



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2024 – 01:58 PM EST

PDB ID : 3J7P
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 : 3J3B, 3J3D, 3J3F, 3J3A

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.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

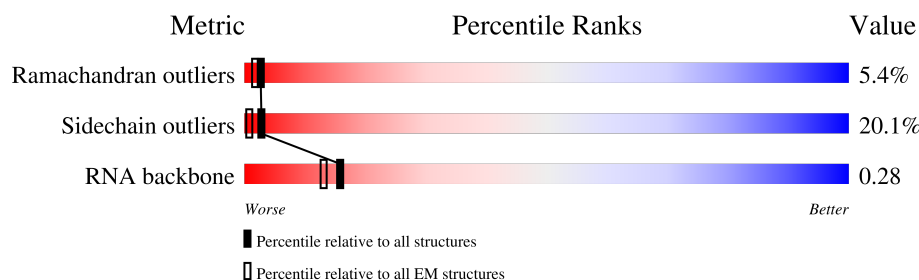
1 Overall quality at a glance

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.






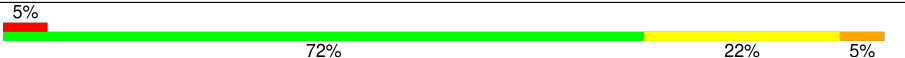

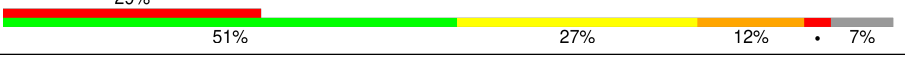


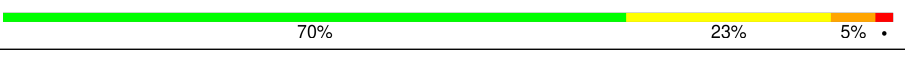


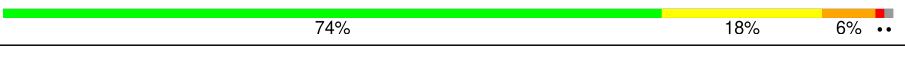





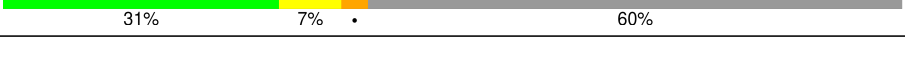

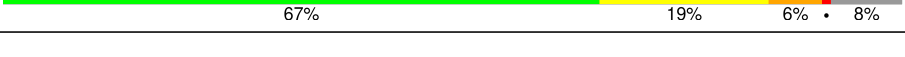
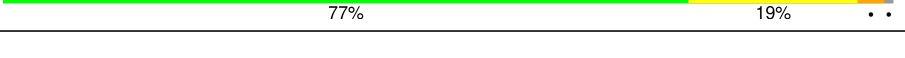
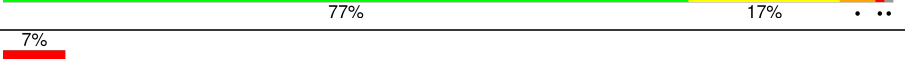

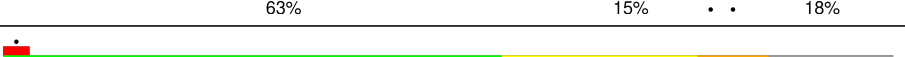

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	<div> <div>5%</div> <div>47%</div> <div>40%</div> <div>10%</div> <div>.</div> </div>
2	7	120	<div> <div>69%</div> <div>24%</div> <div>6%</div> <div>.</div> </div>
3	8	156	<div> <div>53%</div> <div>33%</div> <div>8%</div> <div>5%</div> </div>
4	A	257	<div> <div>71%</div> <div>18%</div> <div>5%</div> <div>5%</div> </div>
5	B	394	<div> <div>74%</div> <div>21%</div> <div>.</div> <div>.</div> </div>
6	C	367	<div> <div>77%</div> <div>19%</div> <div>.</div> <div>.</div> </div>
7	D	297	<div> <div>68%</div> <div>25%</div> <div>.</div> <div>.</div> <div>.</div> </div>
8	E	236	<div> <div>7%</div> <div>64%</div> <div>26%</div> <div>9%</div> <div>.</div> </div>


























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Mol	Chain	Length	Quality of chain
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	
29	Z	136	
30	a	148	
31	b	160	
32	c	115	
33	d	125	

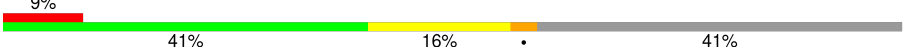


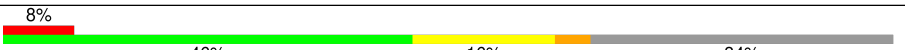
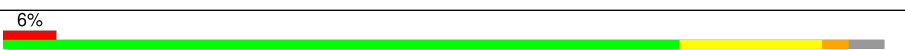

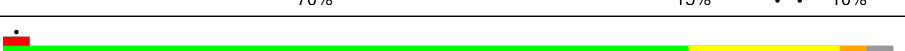
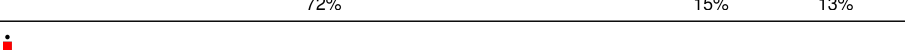
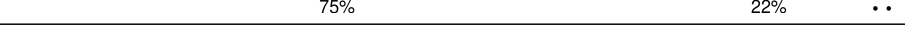
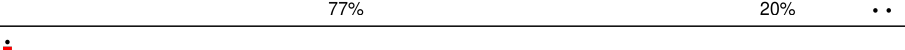
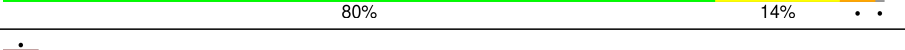
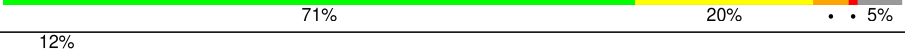
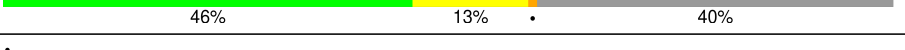

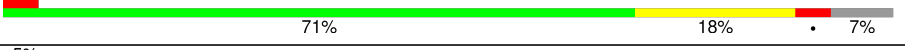


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Mol	Chain	Length	Quality of chain
34	e	135	
35	f	110	
36	g	117	
37	h	123	
38	i	105	
39	j	86	
40	k	70	
41	l	51	
42	m	128	
43	n	25	
44	o	106	
45	p	91	
46	q	202	
47	r	125	
48	4	856	
49	S2	1742	
50	SA	295	
51	SB	264	
52	SC	218	
53	SD	243	
54	SE	263	
55	SF	204	
56	SG	249	
57	SH	194	
58	SI	208	

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

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 (three-letter code: 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

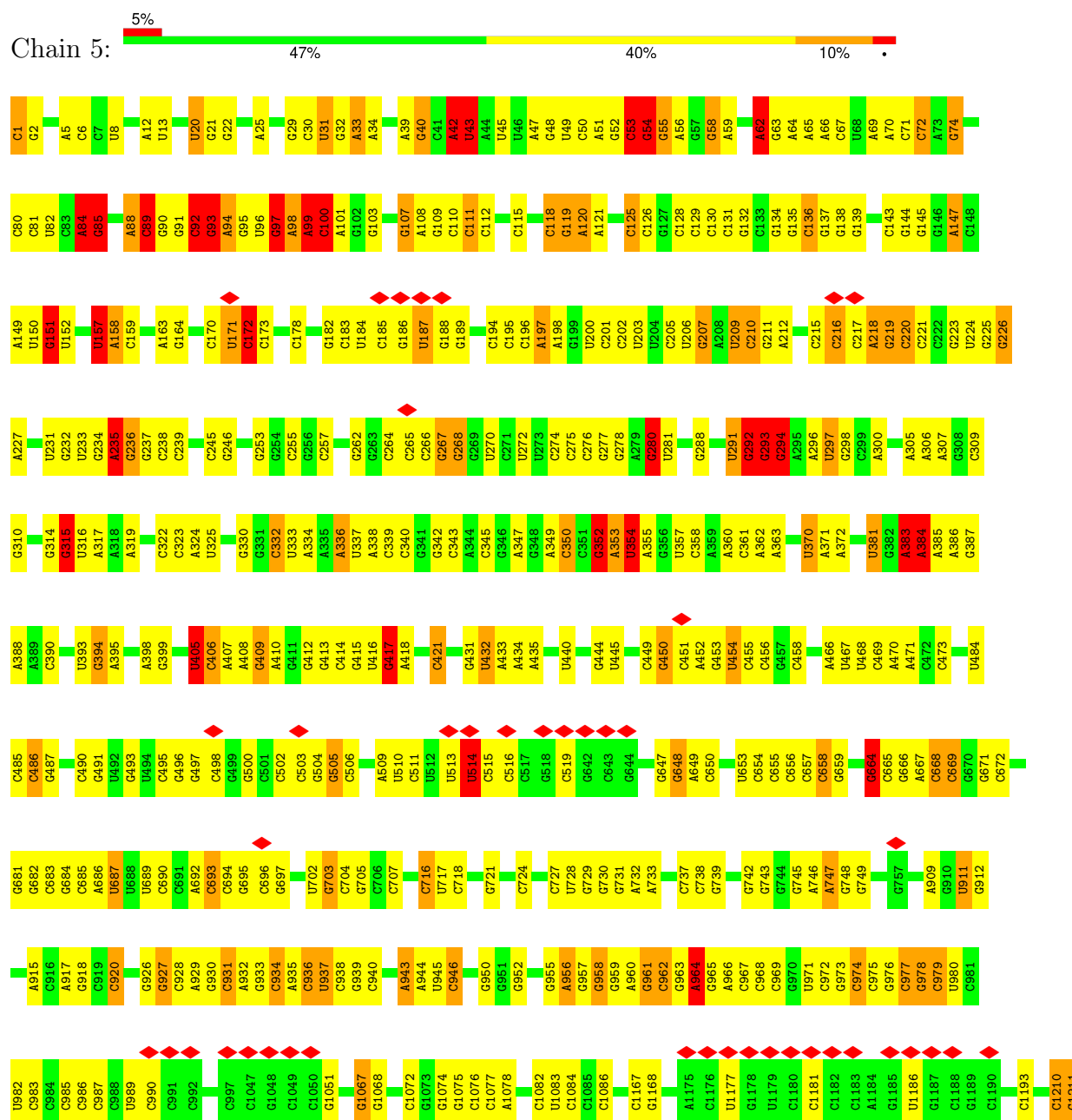
- Molecule 84 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

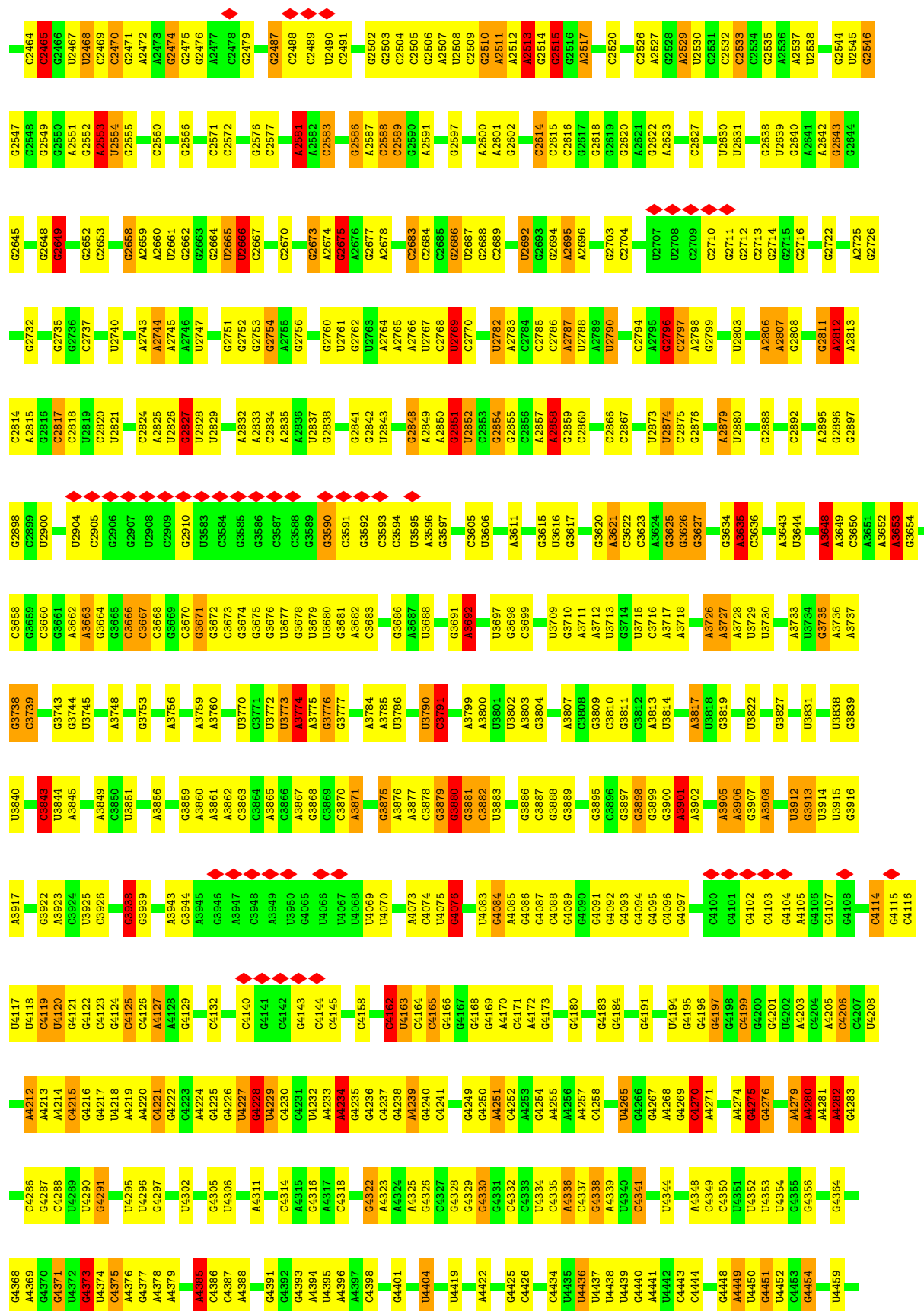
3 Residue-property plots

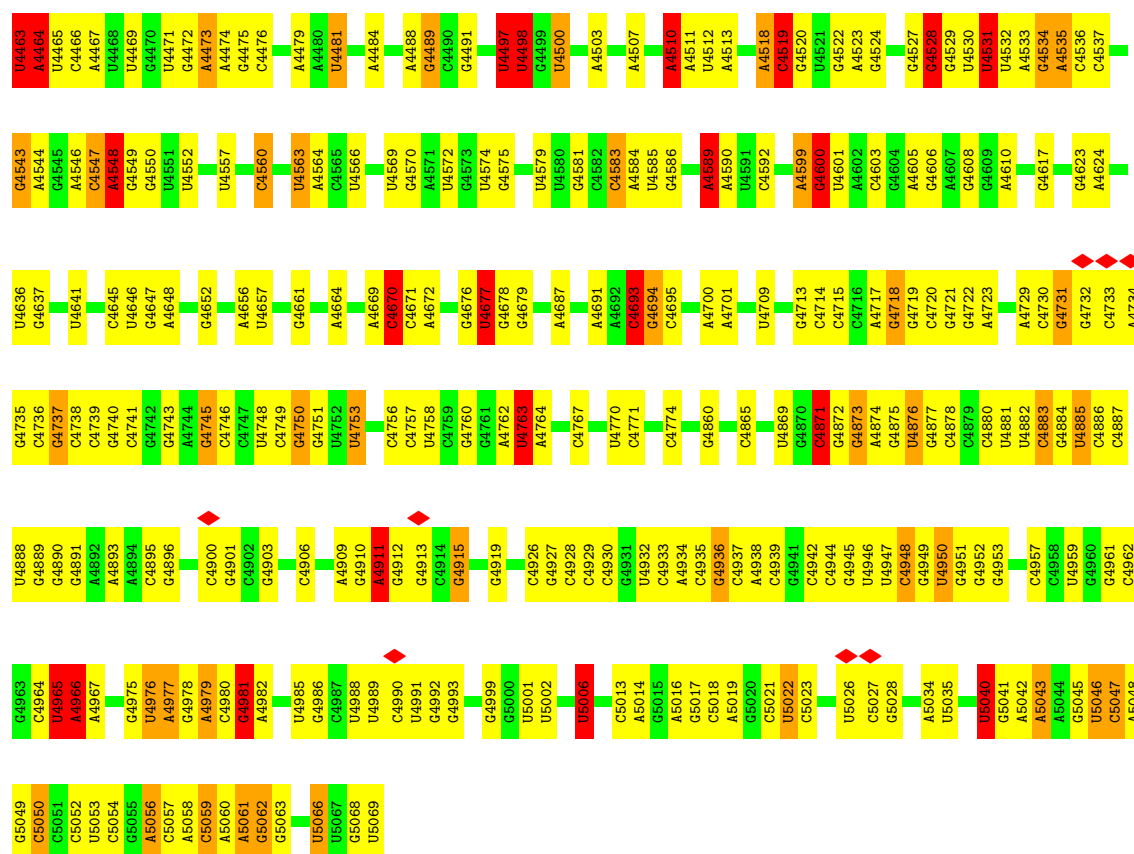
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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





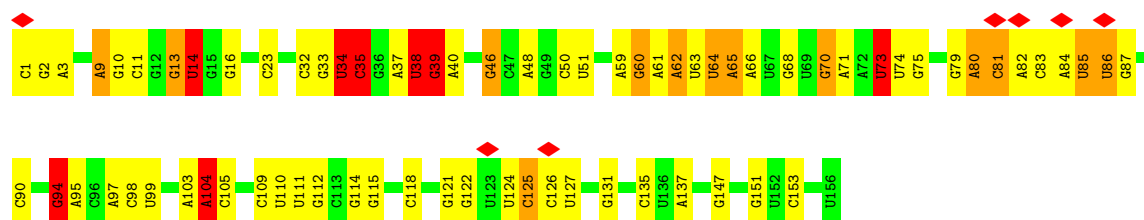




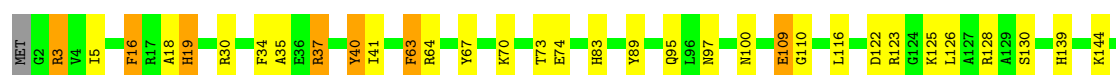
• Molecule 2: 5S ribosomal RNA

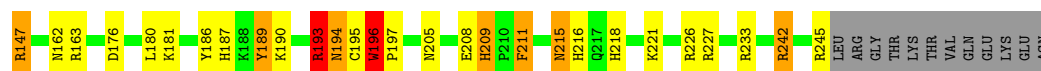


• Molecule 3: 5.8S ribosomal RNA



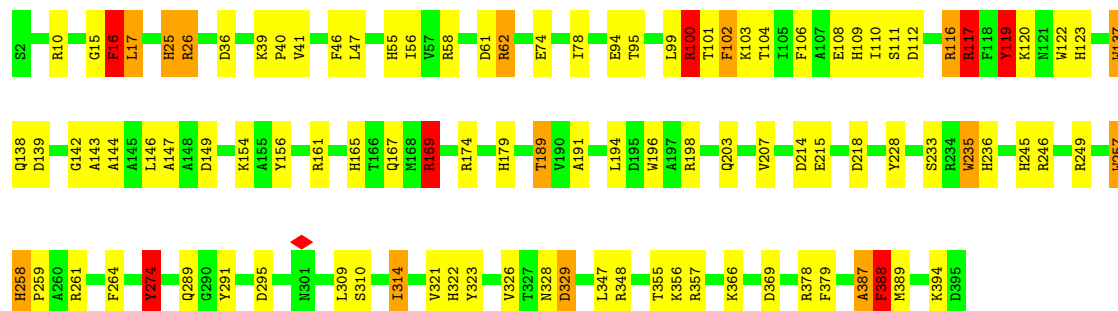
• Molecule 4: Ribosomal protein uL2





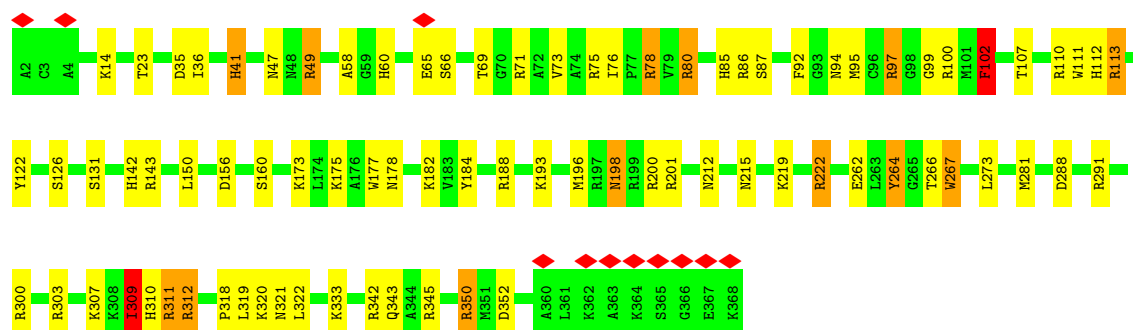
• Molecule 5: Ribosomal protein uL3

Chain B: 74% 21% . .



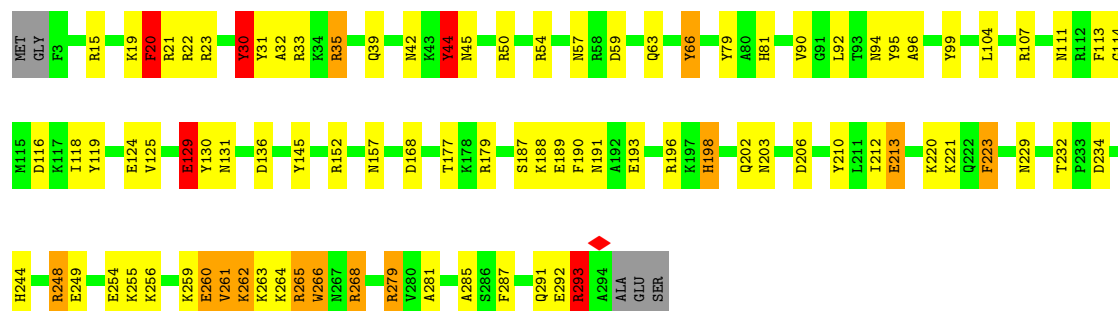
• Molecule 6: Ribosomal protein uL4

Chain C: 77% 19% . .



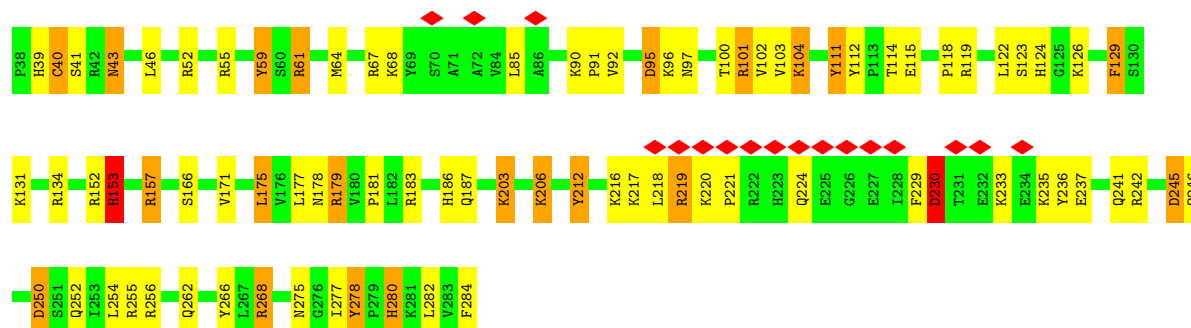
• Molecule 7: Ribosomal protein uL18

Chain D: 68% 25% . .



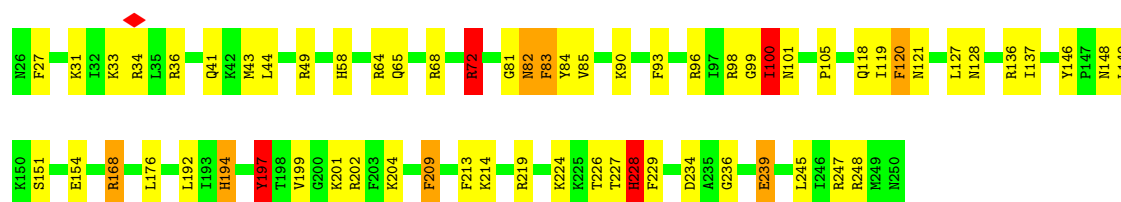
• Molecule 8: Ribosomal protein eL6

Chain E: 7% 64% 26% 9% .



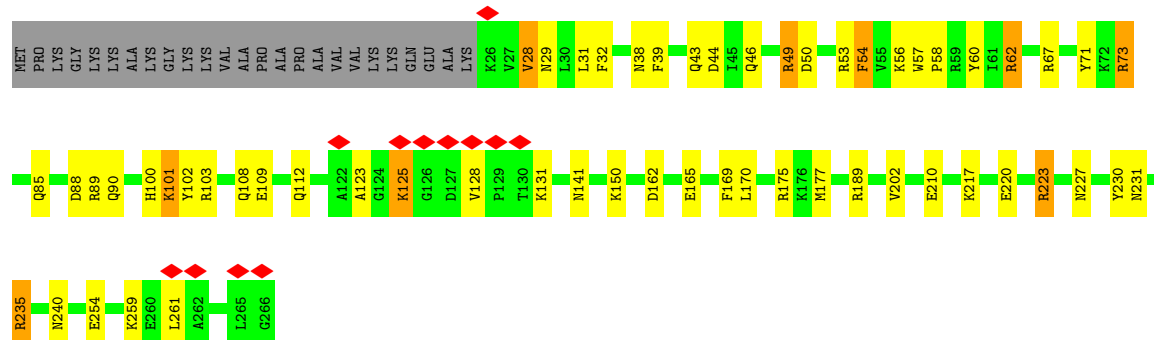
• Molecule 9: Ribosomal protein uL30

Chain F: 72% 24% 5%



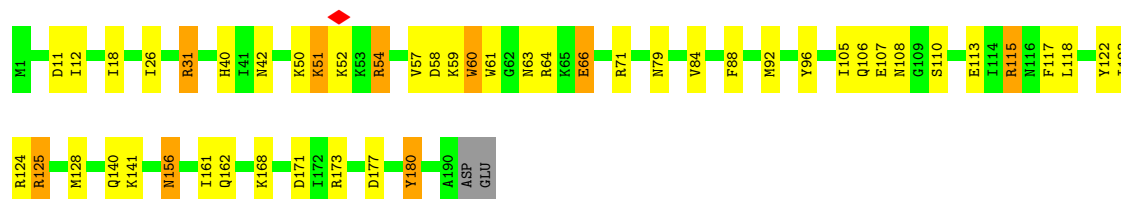
• Molecule 10: Ribosomal protein eL8

Chain G: 69% 18% 9%



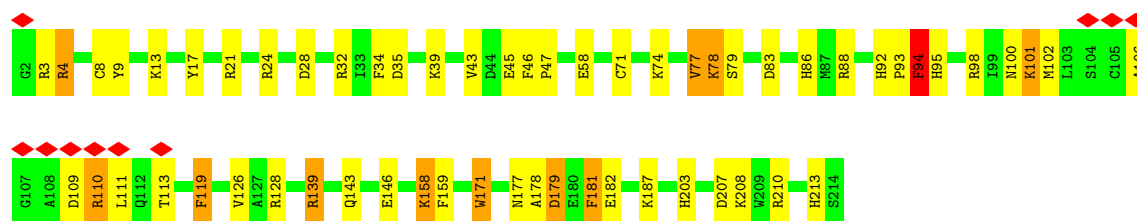
• Molecule 11: Ribosomal protein uL6

Chain H: 73% 21% 5%



• Molecule 12: Ribosomal protein uL16

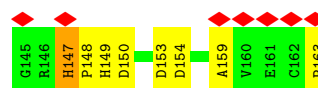
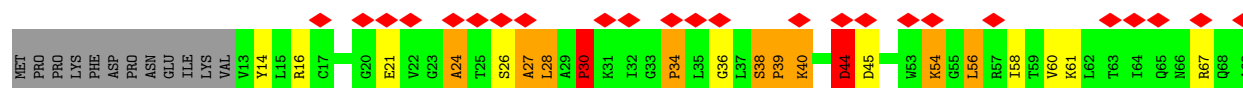
Chain I: 72% 22% 5%



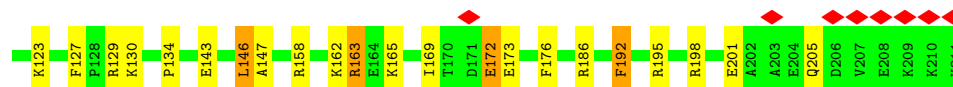
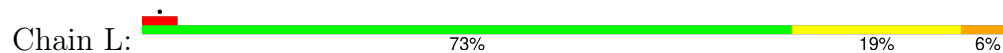
• Molecule 13: Ribosomal protein uL5



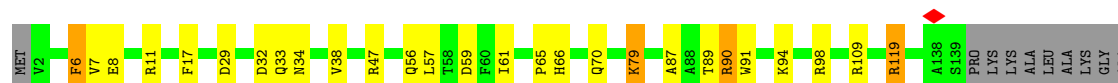
• Molecule 14: Ribosomal protein uL11



• Molecule 15: Ribosomal protein eL13

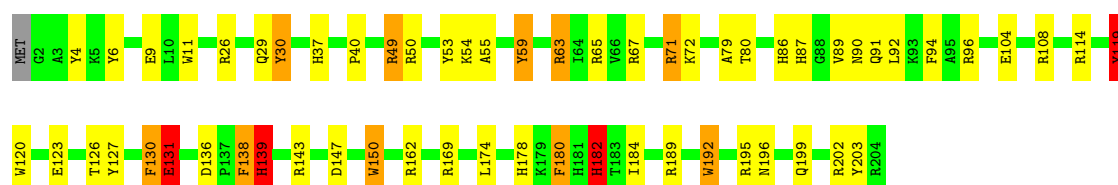


• Molecule 16: Ribosomal protein eL14

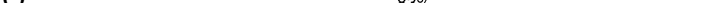


- Molecule 17: Ribosomal protein eL15

Chain N:  70% 23% 5%

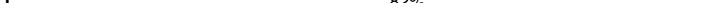


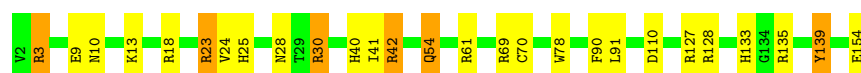
- Molecule 18: Ribosomal protein uL13

Chain O:  83% 12% ..



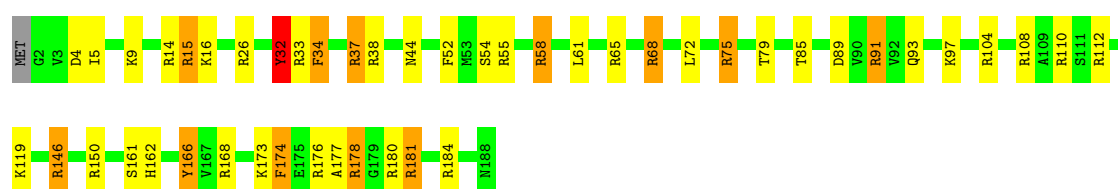
- Molecule 19: Ribosomal protein uL22

Chain P:  82% 14% .



- Molecule 20: Ribosomal protein eL18

Chain Q: 74% 18% 6%



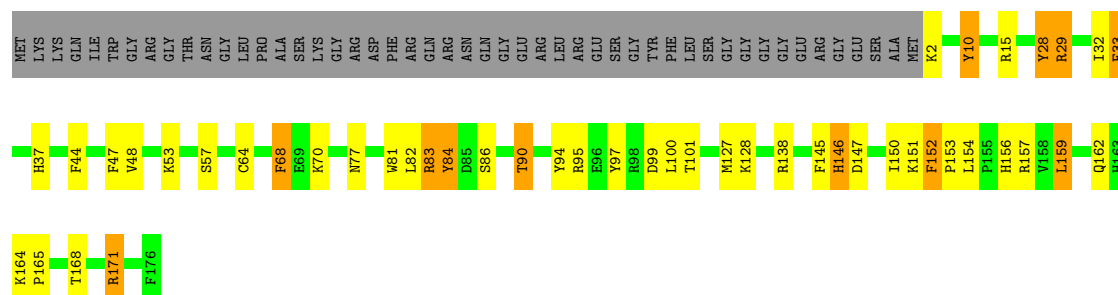
- Molecule 21: Ribosomal protein eL19

Chain R: 

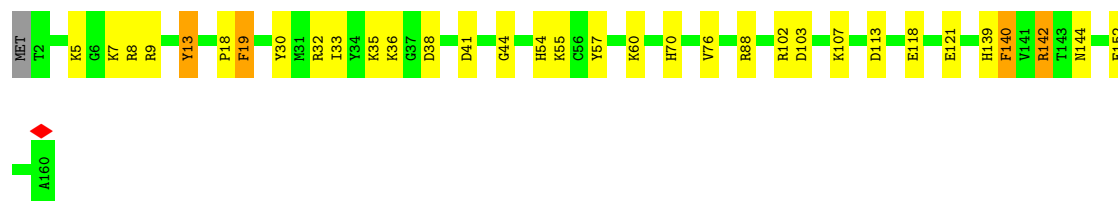
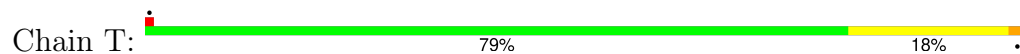




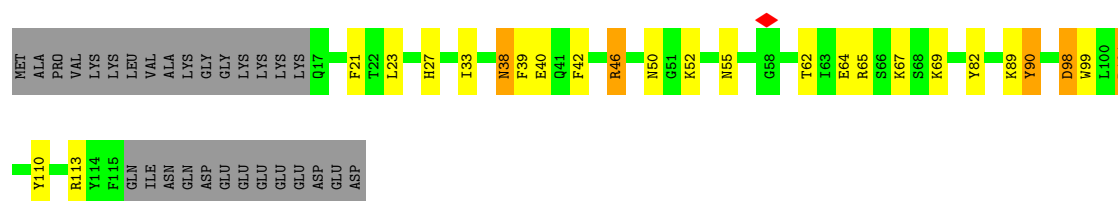
• Molecule 22: Ribosomal protein eL20



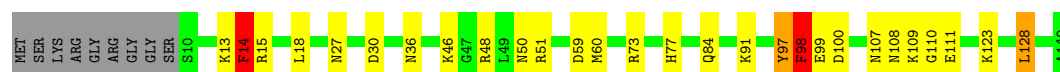
• Molecule 23: Ribosomal protein eL21



• Molecule 24: Ribosomal protein eL22



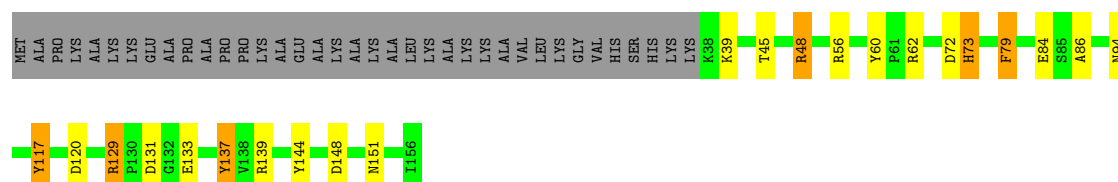
• Molecule 25: Ribosomal protein uL14



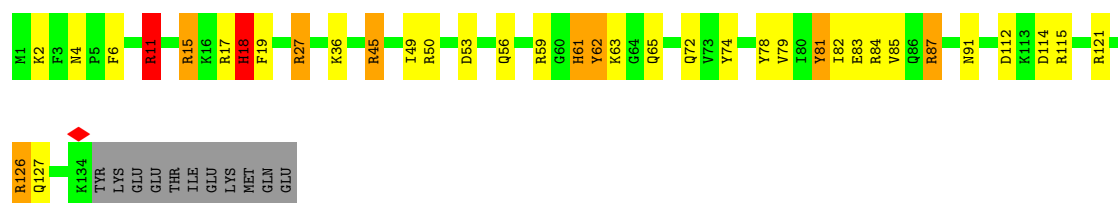
• Molecule 26: Ribosomal protein eL24



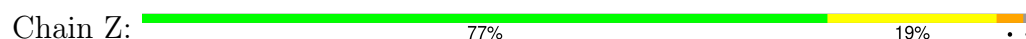
- Molecule 27: Ribosomal protein uL23



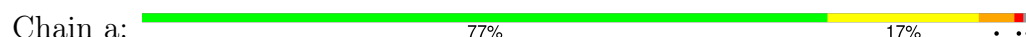
- Molecule 28: Ribosomal protein uL24



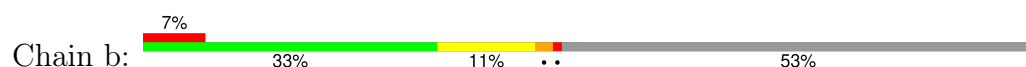
- Molecule 29: Ribosomal protein eL27

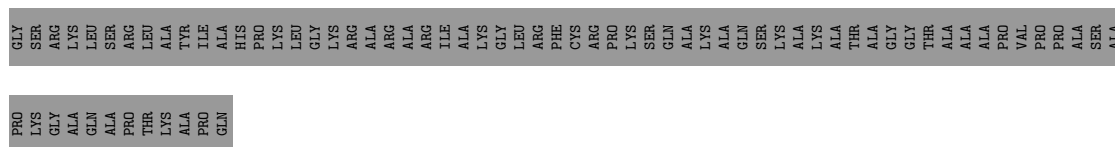


- Molecule 30: Ribosomal protein uL15

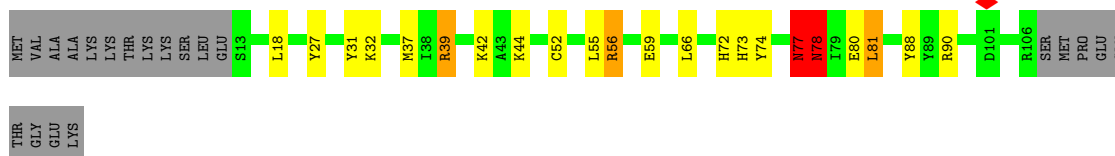


- Molecule 31: Ribosomal protein eL29

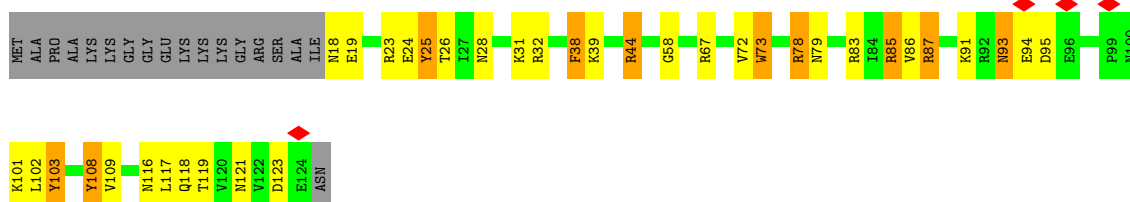




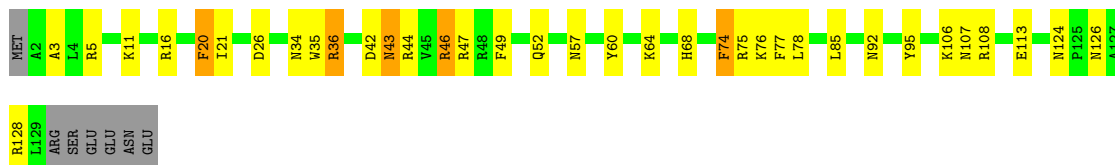
• Molecule 32: Ribosomal protein eL30



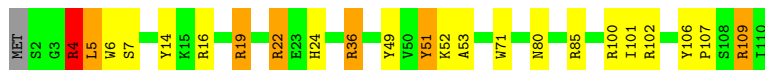
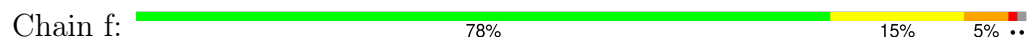
• Molecule 33: Ribosomal protein eL31



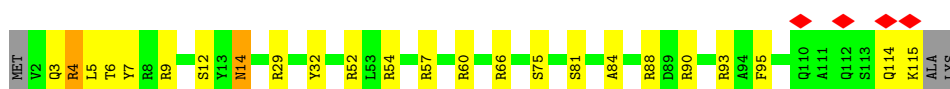
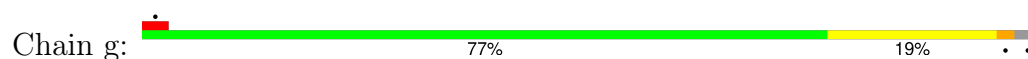
• Molecule 34: Ribosomal protein eL32




• Molecule 35: Ribosomal protein eL33

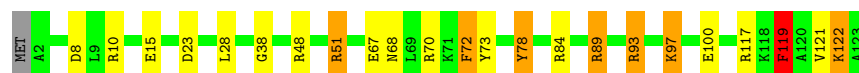


• Molecule 36: Ribosomal protein eL34



- Molecule 37: Ribosomal protein uL29

Chain h:  80% 12% 6% .



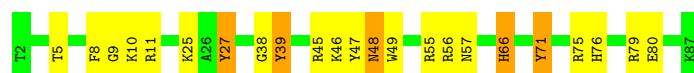
- Molecule 38: Ribosomal protein eL36

Chain i: 76% 17% • •



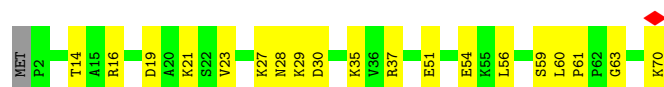
- Molecule 39: Ribosomal protein eL37

Chain j: 73% 21% 6%



- Molecule 40: Ribosomal protein eL38

Chain k:  71% 27%



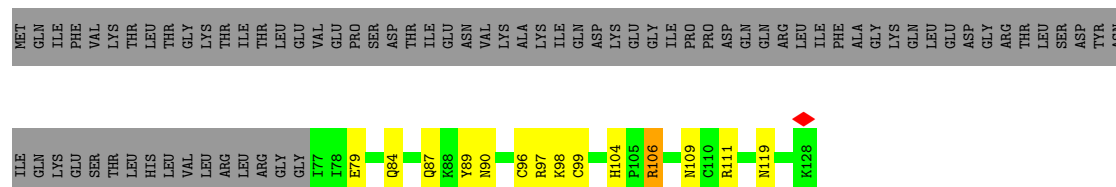
- Molecule 41: Ribosomal protein eL39

Chain 1: 76% 18% 6%



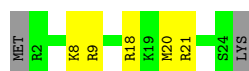
- Molecule 42: Ribosomal protein eL40

Chain m: 

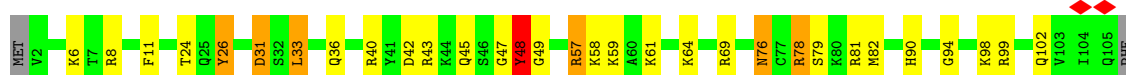


- Molecule 43: Ribosomal protein eL41

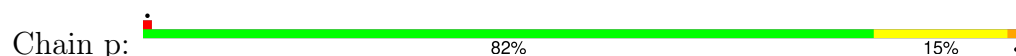
Chain n: 72% 20% 8%



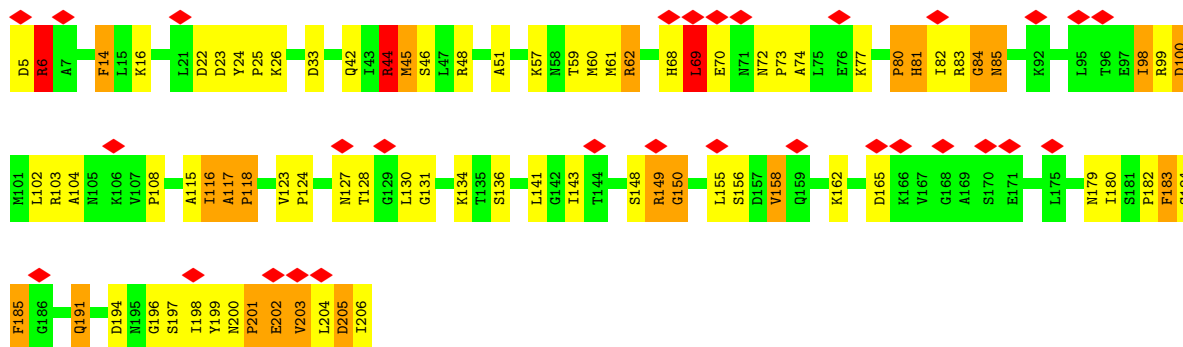
- Molecule 44: Ribosomal protein eL42



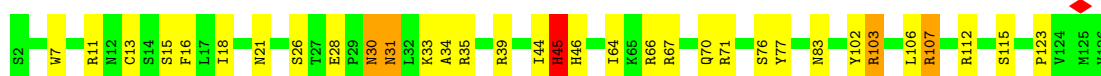
- Molecule 45: Ribosomal protein eL43



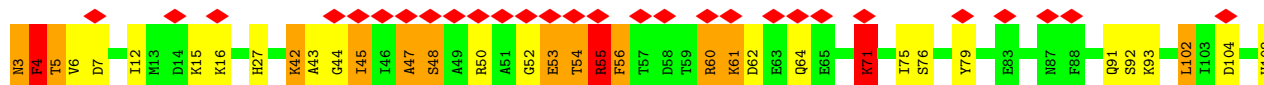
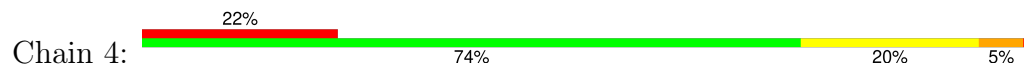
- Molecule 46: Ribosomal protein uL10

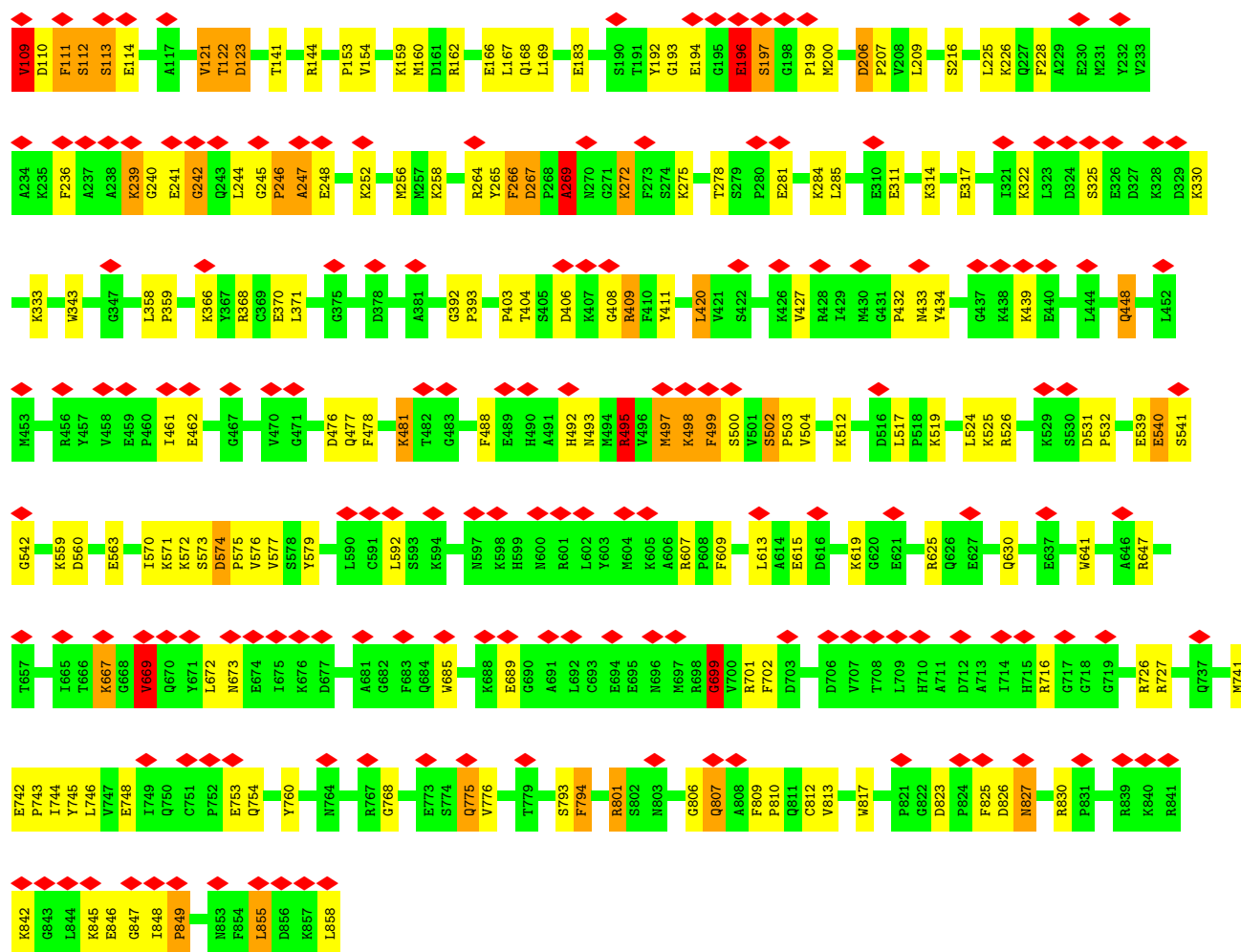


- Molecule 47: Ribosomal protein eL28

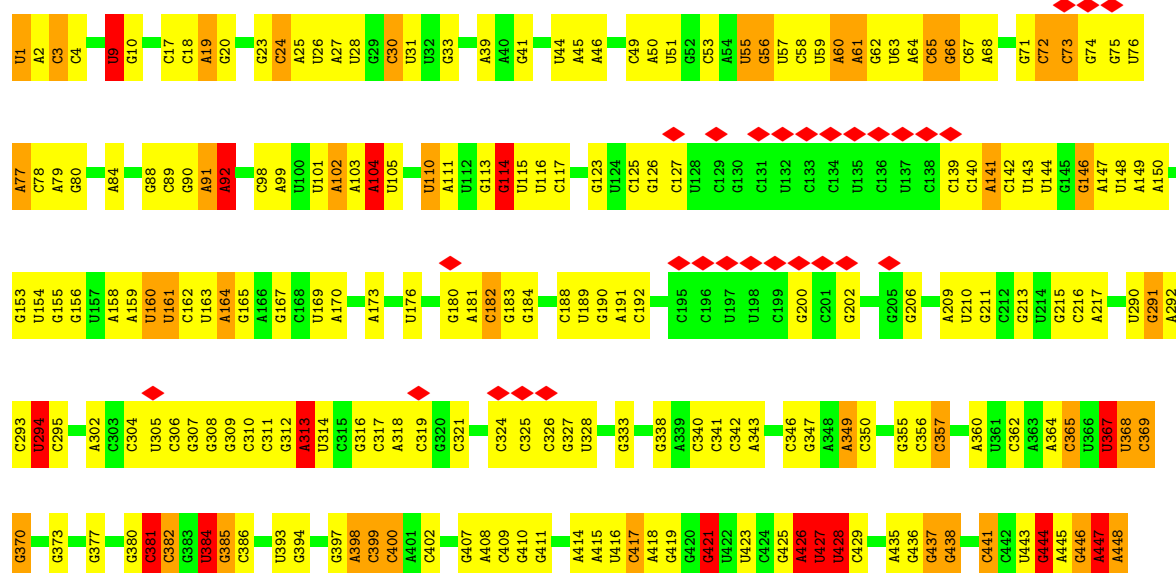


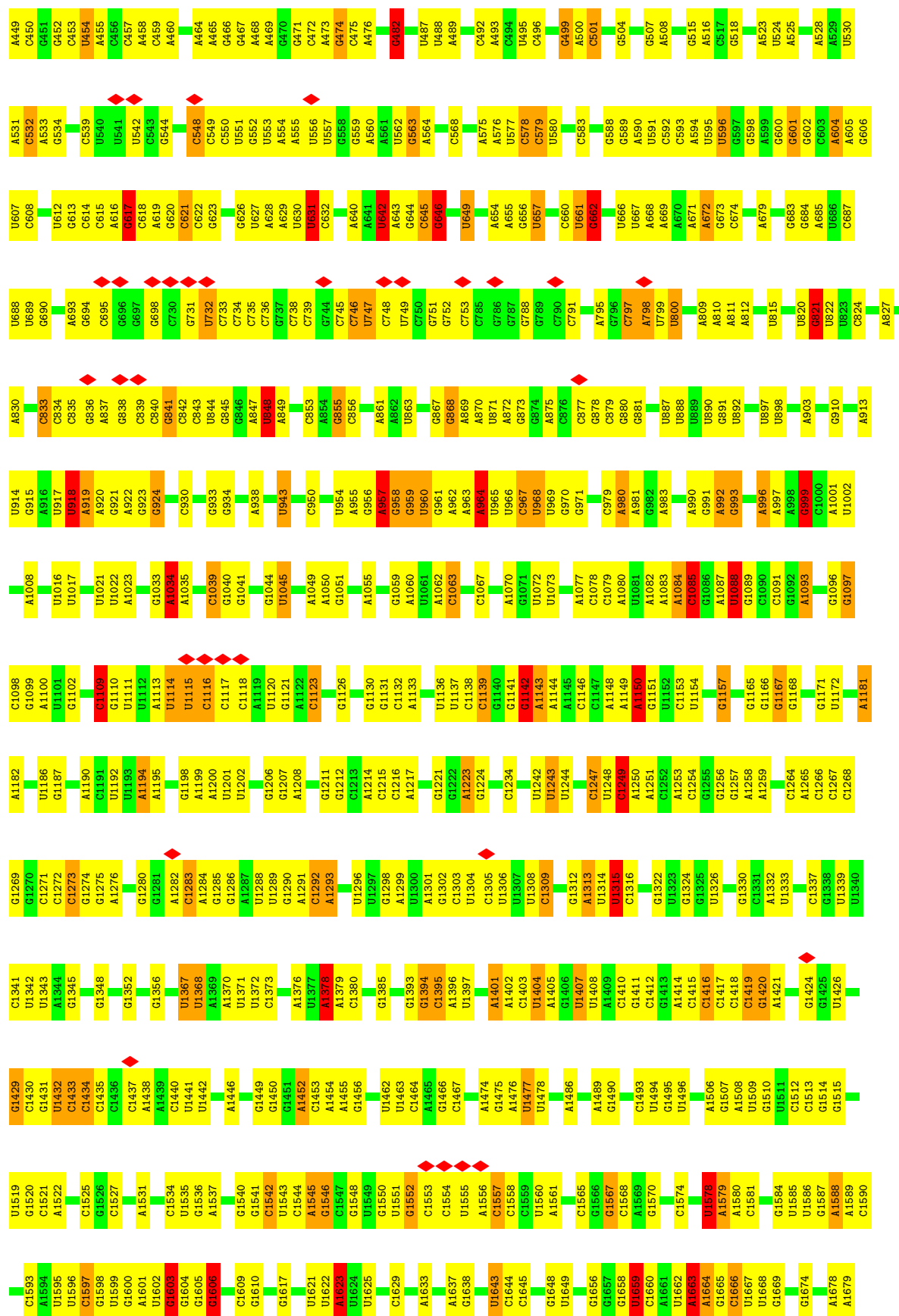
- Molecule 48: Eukaryotic elongation factor 2

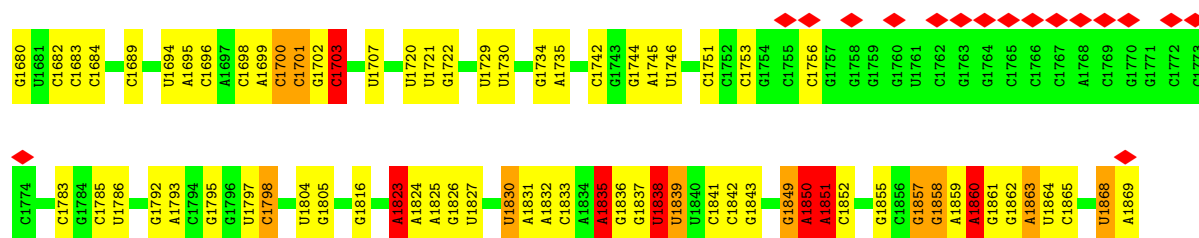




• Molecule 49: 18S ribosomal RNA

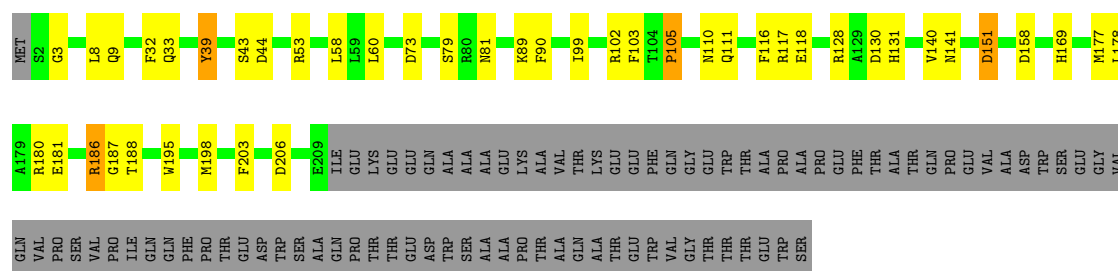






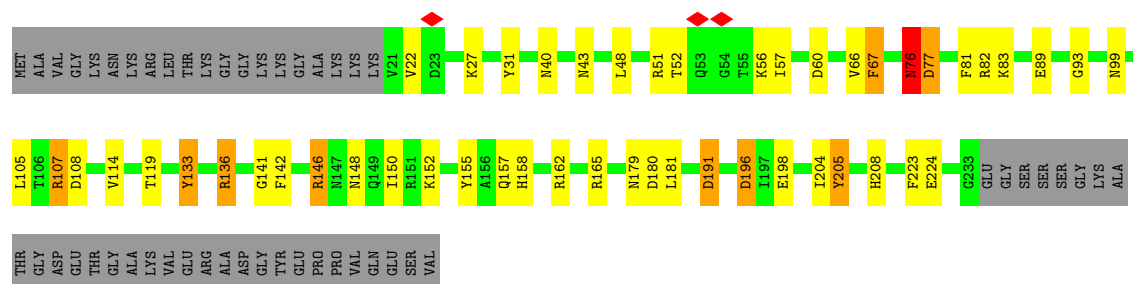
• Molecule 50: Ribosomal protein uS2

Chain SA: 56% 14% 29%



• Molecule 51: Ribosomal protein eS1

Chain SB: 62% 15% 19%



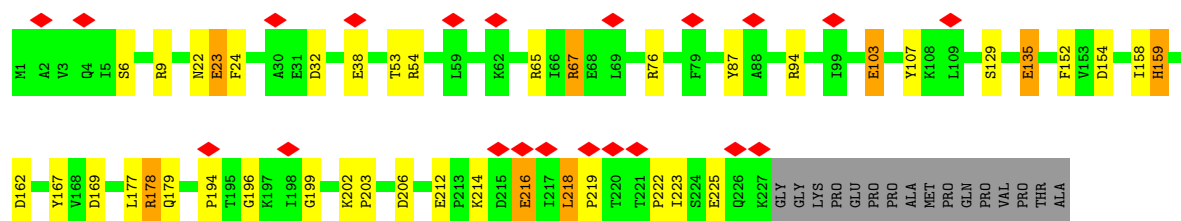
• Molecule 52: Ribosomal protein uS5

Chain SC: 79% 17% 4%

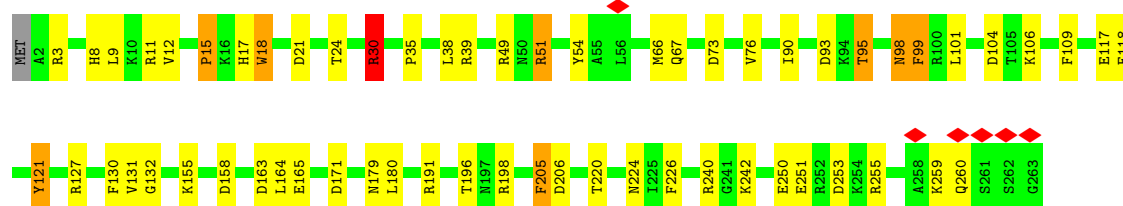
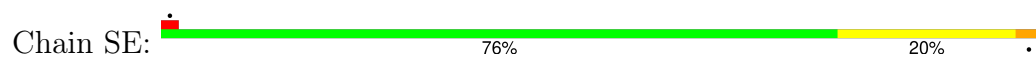


• Molecule 53: Ribosomal protein uS3

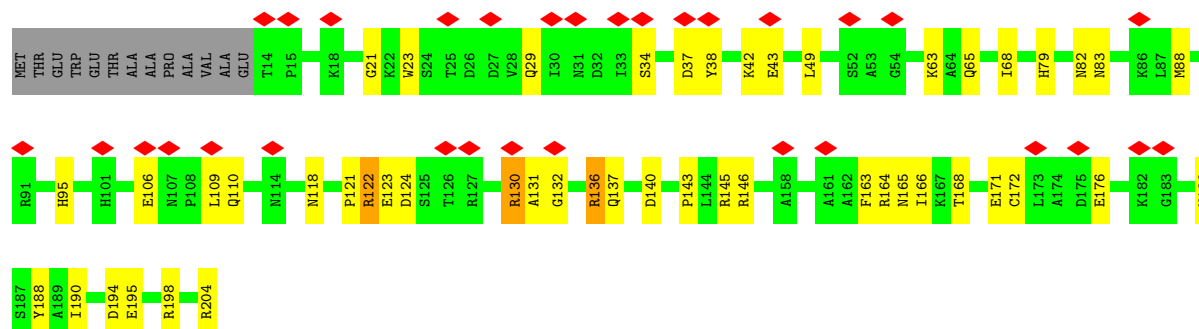
Chain SD: 9% 76% 14% 1%



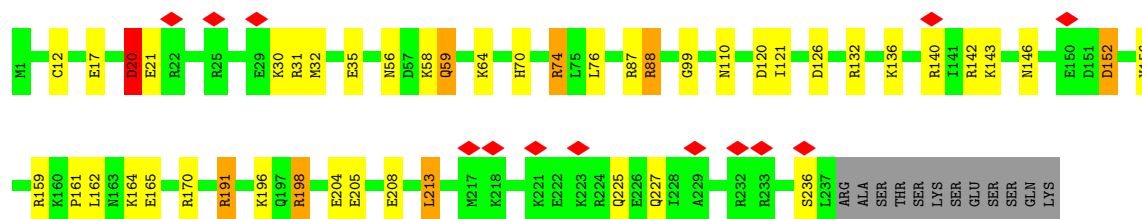
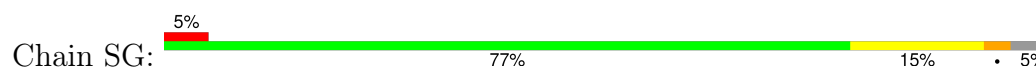
• Molecule 54: Ribosomal protein eS4



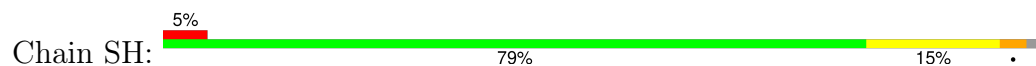
• Molecule 55: Ribosomal protein uS7

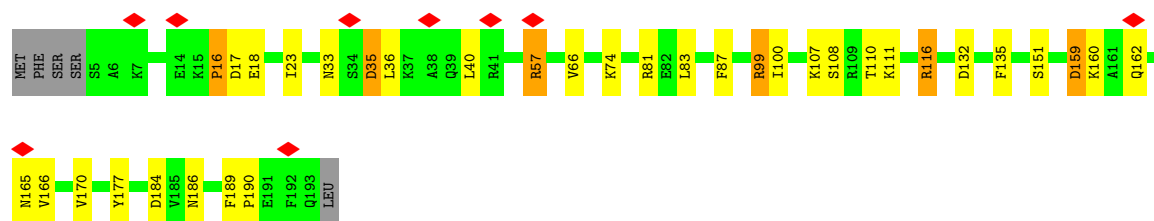


• Molecule 56: Ribosomal protein eS6

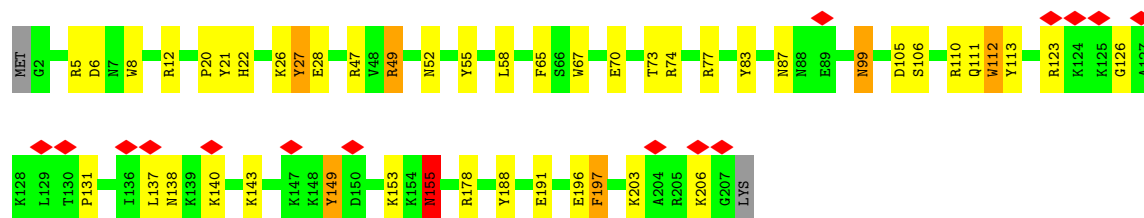
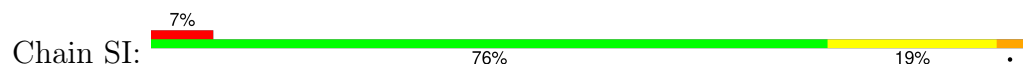


• Molecule 57: Ribosomal protein eS7

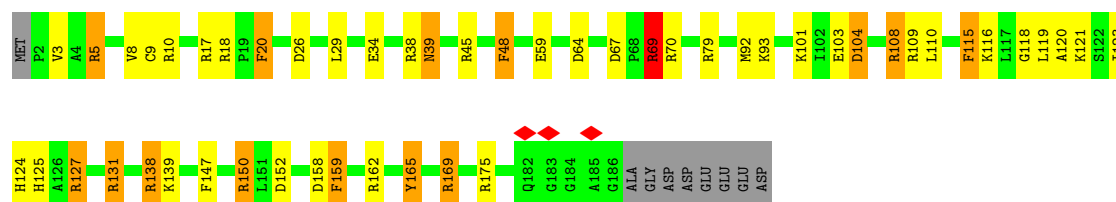




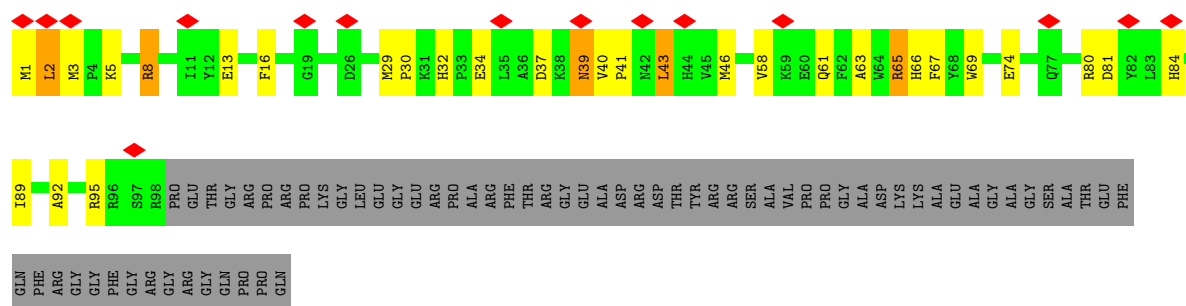
• Molecule 58: Ribosomal protein eS8



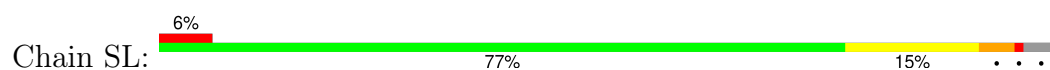
• Molecule 59: Ribosomal protein uS4

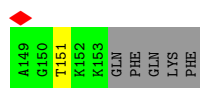


• Molecule 60: Ribosomal protein eS10

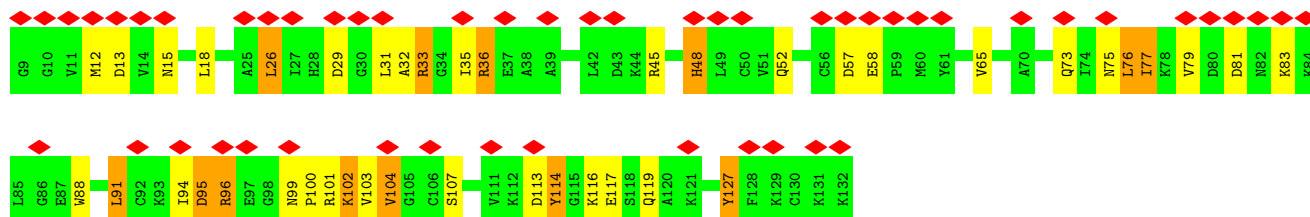
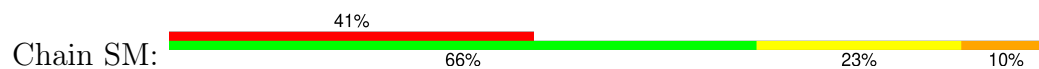


• Molecule 61: Ribosomal protein uS17

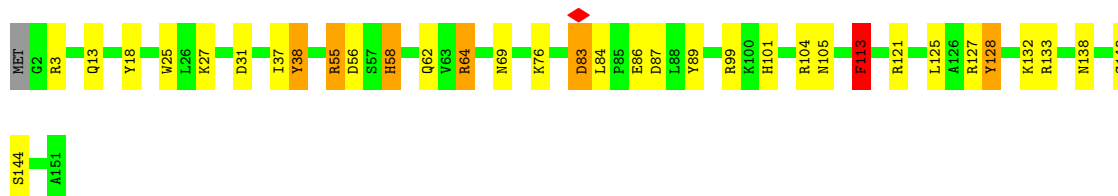
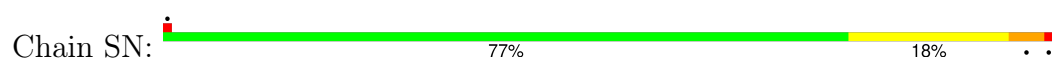




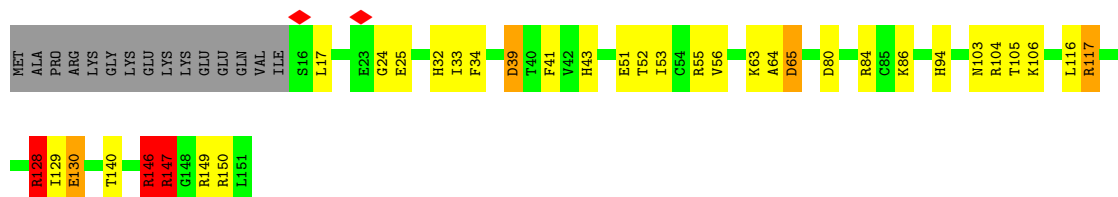
- Molecule 62: Ribosomal protein eS12



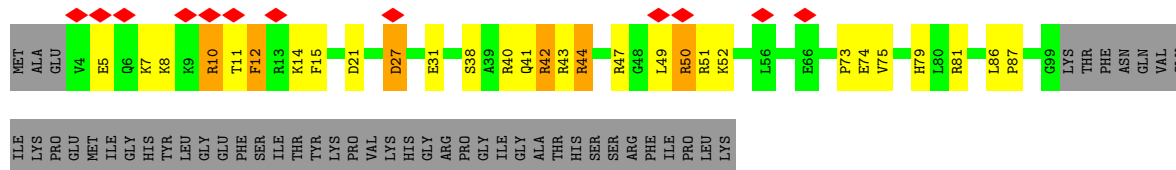
- Molecule 63: Ribosomal protein uS15



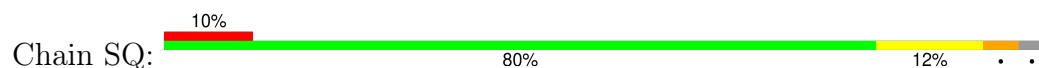
- Molecule 64: Ribosomal protein uS11

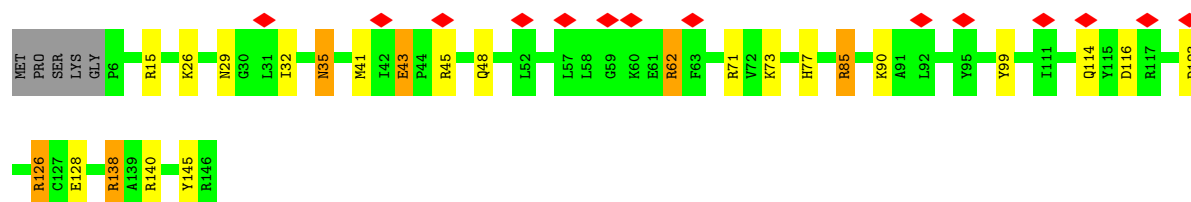


- Molecule 65: Ribosomal protein uS19

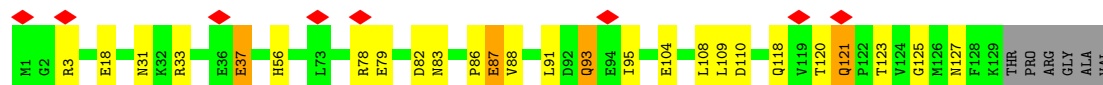
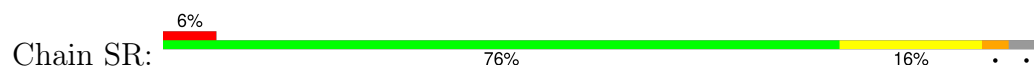


- Molecule 66: Ribosomal protein uS9

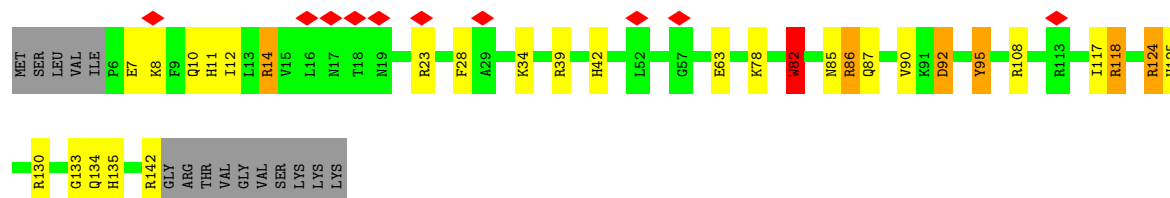




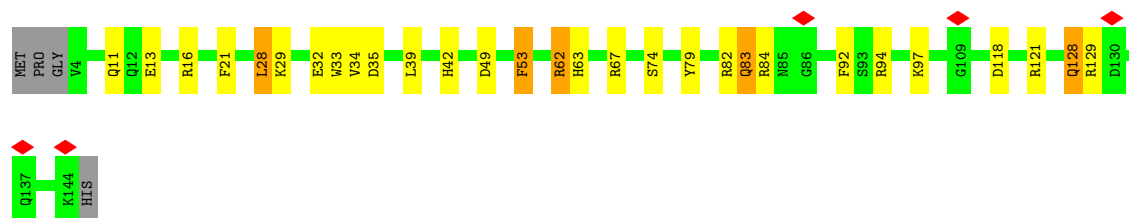
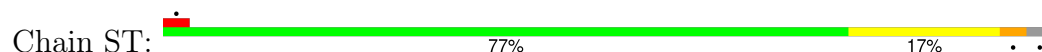
- Molecule 67: Ribosomal protein eS17



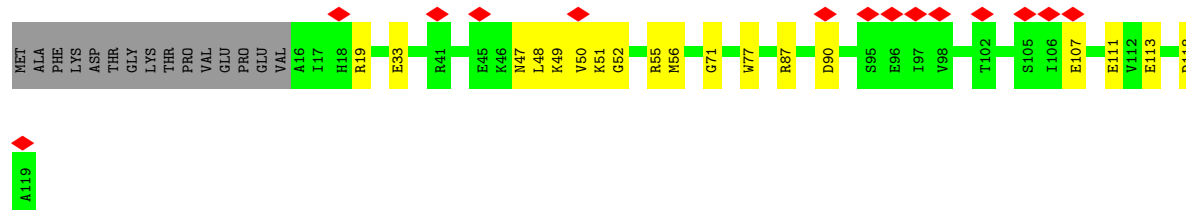
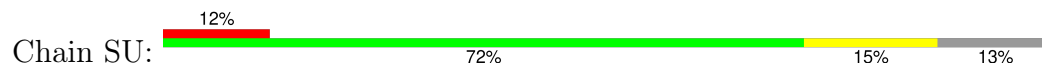
- Molecule 68: Ribosomal protein uS13




- Molecule 69: Ribosomal protein eS19



- Molecule 70: Ribosomal protein uS10




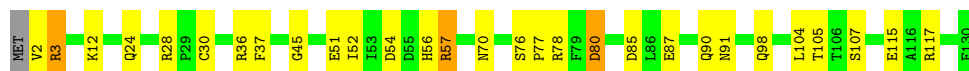
- Molecule 71: Ribosomal protein eS21

Chain SV:  75% 22% ..




- Molecule 72: Ribosomal protein uS8

Chain SW:  77% 20% ..



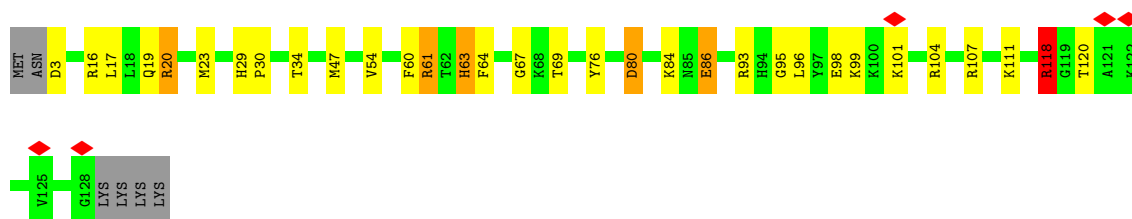
- Molecule 73: Ribosomal protein uS12

Chain SX:  80% 14% ..



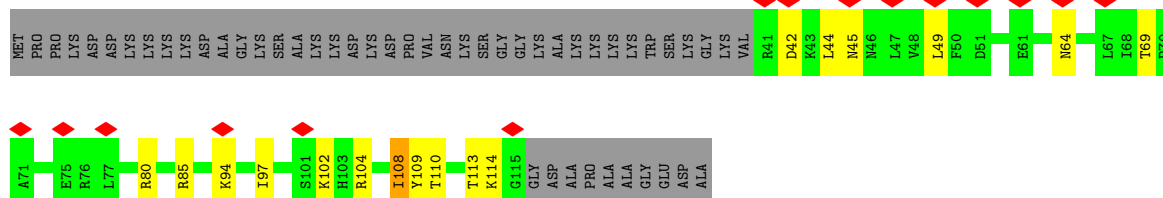
- Molecule 74: Ribosomal protein eS24

Chain SY:  71% 20% 5%



- Molecule 75: Ribosomal protein es25

Chain SZ:  12% 46% 13% 40%




- Molecule 76: Ribosomal protein eS26

Chain Sa:  70% 13% 15%




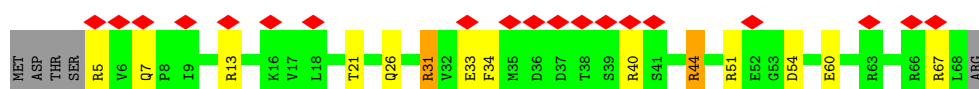
- Molecule 77: Ribosomal protein eS27

Chain Sb: 



- Molecule 78: Ribosomal protein eS28

Chain Sc: 




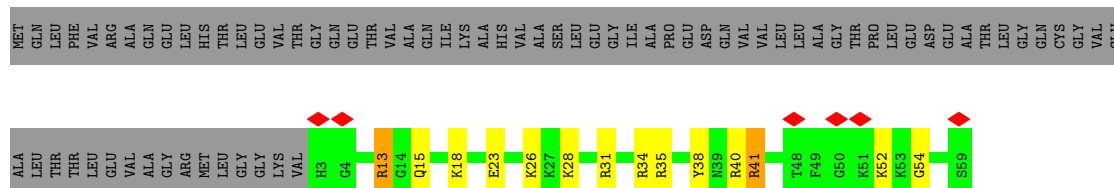
- Molecule 79: Ribosomal protein uS14

Chain Sd: 




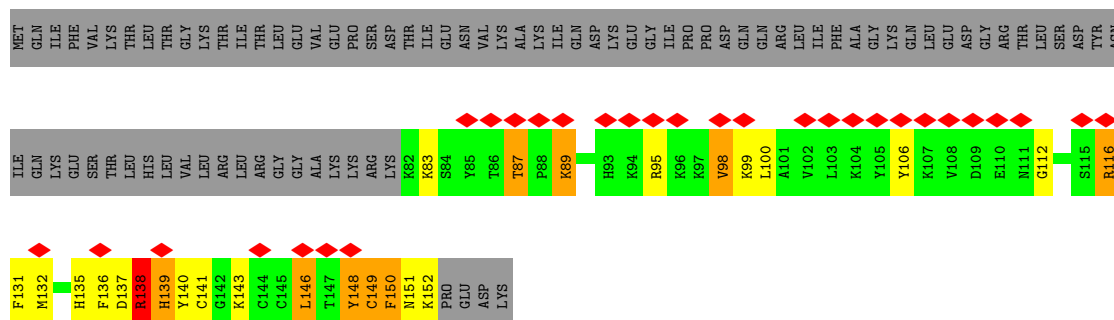
- Molecule 80: Ribosomal protein eS30

Chain Se: 




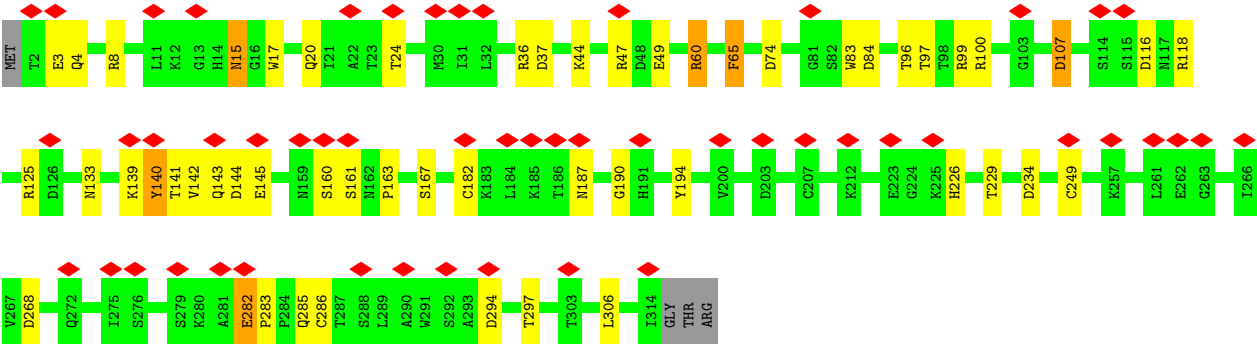
- Molecule 81: Ribosomal protein eS31

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 (\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 (\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	0.64	75/87792 (0.1%)	1.12	729/136945 (0.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
3	8	0.68	3/3701 (0.1%)	1.19	42/5766 (0.7%)
4	A	0.80	3/1906 (0.2%)	1.26	21/2556 (0.8%)
5	B	0.81	8/3214 (0.2%)	1.16	25/4308 (0.6%)
6	C	0.73	3/2973 (0.1%)	1.12	18/3990 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	26/3252 (0.8%)
8	E	0.73	5/1941 (0.3%)	1.21	20/2601 (0.8%)
9	F	0.80	2/1905 (0.1%)	1.27	27/2539 (1.1%)
10	G	0.76	4/1966 (0.2%)	1.09	14/2645 (0.5%)
11	H	0.77	3/1537 (0.2%)	1.17	10/2066 (0.5%)
12	I	0.66	1/1753 (0.1%)	1.11	12/2343 (0.5%)
13	J	0.63	1/1382 (0.1%)	1.04	12/1849 (0.6%)
14	K	1.04	11/1154 (1.0%)	1.78	54/1555 (3.5%)
15	L	0.70	2/1734 (0.1%)	1.12	15/2318 (0.6%)
16	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
17	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
18	O	0.72	3/1684 (0.2%)	1.10	12/2251 (0.5%)
19	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
20	Q	0.69	0/1530	1.35	31/2041 (1.5%)
21	R	0.79	3/1524 (0.2%)	1.27	20/2013 (1.0%)
22	S	0.95	8/1493 (0.5%)	1.30	19/2002 (0.9%)
23	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
24	U	0.63	1/822 (0.1%)	1.03	3/1103 (0.3%)
25	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
26	W	0.71	0/541	1.23	5/720 (0.7%)
27	X	0.64	0/993	1.09	10/1334 (0.7%)
28	Y	0.72	0/1132	1.24	19/1504 (1.3%)
29	Z	0.63	0/1130	1.11	10/1507 (0.7%)
30	a	0.93	6/1192 (0.5%)	1.37	17/1591 (1.1%)
31	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
32	c	0.70	0/742	1.14	5/996 (0.5%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)
34	e	0.90	3/1071 (0.3%)	1.23	15/1429 (1.0%)
35	f	1.01	2/895 (0.2%)	1.34	17/1198 (1.4%)
36	g	0.65	0/916	1.08	5/1220 (0.4%)
37	h	0.63	0/1023	1.21	14/1350 (1.0%)
38	i	0.63	0/843	1.20	8/1115 (0.7%)
39	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)
40	k	0.59	0/575	0.97	1/761 (0.1%)
41	l	0.70	0/454	1.14	4/599 (0.7%)
42	m	0.55	0/435	0.95	1/575 (0.2%)
43	n	0.49	0/223	1.01	0/284
44	o	0.64	0/864	1.27	8/1140 (0.7%)
45	p	0.64	1/718 (0.1%)	1.01	3/953 (0.3%)
46	q	0.81	7/1580 (0.4%)	1.35	37/2133 (1.7%)
47	r	0.68	0/1017	1.12	8/1365 (0.6%)
48	4	0.99	20/6804 (0.3%)	1.41	93/9189 (1.0%)
49	S2	0.65	37/41243 (0.1%)	1.14	330/64257 (0.5%)
50	SA	0.94	4/1679 (0.2%)	1.06	6/2283 (0.3%)
51	SB	0.89	6/1753 (0.3%)	1.15	14/2350 (0.6%)
52	SC	0.99	8/1726 (0.5%)	1.11	9/2332 (0.4%)
53	SD	1.39	12/1793 (0.7%)	1.10	9/2414 (0.4%)
54	SE	0.83	8/2118 (0.4%)	0.98	7/2849 (0.2%)
55	SF	0.74	1/1531 (0.1%)	1.08	9/2059 (0.4%)
56	SG	0.97	9/1946 (0.5%)	1.03	9/2590 (0.3%)
57	SH	0.73	2/1544 (0.1%)	1.02	8/2068 (0.4%)
58	SI	0.97	8/1715 (0.5%)	1.12	12/2287 (0.5%)
59	SJ	1.07	12/1550 (0.8%)	1.28	16/2069 (0.8%)
60	SK	0.75	1/851 (0.1%)	1.00	3/1147 (0.3%)
61	SL	0.85	5/1259 (0.4%)	1.09	7/1684 (0.4%)
62	SM	2.22	2/970 (0.2%)	1.21	8/1300 (0.6%)
63	SN	0.82	4/1232 (0.3%)	1.15	10/1656 (0.6%)
64	SO	1.18	7/1029 (0.7%)	1.38	12/1380 (0.9%)
65	SP	1.52	6/816 (0.7%)	1.29	8/1084 (0.7%)
66	SQ	0.72	2/1142 (0.2%)	1.01	8/1528 (0.5%)
67	SR	0.81	5/1060 (0.5%)	1.02	2/1421 (0.1%)
68	SS	0.66	1/1157 (0.1%)	1.18	13/1548 (0.8%)
69	ST	0.67	2/1119 (0.2%)	1.08	7/1499 (0.5%)
70	SU	0.94	4/828 (0.5%)	0.96	1/1112 (0.1%)
71	SV	0.73	0/631	0.97	0/844
72	SW	1.06	6/1051 (0.6%)	1.22	5/1406 (0.4%)
73	SX	0.99	6/1118 (0.5%)	1.12	12/1493 (0.8%)
74	SY	1.63	5/1040 (0.5%)	1.11	9/1382 (0.7%)
75	SZ	0.56	0/604	0.87	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
76	Sa	0.81	1/794 (0.1%)	1.25	5/1065 (0.5%)
77	Sb	0.59	0/665	0.90	0/891
78	Sc	0.68	0/508	1.13	4/680 (0.6%)
79	Sd	0.79	0/445	1.12	1/589 (0.2%)
80	Se	0.72	1/458 (0.2%)	1.16	5/602 (0.8%)
81	Sf	1.08	6/593 (1.0%)	1.57	12/786 (1.5%)
82	Sg	0.80	11/2493 (0.4%)	0.89	8/3394 (0.2%)
All	All	0.75	379/237633 (0.2%)	1.15	2051/348088 (0.6%)

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	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 379 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
62	SM	58	GLU	CD-OE1	64.43	1.96	1.25
53	SD	216	GLU	CD-OE1	43.67	1.73	1.25
1	5	1823	G	O3'-P	41.55	2.11	1.61
74	SY	86	GLU	CD-OE2	39.60	1.69	1.25
65	SP	21	ASP	CG-OD1	30.90	1.96	1.25

The worst 5 of 2051 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
48	4	699	GLY	CA-C-N	-32.10	46.58	117.20
48	4	699	GLY	C-N-CA	-28.33	50.88	121.70
48	4	768	GLY	O-C-N	21.39	156.93	122.70
72	SW	117	ARG	NE-CZ-NH2	-20.64	109.98	120.30
46	q	205	ASP	CA-C-N	-20.22	72.71	117.20

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 [i](#)

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	A	242/257 (94%)	203 (84%)	30 (12%)	9 (4%)	2	22
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	0	8
6	C	365/367 (100%)	304 (83%)	46 (13%)	15 (4%)	2	20
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	9
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	18
10	G	239/266 (90%)	200 (84%)	32 (13%)	7 (3%)	3	27
11	H	188/192 (98%)	164 (87%)	20 (11%)	4 (2%)	5	32
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	17
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	39
17	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	3	26
18	O	199/204 (98%)	182 (92%)	14 (7%)	3 (2%)	8	39
19	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	10	41
20	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	4	28
21	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	5	31
22	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	7	36
23	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	6	34
24	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	5	32
25	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	5	31
26	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	8	38
27	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	7	36
28	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	2	18

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
29	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	2	21
30	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	1	14
31	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	1	14
32	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	2	19
33	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	2	21
34	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	16	51
35	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	2	17
36	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	7	35
37	h	120/123 (98%)	102 (85%)	15 (12%)	3 (2%)	4	29
38	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	6	33
39	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	17
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	13
45	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	12	45
46	q	200/202 (99%)	133 (66%)	27 (14%)	40 (20%)	0	1
47	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	2	16
48	4	854/856 (100%)	754 (88%)	58 (7%)	42 (5%)	2	16
50	SA	206/295 (70%)	176 (85%)	24 (12%)	6 (3%)	3	27
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	22
53	SD	225/243 (93%)	170 (76%)	44 (20%)	11 (5%)	2	16
54	SE	260/263 (99%)	202 (78%)	41 (16%)	17 (6%)	1	12
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	28
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	24
59	SJ	183/194 (94%)	145 (79%)	24 (13%)	14 (8%)	1	9
60	SK	96/165 (58%)	60 (62%)	26 (27%)	10 (10%)	0	6

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
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	24
64	SO	134/151 (89%)	102 (76%)	18 (13%)	14 (10%)	0	6
65	SP	94/145 (65%)	65 (69%)	18 (19%)	11 (12%)	0	5
66	SQ	139/146 (95%)	112 (81%)	21 (15%)	6 (4%)	2	19
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	13
69	ST	139/145 (96%)	116 (84%)	17 (12%)	6 (4%)	2	19
70	SU	102/119 (86%)	80 (78%)	18 (18%)	4 (4%)	2	21
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	26
73	SX	139/143 (97%)	116 (84%)	18 (13%)	5 (4%)	3	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%)	1	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	13
80	Se	55/133 (41%)	40 (73%)	14 (26%)	1 (2%)	7	35
81	Sf	69/156 (44%)	39 (56%)	21 (30%)	9 (13%)	0	4
82	Sg	311/317 (98%)	250 (80%)	45 (14%)	16 (5%)	1	16
All	All	12341/13747 (90%)	10066 (82%)	1613 (13%)	662 (5%)	3	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%)	139 (74%)	48 (26%)	0	3
5	B	335/335 (100%)	265 (79%)	70 (21%)	1	5
6	C	305/305 (100%)	239 (78%)	66 (22%)	1	4
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	2
8	E	209/209 (100%)	158 (76%)	51 (24%)	0	3
9	F	194/194 (100%)	145 (75%)	49 (25%)	0	3
10	G	206/226 (91%)	158 (77%)	48 (23%)	0	3
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	3
12	I	180/180 (100%)	135 (75%)	45 (25%)	0	3
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	6
14	K	124/136 (91%)	98 (79%)	26 (21%)	1	5
15	L	176/177 (99%)	135 (77%)	41 (23%)	0	3
16	M	116/160 (72%)	95 (82%)	21 (18%)	1	7
17	N	171/172 (99%)	129 (75%)	42 (25%)	0	3
18	O	172/174 (99%)	146 (85%)	26 (15%)	2	14
19	P	134/134 (100%)	112 (84%)	22 (16%)	2	11
20	Q	163/164 (99%)	132 (81%)	31 (19%)	1	6
21	R	159/175 (91%)	120 (76%)	39 (24%)	0	3
22	S	156/192 (81%)	121 (78%)	35 (22%)	1	4
23	T	139/140 (99%)	112 (81%)	27 (19%)	1	6
24	U	89/114 (78%)	67 (75%)	22 (25%)	0	3
25	V	101/107 (94%)	77 (76%)	24 (24%)	0	3
26	W	55/126 (44%)	42 (76%)	13 (24%)	0	3
27	X	107/133 (80%)	89 (83%)	18 (17%)	1	10
28	Y	124/135 (92%)	96 (77%)	28 (23%)	1	4
29	Z	117/118 (99%)	94 (80%)	23 (20%)	1	6

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
30	a	119/120 (99%)	102 (86%)	17 (14%)	2	16
31	b	63/123 (51%)	45 (71%)	18 (29%)	0	2
32	c	79/97 (81%)	60 (76%)	19 (24%)	0	3
33	d	98/110 (89%)	66 (67%)	32 (33%)	0	2
34	e	114/121 (94%)	89 (78%)	25 (22%)	1	4
35	f	88/89 (99%)	73 (83%)	15 (17%)	1	10
36	g	98/100 (98%)	79 (81%)	19 (19%)	1	6
37	h	109/110 (99%)	92 (84%)	17 (16%)	2	13
38	i	86/89 (97%)	71 (83%)	15 (17%)	1	9
39	j	73/73 (100%)	60 (82%)	13 (18%)	1	8
40	k	64/65 (98%)	52 (81%)	12 (19%)	1	6
41	l	47/48 (98%)	39 (83%)	8 (17%)	1	10
42	m	48/116 (41%)	34 (71%)	14 (29%)	0	2
43	n	22/24 (92%)	17 (77%)	5 (23%)	0	4
44	o	92/94 (98%)	70 (76%)	22 (24%)	0	3
45	p	74/74 (100%)	61 (82%)	13 (18%)	1	8
46	q	170/170 (100%)	133 (78%)	37 (22%)	1	4
47	r	109/109 (100%)	86 (79%)	23 (21%)	1	5
48	4	728/728 (100%)	586 (80%)	142 (20%)	1	6
50	SA	174/245 (71%)	141 (81%)	33 (19%)	1	6
51	SB	194/231 (84%)	164 (84%)	30 (16%)	2	13
52	SC	184/184 (100%)	148 (80%)	36 (20%)	1	6
53	SD	190/202 (94%)	163 (86%)	27 (14%)	2	16
54	SE	224/225 (100%)	180 (80%)	44 (20%)	1	6
55	SF	161/170 (95%)	128 (80%)	33 (20%)	1	5
56	SG	207/218 (95%)	171 (83%)	36 (17%)	1	9
57	SH	169/174 (97%)	149 (88%)	20 (12%)	4	21
58	SI	178/180 (99%)	148 (83%)	30 (17%)	1	10
59	SJ	161/168 (96%)	128 (80%)	33 (20%)	1	5
60	SK	89/136 (65%)	68 (76%)	21 (24%)	0	3
61	SL	136/142 (96%)	116 (85%)	20 (15%)	2	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
62	SM	104/104 (100%)	76 (73%)	28 (27%)	0	2
63	SN	130/131 (99%)	101 (78%)	29 (22%)	1	4
64	SO	106/119 (89%)	83 (78%)	23 (22%)	1	4
65	SP	88/130 (68%)	73 (83%)	15 (17%)	1	10
66	SQ	117/121 (97%)	100 (86%)	17 (14%)	2	15
67	SR	117/121 (97%)	102 (87%)	15 (13%)	3	18
68	SS	119/132 (90%)	97 (82%)	22 (18%)	1	7
69	ST	112/115 (97%)	89 (80%)	23 (20%)	1	5
70	SU	94/107 (88%)	84 (89%)	10 (11%)	5	25
71	SV	66/67 (98%)	53 (80%)	13 (20%)	1	6
72	SW	112/113 (99%)	93 (83%)	19 (17%)	1	10
73	SX	113/115 (98%)	97 (86%)	16 (14%)	2	16
74	SY	108/114 (95%)	86 (80%)	22 (20%)	1	5
75	SZ	66/103 (64%)	55 (83%)	11 (17%)	2	10
76	Sa	85/98 (87%)	76 (89%)	9 (11%)	5	25
77	Sb	75/76 (99%)	64 (85%)	11 (15%)	2	15
78	Sc	57/62 (92%)	43 (75%)	14 (25%)	0	3
79	Sd	45/48 (94%)	35 (78%)	10 (22%)	1	4
80	Se	46/105 (44%)	35 (76%)	11 (24%)	0	3
81	Sf	64/140 (46%)	45 (70%)	19 (30%)	0	2
82	Sg	272/275 (99%)	242 (89%)	30 (11%)	5	24
All	All	10721/11706 (92%)	8570 (80%)	2151 (20%)	3	5

5 of 2151 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
64	SO	86	LYS
67	SR	109	LEU
64	SO	80	ASP
78	Sc	67	ARG
22	S	70	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 296 such sidechains are listed below:

Mol	Chain	Res	Type
55	SF	137	GLN
78	Sc	7	GLN
58	SI	44	HIS
68	SS	10	GLN
19	P	72	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3647/3664 (99%)	1616 (44%)	621 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
49	S2	1717/1742 (98%)	745 (43%)	269 (15%)
All	All	5638/5682 (99%)	2453 (43%)	921 (16%)

5 of 2453 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 ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry [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

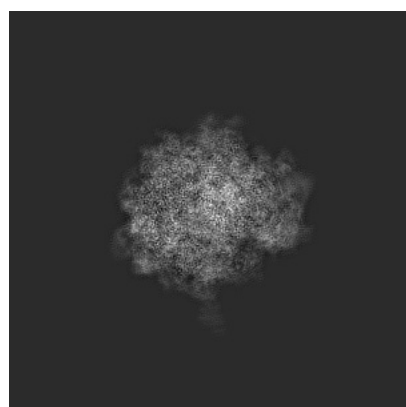
6 Map visualisation [i](#)

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.

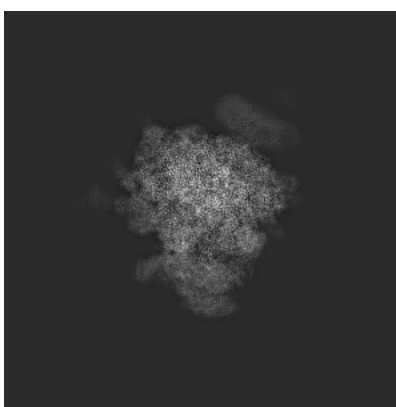
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

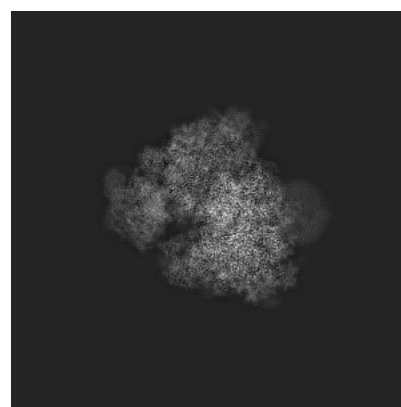
6.1.1 Primary map



X



Y

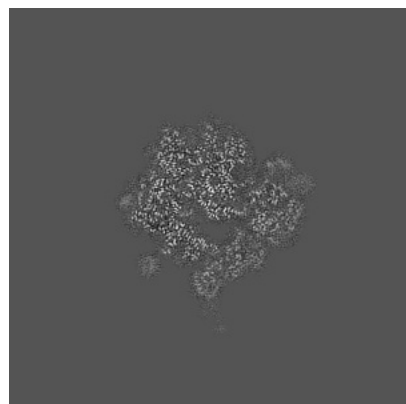


Z

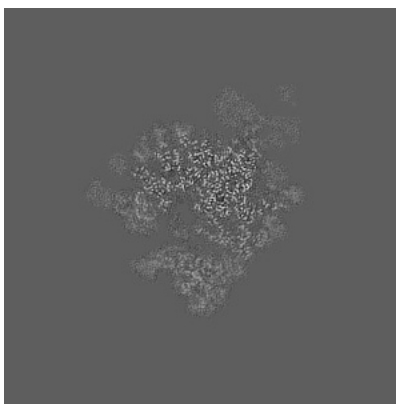
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

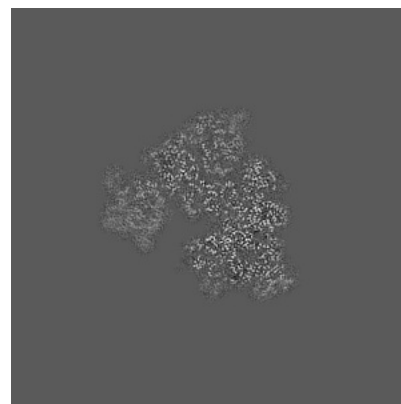
6.2.1 Primary map



X Index: 210



Y Index: 210

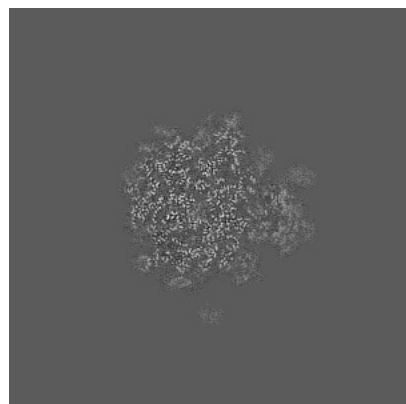


Z Index: 210

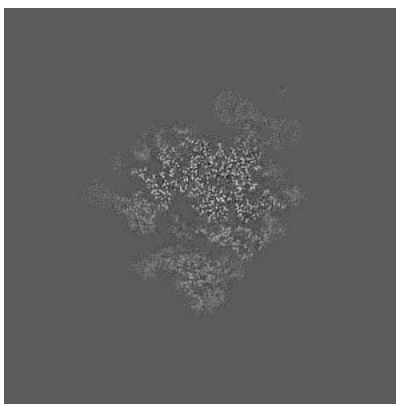
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

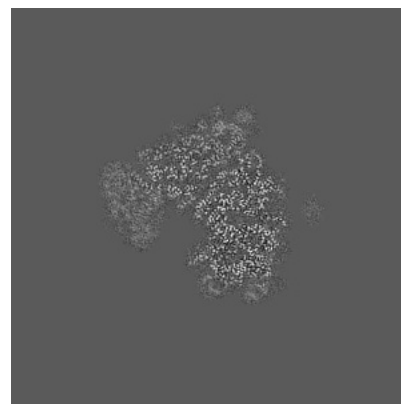
6.3.1 Primary map



X Index: 232



Y Index: 212

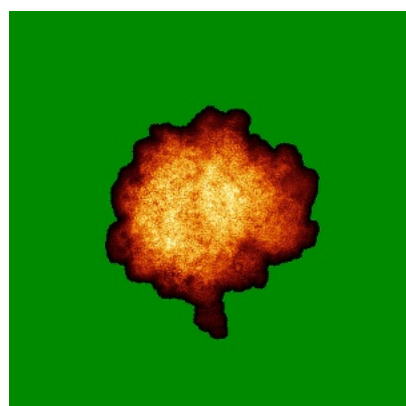


Z Index: 221

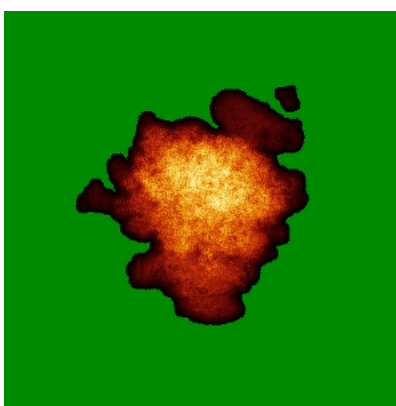
The images above show the largest variance slices of the map in three orthogonal directions.

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

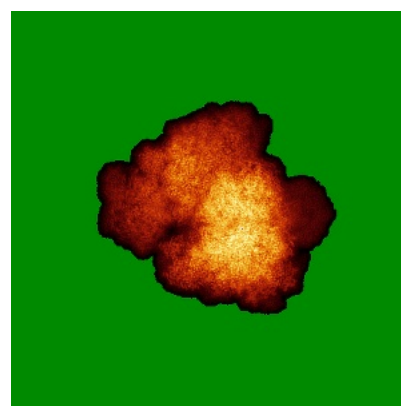
6.4.1 Primary map



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 [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.065. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

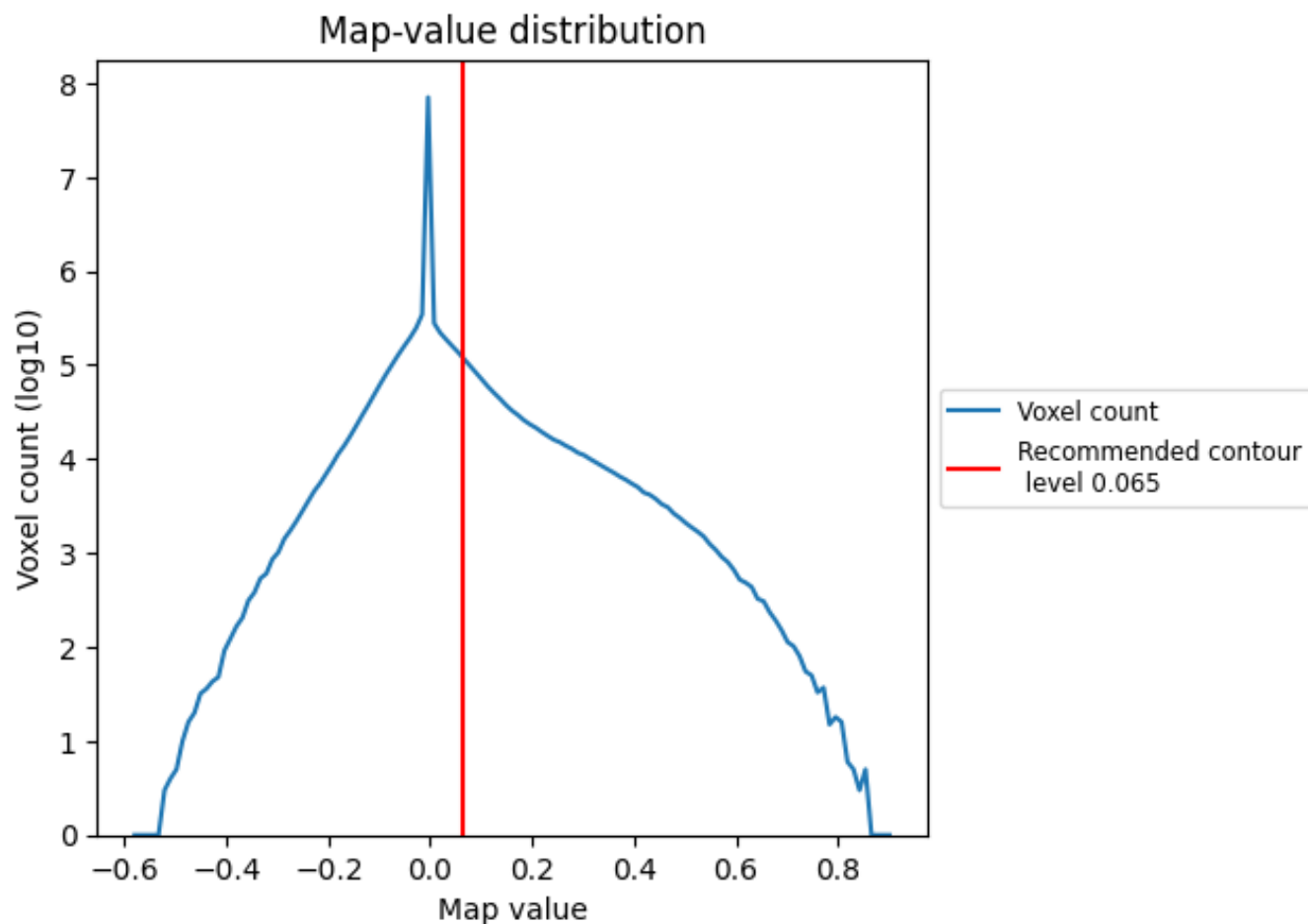
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

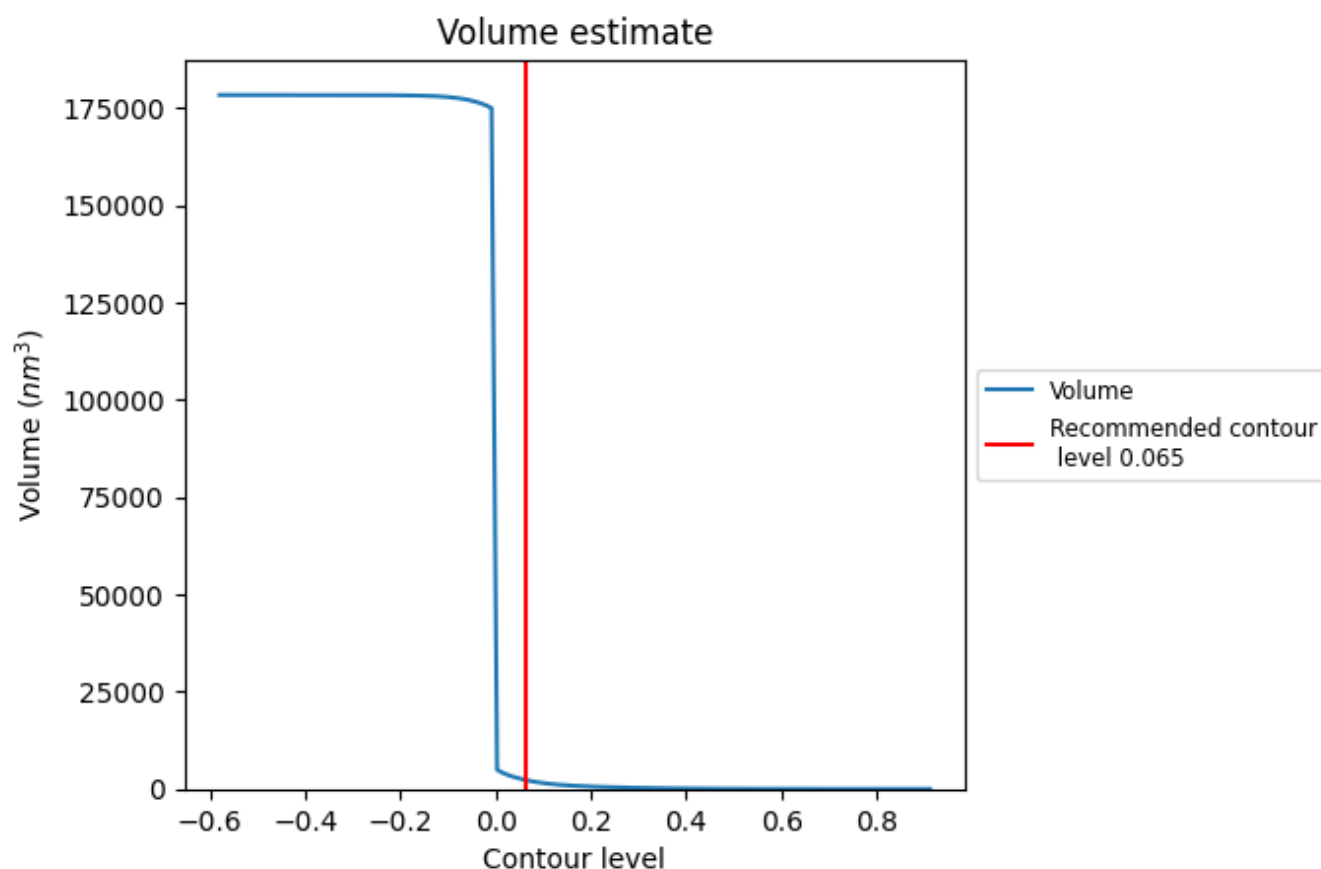
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

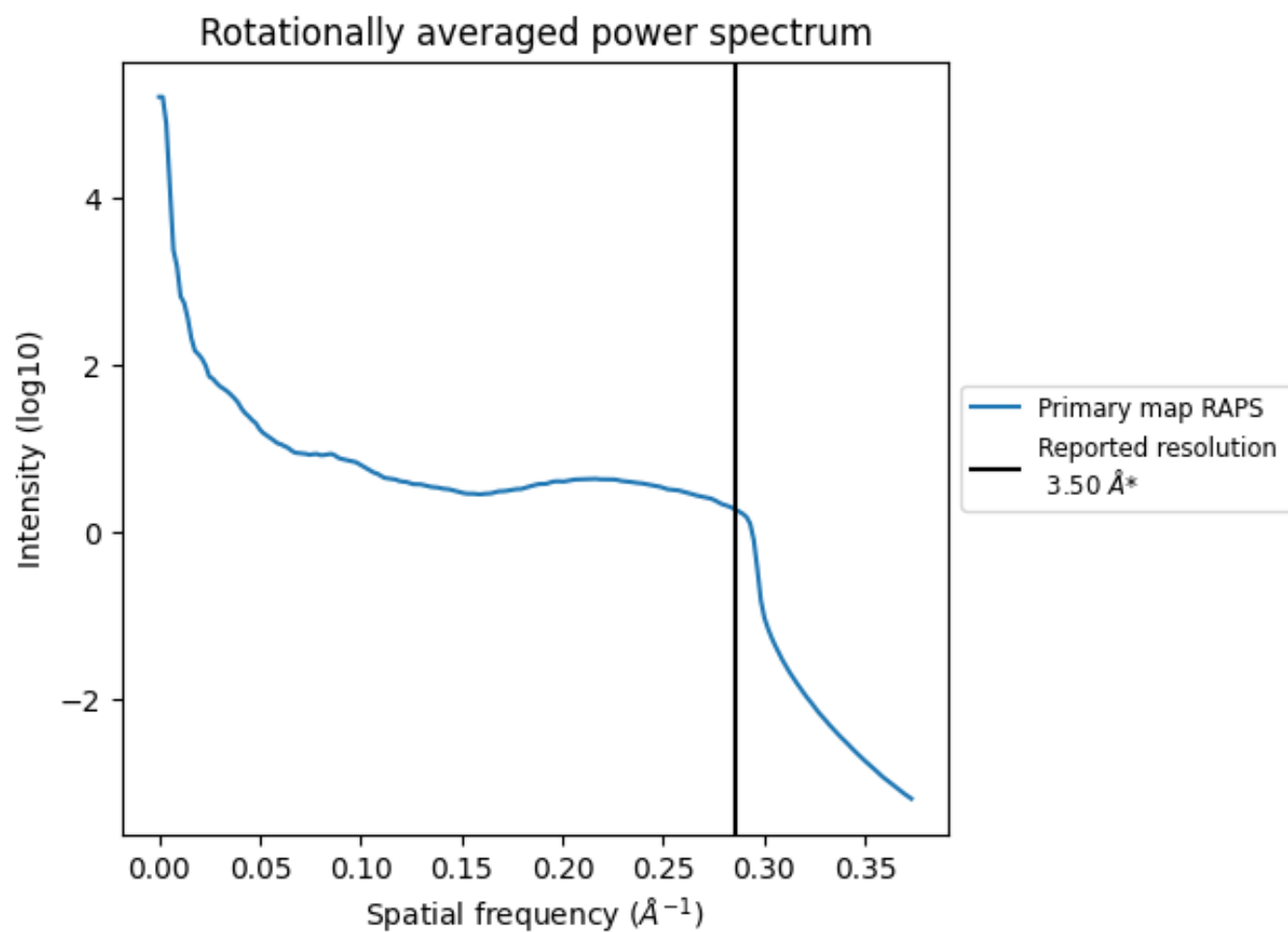
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2236 nm³; 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

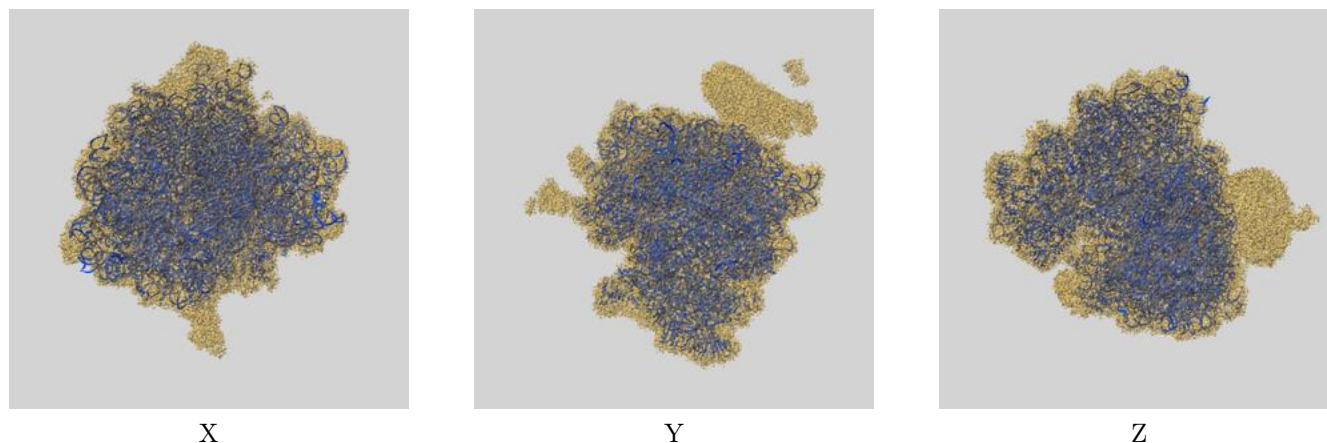
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

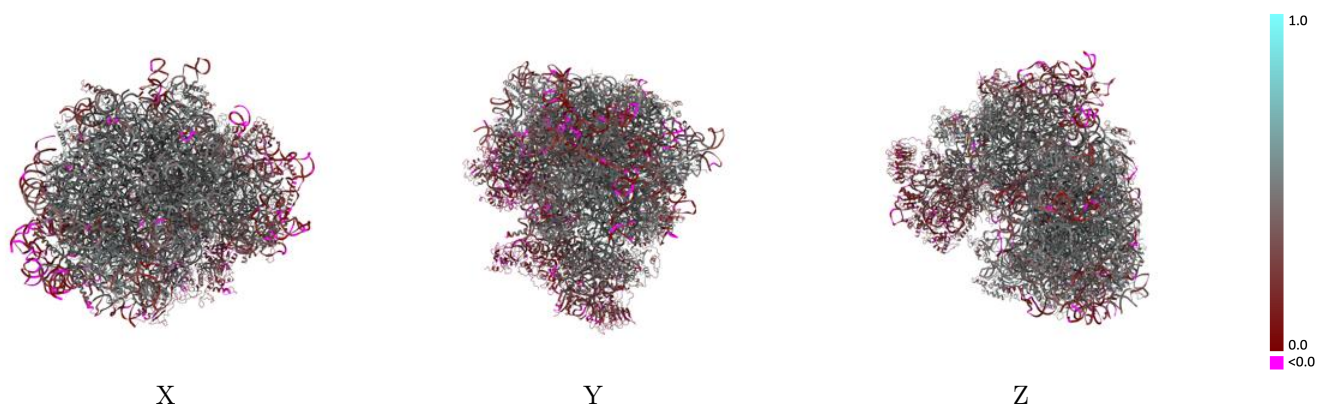
This section contains information regarding the fit between EMDB map EMD-2646 and PDB model 3J7P. Per-residue inclusion information can be found in section [3](#) on page [19](#).

9.1 Map-model overlay [i](#)



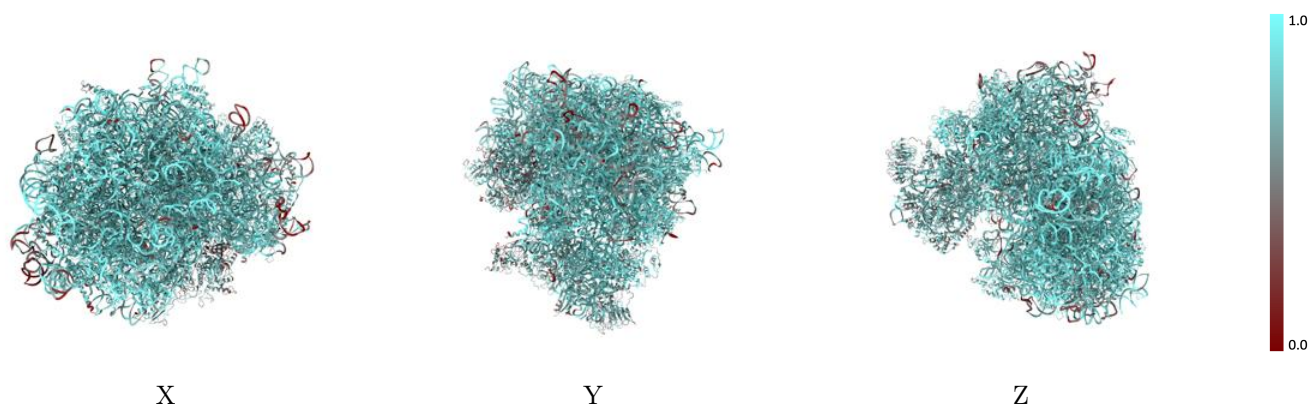
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



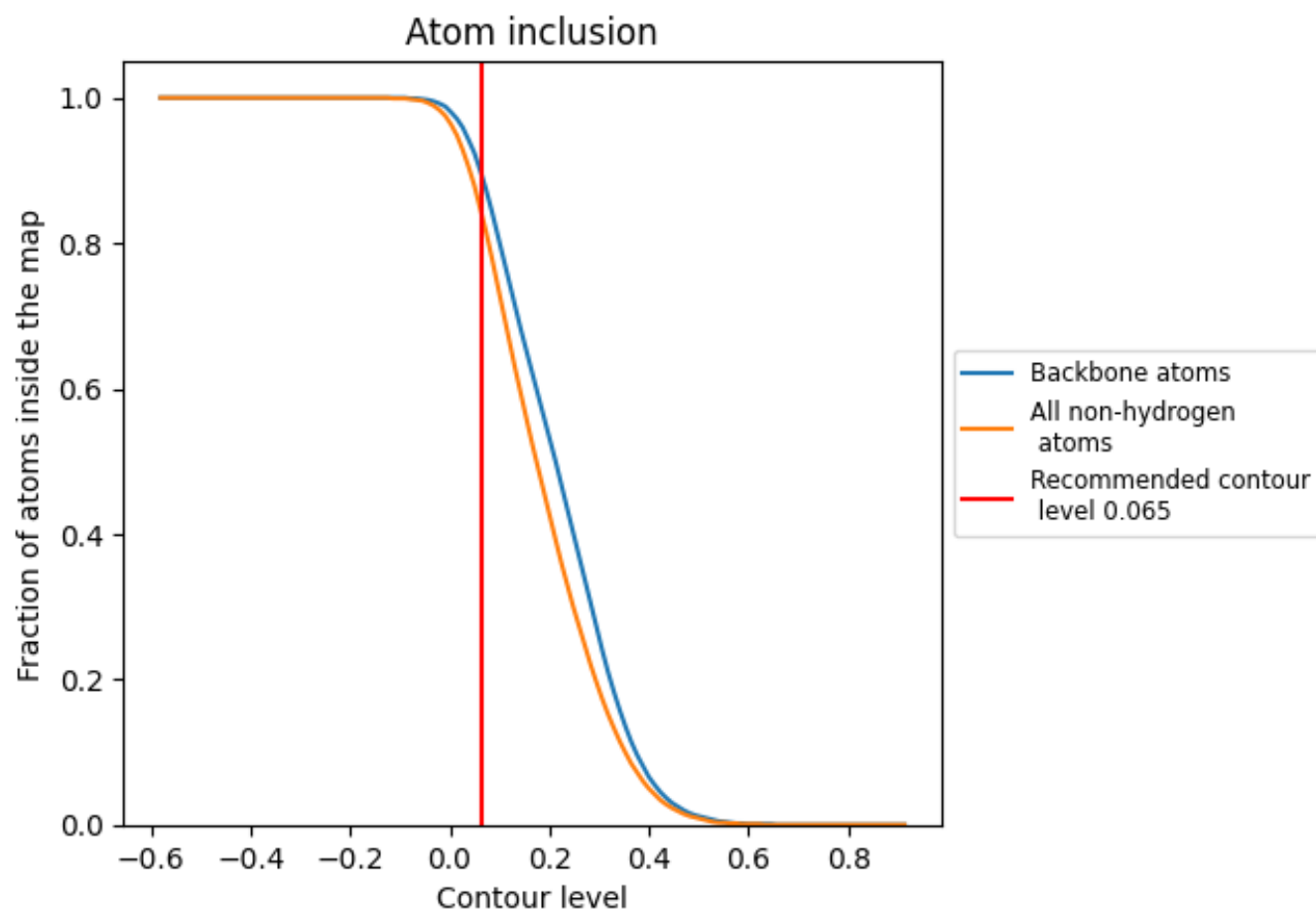
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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




































































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