



wwPDB EM Validation Summary Report ⓘ

Mar 25, 2026 – 10:15 AM UTC

PDB ID : 3J6Y / pdb_00003j6y
EMDB ID : EMD-5943
Title : S. cerevisiae 80S ribosome bound with Taura syndrome virus (TSV) IRES, 2 degree rotation (Class I)
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 : 3U5B, 3U5E, 3U5C, 3U5D

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:

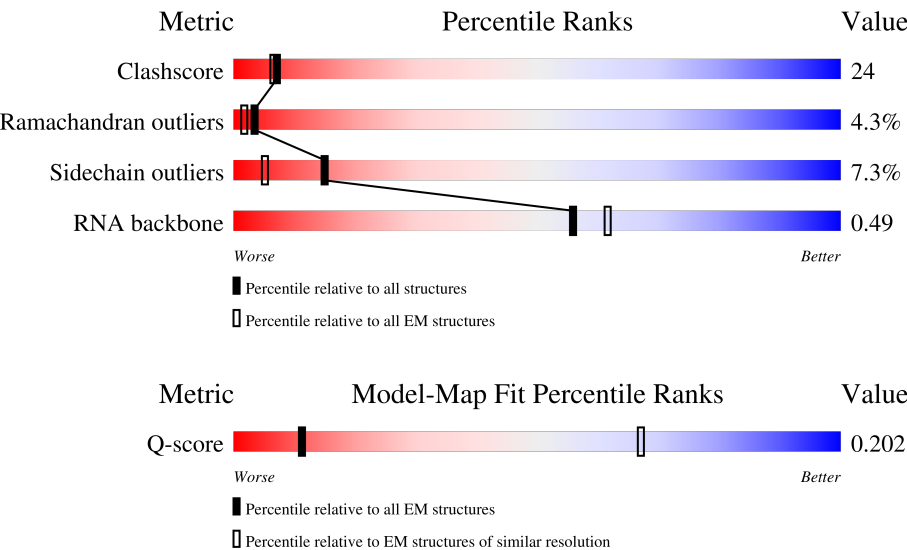
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & 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.



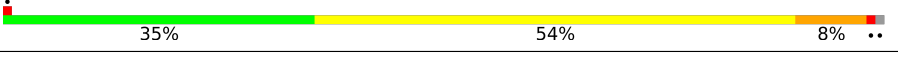
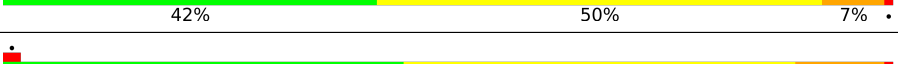
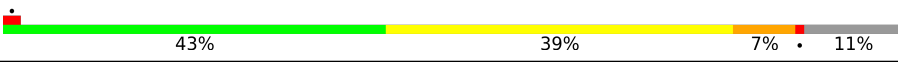
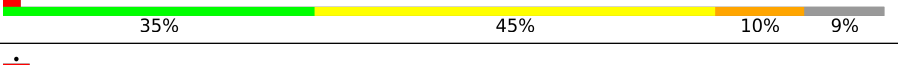
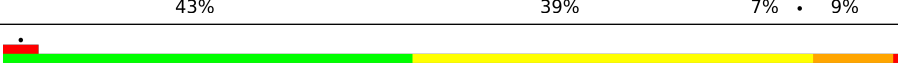
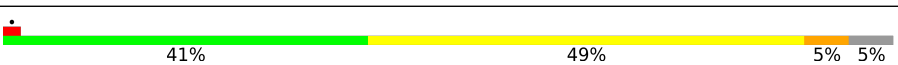
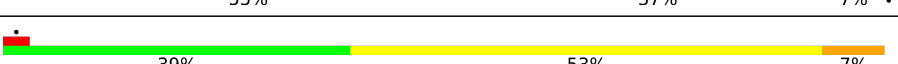
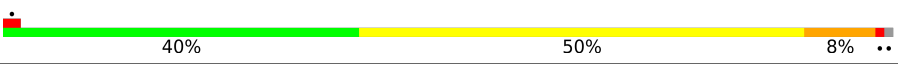
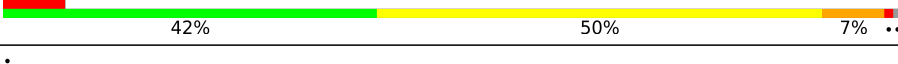
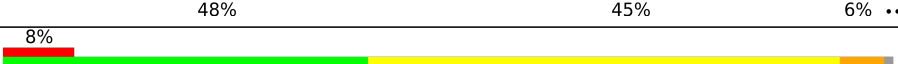
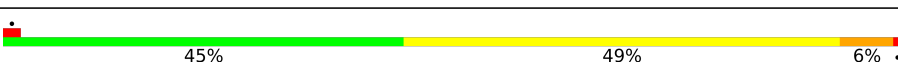
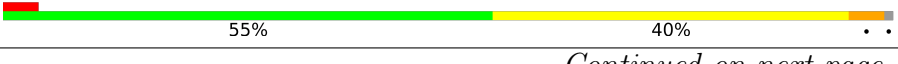
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	531 (5.60 - 6.60)

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	34%52%11% . .
2	8S	158	33%54%9% .
3	5S	121	37%58%5%

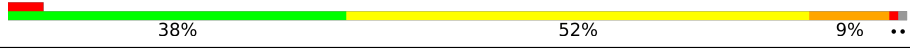
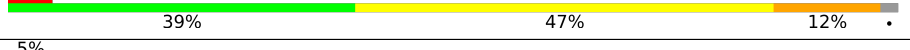
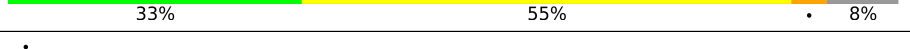
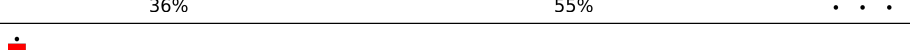
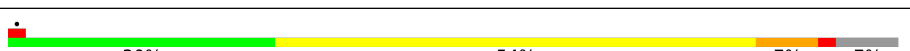
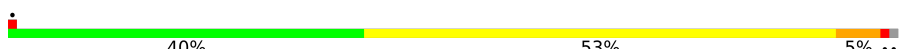
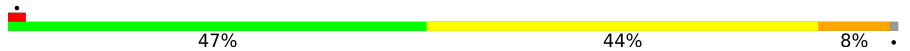
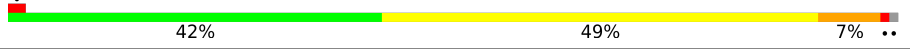
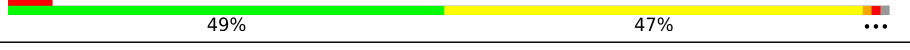
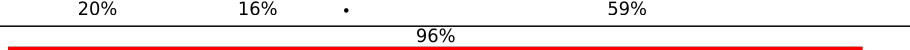
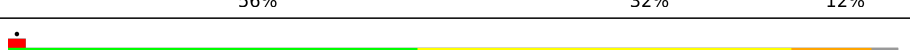
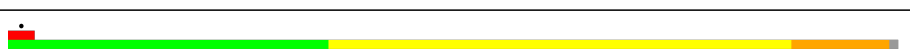
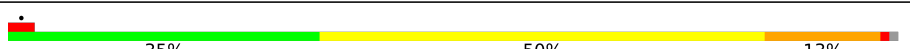
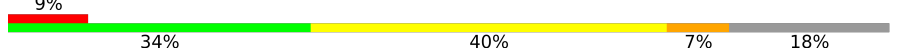
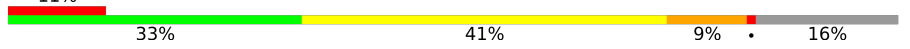
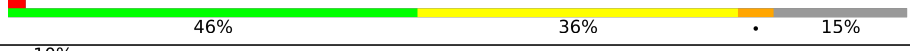
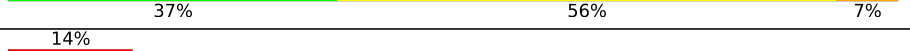
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Mol	Chain	Length	Quality of chain
4	L1	217	
5	L2	254	
6	L3	387	
7	L4	362	
8	L5	297	
9	L6	176	
10	L7	244	
11	L8	256	
12	L9	191	
13	50	221	
14	51	174	
15	53	199	
16	54	138	
17	55	204	
18	56	199	
19	57	184	
20	58	186	
21	59	189	
22	60	172	
23	61	160	
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	21% 47% 50%
80	IR	201	35% 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	0	0
			1522	935	326	261		

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

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

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

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

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

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

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

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

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

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

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

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

- 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.

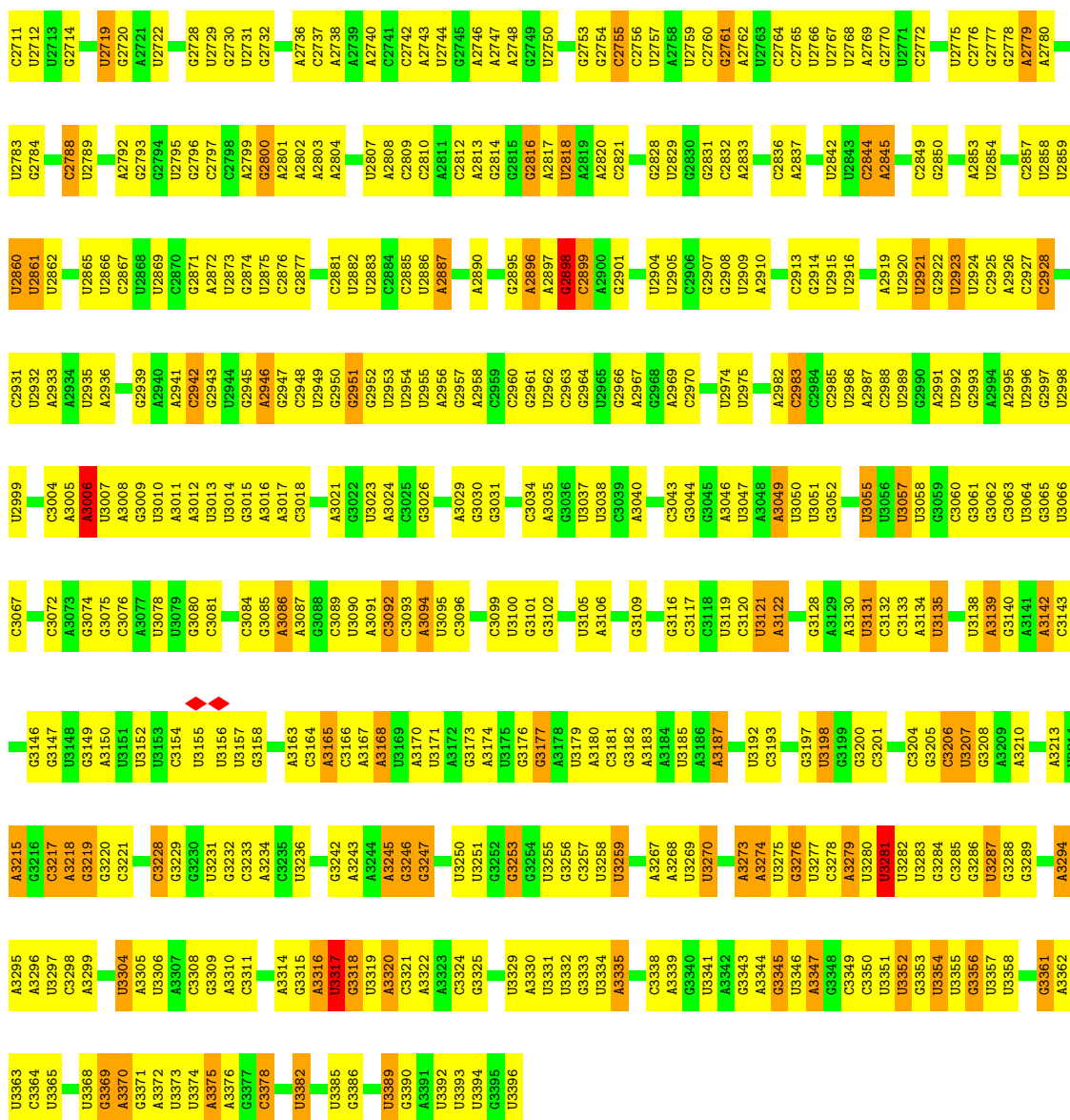
Mol	Chain	Residues	Atoms					AltConf	Trace
79	RA	318	Total	C	N	O	S	0	0
			2445	1546	419	472	8		

- 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		

G1635	G1636	A1637	U1641	A1642	A1643	C1644	G1645	G1646	A1647	A1648	G1649	G1650	G1651	G1652	G1653	A1654	G1655	A1656	G1657	G1658	G1659	G1660	G1661	G1662	C1663	G1664	G1665	G1666	A1667	G1668	G1669	G1670	G1678	A1679	U1682	A1683	G1684	U1688	G1689	C1690	G1691	G1692	G1693	U1694	U1695	A1696	A1697	A1704	U1705	G1706	A1707	C1708	G1709	C1710											
C1563	U1564	G1565	A1566	U1567	U1568	U1569	C1570	A1571	U1572	G1573	C1574	A1575	G1576	C1581	C1582	G1583	A1584	U1585	G1586	A1587	A1588	G1589	G1590	G1591	G1592	G1593	G1594	G1595	U1596	C1597	C1598	C1599	G1602	G1603	G1604	U1607	C1608	G1609	G1610	G1611	A1612	C1615	U1616	G1617	G1618	A1621	U1622	G1623	G1624	A1625	U1626	U1627	G1628	U1629	U1630	C1631	G1634								
A1490	A1491	G1492	G1493	U1494	U1495	C1496	C1497	A1498	C1499	G1500	U1501	A1504	C1505	A1506	C1507	C1508	A1509	U1510	U1511	G1512	G1513	G1517	G1520	G1521	G1522	U1523	U1526	C1527	C1532	U1533	A1534	A1535	G1536	A1537	G1538	A1539	A1545	A1546	G1547	C1548	U1549	C1550	U1553	U1554	U1555	C1556	A1557	U1558	A1559	G1560	C1562														
G1414	U1415	C1416	G1417	A1418	A1419	C1420	G1421	G1422	C1423	U1427	U1430	G1431	C1432	A1433	G1434	C1437	U1438	U1439	G1440	G1441	U1442	G1443	G1444	U1445	A1446	G1447	U1448	A1449	A1452	A1456	U1457	U1458	C1459	A1460	A1461	A1465	G1466	A1475	G1476	A1477	C1478	U1479	G1480	A1481	G1482	G1483	U1484	G1485	G1486	G1487	G1488	A1489													
U1348	G1349	A1350	U1351	A1352	U1353	G1354	U1355	U1356	G1357	C1358	C1359	C1360	C1364	G1365	A1366	G1367	U1368	A1369	G1370	G1371	C1372	C1376	G1377	U1378	G1379	G1380	A1381	G1382	U1383	A1384	C1385	A1386	G1387	U1388	C1391	G1392	A1393	A1394	G1395	C1396	C1397	U1398	A1399	G1400	A1401	C1402	G1403	G1404	U1405	A1406	A1407	G1408	G1409	G1412	G1413										
A1286	A1287	U1288	G1289	A1290	U1291	C1292	U1293	A1294	U1295	G1296	C1297	C1298	U1299	G1300	A1301	A1302	A1303	A1304	U1305	G1306	G1307	A1308	U1309	G1310	G1311	C1312	G1313	C1314	U1315	C1316	A1317	A1318	G1321	U1322	G1323	U1324	U1325	A1326	C1327	C1328	U1329	A1330	U1331	A1332	U1333	U1334	C1335	U1336	A1337	C1338	C1339	G1340	U1341	C1342	G1345	G1346	U1347								
A1204	A1205	G1206	G1207	U1210	U1211	A1212	G1213	U1214	U1215	C1216	A1217	U1220	A1221	G1222	A1223	C1224	A1225	G1226	C1227	U1234	U1235	G1236	G1237	C1238	C1239	A1240	U1241	G1242	G1243	A1244	G1245	G1246	G1250	A1251	C1254	C1257	U1258	A1259	A1260	G1261	A1262	A1263	G1264	U1265	U1269	C1272	G1281	C1284	G1285																
A1132	A1133	G1134	A1135	A1136	C1137	U1138	G1139	U1140	C1141	G1142	A1143	U1144	G1147	A1150	U1151	G1152	A1153	A1154	A1158	A1159	U1167	U1168	A1169	U1170	G1171	G1172	U1173	G1174	C1175	G1176	A1177	G1178	A1179	A1180	U1181	A1182	C1183	G1186	C1187	A1190	U1191	G1192	A1193	G1194	A1195	C1196	A1197	C1198	G1199	A1200	C1201	A1202	A1203												
A1057	A1064	A1065	U1070	U1071	G1072	U1073	G0994	U0995	A0996	A0997	C1000	G1001	A1002	A1003	U1004	U1008	A1009	G1010	A1011	G1012	G1013	U1014	U1015	C1016	C1017	G1018	G1019	G1020	G1024	A1025	A1026	U1028	G1029	U1033	U1034	G1035	A1036	U1039	A1040	C1045	A1046	A1047	C1048	U1049	U1050	U1051	U1052	A1053	A1054	U1056															
U986	U987	U988	A989	U990	G991	A992	G993	G994	A996	A997	C1000	G1001	A1002	A1003	U1004	U1008	A1009	G1010	A1011	G1012	G1013	U1014	U1015	C1016	C1017	G1018	G1019	G1020	G1024	A1025	A1026	U1028	G1029	U1033	U1034	G1035	A1036	U1039	A1040	C1045	A1046	A1047	C1048	U1049	U1050	U1051	U1052	A1053	A1054	U1056															
C923	G924	A925	A926	C927	G928	A929	U930	C931	U932	U935	A936	G937	C938	U939	G940	G941	U942	U943	C944	U946	G947	C948	C949	G950	G953	U954	U955	U956	C957	C958	C959	U960	G961	A962	G963	U964	U965	U966	A967	A970	G971	A972	A973	G974	C975	U976	C977	A978	U979	A980	U981	C982	A983	G984	U985										
U850	C851	U852	G853	G854	U855	G856	G857	A858	G859	G860	C861	U862	G863	C864	U865	U866	U867	U868	A869	U870	U871	U872	U873	U874	G875	U879	C880	C881	A882	U885	C886	G887	U888	A889	C890	G891	U892	C893	G894	A895	U896	U897	U898	G900	G901	U902	U903	A904	U905	A906	G907	G908	A936	A937	G938	C939	A914	A915	G916	A917	C918	U919	A920	A921	A922
U713	G714	A715	G718	U719	A720	G721	G722	U723	G724	U725	G726	G727	G728	C729	C730	A736	G737	A738	G739	A743	A744	C745	A746	G747	G748	C749	C753	G754	A755	U758	C759	G760	G763	U764	C765	A766	U767	C768	G769	G770	A771	U772	G773	U776	U777	U778	G779	A780	G781	U782	A783	A784													

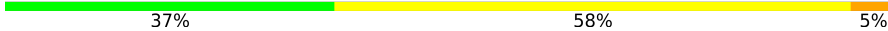


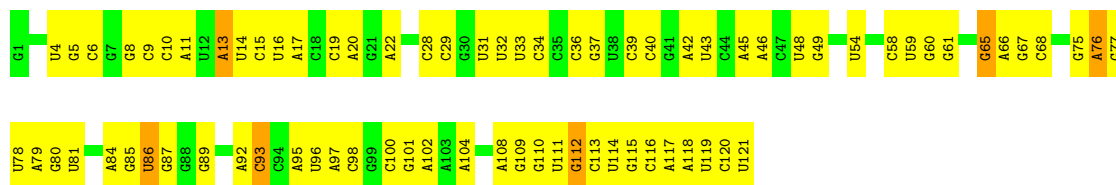


• Molecule 2: 5.8S ribosomal RNA



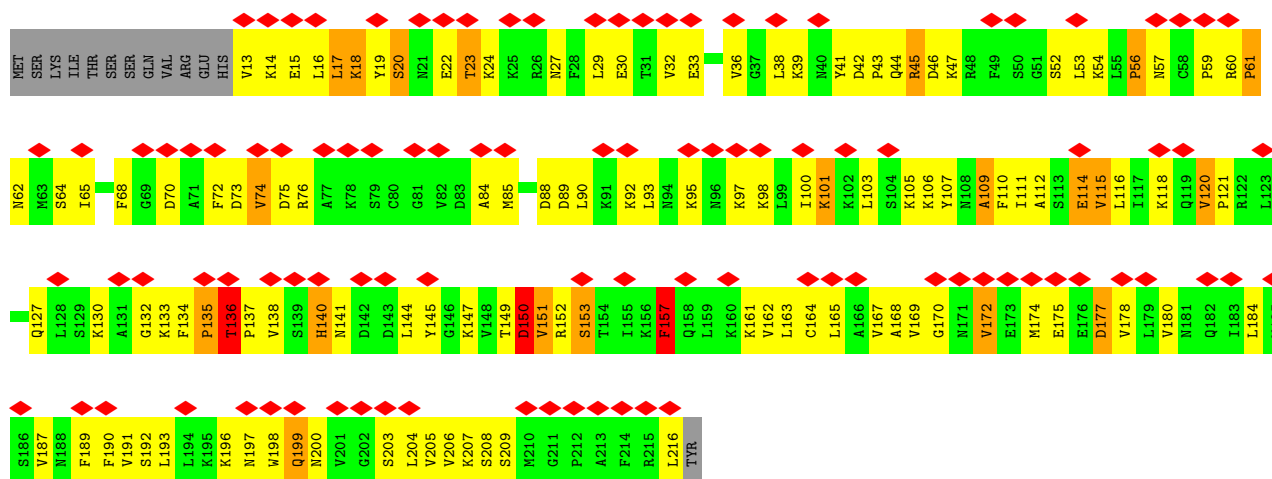
• Molecule 3: 5S ribosomal RNA

Chain 5S: 



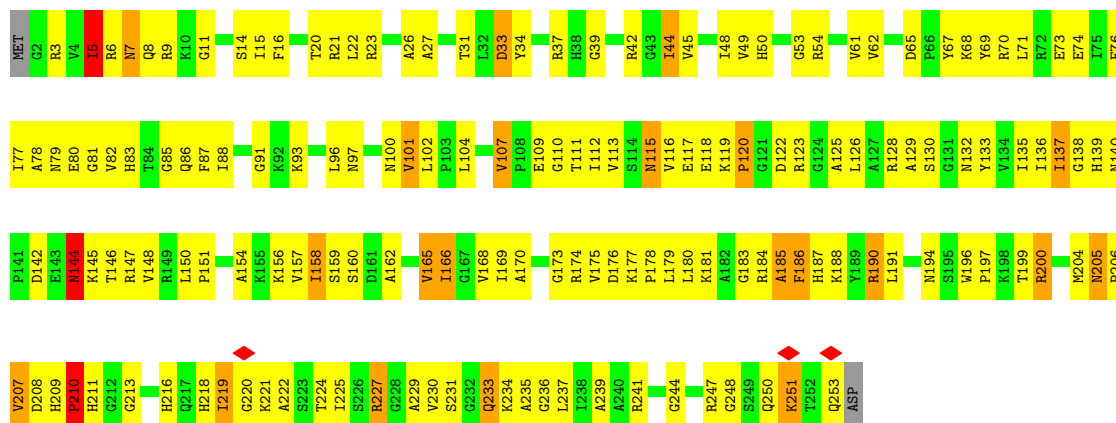
• Molecule 4: 60S ribosomal protein L1

Chain L1: 



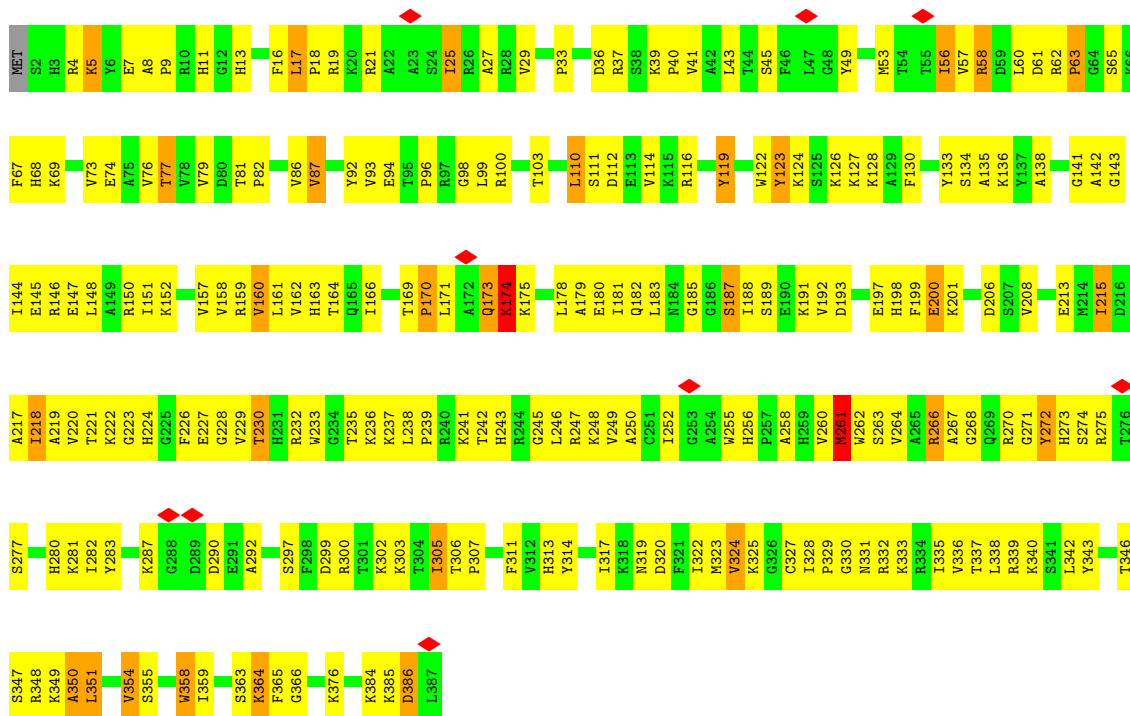
• Molecule 5: 60S ribosomal protein L2

Chain L2: 

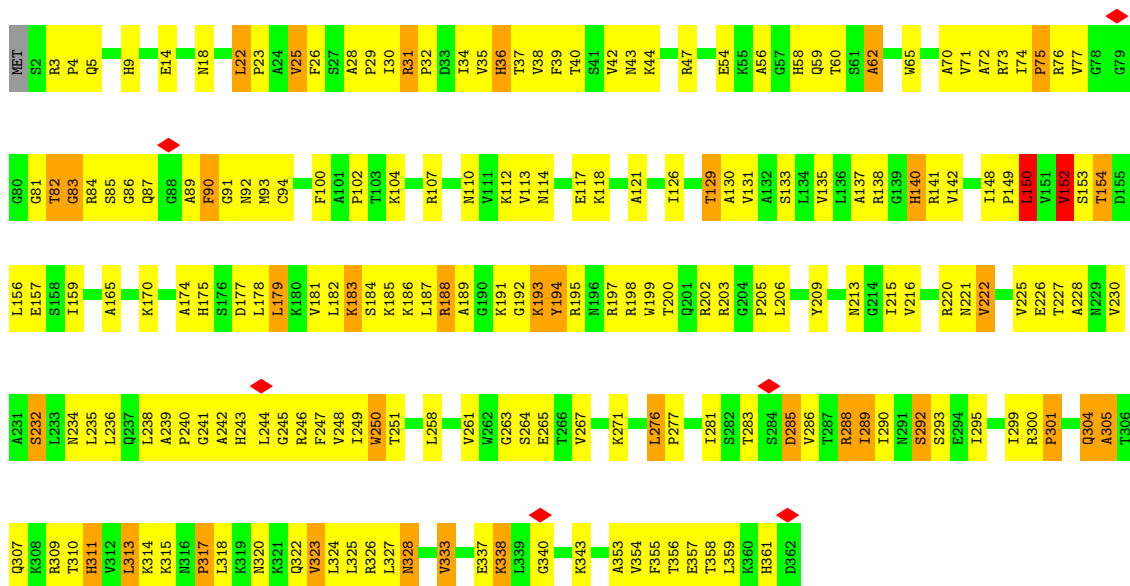


• Molecule 6: 60S ribosomal protein L3

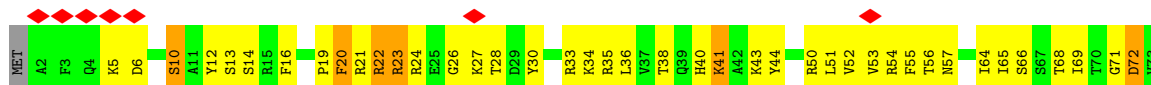
Chain L3: 

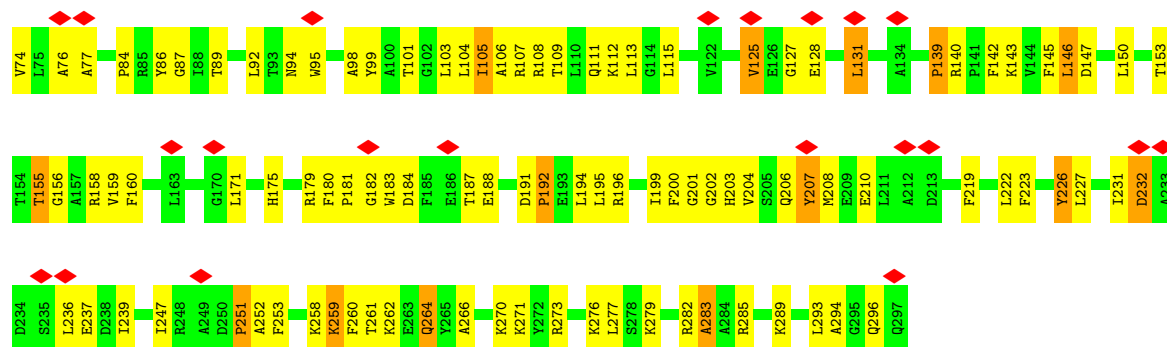


• Molecule 7: 60S ribosomal protein L4

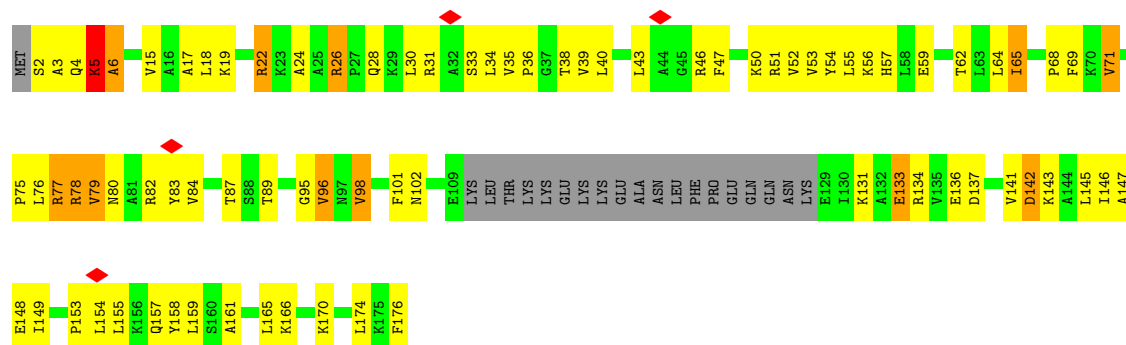


• Molecule 8: 60S ribosomal protein L5

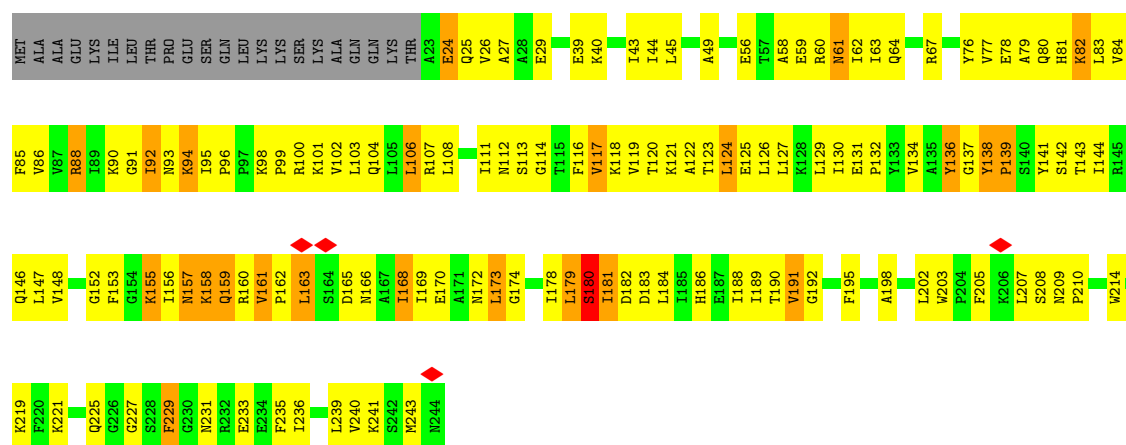




• Molecule 9: 60S ribosomal protein L6

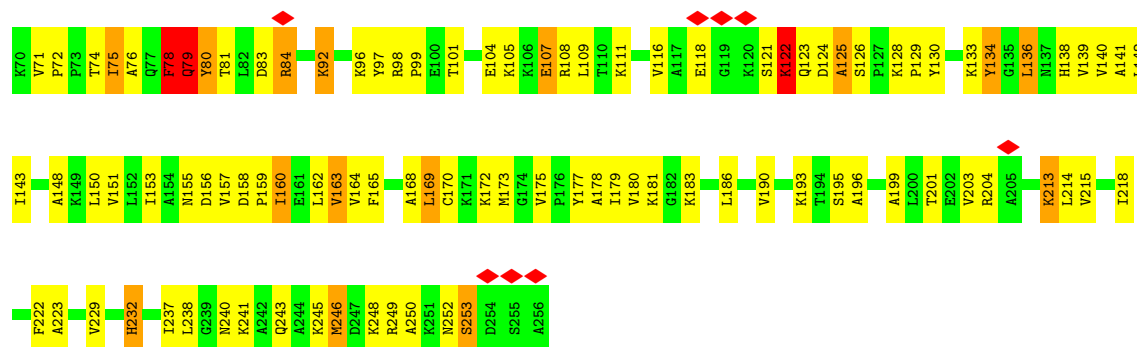


• Molecule 10: 60S ribosomal protein L7



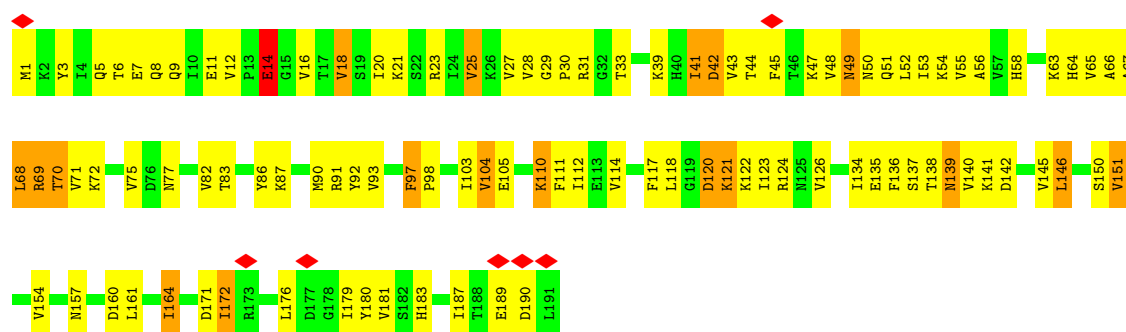
• Molecule 11: 60S ribosomal protein L8





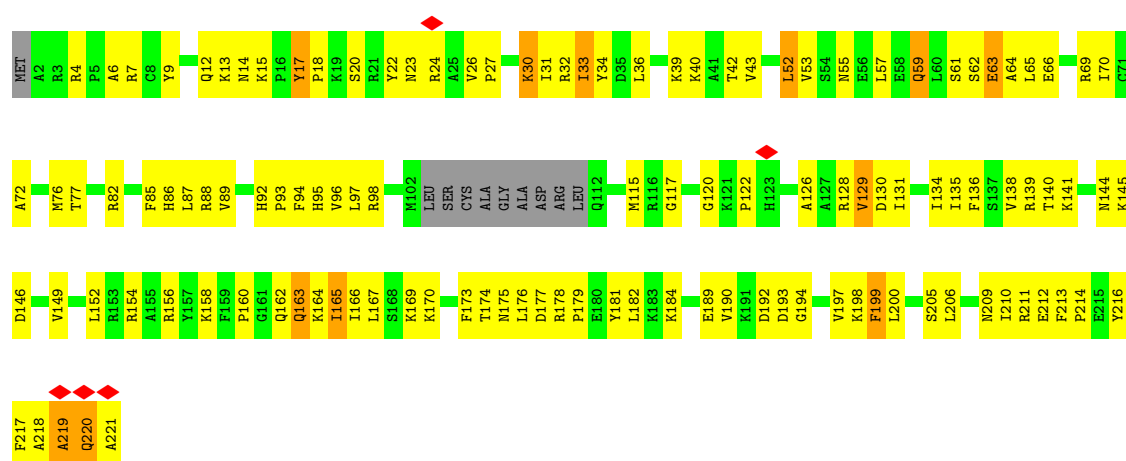
• Molecule 12: 60S ribosomal protein L9

Chain L9: 46% 45% 9%



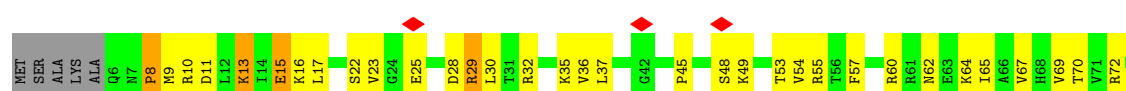
• Molecule 13: 60S ribosomal protein L10

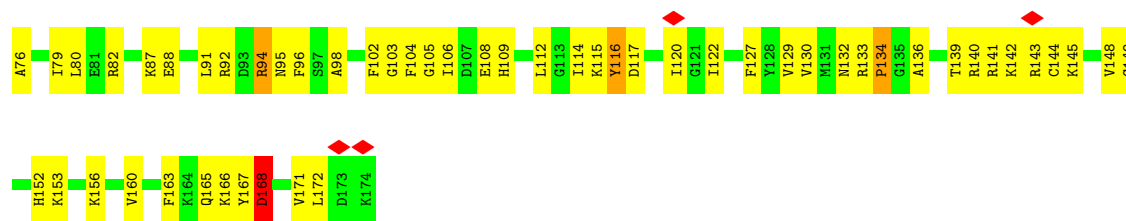
Chain 50: 41% 49% 5% 5%



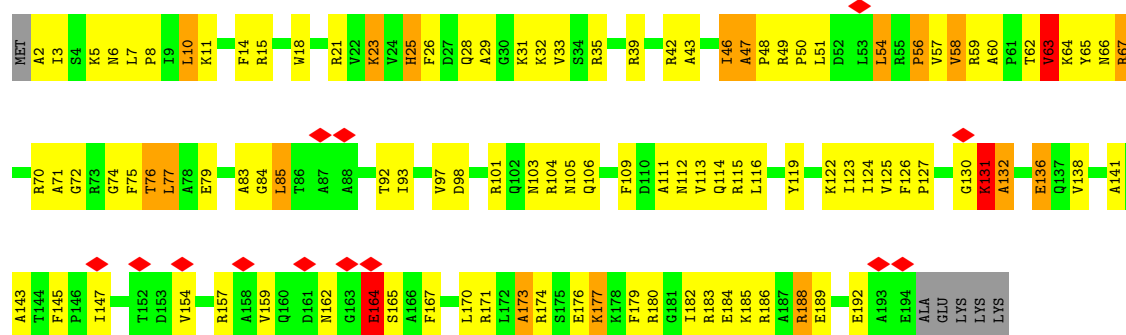
• Molecule 14: 60S ribosomal protein L11

Chain 51: 48% 45% 7%

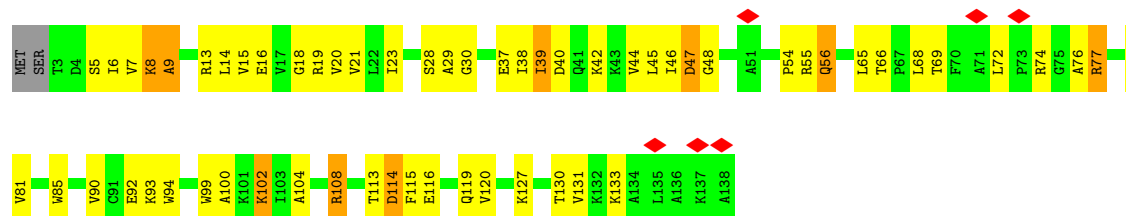




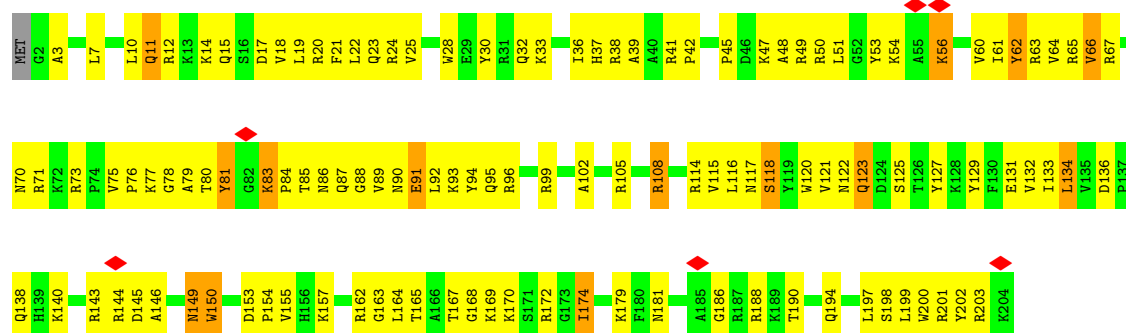
• Molecule 15: 60S ribosomal protein L13



• Molecule 16: 60S ribosomal protein L14

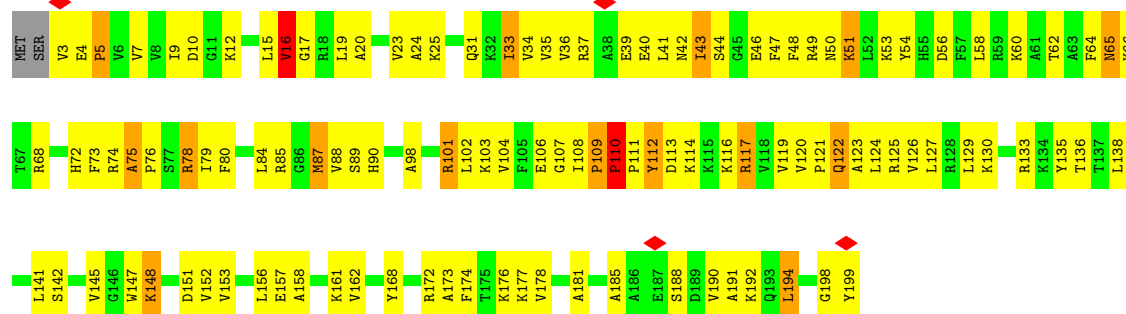


• Molecule 17: 60S ribosomal protein L15



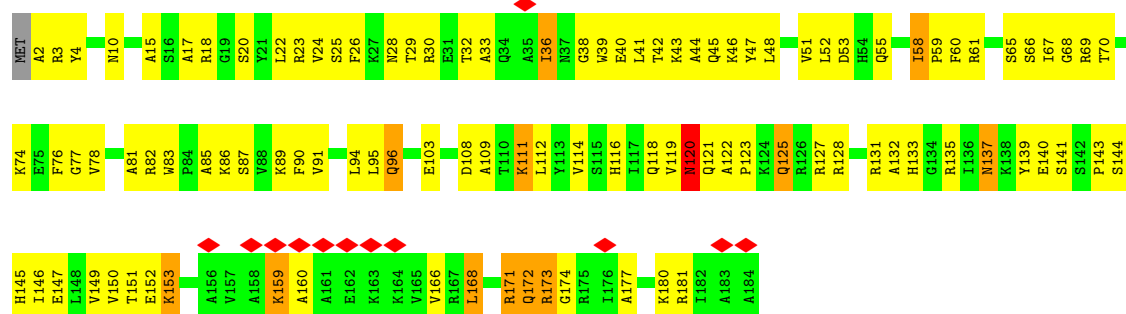
• Molecule 18: 60S ribosomal protein L16

Chain 56: 



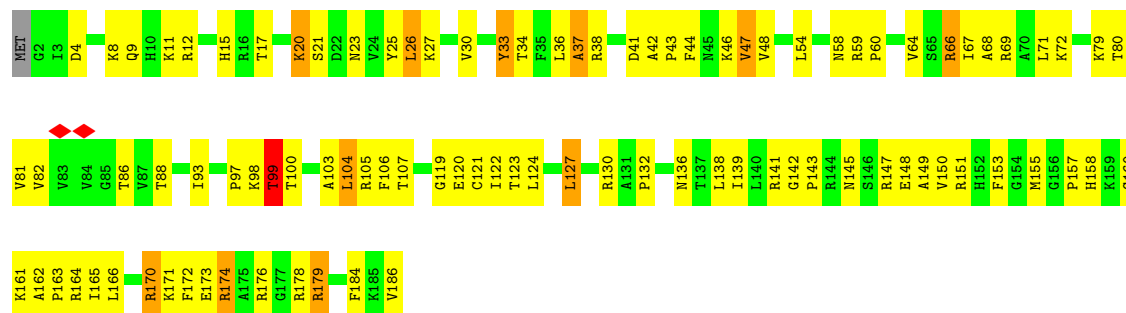
• Molecule 19: 60S ribosomal protein L17

Chain 57: 



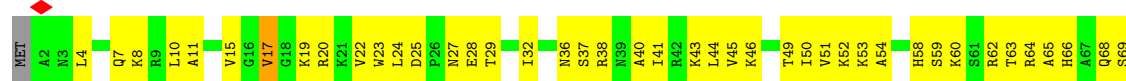
• Molecule 20: 60S ribosomal protein L18

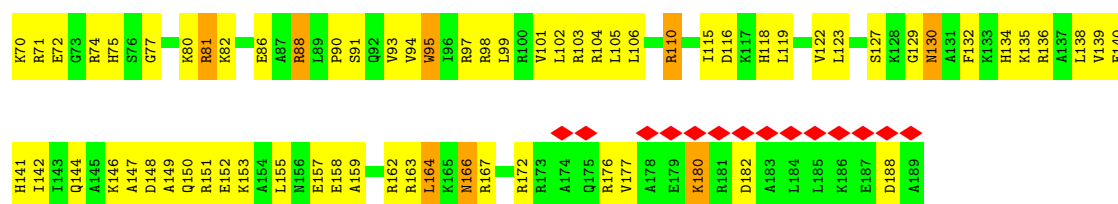
Chain 58: 



• Molecule 21: 60S ribosomal protein L19

Chain 59: 

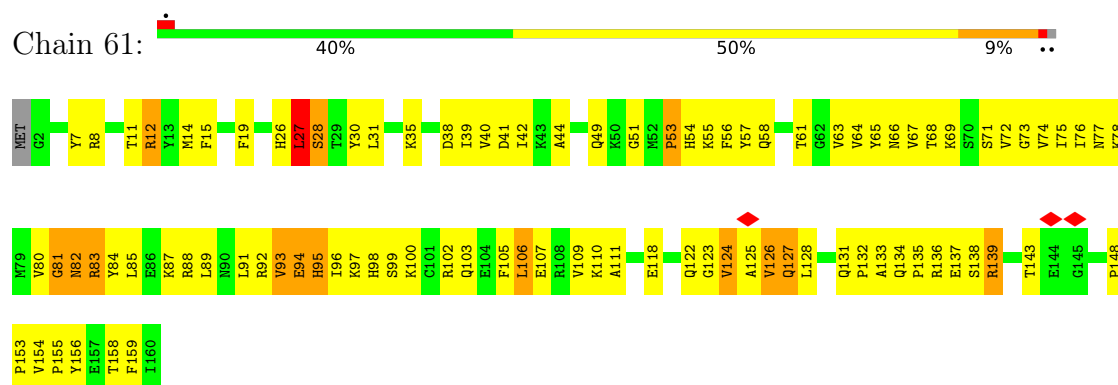




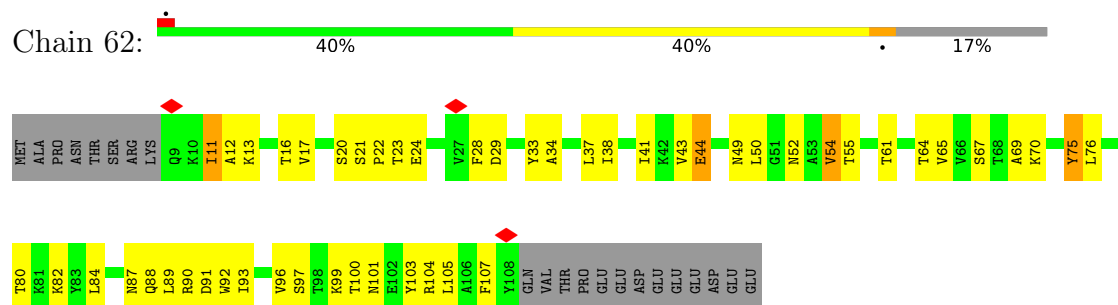
• Molecule 22: 60S ribosomal protein L20



• Molecule 23: 60S ribosomal protein L21

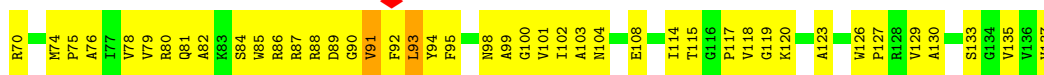


• Molecule 24: 60S ribosomal protein L22

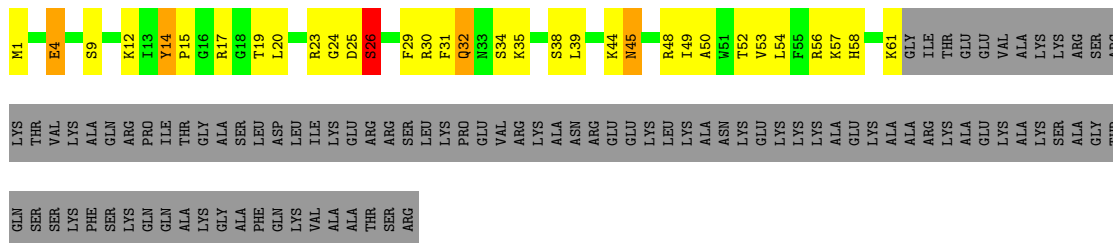


• Molecule 25: 60S ribosomal protein L23

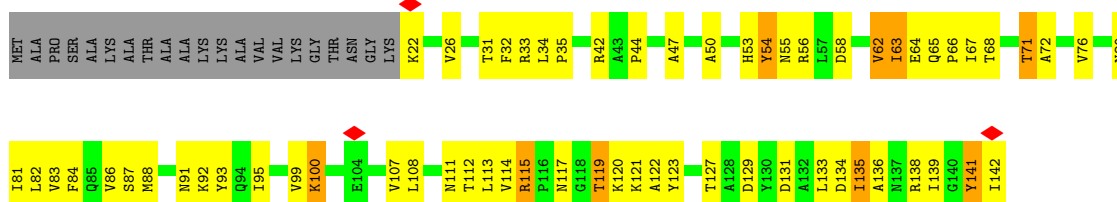




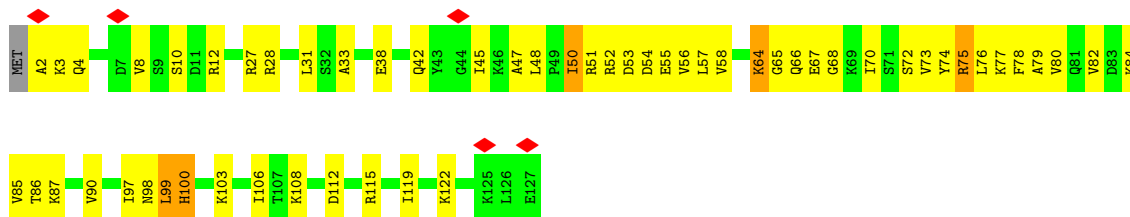
- Molecule 26: 60S ribosomal protein L24



- Molecule 27: 60S ribosomal protein L25



- Molecule 28: 60S ribosomal protein L26

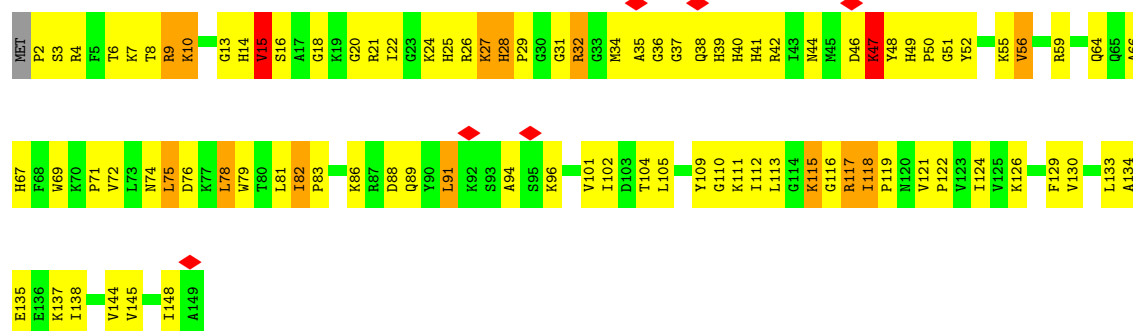
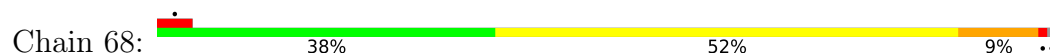


- Molecule 29: 60S ribosomal protein L27





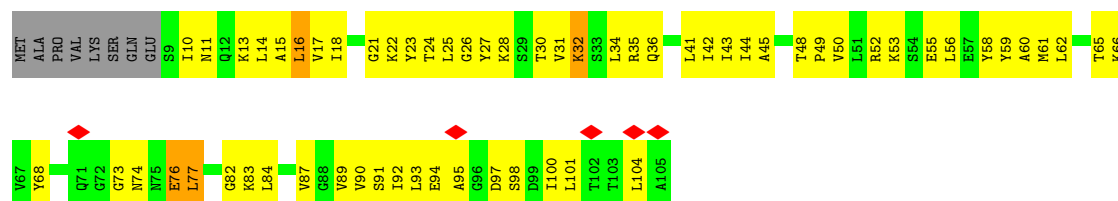
- Molecule 30: 60S ribosomal protein L28



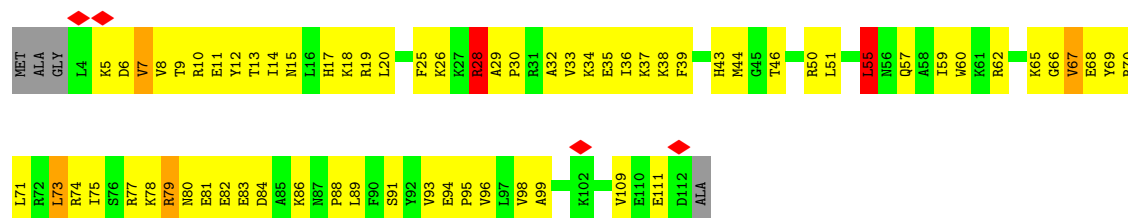
- Molecule 31: 60S ribosomal protein L29



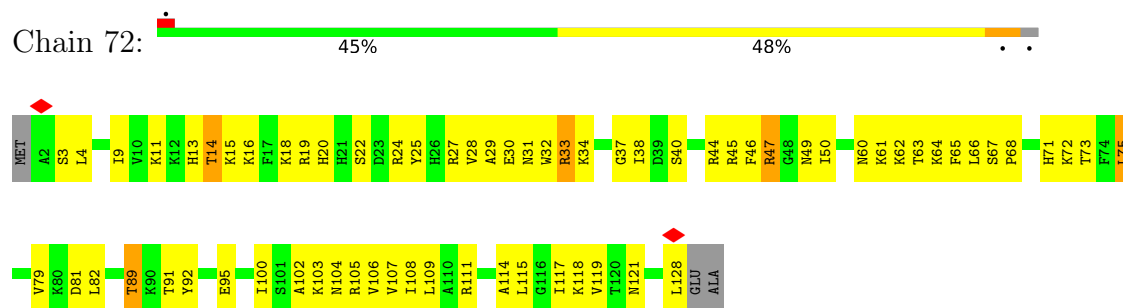
- Molecule 32: 60S ribosomal protein L30



- Molecule 33: 60S ribosomal protein L31



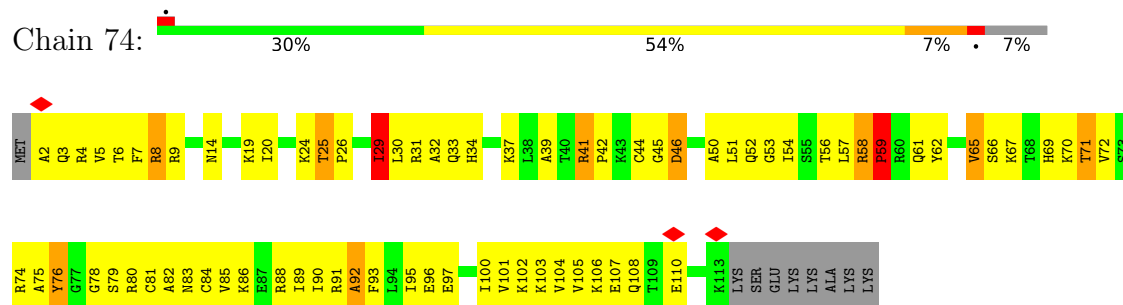
- Molecule 34: 60S ribosomal protein L32



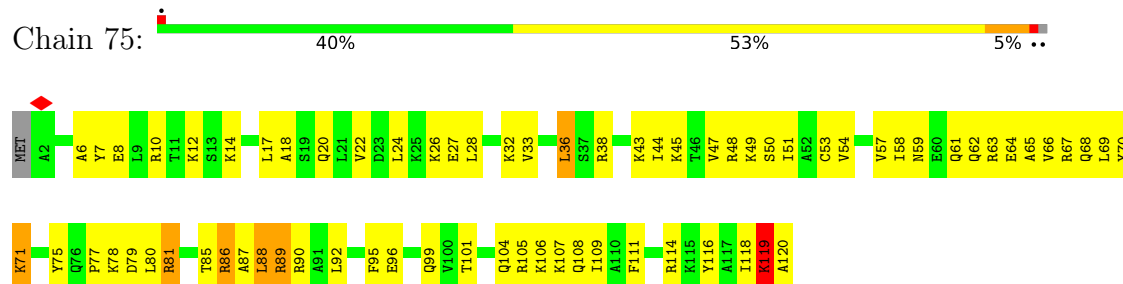
• Molecule 35: 60S ribosomal protein L33



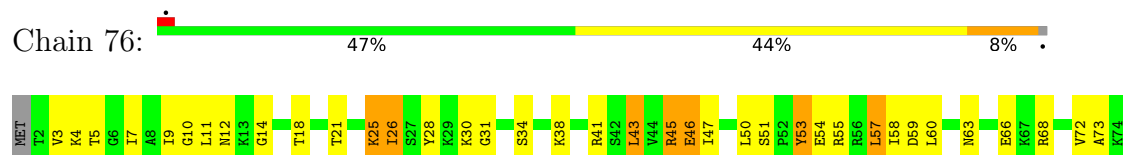
• Molecule 36: 60S ribosomal protein L34



• Molecule 37: 60S ribosomal protein L35



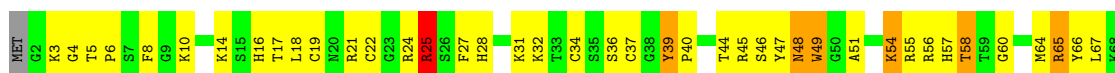
• Molecule 38: 60S ribosomal protein L36





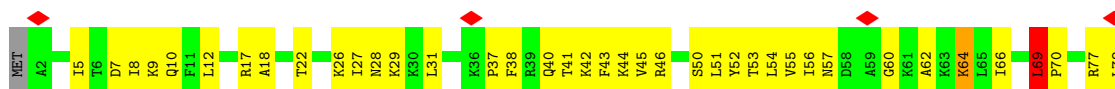
- Molecule 39: 60S ribosomal protein L37

Chain 77: 42% 49% 7% ..



- Molecule 40: 60S ribosomal protein L38

Chain 78: 5% 49% 47% ...



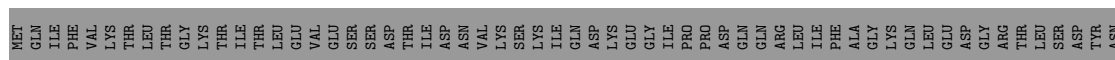
- Molecule 41: 60S ribosomal protein L39

Chain 79: 35% 57% 6% .



- Molecule 42: 60S ribosomal protein L40

Chain 80: 20% 16% . 59%



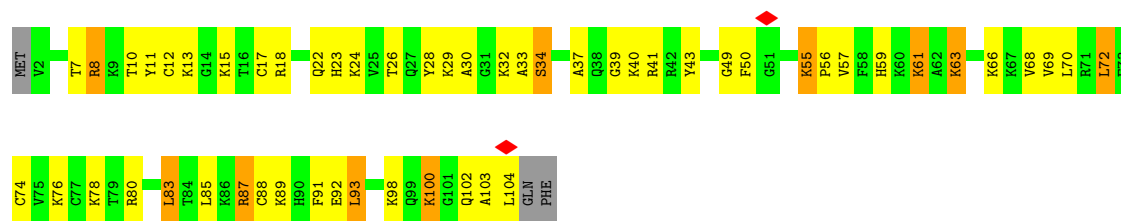
- Molecule 43: 60S ribosomal protein L41

Chain 81: 96% 56% 32% 12%

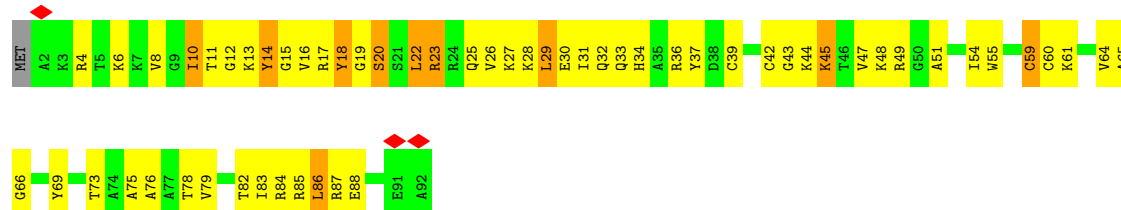


- Molecule 44: 60S ribosomal protein L42

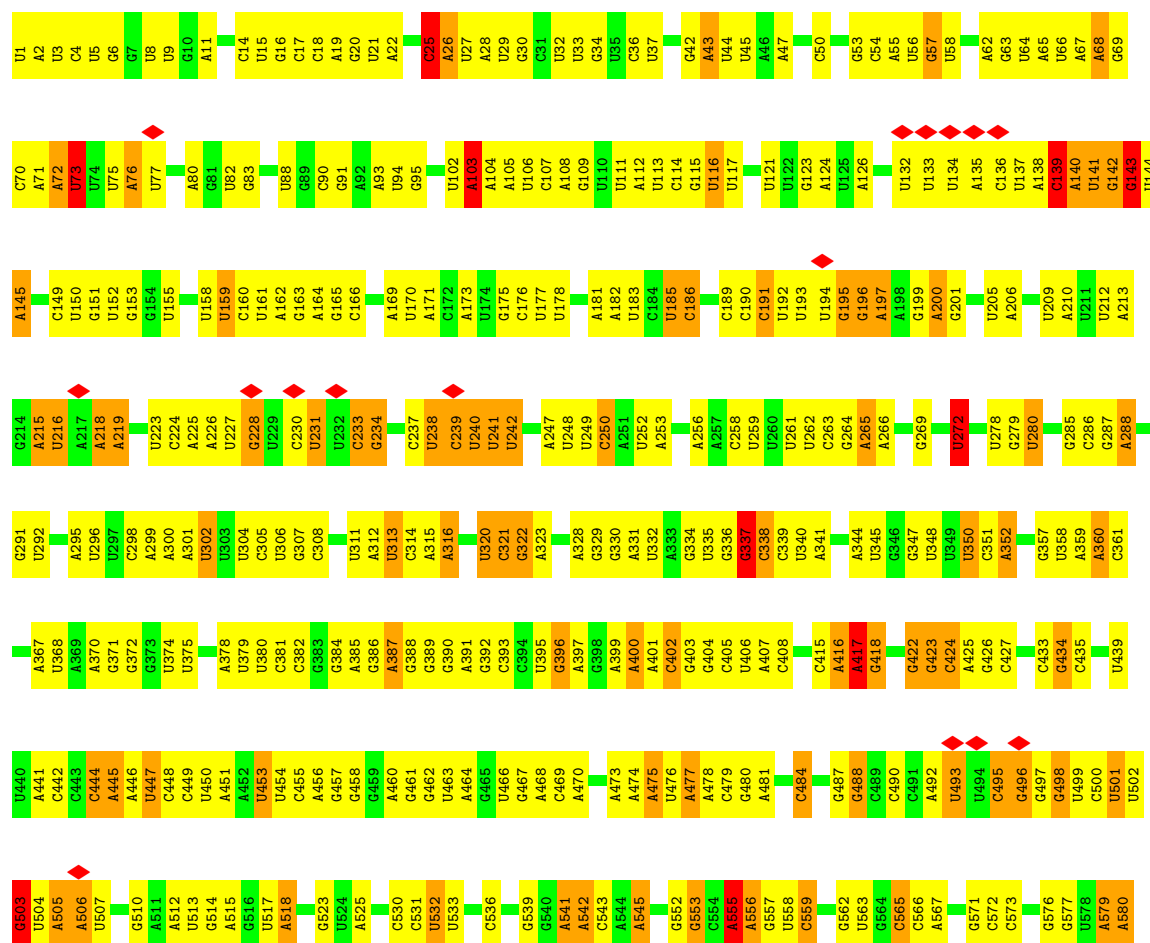
Chain 82: 46% 42% 9% .



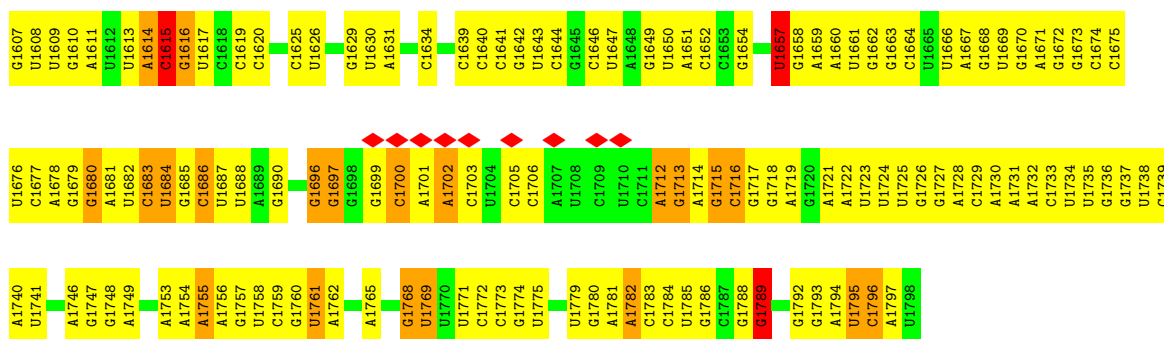
• Molecule 45: 60S ribosomal protein L43



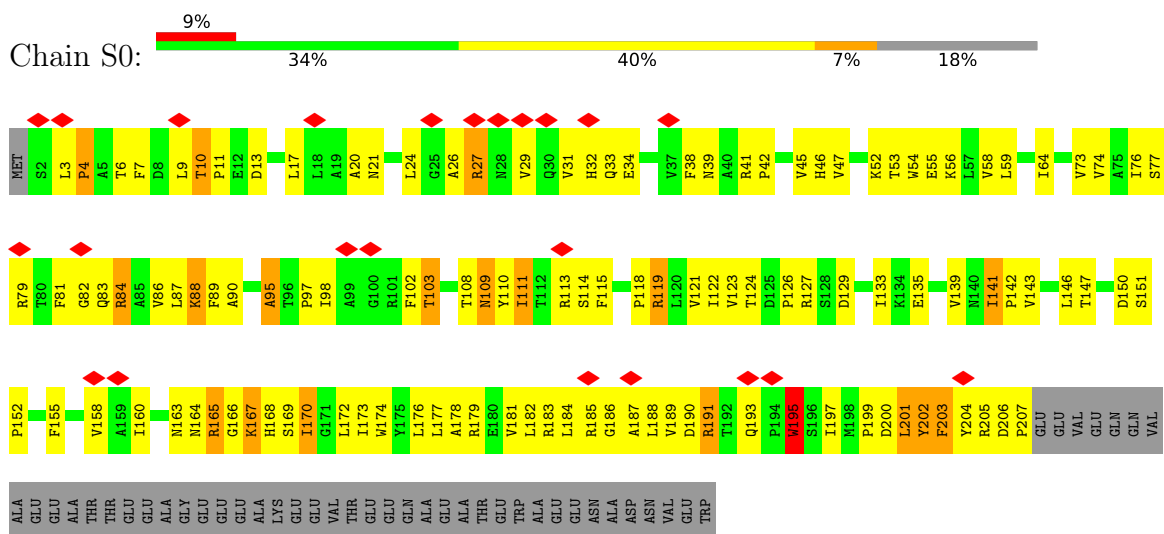
• Molecule 46: 18S ribosomal RNA



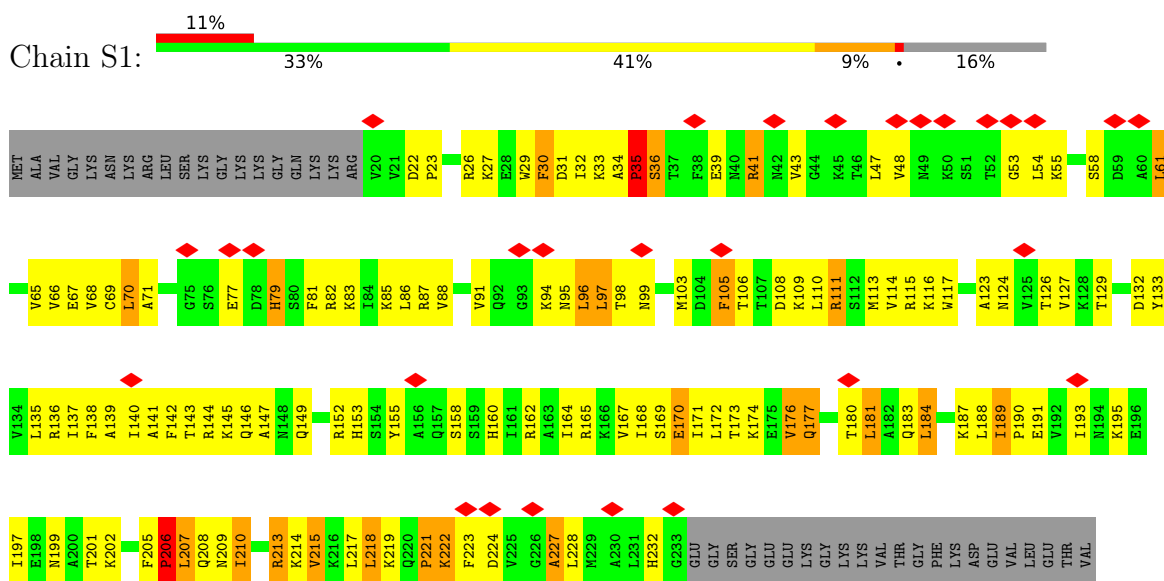




• Molecule 47: 40S ribosomal protein S0

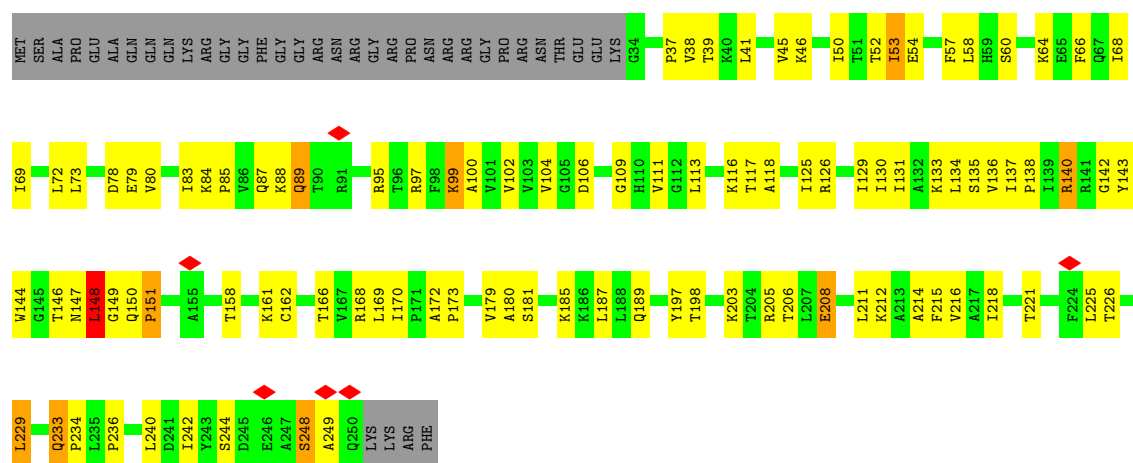


• Molecule 48: 40S ribosomal protein S1

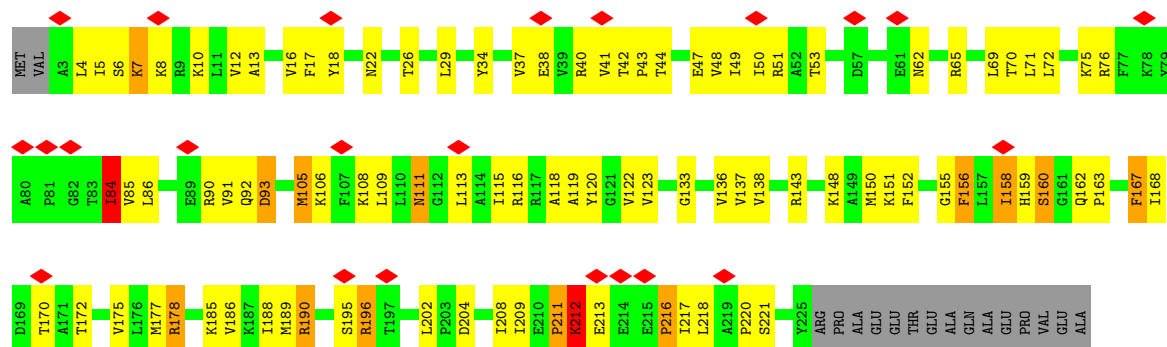


• Molecule 49: 40S ribosomal protein S2

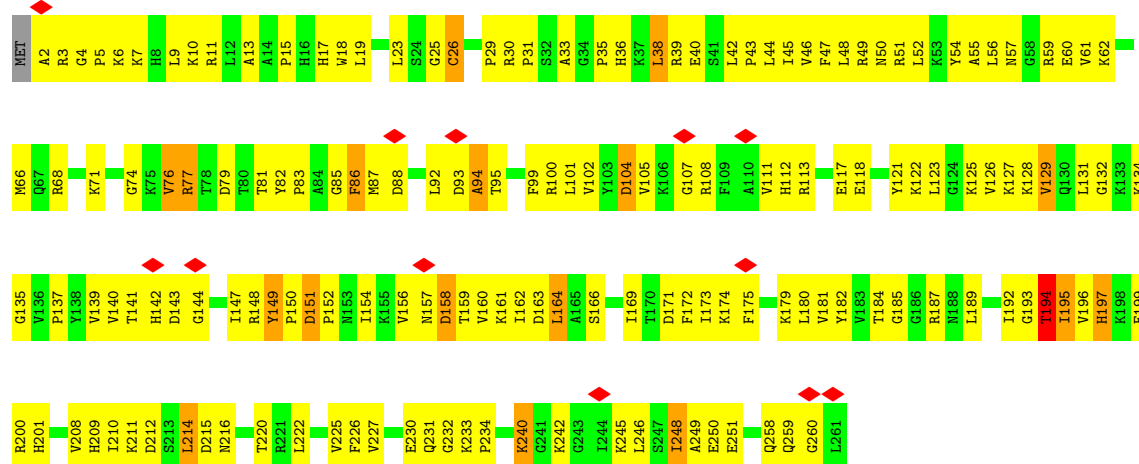




• Molecule 50: 40S ribosomal protein S3

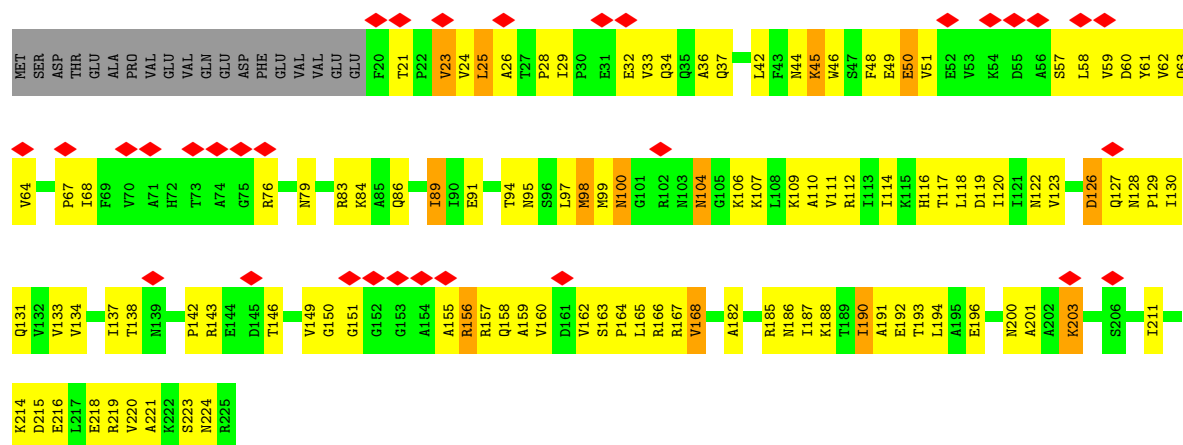


• Molecule 51: 40S ribosomal protein S4

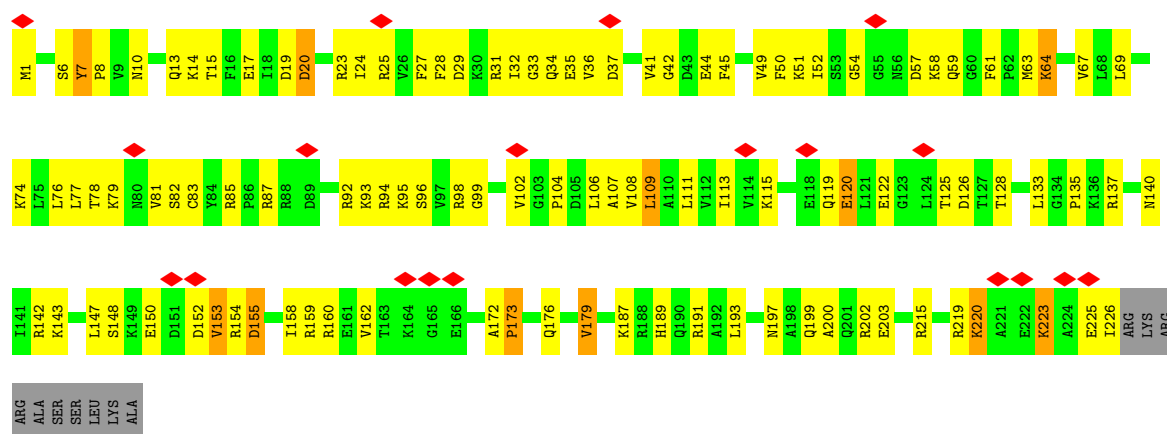


• Molecule 52: 40S ribosomal protein S5

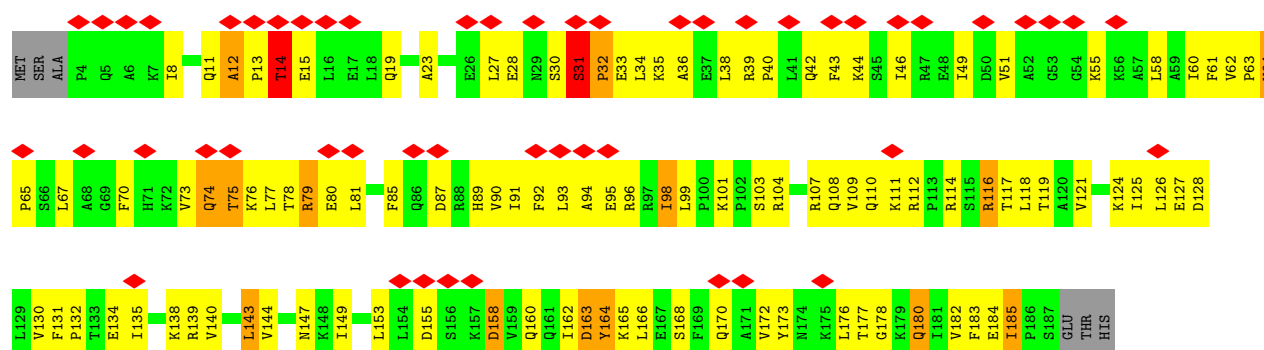




• Molecule 53: 40S ribosomal protein S6

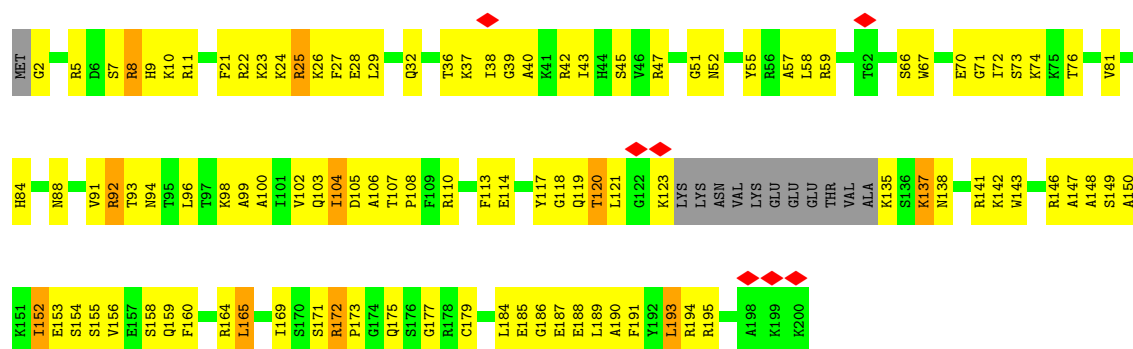


• Molecule 54: 40S ribosomal protein S7

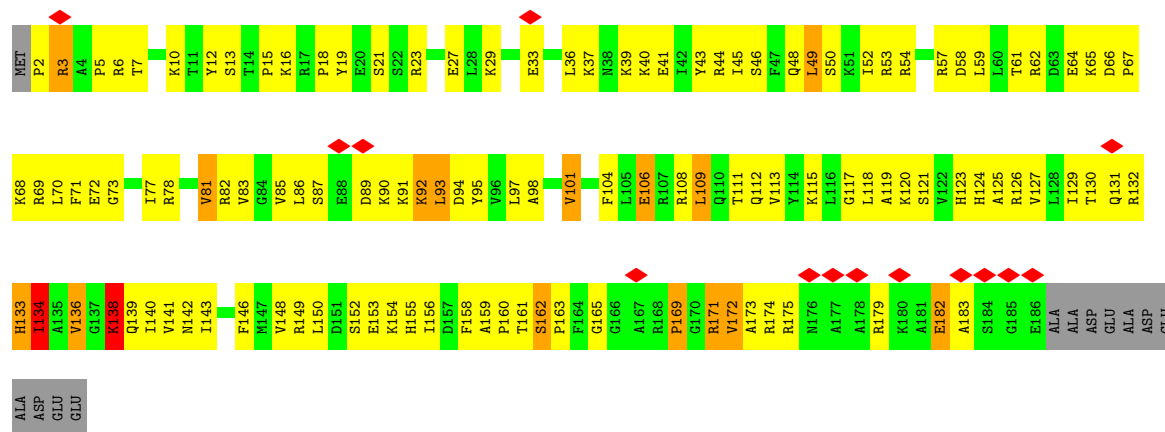


• Molecule 55: 40S ribosomal protein S8



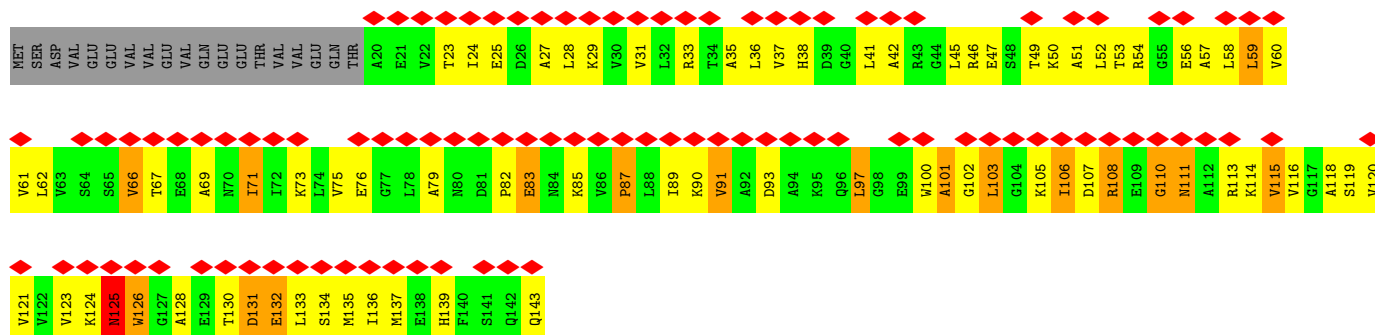


• Molecule 56: 40S ribosomal protein S9

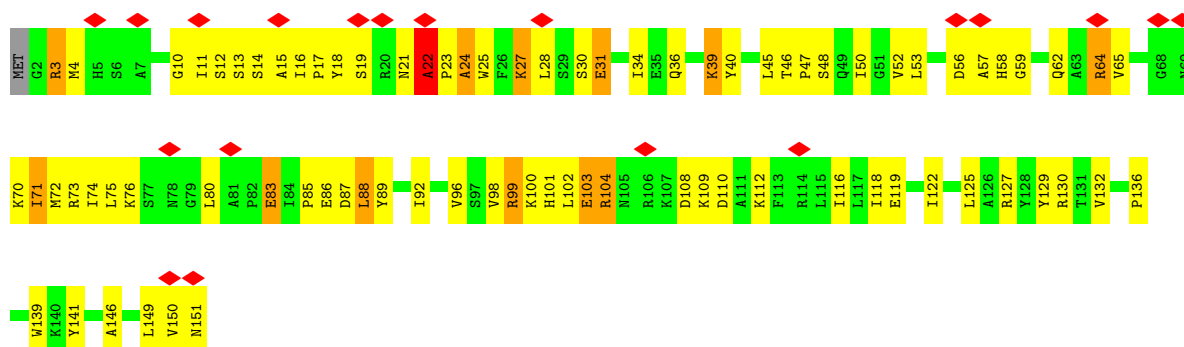
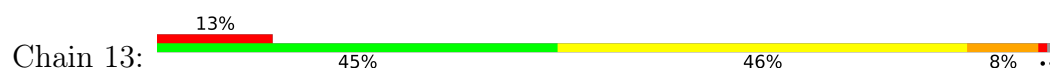




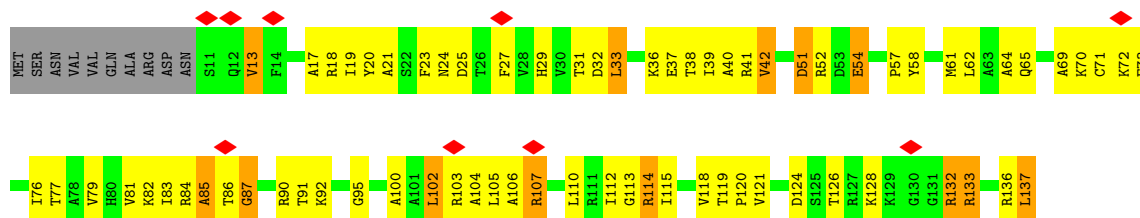
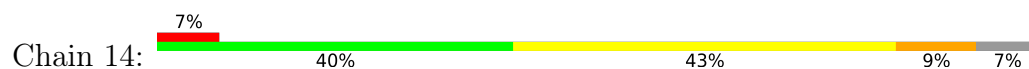
• Molecule 59: 40S ribosomal protein S12



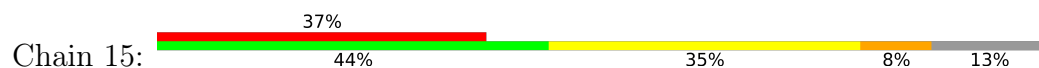
• Molecule 60: 40S ribosomal protein S13

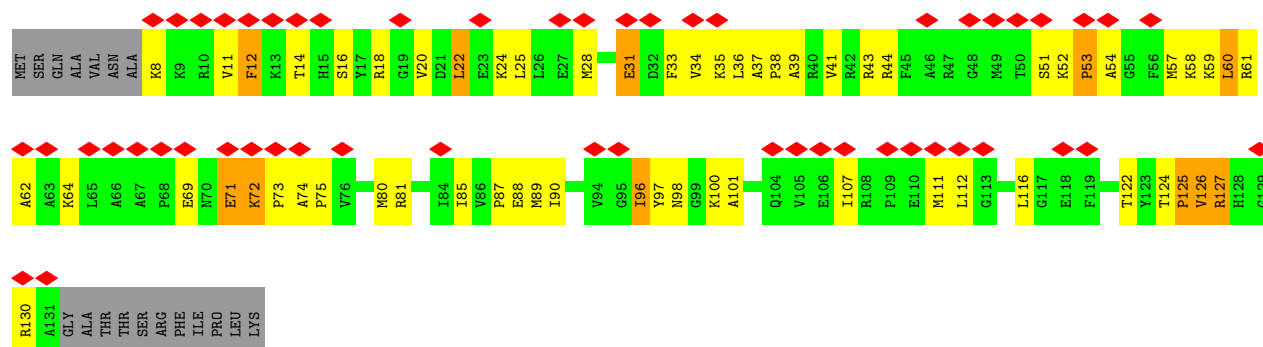


• Molecule 61: 40S ribosomal protein S14

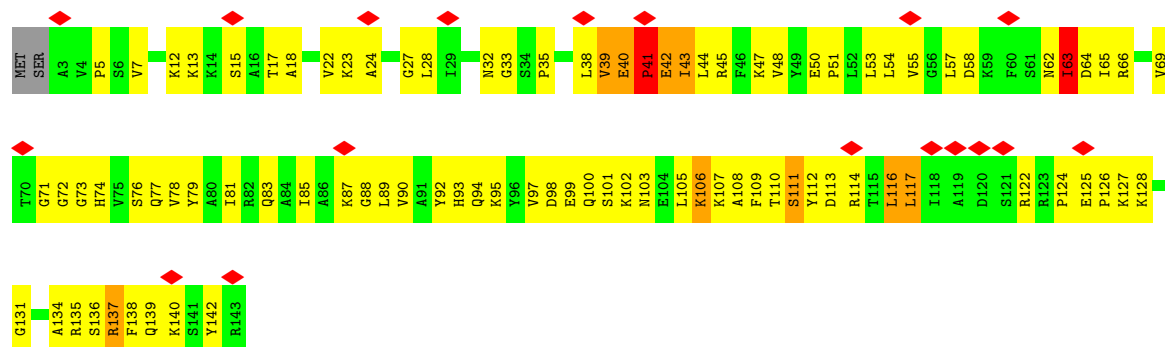


• Molecule 62: 40S ribosomal protein S15

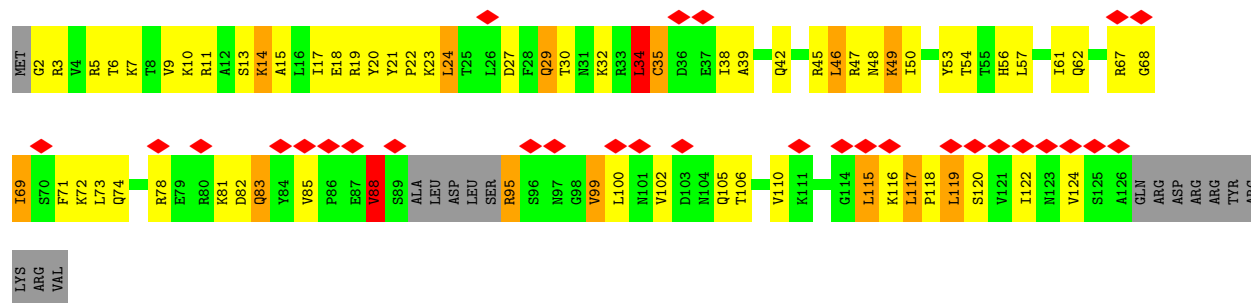




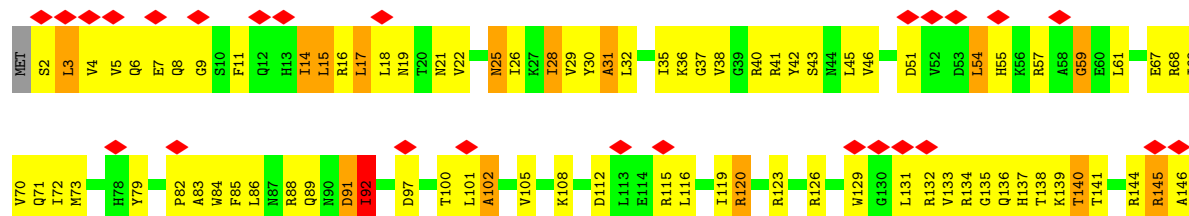
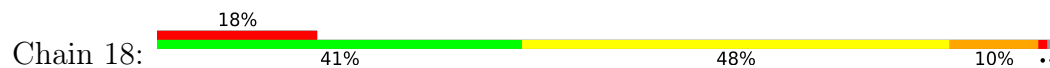
• Molecule 63: 40S ribosomal protein S16



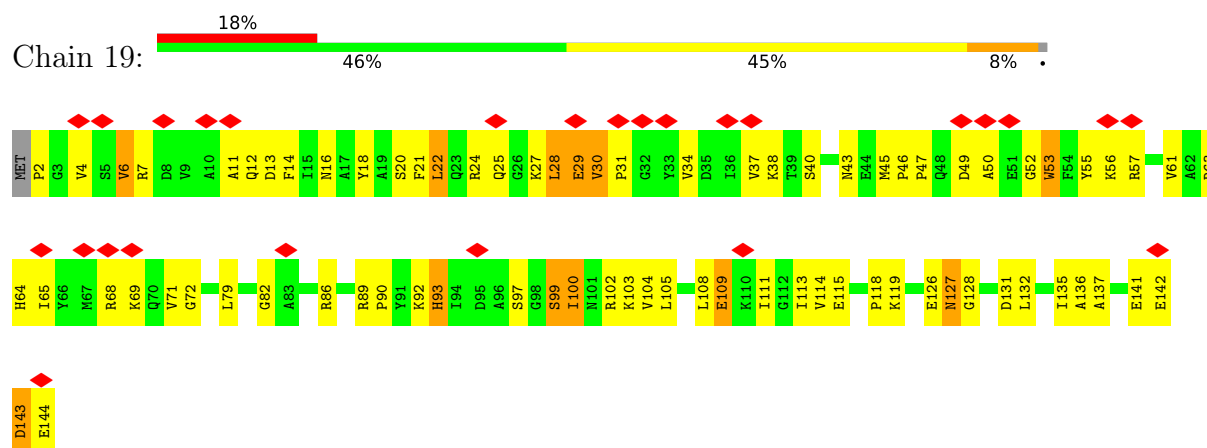
• Molecule 64: 40S ribosomal protein S17



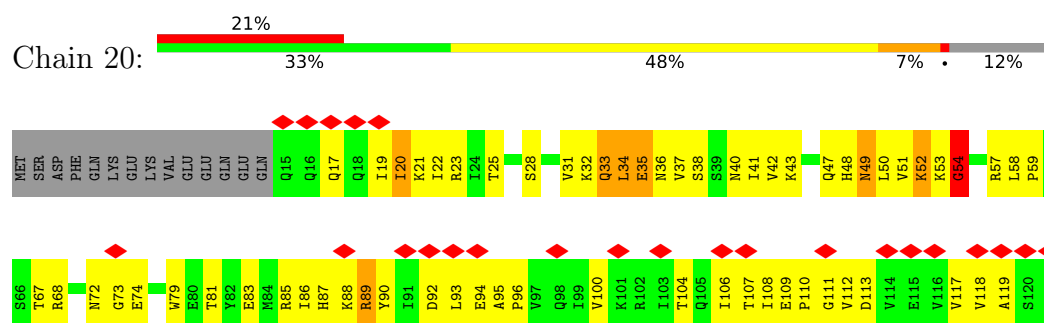
• Molecule 65: 40S ribosomal protein S18



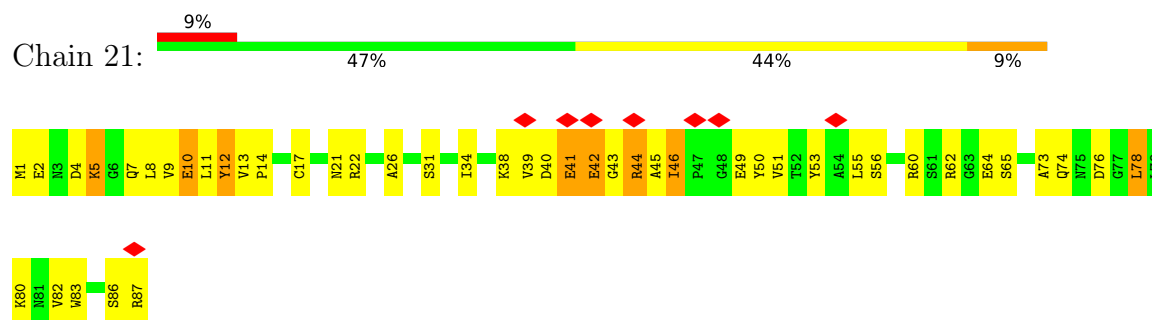
- Molecule 66: 40S ribosomal protein S19



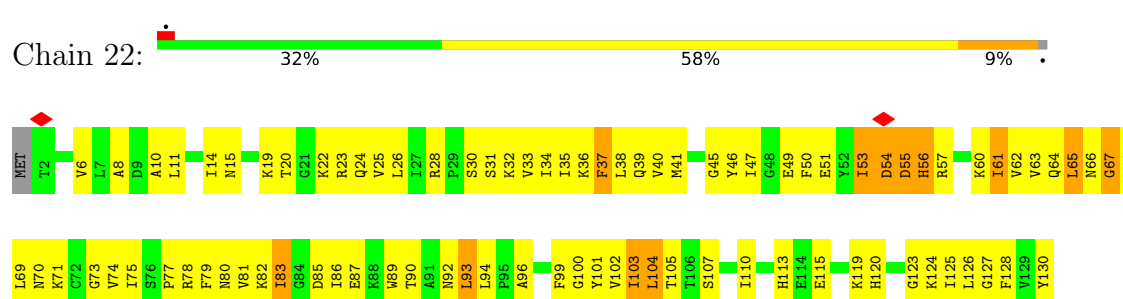
- Molecule 67: 40S ribosomal protein S20



- Molecule 68: 40S ribosomal protein S21

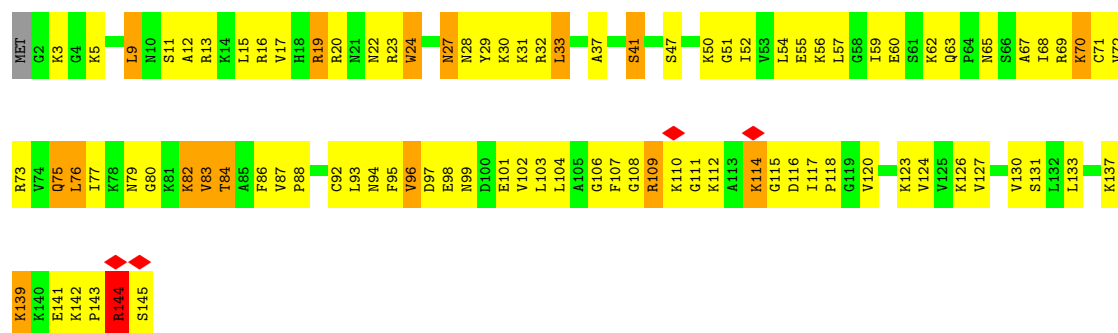


- Molecule 69: 40S ribosomal protein S22



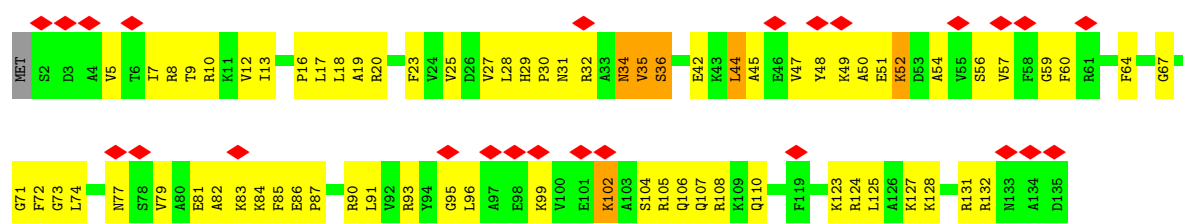
- Molecule 70: 40S ribosomal protein S23

Chain 23: 



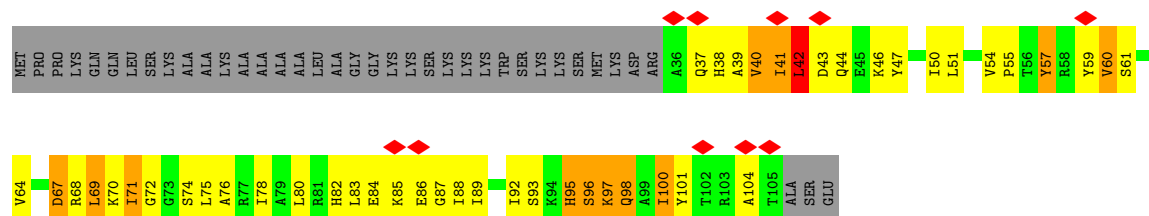
- Molecule 71: 40S ribosomal protein S24

Chain 24: 

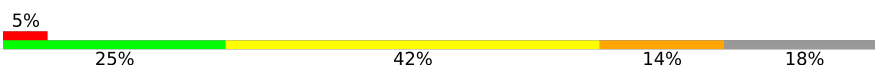


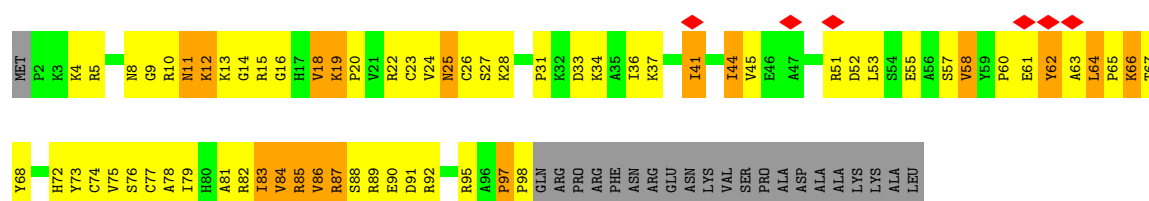
- Molecule 72: 40S ribosomal protein S25

Chain 25: 



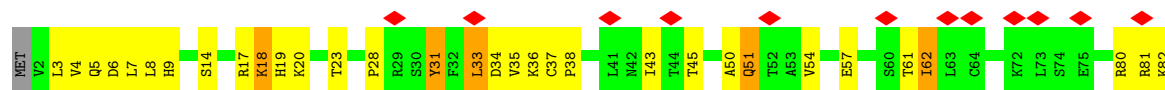
- Molecule 73: 40S ribosomal protein S26

Chain 26: 

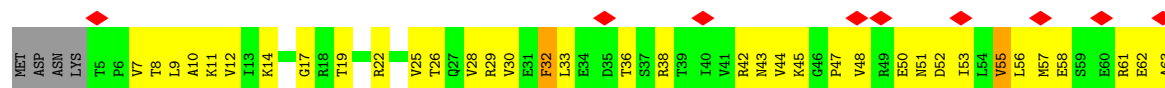


- Molecule 74: 40S ribosomal protein S27

Chain 27: 



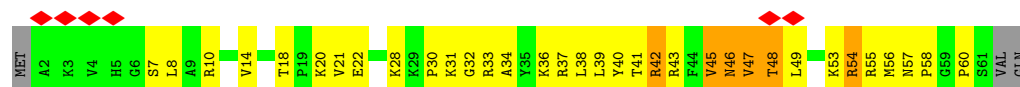
- Molecule 75: 40S ribosomal protein S28



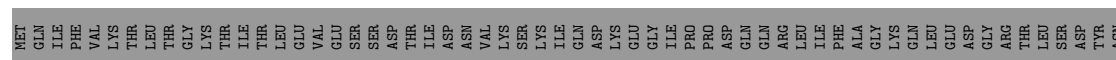
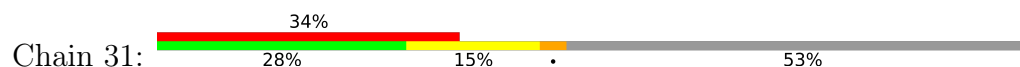
- Molecule 76: 40S ribosomal protein S29



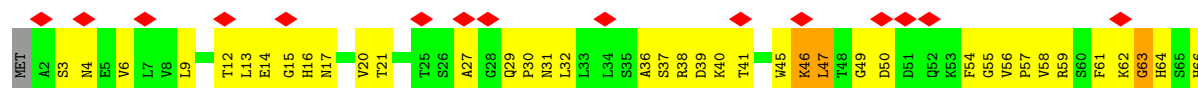
- Molecule 77: 40S ribosomal protein S30

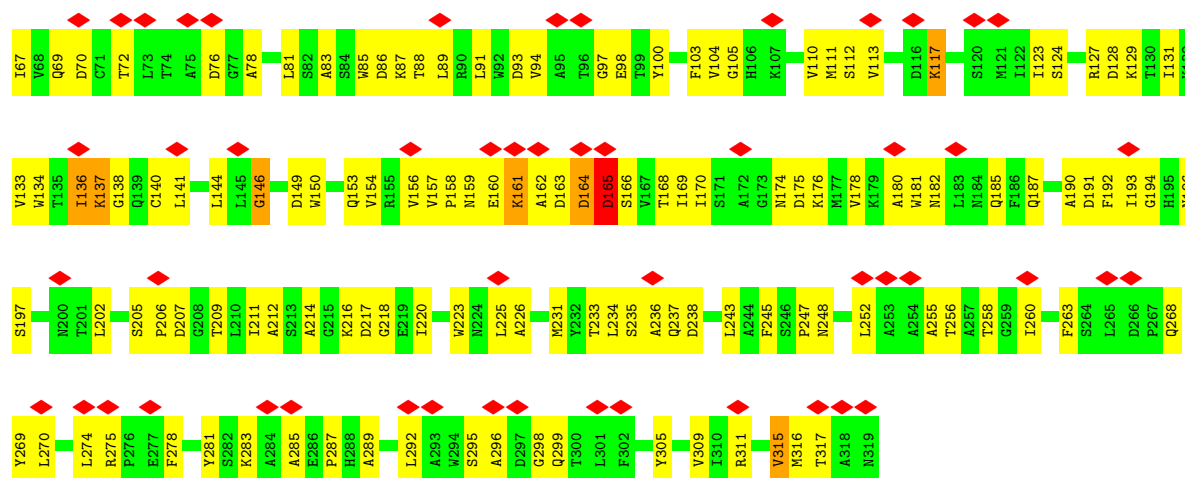


- Molecule 78: 40S ribosomal protein S31

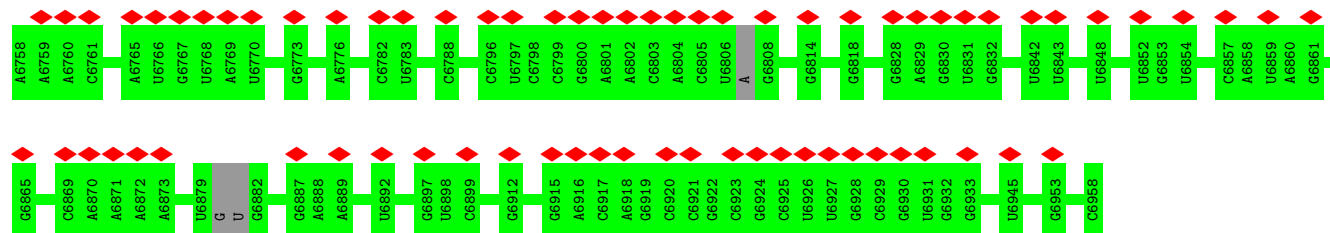


- Molecule 79: Guanine nucleotide-binding protein subunit beta-like protein





• Molecule 80: TSV IRES mRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	51373	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	4.067	Depositor
Minimum map value	-1.662	Depositor
Average map value	0.028	Depositor
Map value standard deviation	0.283	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	0.73	0/79178	0.69	65/123444 (0.1%)
2	8S	0.70	0/3747	0.67	5/5832 (0.1%)
3	5S	0.70	0/2884	0.64	0/4491
4	L1	0.79	0/1634	1.16	17/2195 (0.8%)
5	L2	0.63	0/1952	1.07	12/2622 (0.5%)
6	L3	0.73	0/3153	1.04	21/4239 (0.5%)
7	L4	0.75	0/2802	1.12	17/3792 (0.4%)
8	L5	0.69	1/2426 (0.0%)	0.97	7/3271 (0.2%)
9	L6	0.83	0/1261	1.07	7/1694 (0.4%)
10	L7	0.70	0/1822	1.13	14/2451 (0.6%)
11	L8	0.67	0/1850	1.06	11/2495 (0.4%)
12	L9	0.78	0/1540	1.03	14/2073 (0.7%)
13	50	0.66	0/1754	1.08	11/2350 (0.5%)
14	51	0.67	0/1375	0.93	3/1842 (0.2%)
15	53	0.72	0/1568	1.14	18/2106 (0.9%)
16	54	0.77	0/1069	1.09	6/1438 (0.4%)
17	55	0.63	0/1758	1.04	6/2354 (0.3%)
18	56	0.64	0/1586	1.20	13/2128 (0.6%)
19	57	0.70	0/1466	1.11	14/1968 (0.7%)
20	58	0.72	0/1466	1.07	9/1965 (0.5%)
21	59	0.55	0/1539	1.11	6/2050 (0.3%)
22	60	0.73	0/1482	1.02	5/1990 (0.3%)
23	61	0.72	0/1301	1.06	12/1743 (0.7%)
24	62	0.67	0/812	1.03	5/1099 (0.5%)
25	63	0.70	0/1019	1.03	4/1369 (0.3%)
26	64	0.68	0/521	1.09	8/691 (1.2%)
27	65	0.67	0/984	0.93	1/1325 (0.1%)
28	66	0.74	0/1005	1.09	8/1341 (0.6%)
29	67	0.62	0/1119	1.04	13/1497 (0.9%)
30	68	0.72	0/1205	1.11	12/1612 (0.7%)
31	69	0.60	0/474	1.16	4/629 (0.6%)
32	70	0.58	0/751	0.92	1/1008 (0.1%)
33	71	0.65	0/904	1.01	3/1213 (0.2%)
34	72	0.73	0/1041	1.04	3/1394 (0.2%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	73	0.76	0/869	1.11	11/1168 (0.9%)
36	74	0.63	0/891	1.12	5/1191 (0.4%)
37	75	0.61	0/979	1.10	4/1301 (0.3%)
38	76	0.65	0/779	1.14	7/1034 (0.7%)
39	77	0.61	0/697	0.98	2/923 (0.2%)
40	78	0.66	0/619	1.02	3/826 (0.4%)
41	79	0.59	0/444	0.97	1/588 (0.2%)
42	80	0.76	0/424	1.03	1/562 (0.2%)
43	81	0.93	0/235	1.13	2/300 (0.7%)
44	82	0.68	0/839	0.96	2/1108 (0.2%)
45	83	0.58	0/702	1.09	6/934 (0.6%)
46	1S	0.67	0/42445	0.68	41/66138 (0.1%)
47	S0	0.64	0/1653	1.00	9/2261 (0.4%)
48	S1	0.68	1/1735 (0.1%)	0.91	1/2335 (0.0%)
49	S2	0.59	0/1665	0.97	2/2263 (0.1%)
50	S3	0.67	0/1759	0.99	5/2368 (0.2%)
51	S4	0.64	0/2110	1.00	12/2839 (0.4%)
52	S5	0.67	0/1630	1.05	6/2202 (0.3%)
53	S6	0.65	0/1844	0.99	10/2464 (0.4%)
54	S7	0.67	0/1506	0.98	4/2028 (0.2%)
55	S8	0.60	0/1515	0.96	7/2021 (0.3%)
56	S9	0.55	0/1519	1.01	6/2035 (0.3%)
57	10	0.70	0/837	0.94	2/1131 (0.2%)
58	11	0.68	0/1273	0.99	7/1712 (0.4%)
59	12	0.82	0/943	1.03	3/1274 (0.2%)
60	13	0.64	1/1216 (0.1%)	1.08	7/1638 (0.4%)
61	14	0.64	0/953	1.07	10/1279 (0.8%)
62	15	0.81	0/1012	1.08	7/1356 (0.5%)
63	16	0.68	0/1126	0.98	4/1510 (0.3%)
64	17	0.69	0/974	1.04	4/1304 (0.3%)
65	18	0.69	0/1212	1.01	4/1628 (0.2%)
66	19	0.68	0/1131	1.09	9/1517 (0.6%)
67	20	0.79	0/866	1.00	4/1169 (0.3%)
68	21	0.61	0/694	0.99	2/935 (0.2%)
69	22	0.54	0/1039	0.95	1/1395 (0.1%)
70	23	0.58	0/1140	1.04	7/1518 (0.5%)
71	24	0.63	0/1088	0.97	2/1449 (0.1%)
72	25	0.72	0/571	1.03	2/768 (0.3%)
73	26	0.59	0/782	0.92	3/1047 (0.3%)
74	27	0.70	0/621	1.02	2/838 (0.2%)
75	28	0.67	0/500	0.91	1/670 (0.1%)
76	29	0.63	0/454	0.85	0/602
77	30	0.63	0/483	0.94	0/643

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
78	31	0.79	0/505	1.15	6/682 (0.9%)
79	RA	0.71	0/2498	0.89	7/3398 (0.2%)
All	All	0.70	3/219225 (0.0%)	0.84	596/322063 (0.2%)

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	92
2	8S	0	10
46	1S	1	37
All	All	1	139

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
8	L5	6	ASP	CA-C	5.82	1.55	1.52
60	13	22	ALA	CA-C	5.37	1.59	1.52
48	S1	189	ILE	CA-CB	5.32	1.57	1.54

The worst 5 of 596 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
46	1S	1573	A	C2'-C3'-O3'	12.92	128.88	109.50
46	1S	1761	U	C2'-C3'-O3'	12.00	127.50	109.50
18	56	101	ARG	N-CA-C	-10.94	100.20	114.31
52	S5	168	VAL	N-CA-C	-10.20	103.03	111.81
46	1S	1573	A	C4'-C3'-O3'	9.96	124.33	109.40

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
46	1S	1573	A	C3'

5 of 139 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	2S	148	G	Sidechain
1	2S	26	A	Sidechain

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group
1	2S	40	A	Sidechain
1	2S	59	G	Sidechain
1	2S	91	G	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	2039	0
2	8S	3354	0	1695	102	0
3	5S	2580	0	1304	64	0
4	L1	1609	0	1701	104	0
5	L2	1918	0	1987	170	0
6	L3	3082	0	3165	233	0
7	L4	2750	0	2863	189	0
8	L5	2376	0	2325	115	0
9	L6	1240	0	1326	94	0
10	L7	1785	0	1862	140	0
11	L8	1818	0	1908	112	0
12	L9	1519	0	1587	107	0
13	50	1718	0	1754	94	0
14	51	1354	0	1383	74	0
15	53	1543	0	1608	101	0
16	54	1054	0	1149	58	0
17	55	1721	0	1779	134	0
18	56	1556	0	1659	119	0
19	57	1443	0	1485	108	0
20	58	1442	0	1543	95	0
21	59	1522	0	1617	96	0
22	60	1446	0	1487	99	0
23	61	1277	0	1323	96	0
24	62	796	0	812	42	0
25	63	1004	0	1048	91	0
26	64	509	0	537	22	0
27	65	969	0	1036	67	0
28	66	994	0	1081	56	0
29	67	1093	0	1155	70	0
30	68	1174	0	1215	98	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
31	69	463	0	491	38	0
32	70	743	0	797	60	0
33	71	890	0	938	69	0
34	72	1020	0	1090	58	0
35	73	851	0	880	48	0
36	74	881	0	949	98	0
37	75	970	0	1078	62	0
38	76	772	0	849	48	0
39	77	682	0	687	69	0
40	78	613	0	682	39	0
41	79	437	0	475	29	0
42	80	418	0	459	27	0
43	81	234	0	284	9	0
44	82	827	0	901	47	0
45	83	695	0	738	63	0
46	1S	37949	0	19093	1113	0
47	S0	1612	0	1623	123	0
48	S1	1709	0	1784	129	0
49	S2	1635	0	1723	84	0
50	S3	1734	0	1817	88	0
51	S4	2069	0	2154	163	0
52	S5	1610	0	1675	112	0
53	S6	1820	0	1918	85	0
54	S7	1481	0	1572	102	0
55	S8	1490	0	1525	112	0
56	S9	1494	0	1573	124	0
57	10	817	0	804	66	0
58	11	1245	0	1314	73	0
59	12	935	0	975	65	0
60	13	1193	0	1255	88	0
61	14	942	0	979	90	0
62	15	991	0	1035	51	0
63	16	1106	0	1166	103	0
64	17	965	0	1026	77	0
65	18	1193	0	1222	89	0
66	19	1113	0	1124	71	0
67	20	856	0	917	70	0
68	21	685	0	672	46	0
69	22	1022	0	1060	100	0
70	23	1122	0	1196	103	0
71	24	1074	0	1132	63	0
72	25	563	0	603	52	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
73	26	769	0	818	84	0
74	27	611	0	633	32	0
75	28	498	0	535	47	0
76	29	444	0	436	14	0
77	30	475	0	525	48	0
78	31	498	0	441	13	0
79	RA	2445	0	2401	122	0
80	IR	198	0	0	0	0
All	All	204247	0	150969	8413	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 24.

The worst 5 of 8413 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)
1:2S:250:U:H5'	1:2S:251:G:H5''	1.25	1.16
46:1S:1712:A:H3'	46:1S:1713:G:H5''	1.26	1.15
60:13:22:ALA:HB1	60:13:23:PRO:HA	1.28	1.12
19:57:122:ALA:HB3	19:57:143:PRO:HB2	1.23	1.11
46:1S:845:G:H2'	46:1S:846:G:H5''	1.32	1.11

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%)	133 (66%)	52 (26%)	17 (8%)	0	9
5	L2	250/254 (98%)	199 (80%)	41 (16%)	10 (4%)	2	18
6	L3	384/387 (99%)	321 (84%)	52 (14%)	11 (3%)	3	23

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
7	L4	359/362 (99%)	290 (81%)	47 (13%)	22 (6%)	1	12
8	L5	294/297 (99%)	240 (82%)	41 (14%)	13 (4%)	2	17
9	L6	152/176 (86%)	132 (87%)	16 (10%)	4 (3%)	4	25
10	L7	220/244 (90%)	196 (89%)	19 (9%)	5 (2%)	5	28
11	L8	231/256 (90%)	190 (82%)	31 (13%)	10 (4%)	2	17
12	L9	189/191 (99%)	157 (83%)	27 (14%)	5 (3%)	4	25
13	50	207/221 (94%)	173 (84%)	30 (14%)	4 (2%)	6	32
14	51	167/174 (96%)	131 (78%)	27 (16%)	9 (5%)	1	14
15	53	191/199 (96%)	152 (80%)	25 (13%)	14 (7%)	1	10
16	54	134/138 (97%)	114 (85%)	14 (10%)	6 (4%)	2	16
17	55	201/204 (98%)	168 (84%)	28 (14%)	5 (2%)	4	26
18	56	195/199 (98%)	175 (90%)	15 (8%)	5 (3%)	4	25
19	57	181/184 (98%)	150 (83%)	26 (14%)	5 (3%)	4	24
20	58	183/186 (98%)	154 (84%)	25 (14%)	4 (2%)	5	29
21	59	186/189 (98%)	166 (89%)	16 (9%)	4 (2%)	5	29
22	60	170/172 (99%)	139 (82%)	26 (15%)	5 (3%)	3	23
23	61	157/160 (98%)	126 (80%)	19 (12%)	12 (8%)	1	10
24	62	98/121 (81%)	83 (85%)	12 (12%)	3 (3%)	3	22
25	63	134/137 (98%)	113 (84%)	20 (15%)	1 (1%)	18	56
26	64	59/155 (38%)	44 (75%)	14 (24%)	1 (2%)	7	36
27	65	119/142 (84%)	100 (84%)	16 (13%)	3 (2%)	4	26
28	66	124/127 (98%)	110 (89%)	13 (10%)	1 (1%)	16	54
29	67	133/136 (98%)	106 (80%)	23 (17%)	4 (3%)	3	22
30	68	146/149 (98%)	110 (75%)	27 (18%)	9 (6%)	1	12
31	69	56/59 (95%)	52 (93%)	3 (5%)	1 (2%)	6	34
32	70	95/105 (90%)	89 (94%)	5 (5%)	1 (1%)	11	46
33	71	107/113 (95%)	84 (78%)	20 (19%)	3 (3%)	4	24
34	72	125/130 (96%)	113 (90%)	12 (10%)	0	100	100
35	73	104/107 (97%)	80 (77%)	21 (20%)	3 (3%)	3	23
36	74	110/121 (91%)	92 (84%)	14 (13%)	4 (4%)	2	20
37	75	117/120 (98%)	108 (92%)	8 (7%)	1 (1%)	14	50

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
38	76	97/100 (97%)	81 (84%)	14 (14%)	2 (2%)	5	29
39	77	85/88 (97%)	70 (82%)	13 (15%)	2 (2%)	4	27
40	78	75/78 (96%)	69 (92%)	6 (8%)	0	100	100
41	79	48/51 (94%)	42 (88%)	5 (10%)	1 (2%)	5	29
42	80	50/128 (39%)	40 (80%)	9 (18%)	1 (2%)	6	31
43	81	23/25 (92%)	22 (96%)	1 (4%)	0	100	100
44	82	101/106 (95%)	88 (87%)	9 (9%)	4 (4%)	2	18
45	83	89/92 (97%)	74 (83%)	11 (12%)	4 (4%)	2	16
47	S0	204/252 (81%)	163 (80%)	30 (15%)	11 (5%)	1	14
48	S1	212/255 (83%)	152 (72%)	41 (19%)	19 (9%)	0	8
49	S2	215/254 (85%)	178 (83%)	27 (13%)	10 (5%)	2	16
50	S3	221/240 (92%)	181 (82%)	29 (13%)	11 (5%)	1	15
51	S4	258/261 (99%)	214 (83%)	35 (14%)	9 (4%)	3	20
52	S5	204/225 (91%)	164 (80%)	30 (15%)	10 (5%)	1	15
53	S6	224/236 (95%)	193 (86%)	25 (11%)	6 (3%)	4	25
54	S7	182/190 (96%)	138 (76%)	29 (16%)	15 (8%)	0	9
55	S8	184/200 (92%)	151 (82%)	29 (16%)	4 (2%)	5	29
56	S9	183/197 (93%)	153 (84%)	21 (12%)	9 (5%)	1	15
57	10	94/105 (90%)	75 (80%)	13 (14%)	6 (6%)	1	12
58	11	153/156 (98%)	108 (71%)	36 (24%)	9 (6%)	1	13
59	12	122/143 (85%)	85 (70%)	23 (19%)	14 (12%)	0	5
60	13	148/151 (98%)	123 (83%)	22 (15%)	3 (2%)	6	31
61	14	125/137 (91%)	95 (76%)	24 (19%)	6 (5%)	2	16
62	15	122/142 (86%)	90 (74%)	22 (18%)	10 (8%)	0	9
63	16	139/143 (97%)	114 (82%)	18 (13%)	7 (5%)	1	15
64	17	116/136 (85%)	98 (84%)	14 (12%)	4 (3%)	3	21
65	18	143/146 (98%)	115 (80%)	19 (13%)	9 (6%)	1	12
66	19	141/144 (98%)	117 (83%)	20 (14%)	4 (3%)	4	24
67	20	105/121 (87%)	88 (84%)	13 (12%)	4 (4%)	2	19
68	21	85/87 (98%)	69 (81%)	10 (12%)	6 (7%)	1	10
69	22	127/130 (98%)	108 (85%)	16 (13%)	3 (2%)	4	27

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
70	23	142/145 (98%)	102 (72%)	32 (22%)	8 (6%)	1	14
71	24	132/135 (98%)	103 (78%)	23 (17%)	6 (4%)	2	16
72	25	68/108 (63%)	46 (68%)	16 (24%)	6 (9%)	0	8
73	26	95/119 (80%)	62 (65%)	21 (22%)	12 (13%)	0	4
74	27	79/82 (96%)	59 (75%)	16 (20%)	4 (5%)	1	15
75	28	61/67 (91%)	50 (82%)	10 (16%)	1 (2%)	7	37
76	29	51/56 (91%)	44 (86%)	5 (10%)	2 (4%)	2	18
77	30	58/63 (92%)	42 (72%)	11 (19%)	5 (9%)	0	9
78	31	69/152 (45%)	42 (61%)	18 (26%)	9 (13%)	0	4
79	RA	316/319 (99%)	250 (79%)	53 (17%)	13 (4%)	2	17
All	All	11126/12097 (92%)	9048 (81%)	1604 (14%)	474 (4%)	3	17

5 of 474 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	L1	20	SER
4	L1	153	SER
4	L1	193	LEU
4	L1	199	GLN
4	L1	209	SER

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%)	167 (90%)	18 (10%)	8	25
5	L2	194/196 (99%)	180 (93%)	14 (7%)	13	35
6	L3	322/323 (100%)	300 (93%)	22 (7%)	14	36
7	L4	288/289 (100%)	265 (92%)	23 (8%)	11	31
8	L5	244/245 (100%)	226 (93%)	18 (7%)	13	33
9	L6	134/153 (88%)	124 (92%)	10 (8%)	12	33

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
10	L7	186/205 (91%)	174 (94%)	12 (6%)	15	37
11	L8	191/208 (92%)	173 (91%)	18 (9%)	8	26
12	L9	171/171 (100%)	158 (92%)	13 (8%)	12	33
13	50	180/187 (96%)	168 (93%)	12 (7%)	15	36
14	51	147/150 (98%)	139 (95%)	8 (5%)	20	41
15	53	154/159 (97%)	142 (92%)	12 (8%)	11	32
16	54	107/109 (98%)	102 (95%)	5 (5%)	23	44
17	55	175/176 (99%)	163 (93%)	12 (7%)	14	36
18	56	160/162 (99%)	148 (92%)	12 (8%)	12	33
19	57	145/146 (99%)	134 (92%)	11 (8%)	12	33
20	58	150/151 (99%)	139 (93%)	11 (7%)	13	34
21	59	153/154 (99%)	140 (92%)	13 (8%)	10	29
22	60	156/156 (100%)	147 (94%)	9 (6%)	18	40
23	61	136/137 (99%)	127 (93%)	9 (7%)	15	37
24	62	87/107 (81%)	86 (99%)	1 (1%)	65	76
25	63	104/105 (99%)	96 (92%)	8 (8%)	12	32
26	64	54/129 (42%)	51 (94%)	3 (6%)	19	40
27	65	105/118 (89%)	96 (91%)	9 (9%)	10	29
28	66	109/110 (99%)	106 (97%)	3 (3%)	38	59
29	67	115/116 (99%)	110 (96%)	5 (4%)	26	47
30	68	118/119 (99%)	109 (92%)	9 (8%)	12	33
31	69	46/47 (98%)	40 (87%)	6 (13%)	4	15
32	70	81/88 (92%)	77 (95%)	4 (5%)	22	43
33	71	96/97 (99%)	88 (92%)	8 (8%)	10	30
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%)	87 (92%)	8 (8%)	10	30
37	75	104/105 (99%)	95 (91%)	9 (9%)	9	29
38	76	81/82 (99%)	74 (91%)	7 (9%)	10	29
39	77	70/71 (99%)	62 (89%)	8 (11%)	5	18
40	78	68/69 (99%)	64 (94%)	4 (6%)	18	39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	79	45/46 (98%)	40 (89%)	5 (11%)	6	20
42	80	47/116 (40%)	44 (94%)	3 (6%)	16	37
43	81	23/23 (100%)	19 (83%)	4 (17%)	2	9
44	82	88/91 (97%)	76 (86%)	12 (14%)	3	14
45	83	71/72 (99%)	66 (93%)	5 (7%)	14	35
47	S0	173/210 (82%)	163 (94%)	10 (6%)	18	40
48	S1	191/224 (85%)	174 (91%)	17 (9%)	9	28
49	S2	176/205 (86%)	169 (96%)	7 (4%)	28	49
50	S3	182/195 (93%)	169 (93%)	13 (7%)	13	35
51	S4	221/222 (100%)	204 (92%)	17 (8%)	12	32
52	S5	173/191 (91%)	164 (95%)	9 (5%)	21	42
53	S6	193/201 (96%)	185 (96%)	8 (4%)	27	48
54	S7	165/170 (97%)	154 (93%)	11 (7%)	15	36
55	S8	150/161 (93%)	144 (96%)	6 (4%)	28	49
56	S9	158/166 (95%)	146 (92%)	12 (8%)	12	33
57	10	89/98 (91%)	82 (92%)	7 (8%)	11	32
58	11	136/137 (99%)	128 (94%)	8 (6%)	18	39
59	12	100/119 (84%)	85 (85%)	15 (15%)	3	12
60	13	127/128 (99%)	113 (89%)	14 (11%)	6	20
61	14	96/105 (91%)	92 (96%)	4 (4%)	26	48
62	15	104/118 (88%)	96 (92%)	8 (8%)	12	32
63	16	117/119 (98%)	110 (94%)	7 (6%)	17	39
64	17	109/124 (88%)	94 (86%)	15 (14%)	3	14
65	18	128/129 (99%)	119 (93%)	9 (7%)	14	35
66	19	115/116 (99%)	106 (92%)	9 (8%)	11	32
67	20	100/114 (88%)	94 (94%)	6 (6%)	17	39
68	21	74/74 (100%)	70 (95%)	4 (5%)	20	41
69	22	110/111 (99%)	102 (93%)	8 (7%)	13	34
70	23	119/120 (99%)	103 (87%)	16 (13%)	4	14
71	24	112/113 (99%)	109 (97%)	3 (3%)	39	60
72	25	61/89 (68%)	52 (85%)	9 (15%)	3	13

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
73	26	83/101 (82%)	73 (88%)	10 (12%)	5	17
74	27	70/71 (99%)	69 (99%)	1 (1%)	59	72
75	28	56/60 (93%)	53 (95%)	3 (5%)	20	41
76	29	47/49 (96%)	46 (98%)	1 (2%)	47	65
77	30	51/54 (94%)	48 (94%)	3 (6%)	18	39
78	31	43/135 (32%)	38 (88%)	5 (12%)	5	18
79	RA	261/262 (100%)	245 (94%)	16 (6%)	17	38
All	All	9474/10182 (93%)	8785 (93%)	689 (7%)	15	34

5 of 689 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
52	S5	84	LYS
64	17	34	LEU
53	S6	155	ASP
52	S5	25	LEU
58	11	102	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 327 such sidechains are listed below:

Mol	Chain	Res	Type
52	S5	122	ASN
66	19	127	ASN
53	S6	59	GLN
60	13	21	ASN
71	24	15	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	2S	3304/3395 (97%)	521 (15%)	26 (0%)
2	8S	157/158 (99%)	22 (14%)	1 (0%)
3	5S	120/121 (99%)	10 (8%)	0
46	1S	1779/1798 (98%)	332 (18%)	21 (1%)
80	IR	0/201	-	-
All	All	5360/5673 (94%)	885 (16%)	48 (0%)

5 of 885 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	2S	21	G
1	2S	26	A
1	2S	40	A
1	2S	43	A
1	2S	49	A

5 of 48 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
46	1S	103	A
46	1S	555	A
46	1S	139	C
46	1S	498	G
46	1S	794	U

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.

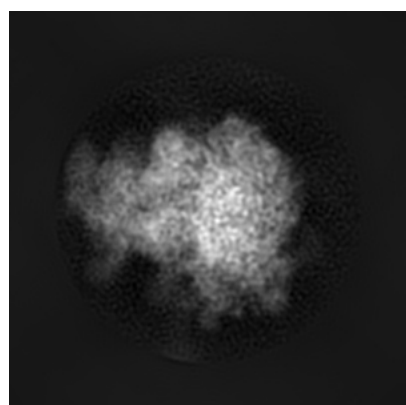
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-5943. These allow visual inspection of the internal detail of the map and identification of artifacts.

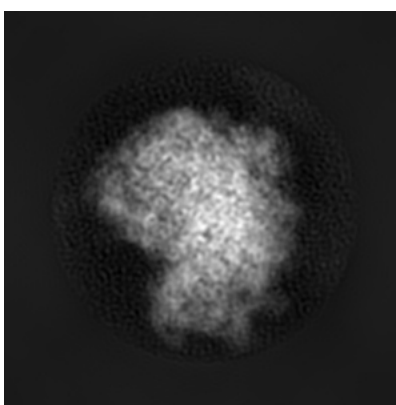
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

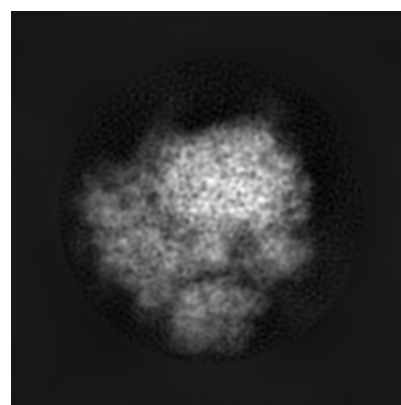
6.1.1 Primary map



X



Y

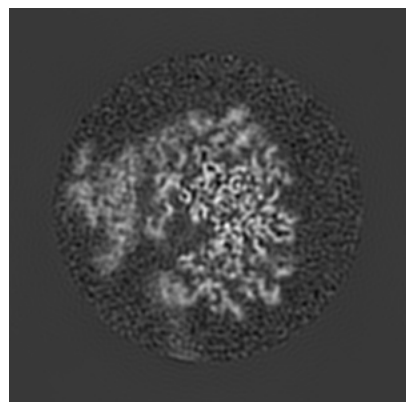


Z

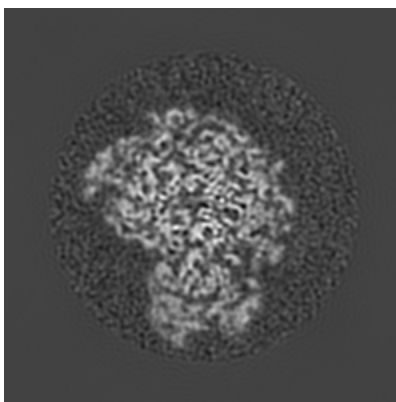
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

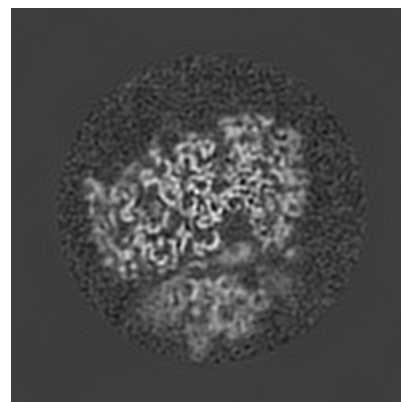
6.2.1 Primary map



X Index: 210



Y Index: 210

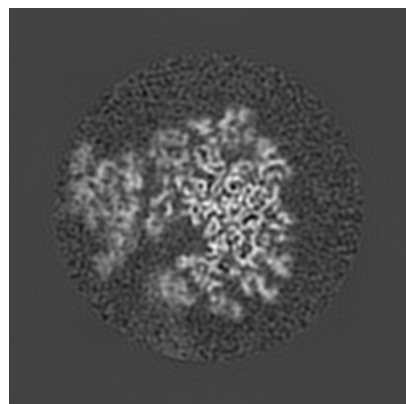


Z Index: 210

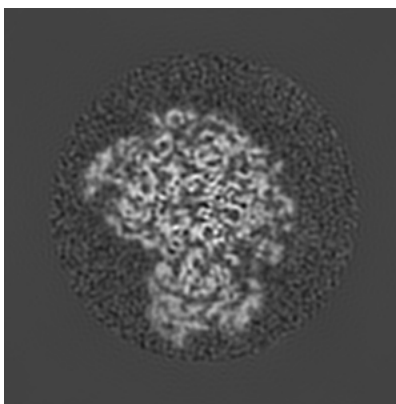
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

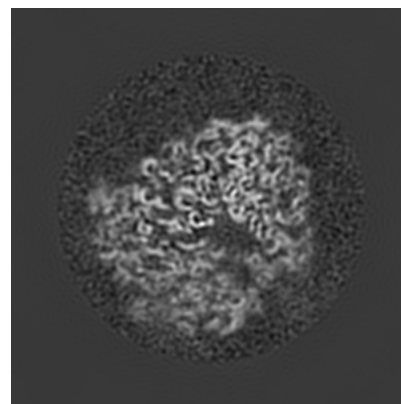
6.3.1 Primary map



X Index: 206



Y Index: 209

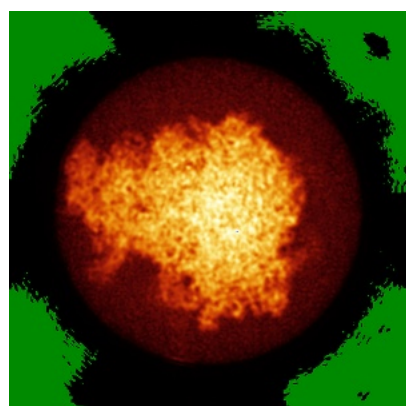


Z Index: 199

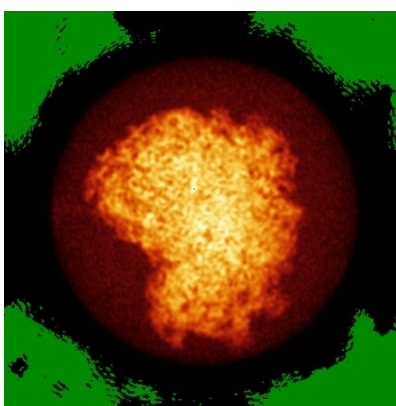
The images above show the largest variance slices of the map in three orthogonal directions.

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

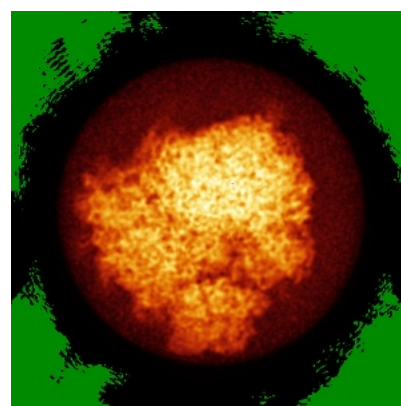
6.4.1 Primary map



X



Y

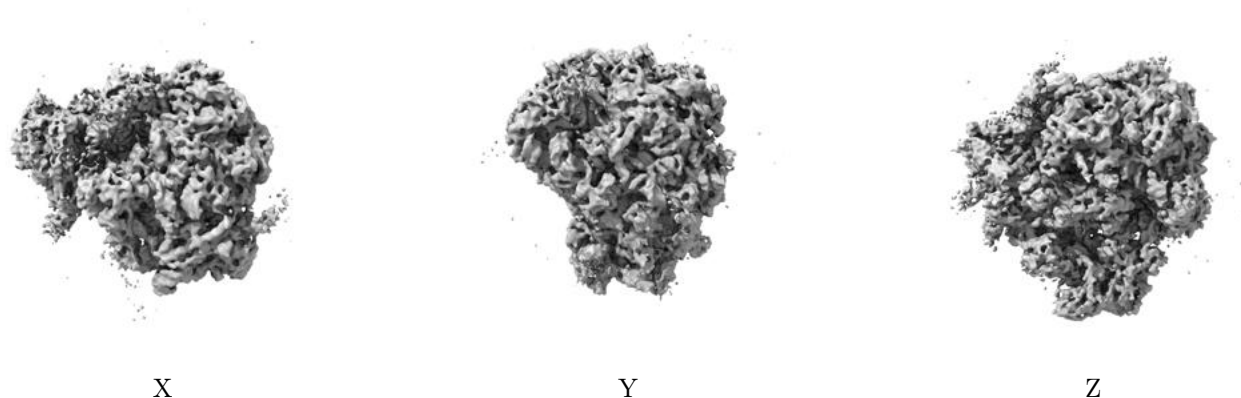


Z

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.

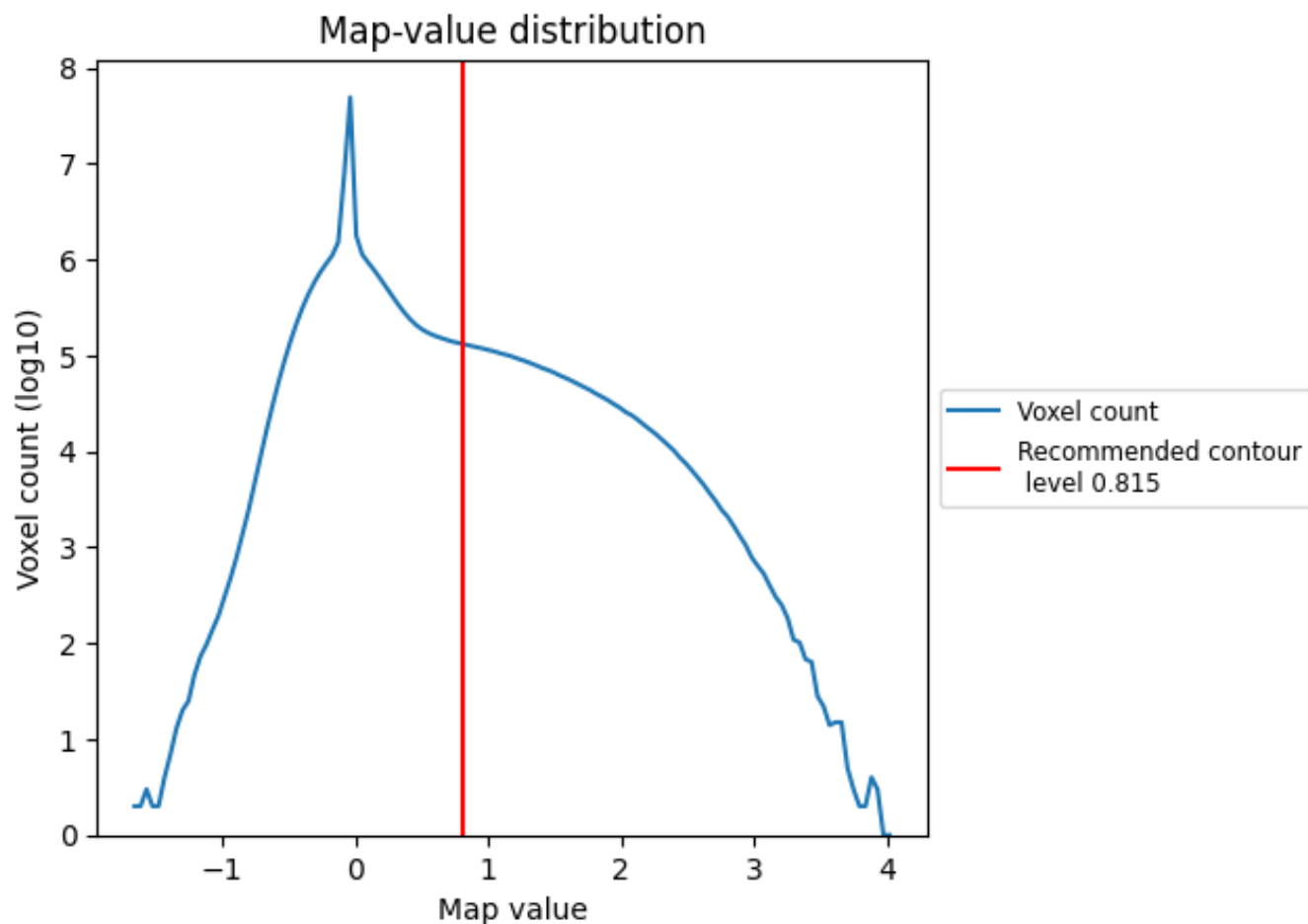
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

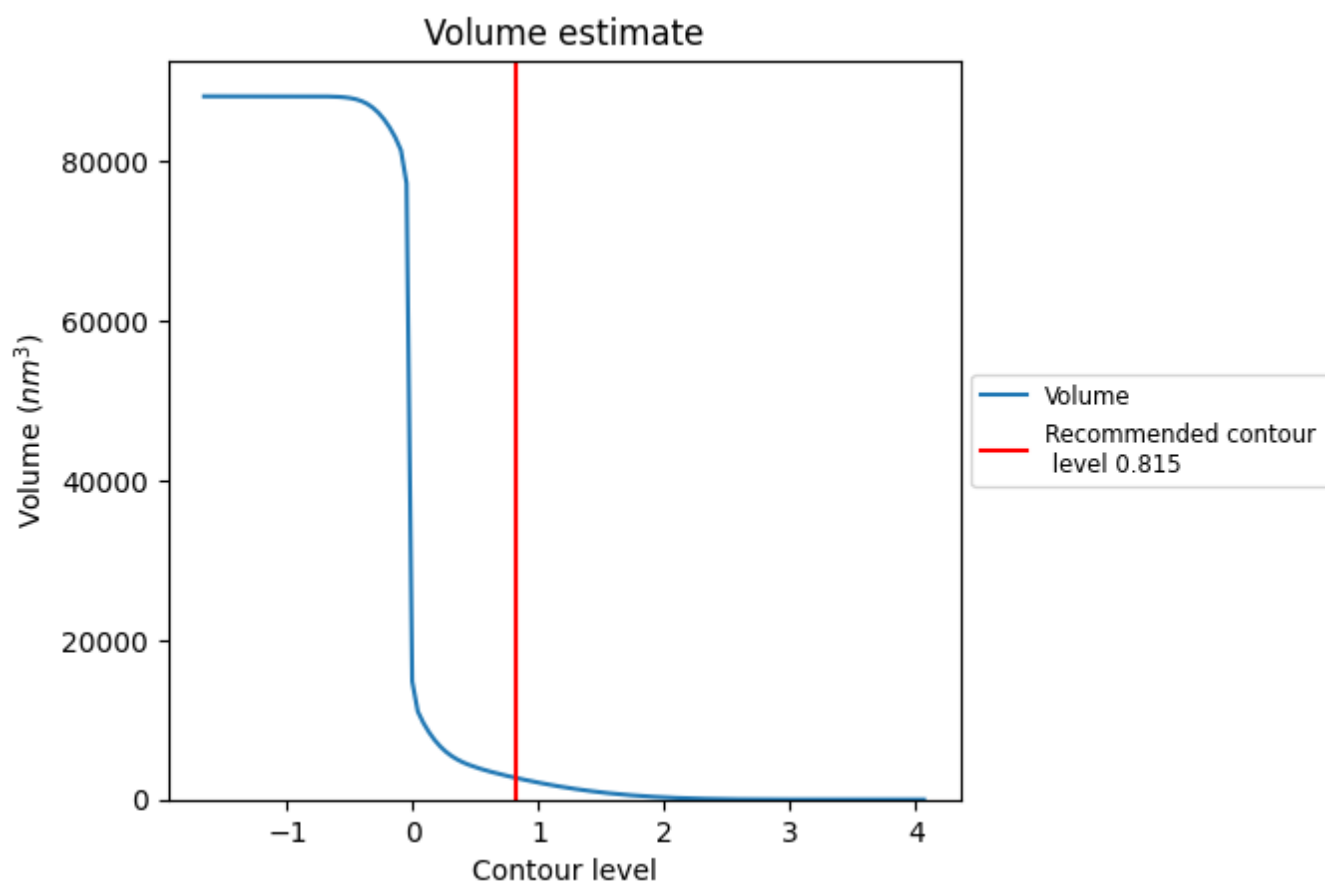
This section contains the results of statistical analysis of the map.

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.

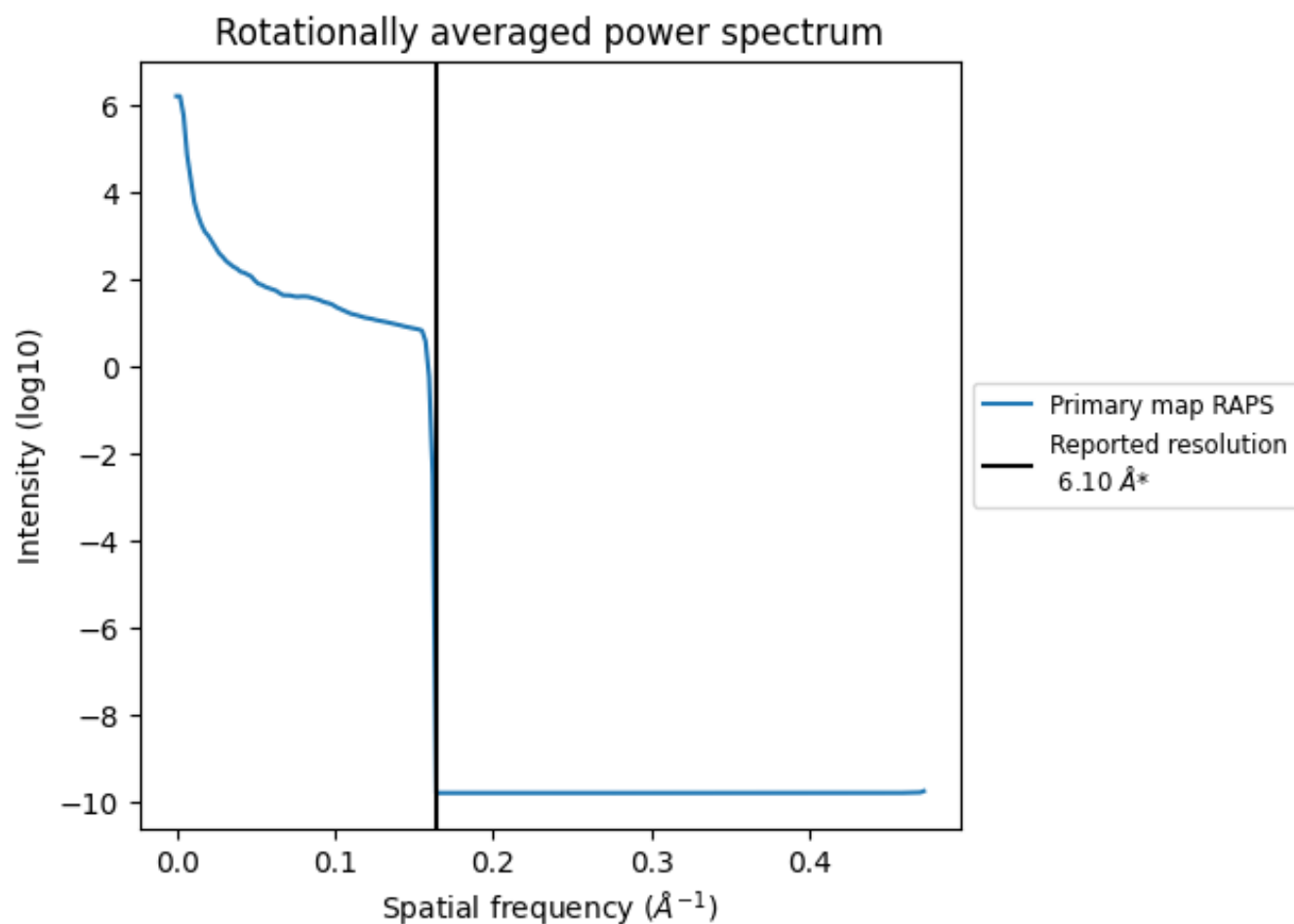
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2733 nm³; this corresponds to an approximate mass of 2468 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 $\text{\AA}^{-1}$

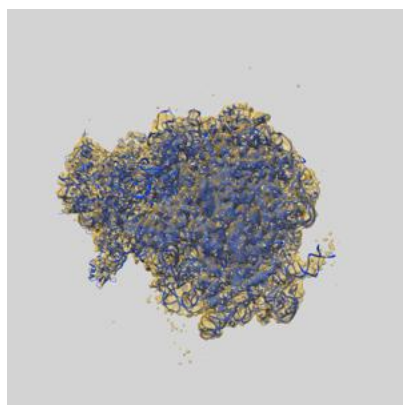
8 Fourier-Shell correlation

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

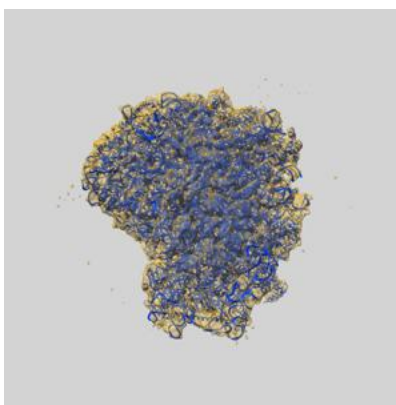
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-5943 and PDB model 3J6Y. Per-residue inclusion information can be found in [section 3](#) on [page 19](#).

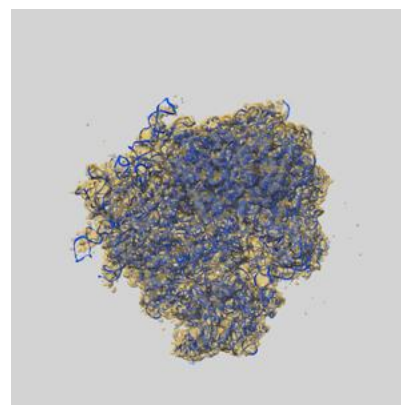
9.1 Map-model overlay [i](#)



X



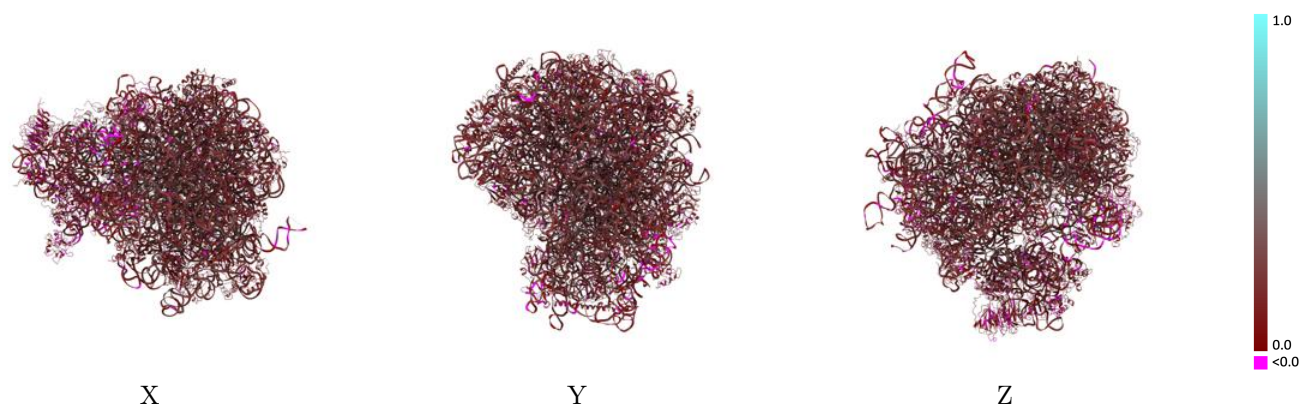
Y



Z

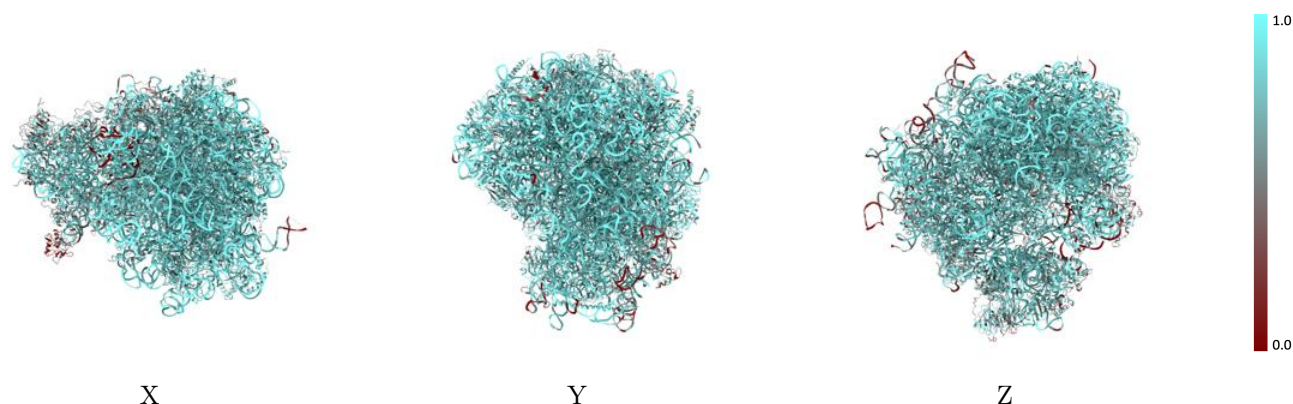
The images above show the 3D surface view of the map at the recommended contour level 0.815 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



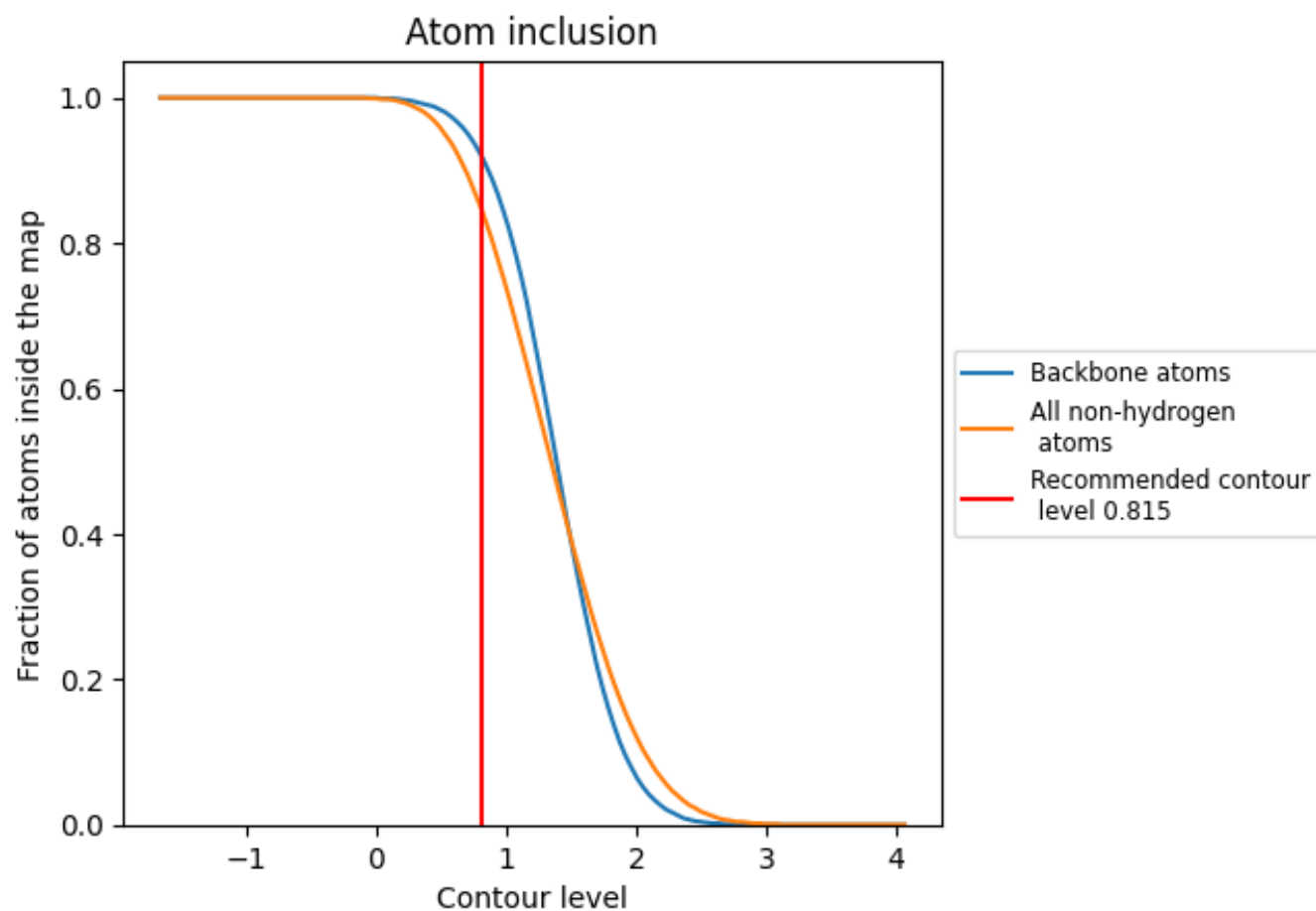
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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



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	 0.8440	 0.2020
10	 0.6900	 0.1580
11	 0.7270	 0.1970
12	 0.1660	 0.1130
13	 0.6980	 0.1670
14	 0.7520	 0.1680
15	 0.5220	 0.1310
16	 0.6880	 0.1380
17	 0.5910	 0.1590
18	 0.6440	 0.1380
19	 0.6520	 0.1110
1S	 0.9160	 0.2110
20	 0.6120	 0.1440
21	 0.7070	 0.1910
22	 0.7540	 0.1790
23	 0.7750	 0.1890
24	 0.6710	 0.1500
25	 0.6560	 0.1670
26	 0.7380	 0.1850
27	 0.6730	 0.1710
28	 0.6510	 0.1470
29	 0.6990	 0.1240
2S	 0.9440	 0.2330
30	 0.7450	 0.2020
31	 0.2810	 0.1520
50	 0.7770	 0.1990
51	 0.7460	 0.1640
53	 0.7630	 0.1880
54	 0.7540	 0.1740
55	 0.7670	 0.1580
56	 0.7850	 0.1730
57	 0.7690	 0.1840
58	 0.7760	 0.1800
59	 0.7490	 0.1840
5S	 0.9710	 0.2270



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Chain	Atom inclusion	Q-score
60	 0.7610	 0.1720
61	 0.7940	 0.1990
62	 0.7420	 0.1890
63	 0.7860	 0.1940
64	 0.8010	 0.1850
65	 0.7740	 0.1930
66	 0.7770	 0.1750
67	 0.7500	 0.1800
68	 0.7790	 0.1840
69	 0.7770	 0.2060
70	 0.7520	 0.1950
71	 0.7800	 0.1930
72	 0.8040	 0.1970
73	 0.7930	 0.1680
74	 0.7720	 0.1700
75	 0.7610	 0.1750
76	 0.7450	 0.1760
77	 0.8160	 0.1630
78	 0.7120	 0.1760
79	 0.7740	 0.1920
80	 0.7330	 0.1660
81	 0.0470	 0.0400
82	 0.7720	 0.1930
83	 0.8100	 0.1920
8S	 0.9710	 0.2410
IR	 0.6460	 0.1160
L1	 0.4280	 0.0990
L2	 0.8020	 0.1960
L3	 0.7860	 0.1840
L4	 0.8050	 0.1940
L5	 0.7070	 0.1560
L6	 0.7820	 0.1880
L7	 0.7840	 0.1790
L8	 0.7500	 0.1840
L9	 0.7540	 0.1760
RA	 0.6500	 0.1330
S0	 0.6920	 0.1850
S1	 0.6750	 0.1730
S2	 0.7680	 0.1920
S3	 0.7040	 0.1830
S4	 0.7660	 0.1680
S5	 0.6510	 0.1450

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Chain	Atom inclusion	Q-score
S6	 0.7290	 0.1530
S7	 0.5870	 0.1690
S8	 0.7820	 0.1770
S9	 0.7450	 0.1600