



wwPDB EM Validation Summary Report ⓘ

Nov 13, 2024 – 04:42 PM EST

PDB ID : 3J7R
EMDB ID : EMD-2644
Title : Structure of the translating mammalian ribosome-Sec61 complex
Authors : Voorhees, R.M.; Fernandez, I.S.; Scheres, S.H.W.; Hegde, R.S.
Deposited on : 2014-08-01
Resolution : 3.90 Å(reported)
Based on initial models : 3J3D, 3J3B, 3J3A, 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.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

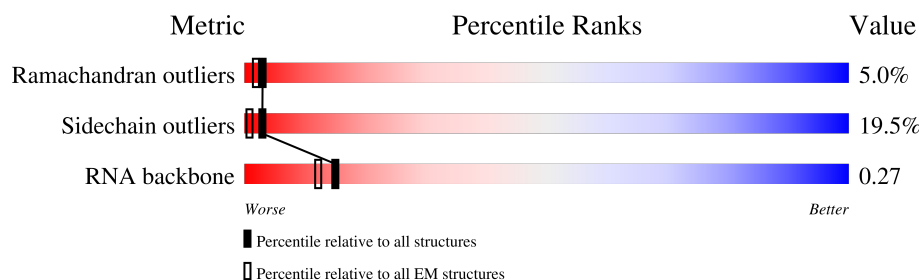
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 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.













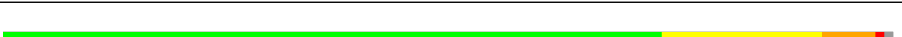


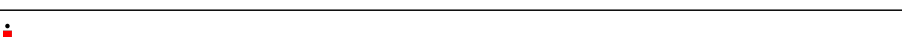
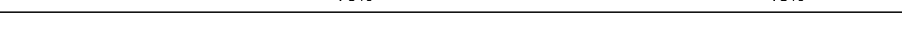
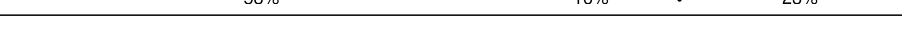



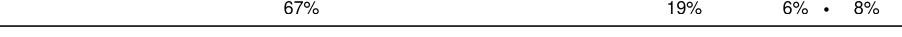





Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415
RNA backbone	6643	2191

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	3722	<div> <div>6%</div> <div>47%</div> <div>40%</div> <div>10%</div> <div>.</div> </div>
2	7	120	<div> <div>.</div> <div>69%</div> <div>24%</div> <div>6%</div> <div>.</div> </div>
3	8	156	<div> <div>5%</div> <div>53%</div> <div>33%</div> <div>8%</div> <div>5%</div> </div>
4	A	257	<div> <div>.</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>.</div> <div>77%</div> <div>19%</div> <div>.</div> <div>.</div> </div>
7	D	297	<div> <div>.</div> <div>68%</div> <div>24%</div> <div>5%</div> <div>.</div> <div>.</div> </div>
8	E	236	<div> <div>6%</div> <div>64%</div> <div>25%</div> <div>9%</div> <div>.</div> </div>









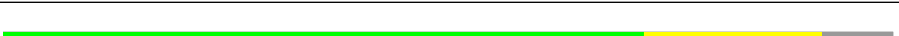

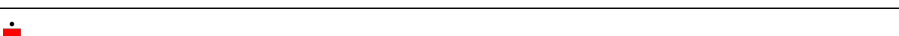
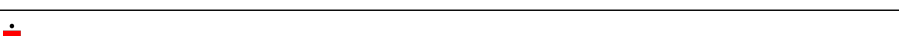

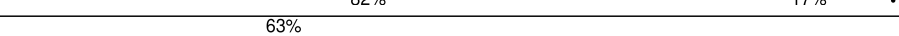
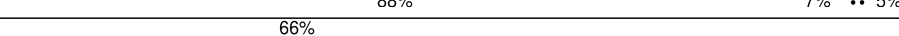
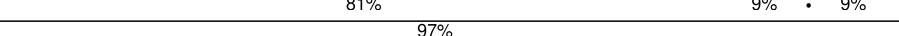
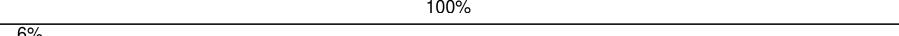








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Mol	Chain	Length	Quality of chain
9	F	225	
10	G	266	
11	H	192	
12	I	213	
13	J	178	
14	L	211	
15	M	213	
16	N	204	
17	O	201	
18	P	153	
19	Q	188	
20	R	196	
21	S	224	
22	T	160	
23	U	128	
24	V	140	
25	W	157	
26	X	156	
27	Y	145	
28	Z	136	
29	a	148	
30	b	160	
31	c	115	
32	d	125	
33	e	135	

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Mol	Chain	Length	Quality of chain
34	f	110	
35	g	117	
36	h	123	
37	i	105	
38	j	86	
39	k	70	
40	l	51	
41	m	128	
42	n	25	
43	o	106	
44	p	91	
45	r	125	
46	z	217	
47	1	393	
48	2	68	
49	3	36	
50	S2	1742	
51	SA	295	
52	SB	264	
53	SC	218	
54	SD	243	
55	SE	263	
56	SF	204	
57	SG	249	
58	SH	194	

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Mol	Chain	Length	Quality of chain
59	SI	208	
60	SJ	194	
61	SK	165	
62	SL	158	
63	SM	124	
64	SN	151	
65	SO	151	
66	SP	145	
67	SQ	146	
68	SR	135	
69	SS	152	
70	ST	145	
71	SU	119	
72	SV	83	
73	SW	130	
74	SX	143	
75	SY	132	
76	SZ	125	
77	Sa	115	
78	Sb	84	
79	Sc	69	
80	Sd	56	
81	Se	133	
82	Sf	156	
83	Sg	317	

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Mol	Chain	Length	Quality of chain
84	S4	10	<div><div></div><div>10%</div><div></div><div>90%</div></div>
85	S5	74	<div><div></div><div>26%</div><div></div><div>32%</div><div></div><div>66%</div><div></div><div></div></div>
86	S6	76	<div><div></div><div>11%</div><div></div><div>29%</div><div></div><div>70%</div><div></div><div></div></div>

2 Entry composition

There are 88 unique types of molecules in this entry. The entry contains 222336 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	3720	Total	C	N	O	P	0	0
			79736	35504	14597	25916	3719		

- 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		

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	85	ILE	VAL	conflict	UNP A0A480L253
B	86	VAL	ILE	conflict	UNP A0A480L253
B	140	ALA	GLU	conflict	UNP A0A480L253

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Chain	Residue	Modelled	Actual	Comment	Reference
B	141	ALA	ASP	conflict	UNP A0A480L253
B	143	ALA	LYS	conflict	UNP A0A480L253
B	144	ALA	LYS	conflict	UNP A0A480L253
B	145	ALA	GLN	conflict	UNP A0A480L253
B	147	ALA	GLU	conflict	UNP A0A480L253
B	148	ALA	ARG	conflict	UNP A0A480L253
B	155	ALA	LYS	conflict	UNP A0A480L253

- 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		

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	354	ALA	-	insertion	UNP A0A287AE76
C	355	ALA	-	insertion	UNP A0A287AE76
C	356	ALA	-	insertion	UNP A0A287AE76

- 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		

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	62	MET	LYS	conflict	UNP Q2YGT9
E	64	MET	LEU	conflict	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	SER	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	?	-	VAL	deletion	UNP Q2YGT9
E	?	-	GLU	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	LYS	deletion	UNP Q2YGT9
E	?	-	VAL	deletion	UNP Q2YGT9
E	?	-	ARG	deletion	UNP Q2YGT9
E	176	VAL	SER	conflict	UNP Q2YGT9
E	206	LYS	GLU	conflict	UNP Q2YGT9

- 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		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	31	LYS	ARG	conflict	UNP A0A480W0U3

- 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		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	53	ARG	CYS	conflict	UNP A0A4X1W808
G	172	ALA	SER	conflict	UNP A0A4X1W808
G	185	LYS	ASN	conflict	UNP A0A4X1W808
G	231	ASN	ASP	conflict	UNP A0A4X1W808

- 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		

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
I	49	GLY	CYS	conflict	UNP Q29195
I	82	ARG	LYS	conflict	UNP Q29195
I	87	MET	ILE	conflict	UNP Q29195
I	145	GLU	LYS	conflict	UNP Q29195
I	187	LYS	GLU	conflict	UNP Q29195
I	189	CYS	ARG	conflict	UNP Q29195
I	200	VAL	ILE	conflict	UNP Q29195
I	203	HIS	ARG	conflict	UNP Q29195
I	211	VAL	ALA	conflict	UNP Q29195

- 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 eL13.

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

- Molecule 15 is a protein called Ribosomal protein eL14.

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

- Molecule 16 is a protein called Ribosomal protein eL15.

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

- Molecule 17 is a protein called Ribosomal protein uL13.

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

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
O	3	GLU	-	variant	UNP A0A480L469
O	4	GLY	-	variant	UNP A0A480L469

- Molecule 18 is a protein called Ribosomal protein uL22.

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

- Molecule 19 is a protein called Ribosomal protein eL18.

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

- Molecule 20 is a protein called Ribosomal protein eL19.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
R	1	TYR	-	variant	UNP A0A480VXS3

- Molecule 21 is a protein called Ribosomal protein eL20.

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

- Molecule 22 is a protein called Ribosomal protein eL21.

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

- Molecule 23 is a protein called Ribosomal protein eL22.

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

- Molecule 24 is a protein called Ribosomal protein uL14.

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

- Molecule 25 is a protein called Ribosomal protein eL24.

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

- Molecule 26 is a protein called Ribosomal protein uL23.

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

- Molecule 27 is a protein called Ribosomal protein uL24.

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

- Molecule 28 is a protein called Ribosomal protein eL27.

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

- Molecule 29 is a protein called Ribosomal protein uL15.

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

- Molecule 30 is a protein called Ribosomal protein eL29.

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

- Molecule 31 is a protein called Ribosomal protein eL30.

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

- Molecule 32 is a protein called Ribosomal protein eL31.

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

- Molecule 33 is a protein called Ribosomal protein eL32.

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

- Molecule 34 is a protein called Ribosomal protein eL33.

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

- Molecule 35 is a protein called Ribosomal protein eL34.

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

- Molecule 36 is a protein called Ribosomal protein uL29.

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

- Molecule 37 is a protein called Ribosomal protein eL36.

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

- Molecule 38 is a protein called Ribosomal protein eL37.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
j	82	ILE	THR	conflict	UNP A0A480UVT3

- Molecule 39 is a protein called Ribosomal protein eL38.

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

- Molecule 40 is a protein called Ribosomal protein eL39.

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

- Molecule 41 is a protein called Ribosomal protein eL40.

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

- Molecule 42 is a protein called Ribosomal protein eL41.

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

- Molecule 43 is a protein called Ribosomal protein eL42.

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

- Molecule 44 is a protein called Ribosomal protein eL43.

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

- Molecule 45 is a protein called Ribosomal protein eL28.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
r	64	ILE	MET	conflict	UNP A0A480YX24

- Molecule 46 is a protein called Ribosomal protein uL1.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	z	217	Total	C	N	O	S	0	0
			1741	1113	312	307	9		

- Molecule 47 is a protein called Sec61 alpha subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	1	375	Total	C	N	O	S	0	0
			2914	1919	469	508	18		

There are 50 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	GLN	deletion	UNP A0A4X1TV07

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Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	ILE	deletion	UNP A0A4X1TV07
1	?	-	PRO	deletion	UNP A0A4X1TV07
1	?	-	LEU	deletion	UNP A0A4X1TV07
1	?	-	PHE	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	ILE	deletion	UNP A0A4X1TV07
1	?	-	MET	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	ASP	deletion	UNP A0A4X1TV07
1	?	-	THR	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	MET	deletion	UNP A0A4X1TV07
1	?	-	TYR	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	ASP	deletion	UNP A0A4X1TV07
1	?	-	PRO	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	GLU	deletion	UNP A0A4X1TV07
1	?	-	MET	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	ALA	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	ILE	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	ASN	deletion	UNP A0A4X1TV07
1	?	-	LEU	deletion	UNP A0A4X1TV07
1	?	-	LEU	deletion	UNP A0A4X1TV07
1	?	-	VAL	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	LEU	deletion	UNP A0A4X1TV07
1	?	-	LEU	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	THR	deletion	UNP A0A4X1TV07
1	?	-	TRP	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	ASP	deletion	UNP A0A4X1TV07
1	?	-	THR	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	SER	deletion	UNP A0A4X1TV07
1	?	-	GLY	deletion	UNP A0A4X1TV07

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Chain	Residue	Modelled	Actual	Comment	Reference
1	?	-	GLY	deletion	UNP A0A4X1TV07
1	?	-	PRO	deletion	UNP A0A4X1TV07
1	?	-	ALA	deletion	UNP A0A4X1TV07
1	?	-	ARG	deletion	UNP A0A4X1TV07
1	?	-	ALA	deletion	UNP A0A4X1TV07
1	?	-	TYR	deletion	UNP A0A4X1TV07
1	343	HIS	TYR	conflict	UNP A0A4X1TV07

- Molecule 48 is a protein called Sec61 gamma subunit.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	2	62	Total	C	N	O	S	0	0
			494	326	86	79	3		

- Molecule 49 is a protein called Sec61 beta subunit.

Mol	Chain	Residues	Atoms				AltConf	Trace
49	3	36	Total	C	N	O	0	0
			180	108	36	36		

- Molecule 50 is a RNA chain called 18S ribosomal RNA.

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

There are 658 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
S2	1	U	-	variant	GB 37956930
S2	2	A	-	variant	GB 37956930
S2	3	C	-	variant	GB 37956930
S2	4	C	-	variant	GB 37956930
S2	5	U	-	variant	GB 37956930
S2	6	G	-	variant	GB 37956930
S2	7	G	-	variant	GB 37956930
S2	8	U	-	variant	GB 37956930
S2	9	U	-	variant	GB 37956930
S2	10	G	-	variant	GB 37956930
S2	11	A	-	variant	GB 37956930
S2	12	U	-	variant	GB 37956930
S2	13	C	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	14	C	-	variant	GB 37956930
S2	15	U	-	variant	GB 37956930
S2	16	G	-	variant	GB 37956930
S2	17	C	-	variant	GB 37956930
S2	18	C	-	variant	GB 37956930
S2	19	A	-	variant	GB 37956930
S2	20	G	-	variant	GB 37956930
S2	21	U	-	variant	GB 37956930
S2	22	A	-	variant	GB 37956930
S2	23	G	-	variant	GB 37956930
S2	24	C	-	variant	GB 37956930
S2	25	A	-	variant	GB 37956930
S2	26	U	-	variant	GB 37956930
S2	27	A	-	variant	GB 37956930
S2	28	U	-	variant	GB 37956930
S2	29	G	-	variant	GB 37956930
S2	30	C	-	variant	GB 37956930
S2	31	U	-	variant	GB 37956930
S2	32	U	-	variant	GB 37956930
S2	33	G	-	variant	GB 37956930
S2	34	U	-	variant	GB 37956930
S2	35	C	-	variant	GB 37956930
S2	36	U	-	variant	GB 37956930
S2	37	C	-	variant	GB 37956930
S2	38	A	-	variant	GB 37956930
S2	39	A	-	variant	GB 37956930
S2	40	A	-	variant	GB 37956930
S2	41	G	-	variant	GB 37956930
S2	42	A	-	variant	GB 37956930
S2	43	U	-	variant	GB 37956930
S2	44	U	-	variant	GB 37956930
S2	45	A	-	variant	GB 37956930
S2	46	A	-	variant	GB 37956930
S2	47	G	-	variant	GB 37956930
S2	48	C	-	variant	GB 37956930
S2	49	C	-	variant	GB 37956930
S2	50	A	-	variant	GB 37956930
S2	51	U	-	variant	GB 37956930
S2	52	G	-	variant	GB 37956930
S2	53	C	-	variant	GB 37956930
S2	54	A	-	variant	GB 37956930
S2	55	U	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	56	G	-	variant	GB 37956930
S2	57	U	-	variant	GB 37956930
S2	58	C	-	variant	GB 37956930
S2	59	U	-	variant	GB 37956930
S2	60	A	-	variant	GB 37956930
S2	61	A	-	variant	GB 37956930
S2	62	G	-	variant	GB 37956930
S2	63	U	-	variant	GB 37956930
S2	64	A	-	variant	GB 37956930
S2	65	C	-	variant	GB 37956930
S2	66	G	-	variant	GB 37956930
S2	67	C	-	variant	GB 37956930
S2	68	A	-	variant	GB 37956930
S2	69	C	-	variant	GB 37956930
S2	70	G	-	variant	GB 37956930
S2	71	G	-	variant	GB 37956930
S2	72	C	-	variant	GB 37956930
S2	73	C	-	variant	GB 37956930
S2	74	G	-	variant	GB 37956930
S2	75	G	-	variant	GB 37956930
S2	76	U	-	variant	GB 37956930
S2	77	A	-	variant	GB 37956930
S2	78	C	-	variant	GB 37956930
S2	79	A	-	variant	GB 37956930
S2	80	G	-	variant	GB 37956930
S2	81	U	-	variant	GB 37956930
S2	82	G	-	variant	GB 37956930
S2	83	A	-	variant	GB 37956930
S2	84	A	-	variant	GB 37956930
S2	85	A	-	variant	GB 37956930
S2	86	C	-	variant	GB 37956930
S2	87	U	-	variant	GB 37956930
S2	88	G	-	variant	GB 37956930
S2	89	C	-	variant	GB 37956930
S2	90	G	-	variant	GB 37956930
S2	91	A	-	variant	GB 37956930
S2	92	A	-	variant	GB 37956930
S2	93	U	-	variant	GB 37956930
S2	94	G	-	variant	GB 37956930
S2	95	G	-	variant	GB 37956930
S2	96	C	-	variant	GB 37956930
S2	97	U	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	98	C	-	variant	GB 37956930
S2	99	A	-	variant	GB 37956930
S2	100	U	-	variant	GB 37956930
S2	101	U	-	variant	GB 37956930
S2	102	A	-	variant	GB 37956930
S2	103	A	-	variant	GB 37956930
S2	104	A	-	variant	GB 37956930
S2	105	U	-	variant	GB 37956930
S2	106	C	-	variant	GB 37956930
S2	107	A	-	variant	GB 37956930
S2	108	G	-	variant	GB 37956930
S2	109	U	-	variant	GB 37956930
S2	110	U	-	variant	GB 37956930
S2	111	A	-	variant	GB 37956930
S2	112	U	-	variant	GB 37956930
S2	113	G	-	variant	GB 37956930
S2	114	G	-	variant	GB 37956930
S2	115	U	-	variant	GB 37956930
S2	116	U	-	variant	GB 37956930
S2	117	C	-	variant	GB 37956930
S2	118	C	-	variant	GB 37956930
S2	119	U	-	variant	GB 37956930
S2	120	U	-	variant	GB 37956930
S2	121	U	-	variant	GB 37956930
S2	122	G	-	variant	GB 37956930
S2	123	G	-	variant	GB 37956930
S2	124	U	-	variant	GB 37956930
S2	125	C	-	variant	GB 37956930
S2	126	G	-	variant	GB 37956930
S2	127	C	-	variant	GB 37956930
S2	128	U	-	variant	GB 37956930
S2	129	C	-	variant	GB 37956930
S2	130	G	-	variant	GB 37956930
S2	131	C	-	variant	GB 37956930
S2	132	U	-	variant	GB 37956930
S2	133	C	-	variant	GB 37956930
S2	134	C	-	variant	GB 37956930
S2	135	U	-	variant	GB 37956930
S2	136	C	-	variant	GB 37956930
S2	137	U	-	variant	GB 37956930
S2	138	C	-	variant	GB 37956930
S2	139	C	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	140	C	-	variant	GB 37956930
S2	141	A	-	variant	GB 37956930
S2	142	C	-	variant	GB 37956930
S2	143	U	-	variant	GB 37956930
S2	144	U	-	variant	GB 37956930
S2	145	G	-	variant	GB 37956930
S2	146	G	-	variant	GB 37956930
S2	147	A	-	variant	GB 37956930
S2	148	U	-	variant	GB 37956930
S2	149	A	-	variant	GB 37956930
S2	150	A	-	variant	GB 37956930
S2	151	C	-	variant	GB 37956930
S2	152	U	-	variant	GB 37956930
S2	153	G	-	variant	GB 37956930
S2	154	U	-	variant	GB 37956930
S2	155	G	-	variant	GB 37956930
S2	156	G	-	variant	GB 37956930
S2	157	U	-	variant	GB 37956930
S2	158	A	-	variant	GB 37956930
S2	159	A	-	variant	GB 37956930
S2	160	U	-	variant	GB 37956930
S2	161	U	-	variant	GB 37956930
S2	162	C	-	variant	GB 37956930
S2	163	U	-	variant	GB 37956930
S2	164	A	-	variant	GB 37956930
S2	165	G	-	variant	GB 37956930
S2	166	A	-	variant	GB 37956930
S2	167	G	-	variant	GB 37956930
S2	168	C	-	variant	GB 37956930
S2	169	U	-	variant	GB 37956930
S2	170	A	-	variant	GB 37956930
S2	171	A	-	variant	GB 37956930
S2	172	U	-	variant	GB 37956930
S2	173	A	-	variant	GB 37956930
S2	174	C	-	variant	GB 37956930
S2	175	A	-	variant	GB 37956930
S2	176	U	-	variant	GB 37956930
S2	177	G	-	variant	GB 37956930
S2	178	C	-	variant	GB 37956930
S2	179	C	-	variant	GB 37956930
S2	180	G	-	variant	GB 37956930
S2	181	A	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	182	C	-	variant	GB 37956930
S2	183	G	-	variant	GB 37956930
S2	184	G	-	variant	GB 37956930
S2	185	G	-	variant	GB 37956930
S2	186	C	-	variant	GB 37956930
S2	187	G	-	variant	GB 37956930
S2	188	C	-	variant	GB 37956930
S2	189	U	-	variant	GB 37956930
S2	190	G	-	variant	GB 37956930
S2	191	A	-	variant	GB 37956930
S2	192	C	-	variant	GB 37956930
S2	193	C	-	variant	GB 37956930
S2	194	C	-	variant	GB 37956930
S2	195	C	-	variant	GB 37956930
S2	196	C	-	variant	GB 37956930
S2	197	U	-	variant	GB 37956930
S2	198	U	-	variant	GB 37956930
S2	199	C	-	variant	GB 37956930
S2	200	G	-	variant	GB 37956930
S2	201	C	-	variant	GB 37956930
S2	202	G	-	variant	GB 37956930
S2	203	G	-	variant	GB 37956930
S2	204	G	-	variant	GB 37956930
S2	205	G	-	variant	GB 37956930
S2	206	G	-	variant	GB 37956930
S2	207	G	-	variant	GB 37956930
S2	208	G	-	variant	GB 37956930
S2	209	A	-	variant	GB 37956930
S2	210	U	-	variant	GB 37956930
S2	211	G	-	variant	GB 37956930
S2	212	C	-	variant	GB 37956930
S2	213	G	-	variant	GB 37956930
S2	214	U	-	variant	GB 37956930
S2	215	G	-	variant	GB 37956930
S2	216	C	-	variant	GB 37956930
S2	217	A	-	variant	GB 37956930
S2	218	U	-	variant	GB 37956930
S2	219	U	-	variant	GB 37956930
S2	220	U	-	variant	GB 37956930
S2	221	A	-	variant	GB 37956930
S2	222	U	-	variant	GB 37956930
S2	223	C	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	224	A	-	variant	GB 37956930
S2	225	G	-	variant	GB 37956930
S2	287	U	-	variant	GB 37956930
S2	288	G	-	variant	GB 37956930
S2	289	G	-	variant	GB 37956930
S2	290	U	-	variant	GB 37956930
S2	291	G	-	variant	GB 37956930
S2	292	A	-	variant	GB 37956930
S2	293	C	-	variant	GB 37956930
S2	294	U	-	variant	GB 37956930
S2	295	C	-	variant	GB 37956930
S2	296	U	-	variant	GB 37956930
S2	297	A	-	variant	GB 37956930
S2	298	G	-	variant	GB 37956930
S2	299	A	-	variant	GB 37956930
S2	300	U	-	variant	GB 37956930
S2	301	A	-	variant	GB 37956930
S2	302	A	-	variant	GB 37956930
S2	303	C	-	variant	GB 37956930
S2	304	C	-	variant	GB 37956930
S2	305	U	-	variant	GB 37956930
S2	306	C	-	variant	GB 37956930
S2	307	G	-	variant	GB 37956930
S2	308	G	-	variant	GB 37956930
S2	309	G	-	variant	GB 37956930
S2	310	C	-	variant	GB 37956930
S2	311	C	-	variant	GB 37956930
S2	312	G	-	variant	GB 37956930
S2	313	A	-	variant	GB 37956930
S2	314	U	-	variant	GB 37956930
S2	315	C	-	variant	GB 37956930
S2	316	G	-	variant	GB 37956930
S2	317	C	-	variant	GB 37956930
S2	318	A	-	variant	GB 37956930
S2	319	C	-	variant	GB 37956930
S2	320	G	-	variant	GB 37956930
S2	321	C	-	variant	GB 37956930
S2	322	C	-	variant	GB 37956930
S2	323	C	-	variant	GB 37956930
S2	324	C	-	variant	GB 37956930
S2	325	C	-	variant	GB 37956930
S2	326	C	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	327	G	-	variant	GB 37956930
S2	328	U	-	variant	GB 37956930
S2	329	G	-	variant	GB 37956930
S2	330	G	-	variant	GB 37956930
S2	331	C	-	variant	GB 37956930
S2	332	G	-	variant	GB 37956930
S2	333	G	-	variant	GB 37956930
S2	334	C	-	variant	GB 37956930
S2	335	G	-	variant	GB 37956930
S2	336	A	-	variant	GB 37956930
S2	337	C	-	variant	GB 37956930
S2	338	G	-	variant	GB 37956930
S2	339	A	-	variant	GB 37956930
S2	340	C	-	variant	GB 37956930
S2	341	C	-	variant	GB 37956930
S2	342	C	-	variant	GB 37956930
S2	343	A	-	variant	GB 37956930
S2	344	U	-	variant	GB 37956930
S2	345	U	-	variant	GB 37956930
S2	346	C	-	variant	GB 37956930
S2	347	G	-	variant	GB 37956930
S2	348	A	-	variant	GB 37956930
S2	349	A	-	variant	GB 37956930
S2	350	C	-	variant	GB 37956930
S2	351	G	-	variant	GB 37956930
S2	352	U	-	variant	GB 37956930
S2	353	C	-	variant	GB 37956930
S2	354	U	-	variant	GB 37956930
S2	355	G	-	variant	GB 37956930
S2	356	C	-	variant	GB 37956930
S2	357	C	-	variant	GB 37956930
S2	358	C	-	variant	GB 37956930
S2	359	U	-	variant	GB 37956930
S2	360	A	-	variant	GB 37956930
S2	361	U	-	variant	GB 37956930
S2	362	C	-	variant	GB 37956930
S2	363	A	-	variant	GB 37956930
S2	364	A	-	variant	GB 37956930
S2	365	C	-	variant	GB 37956930
S2	366	U	-	variant	GB 37956930
S2	367	U	-	variant	GB 37956930
S2	368	U	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	369	C	-	variant	GB 37956930
S2	370	G	-	variant	GB 37956930
S2	371	A	-	variant	GB 37956930
S2	372	U	-	variant	GB 37956930
S2	373	G	-	variant	GB 37956930
S2	374	G	-	variant	GB 37956930
S2	375	U	-	variant	GB 37956930
S2	376	A	-	variant	GB 37956930
S2	377	G	-	variant	GB 37956930
S2	378	U	-	variant	GB 37956930
S2	379	C	-	variant	GB 37956930
S2	380	G	-	variant	GB 37956930
S2	381	C	-	variant	GB 37956930
S2	382	C	-	variant	GB 37956930
S2	383	G	-	variant	GB 37956930
S2	384	U	-	variant	GB 37956930
S2	385	G	-	variant	GB 37956930
S2	386	C	-	variant	GB 37956930
S2	387	C	-	variant	GB 37956930
S2	388	U	-	variant	GB 37956930
S2	389	A	-	variant	GB 37956930
S2	390	C	-	variant	GB 37956930
S2	391	C	-	variant	GB 37956930
S2	392	A	-	variant	GB 37956930
S2	393	U	-	variant	GB 37956930
S2	394	G	-	variant	GB 37956930
S2	395	G	-	variant	GB 37956930
S2	396	U	-	variant	GB 37956930
S2	397	G	-	variant	GB 37956930
S2	398	A	-	variant	GB 37956930
S2	399	C	-	variant	GB 37956930
S2	400	C	-	variant	GB 37956930
S2	401	A	-	variant	GB 37956930
S2	402	C	-	variant	GB 37956930
S2	403	G	-	variant	GB 37956930
S2	404	G	-	variant	GB 37956930
S2	405	G	-	variant	GB 37956930
S2	406	U	-	variant	GB 37956930
S2	407	G	-	variant	GB 37956930
S2	408	A	-	variant	GB 37956930
S2	409	C	-	variant	GB 37956930
S2	410	G	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	411	G	-	variant	GB 37956930
S2	412	G	-	variant	GB 37956930
S2	413	G	-	variant	GB 37956930
S2	414	A	-	variant	GB 37956930
S2	415	A	-	variant	GB 37956930
S2	416	U	-	variant	GB 37956930
S2	417	C	-	variant	GB 37956930
S2	418	A	-	variant	GB 37956930
S2	419	G	-	variant	GB 37956930
S2	420	G	-	variant	GB 37956930
S2	421	G	-	variant	GB 37956930
S2	422	U	-	variant	GB 37956930
S2	423	U	-	variant	GB 37956930
S2	424	C	-	variant	GB 37956930
S2	425	G	-	variant	GB 37956930
S2	426	A	-	variant	GB 37956930
S2	427	U	-	variant	GB 37956930
S2	428	U	-	variant	GB 37956930
S2	429	C	-	variant	GB 37956930
S2	430	C	-	variant	GB 37956930
S2	431	G	-	variant	GB 37956930
S2	432	G	-	variant	GB 37956930
S2	433	A	-	variant	GB 37956930
S2	434	G	-	variant	GB 37956930
S2	435	A	-	variant	GB 37956930
S2	436	G	-	variant	GB 37956930
S2	437	G	-	variant	GB 37956930
S2	438	G	-	variant	GB 37956930
S2	439	A	-	variant	GB 37956930
S2	440	G	-	variant	GB 37956930
S2	441	C	-	variant	GB 37956930
S2	442	C	-	variant	GB 37956930
S2	443	U	-	variant	GB 37956930
S2	444	G	-	variant	GB 37956930
S2	445	A	-	variant	GB 37956930
S2	446	G	-	variant	GB 37956930
S2	447	A	-	variant	GB 37956930
S2	448	A	-	variant	GB 37956930
S2	449	A	-	variant	GB 37956930
S2	450	C	-	variant	GB 37956930
S2	451	G	-	variant	GB 37956930
S2	452	G	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	453	C	-	variant	GB 37956930
S2	454	U	-	variant	GB 37956930
S2	455	A	-	variant	GB 37956930
S2	456	C	-	variant	GB 37956930
S2	457	C	-	variant	GB 37956930
S2	458	A	-	variant	GB 37956930
S2	459	C	-	variant	GB 37956930
S2	460	A	-	variant	GB 37956930
S2	461	U	-	variant	GB 37956930
S2	462	C	-	variant	GB 37956930
S2	463	C	-	variant	GB 37956930
S2	464	A	-	variant	GB 37956930
S2	465	A	-	variant	GB 37956930
S2	466	G	-	variant	GB 37956930
S2	467	G	-	variant	GB 37956930
S2	468	A	-	variant	GB 37956930
S2	469	A	-	variant	GB 37956930
S2	470	G	-	variant	GB 37956930
S2	471	G	-	variant	GB 37956930
S2	472	C	-	variant	GB 37956930
S2	473	A	-	variant	GB 37956930
S2	474	G	-	variant	GB 37956930
S2	475	C	-	variant	GB 37956930
S2	476	A	-	variant	GB 37956930
S2	477	G	-	variant	GB 37956930
S2	478	G	-	variant	GB 37956930
S2	479	C	-	variant	GB 37956930
S2	480	G	-	variant	GB 37956930
S2	481	C	-	variant	GB 37956930
S2	482	G	-	variant	GB 37956930
S2	483	C	-	variant	GB 37956930
S2	484	A	-	variant	GB 37956930
S2	485	A	-	variant	GB 37956930
S2	486	A	-	variant	GB 37956930
S2	487	U	-	variant	GB 37956930
S2	488	U	-	variant	GB 37956930
S2	489	A	-	variant	GB 37956930
S2	490	C	-	variant	GB 37956930
S2	491	C	-	variant	GB 37956930
S2	492	C	-	variant	GB 37956930
S2	493	A	-	variant	GB 37956930
S2	494	C	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	495	U	-	variant	GB 37956930
S2	496	C	-	variant	GB 37956930
S2	497	C	-	variant	GB 37956930
S2	498	C	-	variant	GB 37956930
S2	499	G	-	variant	GB 37956930
S2	500	A	-	variant	GB 37956930
S2	501	C	-	variant	GB 37956930
S2	502	C	-	variant	GB 37956930
S2	503	C	-	variant	GB 37956930
S2	504	G	-	variant	GB 37956930
S2	505	G	-	variant	GB 37956930
S2	506	G	-	variant	GB 37956930
S2	507	G	-	variant	GB 37956930
S2	508	A	-	variant	GB 37956930
S2	509	G	-	variant	GB 37956930
S2	510	G	-	variant	GB 37956930
S2	511	U	-	variant	GB 37956930
S2	512	A	-	variant	GB 37956930
S2	513	G	-	variant	GB 37956930
S2	514	U	-	variant	GB 37956930
S2	515	G	-	variant	GB 37956930
S2	516	A	-	variant	GB 37956930
S2	517	C	-	variant	GB 37956930
S2	518	G	-	variant	GB 37956930
S2	519	A	-	variant	GB 37956930
S2	520	A	-	variant	GB 37956930
S2	521	A	-	variant	GB 37956930
S2	522	A	-	variant	GB 37956930
S2	523	A	-	variant	GB 37956930
S2	524	U	-	variant	GB 37956930
S2	525	A	-	variant	GB 37956930
S2	526	A	-	variant	GB 37956930
S2	527	C	-	variant	GB 37956930
S2	528	A	-	variant	GB 37956930
S2	529	A	-	variant	GB 37956930
S2	530	U	-	variant	GB 37956930
S2	531	A	-	variant	GB 37956930
S2	532	C	-	variant	GB 37956930
S2	533	A	-	variant	GB 37956930
S2	534	G	-	variant	GB 37956930
S2	535	G	-	variant	GB 37956930
S2	536	A	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	537	C	-	variant	GB 37956930
S2	538	U	-	variant	GB 37956930
S2	539	C	-	variant	GB 37956930
S2	540	U	-	variant	GB 37956930
S2	541	U	-	variant	GB 37956930
S2	542	U	-	variant	GB 37956930
S2	543	C	-	variant	GB 37956930
S2	544	G	-	variant	GB 37956930
S2	545	A	-	variant	GB 37956930
S2	546	G	-	variant	GB 37956930
S2	547	G	-	variant	GB 37956930
S2	548	C	-	variant	GB 37956930
S2	549	C	-	variant	GB 37956930
S2	550	C	-	variant	GB 37956930
S2	551	U	-	variant	GB 37956930
S2	552	G	-	variant	GB 37956930
S2	553	U	-	variant	GB 37956930
S2	554	A	-	variant	GB 37956930
S2	555	A	-	variant	GB 37956930
S2	556	U	-	variant	GB 37956930
S2	557	U	-	variant	GB 37956930
S2	558	G	-	variant	GB 37956930
S2	559	G	-	variant	GB 37956930
S2	560	A	-	variant	GB 37956930
S2	561	A	-	variant	GB 37956930
S2	562	U	-	variant	GB 37956930
S2	563	G	-	variant	GB 37956930
S2	564	A	-	variant	GB 37956930
S2	565	G	-	variant	GB 37956930
S2	566	U	-	variant	GB 37956930
S2	567	C	-	variant	GB 37956930
S2	568	C	-	variant	GB 37956930
S2	569	A	-	variant	GB 37956930
S2	570	C	-	variant	GB 37956930
S2	571	U	-	variant	GB 37956930
S2	572	U	-	variant	GB 37956930
S2	573	U	-	variant	GB 37956930
S2	574	A	-	variant	GB 37956930
S2	575	A	-	variant	GB 37956930
S2	576	A	-	variant	GB 37956930
S2	577	U	-	variant	GB 37956930
S2	578	C	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	579	C	-	variant	GB 37956930
S2	580	U	-	variant	GB 37956930
S2	581	U	-	variant	GB 37956930
S2	582	C	-	variant	GB 37956930
S2	583	C	-	variant	GB 37956930
S2	584	G	-	variant	GB 37956930
S2	585	C	-	variant	GB 37956930
S2	586	G	-	variant	GB 37956930
S2	587	A	-	variant	GB 37956930
S2	588	G	-	variant	GB 37956930
S2	589	G	-	variant	GB 37956930
S2	590	A	-	variant	GB 37956930
S2	591	U	-	variant	GB 37956930
S2	592	C	-	variant	GB 37956930
S2	593	C	-	variant	GB 37956930
S2	594	A	-	variant	GB 37956930
S2	595	U	-	variant	GB 37956930
S2	596	U	-	variant	GB 37956930
S2	597	G	-	variant	GB 37956930
S2	598	G	-	variant	GB 37956930
S2	599	A	-	variant	GB 37956930
S2	600	G	-	variant	GB 37956930
S2	601	G	-	variant	GB 37956930
S2	602	G	-	variant	GB 37956930
S2	603	C	-	variant	GB 37956930
S2	604	A	-	variant	GB 37956930
S2	605	A	-	variant	GB 37956930
S2	606	G	-	variant	GB 37956930
S2	607	U	-	variant	GB 37956930
S2	608	C	-	variant	GB 37956930
S2	609	U	-	variant	GB 37956930
S2	610	G	-	variant	GB 37956930
S2	611	G	-	variant	GB 37956930
S2	612	U	-	variant	GB 37956930
S2	613	G	-	variant	GB 37956930
S2	614	C	-	variant	GB 37956930
S2	615	C	-	variant	GB 37956930
S2	616	A	-	variant	GB 37956930
S2	617	G	-	variant	GB 37956930
S2	618	C	-	variant	GB 37956930
S2	619	A	-	variant	GB 37956930
S2	620	G	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	621	C	-	variant	GB 37956930
S2	622	C	-	variant	GB 37956930
S2	623	G	-	variant	GB 37956930
S2	624	C	-	variant	GB 37956930
S2	625	G	-	variant	GB 37956930
S2	626	G	-	variant	GB 37956930
S2	627	U	-	variant	GB 37956930
S2	628	A	-	variant	GB 37956930
S2	629	A	-	variant	GB 37956930
S2	630	U	-	variant	GB 37956930
S2	631	U	-	variant	GB 37956930
S2	632	C	-	variant	GB 37956930
S2	633	C	-	variant	GB 37956930
S2	634	A	-	variant	GB 37956930
S2	635	G	-	variant	GB 37956930
S2	636	C	-	variant	GB 37956930
S2	637	U	-	variant	GB 37956930
S2	638	C	-	variant	GB 37956930
S2	639	C	-	variant	GB 37956930
S2	640	A	-	variant	GB 37956930
S2	641	A	-	variant	GB 37956930
S2	642	U	-	variant	GB 37956930
S2	643	A	-	variant	GB 37956930
S2	644	G	-	variant	GB 37956930
S2	645	C	-	variant	GB 37956930
S2	646	G	-	variant	GB 37956930
S2	647	U	-	variant	GB 37956930
S2	648	A	-	variant	GB 37956930
S2	649	U	-	variant	GB 37956930
S2	650	A	-	variant	GB 37956930
S2	651	U	-	variant	GB 37956930
S2	652	U	-	variant	GB 37956930
S2	653	A	-	variant	GB 37956930
S2	654	A	-	variant	GB 37956930
S2	655	A	-	variant	GB 37956930
S2	656	G	-	variant	GB 37956930
S2	657	U	-	variant	GB 37956930
S2	658	U	-	variant	GB 37956930
S2	659	G	-	variant	GB 37956930
S2	660	C	-	variant	GB 37956930
S2	661	U	-	variant	GB 37956930
S2	662	G	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	663	C	-	variant	GB 37956930
S2	664	A	-	variant	GB 37956930
S2	665	G	-	variant	GB 37956930
S2	666	U	-	variant	GB 37956930
S2	667	U	-	variant	GB 37956930
S2	668	A	-	variant	GB 37956930
S2	669	A	-	variant	GB 37956930
S2	670	A	-	variant	GB 37956930
S2	671	A	-	variant	GB 37956930
S2	672	A	-	variant	GB 37956930
S2	673	G	-	variant	GB 37956930
S2	674	C	-	variant	GB 37956930
S2	675	U	-	variant	GB 37956930
S2	676	C	-	variant	GB 37956930
S2	677	G	-	variant	GB 37956930
S2	678	U	-	variant	GB 37956930
S2	679	A	-	variant	GB 37956930
S2	680	G	-	variant	GB 37956930
S2	681	U	-	variant	GB 37956930
S2	682	U	-	variant	GB 37956930
S2	683	G	-	variant	GB 37956930
S2	684	G	-	variant	GB 37956930
S2	685	A	-	variant	GB 37956930
S2	686	U	-	variant	GB 37956930
S2	687	C	-	variant	GB 37956930
S2	688	U	-	variant	GB 37956930
S2	689	U	-	variant	GB 37956930
S2	690	G	-	variant	GB 37956930
S2	691	G	-	variant	GB 37956930
S2	692	G	-	variant	GB 37956930
S2	693	A	-	variant	GB 37956930
S2	694	G	-	variant	GB 37956930
S2	695	C	-	variant	GB 37956930
S2	696	G	-	variant	GB 37956930
S2	697	G	-	variant	GB 37956930
S2	698	G	-	variant	GB 37956930
S2	730	C	-	variant	GB 37956930
S2	731	G	-	variant	GB 37956930
S2	732	U	-	variant	GB 37956930
S2	733	C	-	variant	GB 37956930
S2	734	C	-	variant	GB 37956930
S2	735	C	-	variant	GB 37956930

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Chain	Residue	Modelled	Actual	Comment	Reference
S2	736	C	-	variant	GB 37956930
S2	737	G	-	variant	GB 37956930
S2	738	C	-	variant	GB 37956930
S2	739	C	-	variant	GB 37956930
S2	744	G	-	variant	GB 37956930
S2	745	C	-	variant	GB 37956930
S2	746	C	-	variant	GB 37956930
S2	747	U	-	variant	GB 37956930
S2	748	C	-	variant	GB 37956930
S2	749	U	-	variant	GB 37956930
S2	750	C	-	variant	GB 37956930
S2	751	G	-	variant	GB 37956930
S2	752	G	-	variant	GB 37956930
S2	753	C	-	variant	GB 37956930
S2	798	A	G	conflict	GB 37956930

- Molecule 51 is a protein called Ribosomal protein uS2.

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

- Molecule 52 is a protein called Ribosomal protein eS1.

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

- Molecule 53 is a protein called Ribosomal protein uS5.

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

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SC	61	MET	LEU	conflict	UNP I3LJ87

- Molecule 54 is a protein called Ribosomal protein uS3.

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

- Molecule 55 is a protein called Ribosomal protein eS4.

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

- Molecule 56 is a protein called Ribosomal protein uS7.

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

- Molecule 57 is a protein called Ribosomal protein eS6.

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

- Molecule 58 is a protein called Ribosomal protein eS7.

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

- Molecule 59 is a protein called Ribosomal protein eS8.

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

- Molecule 60 is a protein called Ribosomal protein uS4.

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

- Molecule 61 is a protein called Ribosomal protein eS10.

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

- Molecule 62 is a protein called Ribosomal protein uS17.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	SL	156	Total	C	N	O	S	0	0
			1276	813	239	218	6		

- Molecule 63 is a protein called Ribosomal protein eS12.

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

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
SM	52	GLN	LEU	conflict	UNP P46405
SM	69	LEU	CYS	conflict	UNP P46405
SM	99	ASN	LYS	conflict	UNP P46405

- Molecule 64 is a protein called Ribosomal protein uS15.

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

- Molecule 65 is a protein called Ribosomal protein uS11.

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

- Molecule 66 is a protein called Ribosomal protein uS19.

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

- Molecule 67 is a protein called Ribosomal protein uS9.

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

- Molecule 68 is a protein called Ribosomal protein eS17.

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

- Molecule 69 is a protein called Ribosomal protein uS13.

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

- Molecule 70 is a protein called Ribosomal protein eS19.

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

- Molecule 71 is a protein called Ribosomal protein uS10.

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

- Molecule 72 is a protein called Ribosomal protein eS21.

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

- Molecule 73 is a protein called Ribosomal protein uS8.

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

- Molecule 74 is a protein called Ribosomal protein uS12.

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

- Molecule 75 is a protein called Ribosomal protein eS24.

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

- Molecule 76 is a protein called Ribosomal protein es25.

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

- Molecule 77 is a protein called Ribosomal protein eS26.

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

- Molecule 78 is a protein called Ribosomal protein eS27.

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

- Molecule 79 is a protein called Ribosomal protein eS28.

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

- Molecule 80 is a protein called Ribosomal protein uS14.

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

- Molecule 81 is a protein called Ribosomal protein eS30.

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

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
Se	-33	VAL	LEU	conflict	UNP A0A480W155
Se	-23	GLU	ASP	conflict	UNP A0A480W155
Se	-21	THR	ILE	conflict	UNP A0A480W155
Se	-11	THR	ARG	conflict	UNP A0A480W155

- Molecule 82 is a protein called Ribosomal protein eS31.

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

- Molecule 83 is a protein called Ribosomal protein RACK1.

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

- Molecule 84 is a RNA chain called Messenger RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
84	S4	10	Total	C	N	O	P	0	0
			201	91	23	78	9		

- Molecule 85 is a RNA chain called A/P tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
85	S5	74	Total	C	N	O	P	0	0
			1579	705	285	516	73		

- Molecule 86 is a RNA chain called P/E tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
86	S6	76	Total	C	N	O	P	0	0
			1622	723	291	532	76		

- Molecule 87 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
87	5	120	Total 120	Mg 120	0
87	7	5	Total 5	Mg 5	0
87	8	3	Total 3	Mg 3	0
87	P	1	Total 1	Mg 1	0
87	V	1	Total 1	Mg 1	0
87	S2	36	Total 36	Mg 36	0

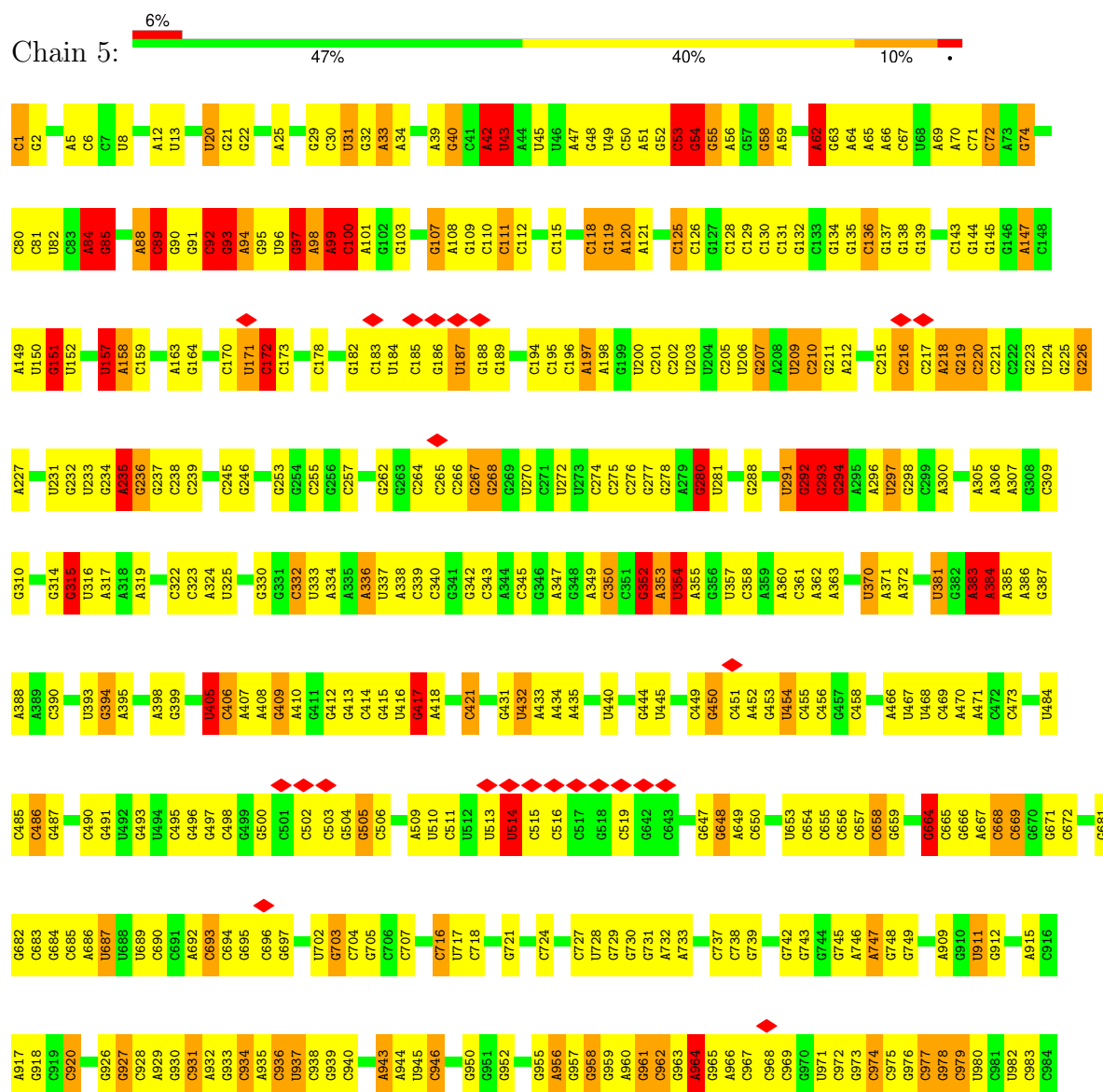
- Molecule 88 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

3 Residue-property plots [i](#)

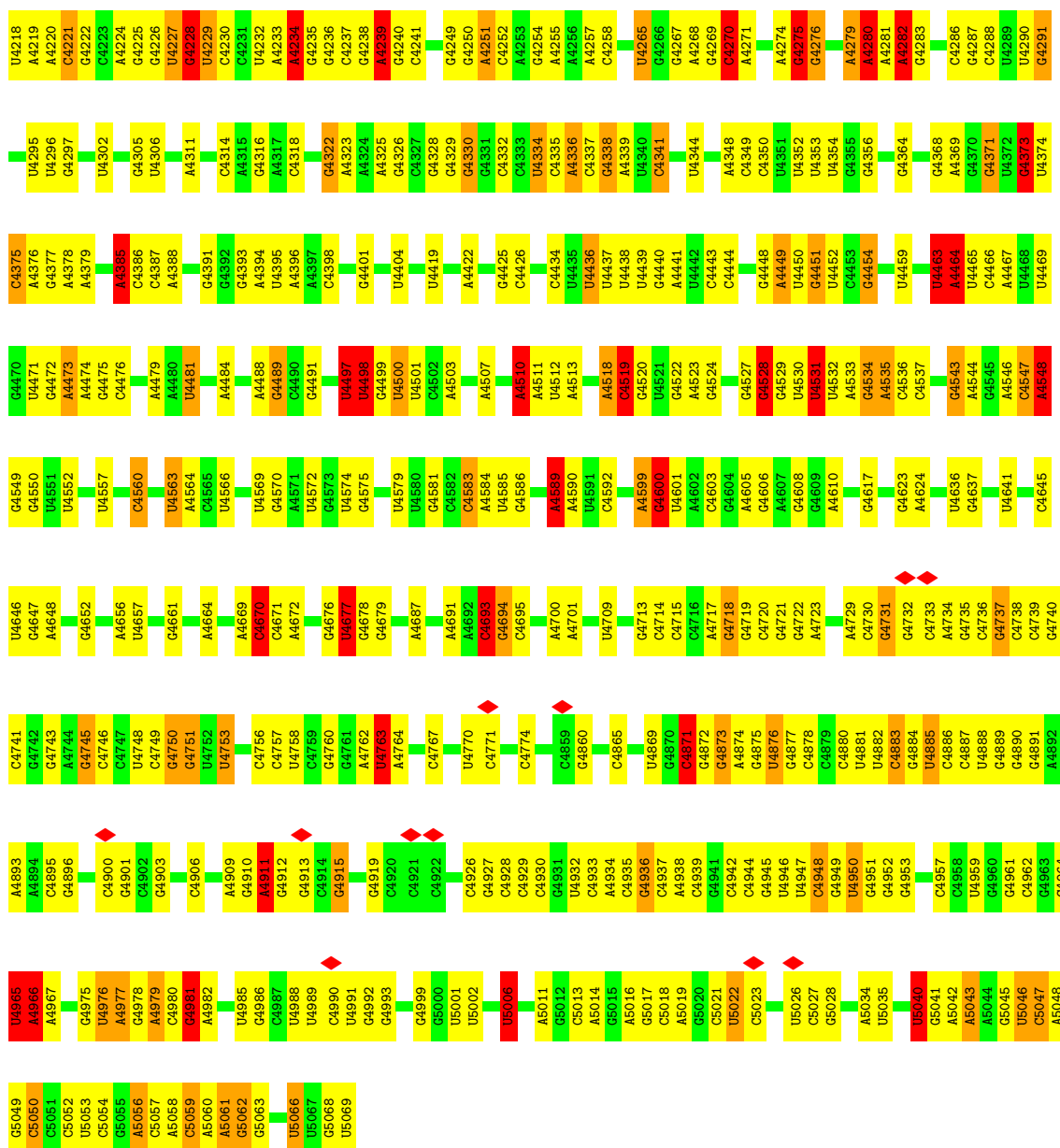
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 28S ribosomal RNA





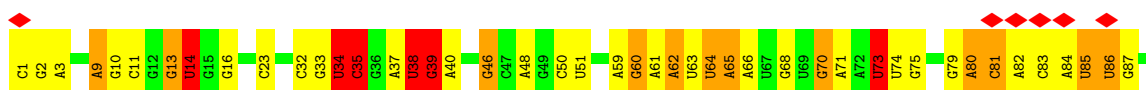




• Molecule 2: 5S ribosomal RNA

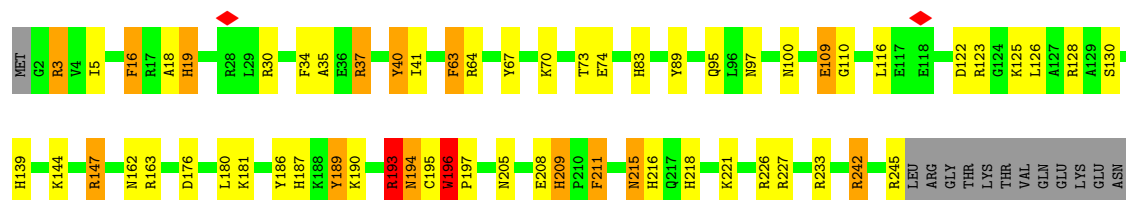


• Molecule 3: 5.8S ribosomal RNA

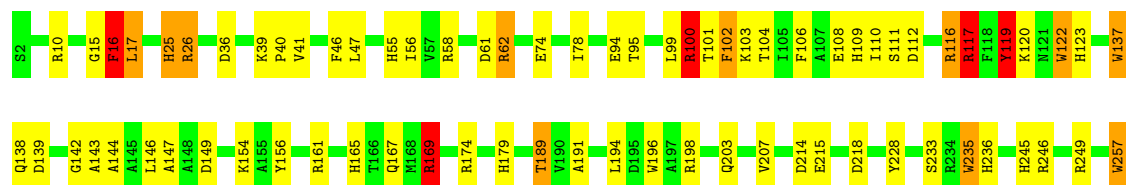




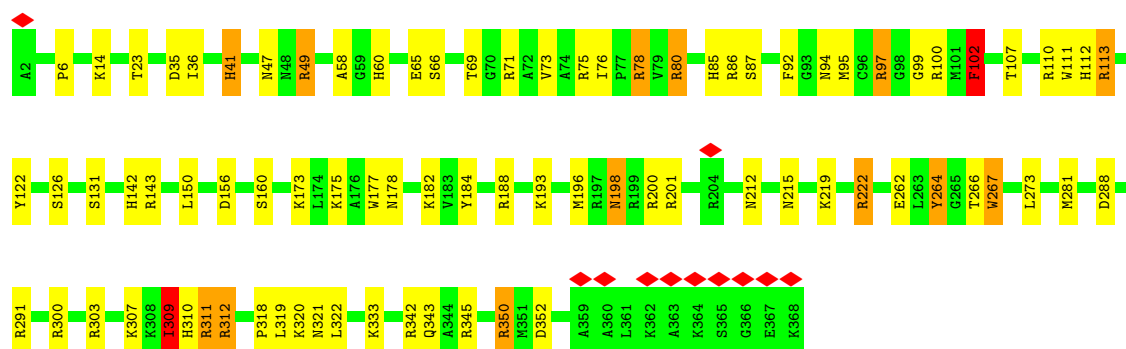
• Molecule 4: Ribosomal protein uL2



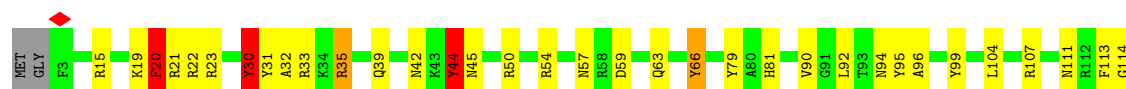
• Molecule 5: Ribosomal protein uL3

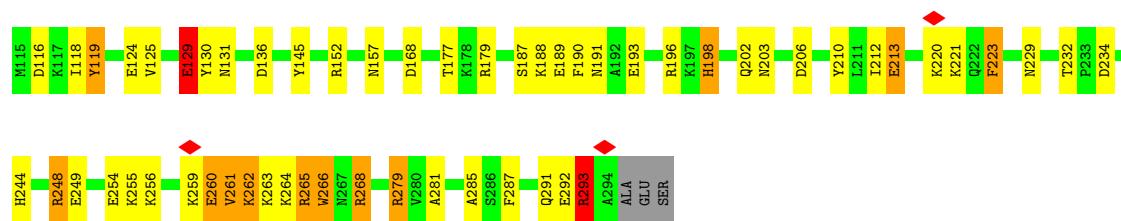


• Molecule 6: Ribosomal protein uL4

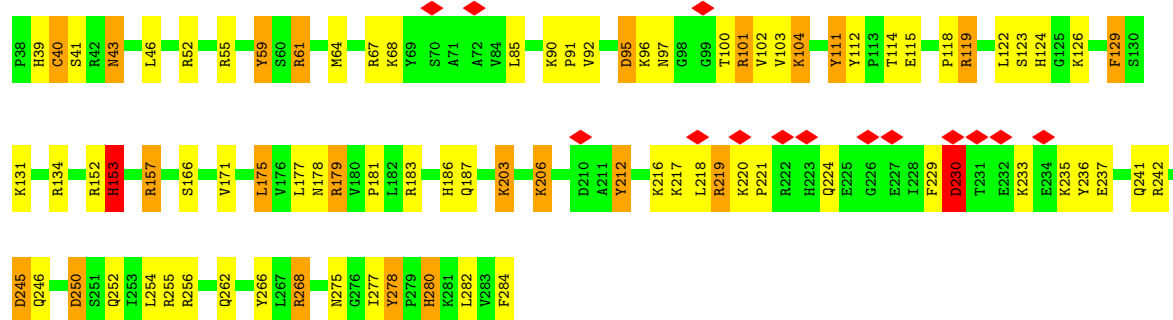


• Molecule 7: Ribosomal protein uL18

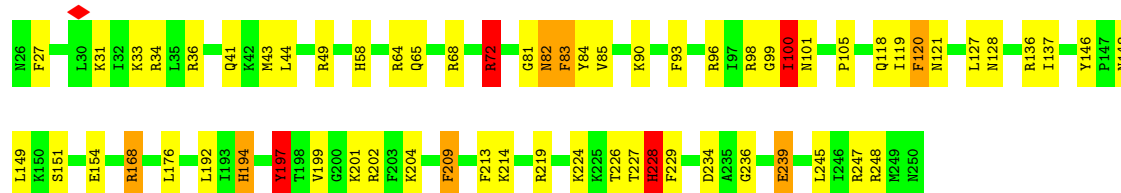




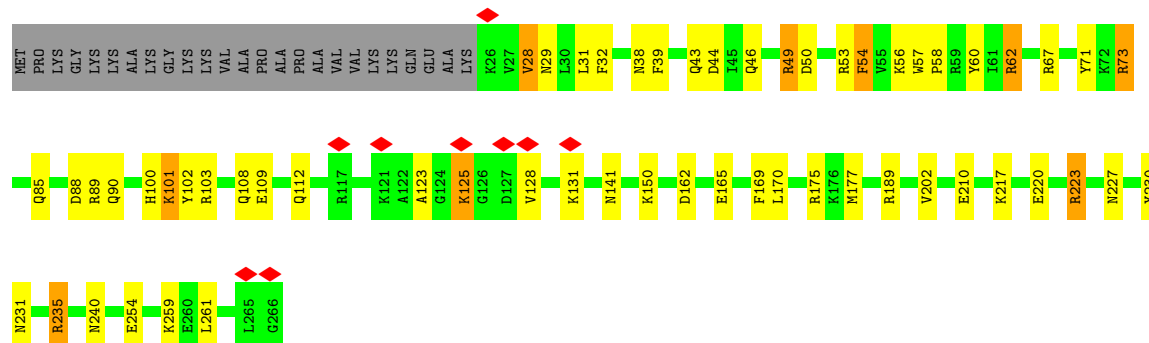
• Molecule 8: Ribosomal protein eL6



• Molecule 9: Ribosomal protein uL30

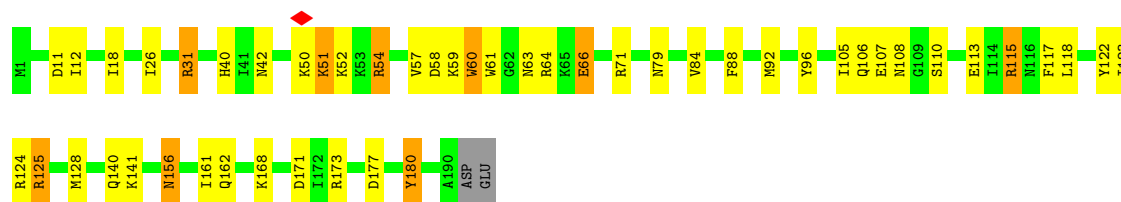


• Molecule 10: Ribosomal protein eL8

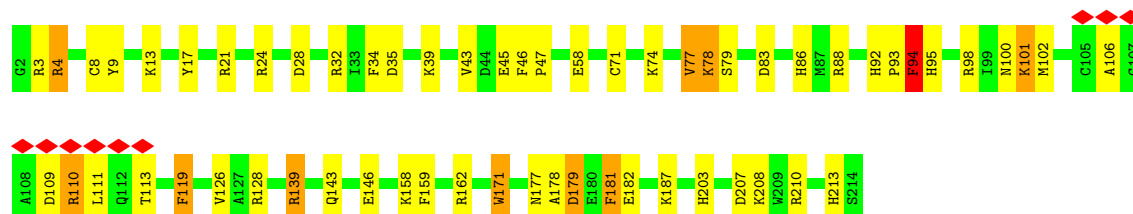


• Molecule 11: Ribosomal protein uL6

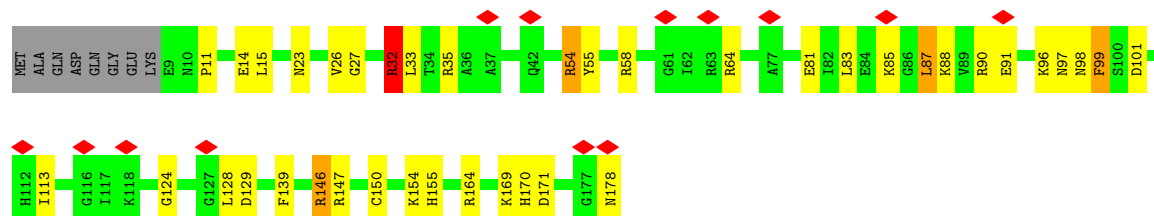




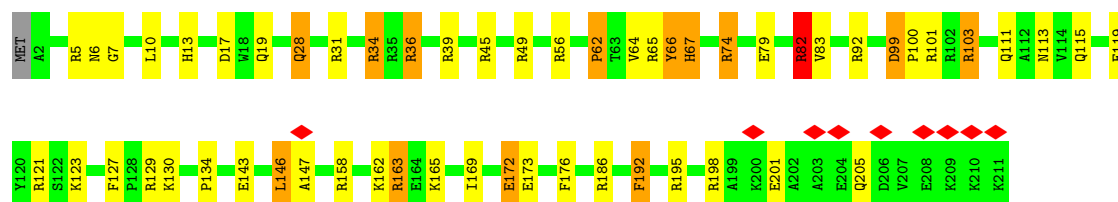
• Molecule 12: Ribosomal protein uL16



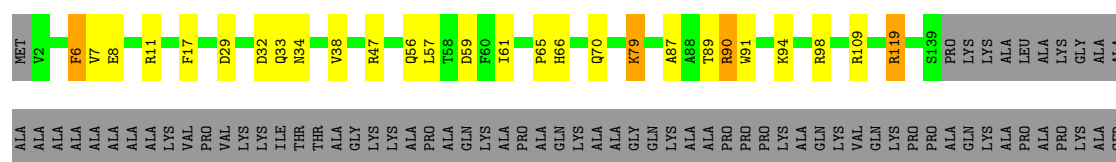
• Molecule 13: Ribosomal protein uL5



• Molecule 14: Ribosomal protein eL13



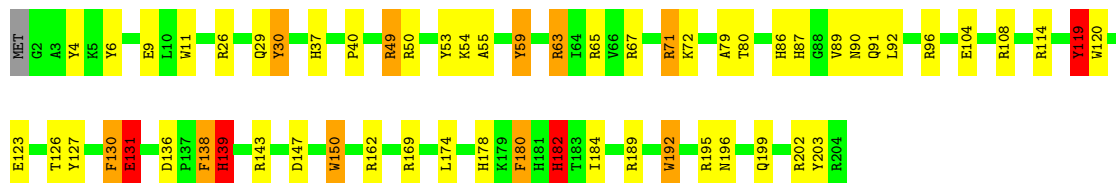
• Molecule 15: Ribosomal protein eL14




GLY
GLU
LYS
ALA

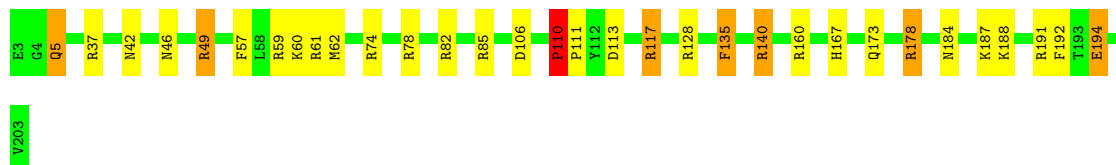
• Molecule 16: Ribosomal protein eL15

Chain N:  71% 22% 5% •




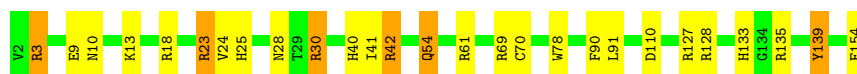
• Molecule 17: Ribosomal protein uL13

Chain O:  84% 12% •



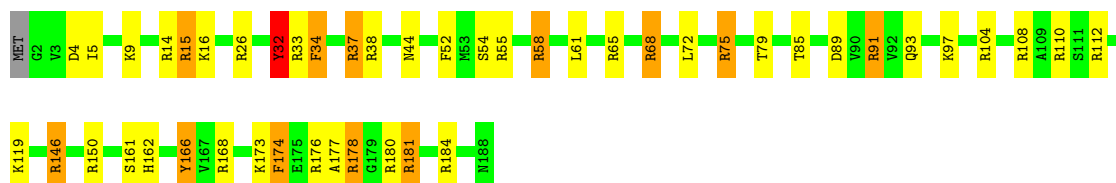
• Molecule 18: Ribosomal protein uL22

Chain P:  82% 14% •



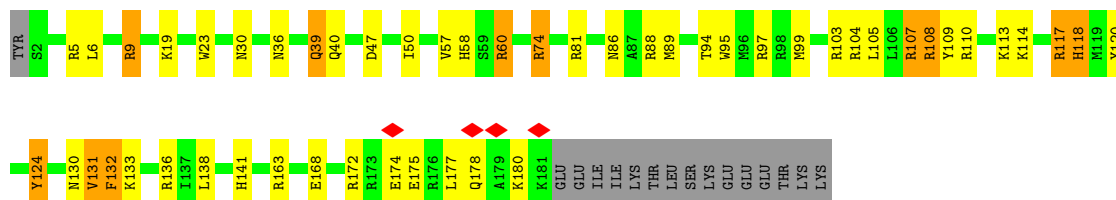
• Molecule 19: Ribosomal protein eL18

Chain Q:  74% 18% 6% ••

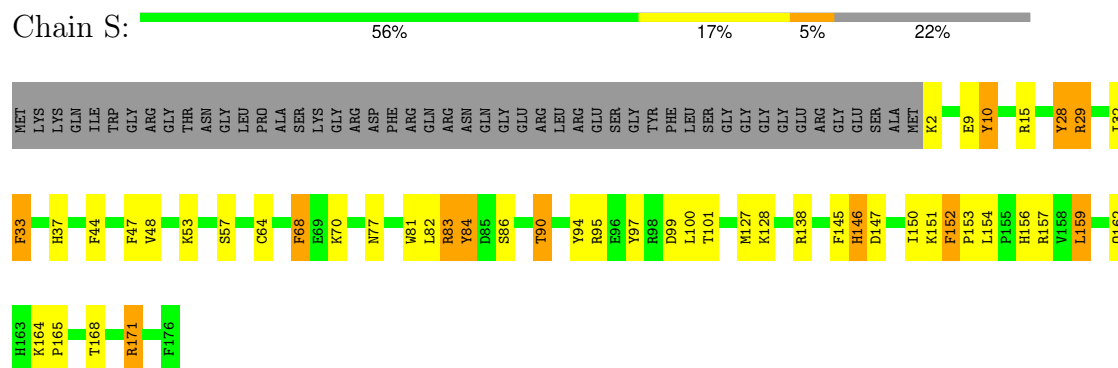


• Molecule 20: Ribosomal protein eL19

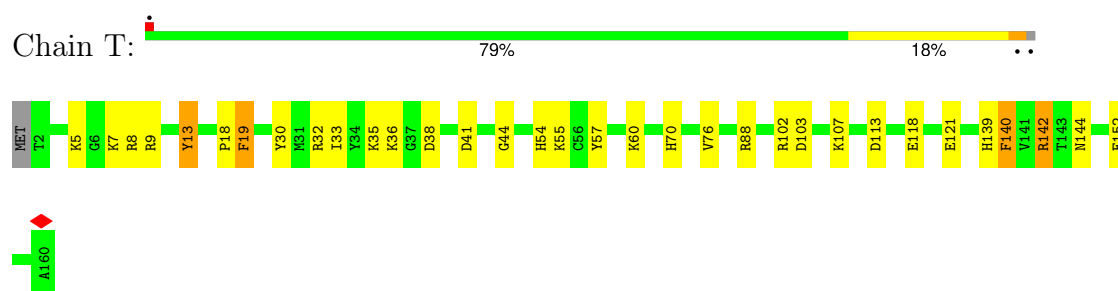
Chain R:  66% 20% 6% 8%



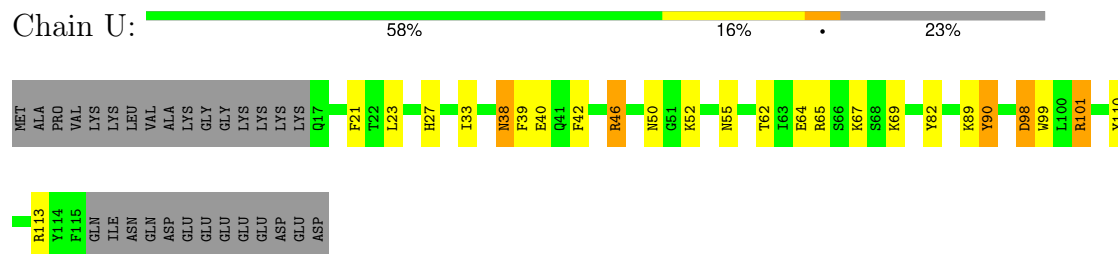
- Molecule 21: Ribosomal protein eL20



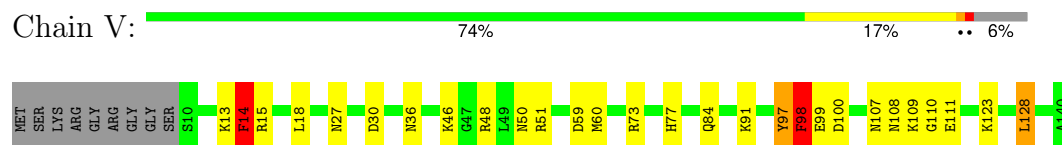
- Molecule 22: Ribosomal protein eL21



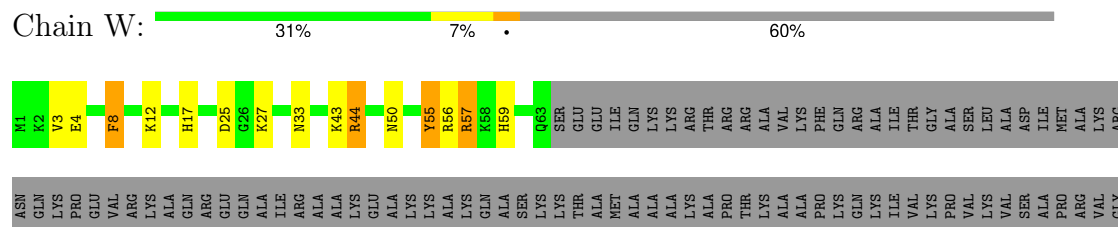
- Molecule 23: Ribosomal protein eL22



- Molecule 24: Ribosomal protein uL14



- Molecule 25: Ribosomal protein eL24



LYS
GLY
ALA
GLN
ALA
PRO
THR
LYS
ALA
PRO
GLN

• Molecule 31: Ribosomal protein eL30

Chain c:  63% 15% 18%

MET VAL ALA ALA LYS LYS THR LYS LYS SER LEU GLU S13 L18 Y27 Y31 K32 M37 I38 R39 K42 A43 K44 C52 L55 R56 E59 L66 H72 H73 Y74 M77 M78 I79 E80 L81 Y88 Y89 R90 D101 R106 SER MET PRO GLU GLN

THR GLY GLU LYS

• Molecule 32: Ribosomal protein eL31

Chain d:  56% 22% 8% 14%

MET ALA PRO ALA LYS LYS GLY GLY LYS LYS LYS GLY ARG SER ALA ILE N18 E19 R23 E24 Y25 T26 I27 N28 K31 R32 F38 K39 R44 G58 R67 V72 M73 R78 M79 R83 I84 R85 V86 R87 K91 R92 N93 E94 D95 E96 D97 K101

L102 Y103 Y108 L4 Y109 N116 L117 Q118 T119 N121 N122 D123 E124 ASN

• Molecule 33: Ribosomal protein eL32

Chain e:  69% 22% 5%

MET A2 A3 L4 R5 K11 R16 F20 I21 D26 N34 W35 R36 D42 M43 R46 R47 R48 F49 Q52 N57 Y60 K64 H68 F74 R75 K76 F77 L78 L85 N92 Y95 K106 N107 R108 E113 N124 P125 N126 A127 R128


L129 ARG SER GLU ASN GLU

• Molecule 34: Ribosomal protein eL33

Chain f:  78% 15% 5% 2%

MET S2 Q3 R4 L5 W6 S7 Y14 R15 R16 R19 R22 E23 H24 R36 Y49 V50 Y51 K52 A53 W71 N80 R85 R100 I101 R102 Y106 P107 S108 R109 I110

• Molecule 35: Ribosomal protein eL34

Chain g:  6% 77% 19% 2%

MET V2 Q3 R4 L5 W6 S7 R8 S12 Y13 N14 R29 Y32 Y33 R52 R53 R54 R55 R56 R57 R60 R66 S75 S81 A84 R88 D89 R90 R93 A94 F95 K108 A109 Q110 A111 Q112 S113 Q114 K115 ALA LYS

• Molecule 36: Ribosomal protein uL29

Amino Acid	Count
MET	1
A2	2
D8	8
L9	9
R10	10
E15	15
D23	23
L28	28
G38	38
R48	48
R51	51
E67	67
M68	68
L69	69
R70	70
K71	71
F72	72
Y73	73
Y78	78
R84	84
R89	89
R93	93
K97	97
E100	100
R117	117
K118	118
F119	119
A120	120
V121	121
K122	122
A123	123
A133	133

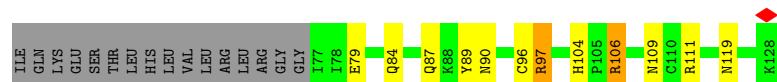
-
- Figure 1: A horizontal bar chart showing the distribution of amino acid types in the protein sequences. The x-axis represents the percentage of sequences, ranging from 0% to 100%. The y-axis lists 20 amino acid types: MET, A2, L3, R4, N12, N20, H26, S27, R28, R29, R30, L33, F39, D42, E46, G49, F50, E54, V63, S64, K65, D66, K67, R68, R85, E88, A102, K103, LYS, and ASP. The bars are color-coded: MET (grey), A2 (green), L3 (light green), R4 (orange), N12 (yellow), N20 (light yellow), H26 (dark orange), S27 (light orange), R28 (yellow), R29 (light yellow), R30 (yellow), L33 (light yellow), F39 (dark orange), D42 (light yellow), E46 (yellow), G49 (light yellow), F50 (yellow), E54 (light yellow), V63 (yellow), S64 (light yellow), K65 (yellow), D66 (yellow), K67 (yellow), R68 (yellow), R85 (orange), E88 (yellow), A102 (green), K103 (grey), LYS (grey), and ASP (grey). Red diamonds are placed above the bars for MET, A2, and A102.

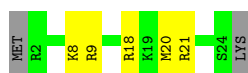
- | | | | | | | | | | | | | | | | | | | | | | | | | | |
|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| T2 | T5 | F8 | G9 | K10 | R11 | K25 | A26 | Y27 | G38 | Y39 | R45 | K46 | Y47 | N48 | W49 | R55 | R56 | N57 | H66 | Y71 | R75 | H76 | R79 | E80 | K87 |
|----|----|----|----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

-
- | Category | Count |
|----------|-------|
| NET | 100 |
| P2 | 100 |
| T14 | 100 |
| A15 | 100 |
| R16 | 100 |
| D19 | 100 |
| A20 | 100 |
| K21 | 100 |
| S22 | 100 |
| V23 | 100 |
| K27 | 100 |
| N28 | 100 |
| K29 | 100 |
| D30 | 100 |
| K35 | 100 |
| V36 | 100 |
| R37 | 100 |
| E51 | 100 |
| E54 | 100 |
| K55 | 100 |
| L56 | 100 |
| S59 | 100 |
| L60 | 100 |
| P61 | 100 |
| P62 | 100 |
| G63 | 100 |
| K70 | 100 |

-
- Diagram illustrating a 16-bit bus architecture. The components are arranged in a sequence: MET, S2, R11, F12, K16, Q17, R21, P22, K34, I35, R36, R45, R46, T47, K48, L49, G50, and L51. Red diamonds indicate connections between K34 and K48, and between L49 and G50.

- | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| MET | GLN | ILE | PHE | VAL | LYS | THR | LEU | THR | GLY | LYS | THR | ILE | THR | LEU | GLU | VAL | GLU | GLU | PRO | SER | ASP | THR | ILE | GLU | ASN | GLN | LYS | LYS | LYS | GLN | ASP | ASP | GLN | GLN | ARG | LEU | LEU | PHE | ILE | GLY | LYS | GLN | THR | LEU | SER | ASP | THR | TYR |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|

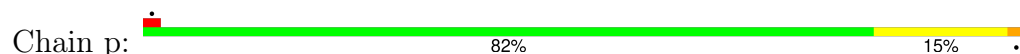




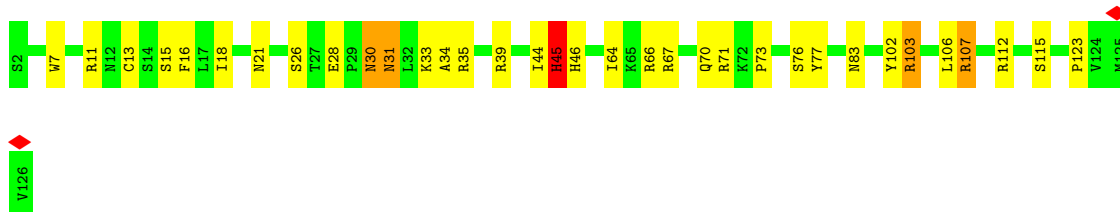
• Molecule 43: Ribosomal protein eL42



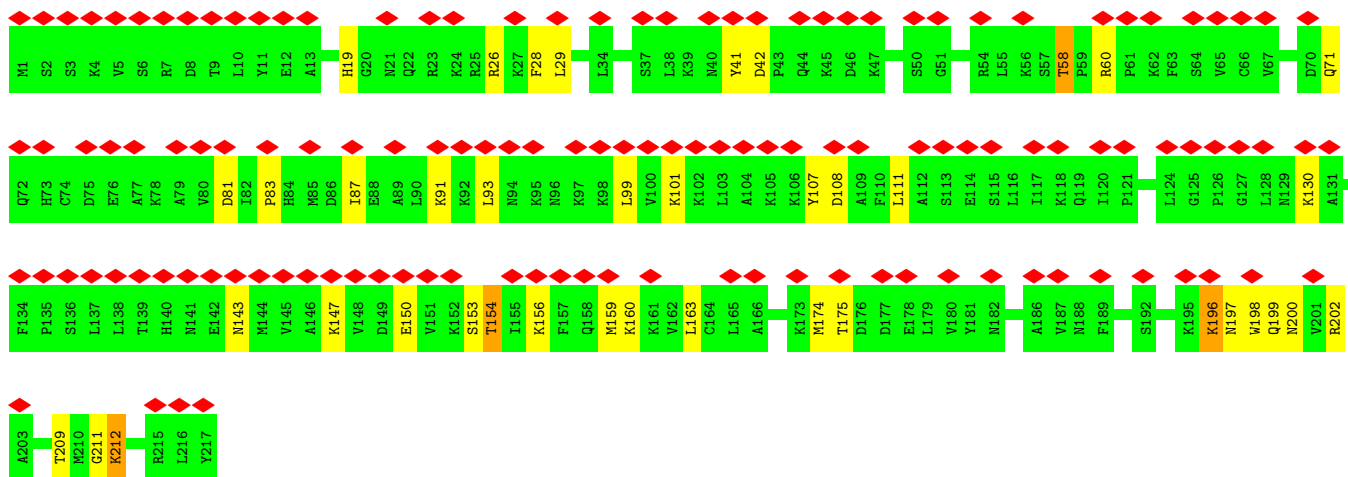
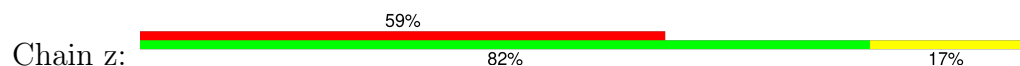
• Molecule 44: Ribosomal protein eL43




• Molecule 45: Ribosomal protein eL28

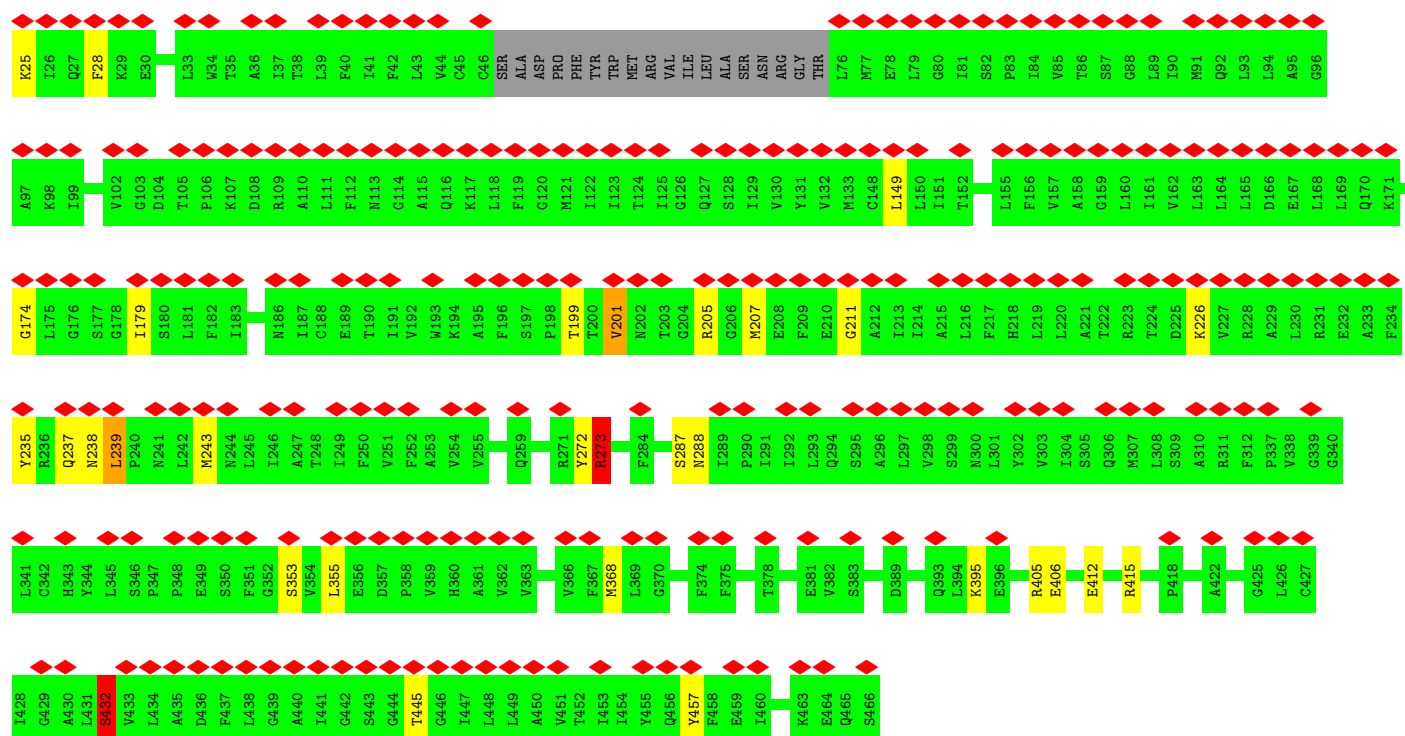


• Molecule 46: Ribosomal protein uL1




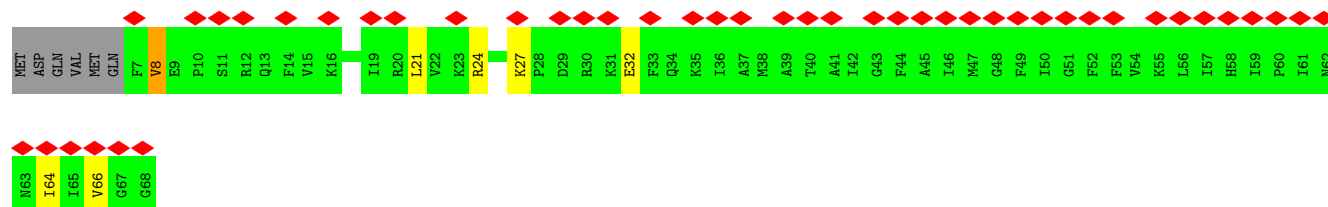
• Molecule 47: Sec61 alpha subunit

Chain 1: 



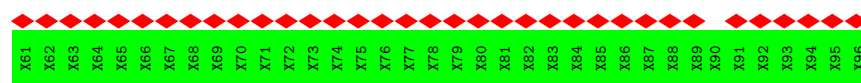
• Molecule 48: Sec61 gamma subunit

Chain 2: 



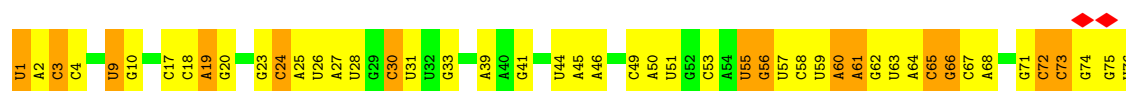
• Molecule 49: Sec61 beta subunit

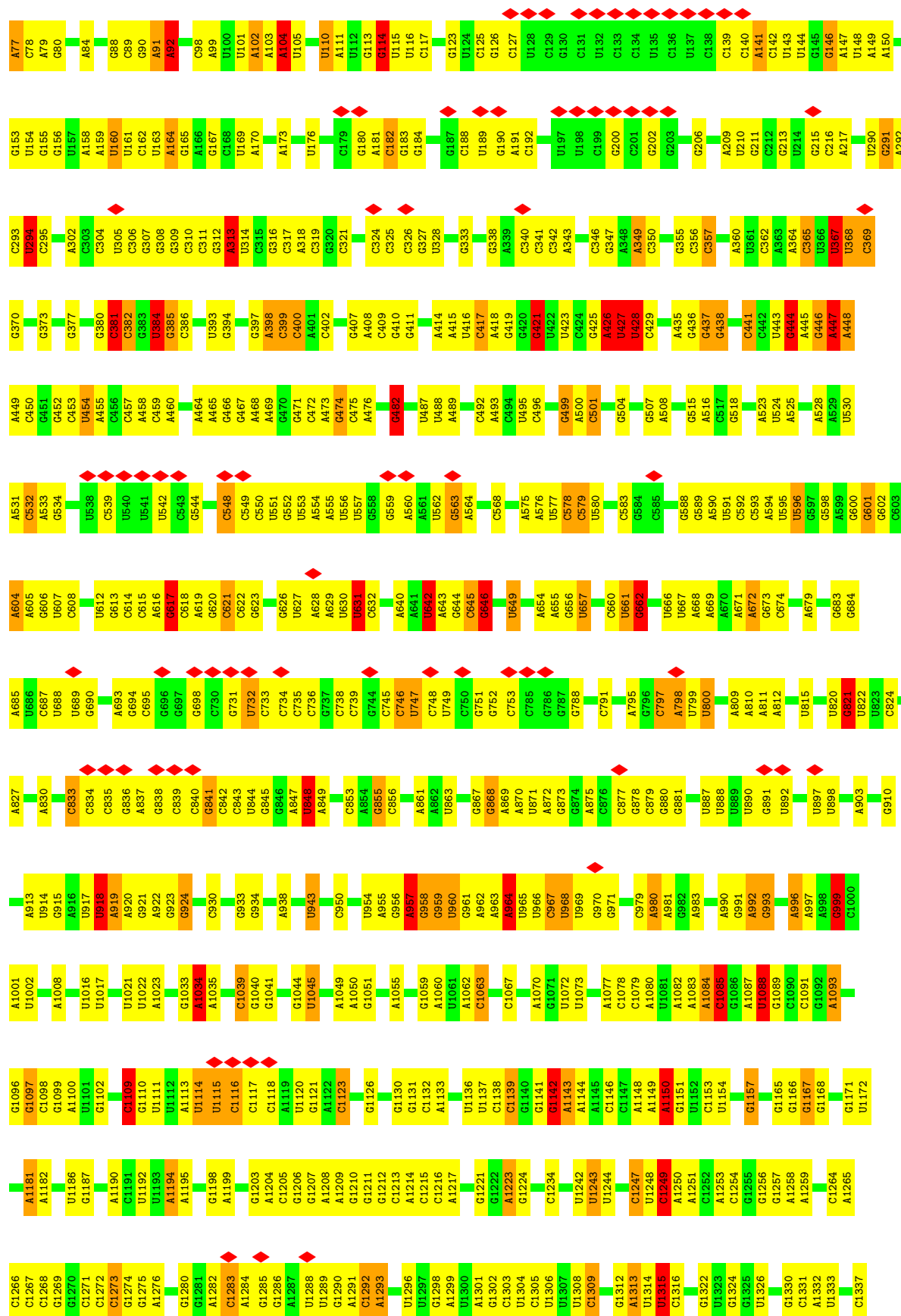
Chain 3: 

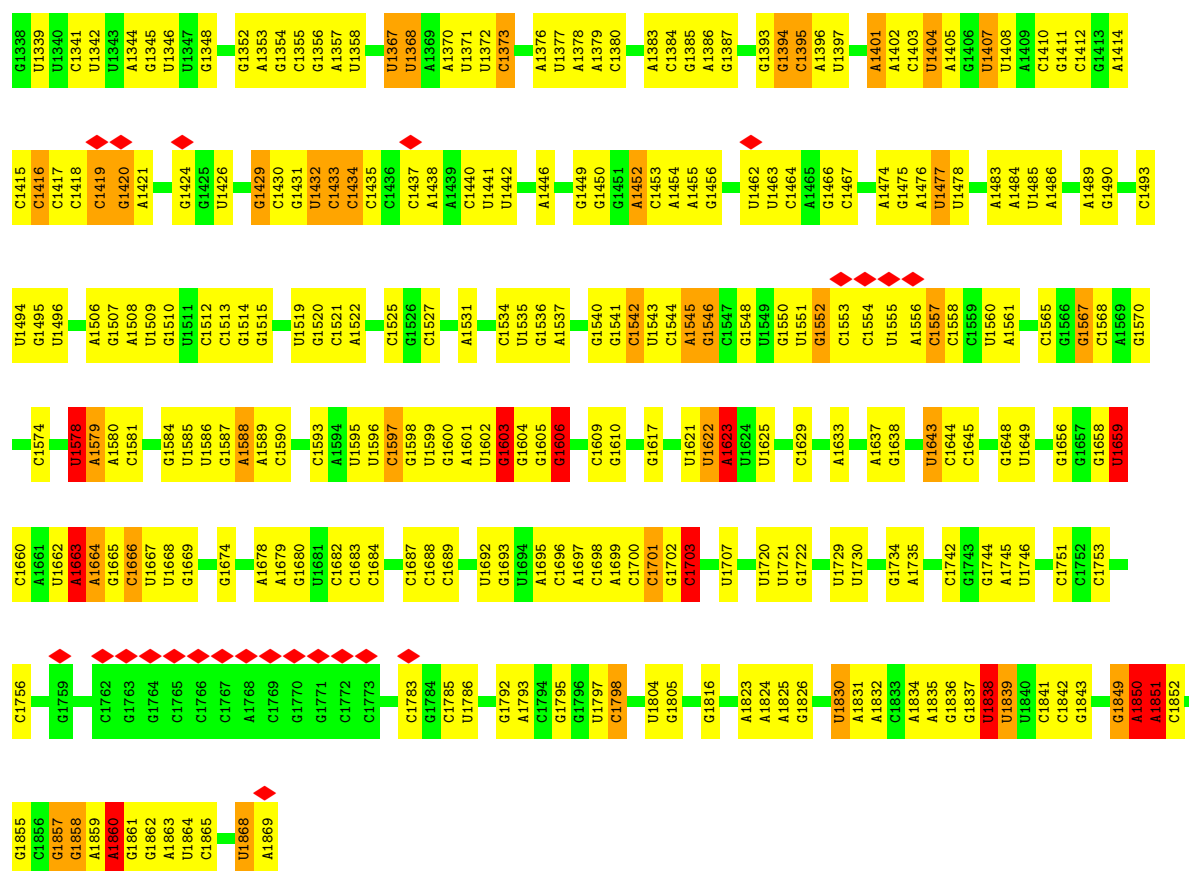


• Molecule 50: 18S ribosomal RNA

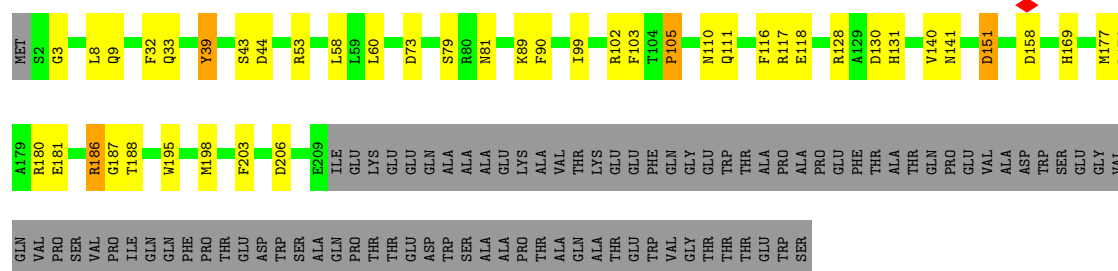
Chain S2: 



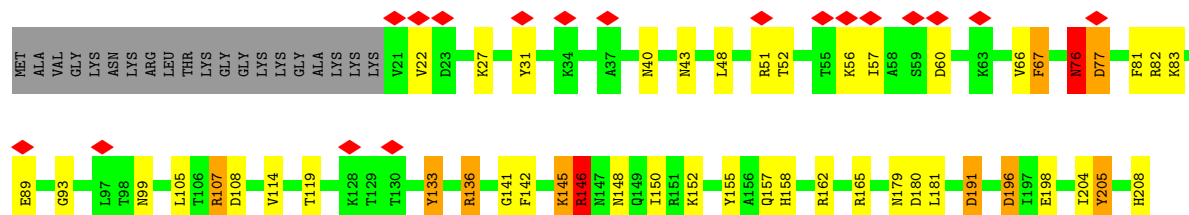


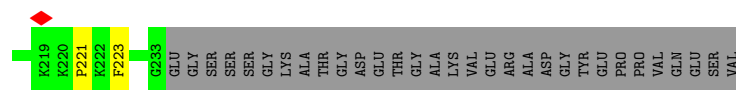


• Molecule 51: Ribosomal protein uS2

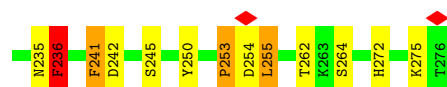
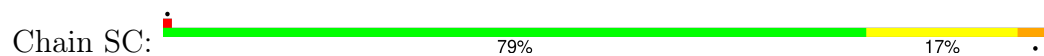


• Molecule 52: Ribosomal protein eS1

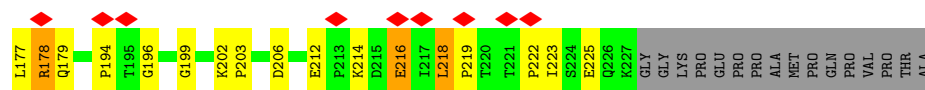
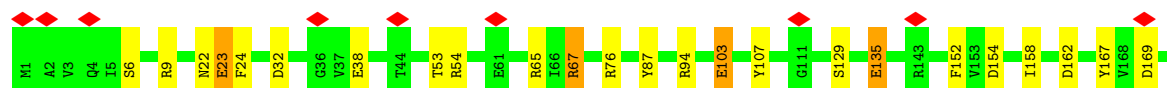
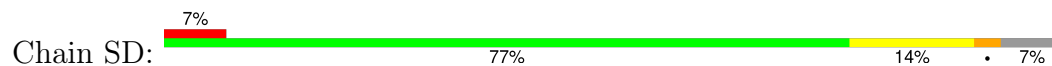




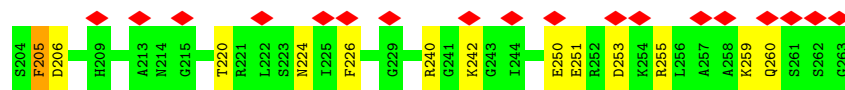
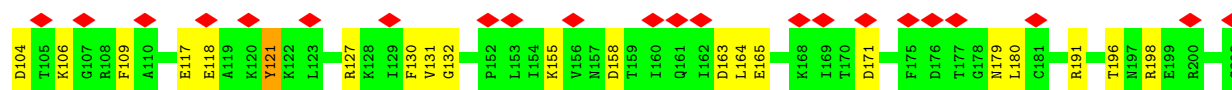
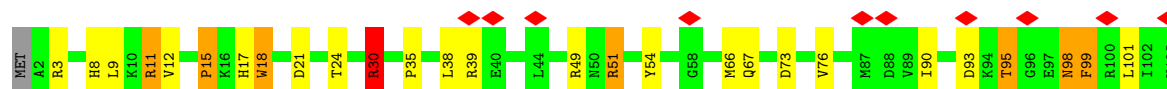
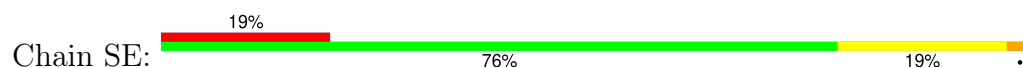
• Molecule 53: Ribosomal protein uS5



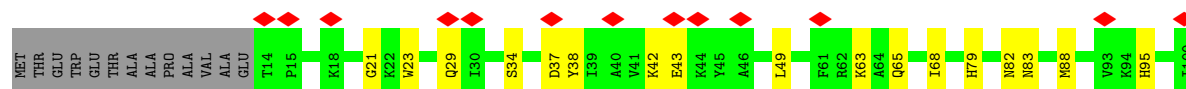
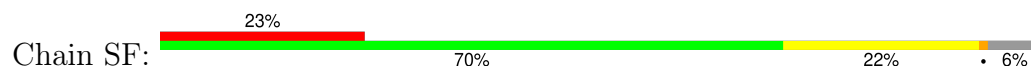
• Molecule 54: Ribosomal protein uS3

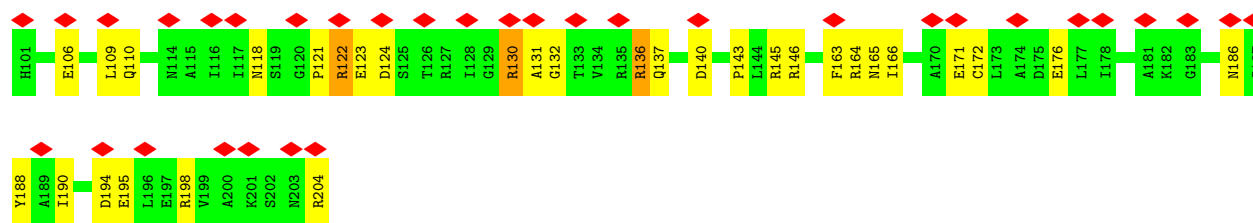


• Molecule 55: Ribosomal protein eS4

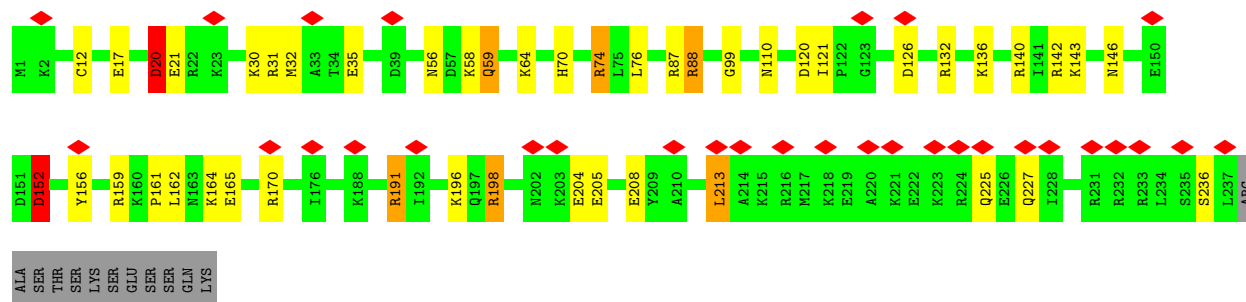
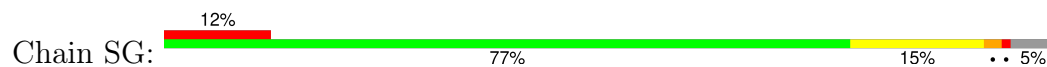


• Molecule 56: Ribosomal protein uS7

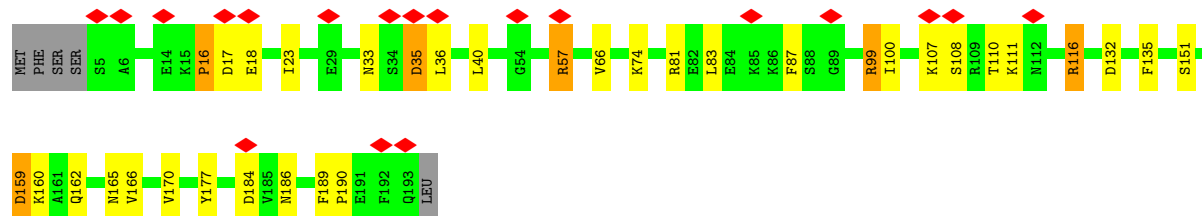
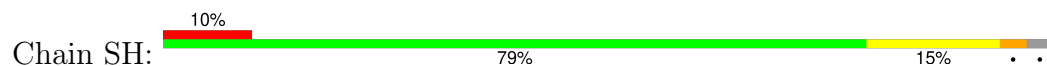




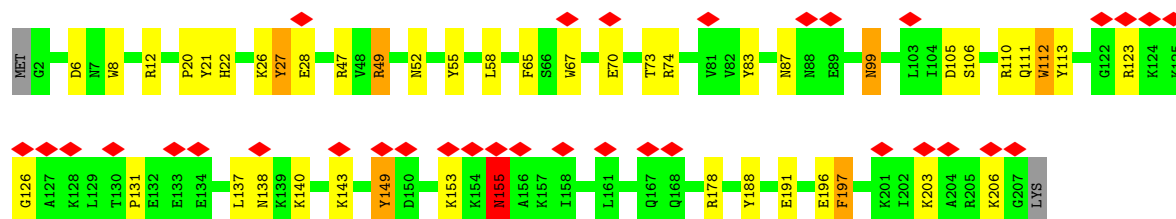
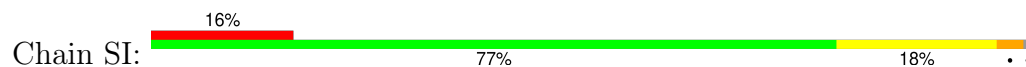
• Molecule 57: Ribosomal protein eS6



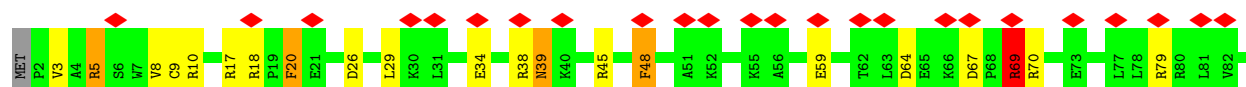
• Molecule 58: Ribosomal protein eS7



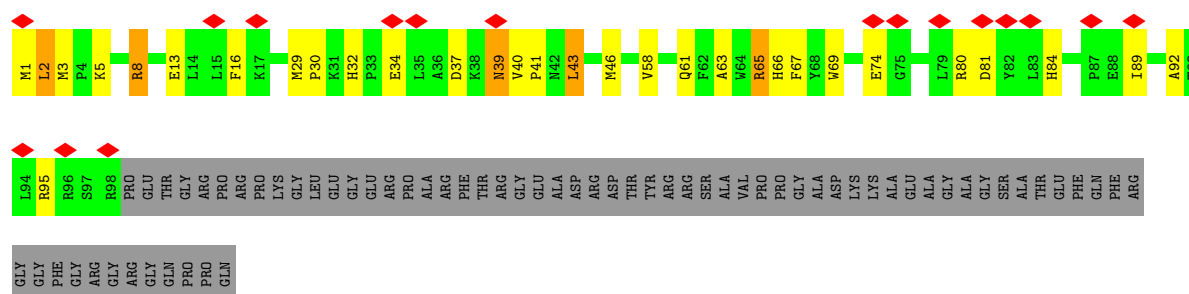
• Molecule 59: Ribosomal protein eS8



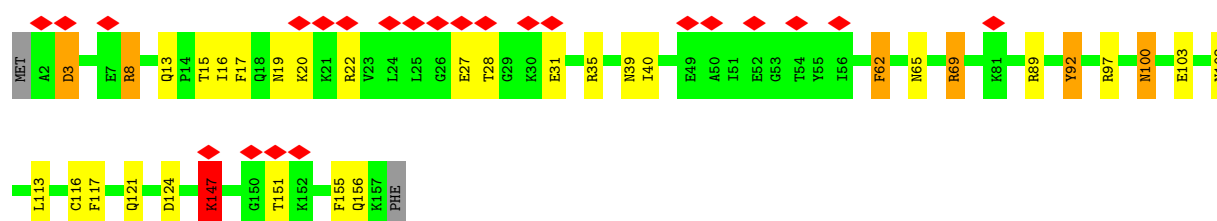
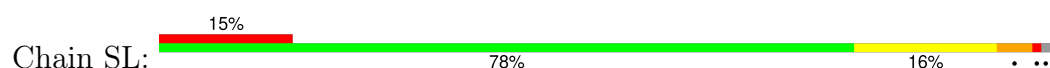
• Molecule 60: Ribosomal protein uS4



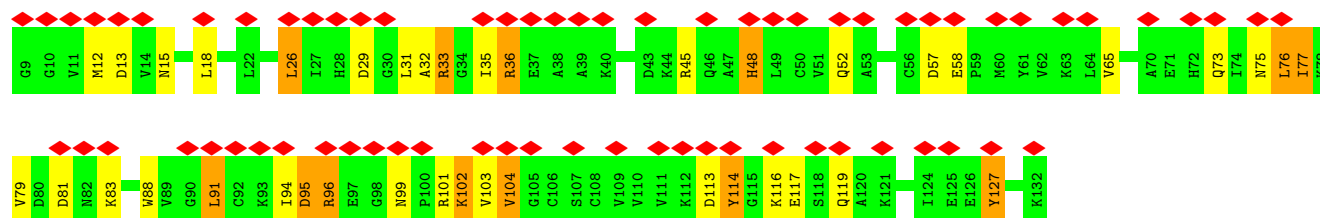
- Molecule 61: Ribosomal protein eS10



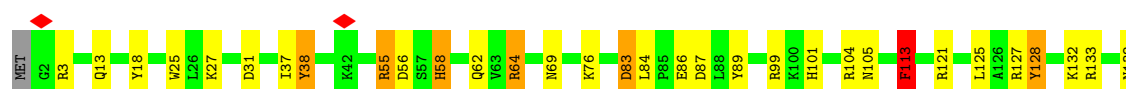
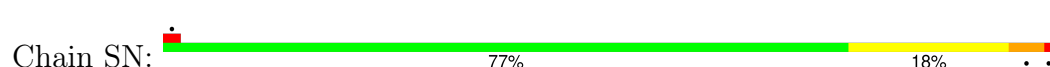
- Molecule 62: Ribosomal protein uS17

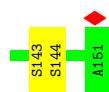


- Molecule 63: Ribosomal protein eS12



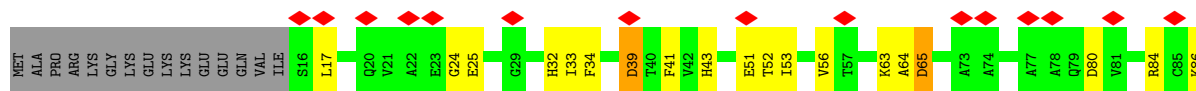
- Molecule 64: Ribosomal protein uS15





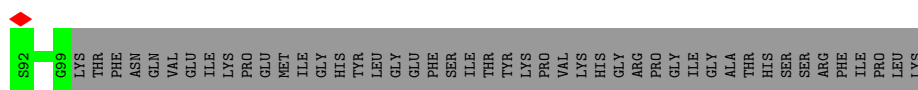
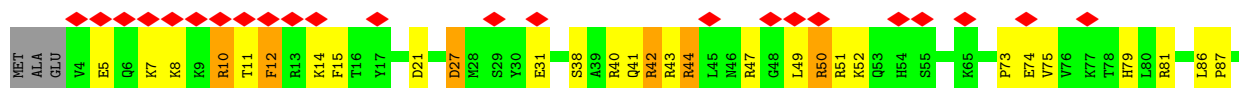
• Molecule 65: Ribosomal protein uS11

Chain SO: 11% 67% 18% 10%



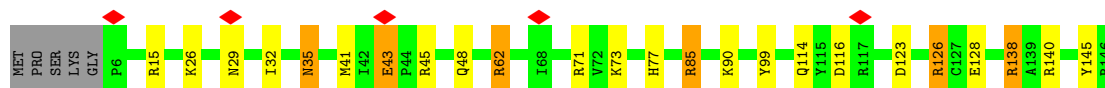
• Molecule 66: Ribosomal protein uS19

Chain SP: 17% 46% 16% 34%



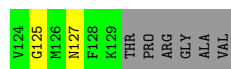
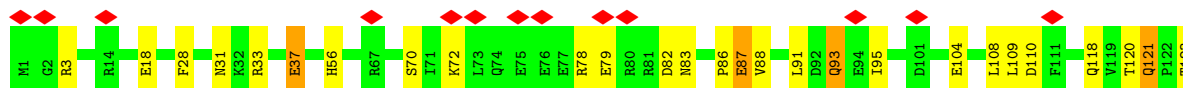
• Molecule 67: Ribosomal protein uS9

Chain SQ: 80% 12%



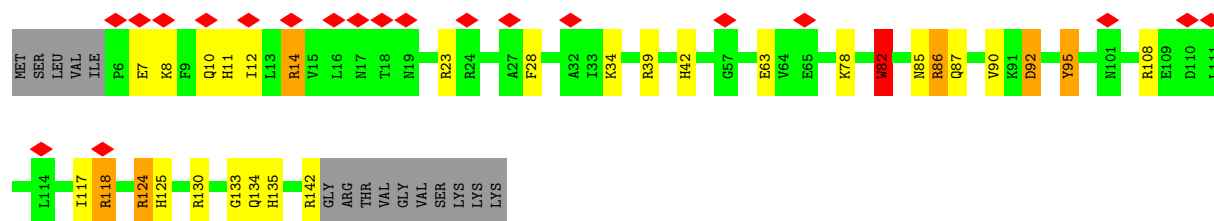
• Molecule 68: Ribosomal protein eS17

Chain SR: 10% 74% 19%

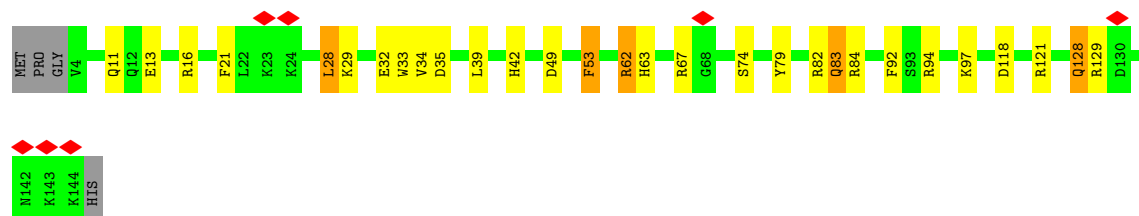
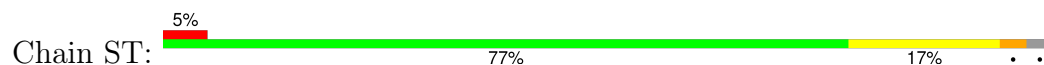


• Molecule 69: Ribosomal protein uS13

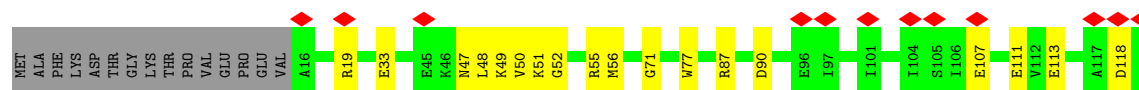
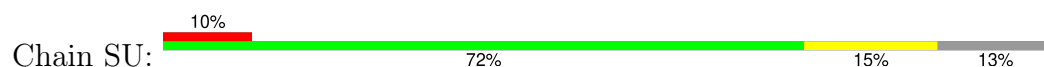
Chain SS: 13% 70% 15% 10%



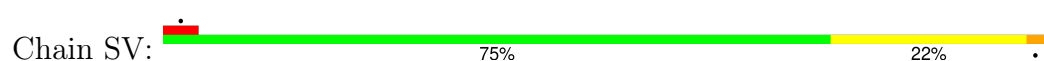
- Molecule 70: Ribosomal protein eS19



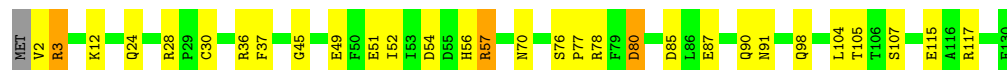
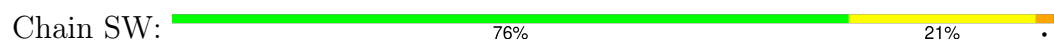
- Molecule 71: Ribosomal protein uS10



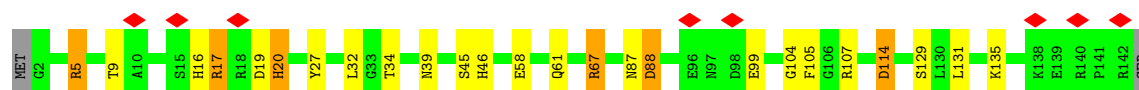
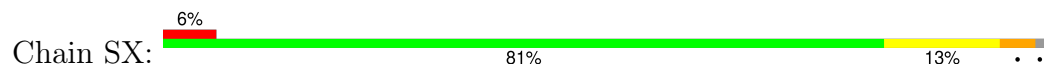
- Molecule 72: Ribosomal protein eS21



- Molecule 73: Ribosomal protein uS8

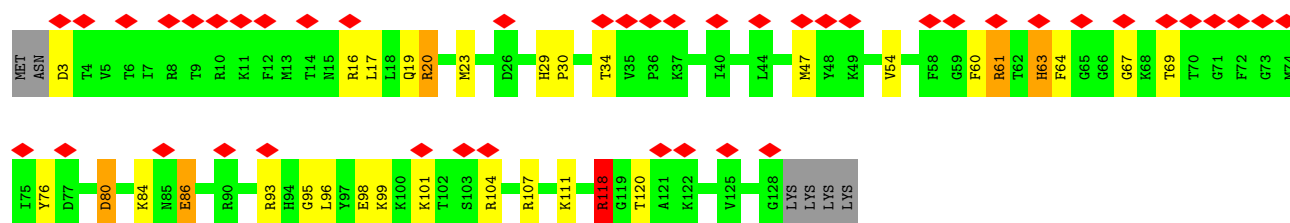


- Molecule 74: Ribosomal protein uS12



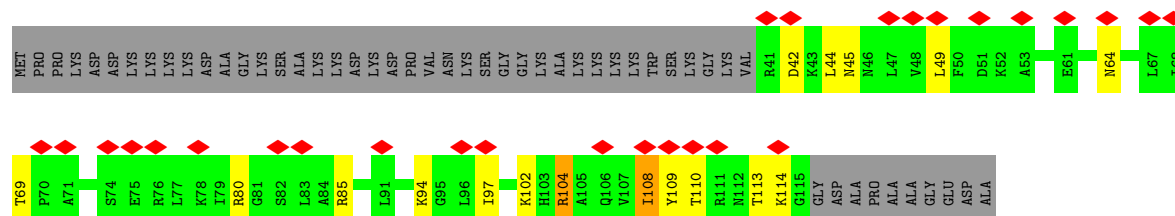
- Molecule 75: Ribosomal protein eS24

Chain SY: 



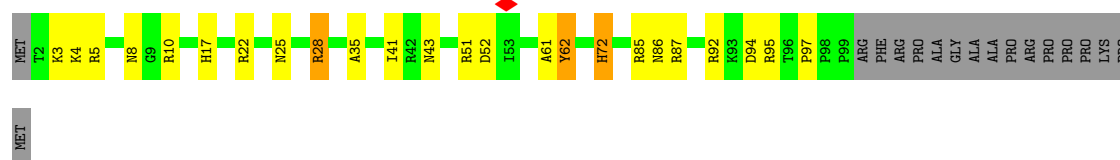
- Molecule 76: Ribosomal protein es25

Chain SZ: 




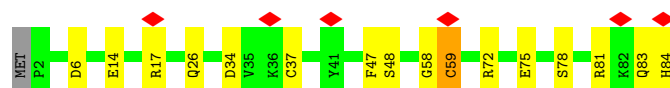
- Molecule 77: Ribosomal protein eS26

Chain Sa: 




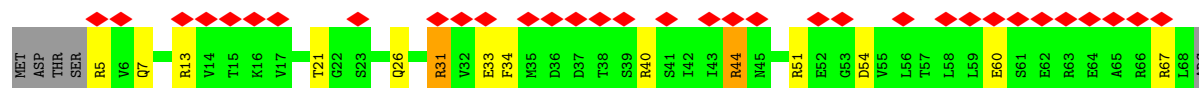
- Molecule 78: Ribosomal protein eS27

Chain Sb: 



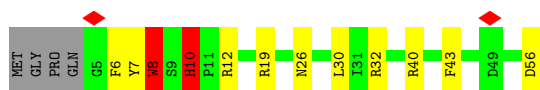
- Molecule 79: Ribosomal protein eS28

Chain Sc: 

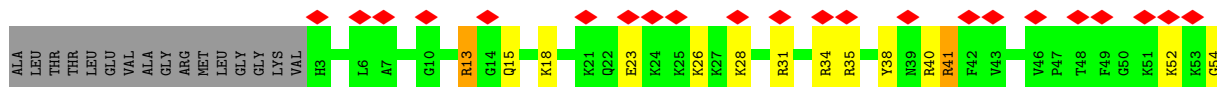
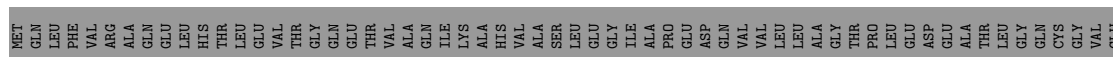
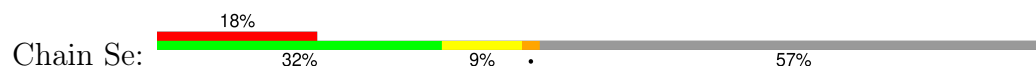


- Molecule 80: Ribosomal protein uS14

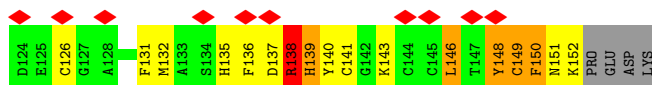
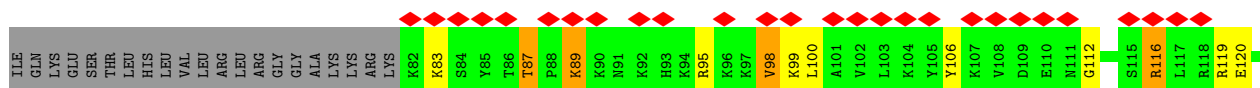
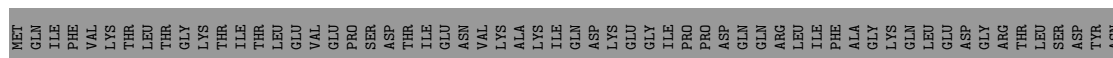
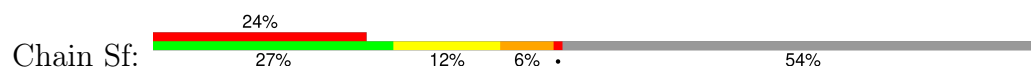
Chain Sd: 



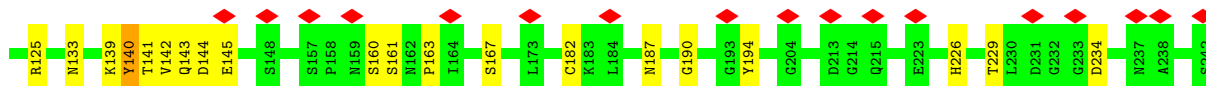
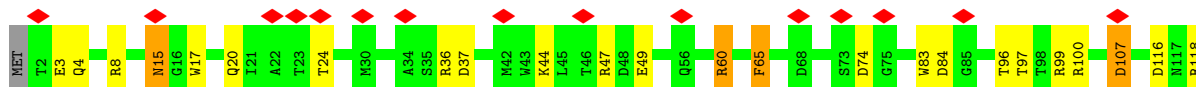
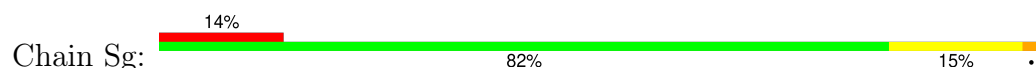
• Molecule 81: Ribosomal protein eS30



• Molecule 82: Ribosomal protein eS31

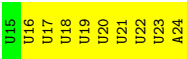


• Molecule 83: Ribosomal protein RACK1

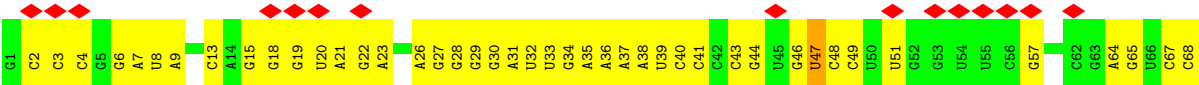


• Molecule 84: Messenger RNA

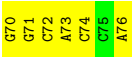
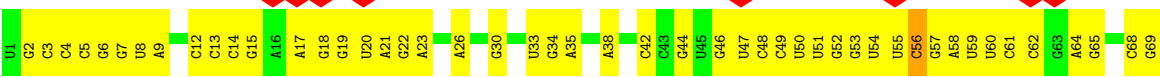




● Molecule 85: A/P tRNA



● Molecule 86: P/E tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	14723	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	0.675	Depositor
Minimum map value	-0.394	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.022	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: MG, ZN

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	0.70	83/89191 (0.1%)	1.13	754/139124 (0.5%)
2	7	0.54	1/2858 (0.0%)	0.96	9/4455 (0.2%)
3	8	0.68	3/3701 (0.1%)	1.20	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	26/4308 (0.6%)
6	C	0.73	4/2973 (0.1%)	1.12	18/3990 (0.5%)
7	D	0.73	2/2426 (0.1%)	1.23	27/3252 (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	13/2645 (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	13/2343 (0.6%)
13	J	0.63	1/1382 (0.1%)	1.04	10/1849 (0.5%)
14	L	0.71	2/1734 (0.1%)	1.12	16/2318 (0.7%)
15	M	0.76	2/1152 (0.2%)	1.11	5/1539 (0.3%)
16	N	0.84	4/1746 (0.2%)	1.33	23/2338 (1.0%)
17	O	0.72	3/1684 (0.2%)	1.11	12/2251 (0.5%)
18	P	0.74	2/1268 (0.2%)	1.10	9/1701 (0.5%)
19	Q	0.69	0/1530	1.35	31/2041 (1.5%)
20	R	0.79	3/1524 (0.2%)	1.27	20/2013 (1.0%)
21	S	0.95	8/1493 (0.5%)	1.30	20/2002 (1.0%)
22	T	0.67	1/1326 (0.1%)	1.04	7/1770 (0.4%)
23	U	0.63	1/822 (0.1%)	1.03	3/1103 (0.3%)
24	V	0.89	4/993 (0.4%)	1.11	7/1332 (0.5%)
25	W	0.72	0/541	1.23	5/720 (0.7%)
26	X	0.64	0/993	1.09	10/1334 (0.7%)
27	Y	0.72	0/1132	1.24	20/1504 (1.3%)
28	Z	0.63	0/1130	1.11	9/1507 (0.6%)
29	a	0.93	6/1192 (0.5%)	1.37	16/1591 (1.0%)
30	b	0.88	2/620 (0.3%)	1.17	5/819 (0.6%)
31	c	0.70	0/742	1.14	5/996 (0.5%)
32	d	0.84	3/903 (0.3%)	1.37	16/1216 (1.3%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
33	e	0.90	3/1071 (0.3%)	1.23	14/1429 (1.0%)
34	f	1.02	2/895 (0.2%)	1.34	17/1198 (1.4%)
35	g	0.65	0/916	1.08	5/1220 (0.4%)
36	h	0.63	0/1023	1.21	13/1350 (1.0%)
37	i	0.63	0/843	1.19	8/1115 (0.7%)
38	j	0.97	1/721 (0.1%)	1.43	11/953 (1.2%)
39	k	0.59	0/575	0.98	1/761 (0.1%)
40	l	0.68	0/454	1.07	3/599 (0.5%)
41	m	0.57	0/435	1.02	3/575 (0.5%)
42	n	0.49	0/223	1.02	0/284
43	o	0.64	0/864	1.27	9/1140 (0.8%)
44	p	0.64	1/718 (0.1%)	1.00	3/953 (0.3%)
45	r	0.68	0/1017	1.12	8/1365 (0.6%)
46	z	0.46	0/1768	0.73	0/2368
47	1	0.59	2/2969 (0.1%)	0.72	3/4014 (0.1%)
48	2	0.46	0/504	0.62	0/673
50	S2	0.68	37/41243 (0.1%)	1.12	315/64257 (0.5%)
51	SA	0.94	4/1679 (0.2%)	1.06	6/2283 (0.3%)
52	SB	1.42	7/1752 (0.4%)	1.63	20/2347 (0.9%)
53	SC	0.98	8/1726 (0.5%)	1.09	9/2332 (0.4%)
54	SD	1.39	12/1793 (0.7%)	1.08	9/2414 (0.4%)
55	SE	0.83	8/2118 (0.4%)	0.98	8/2849 (0.3%)
56	SF	0.74	1/1531 (0.1%)	1.08	11/2059 (0.5%)
57	SG	0.97	10/1946 (0.5%)	1.03	9/2590 (0.3%)
58	SH	0.73	2/1544 (0.1%)	1.02	8/2068 (0.4%)
59	SI	0.97	8/1715 (0.5%)	1.12	10/2287 (0.4%)
60	SJ	1.07	12/1550 (0.8%)	1.28	16/2069 (0.8%)
61	SK	0.75	1/851 (0.1%)	1.00	3/1147 (0.3%)
62	SL	0.85	5/1298 (0.4%)	1.08	7/1735 (0.4%)
63	SM	2.22	2/970 (0.2%)	1.21	8/1300 (0.6%)
64	SN	0.82	4/1232 (0.3%)	1.15	10/1656 (0.6%)
65	SO	1.18	7/1029 (0.7%)	1.38	11/1380 (0.8%)
66	SP	1.52	6/816 (0.7%)	1.29	8/1084 (0.7%)
67	SQ	0.72	2/1142 (0.2%)	1.01	8/1528 (0.5%)
68	SR	0.82	5/1060 (0.5%)	1.08	5/1421 (0.4%)
69	SS	0.66	1/1157 (0.1%)	1.18	13/1548 (0.8%)
70	ST	0.67	2/1119 (0.2%)	1.08	7/1499 (0.5%)
71	SU	0.94	4/828 (0.5%)	0.96	1/1112 (0.1%)
72	SV	0.73	0/631	0.97	0/844
73	SW	1.06	7/1051 (0.7%)	1.22	5/1406 (0.4%)
74	SX	0.95	6/1118 (0.5%)	1.10	11/1493 (0.7%)
75	SY	1.64	5/1040 (0.5%)	1.11	9/1382 (0.7%)
76	SZ	0.56	0/604	0.87	0/810

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
77	Sa	0.81	1/794 (0.1%)	1.20	4/1065 (0.4%)
78	Sb	0.59	0/665	0.90	0/891
79	Sc	0.68	0/508	1.13	4/680 (0.6%)
80	Sd	0.79	0/445	1.12	1/589 (0.2%)
81	Se	0.72	1/458 (0.2%)	1.17	5/602 (0.8%)
82	Sf	1.08	6/593 (1.0%)	1.57	12/786 (1.5%)
83	Sg	0.80	11/2493 (0.4%)	0.89	8/3394 (0.2%)
84	S4	0.23	0/219	0.63	0/337
85	S5	1.22	1/1762 (0.1%)	0.80	2/2739 (0.1%)
86	S6	0.31	1/1812 (0.1%)	1.00	5/2823 (0.2%)
All	All	0.77	357/238566 (0.1%)	1.13	1895/350392 (0.5%)

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	1	157
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	5
13	J	0	2
14	L	0	5
15	M	0	4
16	N	0	10
17	O	0	3
18	P	0	1
19	Q	0	5
20	R	0	6
21	S	0	11
22	T	0	2
23	U	0	2
24	V	0	3

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

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Mol	Chain	#Chirality outliers	#Planarity outliers
77	Sa	0	1
78	Sb	0	1
80	Sd	0	2
82	Sf	0	4
All	All	2	455

The worst 5 of 357 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	5	2037	C	O3'-P	-68.26	0.79	1.61
63	SM	58	GLU	CD-OE1	64.53	1.96	1.25
85	S5	47	U	O3'-P	-49.36	1.01	1.61
52	SB	145	LYS	C-N	-44.69	0.31	1.34
54	SD	216	GLU	CD-OE1	43.79	1.73	1.25

The worst 5 of 1895 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
52	SB	145	LYS	CA-C-N	-33.88	42.66	117.20
1	5	4116	C	P-O3'-C3'	33.09	159.40	119.70
52	SB	145	LYS	O-C-N	-27.76	78.29	122.70
1	5	4116	C	O3'-P-O5'	-27.74	51.30	104.00
86	S6	55	U	OP2-P-O3'	27.36	165.39	105.20

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	5	1992	U	C1'
50	S2	1109	C	C1'

5 of 455 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 ⓘ

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	23
5	B	392/394 (100%)	319 (81%)	40 (10%)	33 (8%)	0	10
6	C	365/367 (100%)	304 (83%)	45 (12%)	16 (4%)	2	21
7	D	290/297 (98%)	235 (81%)	33 (11%)	22 (8%)	1	13
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	20
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	33
12	I	211/213 (99%)	168 (80%)	30 (14%)	13 (6%)	1	16
13	J	168/178 (94%)	136 (81%)	24 (14%)	8 (5%)	2	19
14	L	208/211 (99%)	171 (82%)	26 (12%)	11 (5%)	1	18
15	M	136/213 (64%)	118 (87%)	16 (12%)	2 (2%)	8	39
16	N	201/204 (98%)	172 (86%)	23 (11%)	6 (3%)	3	27
17	O	199/201 (99%)	182 (92%)	14 (7%)	3 (2%)	8	39
18	P	151/153 (99%)	140 (93%)	9 (6%)	2 (1%)	10	41
19	Q	185/188 (98%)	160 (86%)	20 (11%)	5 (3%)	4	29
20	R	178/196 (91%)	153 (86%)	21 (12%)	4 (2%)	5	32
21	S	173/224 (77%)	146 (84%)	24 (14%)	3 (2%)	7	36
22	T	157/160 (98%)	128 (82%)	26 (17%)	3 (2%)	6	34
23	U	97/128 (76%)	74 (76%)	21 (22%)	2 (2%)	5	33
24	V	129/140 (92%)	112 (87%)	14 (11%)	3 (2%)	5	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
25	W	61/157 (39%)	57 (93%)	3 (5%)	1 (2%)	8	37
26	X	117/156 (75%)	108 (92%)	7 (6%)	2 (2%)	7	36
27	Y	132/145 (91%)	112 (85%)	14 (11%)	6 (4%)	2	20
28	Z	133/136 (98%)	113 (85%)	15 (11%)	5 (4%)	2	23
29	a	145/148 (98%)	111 (77%)	26 (18%)	8 (6%)	1	18
30	b	73/160 (46%)	58 (80%)	11 (15%)	4 (6%)	1	18
31	c	92/115 (80%)	78 (85%)	10 (11%)	4 (4%)	2	21
32	d	105/125 (84%)	85 (81%)	16 (15%)	4 (4%)	2	23
33	e	126/135 (93%)	110 (87%)	15 (12%)	1 (1%)	16	51
34	f	107/110 (97%)	95 (89%)	7 (6%)	5 (5%)	2	20
35	g	112/117 (96%)	103 (92%)	7 (6%)	2 (2%)	7	35
36	h	120/123 (98%)	103 (86%)	14 (12%)	3 (2%)	4	30
37	i	100/105 (95%)	91 (91%)	7 (7%)	2 (2%)	6	33
38	j	84/86 (98%)	67 (80%)	13 (16%)	4 (5%)	2	19
39	k	67/70 (96%)	55 (82%)	7 (10%)	5 (8%)	1	13
40	l	48/51 (94%)	42 (88%)	4 (8%)	2 (4%)	2	21
41	m	50/128 (39%)	44 (88%)	6 (12%)	0	100	100
42	n	21/25 (84%)	21 (100%)	0	0	100	100
43	o	102/106 (96%)	85 (83%)	11 (11%)	6 (6%)	1	16
44	p	89/91 (98%)	79 (89%)	9 (10%)	1 (1%)	12	45
45	r	123/125 (98%)	97 (79%)	20 (16%)	6 (5%)	2	19
46	z	213/217 (98%)	166 (78%)	29 (14%)	18 (8%)	0	10
47	1	363/393 (92%)	312 (86%)	36 (10%)	15 (4%)	2	22
48	2	60/68 (88%)	49 (82%)	7 (12%)	4 (7%)	1	15
51	SA	206/295 (70%)	176 (85%)	24 (12%)	6 (3%)	3	27
52	SB	209/264 (79%)	168 (80%)	26 (12%)	15 (7%)	1	14
53	SC	216/218 (99%)	188 (87%)	20 (9%)	8 (4%)	2	23
54	SD	225/243 (93%)	170 (76%)	44 (20%)	11 (5%)	2	19
55	SE	260/263 (99%)	202 (78%)	41 (16%)	17 (6%)	1	15
56	SF	189/204 (93%)	160 (85%)	19 (10%)	10 (5%)	1	18
57	SG	235/249 (94%)	194 (83%)	35 (15%)	6 (3%)	4	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
58	SH	187/194 (96%)	143 (76%)	29 (16%)	15 (8%)	1	12
59	SI	204/208 (98%)	176 (86%)	21 (10%)	7 (3%)	3	25
60	SJ	183/194 (94%)	145 (79%)	24 (13%)	14 (8%)	1	12
61	SK	96/165 (58%)	60 (62%)	26 (27%)	10 (10%)	0	7
62	SL	154/158 (98%)	124 (80%)	23 (15%)	7 (4%)	2	20
63	SM	122/124 (98%)	77 (63%)	25 (20%)	20 (16%)	0	3
64	SN	148/151 (98%)	115 (78%)	28 (19%)	5 (3%)	3	25
65	SO	134/151 (89%)	102 (76%)	18 (13%)	14 (10%)	0	7
66	SP	94/145 (65%)	65 (69%)	18 (19%)	11 (12%)	0	5
67	SQ	139/146 (95%)	112 (81%)	21 (15%)	6 (4%)	2	21
68	SR	127/135 (94%)	95 (75%)	22 (17%)	10 (8%)	1	12
69	SS	135/152 (89%)	104 (77%)	23 (17%)	8 (6%)	1	16
70	ST	139/145 (96%)	116 (84%)	17 (12%)	6 (4%)	2	21
71	SU	102/119 (86%)	80 (78%)	18 (18%)	4 (4%)	2	22
72	SV	80/83 (96%)	63 (79%)	10 (12%)	7 (9%)	0	10
73	SW	127/130 (98%)	112 (88%)	11 (9%)	4 (3%)	3	26
74	SX	139/143 (97%)	115 (83%)	19 (14%)	5 (4%)	3	24
75	SY	124/132 (94%)	92 (74%)	23 (18%)	9 (7%)	1	13
76	SZ	73/125 (58%)	54 (74%)	13 (18%)	6 (8%)	1	11
77	Sa	96/115 (84%)	71 (74%)	17 (18%)	8 (8%)	0	11
78	Sb	81/84 (96%)	61 (75%)	15 (18%)	5 (6%)	1	16
79	Sc	62/69 (90%)	46 (74%)	16 (26%)	0	100	100
80	Sd	50/56 (89%)	38 (76%)	9 (18%)	3 (6%)	1	16
81	Se	55/133 (41%)	40 (73%)	14 (26%)	1 (2%)	7	35
82	Sf	69/156 (44%)	39 (56%)	21 (30%)	9 (13%)	0	4
83	Sg	311/317 (98%)	250 (80%)	45 (14%)	16 (5%)	1	18
All	All	11778/13201 (89%)	9619 (82%)	1571 (13%)	588 (5%)	3	19

5 of 588 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	A	19	HIS
4	A	197	PRO

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Mol	Chain	Res	Type
5	B	16	PHE
5	B	40	PRO
5	B	47	LEU

5.3.2 Protein sidechains [i](#)

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	5
7	D	246/250 (98%)	178 (72%)	68 (28%)	0	2
8	E	209/209 (100%)	157 (75%)	52 (25%)	0	3
9	F	194/194 (100%)	145 (75%)	49 (25%)	0	3
10	G	206/226 (91%)	158 (77%)	48 (23%)	0	4
11	H	169/171 (99%)	125 (74%)	44 (26%)	0	3
12	I	180/180 (100%)	136 (76%)	44 (24%)	0	4
13	J	143/149 (96%)	115 (80%)	28 (20%)	1	7
14	L	176/177 (99%)	135 (77%)	41 (23%)	0	4
15	M	116/160 (72%)	95 (82%)	21 (18%)	1	9
16	N	171/172 (99%)	129 (75%)	42 (25%)	0	3
17	O	172/172 (100%)	146 (85%)	26 (15%)	2	14
18	P	134/134 (100%)	112 (84%)	22 (16%)	2	12
19	Q	163/164 (99%)	132 (81%)	31 (19%)	1	7
20	R	159/175 (91%)	120 (76%)	39 (24%)	0	3
21	S	156/192 (81%)	121 (78%)	35 (22%)	1	5
22	T	139/140 (99%)	112 (81%)	27 (19%)	1	7
23	U	89/114 (78%)	67 (75%)	22 (25%)	0	3
24	V	101/107 (94%)	77 (76%)	24 (24%)	0	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	W	55/126 (44%)	42 (76%)	13 (24%)	0	4
26	X	107/133 (80%)	89 (83%)	18 (17%)	1	11
27	Y	124/135 (92%)	96 (77%)	28 (23%)	1	5
28	Z	117/118 (99%)	93 (80%)	24 (20%)	1	6
29	a	119/120 (99%)	102 (86%)	17 (14%)	2	16
30	b	63/123 (51%)	45 (71%)	18 (29%)	0	2
31	c	79/97 (81%)	60 (76%)	19 (24%)	0	4
32	d	98/110 (89%)	66 (67%)	32 (33%)	0	1
33	e	114/121 (94%)	89 (78%)	25 (22%)	1	5
34	f	88/89 (99%)	73 (83%)	15 (17%)	1	11
35	g	98/100 (98%)	79 (81%)	19 (19%)	1	7
36	h	109/110 (99%)	92 (84%)	17 (16%)	2	13
37	i	86/89 (97%)	71 (83%)	15 (17%)	1	10
38	j	73/73 (100%)	60 (82%)	13 (18%)	1	10
39	k	64/65 (98%)	52 (81%)	12 (19%)	1	8
40	l	47/48 (98%)	39 (83%)	8 (17%)	1	11
41	m	48/116 (41%)	36 (75%)	12 (25%)	0	3
42	n	22/24 (92%)	17 (77%)	5 (23%)	0	4
43	o	92/94 (98%)	70 (76%)	22 (24%)	0	4
44	p	74/74 (100%)	61 (82%)	13 (18%)	1	10
45	r	109/109 (100%)	85 (78%)	24 (22%)	1	5
46	z	195/196 (100%)	169 (87%)	26 (13%)	3	18
47	1	316/331 (96%)	300 (95%)	16 (5%)	20	45
48	2	53/59 (90%)	49 (92%)	4 (8%)	11	34
51	SA	174/245 (71%)	141 (81%)	33 (19%)	1	7
52	SB	194/231 (84%)	164 (84%)	30 (16%)	2	13
53	SC	184/184 (100%)	148 (80%)	36 (20%)	1	7
54	SD	190/202 (94%)	163 (86%)	27 (14%)	2	16
55	SE	224/225 (100%)	180 (80%)	44 (20%)	1	7
56	SF	161/170 (95%)	129 (80%)	32 (20%)	1	6
57	SG	207/218 (95%)	171 (83%)	36 (17%)	1	10

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
58	SH	169/174 (97%)	149 (88%)	20 (12%)	4	20
59	SI	178/180 (99%)	148 (83%)	30 (17%)	1	11
60	SJ	161/168 (96%)	128 (80%)	33 (20%)	1	6
61	SK	89/136 (65%)	68 (76%)	21 (24%)	0	4
62	SL	140/142 (99%)	118 (84%)	22 (16%)	2	13
63	SM	104/104 (100%)	76 (73%)	28 (27%)	0	3
64	SN	130/131 (99%)	101 (78%)	29 (22%)	1	5
65	SO	106/119 (89%)	83 (78%)	23 (22%)	1	5
66	SP	88/130 (68%)	73 (83%)	15 (17%)	1	11
67	SQ	117/121 (97%)	100 (86%)	17 (14%)	2	15
68	SR	117/121 (97%)	102 (87%)	15 (13%)	3	18
69	SS	119/132 (90%)	97 (82%)	22 (18%)	1	8
70	ST	112/115 (97%)	89 (80%)	23 (20%)	1	6
71	SU	94/107 (88%)	84 (89%)	10 (11%)	5	22
72	SV	66/67 (98%)	53 (80%)	13 (20%)	1	7
73	SW	112/113 (99%)	93 (83%)	19 (17%)	1	11
74	SX	113/115 (98%)	98 (87%)	15 (13%)	3	18
75	SY	108/114 (95%)	86 (80%)	22 (20%)	1	6
76	SZ	66/103 (64%)	54 (82%)	12 (18%)	1	9
77	Sa	85/98 (87%)	70 (82%)	15 (18%)	1	10
78	Sb	75/76 (99%)	64 (85%)	11 (15%)	2	15
79	Sc	57/62 (92%)	43 (75%)	14 (25%)	0	3
80	Sd	45/48 (94%)	35 (78%)	10 (22%)	1	5
81	Se	46/105 (44%)	35 (76%)	11 (24%)	0	4
82	Sf	64/140 (46%)	45 (70%)	19 (30%)	0	2
83	Sg	272/275 (99%)	242 (89%)	30 (11%)	5	21
All	All	10267/11256 (91%)	8268 (80%)	1999 (20%)	3	7

5 of 1999 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
28	Z	112	ARG
69	SS	135	HIS

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Mol	Chain	Res	Type
41	m	97	ARG
69	SS	10	GLN
77	Sa	41	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 278 such sidechains are listed below:

Mol	Chain	Res	Type
63	SM	19	GLN
66	SP	46	ASN
74	SX	63	ASN
18	P	80	GLN
18	P	54	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	5	3703/3722 (99%)	1640 (44%)	636 (17%)
2	7	119/120 (99%)	31 (26%)	9 (7%)
3	8	155/156 (99%)	61 (39%)	22 (14%)
50	S2	1717/1742 (98%)	771 (44%)	273 (15%)
84	S4	9/10 (90%)	9 (100%)	0
85	S5	71/74 (95%)	47 (66%)	10 (14%)
86	S6	75/76 (98%)	53 (70%)	8 (10%)
All	All	5849/5900 (99%)	2612 (44%)	958 (16%)

5 of 2612 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 958 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	5	3876	A
50	S2	1506	A
1	5	4548	A

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Mol	Chain	Res	Type
50	S2	1454	A
85	S5	38	A

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

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

5.5 Carbohydrates [i](#)

There are no 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	18
47	1	6
50	S2	5
85	S5	4
52	SB	3
8	E	1

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Mol	Chain	Number of breaks
46	z	1

The worst 5 of 38 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

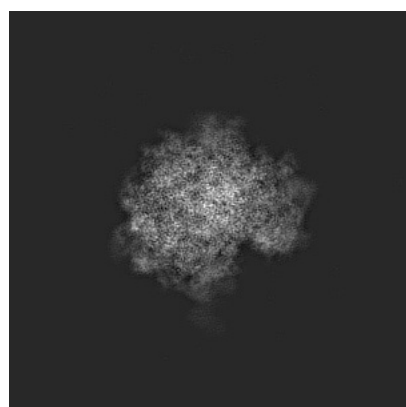
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-2644. These allow visual inspection of the internal detail of the map and identification of artifacts.

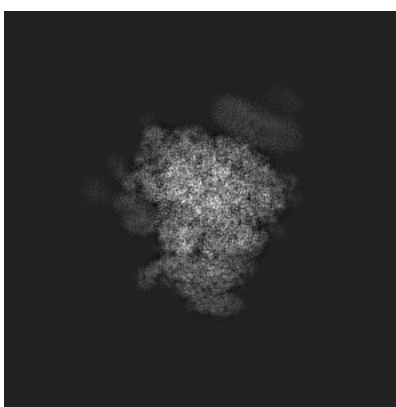
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

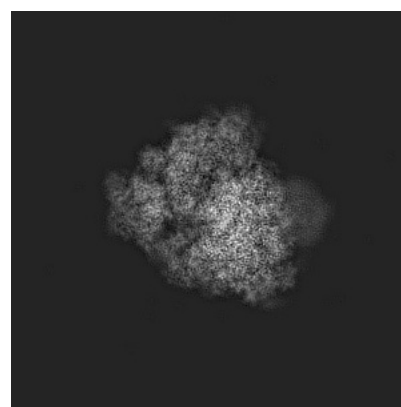
6.1.1 Primary map



X



Y

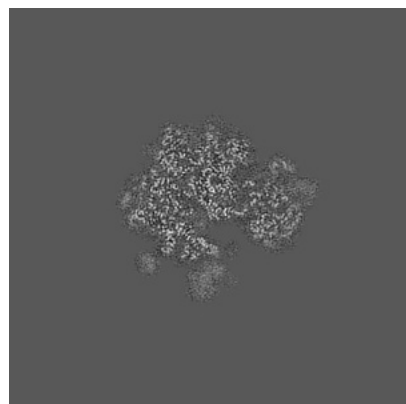


Z

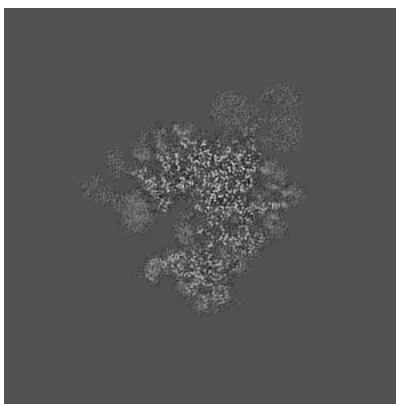
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

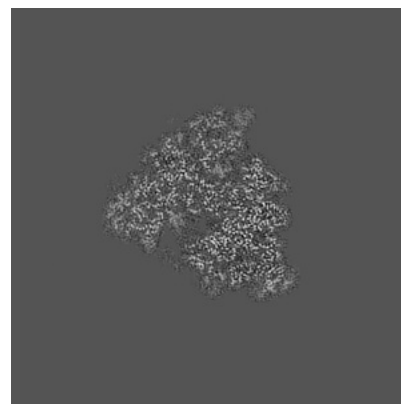
6.2.1 Primary map



X Index: 210



Y Index: 210

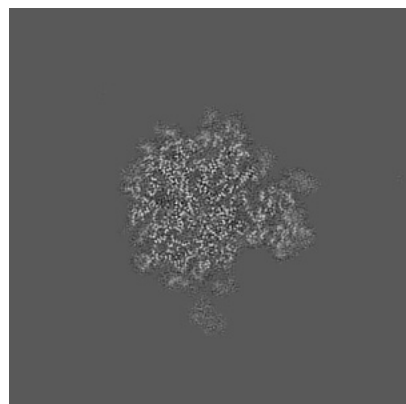


Z Index: 210

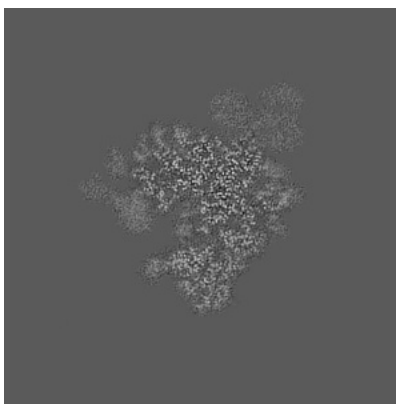
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

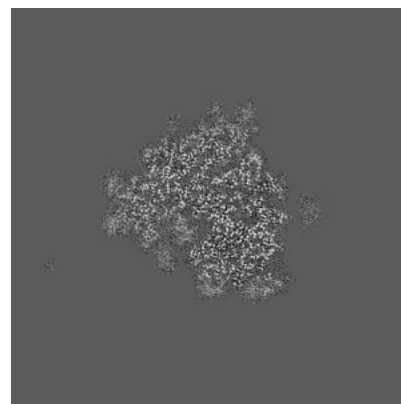
6.3.1 Primary map



X Index: 230



Y Index: 208

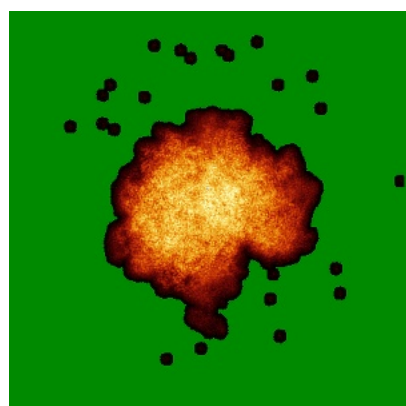


Z Index: 218

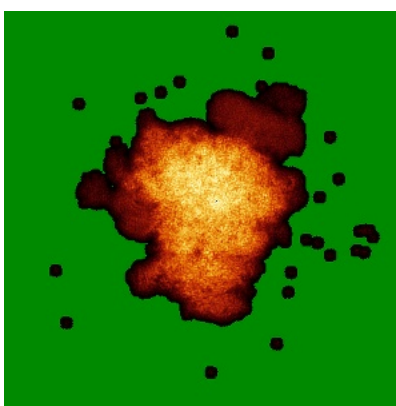
The images above show the largest variance slices of the map in three orthogonal directions.

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

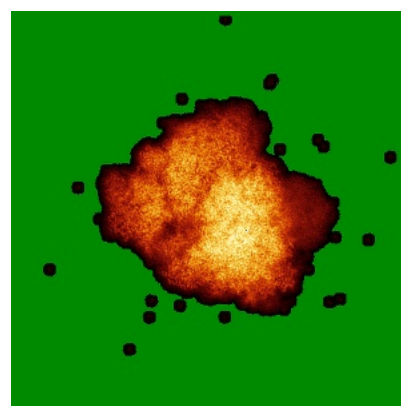
6.4.1 Primary map



X



Y

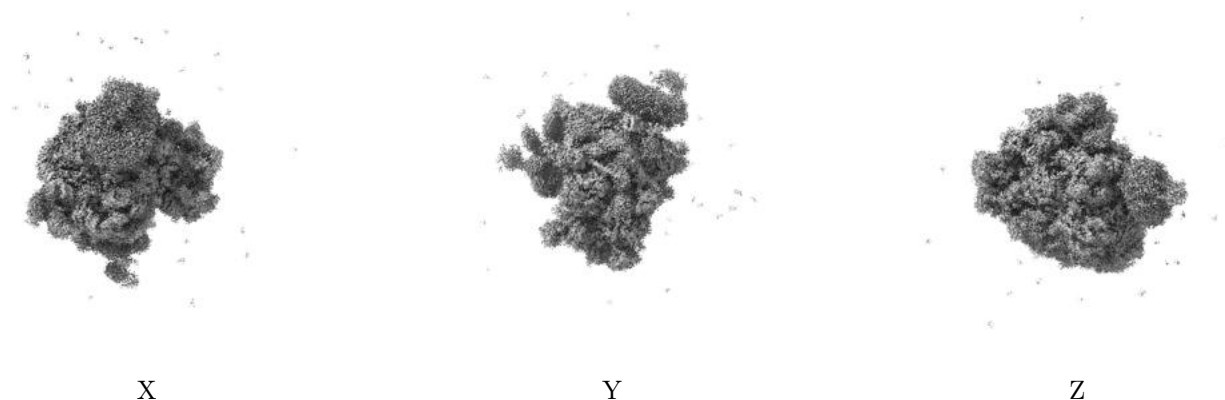


Z

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.

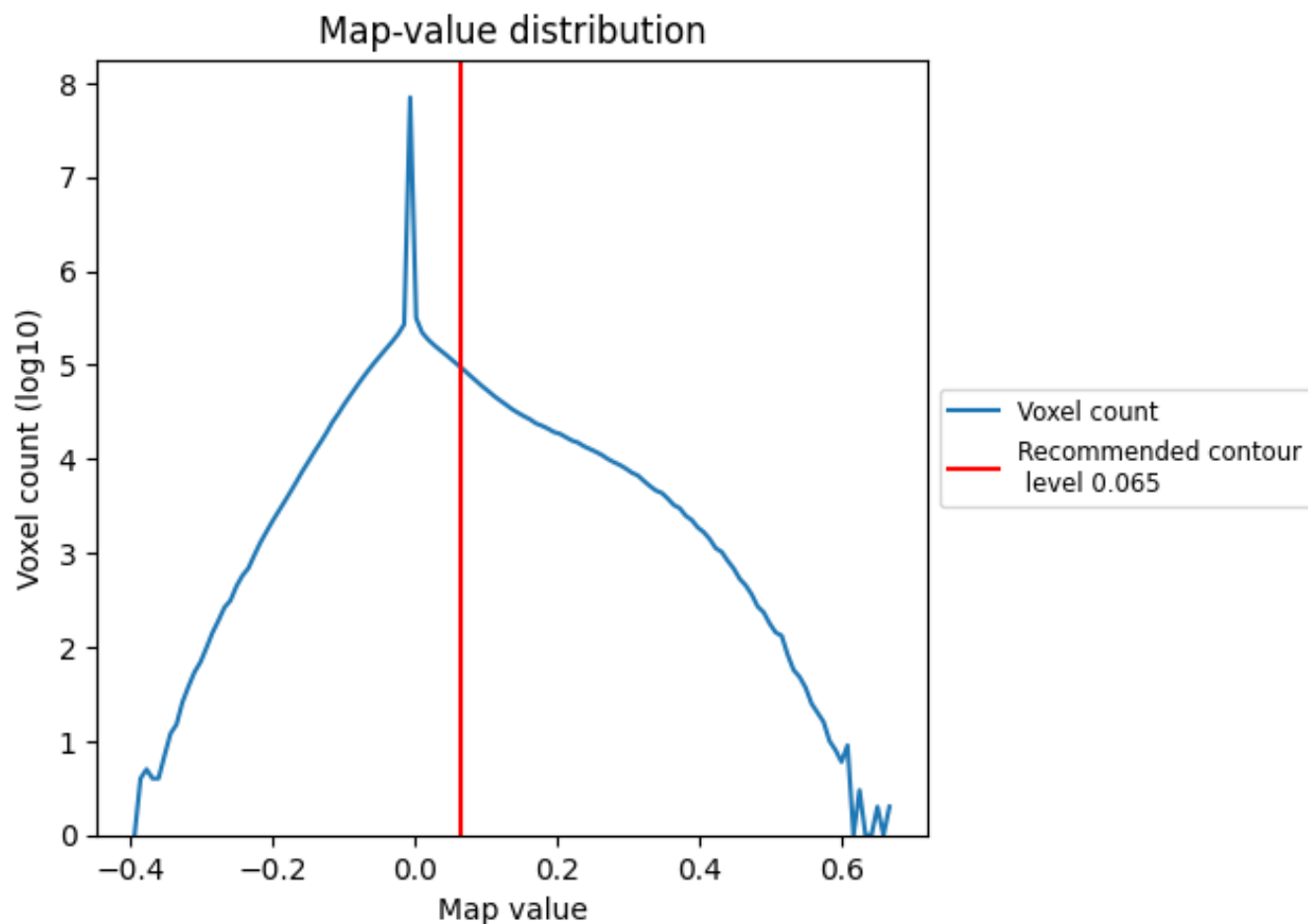
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

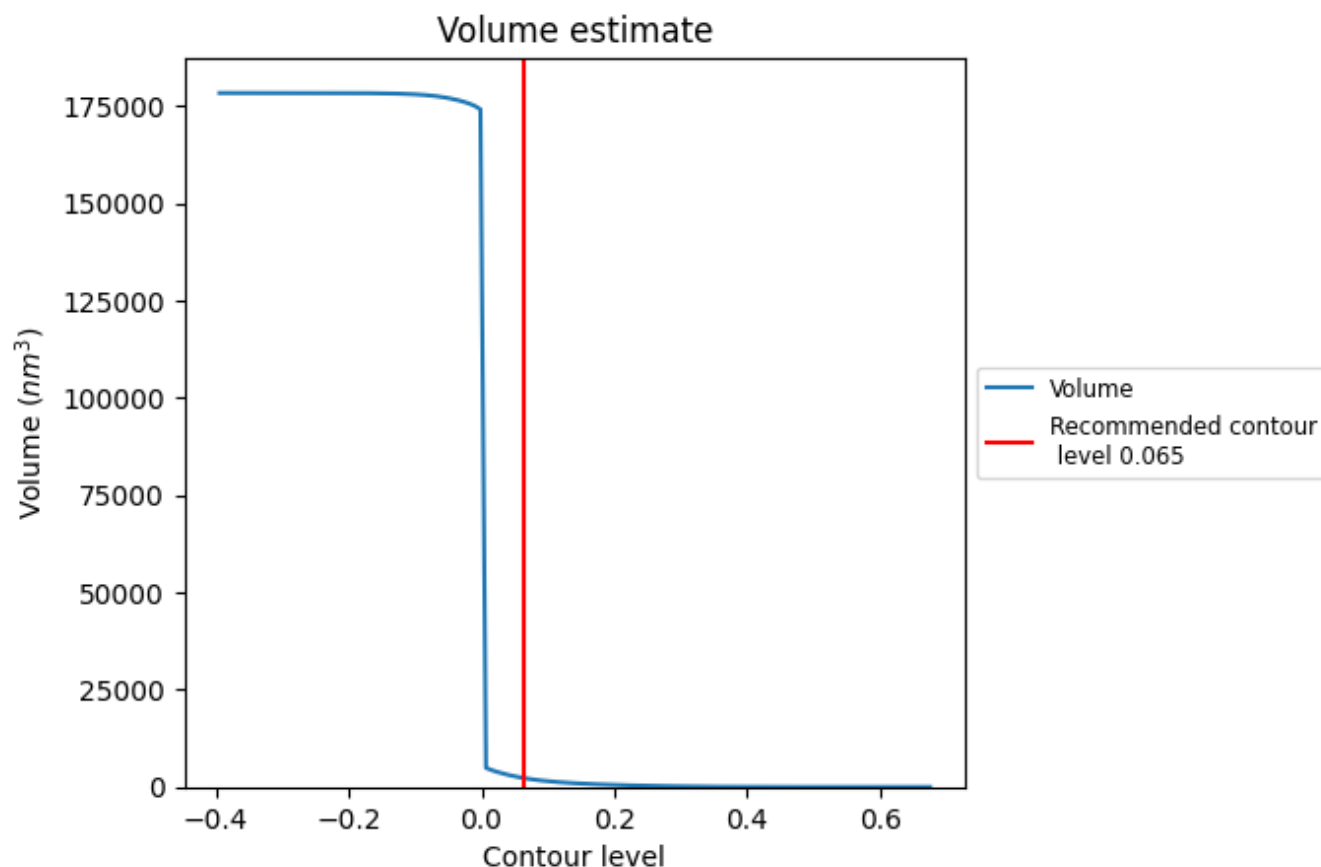
This section contains the results of statistical analysis of the map.

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.

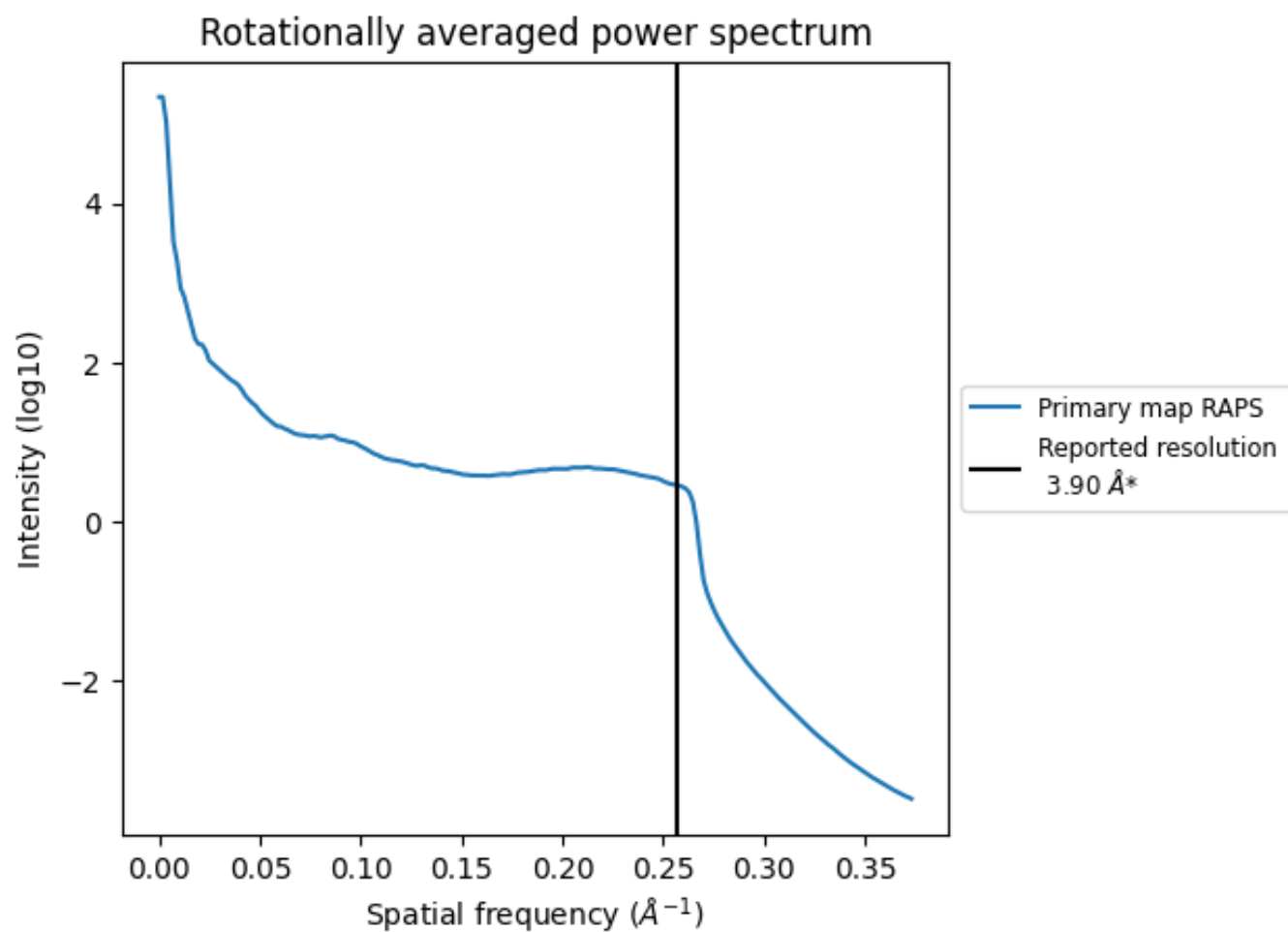
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2249 nm^3 ; this corresponds to an approximate mass of 2032 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 0.256 Å⁻¹

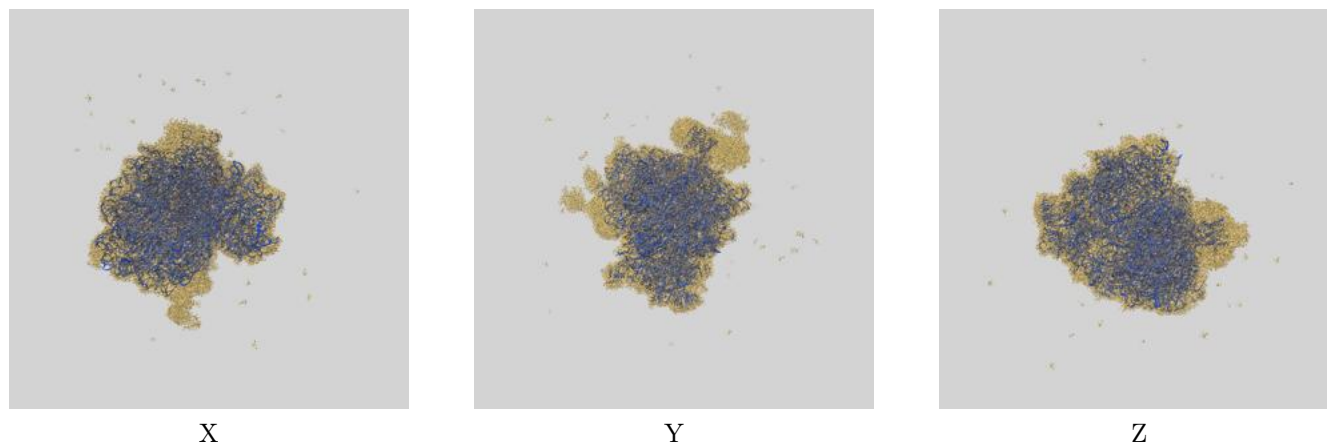
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

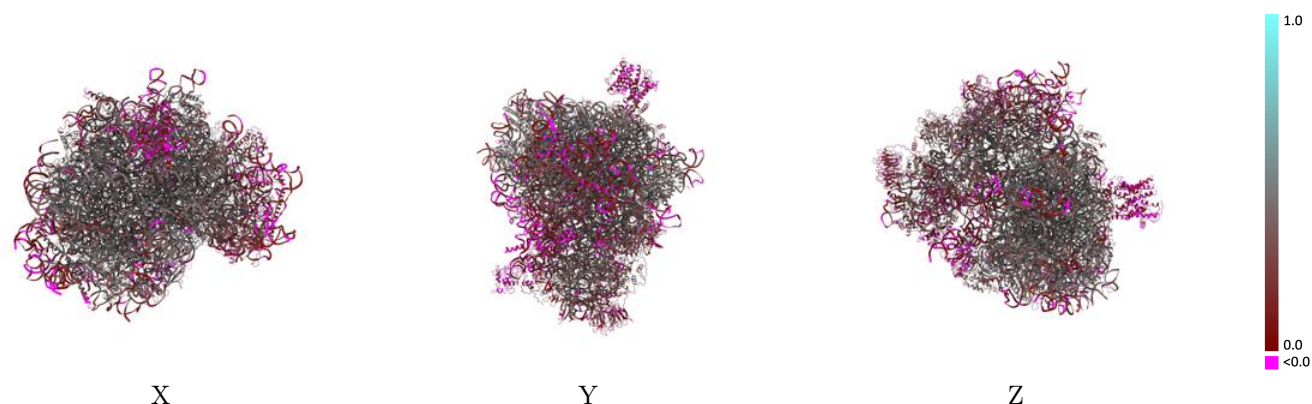
This section contains information regarding the fit between EMDB map EMD-2644 and PDB model 3J7R. Per-residue inclusion information can be found in [section 3](#) on [page 40](#).

9.1 Map-model overlay [i](#)



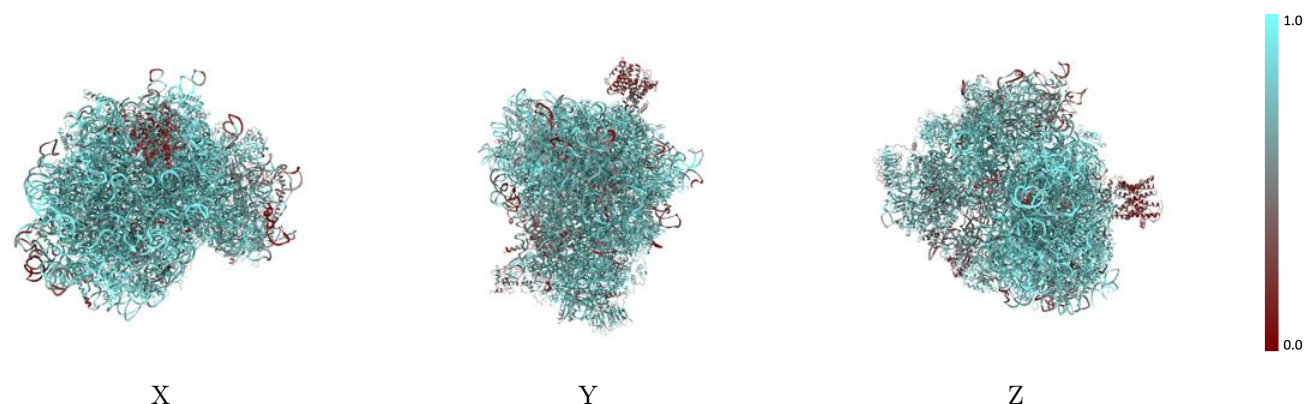
The images above show the 3D surface view of the map at the recommended contour level 0.065 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



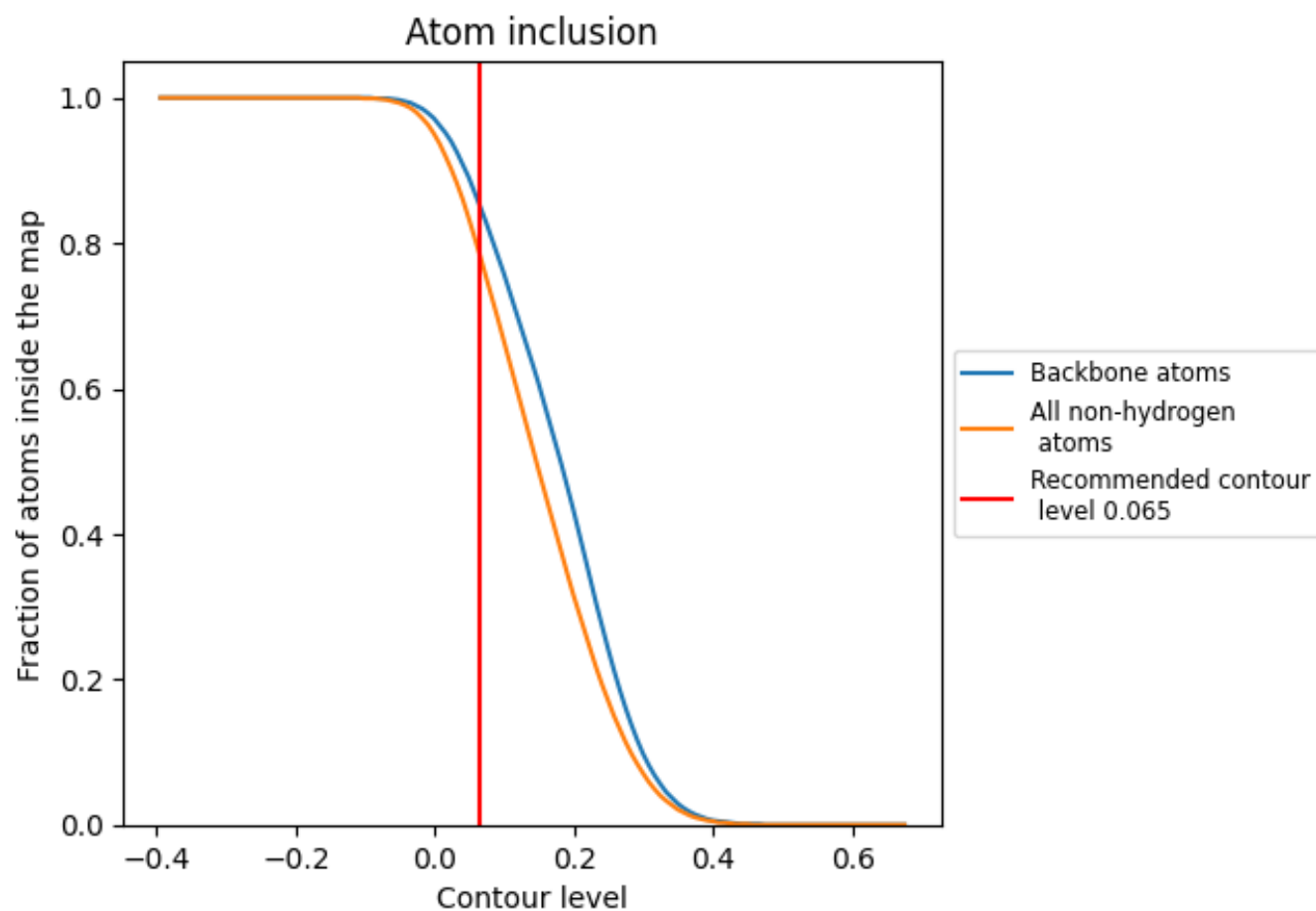
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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, 85% of all backbone atoms, 78% 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	 0.7830	 0.3280
1	 0.3180	 0.0870
2	 0.2760	 0.0550
3	 0.1500	 0.0260
5	 0.8370	 0.3450
7	 0.9290	 0.4110
8	 0.8700	 0.3830
A	 0.8350	 0.4610
B	 0.8450	 0.4450
C	 0.8150	 0.4310
D	 0.7970	 0.3500
E	 0.7770	 0.3780
F	 0.8250	 0.4320
G	 0.7880	 0.3800
H	 0.8220	 0.4230
I	 0.8110	 0.4170
J	 0.7150	 0.2960
L	 0.7930	 0.4020
M	 0.8490	 0.4300
N	 0.8420	 0.4500
O	 0.8380	 0.4490
P	 0.8420	 0.4540
Q	 0.8500	 0.4570
R	 0.7940	 0.3910
S	 0.8460	 0.4380
S2	 0.8050	 0.2890
S4	 0.9350	 0.4180
S5	 0.5760	 0.1580
S6	 0.7030	 0.1880
SA	 0.8010	 0.3670
SB	 0.7190	 0.2930
SC	 0.8100	 0.3880
SD	 0.7190	 0.3080
SE	 0.6020	 0.1750
SF	 0.5930	 0.1730























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Chain	Atom inclusion	Q-score
SG	 0.6640	 0.2190
SH	 0.6940	 0.2780
SI	 0.6460	 0.2250
SJ	 0.4990	 0.0670
SK	 0.6500	 0.1850
SL	 0.6460	 0.2660
SM	 0.4030	 0.0090
SN	 0.7810	 0.3620
SO	 0.6720	 0.2480
SP	 0.5760	 0.1370
SQ	 0.7480	 0.3180
SR	 0.6830	 0.2750
SS	 0.6520	 0.2000
ST	 0.7320	 0.2990
SU	 0.7010	 0.2960
SV	 0.8020	 0.3830
SW	 0.8010	 0.3940
SX	 0.7250	 0.3160
SY	 0.4960	 0.0490
SZ	 0.4730	 0.0290
Sa	 0.8010	 0.3960
Sb	 0.7230	 0.3230
Sc	 0.4320	 0.1010
Sd	 0.7740	 0.3550
Se	 0.4460	 0.1010
Sf	 0.4060	 0.0160
Sg	 0.6410	 0.1780
T	 0.8300	 0.4420
U	 0.7780	 0.3480
V	 0.7980	 0.4380
W	 0.8090	 0.4100
X	 0.7930	 0.4320
Y	 0.8000	 0.4190
Z	 0.8340	 0.4270
a	 0.8440	 0.4470
b	 0.7520	 0.3750
c	 0.8100	 0.4130
d	 0.7860	 0.4040
e	 0.8430	 0.4530
f	 0.8590	 0.4610
g	 0.8010	 0.4170
h	 0.7970	 0.4150

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Chain	Atom inclusion	Q-score
i	 0.7940	 0.3990
j	 0.8810	 0.4600
k	 0.7520	 0.3590
l	 0.8250	 0.4470
m	 0.8460	 0.4230
n	 0.7710	 0.3940
o	 0.7880	 0.4210
p	 0.8140	 0.4420
r	 0.8470	 0.4490
z	 0.3580	 0.0590