680	G1742	G1500	G1500	A1438	U1377	U1313	C1254	U1073	U1013	U1013
U1681	G1743	C1501	C1502	C1439	A1378	U1314	G1255	C1074	G1014	G1014
A1682	G1744	C1503	C1504	U1440	A1379	U1315	G1256	G1075	U1015	U1015
C1683	A1745	C1505	U1504	U1441	C1380	C1316	G1257	G1076	A1016	A1016
G1684	U1746	U1506	G1506	U1442	A1381	C1317	A1258	U1077	U1017	U1017
U1685	C1747	U1507	U1507	C1443	A1382	G1318	A1259	G1078	U1018	U1018
G1686	U1748	U1508	U1508	U1444	A1383	U1319	A1260	C1079	C1019	C1019
C1687	G1749	G1509	G1509	U1445	C1384	G1320	C1261	A1080	A1020	A1020
U1688	C1627	U1510	U1510	A1446	C1385	G1321	G1262	U1081	U1021	U1021
C1689	C1628	U1511	U1511	G1447	G1386	G1322	U1263	A1082	U1022	U1022
U1692	C1629	C1512	C1512	A1448	G1387	U1323	C1264	A1083	A1023	A1023
G1693	A1630	G1513	G1513	G1449	A1388	G1324	A1265	A1084	A1024	A1024
U1694	U1631	C1514	C1514	U1451	U1392	U1325	C1266	G1085	U1025	U1025
A1695	G1632	G1515	G1515	G1452	U1326	G1327	G1267	G1086	C1026	C1026
C1696	A1633	G1516	G1516	A1453	G1393	G1327	C1268	A1087	A1027	A1027
U1697	C1634	G1517	G1517	C1454	G1394	G1328	G1269	U1088	A1028	A1028
G1698	A1635	G1518	G1518	A1455	C1395	C1331	G1270	G1089	G1029	G1029
C1699	U1636	G1519	G1519	A1456	A1396	C1332	A1271	A1148	A1030	A1030
U1700	G1637	U1519	U1519	G1457	U1397	U1333	C1272	A1149	C1090	C1090
C1701	G1638	U1520	G1520	U1458	G1398	G1334	C1273	G1151	A1031	A1031
A1823	A1640	C1521	C1521	G1459	C1399	G1335	G1274	U1152	G1033	G1033
G1762	U1641	A1522	A1522	C1460	U1400	G1336	A1275	A1094	A1034	A1034
A1825	C1703	G1523	G1523	U1461	A1401	C1337	G1276	U1095	A1035	A1035
G1826	G1764	C1524	C1524	G1462	A1402	G1338	C1277	G1096	G1096	G1096
U1827	C1765	U1525	U1525	U1462	U1402	U1462	U1462	U1155	U1155	U1155
G1828	G1766	C1526	C1526	U1462	U1402	U1462	U1462	U1156	U1156	U1156
G1829	C1767	U1527	U1527	U1462	U1402	U1462	U1462	U1157	U1157	U1157



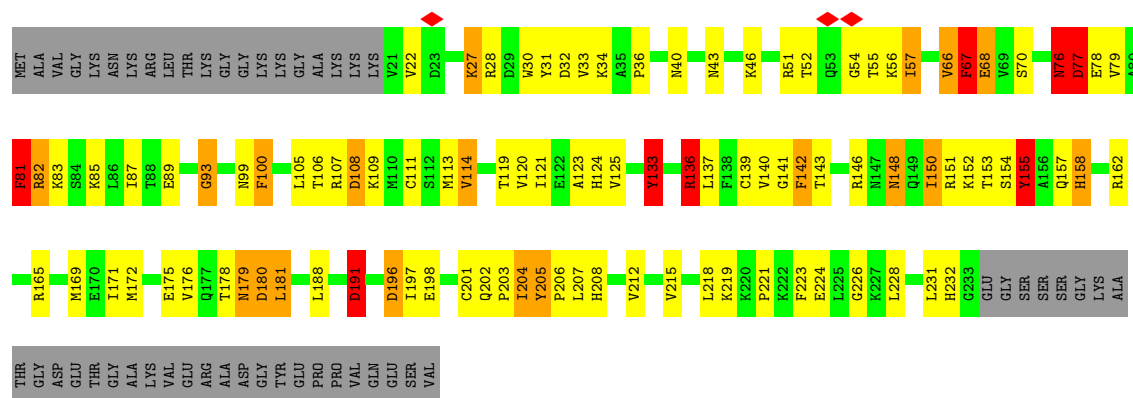
• Molecule 50: Ribosomal protein uS2

Chain SA: 35% 25% 8% 29%



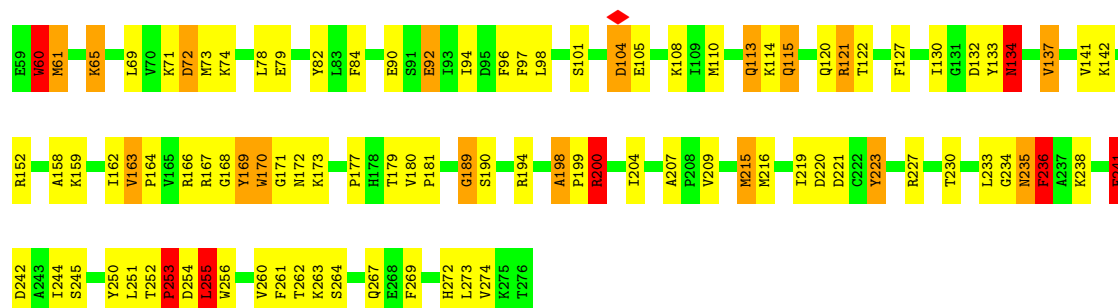
• Molecule 51: Ribosomal protein eS1

Chain SB: 42% 28% 7% 19%

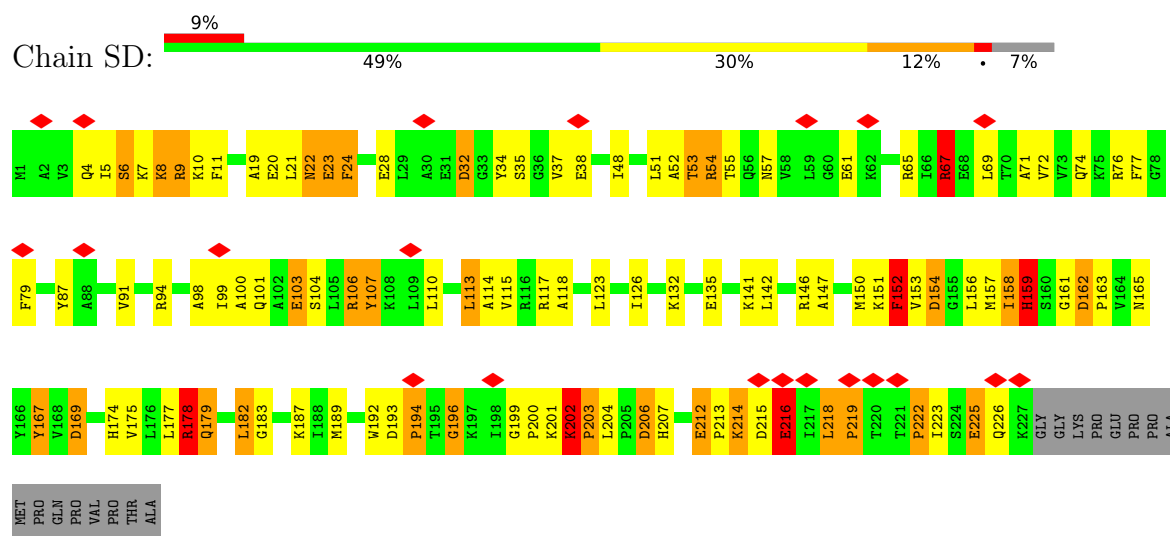


• Molecule 52: Ribosomal protein uS5

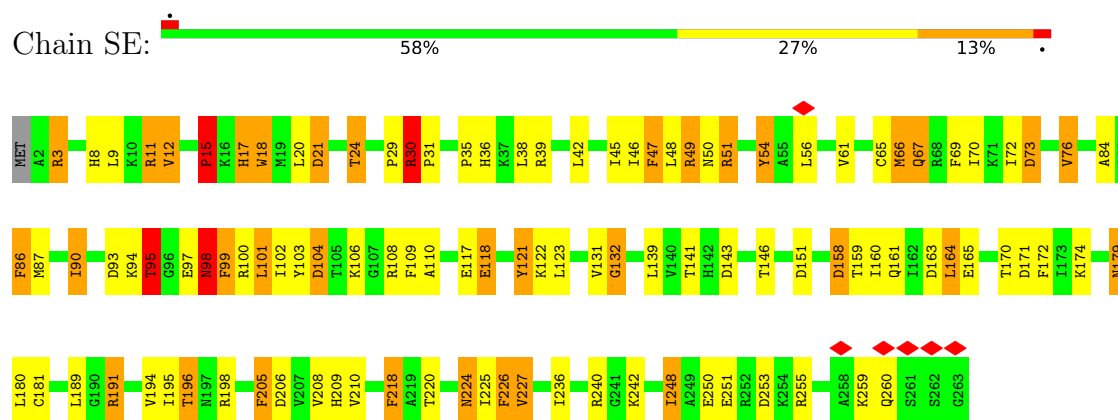
Chain SC: 55% 34% 8%



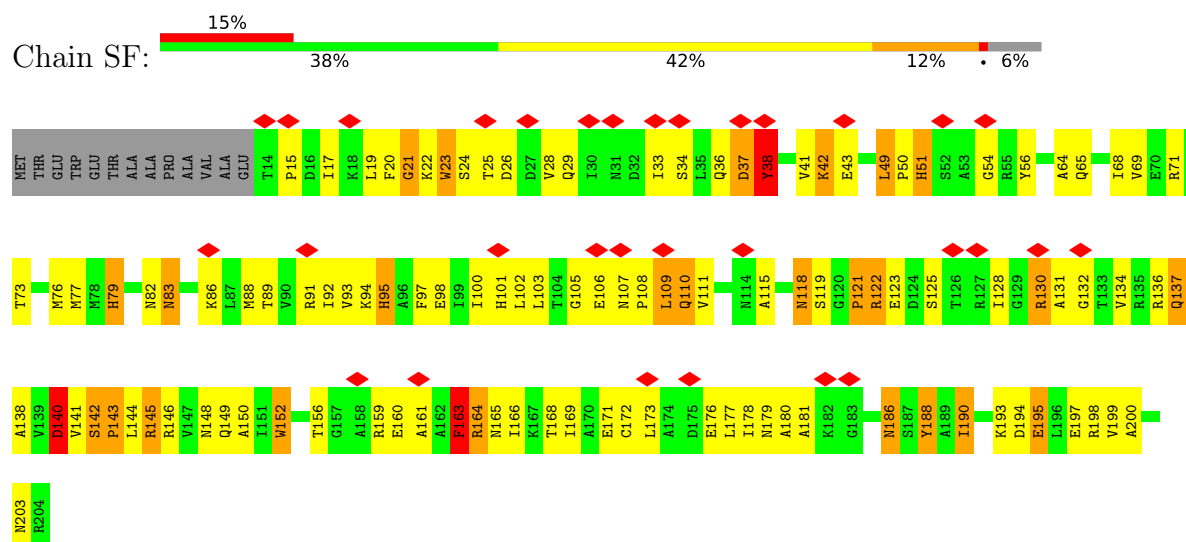
- Molecule 53: Ribosomal protein uS3



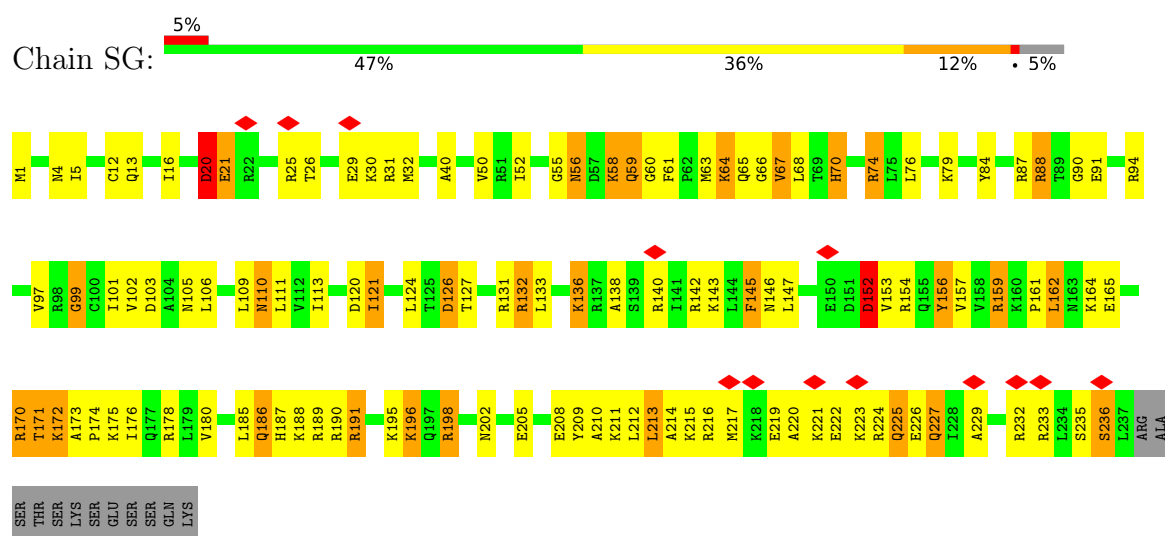
- Molecule 54: Ribosomal protein eS4



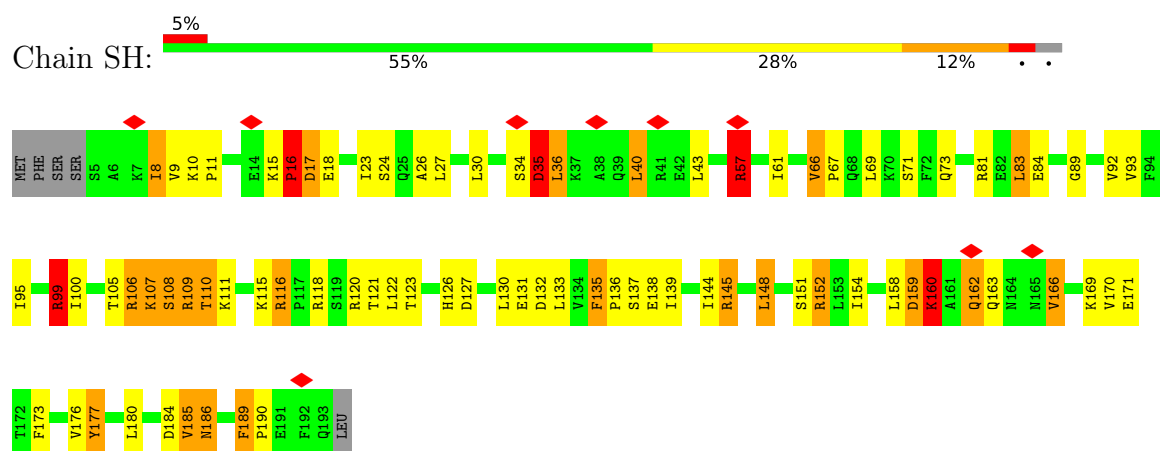
- Molecule 55: Ribosomal protein uS7



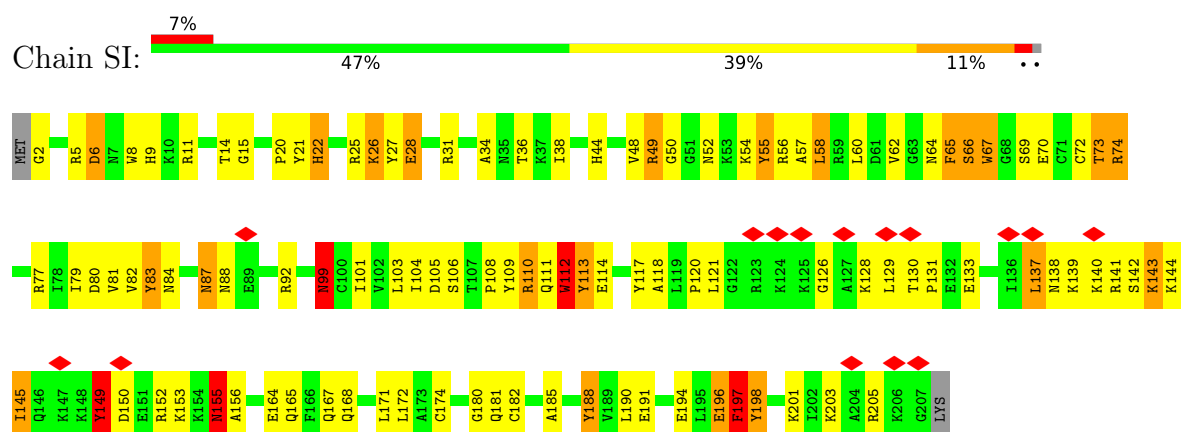
- Molecule 56: Ribosomal protein eS6



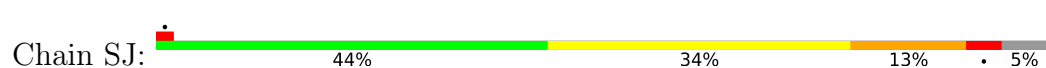
• Molecule 57: Ribosomal protein eS7

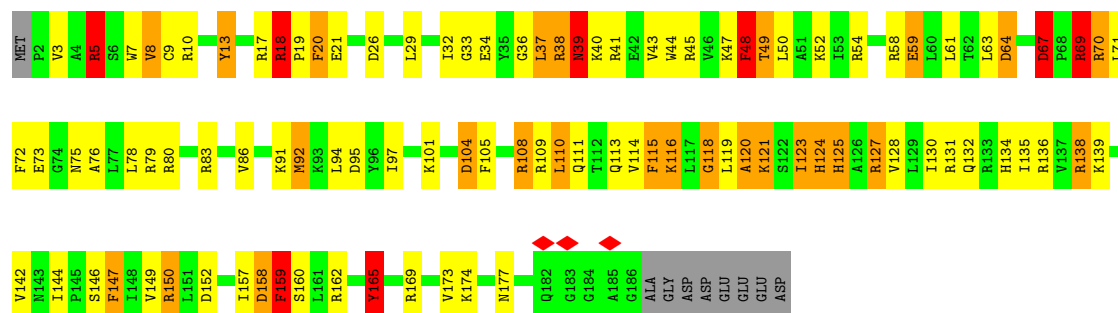


• Molecule 58: Ribosomal protein eS8

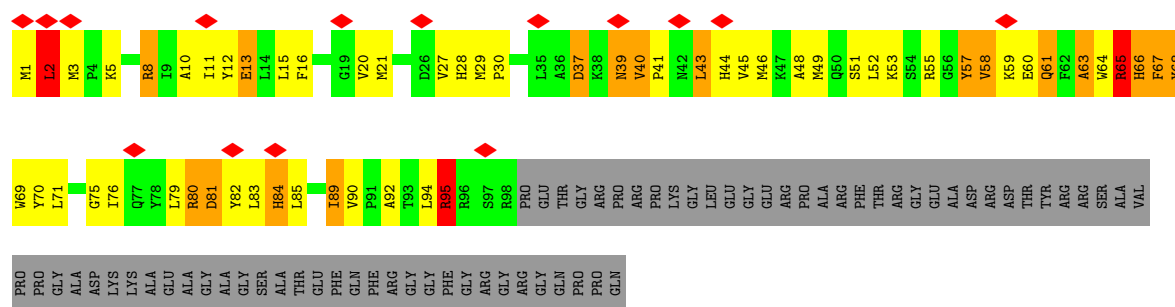
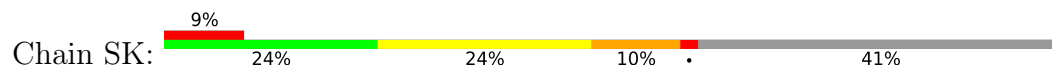


• Molecule 59: Ribosomal protein uS4

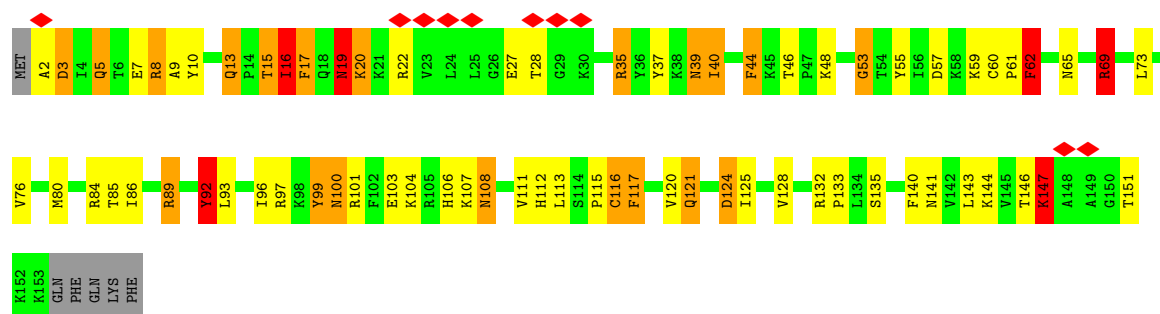




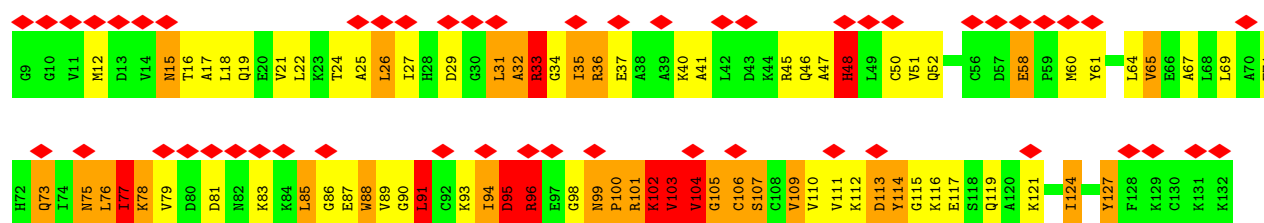
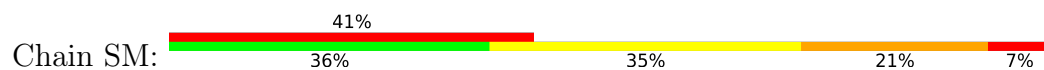
• Molecule 60: Ribosomal protein eS10



• Molecule 61: Ribosomal protein uS17

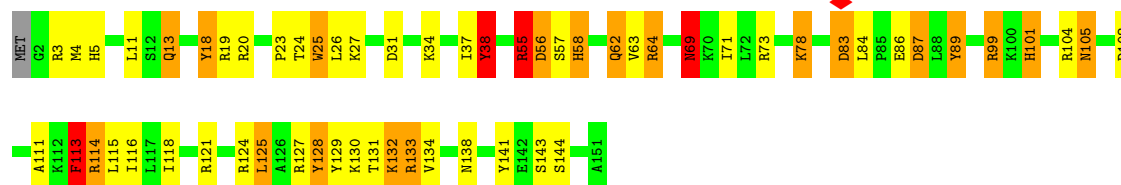


• Molecule 62: Ribosomal protein eS12



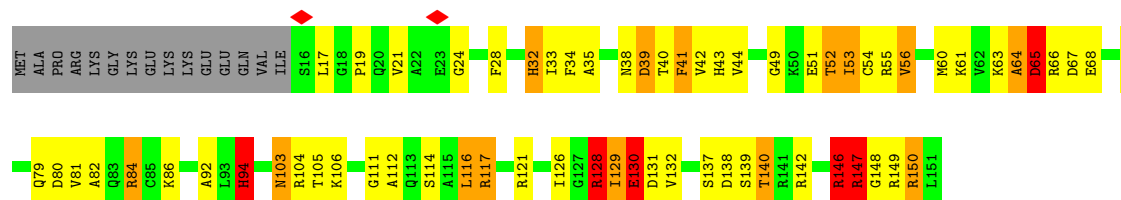
• Molecule 63: Ribosomal protein uS15

Chain SN: 

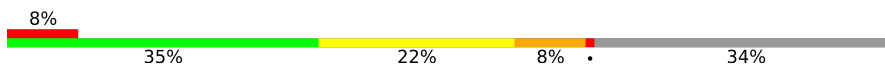


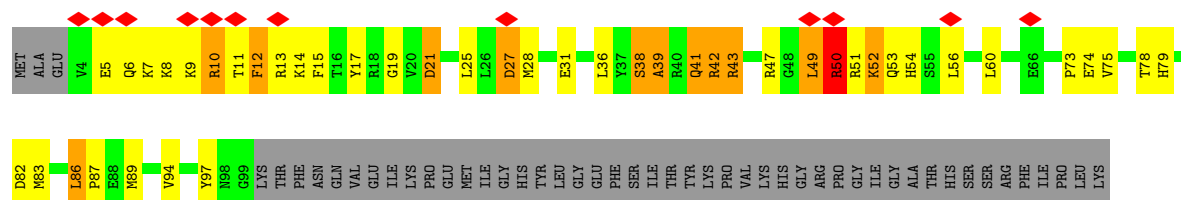
• Molecule 64: Ribosomal protein uS11

Chain SO: 



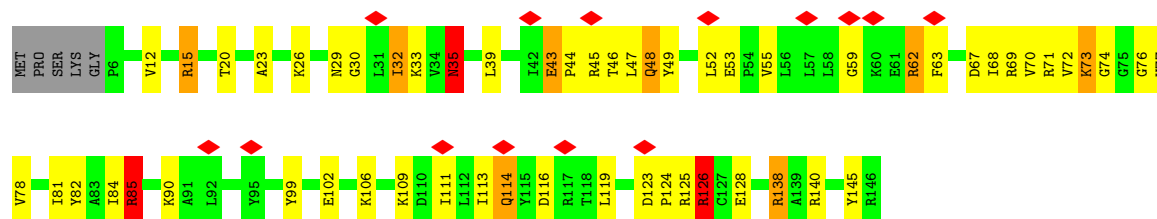
• Molecule 65: Ribosomal protein uS19

Chain SP: 

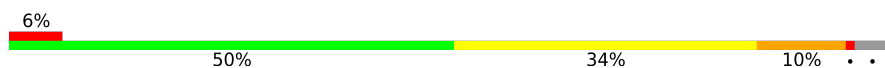


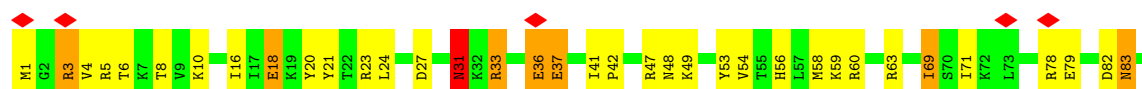
• Molecule 66: Ribosomal protein uS9

Chain SQ: 



• Molecule 67: Ribosomal protein eS17

Chain SR: 





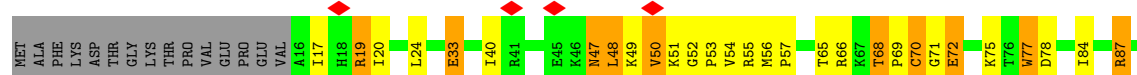
• Molecule 68: Ribosomal protein uS13



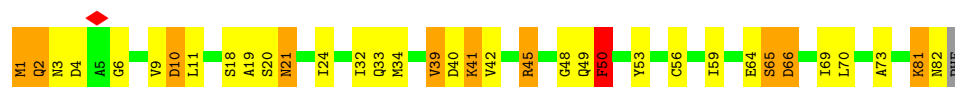
• Molecule 69: Ribosomal protein eS19



• Molecule 70: Ribosomal protein uS10

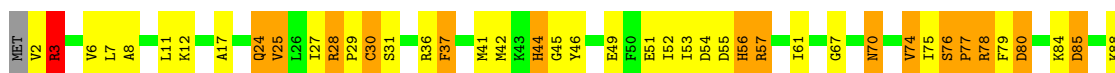


• Molecule 71: Ribosomal protein eS21



• Molecule 72: Ribosomal protein uS8

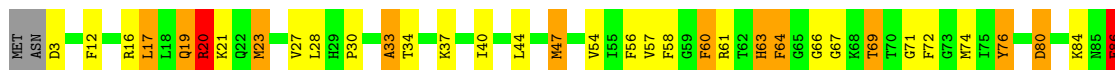




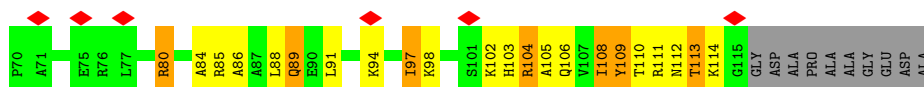
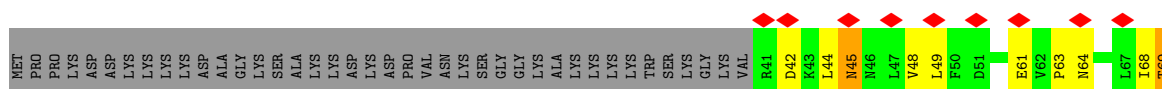
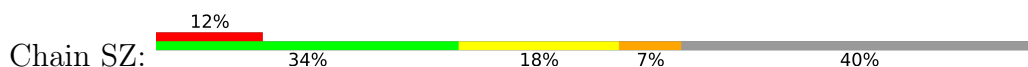
• Molecule 73: Ribosomal protein uS12



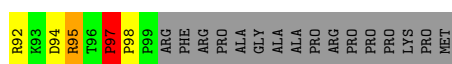
• Molecule 74: Ribosomal protein eS24



• Molecule 75: Ribosomal protein es25

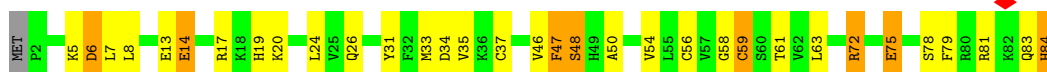


• Molecule 76: Ribosomal protein eS26



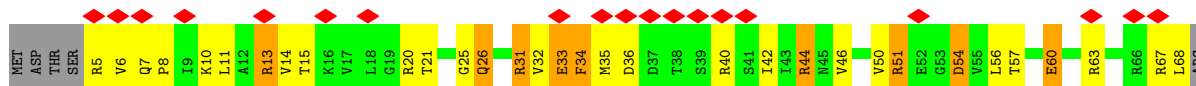
• Molecule 77: Ribosomal protein eS27

Chain Sb: 



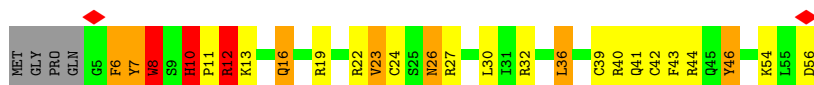
- Molecule 78: Ribosomal protein eS28

Chain Sc: 



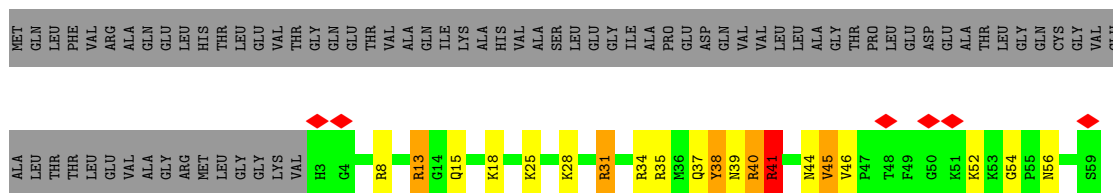
- Molecule 79: Ribosomal protein uS14

Chain Sd: 



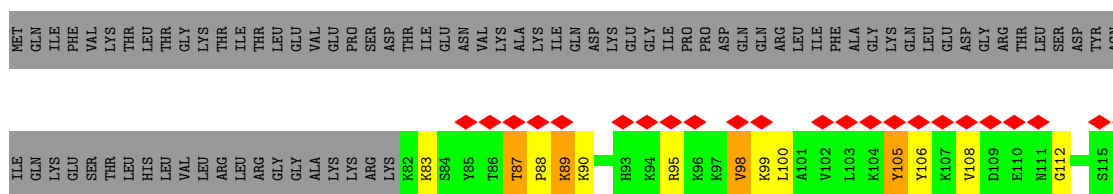
- Molecule 80: Ribosomal protein eS30

Chain Se: 



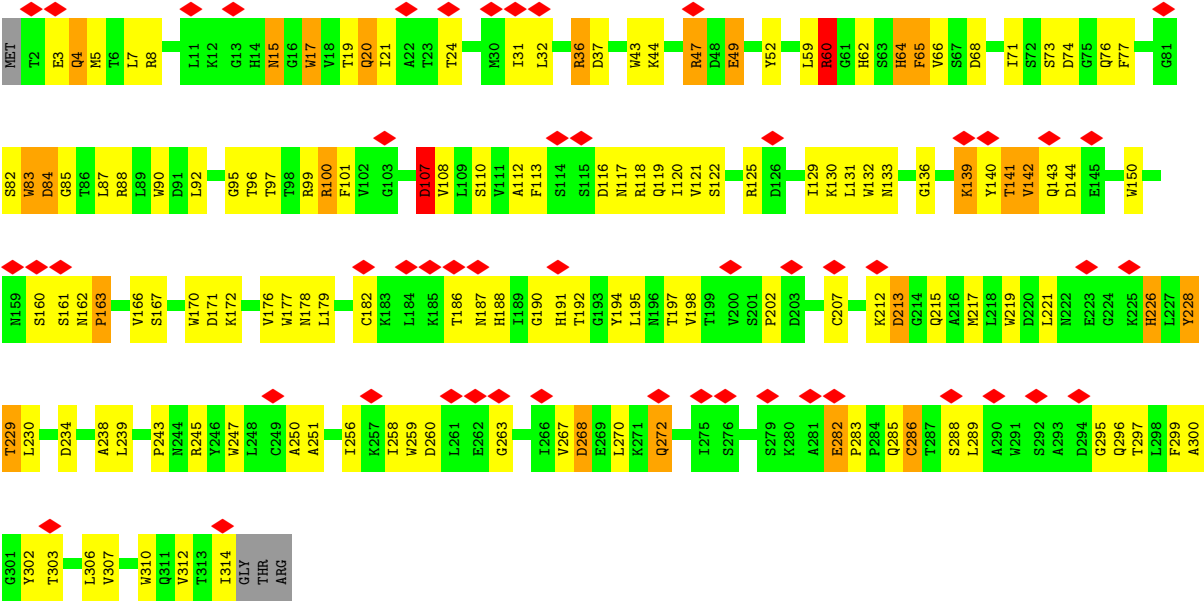
- Molecule 81: Ribosomal protein eS31

Chain Sf: 



- Molecule 82: Ribosomal protein RACK1

Chain Sg: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	36667	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	Each particle	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	27	Depositor
Minimum defocus (nm)	2500	Depositor
Maximum defocus (nm)	3500	Depositor
Magnification	104478	Depositor
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.913	Depositor
Minimum map value	-0.580	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.025	Depositor
Recommended contour level	0.065	Depositor
Map size ($\text{\AA}$)	562.8, 562.8, 562.8	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.3399999, 1.3399999, 1.3399999	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	5	0.59	24/87792 (0.0%)	1.26	1272/136945 (0.9%)
2	7	0.51	1/2858 (0.0%)	1.11	16/4455 (0.4%)
3	8	0.62	0/3701	1.30	64/5766 (1.1%)
4	A	1.06	8/1906 (0.4%)	1.40	32/2556 (1.3%)
5	B	1.02	11/3214 (0.3%)	1.30	33/4308 (0.8%)
6	C	0.95	4/2973 (0.1%)	1.24	19/3990 (0.5%)
7	D	0.95	9/2426 (0.4%)	1.39	30/3252 (0.9%)
8	E	0.99	7/1941 (0.4%)	1.39	19/2601 (0.7%)
9	F	1.03	2/1905 (0.1%)	1.51	36/2539 (1.4%)
10	G	0.90	4/1966 (0.2%)	1.25	15/2645 (0.6%)
11	H	0.90	2/1537 (0.1%)	1.29	11/2066 (0.5%)
12	I	0.84	2/1753 (0.1%)	1.28	21/2343 (0.9%)
13	J	0.76	1/1382 (0.1%)	1.10	8/1849 (0.4%)
14	K	1.51	29/1154 (2.5%)	2.26	72/1555 (4.6%)
15	L	0.93	3/1734 (0.2%)	1.26	15/2318 (0.6%)
16	M	0.92	2/1152 (0.2%)	1.27	12/1539 (0.8%)
17	N	1.02	5/1746 (0.3%)	1.49	30/2338 (1.3%)
18	O	0.93	2/1684 (0.1%)	1.30	14/2251 (0.6%)
19	P	0.97	1/1268 (0.1%)	1.21	8/1701 (0.5%)
20	Q	0.89	1/1530 (0.1%)	1.41	23/2041 (1.1%)
21	R	0.97	7/1524 (0.5%)	1.42	22/2013 (1.1%)
22	S	1.20	8/1493 (0.5%)	1.45	28/2002 (1.4%)
23	T	0.88	1/1326 (0.1%)	1.21	12/1770 (0.7%)
24	U	0.83	3/822 (0.4%)	1.12	4/1103 (0.4%)
25	V	1.08	5/993 (0.5%)	1.26	6/1332 (0.5%)
26	W	0.91	1/541 (0.2%)	1.28	0/720
27	X	0.85	3/993 (0.3%)	1.26	7/1334 (0.5%)
28	Y	0.94	3/1132 (0.3%)	1.32	15/1504 (1.0%)
29	Z	0.84	0/1130	1.21	6/1507 (0.4%)
30	a	1.20	7/1192 (0.6%)	1.57	20/1591 (1.3%)
31	b	0.99	3/620 (0.5%)	1.45	11/819 (1.3%)
32	c	0.94	3/742 (0.4%)	1.31	9/996 (0.9%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	1.08	6/903 (0.7%)	1.46	14/1216 (1.2%)
34	e	1.05	5/1071 (0.5%)	1.39	20/1429 (1.4%)
35	f	1.15	4/895 (0.4%)	1.38	16/1198 (1.3%)
36	g	0.87	0/916	1.22	8/1220 (0.7%)
37	h	0.82	1/1023 (0.1%)	1.26	9/1350 (0.7%)
38	i	0.85	2/843 (0.2%)	1.29	8/1115 (0.7%)
39	j	1.13	4/721 (0.6%)	1.57	16/953 (1.7%)
40	k	0.74	1/575 (0.2%)	1.15	3/761 (0.4%)
41	l	0.85	0/454	1.25	6/599 (1.0%)
42	m	0.75	0/435	1.10	1/575 (0.2%)
43	n	0.63	0/223	1.10	0/284
44	o	0.83	1/864 (0.1%)	1.34	8/1140 (0.7%)
45	p	0.80	0/718	1.22	7/953 (0.7%)
46	q	1.17	25/1580 (1.6%)	1.77	55/2133 (2.6%)
47	r	0.89	1/1017 (0.1%)	1.32	13/1365 (1.0%)
48	4	1.48	53/6804 (0.8%)	2.15	243/9189 (2.6%)
49	S2	0.60	17/41243 (0.0%)	1.28	612/64257 (1.0%)
50	SA	1.06	7/1679 (0.4%)	1.25	14/2283 (0.6%)
51	SB	1.04	7/1753 (0.4%)	1.33	15/2350 (0.6%)
52	SC	1.20	9/1726 (0.5%)	1.30	14/2332 (0.6%)
53	SD	1.20	7/1793 (0.4%)	1.22	13/2414 (0.5%)
54	SE	0.92	8/2118 (0.4%)	1.13	9/2849 (0.3%)
55	SF	0.96	2/1531 (0.1%)	1.26	10/2059 (0.5%)
56	SG	0.96	8/1946 (0.4%)	1.09	5/2590 (0.2%)
57	SH	0.91	2/1544 (0.1%)	1.18	9/2068 (0.4%)
58	SI	1.06	7/1715 (0.4%)	1.23	11/2287 (0.5%)
59	SJ	1.15	11/1550 (0.7%)	1.33	13/2069 (0.6%)
60	SK	0.93	1/851 (0.1%)	1.14	4/1147 (0.3%)
61	SL	1.03	5/1259 (0.4%)	1.32	19/1684 (1.1%)
62	SM	1.69	5/970 (0.5%)	1.38	9/1300 (0.7%)
63	SN	1.05	6/1232 (0.5%)	1.33	9/1656 (0.5%)
64	SO	1.19	5/1029 (0.5%)	1.32	7/1380 (0.5%)
65	SP	1.74	7/816 (0.9%)	1.22	5/1084 (0.5%)
66	SQ	0.87	3/1142 (0.3%)	1.11	3/1528 (0.2%)
67	SR	0.91	5/1060 (0.5%)	1.23	4/1421 (0.3%)
68	SS	0.91	1/1157 (0.1%)	1.29	12/1548 (0.8%)
69	ST	0.83	1/1119 (0.1%)	1.27	6/1499 (0.4%)
70	SU	0.94	3/828 (0.4%)	1.10	4/1112 (0.4%)
71	SV	0.91	0/631	1.10	2/844 (0.2%)
72	SW	1.32	4/1051 (0.4%)	1.28	7/1406 (0.5%)
73	SX	1.22	6/1118 (0.5%)	1.22	10/1493 (0.7%)
74	SY	1.25	5/1040 (0.5%)	1.22	10/1382 (0.7%)
75	SZ	0.85	0/604	1.11	4/810 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sa	1.06	2/794 (0.3%)	1.29	5/1065 (0.5%)
77	Sb	0.79	0/665	0.99	0/891
78	Sc	0.86	0/508	1.12	2/680 (0.3%)
79	Sd	1.01	3/445 (0.7%)	1.17	1/589 (0.2%)
80	Se	0.86	0/458	1.17	4/602 (0.7%)
81	Sf	1.44	9/593 (1.5%)	1.72	15/786 (1.9%)
82	Sg	0.93	11/2493 (0.4%)	1.02	10/3394 (0.3%)
All	All	0.83	432/237633 (0.2%)	1.31	3194/348088 (0.9%)

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	5	0	154
2	7	0	2
3	8	0	11
4	A	0	6
5	B	0	13
6	C	0	5
7	D	0	8
8	E	0	12
9	F	0	5
10	G	0	3
11	H	0	3
12	I	0	4
13	J	0	2
14	K	0	5
15	L	0	5
16	M	0	4
17	N	0	11
18	O	0	3
19	P	0	1
20	Q	0	5
21	R	0	6
22	S	0	11
23	T	0	2
24	U	0	2
25	V	0	3
26	W	0	1
27	X	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
28	Y	0	4
30	a	0	9
31	b	0	1
32	c	0	2
33	d	0	4
34	e	0	4
35	f	0	2
36	g	0	1
37	h	0	3
38	i	0	3
39	j	0	4
40	k	0	1
44	o	0	6
45	p	0	1
46	q	0	7
47	r	0	5
48	4	0	40
49	S2	1	66
50	SA	0	2
51	SB	0	4
52	SC	0	4
53	SD	0	3
54	SE	0	2
55	SF	0	1
57	SH	0	1
58	SI	0	6
59	SJ	0	2
60	SK	0	1
61	SL	0	4
62	SM	0	3
63	SN	0	1
64	SO	0	1
65	SP	0	1
66	SQ	0	1
67	SR	0	2
70	SU	0	1
71	SV	0	2
72	SW	0	2
73	SX	0	2
74	SY	0	1
75	SZ	0	1
76	Sa	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
77	Sb	0	1
79	Sd	0	2
81	Sf	0	4
All	All	1	507

The worst 5 of 432 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
48	4	267	ASP	CA-C	37.55	1.88	1.52
62	SM	58	GLU	CD-OE1	37.46	1.96	1.25
65	SP	21	ASP	CG-OD1	37.40	1.96	1.25
48	4	267	ASP	N-CA	35.69	1.77	1.46
1	5	1823	G	O3'-P	33.24	2.11	1.61

The worst 5 of 3194 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	4	699	GLY	CA-C-N	-52.45	50.88	120.63
48	4	699	GLY	C-N-CA	-52.45	50.88	120.63
48	4	768	GLY	O-C-N	43.87	156.93	122.71
48	4	111	PHE	CA-CB-CG	25.41	139.21	113.80
48	4	267	ASP	N-CA-C	24.23	136.01	108.14

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
49	S2	1109	C	C1'

5 of 507 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	5	22	G	Sidechain
1	5	31	U	Sidechain
1	5	42	A	Sidechain
1	5	43	U	Sidechain
1	5	53	C	Sidechain

5.2 Too-close contacts

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	5	78486	0	39660	10608	0
2	7	2558	0	1296	310	0
3	8	3314	0	1683	500	0
4	A	1868	0	1959	166	0
5	B	3147	0	3280	225	0
6	C	2919	0	3100	178	0
7	D	2380	0	2412	184	0
8	E	1904	0	2055	148	0
9	F	1870	0	1996	180	0
10	G	1934	0	2086	132	0
11	H	1518	0	1601	87	0
12	I	1713	0	1752	110	0
13	J	1359	0	1389	70	0
14	K	1140	0	1189	601	0
15	L	1703	0	1818	102	0
16	M	1131	0	1209	75	0
17	N	1701	0	1749	129	0
18	O	1651	0	1786	89	0
19	P	1242	0	1269	56	0
20	Q	1506	0	1623	78	0
21	R	1508	0	1664	101	0
22	S	1454	0	1496	128	0
23	T	1298	0	1366	85	0
24	U	808	0	831	27	0
25	V	979	0	1039	54	0
26	W	528	0	541	52	0
27	X	976	0	1053	38	0
28	Y	1115	0	1205	64	0
29	Z	1107	0	1182	56	0
30	a	1163	0	1211	110	0
31	b	610	0	650	48	0
32	c	732	0	769	41	0
33	d	888	0	930	66	0
34	e	1053	0	1147	91	0
35	f	876	0	912	56	0
36	g	906	0	1002	56	0
37	h	1015	0	1149	56	0
38	i	832	0	917	30	0
39	j	706	0	743	53	0
40	k	569	0	637	21	0
41	l	444	0	483	13	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	m	429	0	466	31	0
43	n	222	0	261	10	0
44	o	851	0	922	45	0
45	p	708	0	760	28	0
46	q	1556	0	1604	668	0
47	r	1001	0	1062	74	0
48	4	6673	0	6739	2124	0
49	S2	36900	0	18598	5448	0
50	SA	1642	0	1646	107	0
51	SB	1725	0	1797	81	0
52	SC	1690	0	1777	74	0
53	SD	1765	0	1865	104	0
54	SE	2076	0	2177	80	0
55	SF	1509	0	1563	70	0
56	SG	1923	0	2089	101	0
57	SH	1521	0	1616	90	0
58	SI	1686	0	1772	110	0
59	SJ	1525	0	1640	103	0
60	SK	827	0	854	58	0
61	SL	1238	0	1315	59	0
62	SM	960	0	989	114	0
63	SN	1208	0	1294	66	0
64	SO	1016	0	1039	68	0
65	SP	805	0	861	27	0
66	SQ	1124	0	1193	47	0
67	SR	1047	0	1103	51	0
68	SS	1139	0	1191	79	0
69	ST	1101	0	1135	73	0
70	SU	818	0	883	27	0
71	SV	625	0	628	25	0
72	SW	1034	0	1080	57	0
73	SX	1099	0	1166	67	0
74	SY	1023	0	1090	58	0
75	SZ	598	0	656	16	0
76	Sa	781	0	830	56	0
77	Sb	651	0	672	20	0
78	Sc	506	0	536	23	0
79	Sd	434	0	427	38	0
80	Se	452	0	494	19	0
81	Sf	581	0	599	222	0
82	Sg	2436	0	2393	116	0
83	4	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
83	5	118	0	0	0	0
83	7	5	0	0	0	0
83	8	4	0	0	0	0
83	P	1	0	0	0	0
83	S2	36	0	0	0	0
83	V	1	0	0	0	0
84	Sa	1	0	0	3	0
84	j	1	0	0	1	0
84	m	1	0	0	2	0
84	o	1	0	0	1	0
All	All	221686	0	166621	23711	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 61.

The worst 5 of 23711 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)
48:4:753:GLU:HA	48:4:782:PHE:CE1	1.25	1.71
48:4:236:PHE:CE2	48:4:273:PHE:CZ	1.79	1.71
10:G:261:LEU:CD2	10:G:264:LYS:HE2	1.21	1.66
1:5:4413:C:H4'	12:I:157:PHE:CE2	1.13	1.65
48:4:751:CYS:CB	48:4:755:VAL:HB	1.23	1.64

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
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	2 21
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	0 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	2	19
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	8
8	E	232/236 (98%)	150 (65%)	51 (22%)	31 (13%)	0	3
9	F	223/225 (99%)	190 (85%)	23 (10%)	10 (4%)	2	17
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	3	26
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	5	31
12	I	211/213 (99%)	166 (79%)	31 (15%)	14 (7%)	1	11
13	J	168/178 (94%)	137 (82%)	23 (14%)	8 (5%)	2	16
14	K	147/163 (90%)	83 (56%)	31 (21%)	33 (22%)	0	1
15	L	208/211 (99%)	172 (83%)	25 (12%)	11 (5%)	1	14
16	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	8	37
17	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	3	25
18	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	8	37
19	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	9	39
20	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	4	27
21	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	5	30
22	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	7	35
23	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	6	33
24	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	5	31
25	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	5	30
26	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	7	36
27	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	7	35
28	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	2	17
29	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	2	20
30	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	1	13
31	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	1	13
32	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	2	18
33	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	2	20
34	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	16	49
35	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	2	17
36	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	6	34

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
37	h	120/123 (98%)	102 (85%)	15 (12%)	3 (2%)	4	28
38	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	6	32
39	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	16
40	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	9
41	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	2	19
42	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
43	n	21/25 (84%)	21 (100%)	0	0	100	100
44	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	1	12
45	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	11	43
46	q	200/202 (99%)	133 (66%)	27 (14%)	40 (20%)	0	1
47	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	1	16
48	4	854/856 (100%)	754 (88%)	58 (7%)	42 (5%)	1	16
50	SA	206/295 (70%)	176 (85%)	24 (12%)	6 (3%)	3	26
51	SB	211/264 (80%)	170 (81%)	27 (13%)	14 (7%)	1	11
52	SC	216/218 (99%)	189 (88%)	19 (9%)	8 (4%)	2	21
53	SD	225/243 (93%)	170 (76%)	44 (20%)	11 (5%)	1	16
54	SE	260/263 (99%)	202 (78%)	41 (16%)	17 (6%)	1	11
55	SF	189/204 (93%)	160 (85%)	19 (10%)	10 (5%)	1	14
56	SG	235/249 (94%)	194 (83%)	35 (15%)	6 (3%)	4	27
57	SH	187/194 (96%)	143 (76%)	29 (16%)	15 (8%)	1	8
58	SI	204/208 (98%)	176 (86%)	21 (10%)	7 (3%)	3	23
59	SJ	183/194 (94%)	145 (79%)	24 (13%)	14 (8%)	1	8
60	SK	96/165 (58%)	60 (62%)	26 (27%)	10 (10%)	0	5
61	SL	150/158 (95%)	122 (81%)	21 (14%)	7 (5%)	2	17
62	SM	122/124 (98%)	77 (63%)	25 (20%)	20 (16%)	0	2
63	SN	148/151 (98%)	115 (78%)	28 (19%)	5 (3%)	3	23
64	SO	134/151 (89%)	102 (76%)	18 (13%)	14 (10%)	0	5
65	SP	94/145 (65%)	65 (69%)	18 (19%)	11 (12%)	0	4
66	SQ	139/146 (95%)	112 (81%)	21 (15%)	6 (4%)	2	18
67	SR	127/135 (94%)	95 (75%)	24 (19%)	8 (6%)	1	12
68	SS	135/152 (89%)	104 (77%)	23 (17%)	8 (6%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
69	ST	139/145 (96%)	116 (84%)	17 (12%)	6 (4%)	2	18
70	SU	102/119 (86%)	80 (78%)	18 (18%)	4 (4%)	2	20
71	SV	80/83 (96%)	63 (79%)	10 (12%)	7 (9%)	0	7
72	SW	127/130 (98%)	112 (88%)	11 (9%)	4 (3%)	3	25
73	SX	139/143 (97%)	116 (84%)	18 (13%)	5 (4%)	2	22
74	SY	124/132 (94%)	92 (74%)	23 (18%)	9 (7%)	1	9
75	SZ	73/125 (58%)	54 (74%)	13 (18%)	6 (8%)	0	8
76	Sa	96/115 (84%)	74 (77%)	15 (16%)	7 (7%)	1	9
77	Sb	81/84 (96%)	61 (75%)	15 (18%)	5 (6%)	1	12
78	Sc	62/69 (90%)	46 (74%)	16 (26%)	0	100	100
79	Sd	50/56 (89%)	38 (76%)	9 (18%)	3 (6%)	1	12
80	Se	55/133 (41%)	40 (73%)	14 (26%)	1 (2%)	6	34
81	Sf	69/156 (44%)	39 (56%)	21 (30%)	9 (13%)	0	3
82	Sg	311/317 (98%)	250 (80%)	45 (14%)	16 (5%)	1	15
All	All	12341/13747 (90%)	10066 (82%)	1613 (13%)	662 (5%)	2	14

5 of 662 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO
5	B	16	PHE
5	B	40	PRO
5	B	108	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	
4	A	187/199 (94%)	141 (75%)	46 (25%)	1	4
5	B	335/335 (100%)	267 (80%)	68 (20%)	1	7

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
6	C	305/305 (100%)	242 (79%)	63 (21%)	1	6
7	D	246/250 (98%)	179 (73%)	67 (27%)	0	3
8	E	209/209 (100%)	162 (78%)	47 (22%)	1	5
9	F	194/194 (100%)	143 (74%)	51 (26%)	0	3
10	G	206/226 (91%)	156 (76%)	50 (24%)	1	4
11	H	169/171 (99%)	126 (75%)	43 (25%)	0	3
12	I	180/180 (100%)	138 (77%)	42 (23%)	1	5
13	J	143/149 (96%)	111 (78%)	32 (22%)	1	5
14	K	124/136 (91%)	98 (79%)	26 (21%)	1	6
15	L	176/177 (99%)	135 (77%)	41 (23%)	1	5
16	M	116/160 (72%)	95 (82%)	21 (18%)	2	10
17	N	171/172 (99%)	132 (77%)	39 (23%)	1	5
18	O	172/174 (99%)	144 (84%)	28 (16%)	2	14
19	P	134/134 (100%)	113 (84%)	21 (16%)	2	15
20	Q	163/164 (99%)	133 (82%)	30 (18%)	1	9
21	R	159/175 (91%)	118 (74%)	41 (26%)	0	3
22	S	156/192 (81%)	121 (78%)	35 (22%)	1	5
23	T	139/140 (99%)	117 (84%)	22 (16%)	2	15
24	U	89/114 (78%)	70 (79%)	19 (21%)	1	6
25	V	101/107 (94%)	79 (78%)	22 (22%)	1	6
26	W	55/126 (44%)	42 (76%)	13 (24%)	1	4
27	X	107/133 (80%)	87 (81%)	20 (19%)	1	9
28	Y	124/135 (92%)	92 (74%)	32 (26%)	0	3
29	Z	117/118 (99%)	94 (80%)	23 (20%)	1	8
30	a	119/120 (99%)	104 (87%)	15 (13%)	4	21
31	b	63/123 (51%)	46 (73%)	17 (27%)	0	3
32	c	79/97 (81%)	61 (77%)	18 (23%)	1	5
33	d	98/110 (89%)	66 (67%)	32 (33%)	0	2
34	e	114/121 (94%)	87 (76%)	27 (24%)	1	4
35	f	88/89 (99%)	69 (78%)	19 (22%)	1	6
36	g	98/100 (98%)	80 (82%)	18 (18%)	1	9

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
37	h	109/110 (99%)	91 (84%)	18 (16%)	2	13
38	i	86/89 (97%)	69 (80%)	17 (20%)	1	7
39	j	73/73 (100%)	61 (84%)	12 (16%)	2	14
40	k	64/65 (98%)	54 (84%)	10 (16%)	2	15
41	l	47/48 (98%)	39 (83%)	8 (17%)	2	12
42	m	48/116 (41%)	36 (75%)	12 (25%)	0	4
43	n	22/24 (92%)	19 (86%)	3 (14%)	3	19
44	o	92/94 (98%)	71 (77%)	21 (23%)	1	5
45	p	74/74 (100%)	62 (84%)	12 (16%)	2	14
46	q	170/170 (100%)	130 (76%)	40 (24%)	1	4
47	r	109/109 (100%)	92 (84%)	17 (16%)	2	15
48	4	728/728 (100%)	583 (80%)	145 (20%)	1	7
50	SA	174/245 (71%)	142 (82%)	32 (18%)	1	9
51	SB	194/231 (84%)	163 (84%)	31 (16%)	2	14
52	SC	184/184 (100%)	149 (81%)	35 (19%)	1	8
53	SD	190/202 (94%)	160 (84%)	30 (16%)	2	15
54	SE	224/225 (100%)	180 (80%)	44 (20%)	1	8
55	SF	161/170 (95%)	130 (81%)	31 (19%)	1	8
56	SG	207/218 (95%)	170 (82%)	37 (18%)	2	10
57	SH	169/174 (97%)	149 (88%)	20 (12%)	5	23
58	SI	178/180 (99%)	153 (86%)	25 (14%)	3	19
59	SJ	161/168 (96%)	130 (81%)	31 (19%)	1	8
60	SK	89/136 (65%)	70 (79%)	19 (21%)	1	6
61	SL	136/142 (96%)	114 (84%)	22 (16%)	2	14
62	SM	104/104 (100%)	77 (74%)	27 (26%)	0	3
63	SN	130/131 (99%)	98 (75%)	32 (25%)	1	4
64	SO	106/119 (89%)	82 (77%)	24 (23%)	1	5
65	SP	88/130 (68%)	77 (88%)	11 (12%)	4	22
66	SQ	117/121 (97%)	102 (87%)	15 (13%)	4	21
67	SR	117/121 (97%)	101 (86%)	16 (14%)	3	19
68	SS	119/132 (90%)	100 (84%)	19 (16%)	2	14

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
69	ST	112/115 (97%)	87 (78%)	25 (22%)	1	5
70	SU	94/107 (88%)	83 (88%)	11 (12%)	5	24
71	SV	66/67 (98%)	55 (83%)	11 (17%)	2	13
72	SW	112/113 (99%)	93 (83%)	19 (17%)	2	12
73	SX	113/115 (98%)	96 (85%)	17 (15%)	3	17
74	SY	108/114 (95%)	90 (83%)	18 (17%)	2	13
75	SZ	66/103 (64%)	55 (83%)	11 (17%)	2	13
76	Sa	85/98 (87%)	77 (91%)	8 (9%)	8	31
77	Sb	75/76 (99%)	64 (85%)	11 (15%)	3	17
78	Sc	57/62 (92%)	42 (74%)	15 (26%)	0	3
79	Sd	45/48 (94%)	33 (73%)	12 (27%)	0	3
80	Se	46/105 (44%)	36 (78%)	10 (22%)	1	6
81	Sf	64/140 (46%)	44 (69%)	20 (31%)	0	2
82	Sg	272/275 (99%)	246 (90%)	26 (10%)	8	30
All	All	10721/11706 (92%)	8603 (80%)	2118 (20%)	3	7

5 of 2118 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
65	SP	79	HIS
69	ST	33	TRP
65	SP	50	ARG
81	Sf	131	PHE
22	S	101	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 307 such sidechains are listed below:

Mol	Chain	Res	Type
53	SD	22	ASN
73	SX	87	ASN
55	SF	65	GLN
62	SM	99	ASN
79	Sd	26	ASN

5.3.3 RNA

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3652/3664 (99%)	1671 (45%)	621 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
49	S2	1716/1742 (98%)	770 (44%)	269 (15%)
All	All	5642/5682 (99%)	2533 (44%)	921 (16%)

5 of 2533 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	5	2	G
1	5	5	A
1	5	6	C
1	5	8	U
1	5	12	A

5 of 921 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3922	G
49	S2	1597	C
1	5	4700	A
49	S2	1555	U
49	S2	1097	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 170 ligands modelled in this entry, 170 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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	5	13
49	S2	4
8	E	1
14	K	1
48	4	1

The worst 5 of 20 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	E	72:ALA	C	84:VAL	N	23.51
1	S2	753:C	O3'	785:C	P	22.68
1	S2	698:G	O3'	730:C	P	19.95
1	5	4776:G	O3'	4859:C	P	17.87
1	5	757:G	O3'	906:C	P	16.89

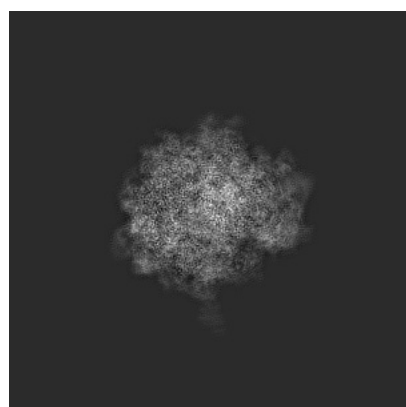
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2646. These allow visual inspection of the internal detail of the map and identification of artifacts.

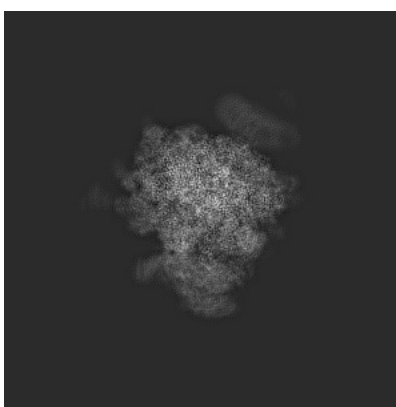
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

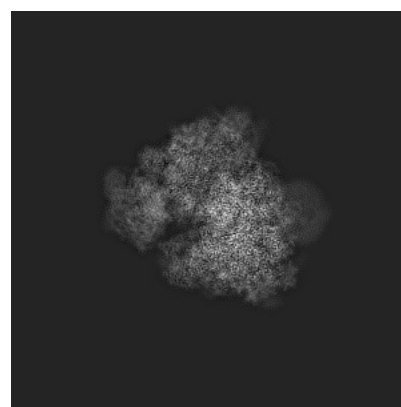
6.1.1 Primary map



X



Y



Z

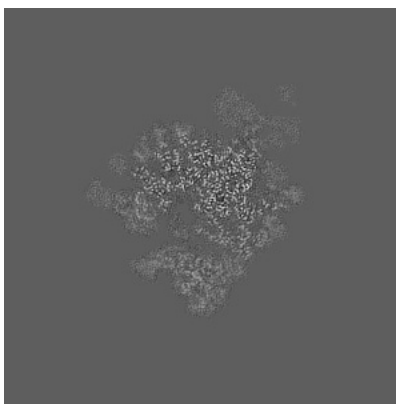
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

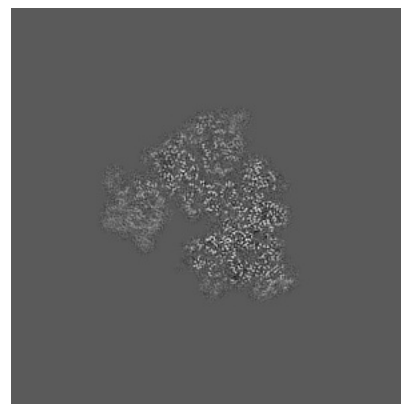
6.2.1 Primary map



X Index: 210



Y Index: 210

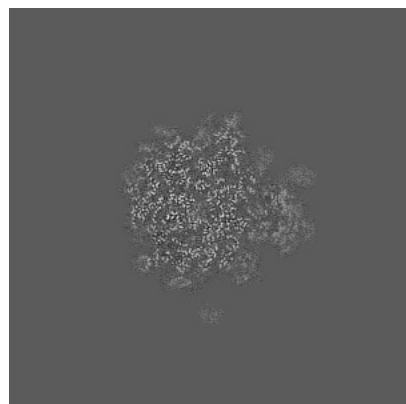


Z Index: 210

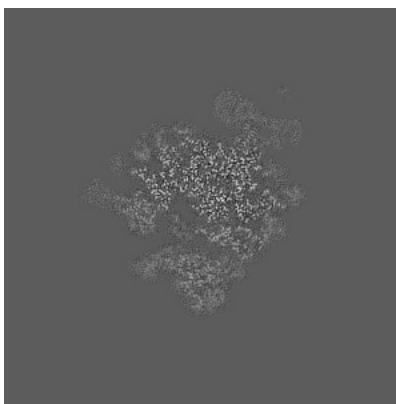
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

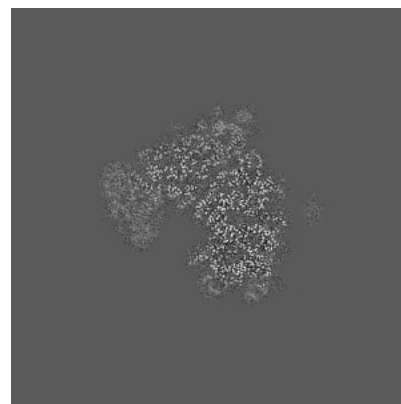
6.3.1 Primary map



X Index: 232



Y Index: 212

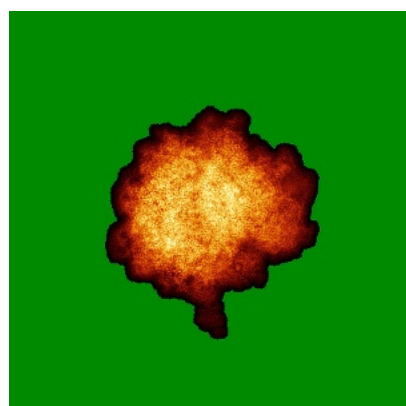


Z Index: 221

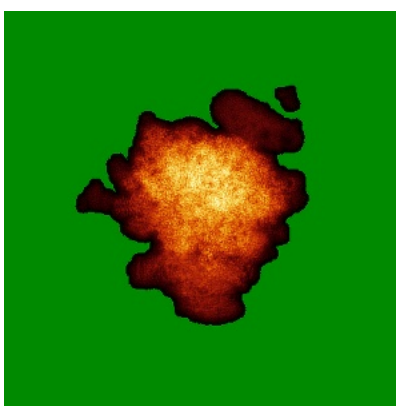
The images above show the largest variance slices of the map in three orthogonal directions.

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

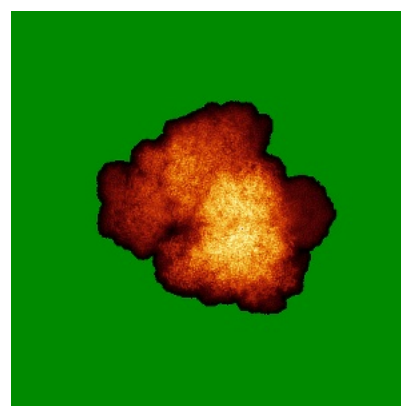
6.4.1 Primary map



X



Y



Z

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

This section was not generated.

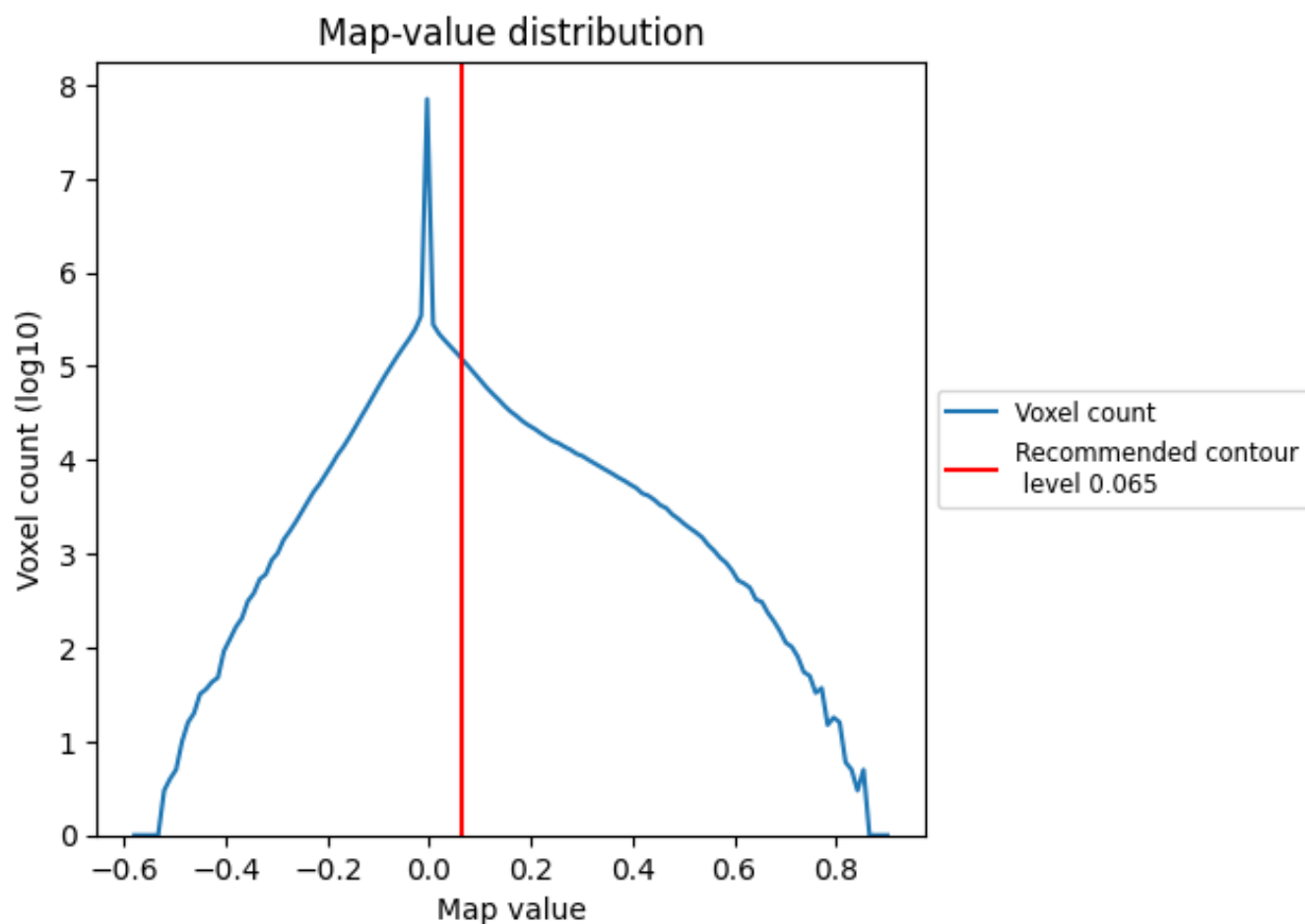
6.6 Mask visualisation

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

7 Map analysis [i](#)

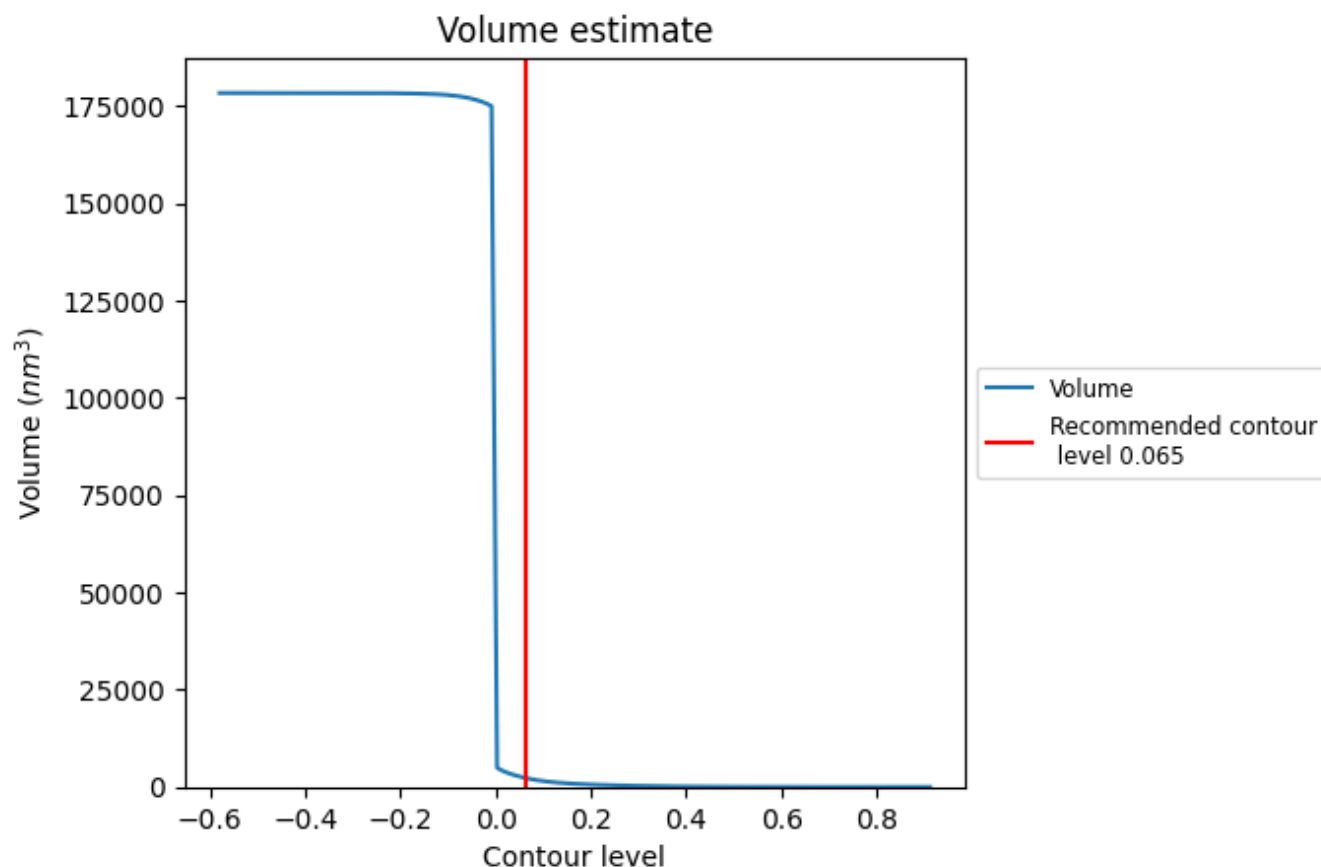
This section contains the results of statistical analysis of the map.

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.

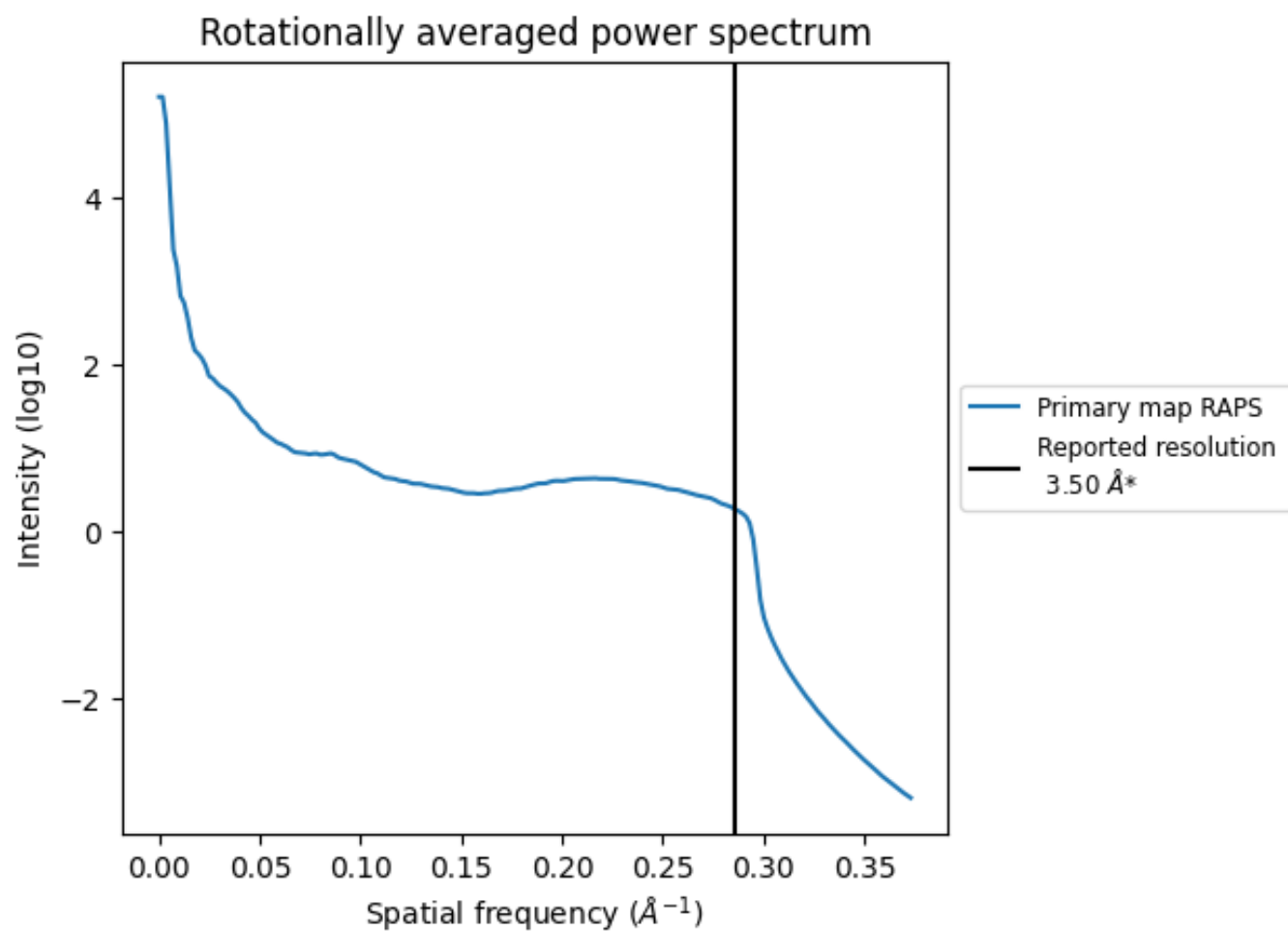
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2236 nm^3 ; this corresponds to an approximate mass of 2020 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 0.286 Å⁻¹

8 Fourier-Shell correlation

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

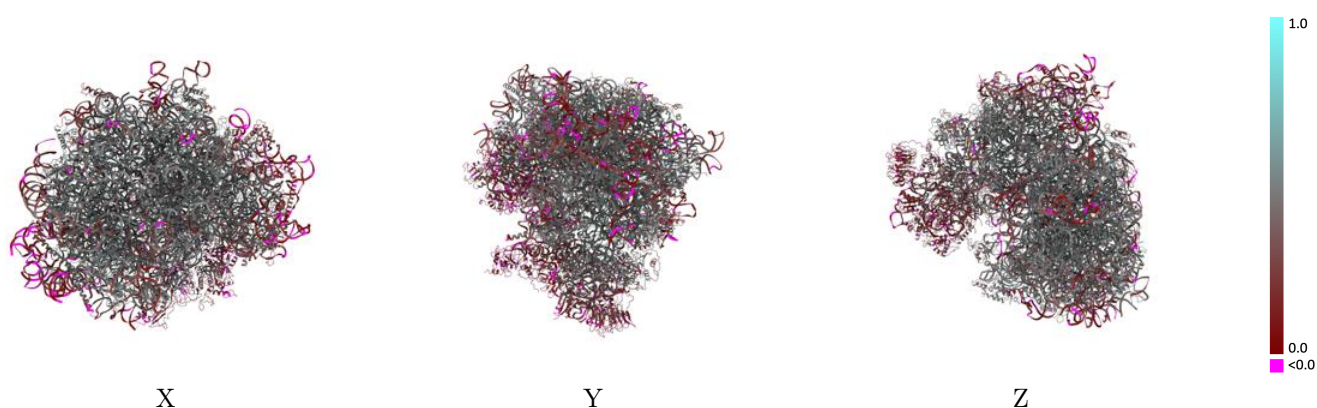
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-2646 and PDB model 3J7P. Per-residue inclusion information can be found in section 3 on page 20.

9.1 Map-model overlay [i](#)

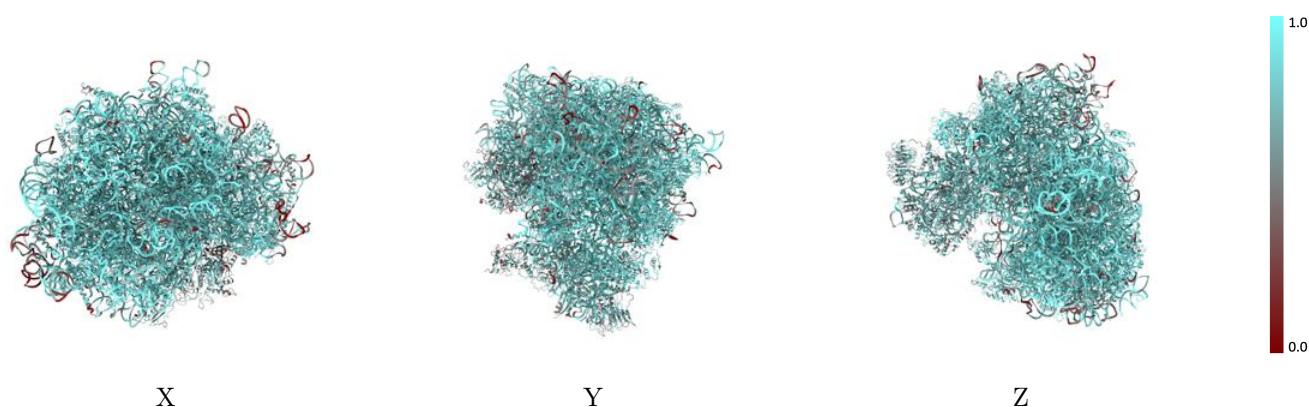
This section was not generated.

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



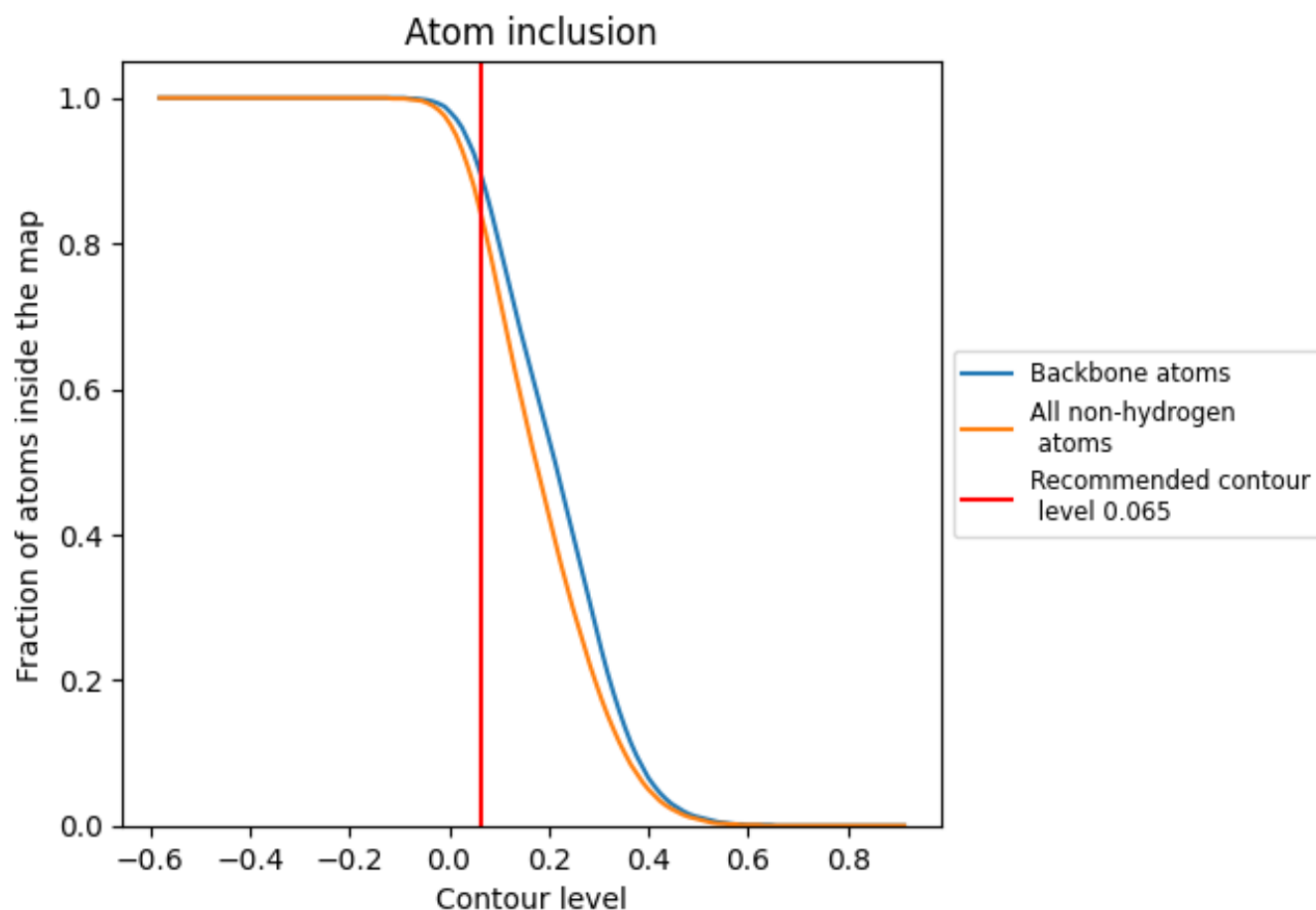
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.065).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% 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 (0.065) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8380	 0.3940
4	 0.5770	 0.2090
5	 0.8680	 0.4020
7	 0.9510	 0.4630
8	 0.8960	 0.4310
A	 0.8930	 0.5000
B	 0.8910	 0.4950
C	 0.8700	 0.4840
D	 0.8730	 0.4340
E	 0.8350	 0.4260
F	 0.8780	 0.4820
G	 0.8430	 0.4340
H	 0.8800	 0.4840
I	 0.8490	 0.4640
J	 0.8300	 0.4140
K	 0.5230	 0.1450
L	 0.8440	 0.4520
M	 0.8800	 0.4790
N	 0.9040	 0.5080
O	 0.8970	 0.5060
P	 0.8870	 0.5030
Q	 0.8970	 0.5060
R	 0.8480	 0.4450
S	 0.9100	 0.4990
S2	 0.8580	 0.3540
SA	 0.8830	 0.4570
SB	 0.8420	 0.4280
SC	 0.8890	 0.4900
SD	 0.7090	 0.2870
SE	 0.8440	 0.4430
SF	 0.6230	 0.2060
SG	 0.7240	 0.2970
SH	 0.7840	 0.3730
SI	 0.7810	 0.3810
SJ	 0.8510	 0.4450



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Chain	Atom inclusion	Q-score
SK	 0.6700	 0.2230
SL	 0.8190	 0.4330
SM	 0.4670	 0.0930
SN	 0.8720	 0.4550
SO	 0.8510	 0.4440
SP	 0.6490	 0.2520
SQ	 0.6910	 0.2540
SR	 0.7290	 0.3230
SS	 0.6950	 0.2300
ST	 0.7390	 0.2670
SU	 0.6980	 0.2790
SV	 0.8640	 0.4650
SW	 0.9160	 0.5060
SX	 0.8760	 0.5020
SY	 0.8080	 0.3850
SZ	 0.6110	 0.1690
Sa	 0.8700	 0.4610
Sb	 0.8780	 0.4540
Sc	 0.5410	 0.2010
Sd	 0.8320	 0.3900
Se	 0.7940	 0.4090
Sf	 0.4120	 0.0550
Sg	 0.6390	 0.2040
T	 0.8790	 0.4820
U	 0.7960	 0.3830
V	 0.8630	 0.4880
W	 0.8550	 0.4750
X	 0.8370	 0.4700
Y	 0.8600	 0.4710
Z	 0.8800	 0.4690
a	 0.8990	 0.5040
b	 0.7610	 0.3830
c	 0.8600	 0.4600
d	 0.8530	 0.4540
e	 0.8920	 0.5010
f	 0.9220	 0.5060
g	 0.8560	 0.4830
h	 0.8500	 0.4650
i	 0.8530	 0.4570
j	 0.9050	 0.4880
k	 0.8100	 0.4220
l	 0.8820	 0.5080

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Chain	Atom inclusion	Q-score
m	 0.8580	 0.4980
n	 0.8860	 0.4620
o	 0.8490	 0.4690
p	 0.8650	 0.4870
q	 0.6420	 0.2130
r	 0.8830	 0.4930