



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 09:43 AM UTC

PDB ID : 3J6X / pdb_00003j6x
EMDB ID : EMD-5942
Title : S. cerevisiae 80S ribosome bound with Taura syndrome virus (TSV) IRES, 5 degree rotation (Class II)
Authors : Koh, C.S.; Brilot, A.F.; Grigorieff, N.; Korostelev, A.A.
Deposited on : 2014-04-16
Resolution : 6.10 Å (reported)
Based on initial models : 3U5C, 3U5D, 3U5B, 3U5E

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

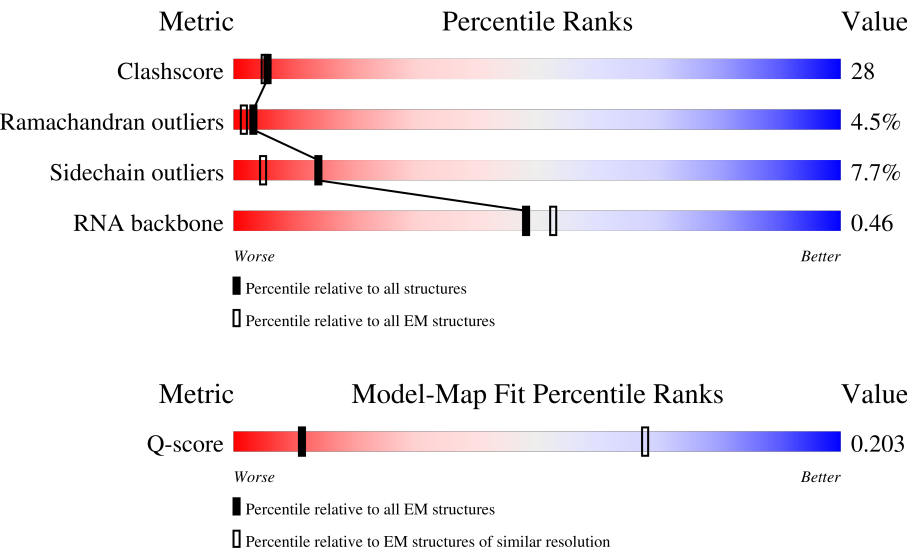
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 6.10 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	531 (5.60 - 6.60)

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	2S	3395	32%53%12% . .
2	8S	158	32%54%13% .
3	5S	121	36%58%7%

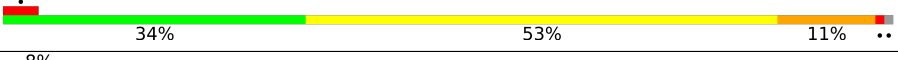
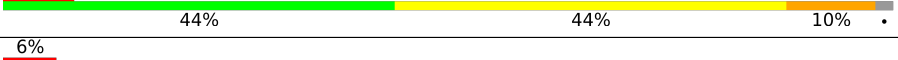
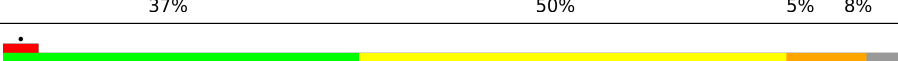
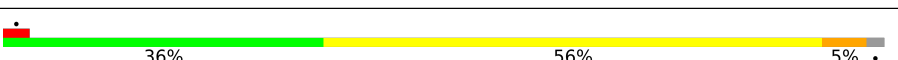
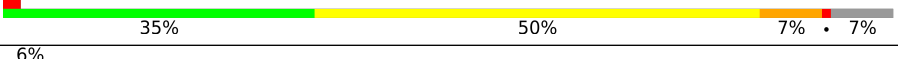
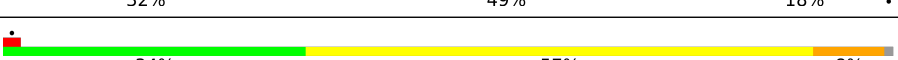
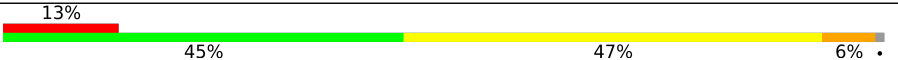
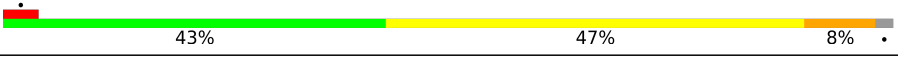
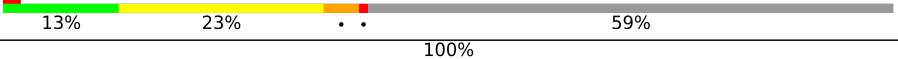
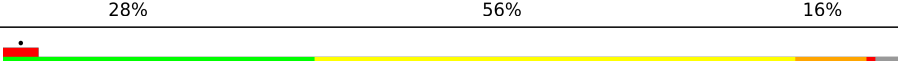
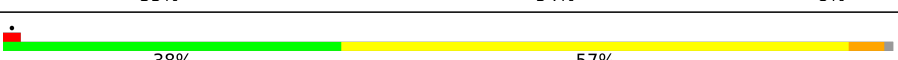
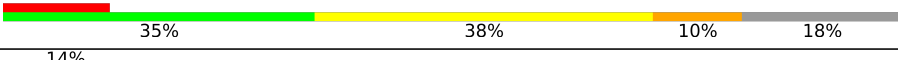
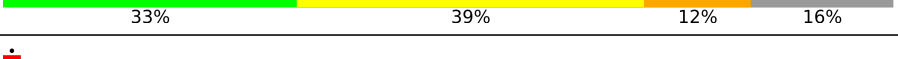
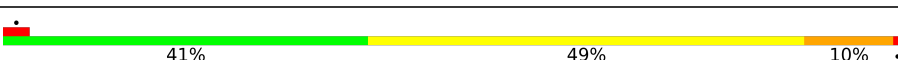
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Mol	Chain	Length	Quality of chain
4	L1	217	
5	L2	254	
6	L3	387	
7	L4	362	
8	L5	297	
9	L6	176	
10	L7	244	
11	L8	256	
12	L9	191	
13	50	221	
14	51	174	
15	53	199	
16	54	138	
17	55	204	
18	56	199	
19	57	184	
20	58	186	
21	59	189	
22	60	172	
23	61	160	
24	62	121	
25	63	137	
26	64	155	
27	65	142	
28	66	127	

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Mol	Chain	Length	Quality of chain
29	67	136	
30	68	149	
31	69	59	
32	70	105	
33	71	113	
34	72	130	
35	73	107	
36	74	121	
37	75	120	
38	76	100	
39	77	88	
40	78	78	
41	79	51	
42	80	128	
43	81	25	
44	82	106	
45	83	92	
46	1S	1798	
47	S0	252	
48	S1	255	
49	S2	254	
50	S3	240	
51	S4	261	
52	S5	225	
53	S6	236	

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Mol	Chain	Length	Quality of chain
54	S7	190	
55	S8	200	
56	S9	197	
57	10	105	
58	11	156	
59	12	143	
60	13	151	
61	14	137	
62	15	142	
63	16	143	
64	17	136	
65	18	146	
66	19	144	
67	20	121	
68	21	87	
69	22	130	
70	23	145	
71	24	135	
72	25	108	
73	26	119	
74	27	82	
75	28	67	
76	29	56	
77	30	63	
78	31	152	

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Mol	Chain	Length	Quality of chain
79	RA	319	22% 53% 39% 7%
80	IR	201	47% 99%

2 Entry composition

There are 80 unique types of molecules in this entry. The entry contains 204247 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 25S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	2S	3308	Total	C	N	O	P	0	0
			70742	31596	12731	23107	3308		

- Molecule 2 is a RNA chain called 5.8S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	8S	158	Total	C	N	O	P	0	0
			3354	1500	586	1110	158		

- Molecule 3 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	5S	121	Total	C	N	O	P	0	0
			2580	1152	461	846	121		

- Molecule 4 is a protein called 60S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	L1	204	Total	C	N	O	S	0	0
			1609	1031	279	290	9		

- Molecule 5 is a protein called 60S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L2	252	Total	C	N	O	S	0	0
			1918	1193	389	335	1		

- Molecule 6 is a protein called 60S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	L3	386	Total	C	N	O	S	0	0
			3082	1956	584	534	8		

- Molecule 7 is a protein called 60S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	L4	361	Total	C	N	O	S	0	0
			2750	1730	522	495	3		

- Molecule 8 is a protein called 60S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	L5	296	Total	C	N	O	S	0	0
			2376	1501	414	459	2		

- Molecule 9 is a protein called 60S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	L6	156	Total	C	N	O	S	0	0
			1240	800	222	217	1		

- Molecule 10 is a protein called 60S ribosomal protein L7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	L7	222	Total	C	N	O	S	0	0
			1785	1151	324	309	1		

- Molecule 11 is a protein called 60S ribosomal protein L8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	L8	233	Total	C	N	O	S	0	0
			1818	1159	326	330	3		

- Molecule 12 is a protein called 60S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L9	191	Total	C	N	O	S	0	0
			1519	963	274	278	4		

- Molecule 13 is a protein called 60S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	50	211	Total	C	N	O	S	0	0
			1718	1089	325	298	6		

- Molecule 14 is a protein called 60S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	51	169	Total	C	N	O	S	0	0
			1354	847	253	250	4		

- Molecule 15 is a protein called 60S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	53	193	Total	C	N	O		0	0
			1543	962	315	266			

- Molecule 16 is a protein called 60S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	54	136	Total	C	N	O	S	0	0
			1054	675	199	178	2		

- Molecule 17 is a protein called 60S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	55	203	Total	C	N	O	S	0	0
			1721	1077	361	282	1		

- Molecule 18 is a protein called 60S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	56	197	Total	C	N	O	S	0	0
			1556	1003	289	263	1		

- Molecule 19 is a protein called 60S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	57	183	Total	C	N	O		0	0
			1443	896	287	260			

- Molecule 20 is a protein called 60S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	58	185	Total	C	N	O	S	0	0
			1442	908	290	242	2		

- Molecule 21 is a protein called 60S ribosomal protein L19.

Mol	Chain	Residues	Atoms				AltConf	Trace
21	59	188	Total	C	N	O		
			1522	935	326	261	0	0

- Molecule 22 is a protein called 60S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	60	172	Total	C	N	O	S		
			1446	930	267	245	4	0	0

- Molecule 23 is a protein called 60S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	61	159	Total	C	N	O	S		
			1277	805	246	222	4	0	0

- Molecule 24 is a protein called 60S ribosomal protein L22.

Mol	Chain	Residues	Atoms				AltConf	Trace
24	62	100	Total	C	N	O		
			796	516	131	149	0	0

- Molecule 25 is a protein called 60S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	63	136	Total	C	N	O	S		
			1004	628	189	180	7	0	0

- Molecule 26 is a protein called 60S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	64	61	Total	C	N	O	S		
			509	328	100	80	1	0	0

- Molecule 27 is a protein called 60S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	65	121	Total	C	N	O	S		
			969	623	170	174	2	0	0

- Molecule 28 is a protein called 60S ribosomal protein L26.

Mol	Chain	Residues	Atoms				AltConf	Trace
28	66	126	Total	C	N	O	0	0
			994	625	192	177		

- Molecule 29 is a protein called 60S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	67	135	Total	C	N	O	0	0
			1093	710	202	181		

- Molecule 30 is a protein called 60S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	68	148	Total	C	N	O	S	0	0
			1174	749	231	191	3		

- Molecule 31 is a protein called 60S ribosomal protein L29.

Mol	Chain	Residues	Atoms				AltConf	Trace
31	69	58	Total	C	N	O	0	0
			463	289	100	74		

- Molecule 32 is a protein called 60S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	70	97	Total	C	N	O	S	0	0
			743	479	124	139	1		

- Molecule 33 is a protein called 60S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	71	109	Total	C	N	O	S	0	0
			890	565	168	156	1		

- Molecule 34 is a protein called 60S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	72	127	Total	C	N	O	S	0	0
			1020	647	205	167	1		

- Molecule 35 is a protein called 60S ribosomal protein L33.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	73	106	Total	C	N	O	S	0	0
			851	540	165	145	1		

- Molecule 36 is a protein called 60S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	74	112	Total	C	N	O	S	0	0
			881	546	179	152	4		

- Molecule 37 is a protein called 60S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	75	119	Total	C	N	O	S	0	0
			970	615	186	168	1		

- Molecule 38 is a protein called 60S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	76	99	Total	C	N	O	S	0	0
			772	481	156	133	2		

- Molecule 39 is a protein called 60S ribosomal protein L37.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	77	87	Total	C	N	O	S	0	0
			682	414	148	115	5		

- Molecule 40 is a protein called 60S ribosomal protein L38.

Mol	Chain	Residues	Atoms				AltConf	Trace
40	78	77	Total	C	N	O	0	0
			613	391	115	107		

- Molecule 41 is a protein called 60S ribosomal protein L39.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	79	50	Total	C	N	O	S	0	0
			437	272	97	66	2		

- Molecule 42 is a protein called 60S ribosomal protein L40.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	80	52	Total	C	N	O	S	0	0
			418	259	86	68	5		

- Molecule 43 is a protein called 60S ribosomal protein L41.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	81	25	Total	C	N	O	S	0	0
			234	142	63	28	1		

- Molecule 44 is a protein called 60S ribosomal protein L42.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	82	103	Total	C	N	O	S	0	0
			827	520	167	135	5		

- Molecule 45 is a protein called 60S ribosomal protein L43.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	83	91	Total	C	N	O	S	0	0
			695	429	138	122	6		

- Molecule 46 is a RNA chain called 18S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	1S	1781	Total	C	N	O	P	0	0
			37949	16965	6715	12488	1781		

- Molecule 47 is a protein called 40S ribosomal protein S0.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	S0	206	Total	C	N	O	S	0	0
			1612	1034	285	291	2		

- Molecule 48 is a protein called 40S ribosomal protein S1.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	S1	214	Total	C	N	O	S	0	0
			1709	1084	310	311	4		

- Molecule 49 is a protein called 40S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	S2	217	Total	C	N	O	S	0	0
			1635	1047	289	297	2		

- Molecule 50 is a protein called 40S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	S3	223	Total	C	N	O	S	0	0
			1734	1101	313	314	6		

- Molecule 51 is a protein called 40S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S4	260	Total	C	N	O	S	0	0
			2069	1316	389	361	3		

- Molecule 52 is a protein called 40S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	S5	206	Total	C	N	O	S	0	0
			1610	1007	300	300	3		

- Molecule 53 is a protein called 40S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	S6	226	Total	C	N	O	S	0	0
			1820	1142	350	325	3		

- Molecule 54 is a protein called 40S ribosomal protein S7.

Mol	Chain	Residues	Atoms				AltConf	Trace
54	S7	184	Total	C	N	O	0	0
			1481	951	265	265		

- Molecule 55 is a protein called 40S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	S8	188	Total	C	N	O	S	0	0
			1490	925	298	265	2		

- Molecule 56 is a protein called 40S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	S9	185	Total	C	N	O	S	0	0
			1494	943	289	261	1		

- Molecule 57 is a protein called 40S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
57	10	96	Total	C	N	O	S	0	0
			817	529	133	153	2		

- Molecule 58 is a protein called 40S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
58	11	155	Total	C	N	O	S	0	0
			1245	798	235	209	3		

- Molecule 59 is a protein called 40S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
59	12	124	Total	C	N	O	S	0	0
			935	587	165	181	2		

- Molecule 60 is a protein called 40S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
60	13	150	Total	C	N	O	S	0	0
			1193	759	224	208	2		

- Molecule 61 is a protein called 40S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
61	14	127	Total	C	N	O	S	0	0
			942	578	186	175	3		

- Molecule 62 is a protein called 40S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
62	15	124	Total	C	N	O	S	0	0
			991	631	187	166	7		

- Molecule 63 is a protein called 40S ribosomal protein S16.

Mol	Chain	Residues	Atoms				AltConf	Trace
63	16	141	Total	C	N	O	0	0
			1106	708	203	195		

- Molecule 64 is a protein called 40S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
64	17	120	Total	C	N	O	S	0	0
			965	603	183	177	2		

- Molecule 65 is a protein called 40S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
65	18	145	Total	C	N	O	S	0	0
			1193	743	237	211	2		

- Molecule 66 is a protein called 40S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
66	19	143	Total	C	N	O	S	0	0
			1113	694	208	209	2		

- Molecule 67 is a protein called 40S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
67	20	107	Total	C	N	O	S	0	0
			856	539	156	160	1		

- Molecule 68 is a protein called 40S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
68	21	87	Total	C	N	O	S	0	0
			685	420	125	138	2		

- Molecule 69 is a protein called 40S ribosomal protein S22.

Mol	Chain	Residues	Atoms					AltConf	Trace
69	22	129	Total	C	N	O	S	0	0
			1022	650	188	181	3		

- Molecule 70 is a protein called 40S ribosomal protein S23.

Mol	Chain	Residues	Atoms					AltConf	Trace
70	23	144	Total	C	N	O	S	0	0
			1122	708	220	192	2		

- Molecule 71 is a protein called 40S ribosomal protein S24.

Mol	Chain	Residues	Atoms					AltConf	Trace
71	24	134	Total	C	N	O		0	0
			1074	676	208	190			

- Molecule 72 is a protein called 40S ribosomal protein S25.

Mol	Chain	Residues	Atoms					AltConf	Trace
72	25	70	Total	C	N	O		0	0
			563	360	104	99			

- Molecule 73 is a protein called 40S ribosomal protein S26.

Mol	Chain	Residues	Atoms					AltConf	Trace
73	26	97	Total	C	N	O	S	0	0
			769	475	160	129	5		

- Molecule 74 is a protein called 40S ribosomal protein S27.

Mol	Chain	Residues	Atoms					AltConf	Trace
74	27	81	Total	C	N	O	S	0	0
			611	382	110	114	5		

- Molecule 75 is a protein called 40S ribosomal protein S28.

Mol	Chain	Residues	Atoms					AltConf	Trace
75	28	63	Total	C	N	O	S	0	0
			498	306	99	92	1		

- Molecule 76 is a protein called 40S ribosomal protein S29.

Mol	Chain	Residues	Atoms					AltConf	Trace
76	29	53	Total	C	N	O	S	0	0
			444	275	92	73	4		

- Molecule 77 is a protein called 40S ribosomal protein S30.

Mol	Chain	Residues	Atoms					AltConf	Trace
77	30	60	Total	C	N	O	S	0	0
			475	299	98	77	1		

- Molecule 78 is a protein called 40S ribosomal protein S31.

Mol	Chain	Residues	Atoms					AltConf	Trace
78	31	71	Total	C	N	O	S	0	0
			498	309	93	92	4		

- Molecule 79 is a protein called Guanine nucleotide-binding protein subunit beta-like protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
79	RA	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

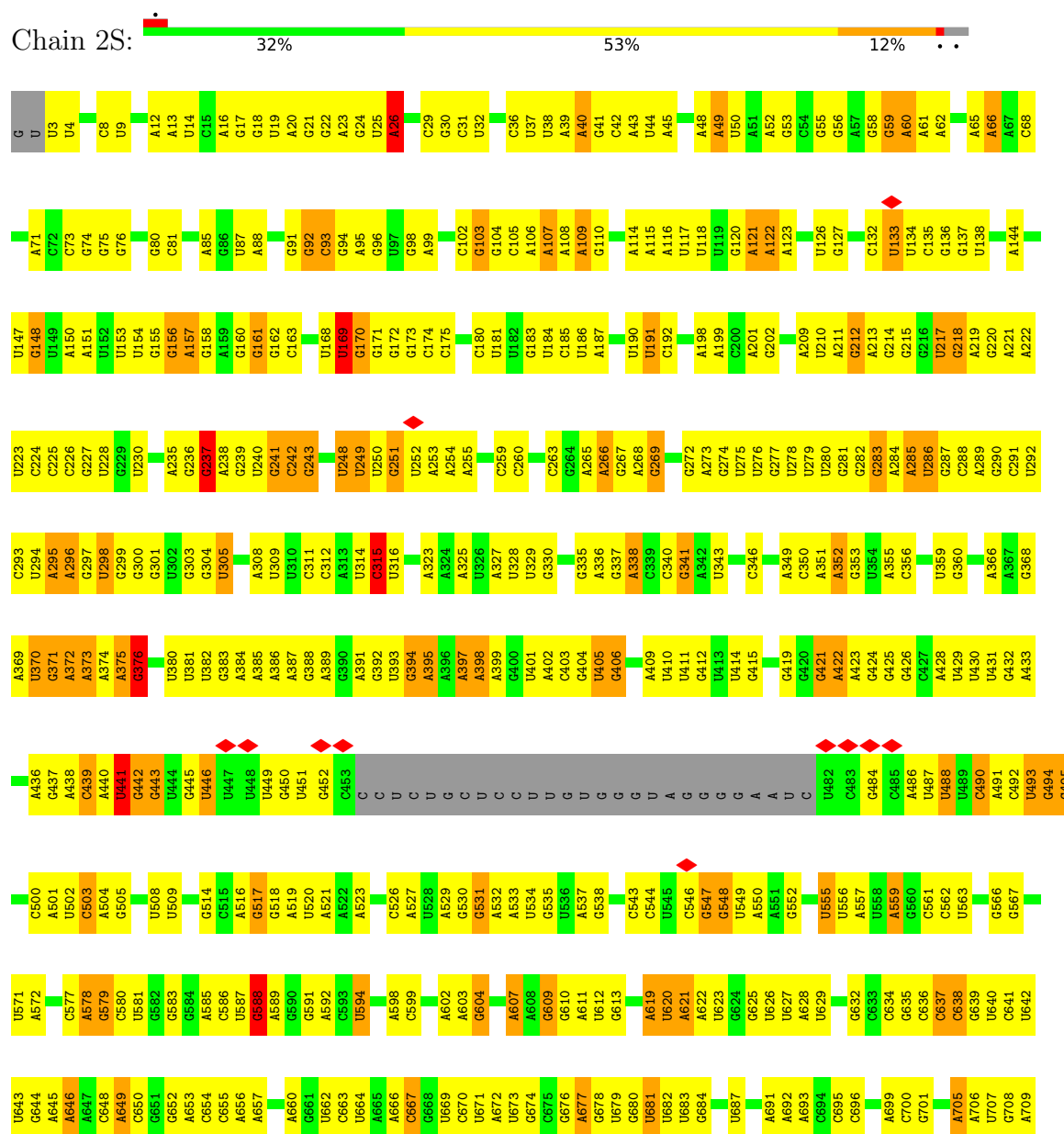
- Molecule 80 is a RNA chain called TSV IRES mRNA.

Mol	Chain	Residues	Atoms		AltConf	Trace
80	IR	198	Total	P	0	198
			198	198		

3 Residue-property plots

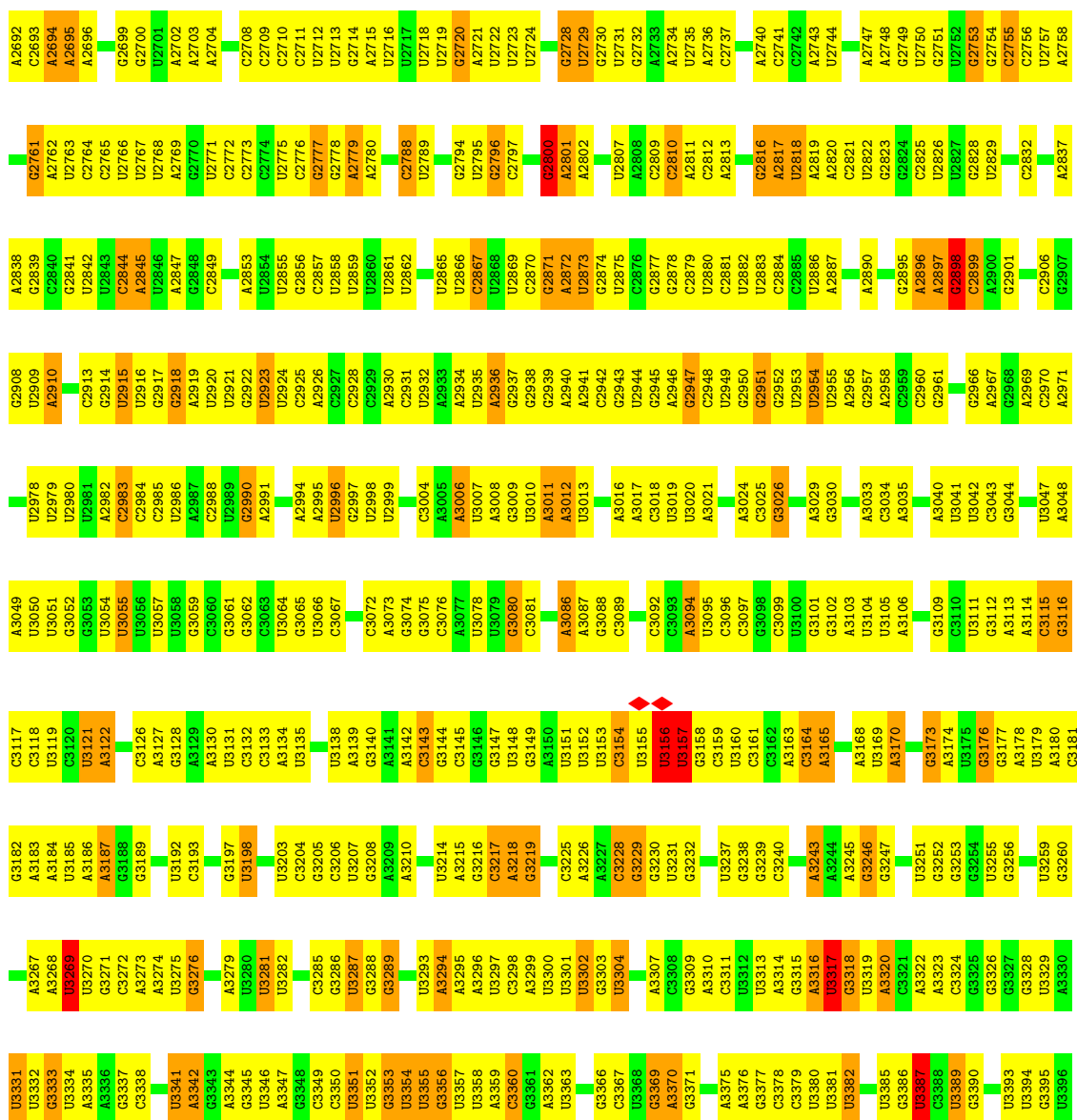
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 25S ribosomal RNA

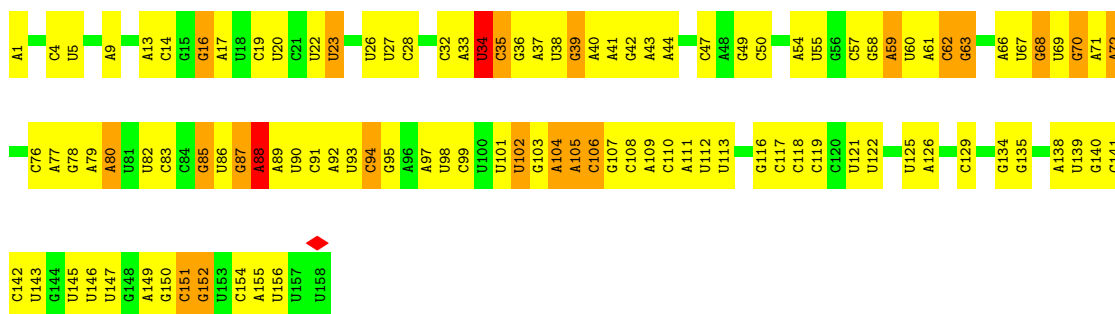


G1635	U1479	U1405	U1334	G1262	C1189	U1124	A1054	C982	U919	C851	G755	A710
A1638	G1480	A1406	C1335	A1263	A1190	U1125	A1055	A983	A920	U852	A766	A711
A1642	A1481	G1408	A1337	U1265	U1191	G1126	U1056	C984	A921	G853	A767	G712
G1643	A1482	G1407	A1336	G1266	C1192	G1127	U1057	U985		G854	A769	U713
C1644	G1483	U1410	C1338	U1276	A1193	U1128	A1057	U986	G924	U855	U790	G714
U1645	G1484	C1411	C1339	C1277	A1195	A1129		U987	A925	G856	A791	A715
G1646			G1340	C1278		A1130	U1060	U988	A926	G857	G792	A716
G1647	G1487	U1415	U1341	C1279	A1200	G1131	A1061	A989	C927	A858	C793	C717
A1648	G1488	C1416	C1342	C1280	C1201	C1132	A1062	U990	C928	G859	U794	G718
U1649	A1489	G1417	G1346	G1281	A1202	A1133	G1063	C991	A929	G860	G795	U719
G1650	A1490	U1347	U1348	G1282	A1203	G1134	A1064	A992	U930	C861	U796	A720
U1651	G1492	C1420	G1349	C1283	A1204	A1135	A1065	G993		U862	U797	
G1652		G1421	A1350	U1284	A1205	A1136	G1066		U932	C863	G798	G725
G1653	C1497	G1422	G1285	G1286	G1206	C1137		A996	A933	C864	G799	G726
A1654	A1498	G1423	G1286	A1287		U1138	G1072	A997	A936	G867	G800	G727
G1655	C1499	C1426	A1287	U1288	G1209	G1139	U1073	A998	A937	A801	G728	
A1656	G1500	U1427	U1353	U1289	U1210	G1140	U1074	C1000	C938	C802	C803	A736
C1657	U1501	A1428	G1354	G1289	U1211	G1142		G1001	U939	G870	C804	G737
G1658	C1502	G1429	A1355	A1290	A1212	A1143	A1079	A1002	G940	U871	G805	A738
U1659	A1503	U1430	U1356	A1291	G1213	U1044	A1080	A1003		U872	A806	G739
C1660	A1504		G1357	C1292	U1214	G1145	U1081	U1004	U942	C873	A807	G740
G1661	A1505		C1358	U1293	U1215	C1146	U1082		U943	U874	A808	U741
A1662	C1506	G1433	C1359	A1294	C1216	G1147	G1083	A1009	C945	A876	G809	G742
U1663	A1507	A1434	U1360	G1295	A1217	G1148		G1010	C946	A877	A810	C743
C1664	G1508	A1435	C1361	C1296	U1218	G1149	U1088	A1011	U946	C877	U811	A744
G1665	A1509	U1436	G1362	G1300	C1219	U1150	G1089	G1012	G947	G878	G812	C745
C1666	C1510	C1437	A1363	A1301	U1220	A1151	G1090	G1013	U948	U879	G813	A746
A1667	A1511	U1438	G1364	A1302	A1221	G1152	A1091	U1014	C949	G880	U821	G754
G1668	U1512	U1439	G1365	G1222	G1223	A1153	C1092	U1015	G950	C881	G815	A747
C1669	G1513		A1366	C1224	C1225	A1154	A1093	C1016	A951	A882	A816	G750
A1676	G1514	G1443	G1367	U1225	A1226	C1155	U1094	C1017	A952	A883	A817	A751
U1677	A1515	G1444	U1368	U1305	G1226	A1158	U1095	G1018	G953	A884	C818	
G1678	C1516	U1445	A1369	G1306	U1227	A1159	U1096	G1019	U954	U885	U819	
A1679	G1517	G1447	G1370	G1307	C1228		G1097	G1020	U956		U820	
G1680		U1448	G1372	U1309	C1229	U1162	A1098		C957	U892	G822	A755
U1681	U1523	A1449	A1373	G1312	G1230	G1166		G1024	C958	G894	C823	G760
U1682	A1524	A1454	G1374	G1313	A1231		A1102	A1025	C959	A896	C824	A761
U1687	U1525	U1455		C1314	U1235	A1169	A1103	A1026	U960	U897	U825	G762
U1688	G1526	A1456	A1381	U1315	G1236	G1170	G1104	U1027	G963	U898	G826	G763
U1689	C1527	A1456		C1316	G1237	G1171	A1105	G1029	G964	U899	A827	U764
C1690	G1528	A1460	U1384	A1317	C1238	G1172	G1106		A965	G900	U828	C765
A1691		A1461	C1385	A1318	C1239	U1173	U1108	U1033	U966	G901	U829	U766
U1694	U1533	A1462		G1319	A1240	G1174	U1109	U1034	A967		A830	U767
A1695	A1535	U1463	G1389	C1320	U1241	C1175	U1110	G1035	G968	U905	G832	C768
U1696	G1536	G1464	A1390	G1321	G1242	C1176	U1111	A1036	C969	A906	G833	G770
A1697	A1537	G1466	C1391	U1322	G1243	C1177	A1112	C1037	A970	G907	U834	A771
U1705	G1538	A1467	G1392	G1323	A1244	G1178	A1113	C1038	G971	G908	G835	U772
A1707	U1541	C1468	A1393	U1324	G1245	A1179	G1113		A972	G909	A836	
A1708	A1545	U1469	A1394	U1325	G1246	U1180	U1114	U1042	A973	G910	G842	G776
C1708	U1546	U1471	U1398	C1327		U1181	G1115	C1043	G974	C911	U777	U778
A1709	G1547	U1472	G1400	U1328	A1252	A1182	G1116	U1044	G975	G912	A843	G779
C1709	C1548	G1473	U1329	A1253	U1254	C1183	C1045	A1046	U976	A913	A846	A780
U1629	U1549	A1401	C1330	C1254	U1255	C1184	A1047	A1047	G977	A915	A847	G781
G1713	C1402	C1403	U1331	C1255		C1185	A1120	A1048	U979	G978	A848	U782
A1714	G1404		A1332	C1256	A1260	G1186	U1121	A1049	A980	A783	C849	A783
			C1333		G1261	U1188	U1122	U1050	U981	C918	U850	A784

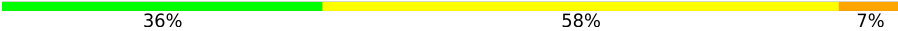


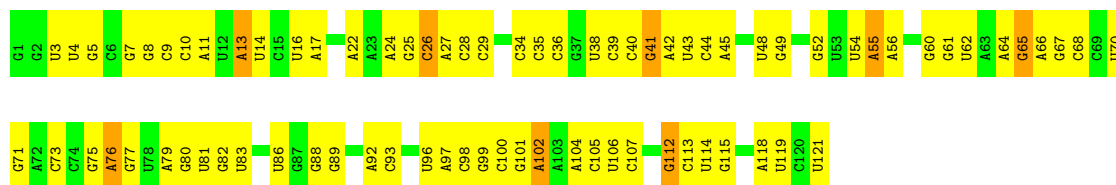


• Molecule 2: 5.8S ribosomal RNA

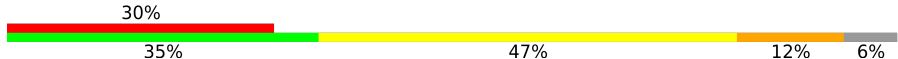


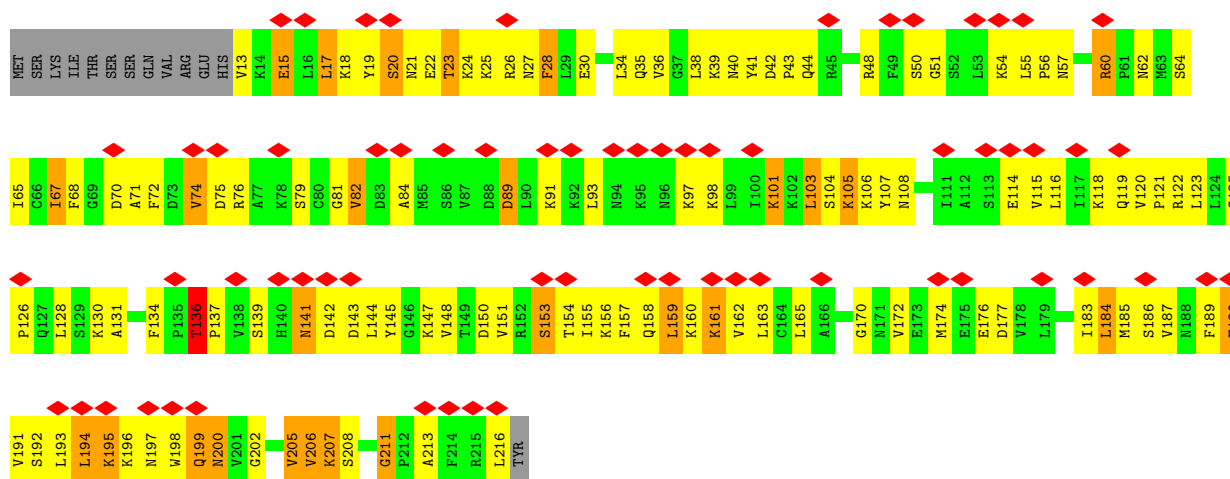
• Molecule 3: 5S ribosomal RNA

Chain 5S: 

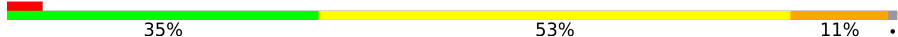


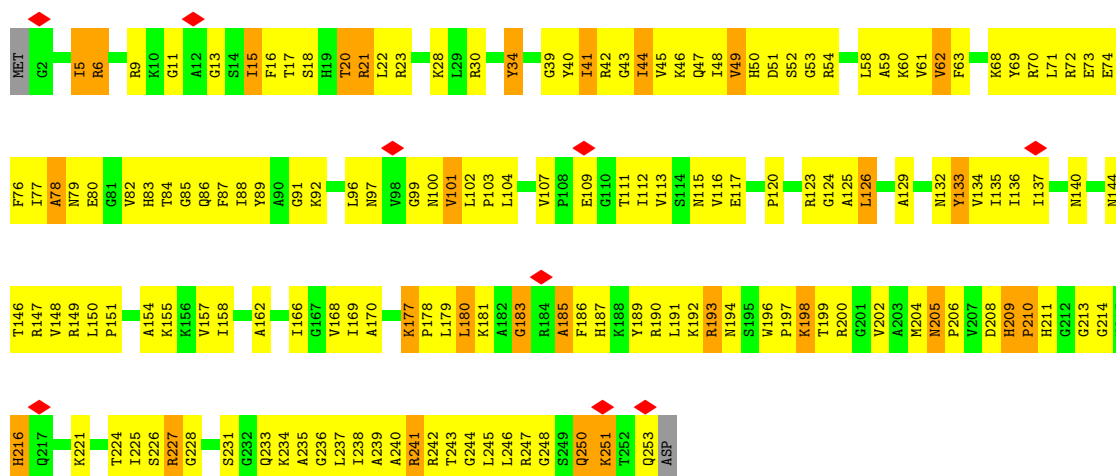
• Molecule 4: 60S ribosomal protein L1

Chain L1: 



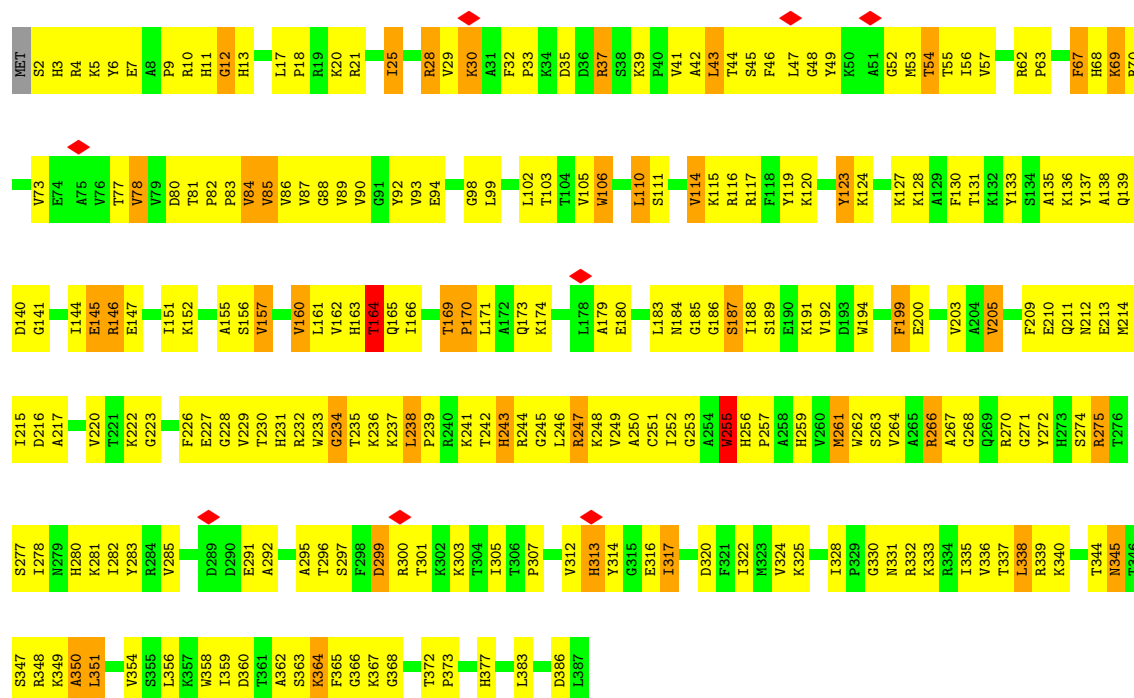
• Molecule 5: 60S ribosomal protein L2

Chain L2: 

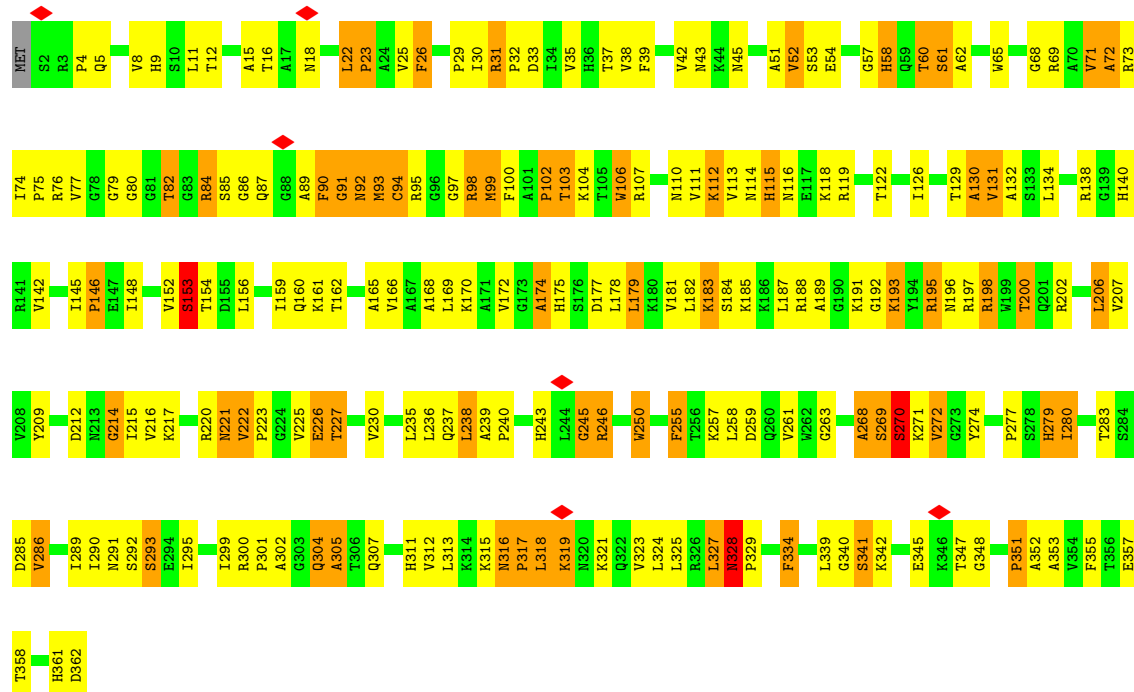


• Molecule 6: 60S ribosomal protein L3

Chain L3: 

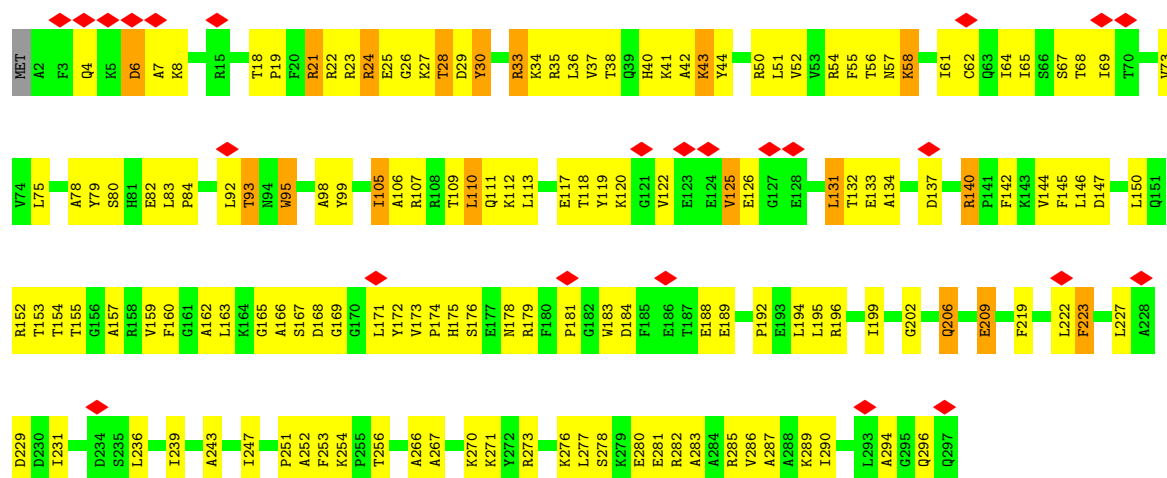


• Molecule 7: 60S ribosomal protein L4

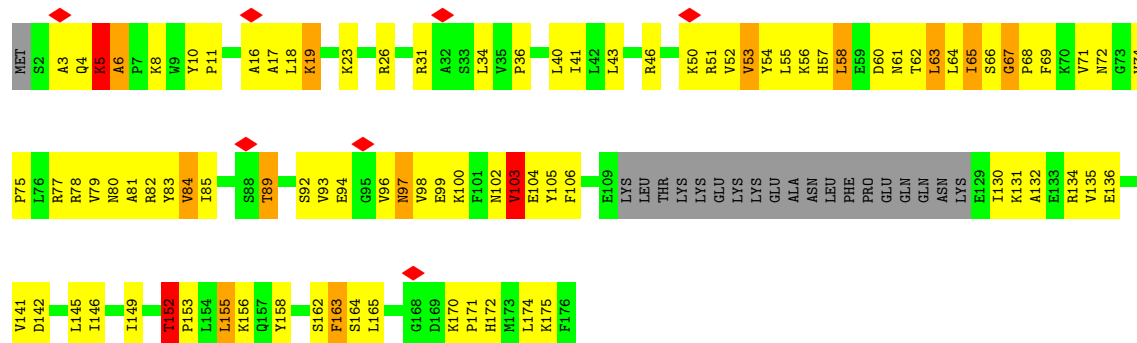


• Molecule 8: 60S ribosomal protein L5

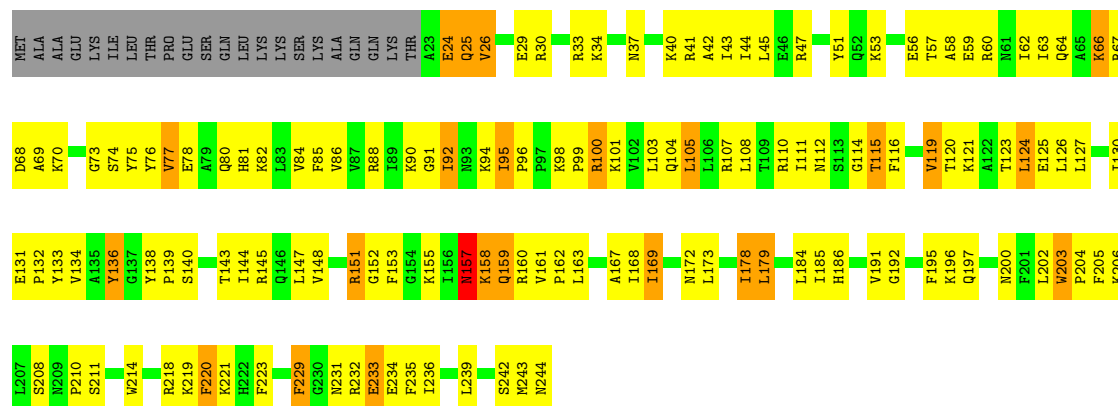




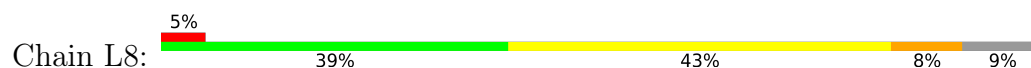
• Molecule 9: 60S ribosomal protein L6

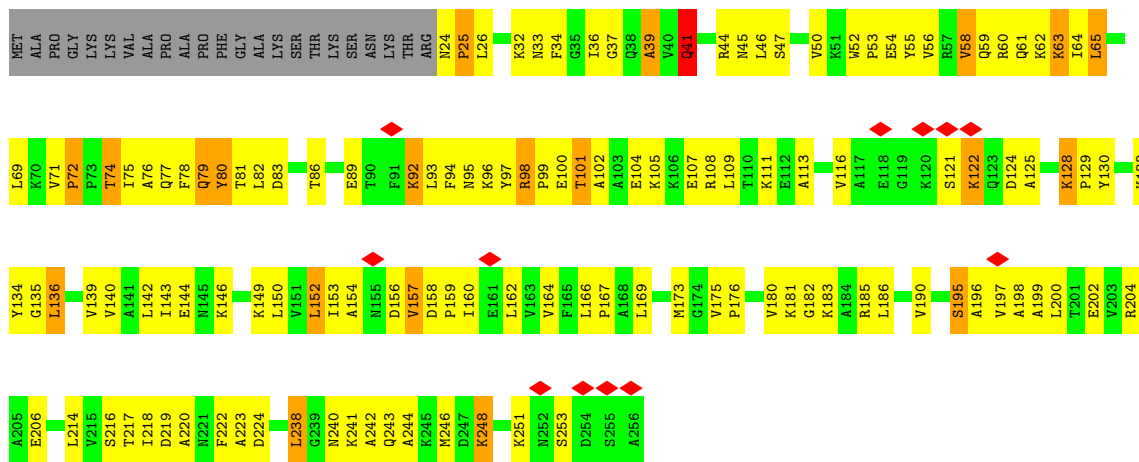


• Molecule 10: 60S ribosomal protein L7

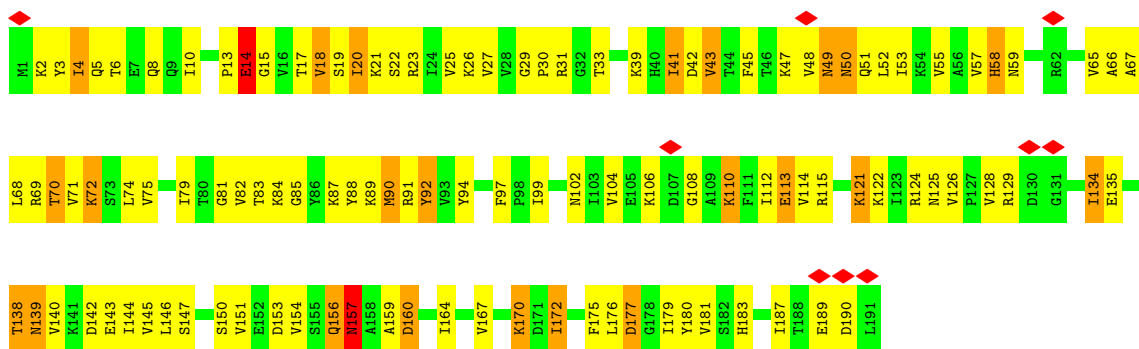


• Molecule 11: 60S ribosomal protein L8

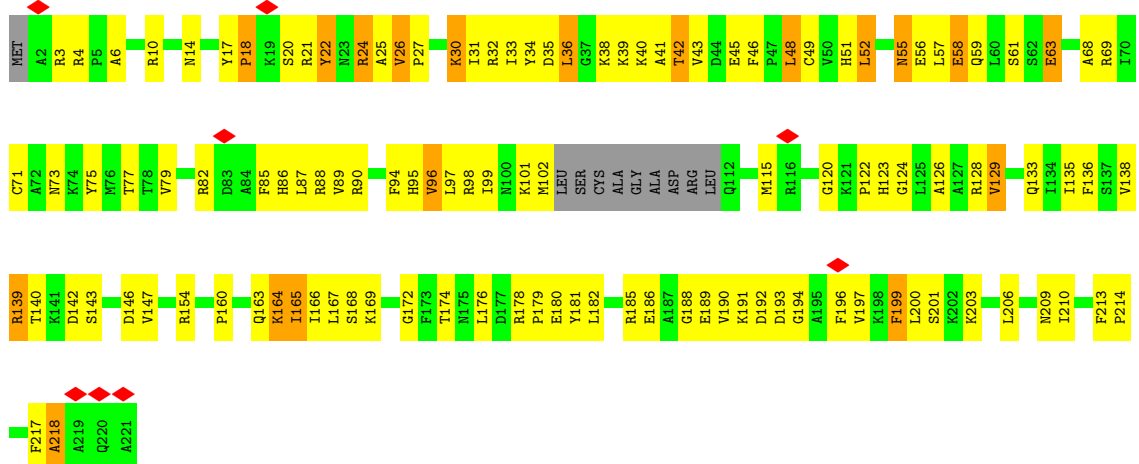




• Molecule 12: 60S ribosomal protein L9

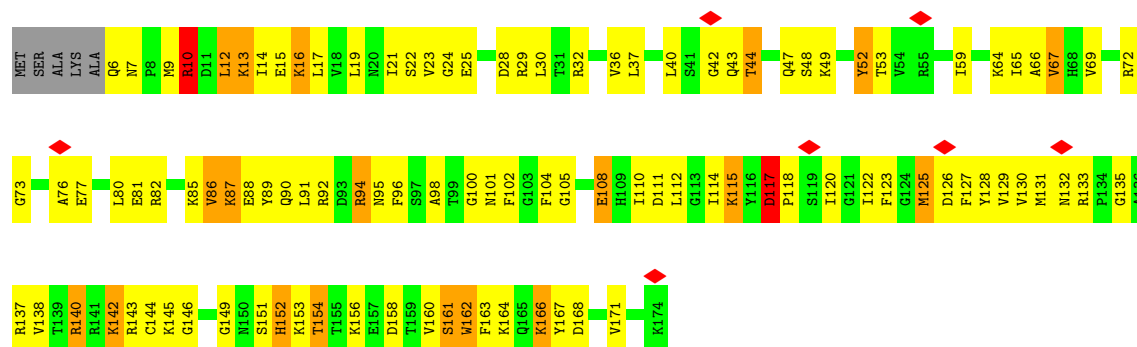


• Molecule 13: 60S ribosomal protein L10

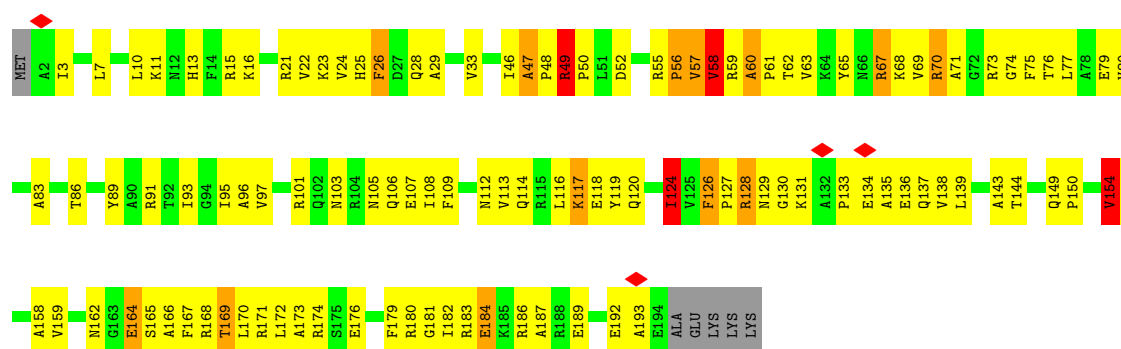


• Molecule 14: 60S ribosomal protein L11

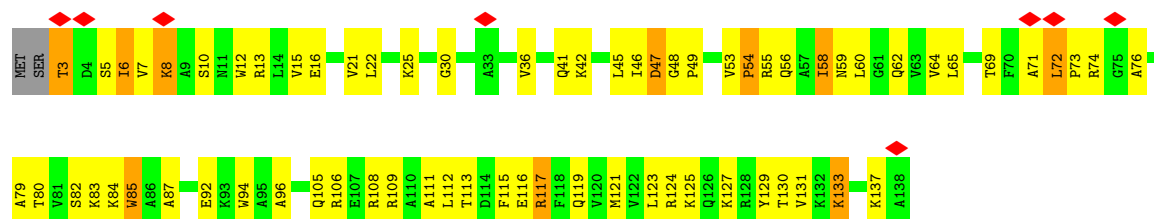




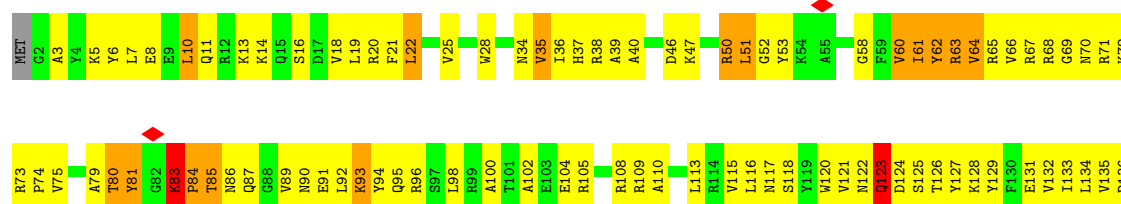
• Molecule 15: 60S ribosomal protein L13



• Molecule 16: 60S ribosomal protein L14

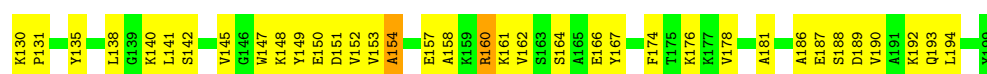
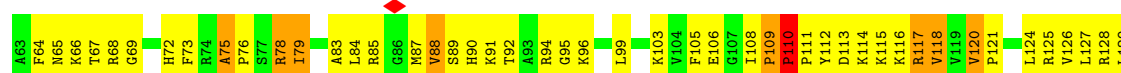
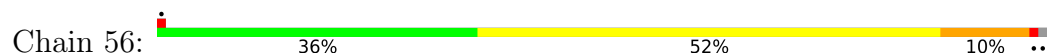


• Molecule 17: 60S ribosomal protein L15

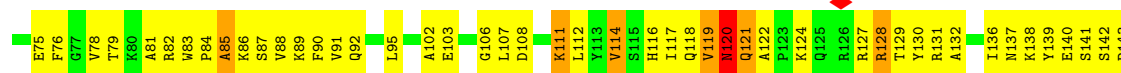
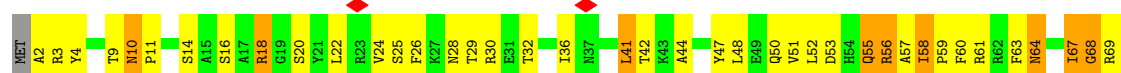




• Molecule 18: 60S ribosomal protein L16



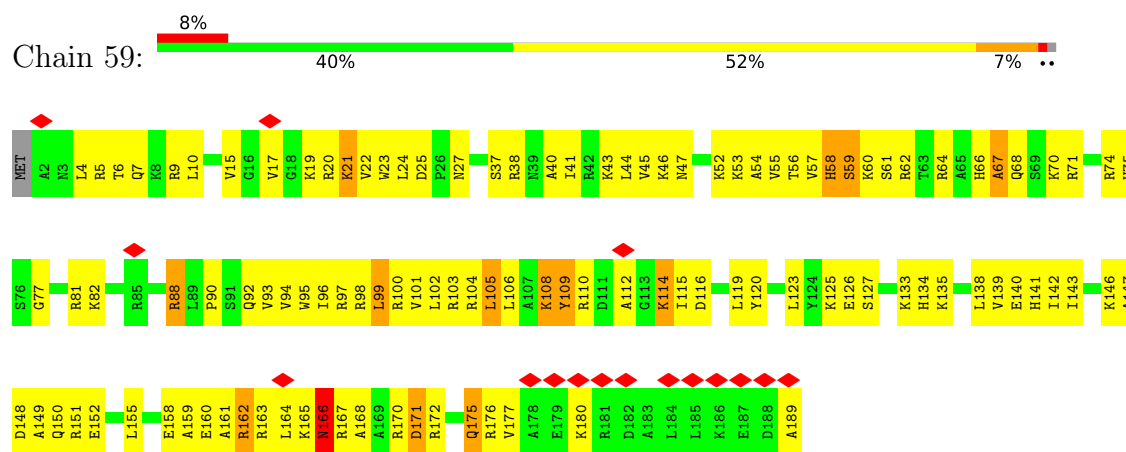
• Molecule 19: 60S ribosomal protein L17



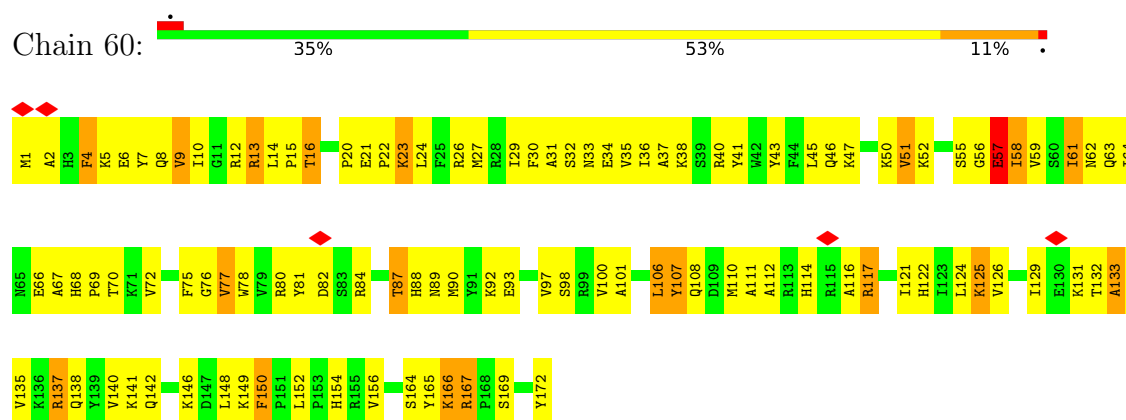
• Molecule 20: 60S ribosomal protein L18



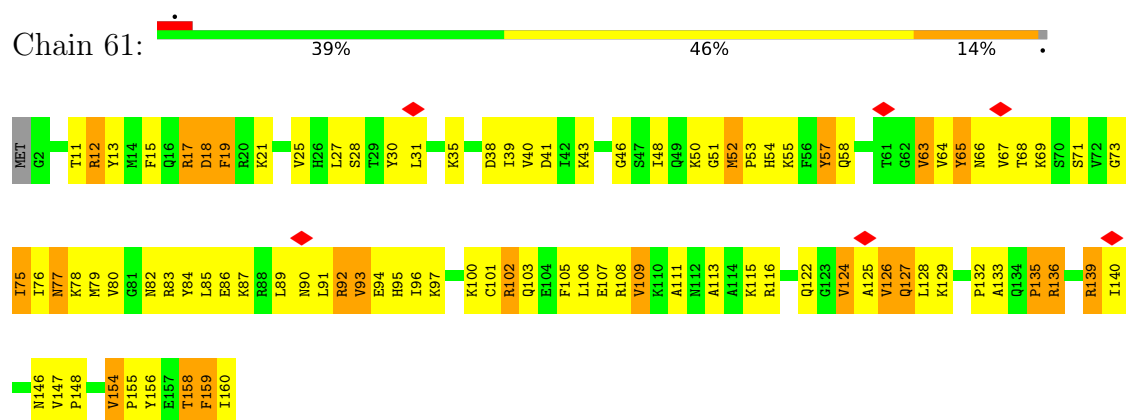
• Molecule 21: 60S ribosomal protein L19



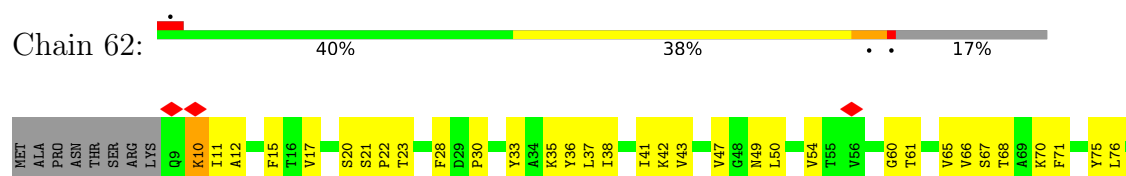
• Molecule 22: 60S ribosomal protein L20

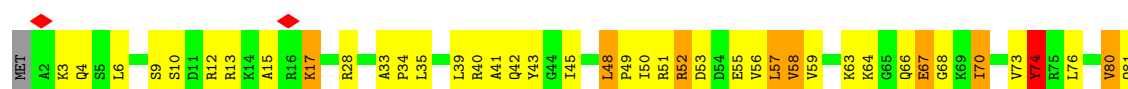


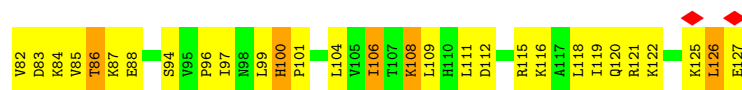
• Molecule 23: 60S ribosomal protein L21



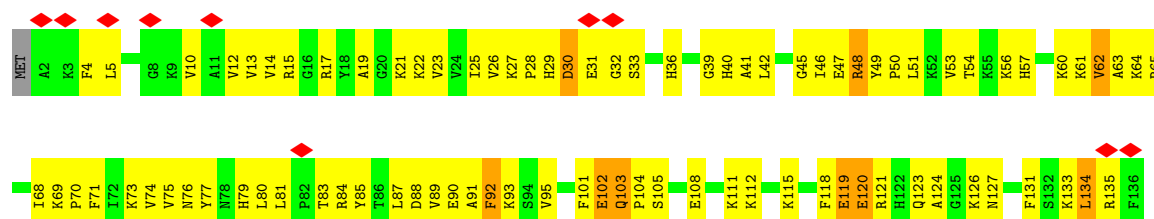
• Molecule 24: 60S ribosomal protein L22



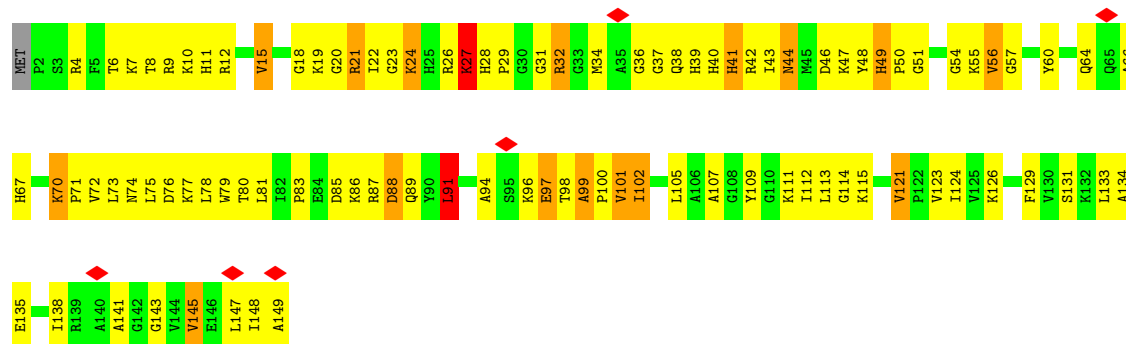




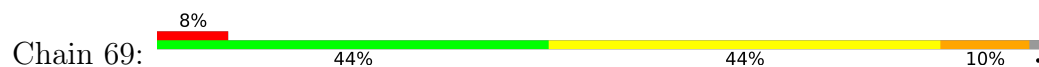
• Molecule 29: 60S ribosomal protein L27



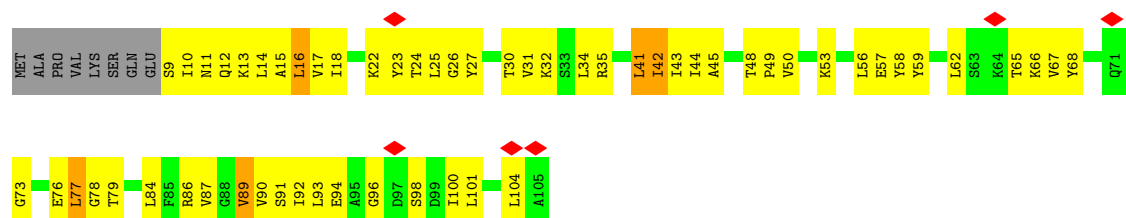
• Molecule 30: 60S ribosomal protein L28



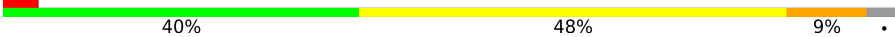
• Molecule 31: 60S ribosomal protein L29

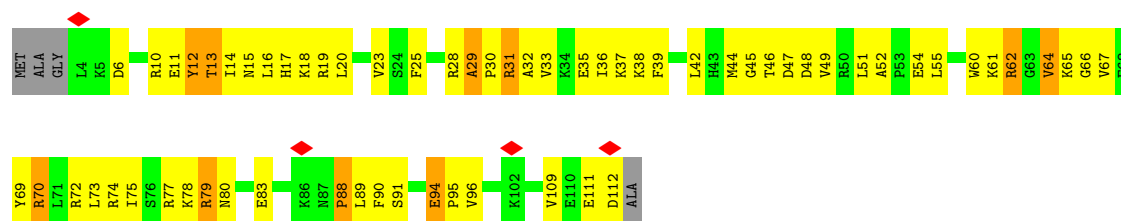


• Molecule 32: 60S ribosomal protein L30



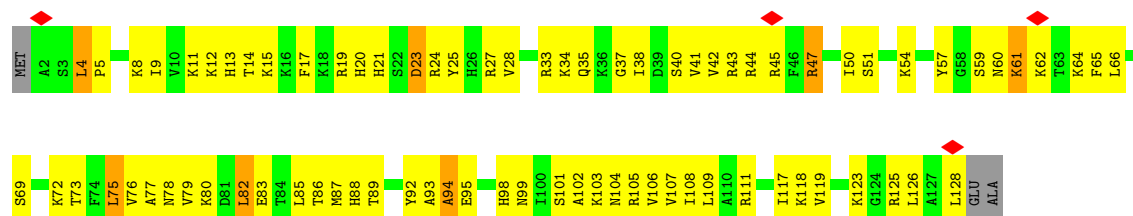
• Molecule 33: 60S ribosomal protein L31

Chain 71:  40% 48% 9% .



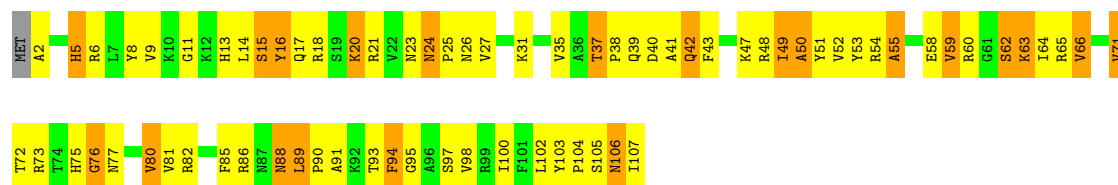
• Molecule 34: 60S ribosomal protein L32

Chain 72:  36% 56% 5% .

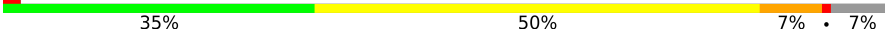


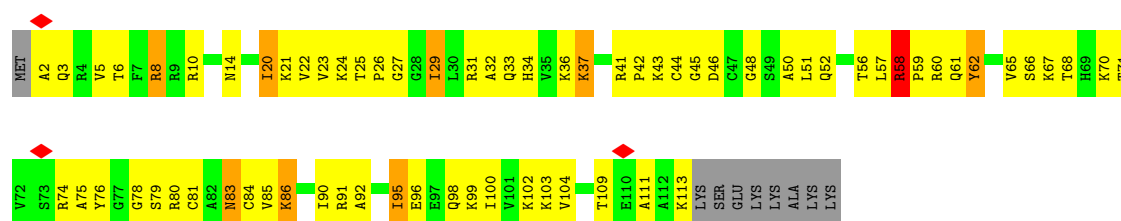
• Molecule 35: 60S ribosomal protein L33

Chain 73:  32% 48% 20% .



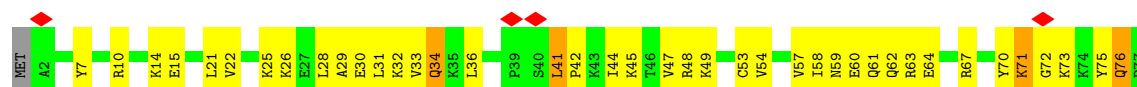
• Molecule 36: 60S ribosomal protein L34

Chain 74:  35% 50% 7% .



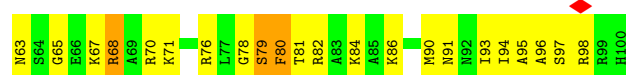
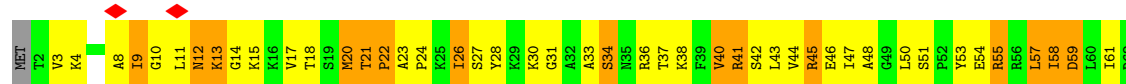
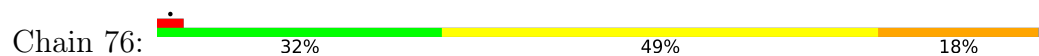
• Molecule 37: 60S ribosomal protein L35

Chain 75:  6% 44% 48% 7% .





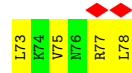
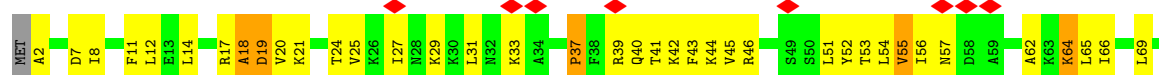
- Molecule 38: 60S ribosomal protein L36



- Molecule 39: 60S ribosomal protein L37



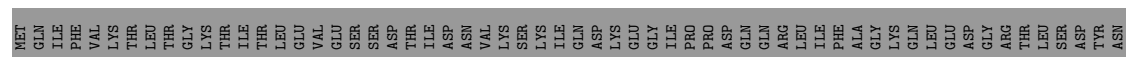
- Molecule 40: 60S ribosomal protein L38

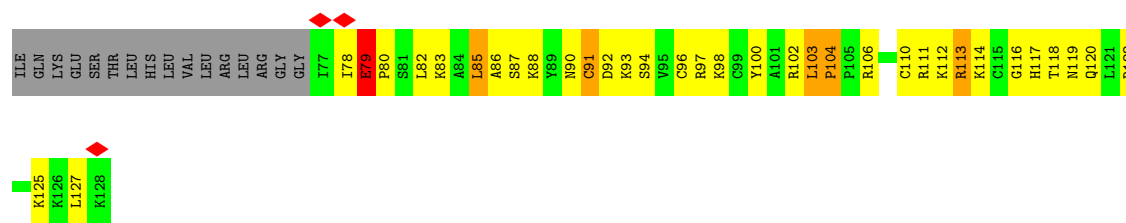


- Molecule 41: 60S ribosomal protein L39



- Molecule 42: 60S ribosomal protein L40

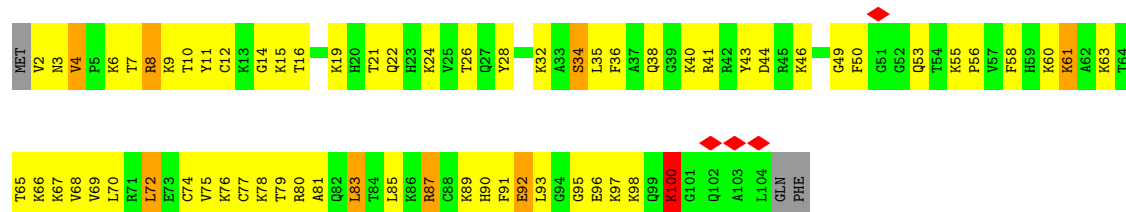




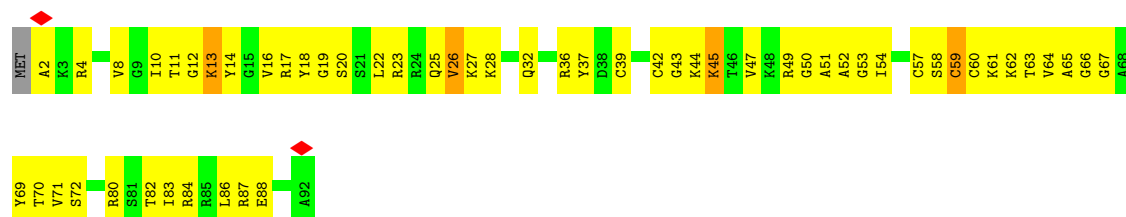
- Molecule 43: 60S ribosomal protein L41



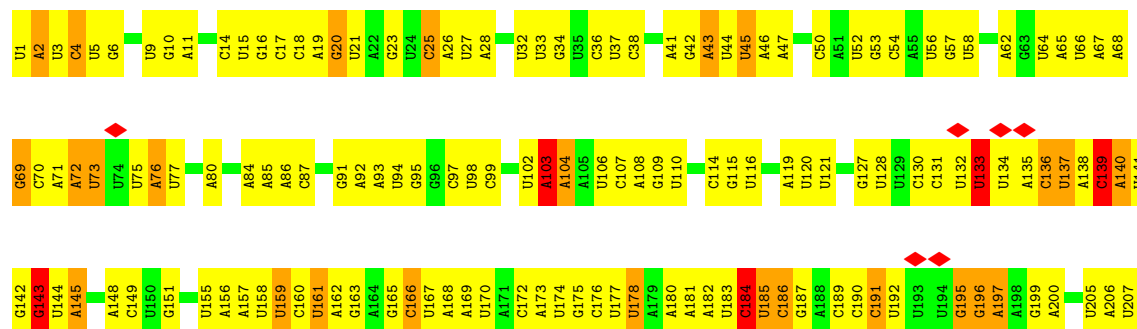
- Molecule 44: 60S ribosomal protein L42

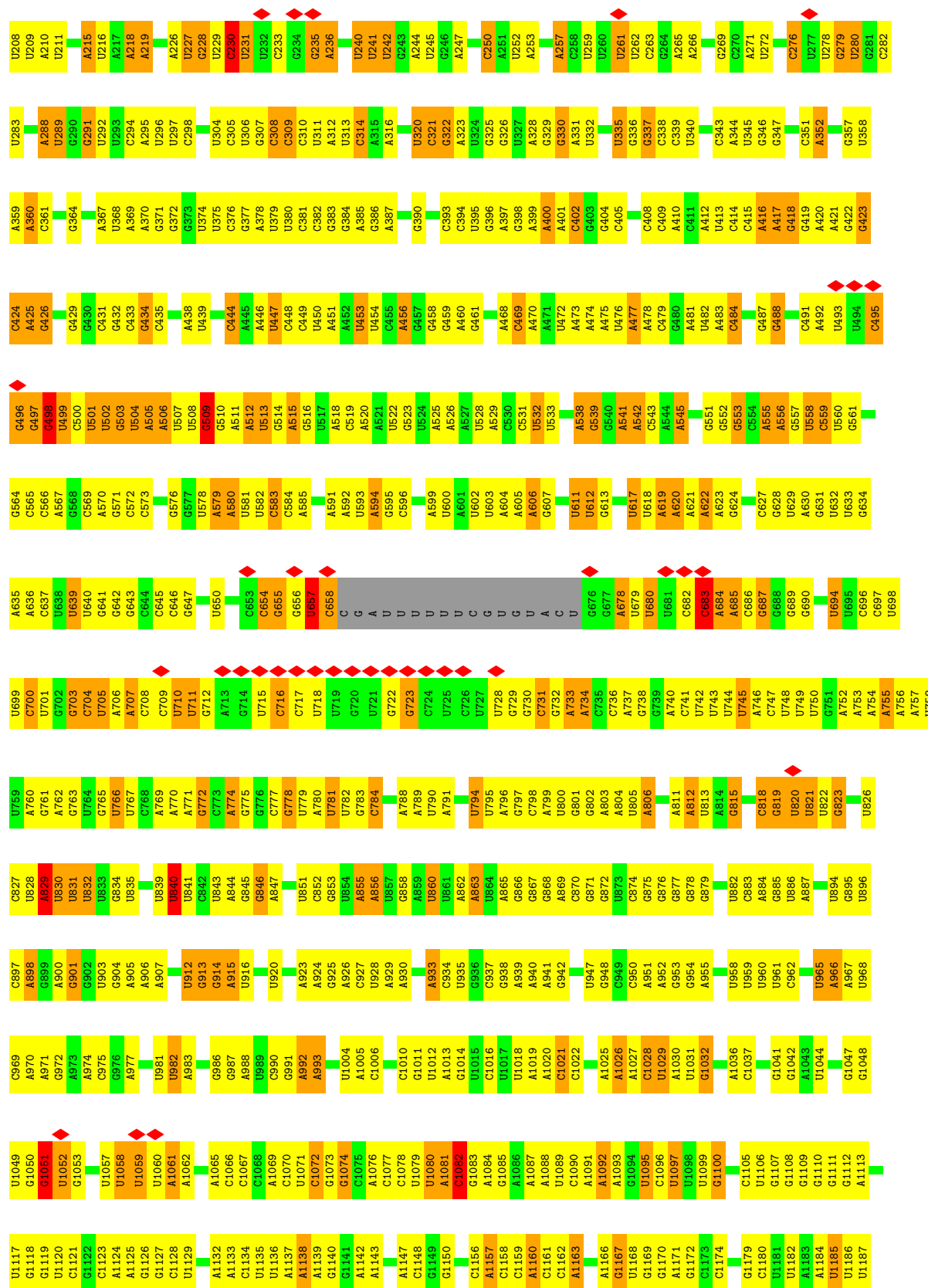


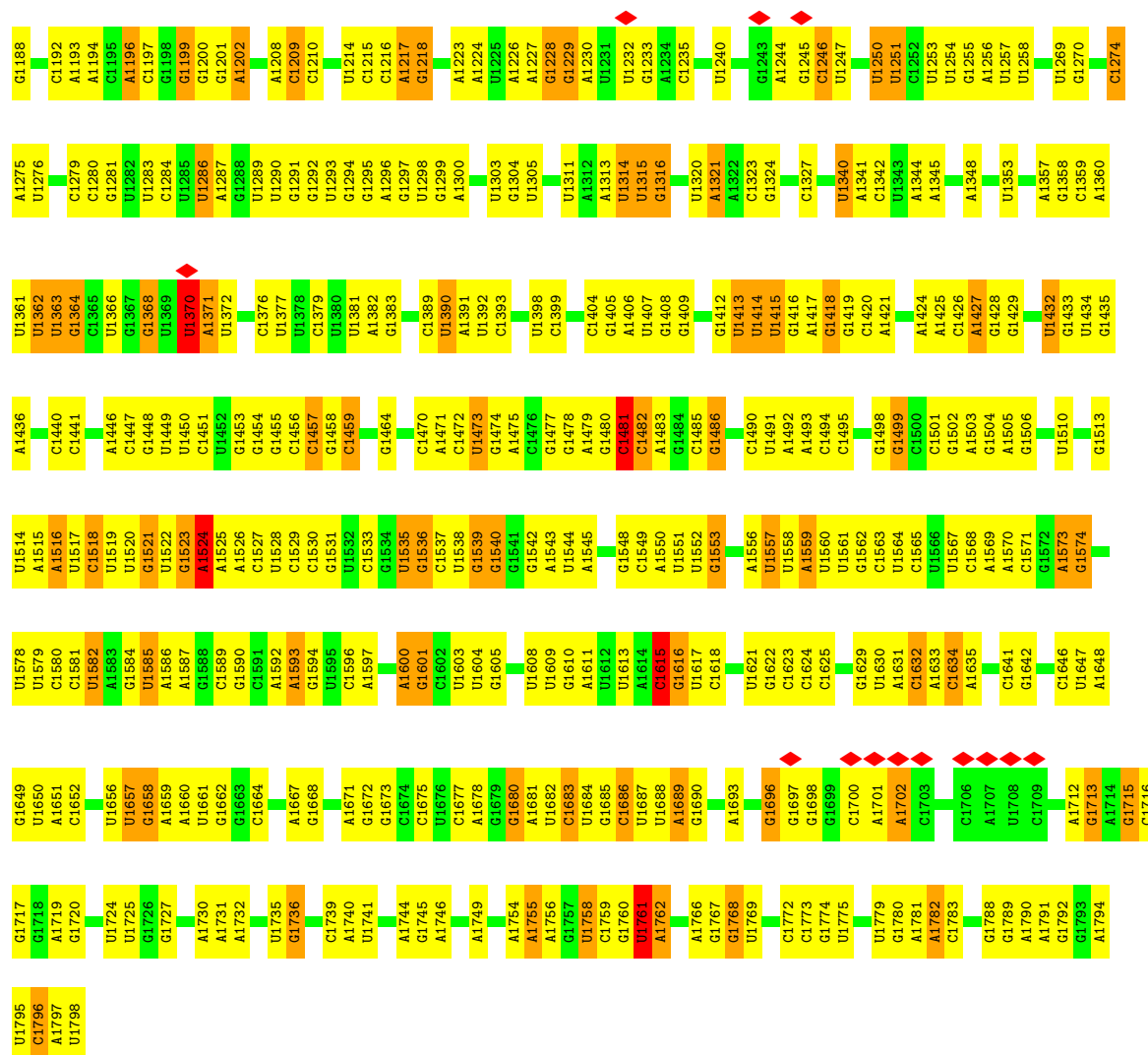
- Molecule 45: 60S ribosomal protein L43



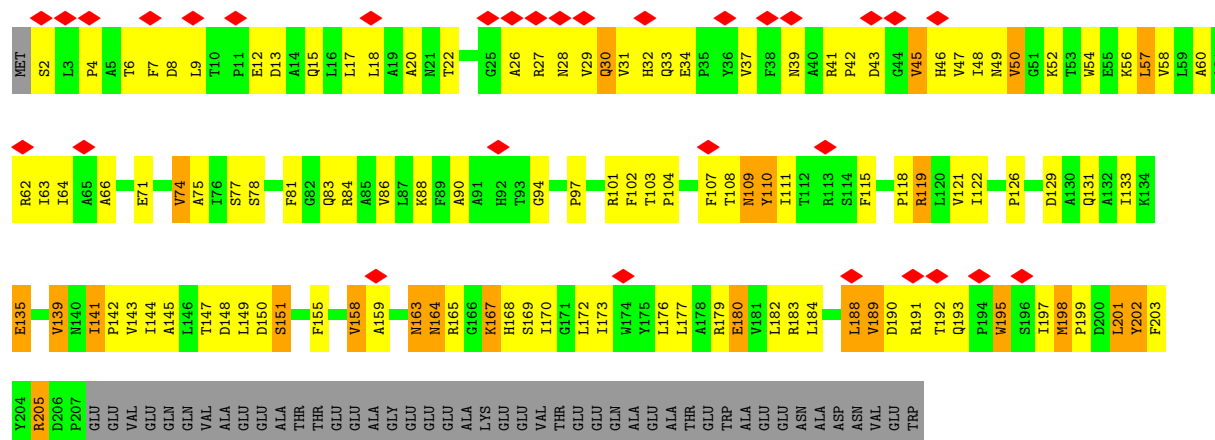
- Molecule 46: 18S ribosomal RNA



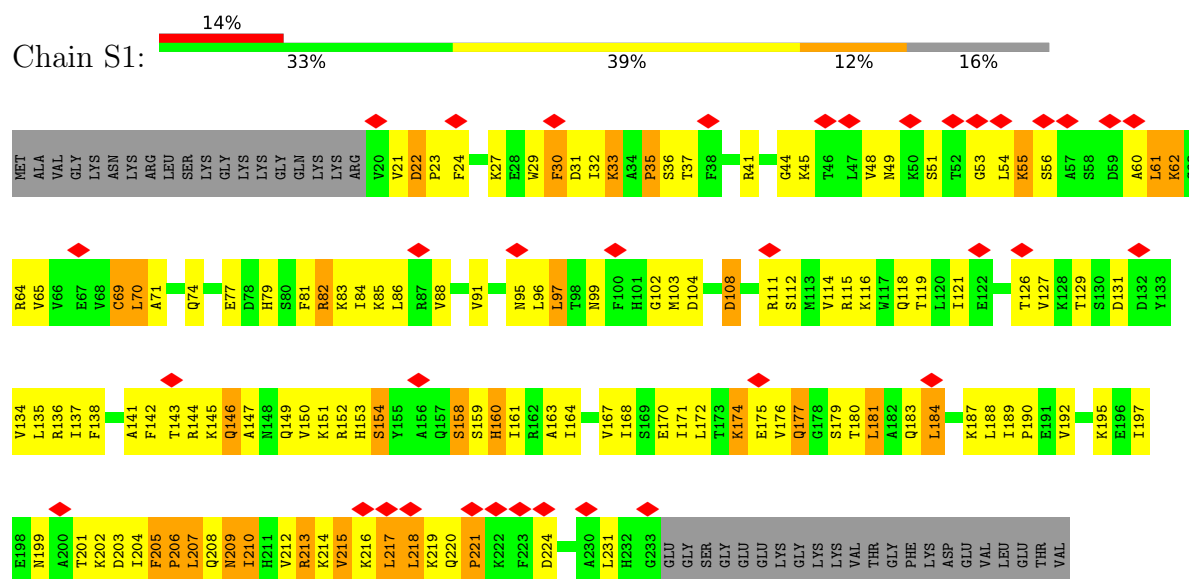




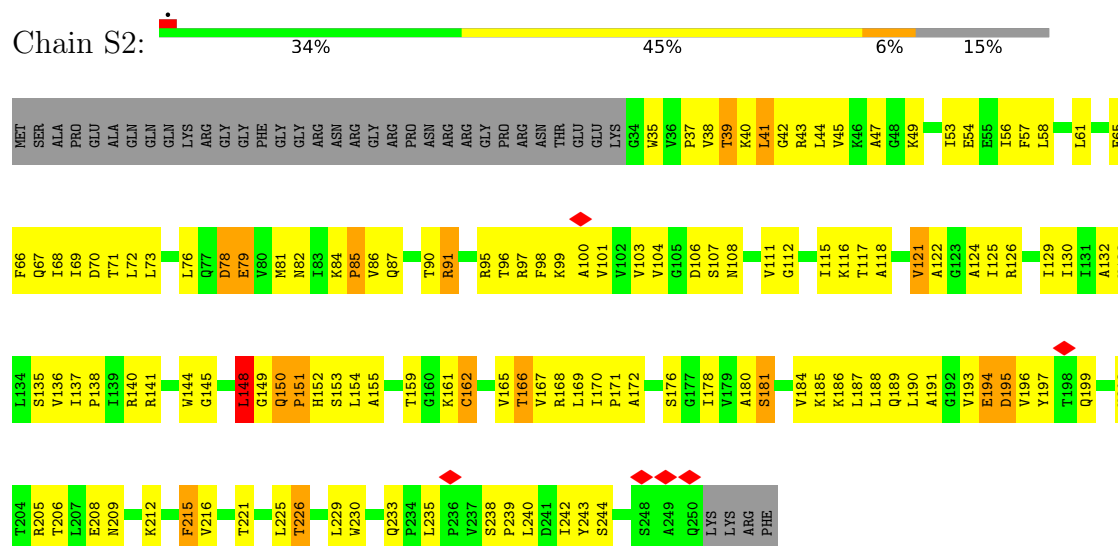
• Molecule 47: 40S ribosomal protein S0

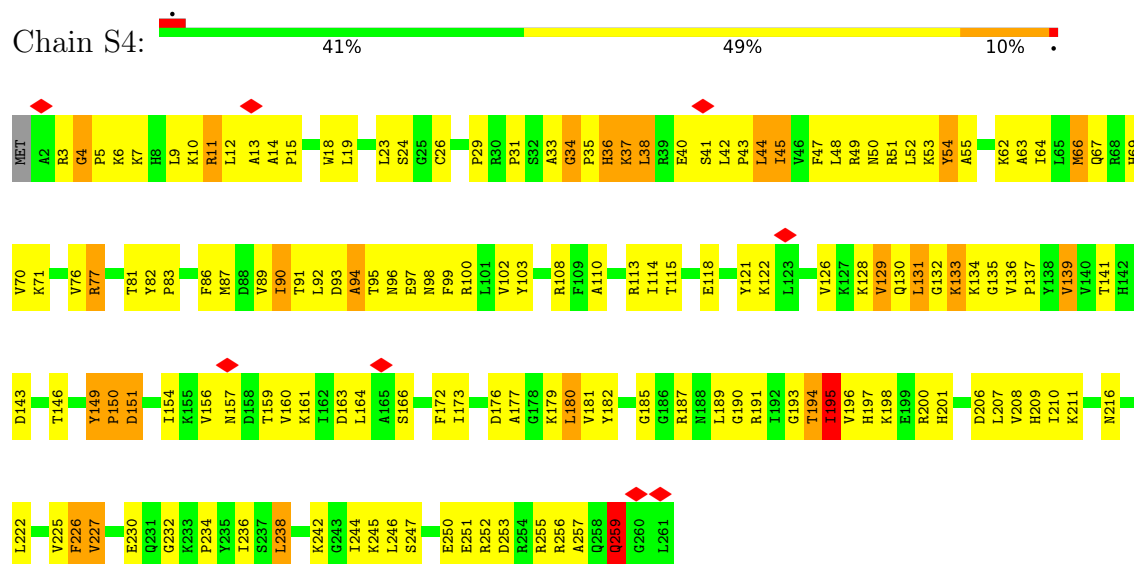


• Molecule 48: 40S ribosomal protein S1

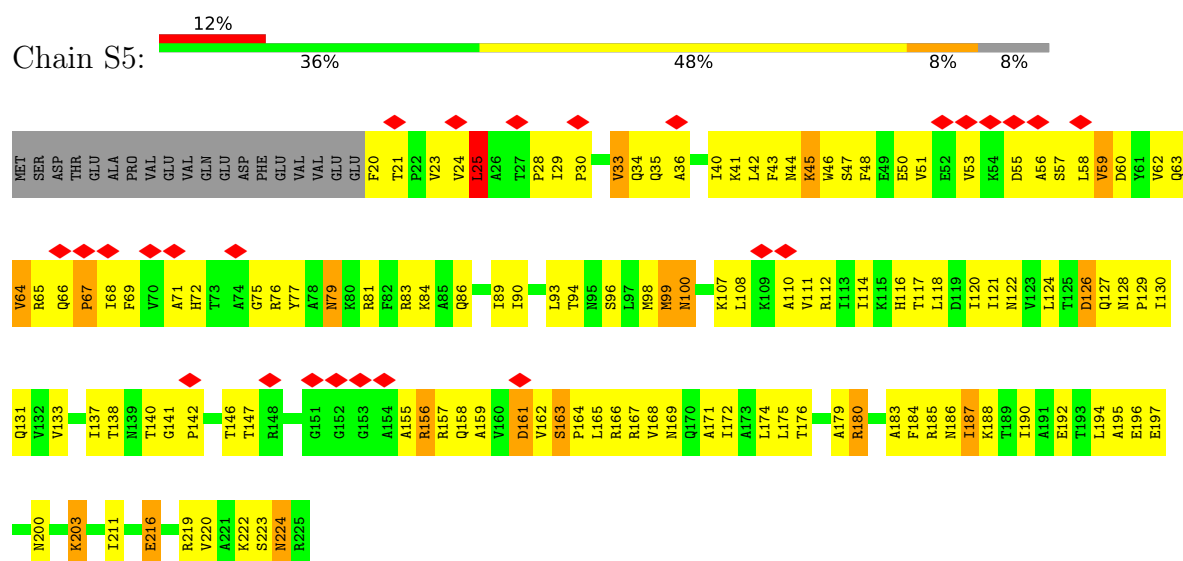


• Molecule 49: 40S ribosomal protein S2

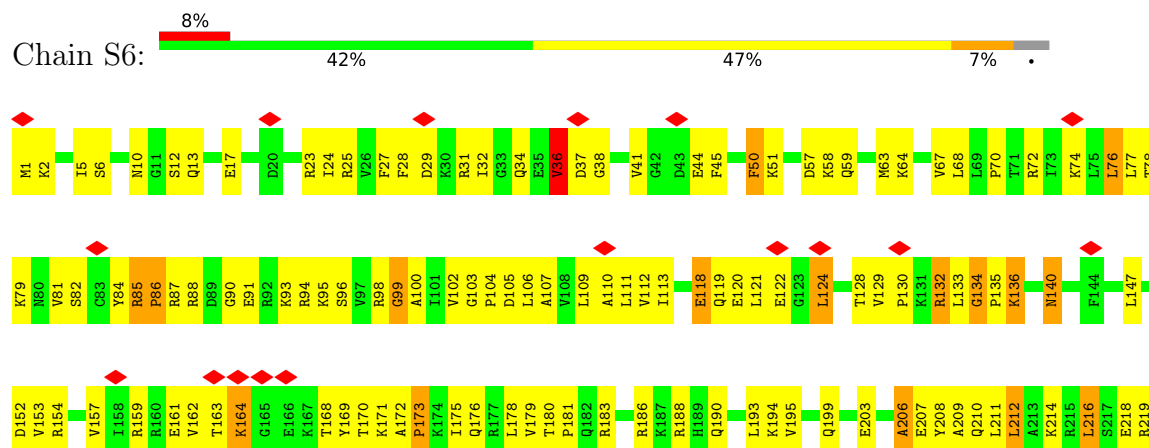


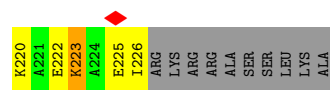


• Molecule 52: 40S ribosomal protein S5

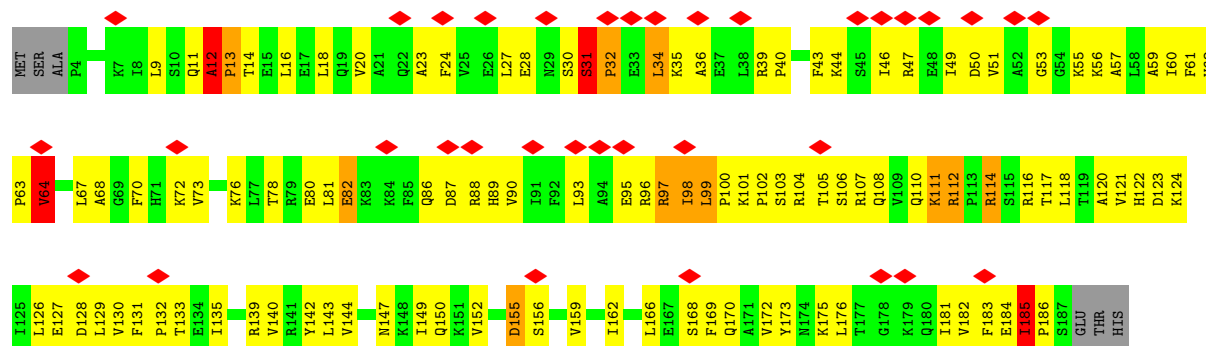


• Molecule 53: 40S ribosomal protein S6

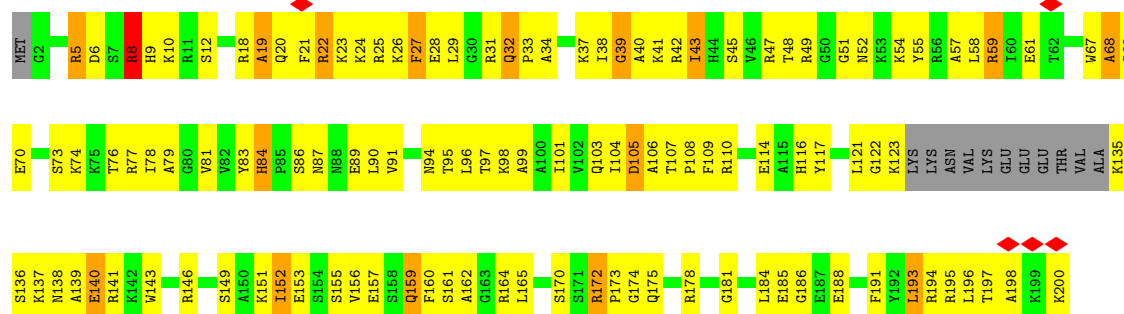




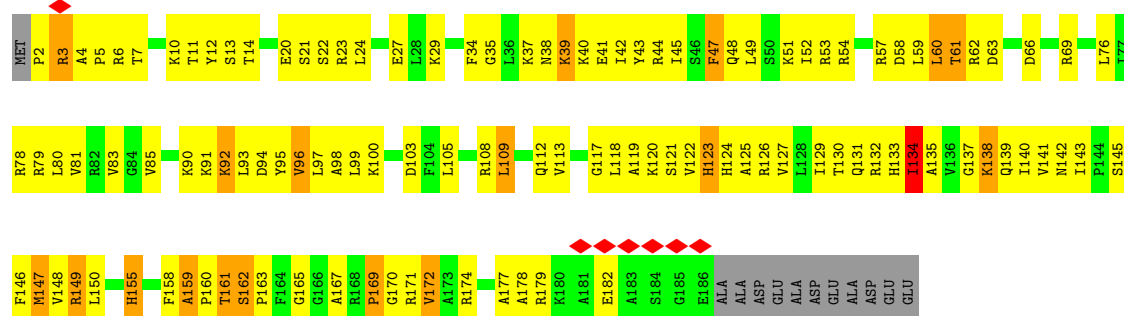
• Molecule 54: 40S ribosomal protein S7



• Molecule 55: 40S ribosomal protein S8



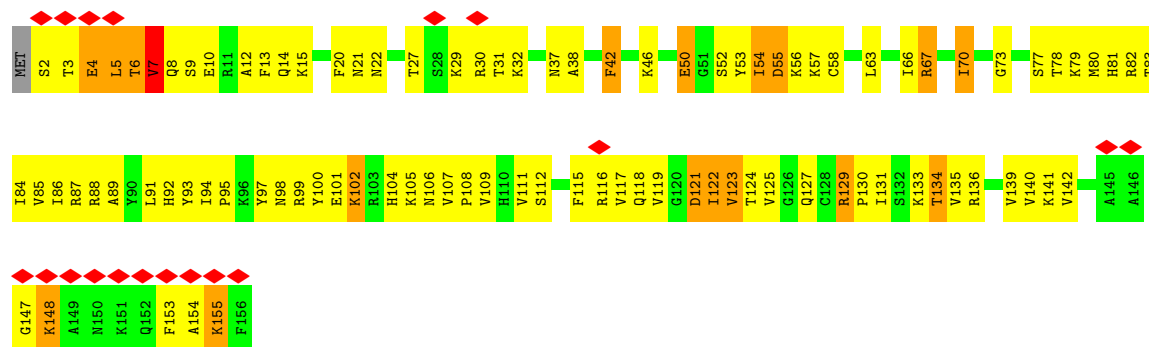
• Molecule 56: 40S ribosomal protein S9



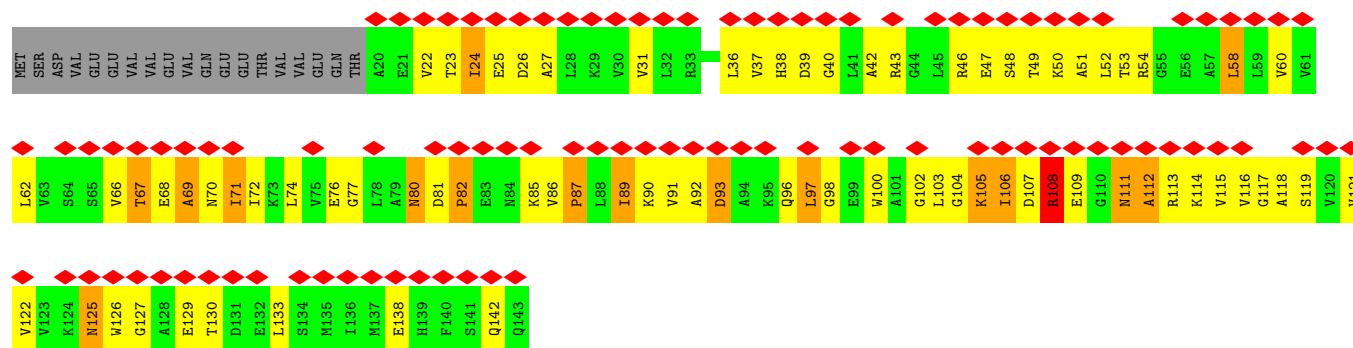
• Molecule 57: 40S ribosomal protein S10



- Molecule 58: 40S ribosomal protein S11

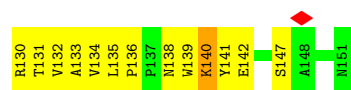


- Molecule 59: 40S ribosomal protein S12

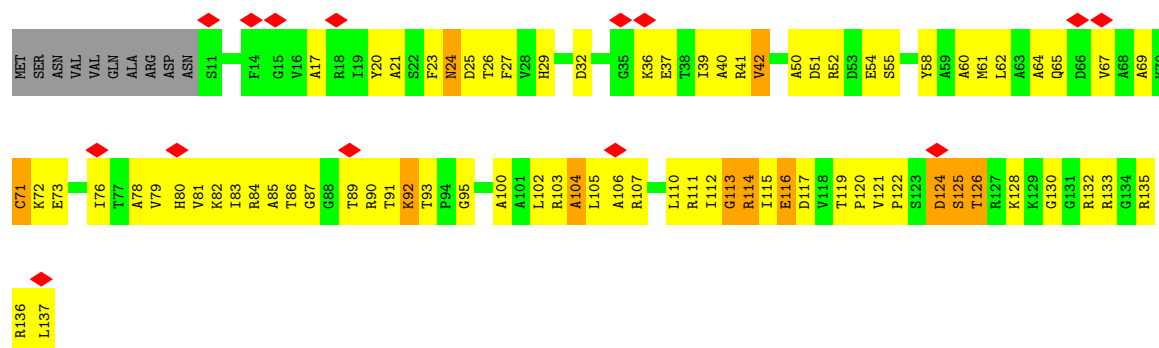


- Molecule 60: 40S ribosomal protein S13

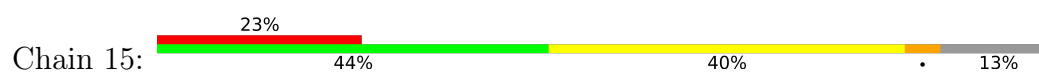




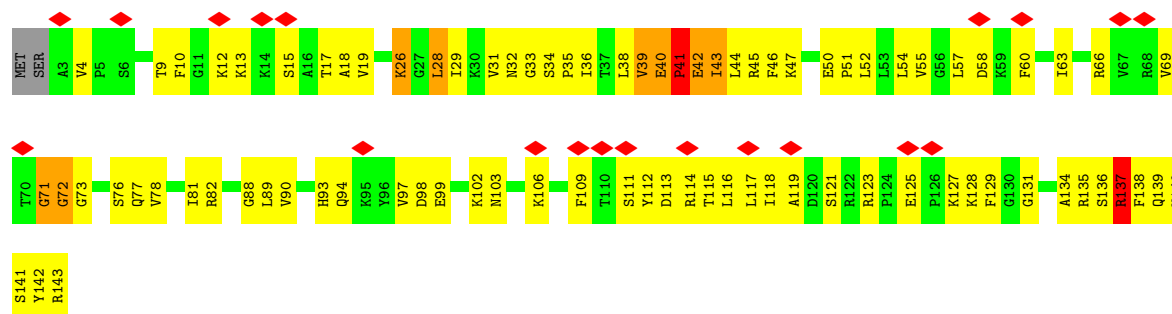
• Molecule 61: 40S ribosomal protein S14



• Molecule 62: 40S ribosomal protein S15

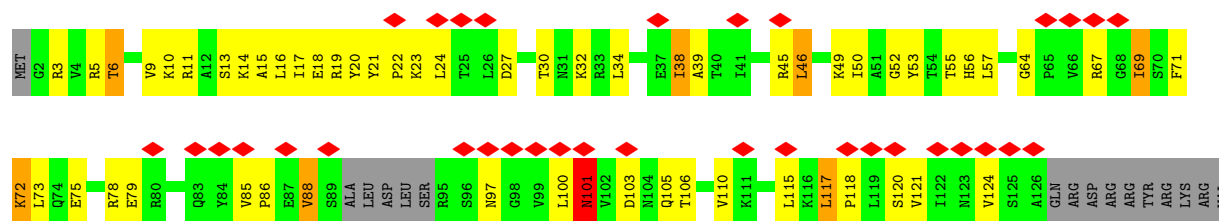


• Molecule 63: 40S ribosomal protein S16

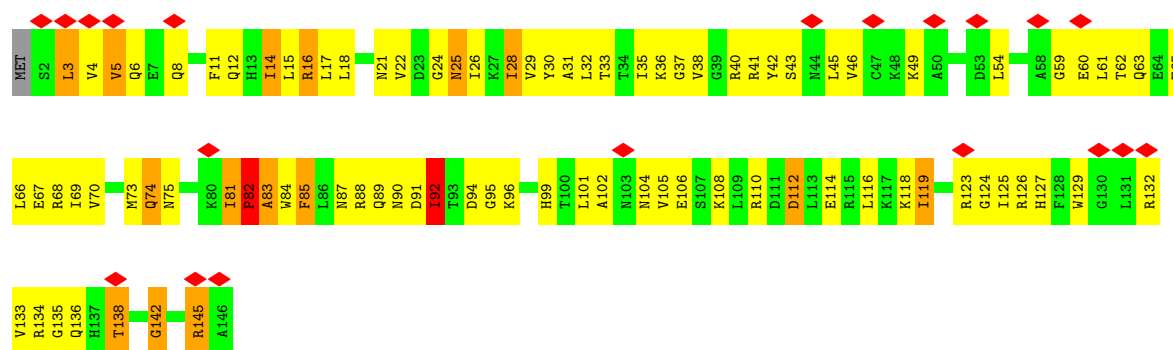


• Molecule 64: 40S ribosomal protein S17

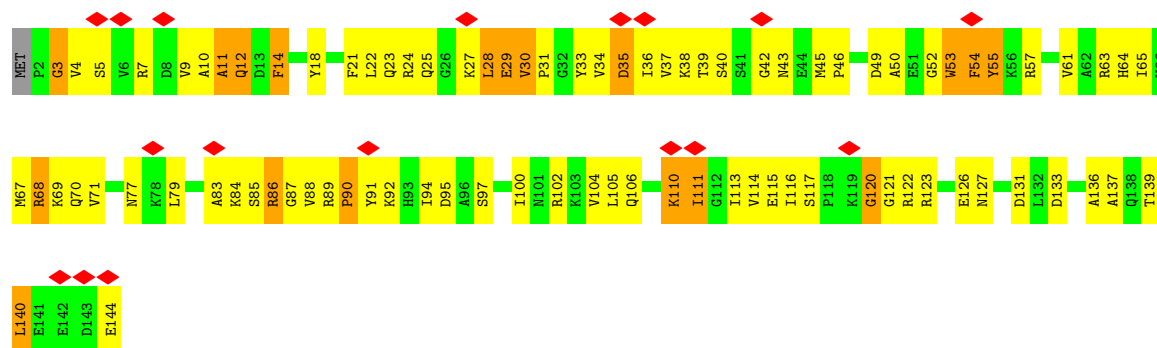




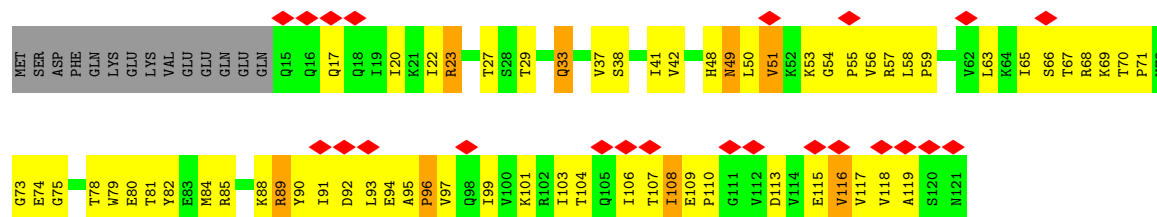
• Molecule 65: 40S ribosomal protein S18



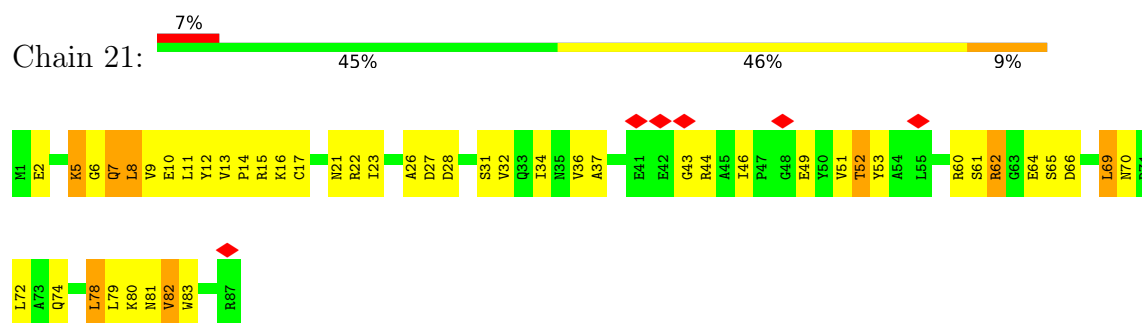
• Molecule 66: 40S ribosomal protein S19



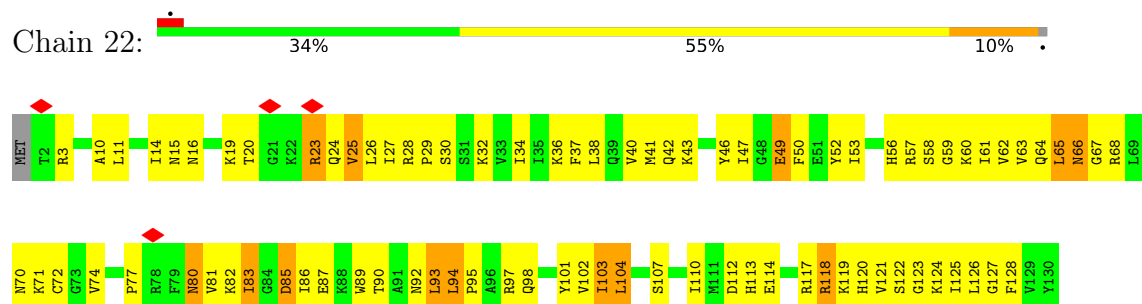
• Molecule 67: 40S ribosomal protein S20



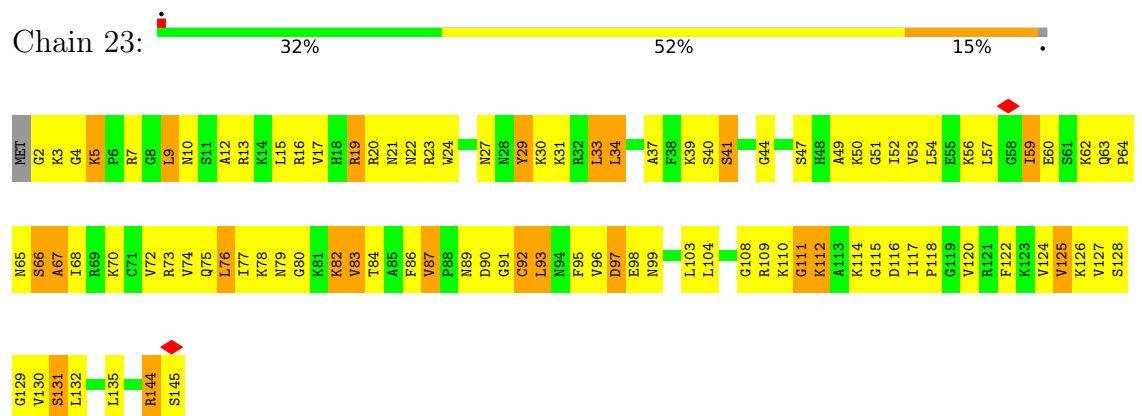
• Molecule 68: 40S ribosomal protein S21



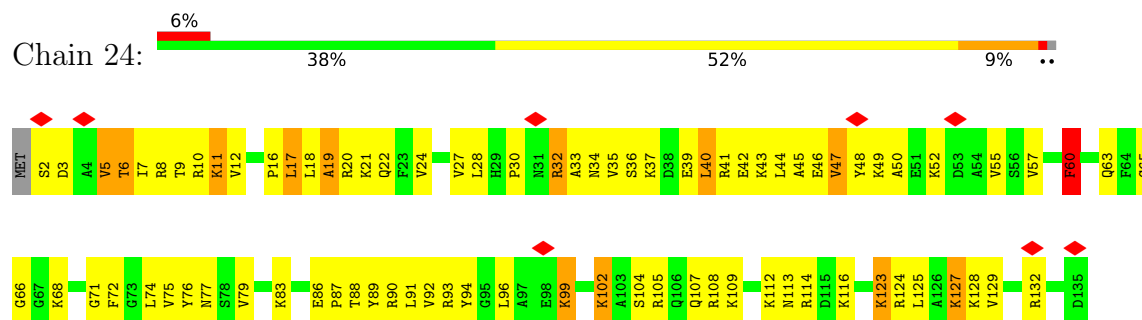
- Molecule 69: 40S ribosomal protein S22



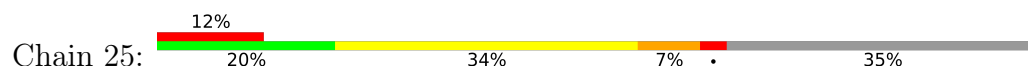
- Molecule 70: 40S ribosomal protein S23



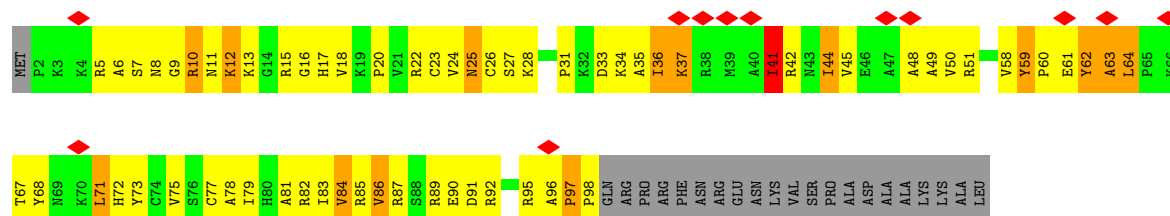
- Molecule 71: 40S ribosomal protein S24



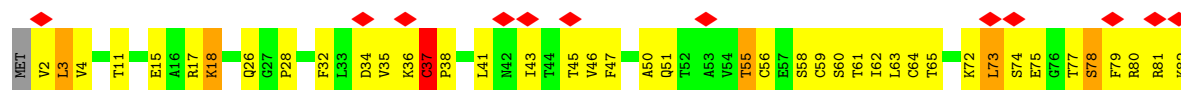
- Molecule 72: 40S ribosomal protein S25



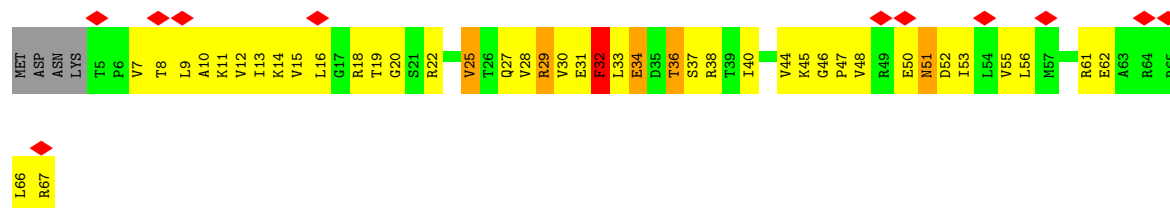
- Molecule 73: 40S ribosomal protein S26



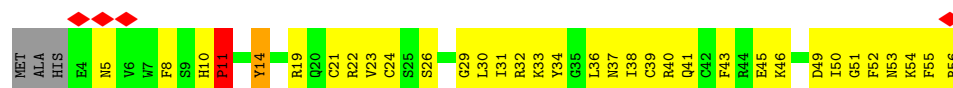
- Molecule 74: 40S ribosomal protein S27



- Molecule 75: 40S ribosomal protein S28



- Molecule 76: 40S ribosomal protein S29



- Molecule 77: 40S ribosomal protein S30



1U6940	1U6952
1U6941	CS953
A6942	CS954
A6943	1U6955
1U6944	A6956
	A6957
	CS958

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	52444	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	CTFFIND3, FREALIGN per micrograph	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	1150	Depositor
Maximum defocus (nm)	6530	Depositor
Magnification	132138	Depositor
Image detector	FEI FALCON I (4k x 4k)	Depositor
Maximum map value	4.026	Depositor
Minimum map value	-1.575	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.284	Depositor
Recommended contour level	0.815	Depositor
Map size ($\text{\AA}$)	444.99, 444.99, 444.99	wwPDB
Map dimensions	420, 420, 420	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.0595, 1.0595, 1.0595	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	2S	0.75	2/79178 (0.0%)	0.73	73/123444 (0.1%)
2	8S	0.73	0/3747	0.70	5/5832 (0.1%)
3	5S	0.73	0/2884	0.68	0/4491
4	L1	0.79	1/1634 (0.1%)	1.16	13/2195 (0.6%)
5	L2	0.68	0/1952	1.15	23/2622 (0.9%)
6	L3	0.73	0/3153	1.12	33/4239 (0.8%)
7	L4	0.76	1/2802 (0.0%)	1.23	34/3792 (0.9%)
8	L5	0.71	0/2426	1.04	16/3271 (0.5%)
9	L6	0.85	0/1261	1.17	14/1694 (0.8%)
10	L7	0.72	0/1822	1.21	17/2451 (0.7%)
11	L8	0.68	0/1850	1.19	18/2495 (0.7%)
12	L9	0.77	0/1540	1.18	17/2073 (0.8%)
13	50	0.68	0/1754	1.13	16/2350 (0.7%)
14	51	0.67	0/1375	1.08	13/1842 (0.7%)
15	53	0.73	0/1568	1.23	19/2106 (0.9%)
16	54	0.84	0/1069	1.16	12/1438 (0.8%)
17	55	0.66	0/1758	1.09	16/2354 (0.7%)
18	56	0.69	0/1586	1.27	25/2128 (1.2%)
19	57	0.77	1/1466 (0.1%)	1.26	21/1968 (1.1%)
20	58	0.74	0/1466	1.17	17/1965 (0.9%)
21	59	0.56	0/1539	1.21	19/2050 (0.9%)
22	60	0.75	0/1482	1.12	19/1990 (1.0%)
23	61	0.74	0/1301	1.15	18/1743 (1.0%)
24	62	0.66	0/812	1.02	0/1099
25	63	0.67	0/1019	1.12	9/1369 (0.7%)
26	64	0.66	0/521	1.15	7/691 (1.0%)
27	65	0.69	0/984	1.20	12/1325 (0.9%)
28	66	0.75	0/1005	1.15	8/1341 (0.6%)
29	67	0.60	0/1119	1.08	8/1497 (0.5%)
30	68	0.74	0/1205	1.21	20/1612 (1.2%)
31	69	0.62	0/474	1.21	7/629 (1.1%)
32	70	0.60	0/751	1.04	3/1008 (0.3%)
33	71	0.68	0/904	1.20	14/1213 (1.2%)
34	72	0.76	0/1041	1.12	8/1394 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	73	0.79	0/869	1.19	12/1168 (1.0%)
36	74	0.67	0/891	1.10	7/1191 (0.6%)
37	75	0.66	0/979	1.16	7/1301 (0.5%)
38	76	0.70	0/779	1.28	9/1034 (0.9%)
39	77	0.68	0/697	1.17	6/923 (0.7%)
40	78	0.68	0/619	1.02	4/826 (0.5%)
41	79	0.58	0/444	1.14	3/588 (0.5%)
42	80	0.69	0/424	1.26	7/562 (1.2%)
43	81	0.93	0/235	1.13	0/300
44	82	0.72	0/839	1.08	6/1108 (0.5%)
45	83	0.63	0/702	1.04	4/934 (0.4%)
46	1S	0.69	0/42445	0.70	34/66138 (0.1%)
47	S0	0.62	0/1653	1.08	11/2261 (0.5%)
48	S1	0.65	0/1735	0.95	5/2335 (0.2%)
49	S2	0.62	0/1665	1.13	19/2263 (0.8%)
50	S3	0.67	0/1759	1.05	11/2368 (0.5%)
51	S4	0.58	0/2110	1.09	22/2839 (0.8%)
52	S5	0.66	1/1630 (0.1%)	1.12	17/2202 (0.8%)
53	S6	0.63	0/1844	1.13	20/2464 (0.8%)
54	S7	0.67	0/1506	1.14	11/2028 (0.5%)
55	S8	0.60	0/1515	1.09	18/2021 (0.9%)
56	S9	0.51	0/1519	1.12	15/2035 (0.7%)
57	10	0.68	0/837	1.04	4/1131 (0.4%)
58	11	0.67	0/1273	1.05	10/1712 (0.6%)
59	12	0.88	0/943	1.09	3/1274 (0.2%)
60	13	0.59	0/1216	1.05	3/1638 (0.2%)
61	14	0.67	0/953	1.05	10/1279 (0.8%)
62	15	0.69	0/1012	1.08	7/1356 (0.5%)
63	16	0.65	0/1126	0.97	5/1510 (0.3%)
64	17	0.67	0/974	1.05	6/1304 (0.5%)
65	18	0.68	0/1212	1.11	9/1628 (0.6%)
66	19	0.67	0/1131	1.12	10/1517 (0.7%)
67	20	0.74	0/866	0.97	3/1169 (0.3%)
68	21	0.61	0/694	1.01	2/935 (0.2%)
69	22	0.56	0/1039	1.11	7/1395 (0.5%)
70	23	0.55	0/1140	1.07	6/1518 (0.4%)
71	24	0.62	0/1088	0.99	4/1449 (0.3%)
72	25	0.70	0/571	1.12	4/768 (0.5%)
73	26	0.60	0/782	0.97	5/1047 (0.5%)
74	27	0.66	0/621	1.04	6/838 (0.7%)
75	28	0.64	0/500	1.03	4/670 (0.6%)
76	29	0.61	0/454	0.94	1/602 (0.2%)
77	30	0.61	0/483	1.06	4/643 (0.6%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	31	0.73	0/505	1.03	3/682 (0.4%)
79	RA	0.72	0/2498	1.00	13/3398 (0.4%)
All	All	0.71	6/219225 (0.0%)	0.89	931/322063 (0.3%)

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	2S	0	108
2	8S	0	5
3	5S	0	1
6	L3	0	1
46	1S	0	45
All	All	0	160

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	L4	222	VAL	CA-CB	6.16	1.58	1.54
1	2S	490	C	O5'-C5'	5.95	1.51	1.42
4	L1	98	LYS	CA-C	5.92	1.55	1.52
1	2S	2094	C	O5'-C5'	5.53	1.51	1.42
19	57	161	ALA	CA-C	5.42	1.55	1.52

The worst 5 of 931 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
27	65	51	VAL	CA-C-N	11.27	131.37	119.76
27	65	51	VAL	C-N-CA	11.27	131.37	119.76
37	75	89	ARG	N-CA-C	-10.99	100.41	114.04
69	22	94	LEU	CA-C-N	10.60	130.42	119.19
69	22	94	LEU	C-N-CA	10.60	130.42	119.19

There are no chirality outliers.

5 of 160 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2S	107	A	Sidechain
1	2S	26	A	Sidechain

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Mol	Chain	Res	Type	Group
1	2S	40	A	Sidechain
1	2S	59	G	Sidechain
1	2S	93	C	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	2S	70742	0	35551	2330	0
2	8S	3354	0	1695	110	0
3	5S	2580	0	1304	88	0
4	L1	1609	0	1701	134	0
5	L2	1918	0	1987	196	0
6	L3	3082	0	3165	282	0
7	L4	2750	0	2863	235	0
8	L5	2376	0	2325	137	0
9	L6	1240	0	1326	102	0
10	L7	1785	0	1862	143	0
11	L8	1818	0	1908	136	0
12	L9	1519	0	1587	124	0
13	50	1718	0	1754	109	0
14	51	1354	0	1383	104	0
15	53	1543	0	1608	139	0
16	54	1054	0	1149	72	0
17	55	1721	0	1779	164	0
18	56	1556	0	1659	125	0
19	57	1443	0	1485	120	0
20	58	1442	0	1543	132	0
21	59	1522	0	1617	105	0
22	60	1446	0	1487	129	0
23	61	1277	0	1323	113	0
24	62	796	0	812	48	0
25	63	1004	0	1048	100	0
26	64	509	0	537	38	0
27	65	969	0	1036	84	0
28	66	994	0	1081	74	0
29	67	1093	0	1155	82	0
30	68	1174	0	1215	112	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	69	463	0	491	32	0
32	70	743	0	797	52	0
33	71	890	0	938	66	0
34	72	1020	0	1090	77	0
35	73	851	0	880	78	0
36	74	881	0	949	77	0
37	75	970	0	1078	70	0
38	76	772	0	849	75	0
39	77	682	0	687	60	0
40	78	613	0	682	37	0
41	79	437	0	475	29	0
42	80	418	0	459	33	0
43	81	234	0	284	24	0
44	82	827	0	901	65	0
45	83	695	0	738	68	0
46	1S	37949	0	19093	1250	0
47	S0	1612	0	1623	103	0
48	S1	1709	0	1784	149	0
49	S2	1635	0	1723	133	0
50	S3	1734	0	1817	106	0
51	S4	2069	0	2154	158	0
52	S5	1610	0	1675	133	0
53	S6	1820	0	1918	127	0
54	S7	1481	0	1572	143	0
55	S8	1490	0	1525	128	0
56	S9	1494	0	1573	121	0
57	10	817	0	804	78	0
58	11	1245	0	1314	110	0
59	12	935	0	975	69	0
60	13	1193	0	1255	114	0
61	14	942	0	979	86	0
62	15	991	0	1035	62	0
63	16	1106	0	1166	82	0
64	17	965	0	1026	64	0
65	18	1193	0	1222	94	0
66	19	1113	0	1124	99	0
67	20	856	0	917	73	0
68	21	685	0	672	44	0
69	22	1022	0	1060	116	0
70	23	1122	0	1196	122	0
71	24	1074	0	1132	83	0
72	25	563	0	603	50	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	26	769	0	818	77	0
74	27	611	0	633	32	0
75	28	498	0	535	46	0
76	29	444	0	436	36	0
77	30	475	0	525	43	0
78	31	498	0	441	25	0
79	RA	2445	0	2401	114	0
80	IR	198	0	0	0	0
All	All	204247	0	150969	9754	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 28.

The worst 5 of 9754 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
50:S3:209:ILE:HG22	64:17:38:ILE:HG13	1.29	1.15
46:1S:1701:A:H3'	46:1S:1702:A:H5''	1.25	1.14
6:L3:86:VAL:HA	6:L3:162:VAL:HG12	1.21	1.13
1:2S:632:G:H5''	18:56:94:ARG:HD2	1.26	1.13
9:L6:43:LEU:HD13	35:73:103:TYR:HB3	1.31	1.13

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	L1	202/217 (93%)	137 (68%)	50 (25%)	15 (7%)	1	10
5	L2	250/254 (98%)	196 (78%)	44 (18%)	10 (4%)	2	18
6	L3	384/387 (99%)	322 (84%)	51 (13%)	11 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	L4	359/362 (99%)	284 (79%)	48 (13%)	27 (8%)	1	10
8	L5	294/297 (99%)	244 (83%)	40 (14%)	10 (3%)	3	21
9	L6	152/176 (86%)	131 (86%)	16 (10%)	5 (3%)	3	21
10	L7	220/244 (90%)	192 (87%)	19 (9%)	9 (4%)	2	17
11	L8	231/256 (90%)	184 (80%)	38 (16%)	9 (4%)	2	18
12	L9	189/191 (99%)	153 (81%)	30 (16%)	6 (3%)	3	21
13	50	207/221 (94%)	166 (80%)	36 (17%)	5 (2%)	4	27
14	51	167/174 (96%)	130 (78%)	29 (17%)	8 (5%)	2	16
15	53	191/199 (96%)	150 (78%)	35 (18%)	6 (3%)	3	22
16	54	134/138 (97%)	114 (85%)	17 (13%)	3 (2%)	5	29
17	55	201/204 (98%)	156 (78%)	36 (18%)	9 (4%)	2	16
18	56	195/199 (98%)	177 (91%)	14 (7%)	4 (2%)	5	29
19	57	181/184 (98%)	143 (79%)	34 (19%)	4 (2%)	5	29
20	58	183/186 (98%)	153 (84%)	23 (13%)	7 (4%)	2	19
21	59	186/189 (98%)	168 (90%)	14 (8%)	4 (2%)	5	29
22	60	170/172 (99%)	140 (82%)	25 (15%)	5 (3%)	3	23
23	61	157/160 (98%)	128 (82%)	19 (12%)	10 (6%)	1	12
24	62	98/121 (81%)	76 (78%)	18 (18%)	4 (4%)	2	17
25	63	134/137 (98%)	105 (78%)	24 (18%)	5 (4%)	2	19
26	64	59/155 (38%)	43 (73%)	13 (22%)	3 (5%)	1	15
27	65	119/142 (84%)	97 (82%)	17 (14%)	5 (4%)	2	17
28	66	124/127 (98%)	104 (84%)	16 (13%)	4 (3%)	3	21
29	67	133/136 (98%)	110 (83%)	20 (15%)	3 (2%)	5	28
30	68	146/149 (98%)	117 (80%)	26 (18%)	3 (2%)	5	29
31	69	56/59 (95%)	43 (77%)	11 (20%)	2 (4%)	2	20
32	70	95/105 (90%)	89 (94%)	4 (4%)	2 (2%)	5	29
33	71	107/113 (95%)	91 (85%)	14 (13%)	2 (2%)	6	32
34	72	125/130 (96%)	109 (87%)	15 (12%)	1 (1%)	16	54
35	73	104/107 (97%)	79 (76%)	17 (16%)	8 (8%)	1	9
36	74	110/121 (91%)	88 (80%)	18 (16%)	4 (4%)	2	20
37	75	117/120 (98%)	107 (92%)	6 (5%)	4 (3%)	3	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	76	97/100 (97%)	76 (78%)	13 (13%)	8 (8%)	0	9
39	77	85/88 (97%)	67 (79%)	16 (19%)	2 (2%)	4	27
40	78	75/78 (96%)	64 (85%)	7 (9%)	4 (5%)	1	14
41	79	48/51 (94%)	39 (81%)	8 (17%)	1 (2%)	5	29
42	80	50/128 (39%)	42 (84%)	6 (12%)	2 (4%)	2	18
43	81	23/25 (92%)	21 (91%)	1 (4%)	1 (4%)	2	17
44	82	101/106 (95%)	79 (78%)	18 (18%)	4 (4%)	2	18
45	83	89/92 (97%)	75 (84%)	13 (15%)	1 (1%)	11	46
47	S0	204/252 (81%)	163 (80%)	29 (14%)	12 (6%)	1	13
48	S1	212/255 (83%)	154 (73%)	45 (21%)	13 (6%)	1	12
49	S2	215/254 (85%)	177 (82%)	30 (14%)	8 (4%)	2	19
50	S3	221/240 (92%)	184 (83%)	24 (11%)	13 (6%)	1	13
51	S4	258/261 (99%)	203 (79%)	45 (17%)	10 (4%)	2	18
52	S5	204/225 (91%)	165 (81%)	32 (16%)	7 (3%)	3	21
53	S6	224/236 (95%)	192 (86%)	26 (12%)	6 (3%)	4	25
54	S7	182/190 (96%)	137 (75%)	34 (19%)	11 (6%)	1	13
55	S8	184/200 (92%)	147 (80%)	28 (15%)	9 (5%)	1	15
56	S9	183/197 (93%)	153 (84%)	21 (12%)	9 (5%)	1	15
57	10	94/105 (90%)	74 (79%)	13 (14%)	7 (7%)	1	10
58	11	153/156 (98%)	107 (70%)	37 (24%)	9 (6%)	1	13
59	12	122/143 (85%)	76 (62%)	29 (24%)	17 (14%)	0	3
60	13	148/151 (98%)	125 (84%)	20 (14%)	3 (2%)	6	31
61	14	125/137 (91%)	96 (77%)	22 (18%)	7 (6%)	1	14
62	15	122/142 (86%)	101 (83%)	16 (13%)	5 (4%)	2	17
63	16	139/143 (97%)	112 (81%)	20 (14%)	7 (5%)	1	15
64	17	116/136 (85%)	92 (79%)	20 (17%)	4 (3%)	3	21
65	18	143/146 (98%)	120 (84%)	16 (11%)	7 (5%)	1	15
66	19	141/144 (98%)	118 (84%)	15 (11%)	8 (6%)	1	14
67	20	105/121 (87%)	85 (81%)	14 (13%)	6 (6%)	1	14
68	21	85/87 (98%)	68 (80%)	13 (15%)	4 (5%)	2	16
69	22	127/130 (98%)	106 (84%)	19 (15%)	2 (2%)	7	37

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	23	142/145 (98%)	108 (76%)	24 (17%)	10 (7%)	1	11
71	24	132/135 (98%)	106 (80%)	20 (15%)	6 (4%)	2	16
72	25	68/108 (63%)	45 (66%)	14 (21%)	9 (13%)	0	4
73	26	95/119 (80%)	64 (67%)	19 (20%)	12 (13%)	0	4
74	27	79/82 (96%)	58 (73%)	15 (19%)	6 (8%)	1	10
75	28	61/67 (91%)	50 (82%)	9 (15%)	2 (3%)	3	21
76	29	51/56 (91%)	44 (86%)	5 (10%)	2 (4%)	2	18
77	30	58/63 (92%)	47 (81%)	8 (14%)	3 (5%)	1	14
78	31	69/152 (45%)	37 (54%)	20 (29%)	12 (17%)	0	2
79	RA	316/319 (99%)	252 (80%)	53 (17%)	11 (4%)	3	20
All	All	11126/12097 (92%)	8955 (80%)	1674 (15%)	497 (4%)	3	16

5 of 497 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L1	15	GLU
4	L1	20	SER
4	L1	23	THR
4	L1	136	THR
4	L1	199	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
4	L1	185/198 (93%)	166 (90%)	19 (10%)	7	23
5	L2	194/196 (99%)	182 (94%)	12 (6%)	16	38
6	L3	322/323 (100%)	291 (90%)	31 (10%)	8	25
7	L4	288/289 (100%)	257 (89%)	31 (11%)	6	21
8	L5	244/245 (100%)	226 (93%)	18 (7%)	13	33
9	L6	134/153 (88%)	126 (94%)	8 (6%)	17	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	L7	186/205 (91%)	173 (93%)	13 (7%)	14	35
11	L8	191/208 (92%)	178 (93%)	13 (7%)	14	36
12	L9	171/171 (100%)	154 (90%)	17 (10%)	7	24
13	50	180/187 (96%)	167 (93%)	13 (7%)	13	35
14	51	147/150 (98%)	133 (90%)	14 (10%)	8	25
15	53	154/159 (97%)	138 (90%)	16 (10%)	7	22
16	54	107/109 (98%)	104 (97%)	3 (3%)	38	59
17	55	175/176 (99%)	161 (92%)	14 (8%)	11	31
18	56	160/162 (99%)	150 (94%)	10 (6%)	16	37
19	57	145/146 (99%)	133 (92%)	12 (8%)	10	30
20	58	150/151 (99%)	140 (93%)	10 (7%)	15	36
21	59	153/154 (99%)	147 (96%)	6 (4%)	28	49
22	60	156/156 (100%)	143 (92%)	13 (8%)	10	30
23	61	136/137 (99%)	128 (94%)	8 (6%)	18	39
24	62	87/107 (81%)	82 (94%)	5 (6%)	18	40
25	63	104/105 (99%)	93 (89%)	11 (11%)	6	21
26	64	54/129 (42%)	51 (94%)	3 (6%)	19	40
27	65	105/118 (89%)	91 (87%)	14 (13%)	4	14
28	66	109/110 (99%)	101 (93%)	8 (7%)	13	34
29	67	115/116 (99%)	110 (96%)	5 (4%)	26	47
30	68	118/119 (99%)	108 (92%)	10 (8%)	10	29
31	69	46/47 (98%)	41 (89%)	5 (11%)	6	21
32	70	81/88 (92%)	77 (95%)	4 (5%)	22	43
33	71	96/97 (99%)	86 (90%)	10 (10%)	7	22
34	72	109/111 (98%)	102 (94%)	7 (6%)	16	37
35	73	90/91 (99%)	82 (91%)	8 (9%)	9	28
36	74	95/103 (92%)	89 (94%)	6 (6%)	16	37
37	75	104/105 (99%)	99 (95%)	5 (5%)	23	44
38	76	81/82 (99%)	71 (88%)	10 (12%)	4	17
39	77	70/71 (99%)	65 (93%)	5 (7%)	13	35
40	78	68/69 (99%)	65 (96%)	3 (4%)	25	47

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	79	45/46 (98%)	41 (91%)	4 (9%)	9	28
42	80	47/116 (40%)	43 (92%)	4 (8%)	10	29
43	81	23/23 (100%)	19 (83%)	4 (17%)	2	9
44	82	88/91 (97%)	80 (91%)	8 (9%)	9	27
45	83	71/72 (99%)	69 (97%)	2 (3%)	38	59
47	S0	173/210 (82%)	159 (92%)	14 (8%)	11	31
48	S1	191/224 (85%)	174 (91%)	17 (9%)	9	28
49	S2	176/205 (86%)	167 (95%)	9 (5%)	21	42
50	S3	182/195 (93%)	173 (95%)	9 (5%)	22	43
51	S4	221/222 (100%)	203 (92%)	18 (8%)	11	31
52	S5	173/191 (91%)	161 (93%)	12 (7%)	14	36
53	S6	193/201 (96%)	180 (93%)	13 (7%)	15	36
54	S7	165/170 (97%)	160 (97%)	5 (3%)	36	57
55	S8	150/161 (93%)	143 (95%)	7 (5%)	23	44
56	S9	158/166 (95%)	145 (92%)	13 (8%)	10	31
57	10	89/98 (91%)	79 (89%)	10 (11%)	6	19
58	11	136/137 (99%)	124 (91%)	12 (9%)	9	28
59	12	100/119 (84%)	86 (86%)	14 (14%)	3	13
60	13	127/128 (99%)	116 (91%)	11 (9%)	9	29
61	14	96/105 (91%)	91 (95%)	5 (5%)	21	42
62	15	104/118 (88%)	101 (97%)	3 (3%)	37	58
63	16	117/119 (98%)	106 (91%)	11 (9%)	8	26
64	17	109/124 (88%)	101 (93%)	8 (7%)	13	34
65	18	128/129 (99%)	113 (88%)	15 (12%)	5	18
66	19	115/116 (99%)	111 (96%)	4 (4%)	32	53
67	20	100/114 (88%)	94 (94%)	6 (6%)	17	39
68	21	74/74 (100%)	66 (89%)	8 (11%)	6	21
69	22	110/111 (99%)	101 (92%)	9 (8%)	10	31
70	23	119/120 (99%)	110 (92%)	9 (8%)	12	33
71	24	112/113 (99%)	104 (93%)	8 (7%)	13	35
72	25	61/89 (68%)	54 (88%)	7 (12%)	5	18

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	26	83/101 (82%)	76 (92%)	7 (8%)	10	30
74	27	70/71 (99%)	68 (97%)	2 (3%)	37	58
75	28	56/60 (93%)	50 (89%)	6 (11%)	6	21
76	29	47/49 (96%)	44 (94%)	3 (6%)	16	37
77	30	51/54 (94%)	45 (88%)	6 (12%)	5	18
78	31	43/135 (32%)	39 (91%)	4 (9%)	8	26
79	RA	261/262 (100%)	239 (92%)	22 (8%)	10	30
All	All	9474/10182 (93%)	8745 (92%)	729 (8%)	14	32

5 of 729 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
50	S3	7	LYS
59	12	116	VAL
51	S4	44	LEU
50	S3	4	LEU
55	S8	8	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 352 such sidechains are listed below:

Mol	Chain	Res	Type
52	S5	128	ASN
63	16	139	GLN
53	S6	185	GLN
57	10	29	GLN
65	18	127	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2S	3304/3395 (97%)	554 (16%)	30 (0%)
2	8S	157/158 (99%)	27 (17%)	1 (0%)
3	5S	120/121 (99%)	12 (10%)	0
46	1S	1779/1798 (98%)	346 (19%)	19 (1%)
80	IR	0/201	-	-
All	All	5360/5673 (94%)	939 (17%)	50 (0%)

5 of 939 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2S	13	A
1	2S	14	U
1	2S	26	A
1	2S	40	A
1	2S	43	A

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	2S	3351	U
46	1S	497	G
46	1S	1761	U
1	2S	3353	G
46	1S	139	C

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](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

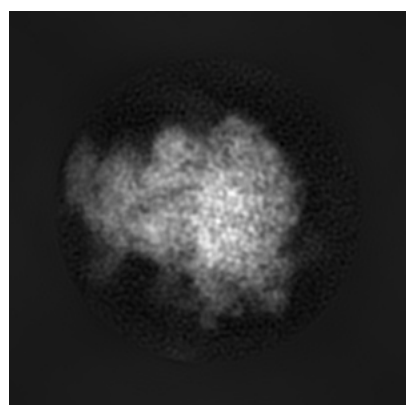
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5942. These allow visual inspection of the internal detail of the map and identification of artifacts.

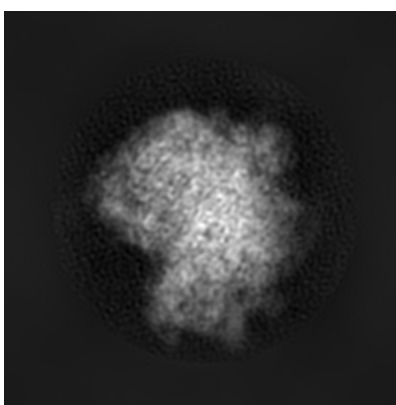
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

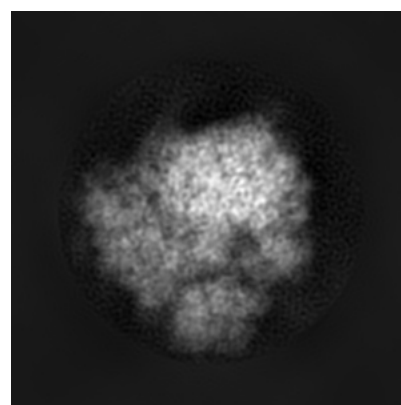
6.1.1 Primary map



X



Y

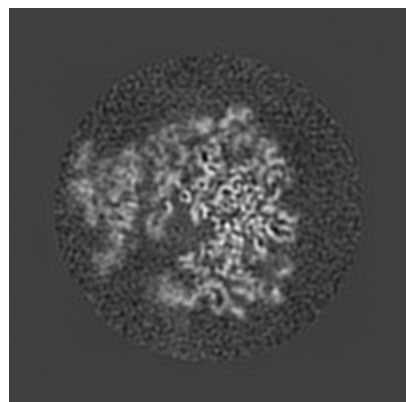


Z

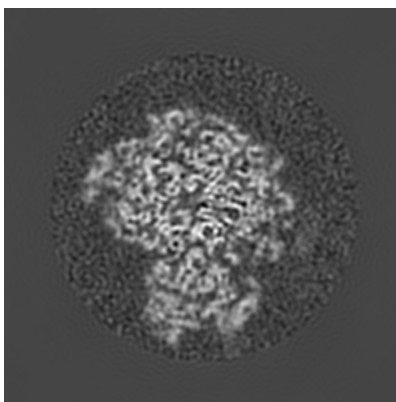
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

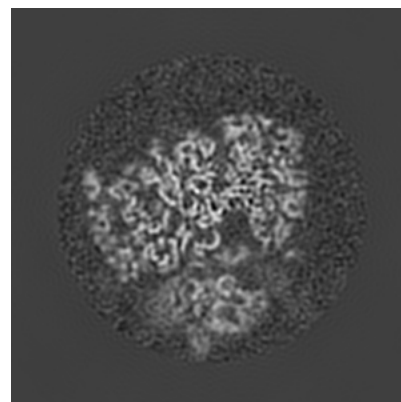
6.2.1 Primary map



X Index: 210



Y Index: 210

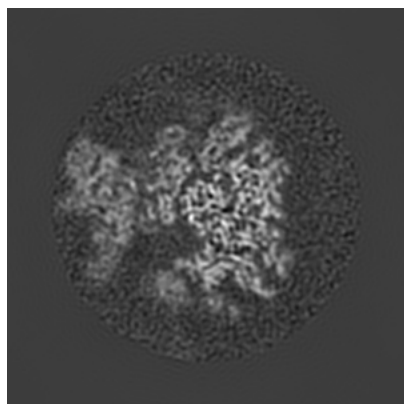


Z Index: 210

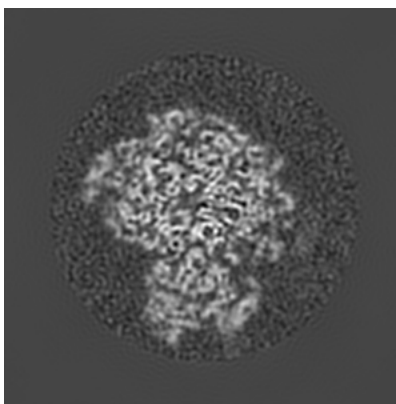
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

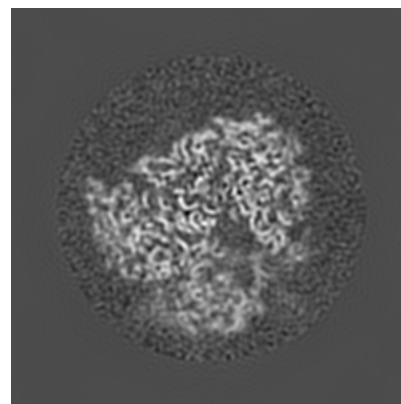
6.3.1 Primary map



X Index: 200



Y Index: 210

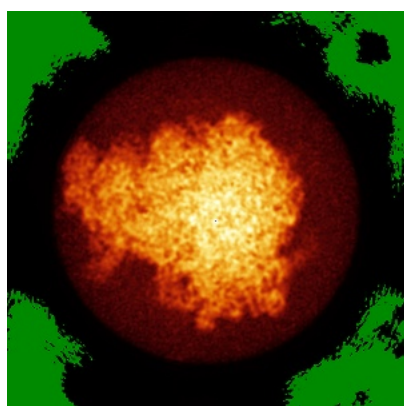


Z Index: 203

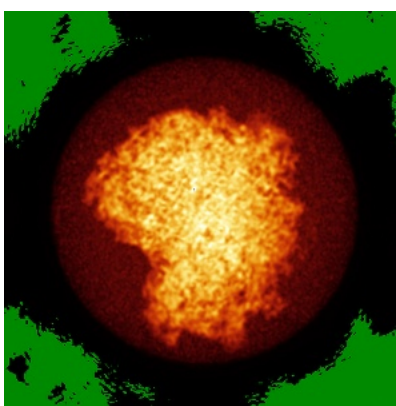
The images above show the largest variance slices of the map in three orthogonal directions.

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

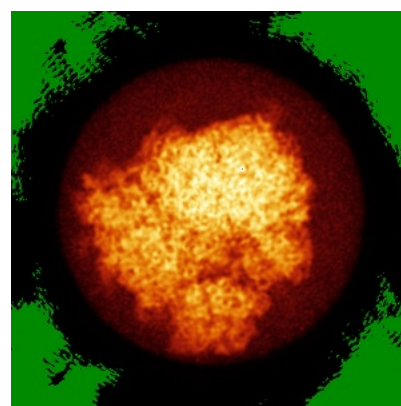
6.4.1 Primary map



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 0.815. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

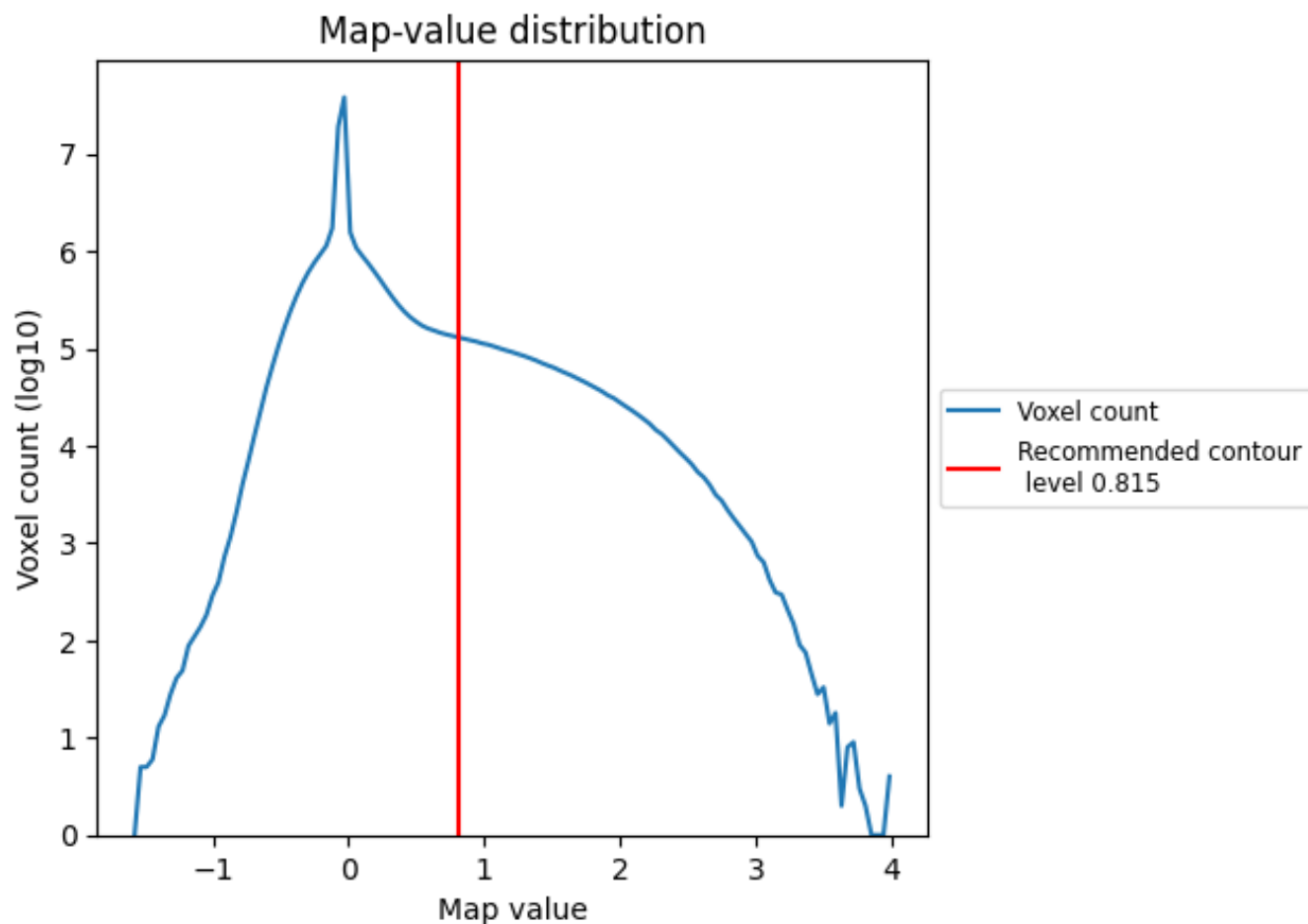
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

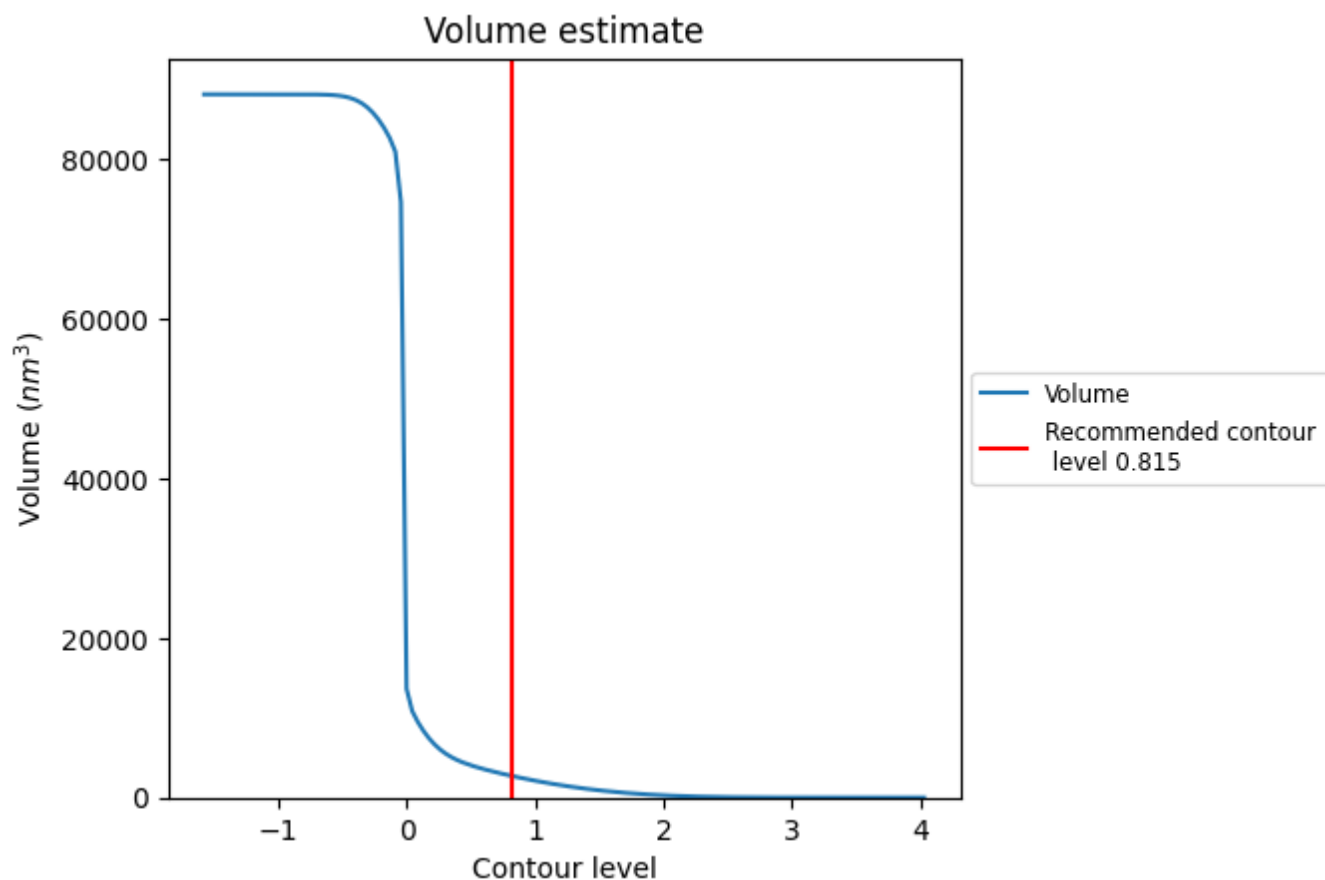
This section contains the results of statistical analysis of the map.

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.

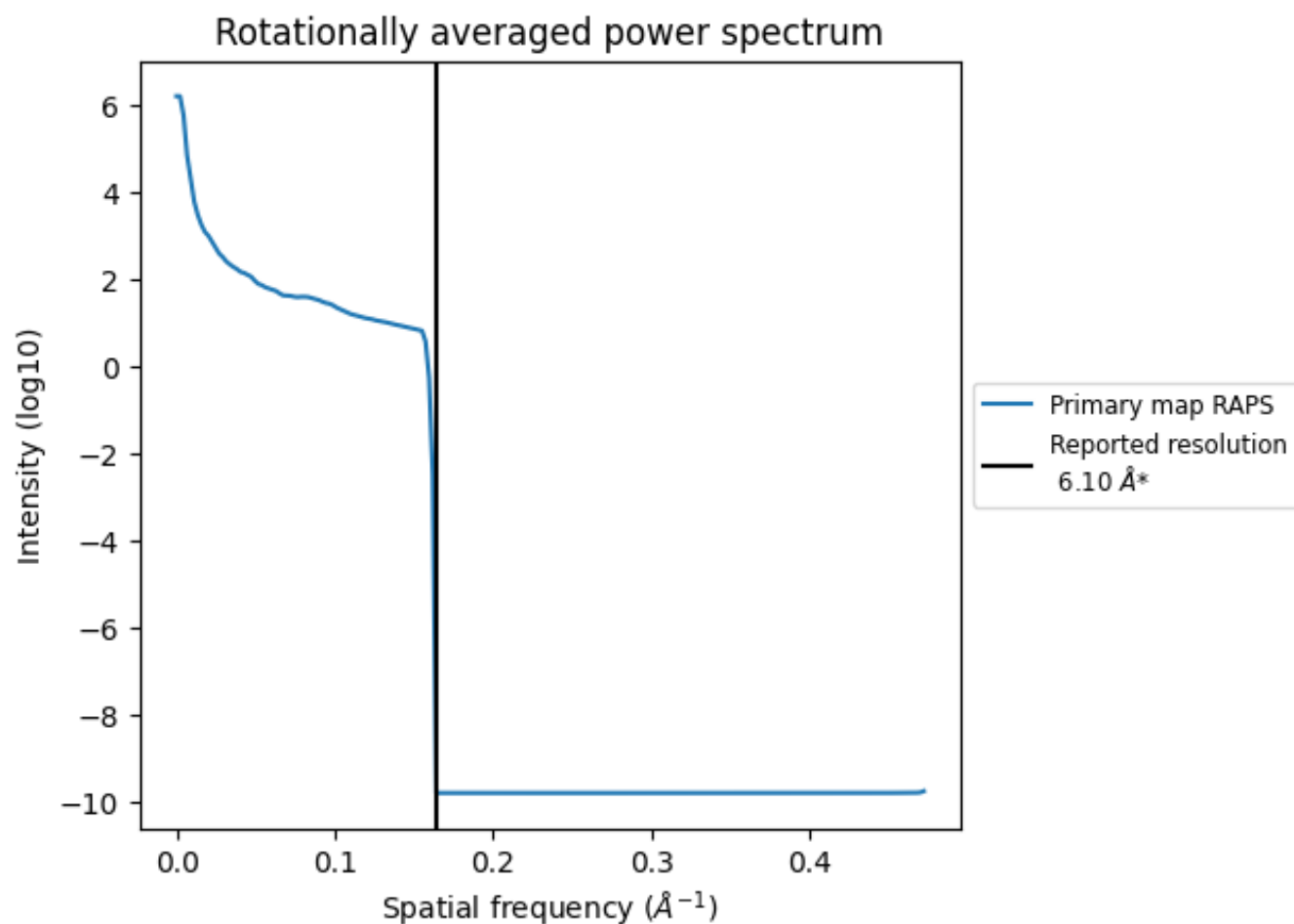
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2726 nm³; this corresponds to an approximate mass of 2462 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 0.164 Å⁻¹

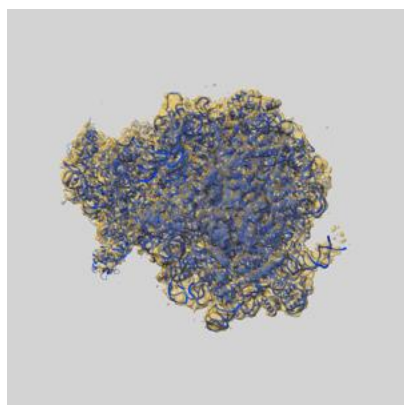
8 Fourier-Shell correlation

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

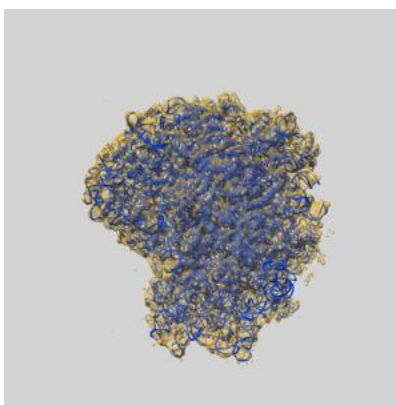
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5942 and PDB model 3J6X. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

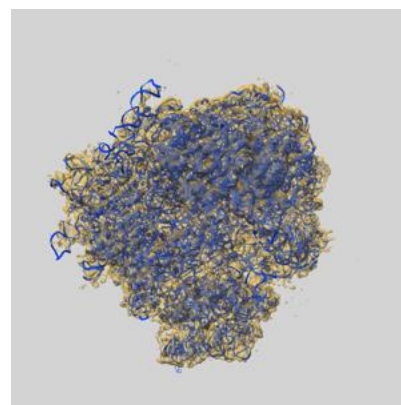
9.1 Map-model overlay [i](#)



X



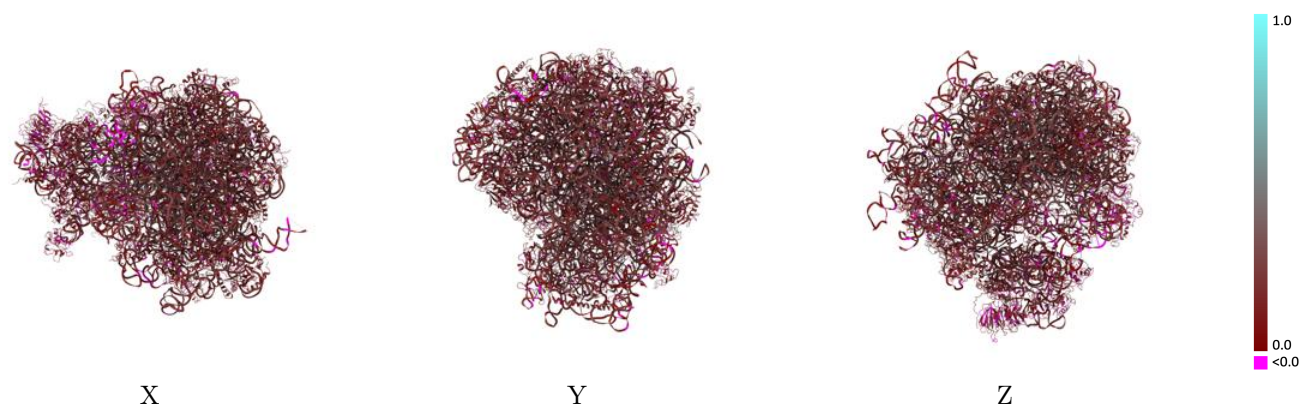
Y



Z

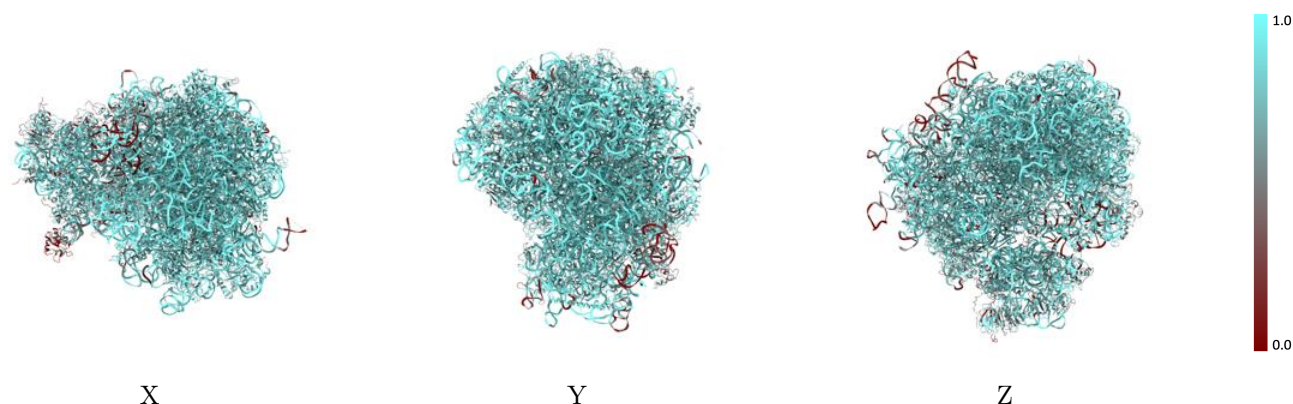
The images above show the 3D surface view of the map at the recommended contour level 0.815 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



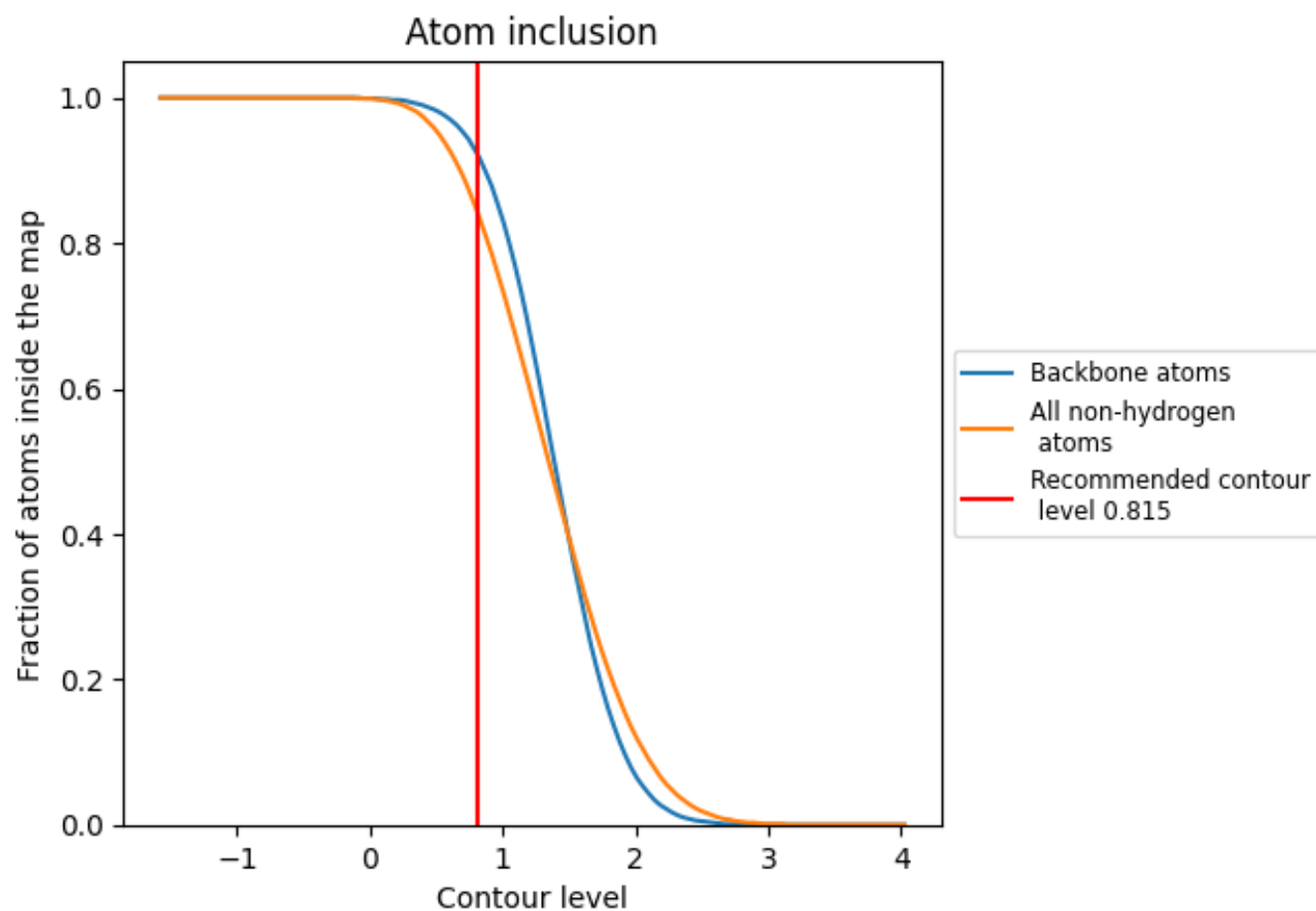
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.815).

9.4 Atom inclusion [i](#)



At the recommended contour level, 92% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.815) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8410	 0.2030
10	 0.6850	 0.1560
11	 0.7110	 0.1900
12	 0.1720	 0.1050
13	 0.7290	 0.1890
14	 0.6900	 0.1560
15	 0.5990	 0.1550
16	 0.6800	 0.1420
17	 0.5650	 0.1670
18	 0.6390	 0.1410
19	 0.7190	 0.1420
1S	 0.9170	 0.2170
20	 0.6010	 0.1460
21	 0.6900	 0.1880
22	 0.7490	 0.1760
23	 0.7840	 0.1960
24	 0.7340	 0.1600
25	 0.6910	 0.1490
26	 0.6810	 0.1960
27	 0.6810	 0.1870
28	 0.6530	 0.1710
29	 0.7410	 0.1490
2S	 0.9370	 0.2340
30	 0.7320	 0.1820
31	 0.2360	 0.1600
50	 0.7930	 0.1840
51	 0.7490	 0.1620
53	 0.7740	 0.1760
54	 0.7550	 0.1750
55	 0.7720	 0.1580
56	 0.7810	 0.1680
57	 0.7540	 0.1820
58	 0.7680	 0.1800
59	 0.7280	 0.1860
5S	 0.9820	 0.2240



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Chain	Atom inclusion	Q-score
60	 0.7650	 0.1710
61	 0.7720	 0.1890
62	 0.7560	 0.1790
63	 0.7800	 0.2000
64	 0.7650	 0.1770
65	 0.7330	 0.1950
66	 0.7960	 0.1830
67	 0.7170	 0.1840
68	 0.7920	 0.1820
69	 0.7700	 0.1990
70	 0.7320	 0.1960
71	 0.7710	 0.1830
72	 0.7920	 0.2050
73	 0.8160	 0.1700
74	 0.7410	 0.1700
75	 0.7390	 0.1720
76	 0.7720	 0.1660
77	 0.8190	 0.1610
78	 0.6200	 0.1860
79	 0.7640	 0.2040
80	 0.7300	 0.1800
81	 0.0380	 0.0060
82	 0.7970	 0.1930
83	 0.7790	 0.1850
8S	 0.9670	 0.2440
IR	 0.5200	 0.1120
L1	 0.5570	 0.1210
L2	 0.8000	 0.1880
L3	 0.7920	 0.1880
L4	 0.7900	 0.1810
L5	 0.7180	 0.1590
L6	 0.7630	 0.1810
L7	 0.7870	 0.1770
L8	 0.7360	 0.1740
L9	 0.7310	 0.1850
RA	 0.6280	 0.1270
S0	 0.6600	 0.1790
S1	 0.6160	 0.1710
S2	 0.7750	 0.1930
S3	 0.7050	 0.1740
S4	 0.7650	 0.1820
S5	 0.6720	 0.1530

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Chain	Atom inclusion	Q-score
S6	 0.7480	 0.1610
S7	 0.5990	 0.1640
S8	 0.7810	 0.1670
S9	 0.7430	 0.1740