



wwPDB EM Validation Summary Report ⓘ

Oct 6, 2024 – 11:27 am BST

PDB ID : 6SPF
EMDB ID : EMD-10284
Title : Pseudomonas aeruginosa 70s ribosome from an aminoglycoside resistant clinical isolate
Authors : Halfon, Y.; Jimenez-Fernande, A.; La Ros, R.; Espinos, R.; Krogh Johansen, H.; Matzov, D.; Eyal, Z.; Bashan, A.; Zimmerman, E.; Belousoff, M.; Molin, S.; Yonath, A.
Deposited on : 2019-09-01
Resolution : 2.89 Å(reported)

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

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

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

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

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

EMDB validation analysis : 0.0.1.dev113
MolProbity : 4.02b-467
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

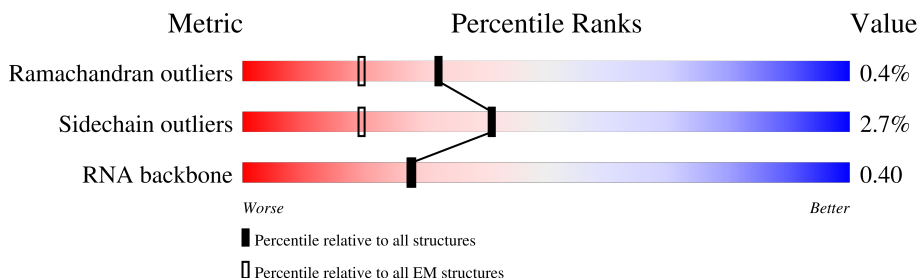
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.89 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	2888	<div> <div>8%</div> <div>64%</div> <div>31%</div> <div>5%</div> </div>
2	B	117	<div> <div>6%</div> <div>54%</div> <div>40%</div> <div>6%</div> </div>
3	C	271	<div> <div>94%</div> <div>6%</div> </div>
4	D	207	<div> <div>80%</div> <div>16%</div> <div>.</div> </div>
5	E	199	<div> <div>98%</div> <div>.</div> </div>
6	F	174	<div> <div>57%</div> <div>96%</div> <div>.</div> </div>
7	G	169	<div> <div>59%</div> <div>99%</div> <div>.</div> </div>
8	H	78	<div> <div>65%</div> <div>99%</div> <div>.</div> </div>

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Mol	Chain	Length	Quality of chain
9	I	140	<div> <div>100%</div> <div>98%</div> </div>
10	J	141	<div> <div>99%</div> </div>
11	K	120	<div> <div>97%</div> </div>
12	L	144	<div> <div>98%</div> </div>
13	M	136	<div> <div>99%</div> </div>
14	N	120	<div> <div>98%</div> </div>
15	O	115	<div> <div>38%</div> <div>96%</div> </div>
16	P	114	<div> <div>97%</div> </div>
17	Q	117	<div> <div>97%</div> </div>
18	R	102	<div> <div>5%</div> <div>95%</div> <div>5%</div> </div>
19	S	110	<div> <div>98%</div> </div>
20	T	94	<div> <div>97%</div> </div>
21	U	103	<div> <div>6%</div> <div>99%</div> </div>
22	V	188	<div> <div>97%</div> </div>
23	W	76	<div> <div>99%</div> </div>
24	X	77	<div> <div>99%</div> </div>
25	Y	60	<div> <div>98%</div> </div>
26	Z	57	<div> <div>96%</div> </div>
27	1	31	<div> <div>100%</div> <div>100%</div> </div>
28	2	53	<div> <div>98%</div> </div>
29	3	50	<div> <div>44%</div> <div>98%</div> </div>
30	4	44	<div> <div>98%</div> </div>
31	5	63	<div> <div>97%</div> </div>
32	6	38	<div> <div>97%</div> </div>
33	a	1521	<div> <div>32%</div> <div>51%</div> <div>38%</div> <div>9%</div> </div>

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Mol	Chain	Length	Quality of chain
34	b	226	80% 94% 99% 100%
35	c	203	76% 98% 70% 97%
36	d	204	87% 99% 97% 98%
37	e	150	58% 95% 91% 97%
38	f	100	99% 99% 99% 99%
39	g	154	83% 98% 72% 97%
40	h	129	93% 95% 98% 98%
41	i	126	59% 91% 46% 99%
42	j	96	34% 96% 82% 98%
43	k	115	29% 100% 97% 96%
44	l	120	29% 100% 97% 96%
45	m	110	29% 100% 97% 96%
46	n	98	29% 100% 97% 96%
47	o	87	29% 100% 97% 96%
48	p	78	29% 100% 97% 96%
49	q	76	29% 100% 97% 96%
50	r	56	29% 100% 97% 96%
51	s	80	29% 100% 97% 96%
52	t	86	29% 100% 97% 96%
53	u	34	29% 100% 97% 96%

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 138296 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 *Pseudomonas aeruginosa* strain PAO1 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	2885	Total	C	N	O	P	0	0
			61899	27618	11351	20046	2884		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	117	Total	C	N	O	P	0	0
			2495	1114	448	816	117		

- Molecule 3 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	271	Total	C	N	O	S	0	0
			2048	1258	422	362	6		

- Molecule 4 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	207	Total	C	N	O	S	0	0
			1549	960	297	287	5		

- Molecule 5 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	E	199	Total	C	N	O	S	0	0
			1509	948	281	278	2		

- Molecule 6 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	F	174	Total	C	N	O	S	0	0
			1278	806	225	244	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	7	LEU	ILE	conflict	UNP A0A072ZMU2

- Molecule 7 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	G	169	Total	C	N	O	S	0	0
			1264	795	233	234	2		

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
G	?	-	GLY	deletion	UNP A0A2V3F3S9
G	?	-	TYR	deletion	UNP A0A2V3F3S9
G	?	-	LYS	deletion	UNP A0A2V3F3S9
G	?	-	ALA	deletion	UNP A0A2V3F3S9

- Molecule 8 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	H	78	Total	C	N	O		0	0
			577	363	104	110			

- Molecule 9 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	I	140	Total	C	N	O	S	0	0
			1026	642	183	198	3		

- Molecule 10 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	141	Total	C	N	O	S	0	0
			1122	713	205	201	3		

- Molecule 11 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	120	Total	C	N	O	S	0	0
			922	576	178	162	6		

- Molecule 12 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	L	144	Total	C	N	O	S	0	0
			1063	653	214	193	3		

- Molecule 13 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	M	136	Total	C	N	O	S	0	0
			1076	684	210	179	3		

- Molecule 14 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	120	Total	C	N	O	S	0	0
			959	600	192	162	5		

- Molecule 15 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	115	Total	C	N	O	S	0	0
			881	544	174	161	2		

- Molecule 16 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	P	114	Total	C	N	O	S	0	0
			901	567	171	162	1		

- Molecule 17 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	117	Total	C	N	O	0	0
			936	592	196	148		

- Molecule 18 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	102	Total	C	N	O	S	0	0
			801	509	154	136	2		

- Molecule 19 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	S	110	Total	C	N	O	S	0	0
			833	515	161	153	4		

- Molecule 20 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	94	Total	C	N	O	S	0	0
			732	469	132	130	1		

- Molecule 21 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	U	103	Total	C	N	O	S	0	0
			801	503	152	144	2		

- Molecule 22 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	V	188	Total	C	N	O	S	0	0
			1397	888	254	253	2		

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	6	VAL	LEU	conflict	UNP A0A072ZBM5
V	71	VAL	ALA	conflict	UNP A0A072ZBM5

- Molecule 23 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
23	W	76	Total	C	N	O	0	0
			574	365	110	99		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
W	40	LEU	GLN	conflict	UNP A0A071LFT4

- Molecule 24 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	X	77	Total	C	N	O	S	0	0
			626	389	134	101	2		

- Molecule 25 is a protein called Ribosomal protein uL29.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	Y	60	Total	C	N	O	S	0	0
			468	286	96	85	1		

- Molecule 26 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	Z	57	Total	C	N	O	S	0	0
			445	277	87	79	2		

- Molecule 27 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	1	31	Total	C	N	O	S	0	0
			232	144	40	45	3		

- Molecule 28 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	2	53	Total	C	N	O	S	0	0
			419	251	89	78	1		

- Molecule 29 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
29	3	50	Total	C	N	O	0	0
			408	262	74	72		

- Molecule 30 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	4	44	Total	C	N	O	S	0	0
			364	222	87	53	2		

- Molecule 31 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	5	63	Total	C	N	O	S	0	0
			502	311	107	81	3		

- Molecule 32 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	6	38	Total	C	N	O	S	0	0
			303	184	69	46	4		

- Molecule 33 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	a	1390	Total	C	N	O	P	0	0
			29826	13303	5479	9654	1390		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
a	101	A	G	conflict	GB 1378074500

- Molecule 34 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	b	221	Total	C	N	O	S	0	0
			1698	1070	309	310	9		

- Molecule 35 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	c	203	Total	C	N	O	S	0	0
			1609	1017	303	284	5		

- Molecule 36 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	d	204	Total	C	N	O	S	0	0
			1596	988	310	293	5		

- Molecule 37 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	e	149	Total	C	N	O	S	0	0
			1092	687	202	197	6		

- Molecule 38 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	f	100	Total	C	N	O	S	0	0
			802	497	152	149	4		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
f	80	ALA	TYR	conflict	UNP A0A069Q263

- Molecule 39 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	g	154	Total	C	N	O	S	0	0
			1190	747	227	211	5		

- Molecule 40 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	h	129	Total	C	N	O	S	0	0
			965	608	171	180	6		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
h	94	ALA	LYS	conflict	UNP E2RXT9

- Molecule 41 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	i	126	Total	C	N	O	S	0	0
			994	616	198	179	1		

- Molecule 42 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	j	96	Total	C	N	O	S	0	0
			763	479	143	140	1		

- Molecule 43 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	k	115	Total	C	N	O	S	0	0
			832	514	160	156	2		

- Molecule 44 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	l	120	Total	C	N	O	S	0	0
			942	577	195	166	4		

- Molecule 45 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	m	109	Total	C	N	O	S	0	0
			847	515	173	155	4		

- Molecule 46 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	n	98	Total	C	N	O	S	0	0
			776	479	163	131	3		

- Molecule 47 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	o	87	Total	C	N	O	S	0	0
			691	428	135	127	1		

- Molecule 48 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	p	78	Total	C	N	O	S	0	0
			609	381	120	107	1		

- Molecule 49 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	q	76	Total	C	N	O	S	0	0
			619	387	120	110	2		

- Molecule 50 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
50	r	56	Total	C	N	O	0	0
			443	283	79	81		

- Molecule 51 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	s	80	Total	C	N	O	S	0	0
			635	405	121	106	3		

- Molecule 52 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	t	86	Total	C	N	O	S	0	0
			662	410	137	113	2		

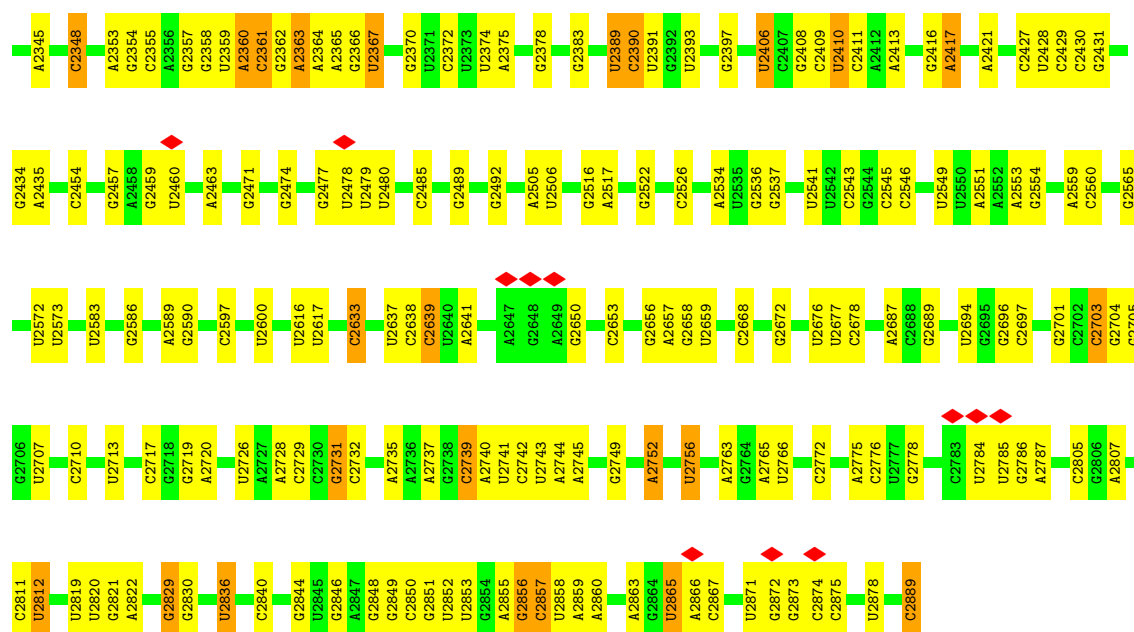
- Molecule 53 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms				AltConf	Trace
53	u	34	Total	C	N	O	0	0
			295	178	70	47		

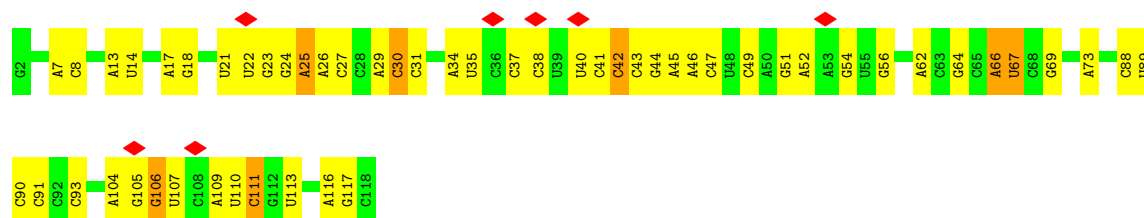
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
u	46	ARG	LYS	conflict	UNP A0A069QC99

A2274	C2094	U1769	G1643	U	G1306	G1199	A1096	U1035
A2275	U2095	A1770	U1652	U	C1307	U1204	G1097	A1036
G2276	U2096	A1771	G1657	A1526	A1308	G1205	U1098	G1037
U2277	G2097	A1774	C1660	G1527	G1311	A1211	C1099	A1038
G2278	U2098	C1775	G1664	A1528	U1316	G1212	G1100	G1041
C2280	G2099	C1780	C1665	U1529	C1317	A1213	A1101	C1042
G2281	U2100	C1787	A1666	U1530	C1320	A1214	U1103	U1043
U2283	A2101	A1788	C1671	A1531	C1322	C1220	A1044	A1044
C2289	G2102	A1789	U1683	C1532	U1327	U1221	G1045	G1045
G2290	G2103	A1790	C1684	U1537	U1328	G1222	G1046	G1046
G2291	A2104	C1791	U1686	G1542	U1331	G1223	A1047	A1047
U2292	U2105	A1795	C1688	U1549	C1332	A1224	G1048	G1048
G2293	A2106	A1796	G1689	U1556	G1333	G1226	G1049	G1049
C2294	G2107	A1802	U1686	A1557	U1334	U1227	U1050	U1050
G2295	U2108	A1797	G1686	C1555	U1339	A1228	G1121	G1121
U2296	G2109	G1798	G1700	U1556	U1346	U1229	U1051	U1051
A2297	A2020	G1801	U1708	A1557	A1346	A1233	G1052	G1052
G2298	U2021	A1802	C1803	A1558	U1463	A1234	G1053	G1053
U2299	G2022	C1803	A1710	U1559	U1468	A1235	A1124	A1124
C2300	C2023	U1807	A1711	A1560	G1469	U1236	C1054	C1054
G2301	U2030	U1814	U1715	U1568	U1352	G1237	U1055	U1055
C2304	C2031	C1817	U1716	G1571	A1355	C1238	U1056	U1056
U2117	G2034	U1817	U1717	C1572	G1356	U1239	A1057	A1057
U2118	A2039	C1820	A1718	U1573	C1357	A1240	G1058	G1058
U2119	C2042	U1823	C1719	U1574	G1361	U1242	A1059	A1059
G2120	G2043	G1829	U1720	A1576	U1362	G1243	A1060	A1060
A2121	A2047	A1834	U1724	A1580	C1363	A1249	G1061	G1061
G2122	G2048	A1835	A1725	U1596	U1366	G1253	C1062	C1062
C2123	U1927	U1835	G1736	C1597	G1367	U1254	A1063	A1063
C2124	U1930	U1838	C1739	A1495	G1368	G1258	G1064	G1064
G2125	U1938	A1841	G1740	A1496	G1369	A1259	C1065	C1065
U2126	G2056	U1841	A1741	A1598	A1370	G1260	C1066	C1066
G2127	U2059	A1853	A1742	A1600	A1372	A1261	A1067	A1067
G2128	C2060	G1854	U1745	C1601	C1373	U1262	C1068	C1068
A2129	U2063	C1855	A1746	G1603	A1382	U1263	C1069	C1069
C2130	A2064	G1856	G1750	G1616	U1507	A1271	C1070	C1070
G2131	G1954	C1857	G1751	A1622	G1508	C1276	U1071	U1071
C2132	U1957	A1858	C1755	A1624	A1509	A1281	U1072	U1072
C2133	G1959	G1860	U1756	C1629	U1510	G1288	U1073	U1073
G2135	U1968	A1862	G1757	C1634	G1511	A1288	A1074	A1074
U2136	A1968	G1863	U1758	G1635	A1515	A1288	A1076	A1076
U2137	U1969	A1864	G1759	C1636	G1516	C1292	G1077	G1077
C2138	C1972	G1865	C1761	U1637	U1517	C1293	A1078	A1078
G2139	U1976	U1871	U1762	U1638	C1518	U1289	A1079	A1079
C2140	U1979	A1872	G1763	G1639	G1519	U1300	A1080	A1080
U2142	G2093	U1873	U1768	A1640	U1520	C1301	G1081	G1081
G2143	C2093	U1873	U1768	A1641	C1521	G1197	C1082	C1082
A2145	U2150	U1873	U1768	A1642	U1522	U1198	G1083	G1083
G2146	C2147	U1873	U1768	A1642	U1522	U1198	U1084	U1084
C2147	C2148	U1873	U1768	A1642	U1522	U1198	A1085	A1085
A2149	U2150	U1873	U1768	A1642	U1522	U1198	A1086	A1086
C2151	C2152	U1873	U1768	A1642	U1522	U1198	U1087	U1087
U2153	U2153	U1873	U1768	A1642	U1522	U1198	A1088	A1088
U2154	U2154	U1873	U1768	A1642	U1522	U1198	G1089	G1089
G2155	U2155	U1873	U1768	A1642	U1522	U1198	U1089	U1089
A2156	U2156	U1873	U1768	A1642	U1522	U1198	A1090	A1090
U2157	U2157	U1873	U1768	A1642	U1522	U1198	U1091	U1091
A2158	U2158	U1873	U1768	A1642	U1522	U1198	C1092	C1092
U2159	U2159	U1873	U1768	A1642	U1522	U1198	A1093	A1093
A2160	U2160	U1873	U1768	A1642	U1522	U1198	C1094	C1094
C2161	U2161	U1873	U1768	A1642	U1522	U1198	U1095	U1095
G2162	U2162	U1873	U1768	A1642	U1522	U1198	U1095	U1095
A2163	U2163	U1873	U1768	A1642	U1522	U1198	U1095	U1095
C2164	U2164	U1873	U1768	A1642	U1522	U1198	U1095	U1095
U2165	U2165	U1873	U1768	A1642	U1522	U1198	U1095	U1095
G2166	U2166	U1873	U1768	A1642	U1522	U1198	U1095	U1095
C2167	U2167	U1873	U1768	A1642	U1522	U1198	U1095	U1095
G2168	U2168	U1873	U1768	A1642	U1522	U1198	U1095	U1095
U2169	U2169	U1873	U1768	A1642	U1522	U1198	U1095	U1095
G2170	U2170	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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C2174	U2174	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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U2177	U2177	U1873	U1768	A1642	U1522	U1198	U1095	U1095
A2178	U2178	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2312	U2312	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2316	U2316	U1873	U1768	A1642	U1522	U1198	U1095	U1095
G2317	U2317	U1873	U1768	A1642	U1522	U1198	U1095	U1095
C2318	U2318	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2321	U2321	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2323	U2323	U1873	U1768	A1642	U1522	U1198	U1095	U1095
G2324	U2324	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2326	U2326	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2330	U2330	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2332	U2332	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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C2334	U2334	U1873	U1768	A1642	U1522	U1198	U1095	U1095
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A2336	U2336	U1873	U1768	A1642	U1522	U1198	U1095	U1095
U2337	U2337	U1873	U1768	A1642	U1522	U1198	U1095	U1095
G2338	U2338	U1873	U1768	A1642	U1522	U1198	U1095	U1095
A2339	U2339	U1873	U1768	A1642	U1522	U1198	U1095	U1095
U2340	U2340	U1873	U1768	A1642	U1522	U1198	U1095	U1095
A2342	U2342	U1873	U1768	A1642	U1522	U1198	U1095	U1095



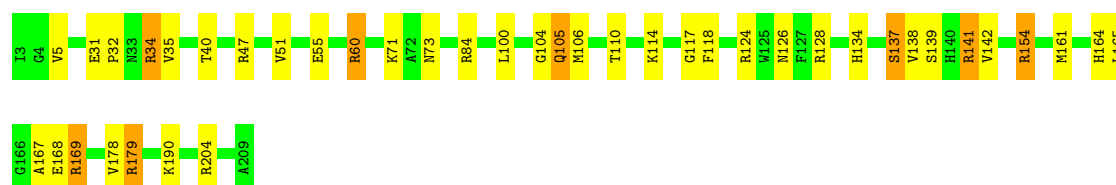
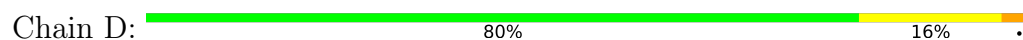
- Molecule 2: 5S rRNA



- Molecule 3: 50S ribosomal protein L2

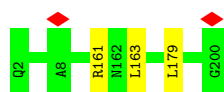


- Molecule 4: 50S ribosomal protein L3



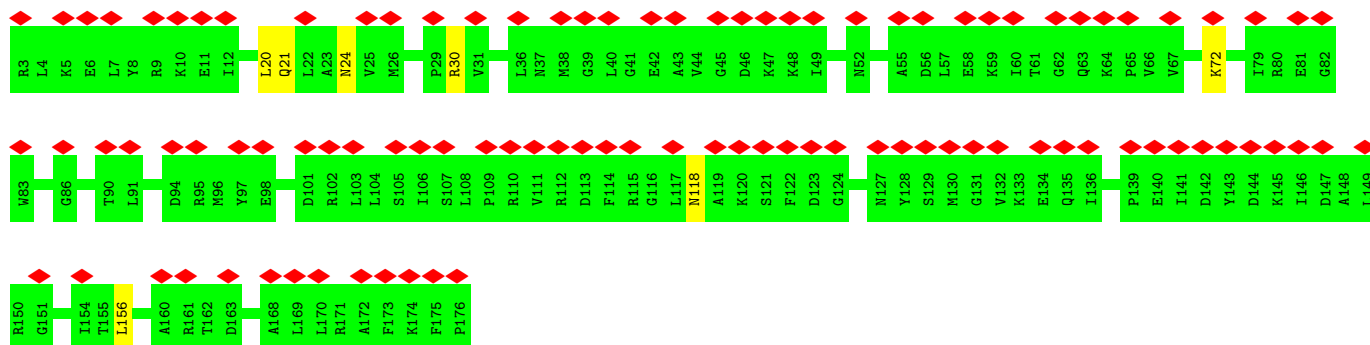
- Molecule 5: 50S ribosomal protein L4

Chain E:  98%



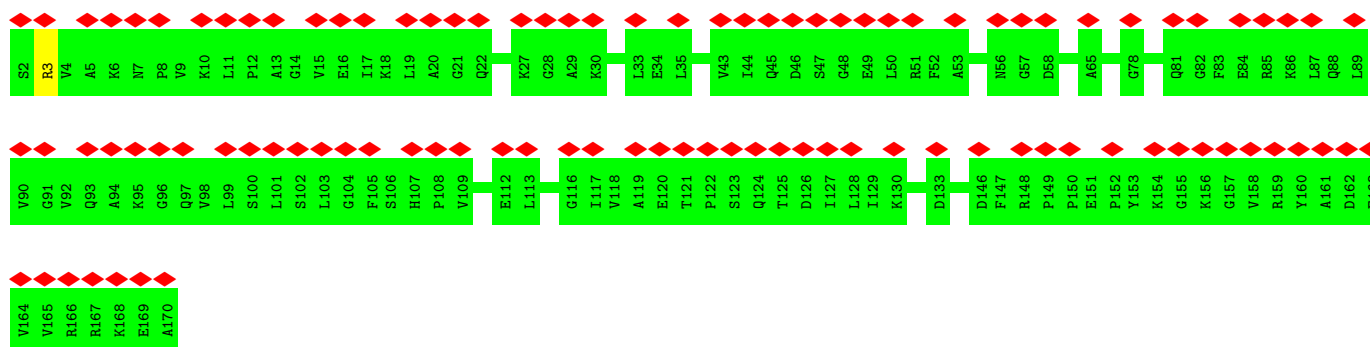
- Molecule 6: 50S ribosomal protein L5

Chain F:  57%
96%



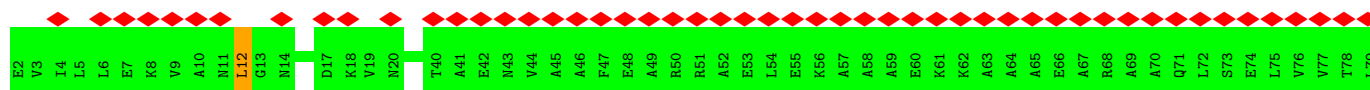
- Molecule 7: 50S ribosomal protein L6

Chain G:  59%
99%



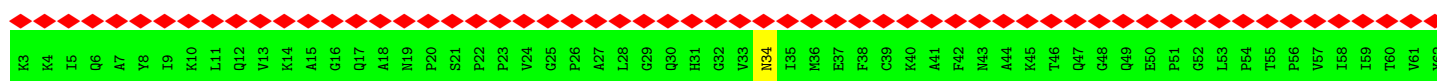
- Molecule 8: 50S ribosomal protein L9

Chain H:  65%
99%



- Molecule 9: 50S ribosomal protein L11

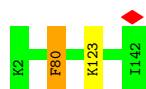
Chain I:  100%
98%





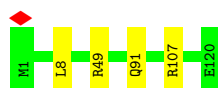
- Molecule 10: 50S ribosomal protein L13

Chain J:  99%



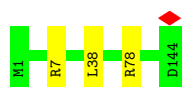
- Molecule 11: 50S ribosomal protein L14

Chain K:  97%



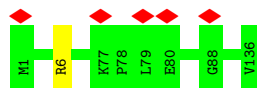
- Molecule 12: 50S ribosomal protein L15

Chain L:  98%



- Molecule 13: 50S ribosomal protein L16

Chain M:  99%




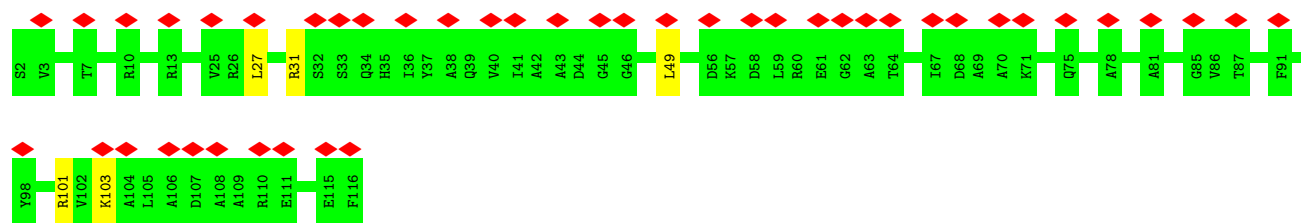
- Molecule 14: 50S ribosomal protein L17

Chain N:  98%



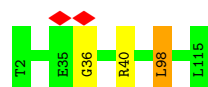
- Molecule 15: 50S ribosomal protein L18

Chain O:  38% 96%



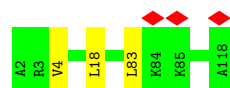
- Molecule 16: 50S ribosomal protein L19

Chain P: 97% ..



- Molecule 17: 50S ribosomal protein L20

Chain Q: 97% .



- Molecule 18: 50S ribosomal protein L21

Chain R: 5% 95% 5%



- Molecule 19: 50S ribosomal protein L22

Chain S: 98% .



- Molecule 20: 50S ribosomal protein L23

Chain T: 97% .



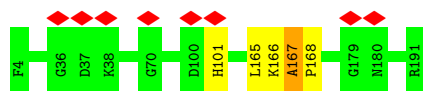
- Molecule 21: 50S ribosomal protein L24

Chain U: 6% 99%



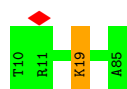
- Molecule 22: 50S ribosomal protein L25

Chain V: 97%



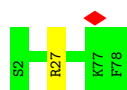
- Molecule 23: 50S ribosomal protein L27

Chain W: 99%



- Molecule 24: 50S ribosomal protein L28

Chain X: 99%



- Molecule 25: Ribosomal protein uL29

Chain Y: 98%



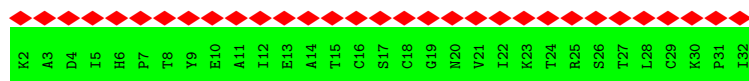
- Molecule 26: 50S ribosomal protein L30

Chain Z: 96%



- Molecule 27: 50S ribosomal protein L31

Chain 1: 100%



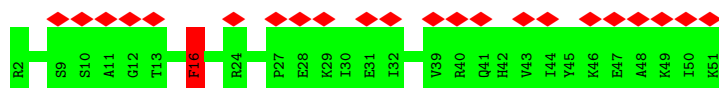
- Molecule 28: 50S ribosomal protein L32

Chain 2:  98% .



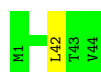
- Molecule 29: 50S ribosomal protein L33

Chain 3:  44% 98% .



- Molecule 30: 50S ribosomal protein L34

Chain 4:  98% .



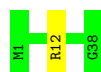
- Molecule 31: 50S ribosomal protein L35

Chain 5:  97% .



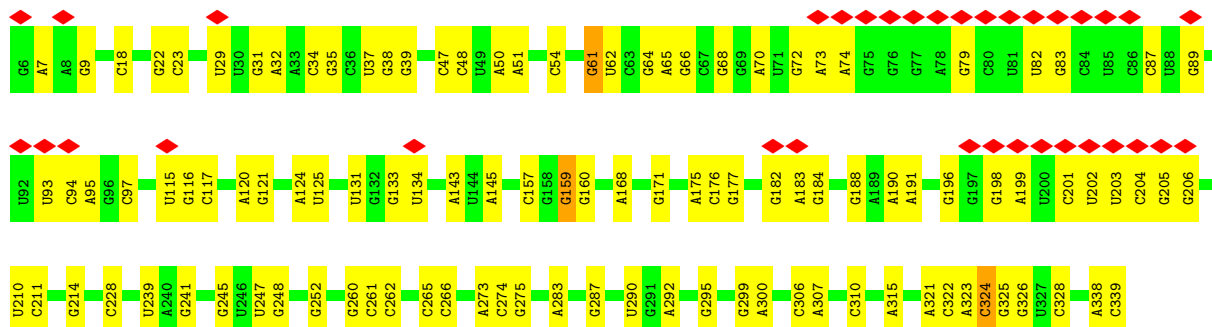
- Molecule 32: 50S ribosomal protein L36

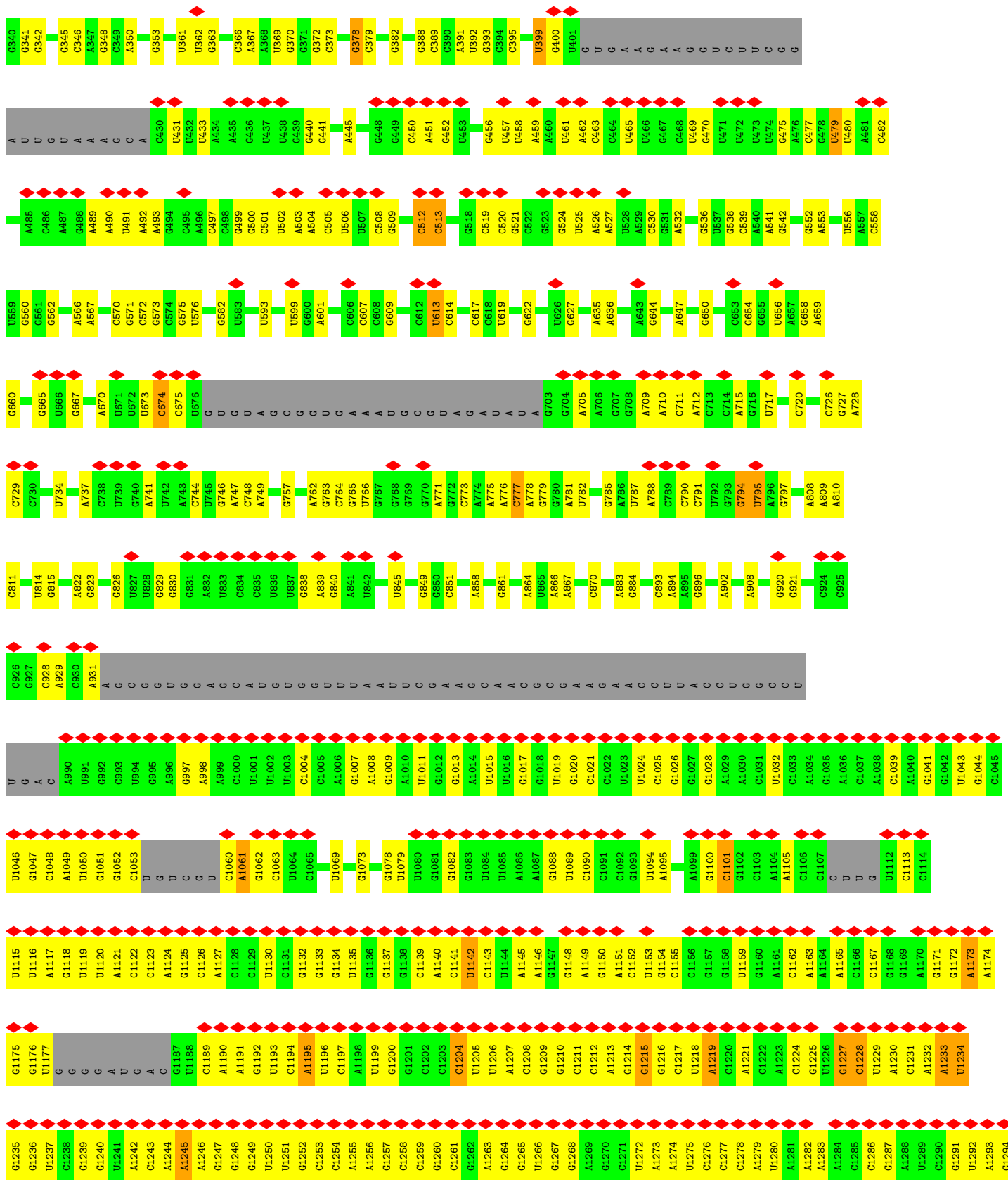
Chain 6:  97% .

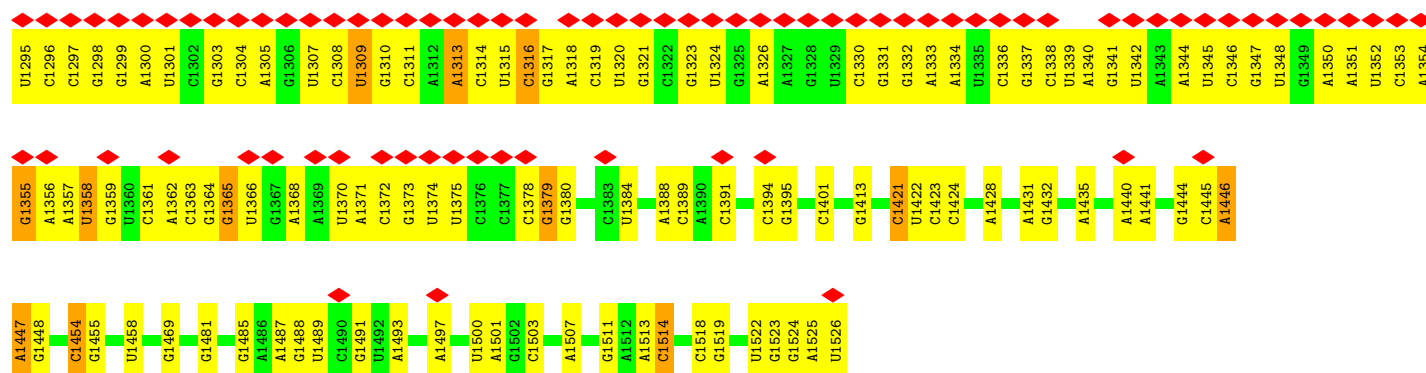


- Molecule 33: 16S rRNA

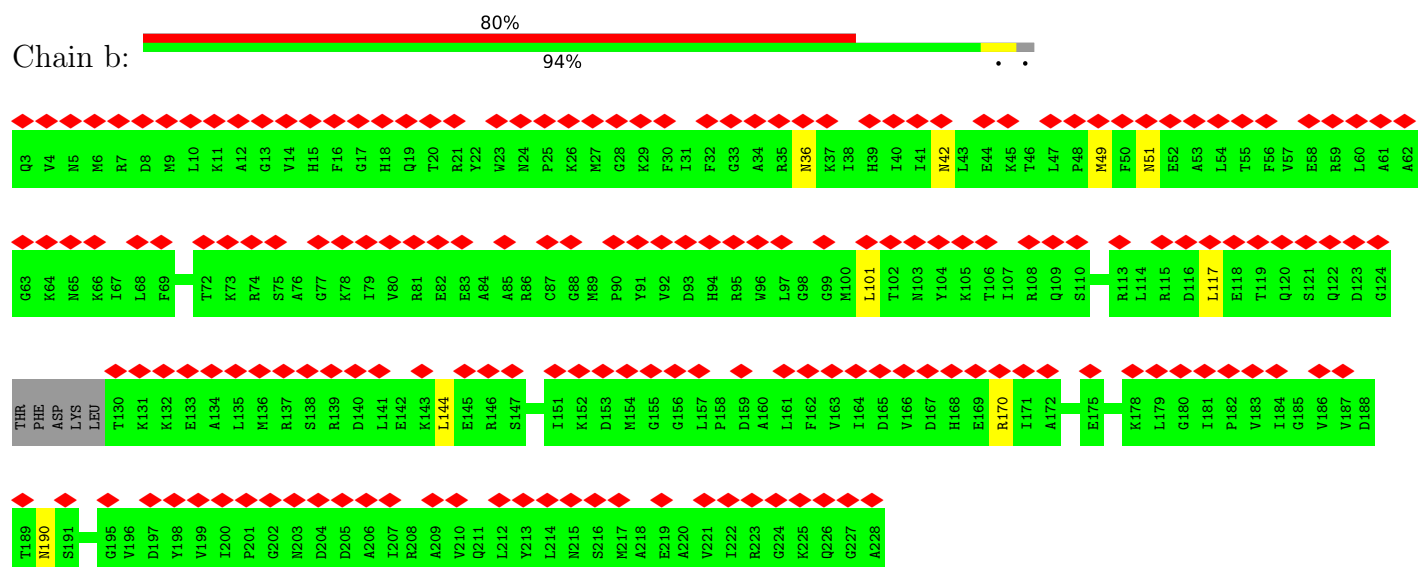
Chain a:  32% 51% 38% 9% .



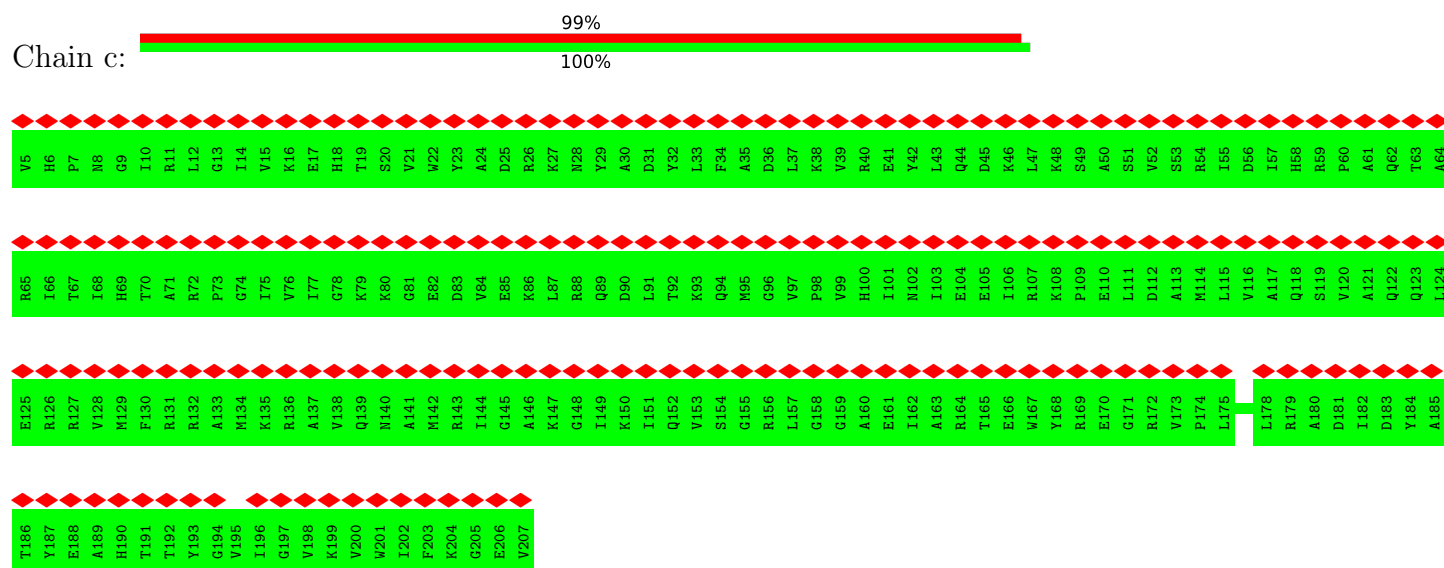




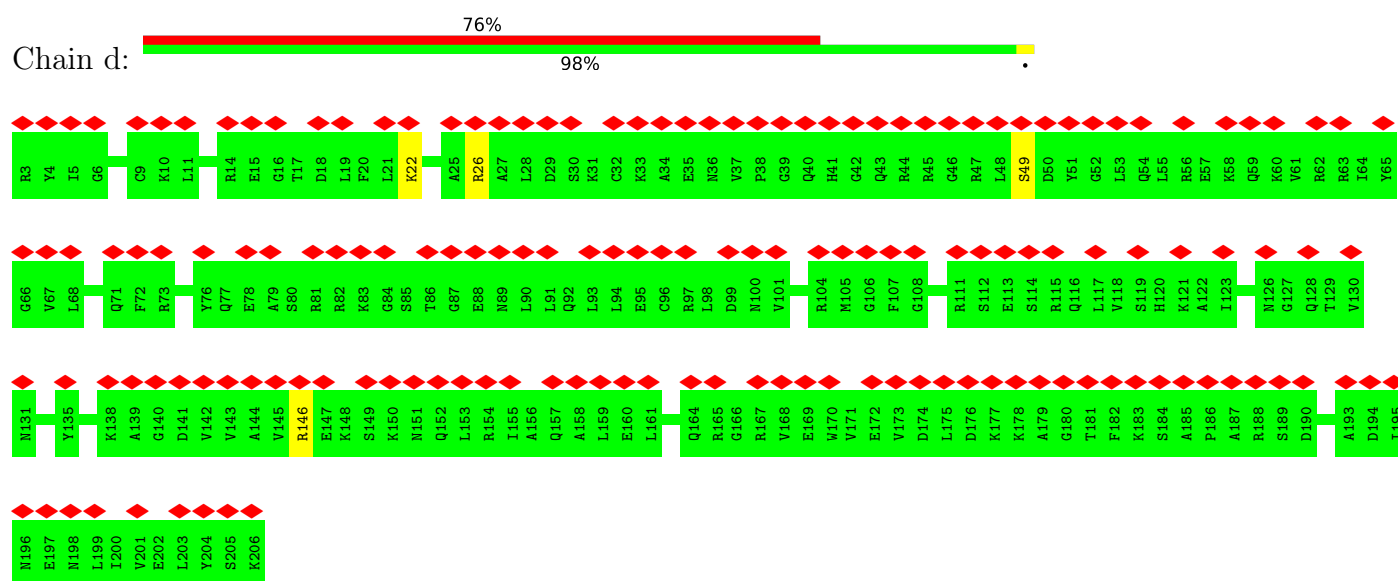
• Molecule 34: 30S ribosomal protein S2



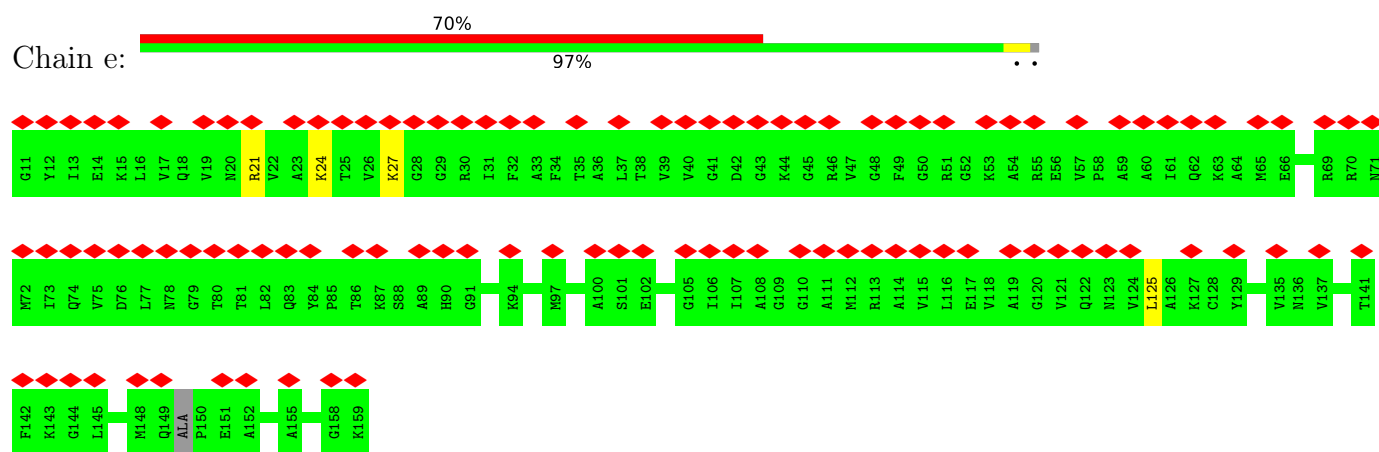
• Molecule 35: 30S ribosomal protein S3



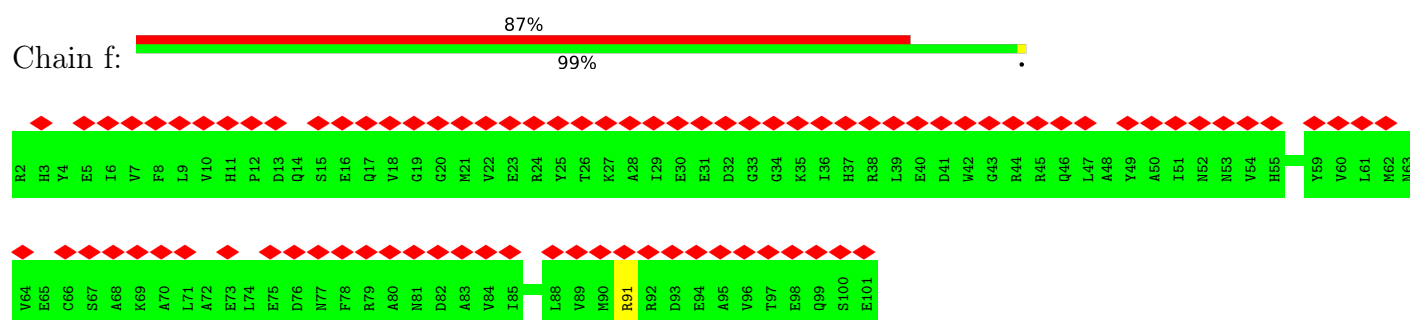
• Molecule 36: 30S ribosomal protein S4



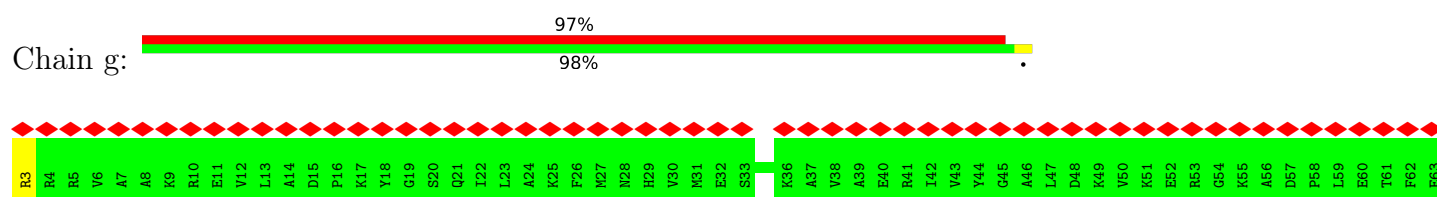
• Molecule 37: 30S ribosomal protein S5



• Molecule 38: 30S ribosomal protein S6

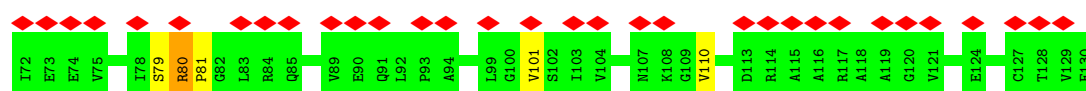
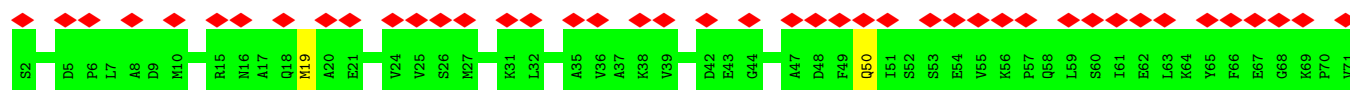
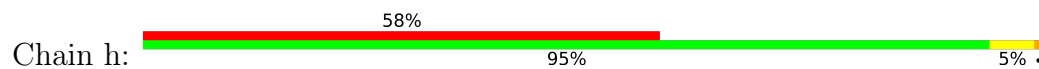


• Molecule 39: 30S ribosomal protein S7

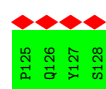
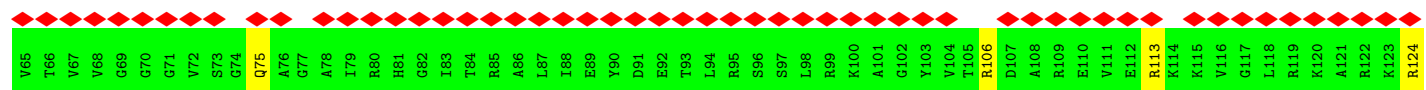
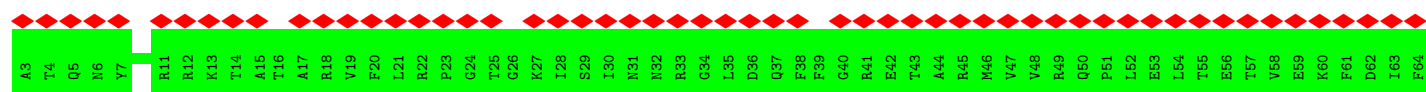




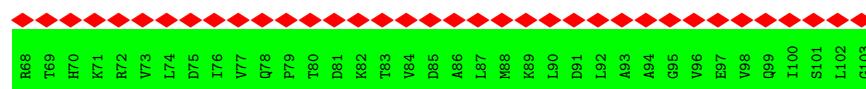
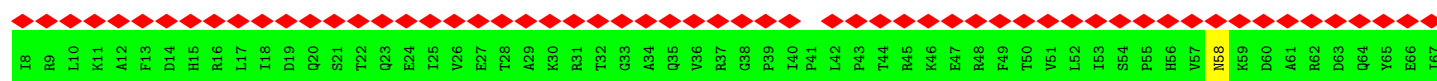
• Molecule 40: 30S ribosomal protein S8



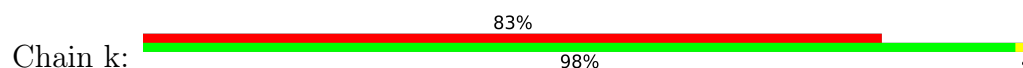
• Molecule 41: 30S ribosomal protein S9

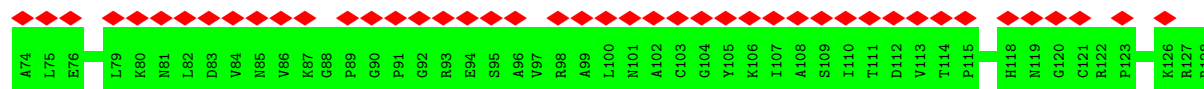
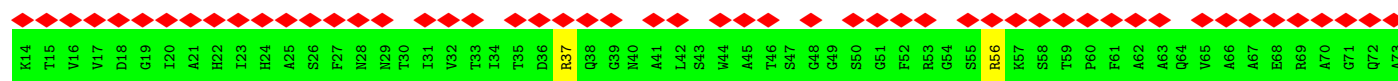


• Molecule 42: 30S ribosomal protein S10

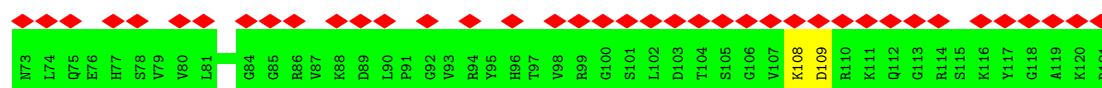
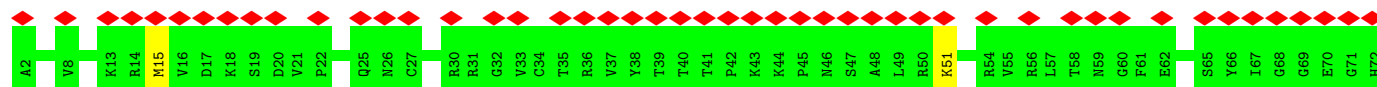


• Molecule 43: 30S ribosomal protein S11

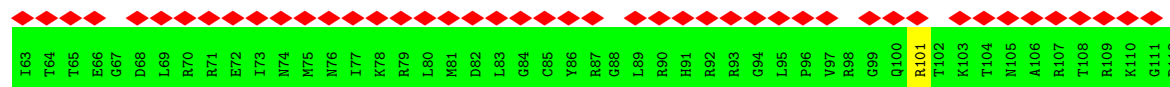




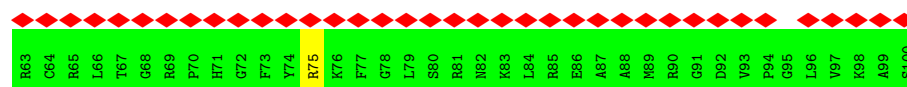
• Molecule 44: 30S ribosomal protein S12



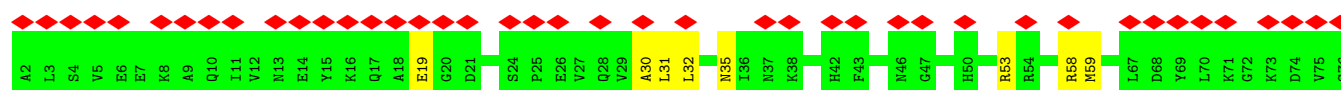
• Molecule 45: 30S ribosomal protein S13

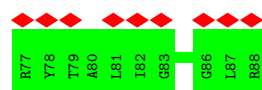


• Molecule 46: 30S ribosomal protein S14

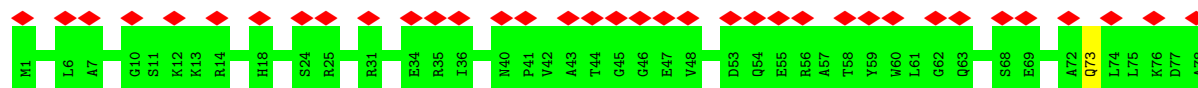


• Molecule 47: 30S ribosomal protein S15

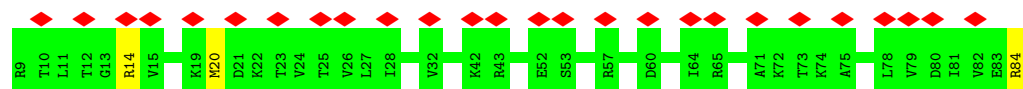




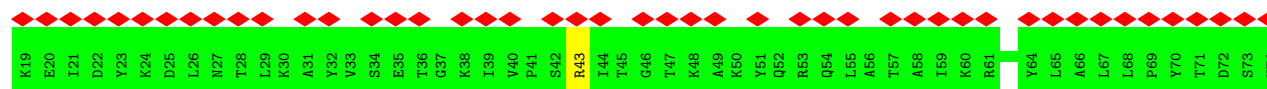
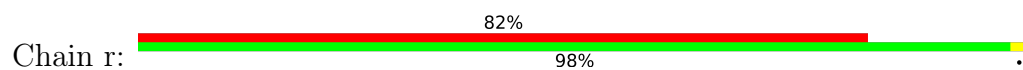
- Molecule 48: 30S ribosomal protein S16



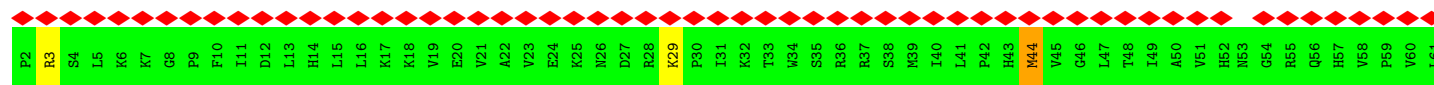
- Molecule 49: 30S ribosomal protein S17



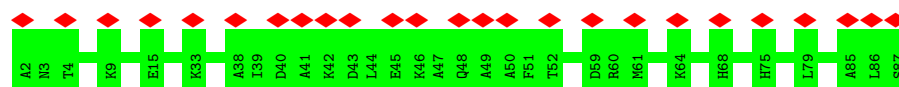
- Molecule 50: 30S ribosomal protein S18



- Molecule 51: 30S ribosomal protein S19



- Molecule 52: 30S ribosomal protein S20



- Molecule 53: 30S ribosomal protein S21



S34	R35	E36	F37	Y38	E39	K40	P41	T42	A43	E44	R45	R46	R47	K48	A49	A50	A51	A52	V53	K54	R55	H56	A57	K58	K59	V60	D61	R62	E63	Q64	R65	R66	R67
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4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	319022	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	1.0	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON II (4k x 4k)	Depositor
Maximum map value	0.788	Depositor
Minimum map value	-0.478	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.017	Depositor
Recommended contour level	0.0491	Depositor
Map size (\AA)	440.0, 440.0, 440.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.1, 1.1, 1.1	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	A	0.96	13/69320 (0.0%)	1.26	713/108135 (0.7%)
2	B	0.61	0/2789	1.23	26/4345 (0.6%)
3	C	0.54	0/2084	0.73	0/2800
4	D	0.59	0/1572	0.82	2/2118 (0.1%)
5	E	0.48	0/1529	0.70	1/2060 (0.0%)
6	F	0.32	0/1294	0.73	0/1754
7	G	0.30	0/1280	0.62	0/1726
8	H	0.30	0/580	0.60	1/781 (0.1%)
9	I	0.32	0/1041	0.66	0/1408
10	J	0.52	0/1148	0.66	1/1549 (0.1%)
11	K	0.58	0/931	0.74	1/1247 (0.1%)
12	L	0.48	0/1075	0.69	1/1432 (0.1%)
13	M	0.37	0/1096	0.60	0/1466
14	N	0.51	0/975	0.71	0/1304
15	O	0.33	0/888	0.74	2/1183 (0.2%)
16	P	0.52	0/910	0.72	1/1218 (0.1%)
17	Q	0.59	0/946	0.71	2/1257 (0.2%)
18	R	0.48	0/814	0.67	0/1091
19	S	0.49	0/837	0.64	0/1114
20	T	0.47	0/742	0.74	2/993 (0.2%)
21	U	0.39	0/809	0.65	0/1079
22	V	0.36	0/1420	0.71	1/1927 (0.1%)
23	W	0.51	0/582	0.87	1/773 (0.1%)
24	X	0.45	0/637	0.62	0/849
25	Y	0.36	0/471	0.71	1/630 (0.2%)
26	Z	0.46	0/449	0.67	0/602
27	1	0.27	0/235	0.51	0/318
28	2	0.51	0/425	0.66	1/568 (0.2%)
29	3	0.38	0/415	0.73	1/554 (0.2%)
30	4	0.60	0/367	0.84	1/482 (0.2%)
31	5	0.40	0/507	0.73	0/664
32	6	0.36	0/304	0.69	0/399
33	a	0.78	11/33391 (0.0%)	1.55	179/52073 (0.3%)
34	b	0.30	0/1724	0.64	2/2319 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	c	0.26	0/1638	0.56	0/2209
36	d	0.28	0/1615	0.60	0/2163
37	e	0.32	0/1106	0.66	0/1488
38	f	0.31	0/815	0.69	0/1098
39	g	0.30	0/1207	0.61	0/1616
40	h	0.29	0/976	0.66	0/1314
41	i	0.30	0/1006	0.65	0/1347
42	j	0.27	0/773	0.58	0/1045
43	k	0.28	0/848	0.57	0/1152
44	l	0.32	0/955	0.66	0/1280
45	m	0.28	0/853	0.66	1/1144 (0.1%)
46	n	0.29	0/786	0.60	0/1047
47	o	0.30	0/698	0.74	2/933 (0.2%)
48	p	0.31	0/620	0.65	0/835
49	q	0.28	0/627	0.59	0/844
50	r	0.27	0/450	0.53	0/608
51	s	4.72	1/649 (0.2%)	0.68	0/874
52	t	0.29	0/669	0.55	0/891
53	u	0.29	0/298	0.46	0/391
All	All	0.84	25/150176 (0.0%)	1.21	943/224497 (0.4%)

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
3	C	0	2
4	D	0	10
5	E	0	1
6	F	0	2
9	I	0	2
16	P	0	1
17	Q	0	1
18	R	0	1
22	V	0	3
29	3	0	1
36	d	0	1
40	h	0	3
41	i	0	1
44	l	0	1
45	m	0	2

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Mol	Chain	#Chirality outliers	#Planarity outliers
46	n	0	1
47	o	0	1
48	p	0	1
51	s	0	1
All	All	0	36

The worst 5 of 25 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
51	s	3	ARG	CB-CG	120.12	4.76	1.52
33	a	1313	A	N3-C4	56.98	1.69	1.34
33	a	1313	A	C6-N1	52.01	1.72	1.35
33	a	1219	A	N9-C4	43.52	1.64	1.37
33	a	1313	A	C5-C4	41.61	1.67	1.38

The worst 5 of 943 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
33	a	1219	A	N7-C8-N9	-145.93	40.83	113.80
33	a	1219	A	C4-C5-N7	-137.41	42.00	110.70
33	a	1219	A	C8-N9-C4	-132.12	52.95	105.80
33	a	1219	A	C5-N7-C8	58.62	133.21	103.90
33	a	1219	A	C6-C5-N7	37.35	158.44	132.30

There are no chirality outliers.

5 of 36 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	C	270	ARG	Sidechain
3	C	271	ARG	Sidechain
4	D	34	ARG	Sidechain
4	D	60	ARG	Sidechain
4	D	84	ARG	Sidechain

5.2 Too-close contacts

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

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	C	269/271 (99%)	239 (89%)	28 (10%)	2 (1%)	19	49
4	D	205/207 (99%)	176 (86%)	19 (9%)	10 (5%)	2	6
5	E	197/199 (99%)	191 (97%)	6 (3%)	0	100	100
6	F	172/174 (99%)	138 (80%)	34 (20%)	0	100	100
7	G	167/169 (99%)	152 (91%)	15 (9%)	0	100	100
8	H	76/78 (97%)	70 (92%)	6 (8%)	0	100	100
9	I	138/140 (99%)	118 (86%)	20 (14%)	0	100	100
10	J	139/141 (99%)	129 (93%)	10 (7%)	0	100	100
11	K	118/120 (98%)	111 (94%)	7 (6%)	0	100	100
12	L	142/144 (99%)	132 (93%)	10 (7%)	0	100	100
13	M	134/136 (98%)	127 (95%)	7 (5%)	0	100	100
14	N	118/120 (98%)	109 (92%)	9 (8%)	0	100	100
15	O	113/115 (98%)	96 (85%)	17 (15%)	0	100	100
16	P	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
17	Q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
18	R	100/102 (98%)	91 (91%)	8 (8%)	1 (1%)	13	40
19	S	108/110 (98%)	104 (96%)	4 (4%)	0	100	100
20	T	92/94 (98%)	84 (91%)	7 (8%)	1 (1%)	12	37
21	U	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	13	40
22	V	186/188 (99%)	158 (85%)	26 (14%)	2 (1%)	12	37
23	W	74/76 (97%)	60 (81%)	13 (18%)	1 (1%)	9	31
24	X	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
25	Y	58/60 (97%)	55 (95%)	3 (5%)	0	100	100
26	Z	55/57 (96%)	53 (96%)	2 (4%)	0	100	100
27	1	29/31 (94%)	26 (90%)	3 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
28	2	51/53 (96%)	48 (94%)	3 (6%)	0	100	100
29	3	48/50 (96%)	36 (75%)	12 (25%)	0	100	100
30	4	42/44 (96%)	41 (98%)	1 (2%)	0	100	100
31	5	61/63 (97%)	55 (90%)	6 (10%)	0	100	100
32	6	36/38 (95%)	31 (86%)	5 (14%)	0	100	100
34	b	217/226 (96%)	199 (92%)	18 (8%)	0	100	100
35	c	201/203 (99%)	174 (87%)	27 (13%)	0	100	100
36	d	202/204 (99%)	177 (88%)	25 (12%)	0	100	100
37	e	147/150 (98%)	138 (94%)	9 (6%)	0	100	100
38	f	98/100 (98%)	88 (90%)	10 (10%)	0	100	100
39	g	152/154 (99%)	134 (88%)	18 (12%)	0	100	100
40	h	127/129 (98%)	111 (87%)	14 (11%)	2 (2%)	8	28
41	i	124/126 (98%)	107 (86%)	17 (14%)	0	100	100
42	j	94/96 (98%)	81 (86%)	13 (14%)	0	100	100
43	k	113/115 (98%)	95 (84%)	18 (16%)	0	100	100
44	l	118/120 (98%)	100 (85%)	17 (14%)	1 (1%)	16	45
45	m	105/110 (96%)	92 (88%)	13 (12%)	0	100	100
46	n	96/98 (98%)	81 (84%)	15 (16%)	0	100	100
47	o	85/87 (98%)	78 (92%)	6 (7%)	1 (1%)	11	35
48	p	76/78 (97%)	68 (90%)	8 (10%)	0	100	100
49	q	74/76 (97%)	71 (96%)	3 (4%)	0	100	100
50	r	54/56 (96%)	50 (93%)	4 (7%)	0	100	100
51	s	78/80 (98%)	59 (76%)	19 (24%)	0	100	100
52	t	84/86 (98%)	83 (99%)	1 (1%)	0	100	100
53	u	32/34 (94%)	32 (100%)	0	0	100	100
All	All	5608/5719 (98%)	5018 (90%)	568 (10%)	22 (0%)	32	60

5 of 22 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	C	120	ILE
4	D	105	GLN
4	D	134	HIS

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Mol	Chain	Res	Type
20	T	3	GLN
22	V	167	ALA

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	
3	C	206/212 (97%)	192 (93%)	14 (7%)	13	38
4	D	157/159 (99%)	129 (82%)	28 (18%)	1	4
5	E	155/157 (99%)	154 (99%)	1 (1%)	84	95
6	F	122/149 (82%)	117 (96%)	5 (4%)	26	60
7	G	131/135 (97%)	130 (99%)	1 (1%)	79	93
8	H	55/55 (100%)	54 (98%)	1 (2%)	54	82
9	I	108/108 (100%)	107 (99%)	1 (1%)	75	92
10	J	118/118 (100%)	116 (98%)	2 (2%)	56	83
11	K	100/100 (100%)	97 (97%)	3 (3%)	36	71
12	L	105/106 (99%)	103 (98%)	2 (2%)	52	81
13	M	109/109 (100%)	108 (99%)	1 (1%)	75	92
14	N	99/99 (100%)	97 (98%)	2 (2%)	50	79
15	O	86/86 (100%)	83 (96%)	3 (4%)	31	66
16	P	96/96 (100%)	94 (98%)	2 (2%)	48	78
17	Q	87/87 (100%)	86 (99%)	1 (1%)	70	90
18	R	82/86 (95%)	79 (96%)	3 (4%)	29	64
19	S	87/87 (100%)	85 (98%)	2 (2%)	45	77
20	T	77/79 (98%)	77 (100%)	0	100	100
21	U	88/88 (100%)	88 (100%)	0	100	100
22	V	144/153 (94%)	144 (100%)	0	100	100
23	W	56/56 (100%)	56 (100%)	0	100	100
24	X	65/66 (98%)	64 (98%)	1 (2%)	60	85

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
25	Y	51/53 (96%)	50 (98%)	1 (2%)	50	79
26	Z	48/48 (100%)	46 (96%)	2 (4%)	25	59
27	1	27/27 (100%)	27 (100%)	0	100	100
28	2	45/46 (98%)	45 (100%)	0	100	100
29	3	44/46 (96%)	43 (98%)	1 (2%)	45	77
30	4	37/37 (100%)	37 (100%)	0	100	100
31	5	53/54 (98%)	51 (96%)	2 (4%)	28	63
32	6	33/34 (97%)	32 (97%)	1 (3%)	36	71
34	b	174/188 (93%)	167 (96%)	7 (4%)	27	61
35	c	163/169 (96%)	163 (100%)	0	100	100
36	d	166/173 (96%)	163 (98%)	3 (2%)	54	82
37	e	108/109 (99%)	104 (96%)	4 (4%)	29	64
38	f	81/85 (95%)	80 (99%)	1 (1%)	67	89
39	g	116/120 (97%)	113 (97%)	3 (3%)	41	74
40	h	104/107 (97%)	101 (97%)	3 (3%)	37	72
41	i	102/102 (100%)	99 (97%)	3 (3%)	37	72
42	j	85/85 (100%)	84 (99%)	1 (1%)	67	89
43	k	83/87 (95%)	81 (98%)	2 (2%)	44	76
44	l	104/104 (100%)	102 (98%)	2 (2%)	52	81
45	m	91/92 (99%)	90 (99%)	1 (1%)	70	90
46	n	78/80 (98%)	77 (99%)	1 (1%)	65	88
47	o	73/73 (100%)	69 (94%)	4 (6%)	18	48
48	p	61/63 (97%)	61 (100%)	0	100	100
49	q	70/70 (100%)	67 (96%)	3 (4%)	25	57
50	r	46/48 (96%)	45 (98%)	1 (2%)	47	78
51	s	69/71 (97%)	67 (97%)	2 (3%)	37	72
52	t	68/68 (100%)	68 (100%)	0	100	100
53	u	28/28 (100%)	28 (100%)	0	100	100
All	All	4541/4658 (98%)	4420 (97%)	121 (3%)	41	73

5 of 121 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
12	L	78	ARG
46	n	75	ARG
19	S	92	ARG
45	m	40	ASN
50	r	43	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 61 such sidechains are listed below:

Mol	Chain	Res	Type
24	X	34	GLN
47	o	42	HIS
34	b	36	ASN
47	o	35	ASN
51	s	57	HIS

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	2883/2888 (99%)	817 (28%)	36 (1%)
2	B	116/117 (99%)	48 (41%)	4 (3%)
33	a	1382/1521 (90%)	573 (41%)	0
All	All	4381/4526 (96%)	1438 (32%)	40 (0%)

5 of 1438 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	10	A
1	A	14	A
1	A	15	G
1	A	22	C
1	A	34	U

5 of 40 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	A	2274	A
1	A	2743	U
1	A	2317	G
1	A	2536	G
2	B	34	A

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
33	a	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	a	1376:C	O3'	1377:C	P	3.50

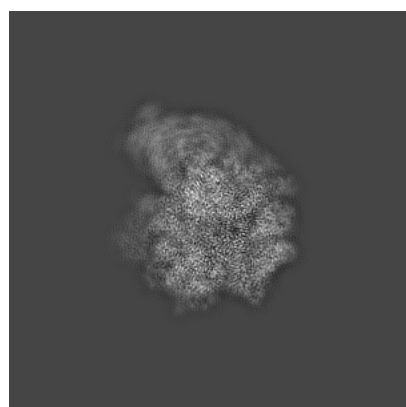
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-10284. These allow visual inspection of the internal detail of the map and identification of artifacts.

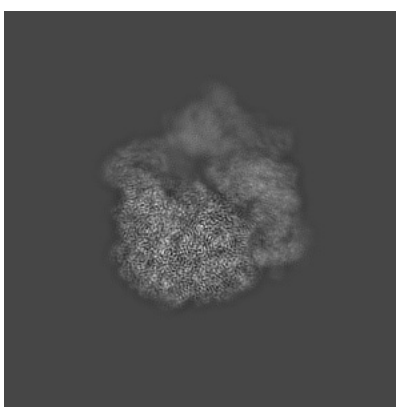
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

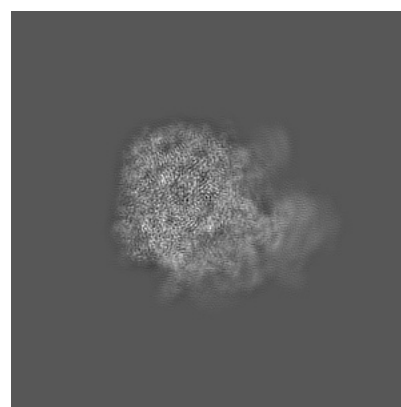
6.1.1 Primary map



X



Y



Z

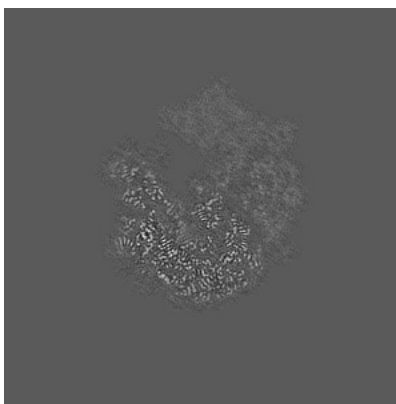
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

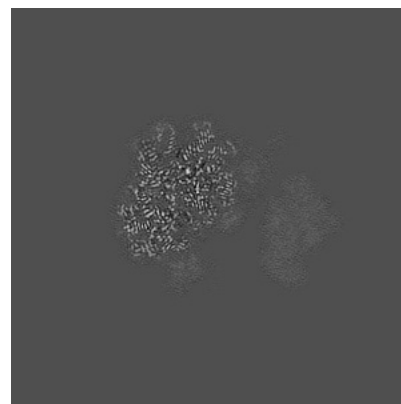
6.2.1 Primary map



X Index: 200



Y Index: 200

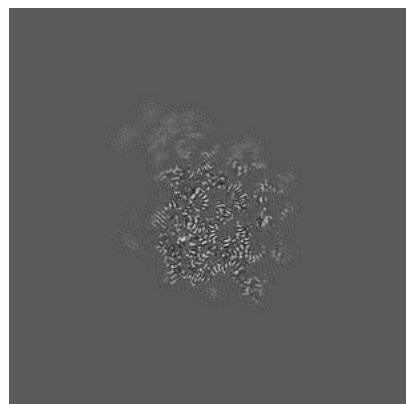


Z Index: 200

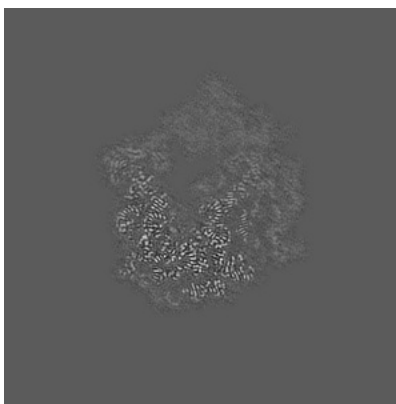
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

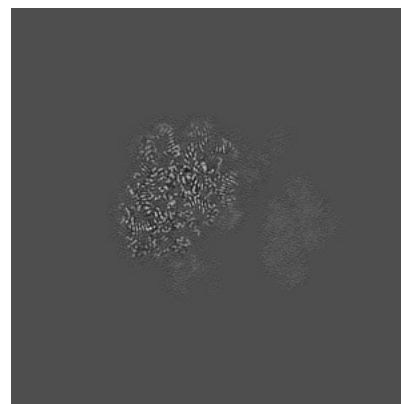
6.3.1 Primary map



X Index: 153



Y Index: 187

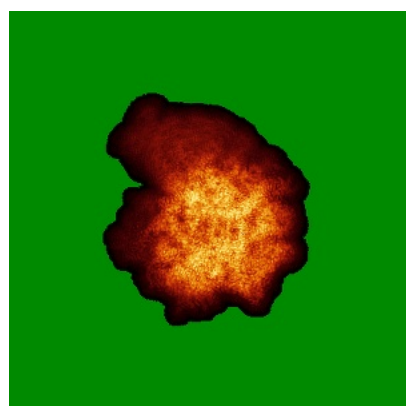


Z Index: 198

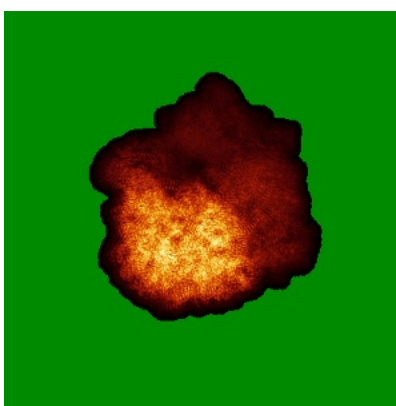
The images above show the largest variance slices of the map in three orthogonal directions.

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

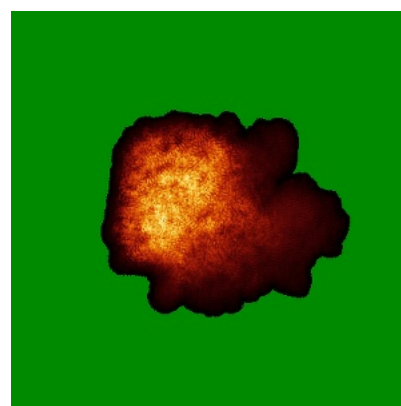
6.4.1 Primary map



X



Y

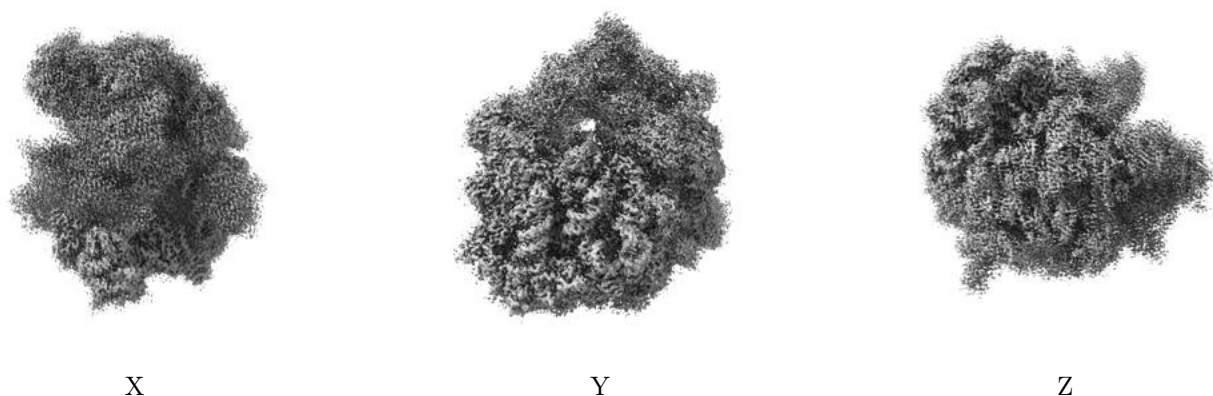


Z

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 0.0491. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

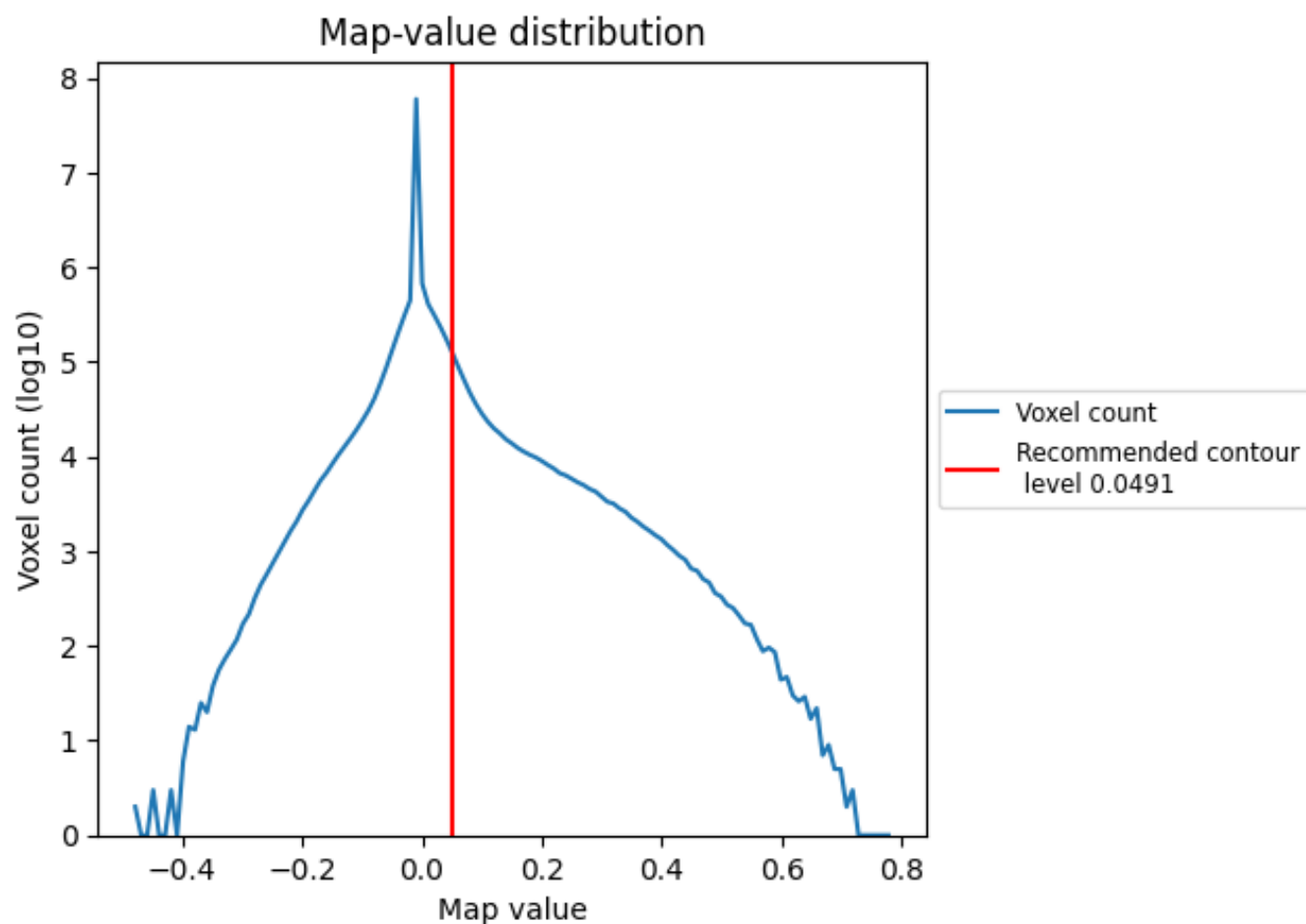
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

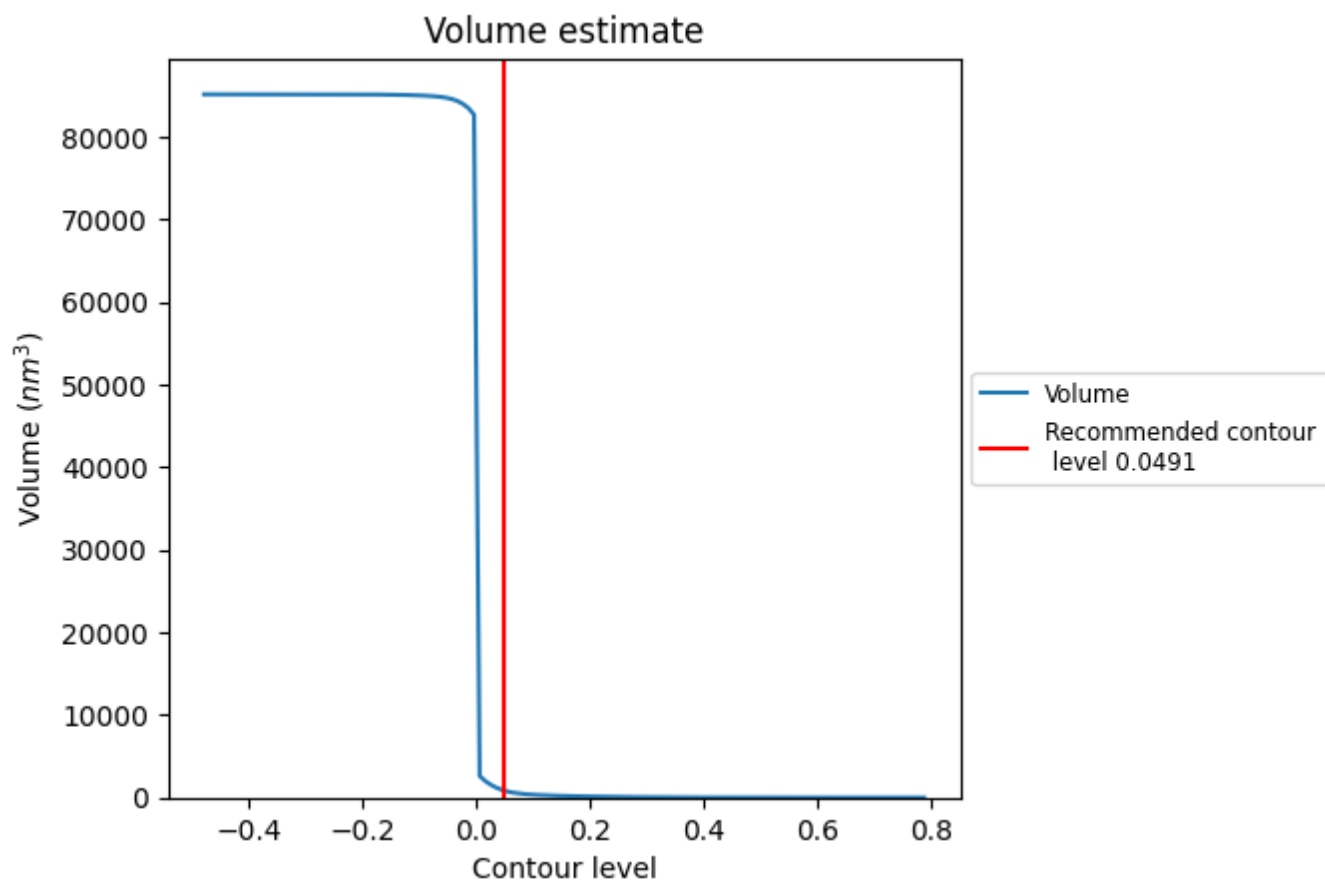
This section contains the results of statistical analysis of the map.

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.

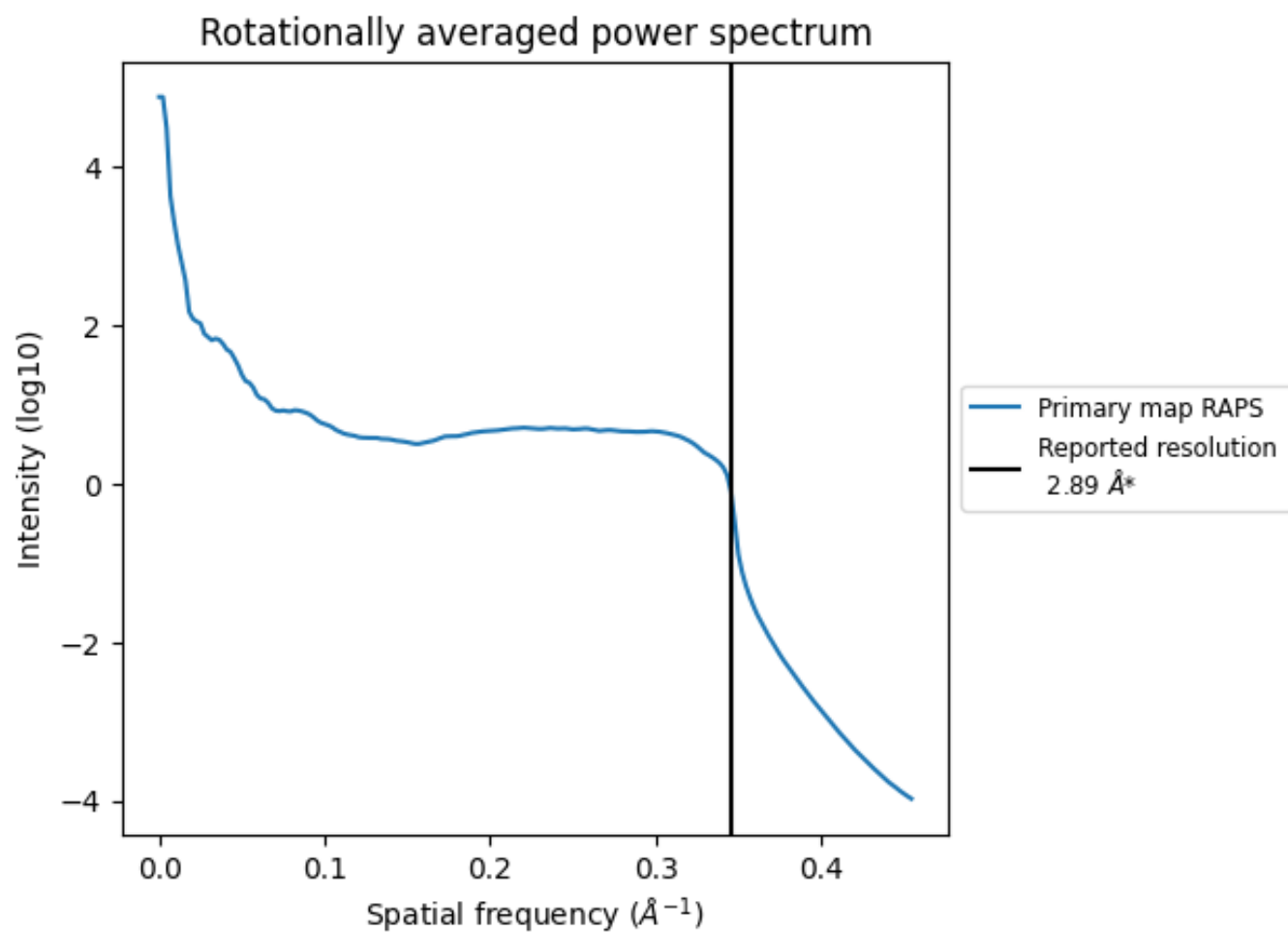
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 861 nm³; this corresponds to an approximate mass of 778 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 0.346 Å⁻¹

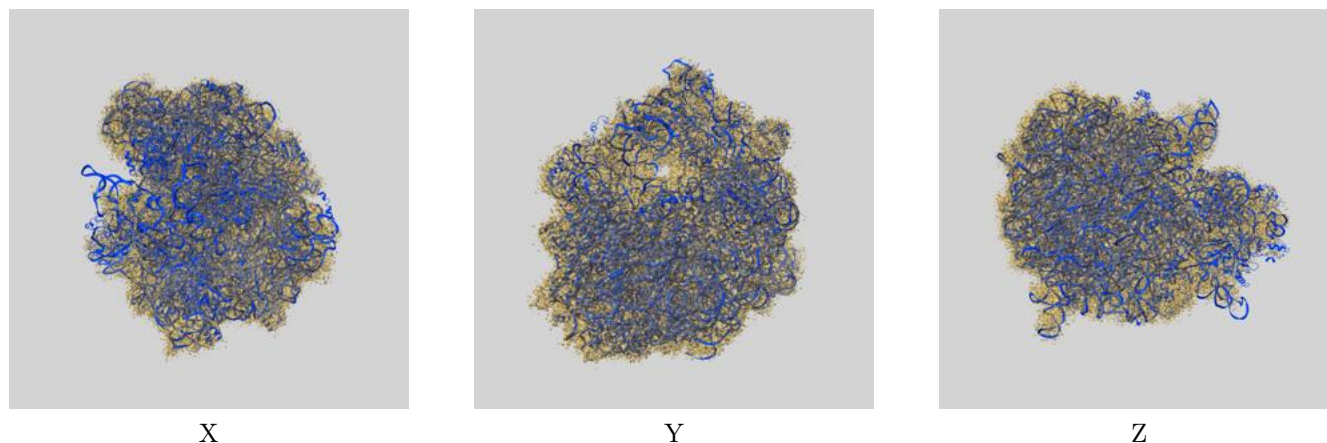
8 Fourier-Shell correlation

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

9 Map-model fit [i](#)

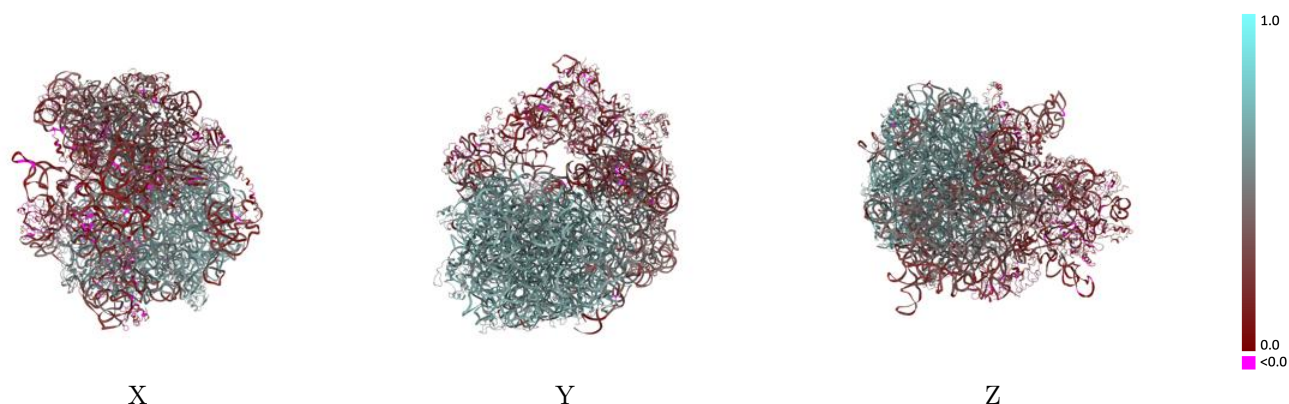
This section contains information regarding the fit between EMDB map EMD-10284 and PDB model 6SPF. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



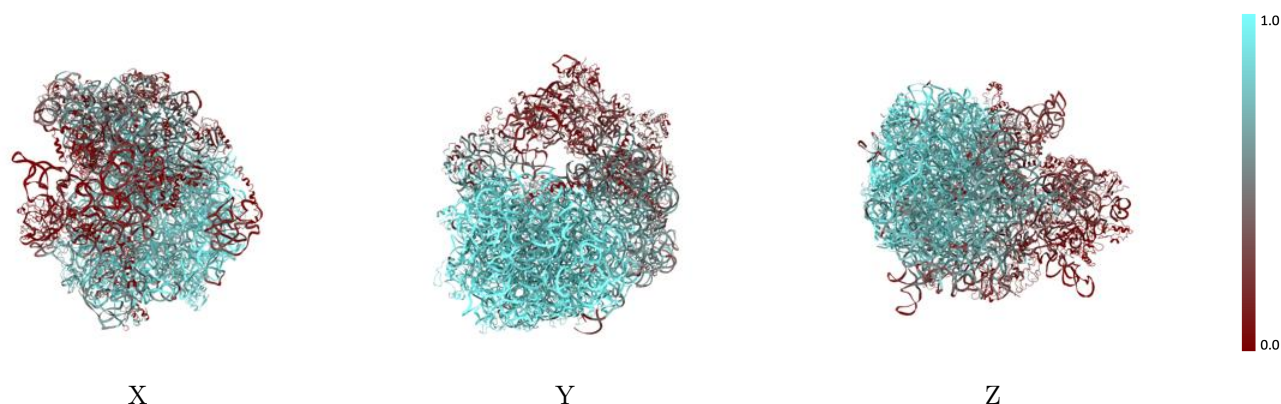
The images above show the 3D surface view of the map at the recommended contour level 0.0491 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



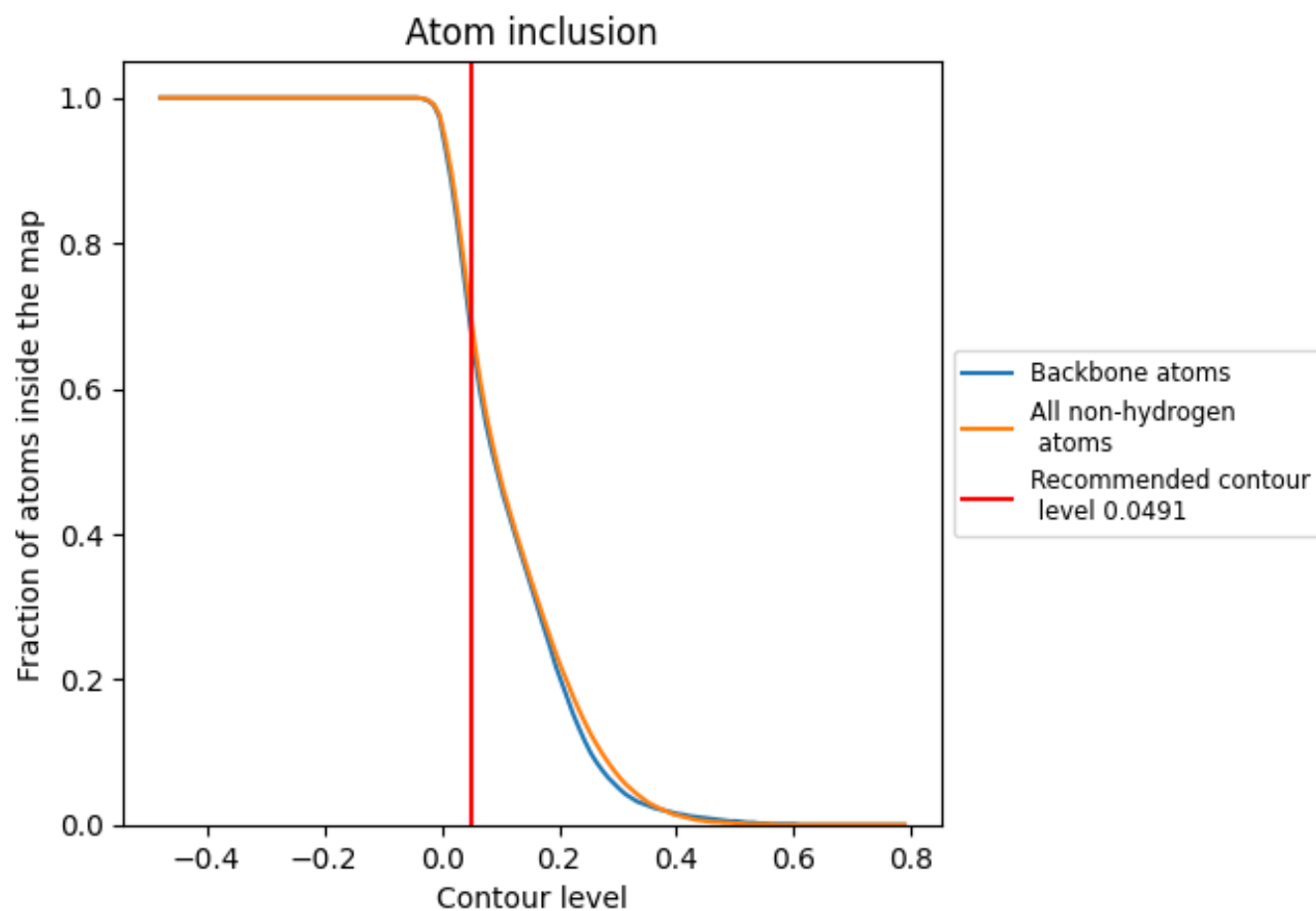
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0491).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 68% of all backbone atoms, 70% 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 (0.0491) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.7030	 0.4610
1	 0.0000	 0.1520
2	 0.9360	 0.6140
3	 0.5090	 0.3640
4	 0.9710	 0.6320
5	 0.8910	 0.5960
6	 0.8200	 0.5610
A	 0.8870	 0.5680
B	 0.7480	 0.3920
C	 0.9330	 0.6170
D	 0.9490	 0.6250
E	 0.9200	 0.5970
F	 0.3800	 0.2220
G	 0.3760	 0.3870
H	 0.3080	 0.2770
I	 0.0290	 0.1110
J	 0.9430	 0.6150
K	 0.9060	 0.6100
L	 0.9130	 0.5920
M	 0.8170	 0.5770
N	 0.9540	 0.6200
O	 0.5130	 0.2330
P	 0.8940	 0.5950
Q	 0.9230	 0.6060
R	 0.8800	 0.5620
S	 0.9230	 0.6200
T	 0.8990	 0.5870
U	 0.8310	 0.5470
V	 0.7330	 0.4960
W	 0.8950	 0.5910
X	 0.9100	 0.6020
Y	 0.8860	 0.5720
Z	 0.9310	 0.6070
a	 0.5370	 0.3220
b	 0.2520	 0.2730



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Chain	Atom inclusion	Q-score
c	 0.0560	 0.1670
d	 0.2680	 0.2390
e	 0.2910	 0.3050
f	 0.2170	 0.2100
g	 0.0940	 0.2300
h	 0.3720	 0.3130
i	 0.1350	 0.1730
j	 0.0630	 0.1880
k	 0.1990	 0.2160
l	 0.2990	 0.3490
m	 0.1090	 0.1710
n	 0.0580	 0.1730
o	 0.3770	 0.2550
p	 0.4440	 0.3410
q	 0.4800	 0.3650
r	 0.2210	 0.1440
s	 0.1340	 0.1910
t	 0.5600	 0.3880
u	 0.1230	 0.2450