



wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 03:18 AM UTC

PDB ID : 6WNV / pdb_00006wnv
EMDB ID : EMD-21857
Title : 70S ribosome without free 5S rRNA and with a perturbed PTC
Authors : Loveland, A.B.; Korostelev, A.A.; Mankin, A.S.; Huang, S.; Aleksashin, N.A.; Klepacki, D.; Reier, K.; Kefi, A.; Szal, A.; Remme, J.; Jaeger, L.; Vazquez-Laslop, N.
Deposited on : 2020-04-23
Resolution : 3.50 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:

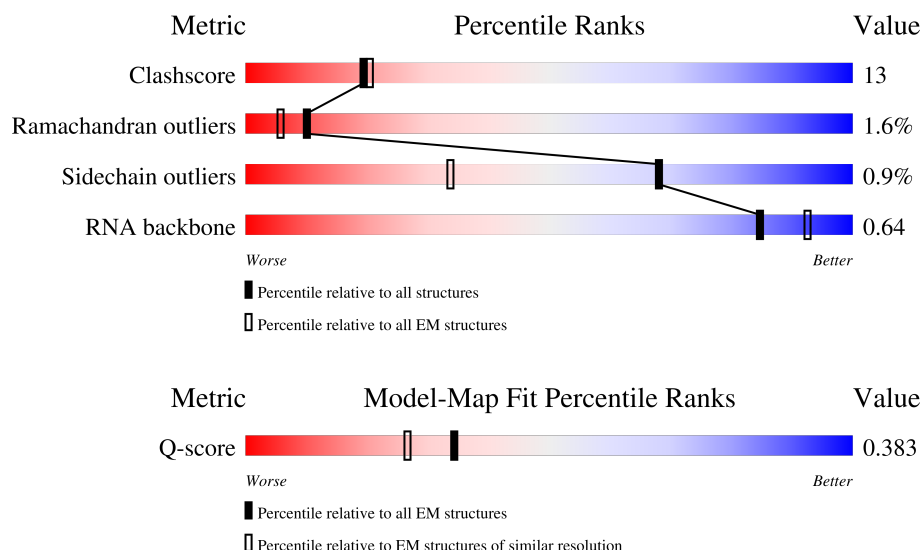
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance

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

The reported resolution of this entry is 3.50 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	13950 (3.00 - 4.00)

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	b	271	
2	c	209	
3	d	201	

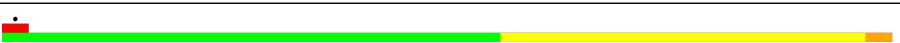
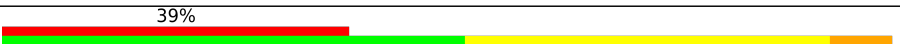
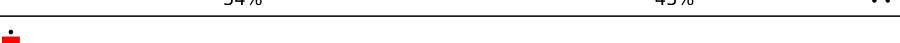
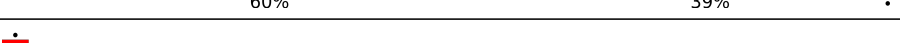
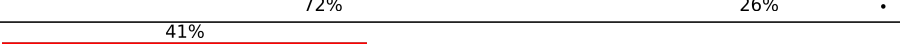
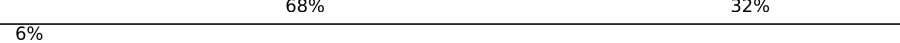
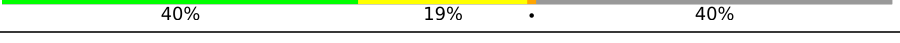
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Mol	Chain	Length	Quality of chain
4	e	177	
5	f	176	
6	g	149	
7	h	131	
8	i	141	
9	j	142	
10	k	122	
11	l	143	
12	n	120	
13	o	116	
14	p	114	
15	q	117	
16	r	103	
17	s	110	
18	t	93	
19	u	102	
20	v	94	
21	w	75	
22	x	77	
23	y	63	
24	z	58	
25	A	70	
26	B	56	
27	D	46	
28	E	64	

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Mol	Chain	Length	Quality of chain
29	F	38	
30	G	225	
31	H	206	
32	I	205	
33	J	157	
34	K	100	
35	L	151	
36	M	129	
37	N	127	
38	O	98	
39	P	116	
40	Q	123	
41	R	114	
42	S	100	
43	T	88	
44	U	82	
45	V	80	
46	W	65	
47	X	79	
48	Y	85	
49	Z	65	
50	a	223	
51	3	1539	
52	4	3031	

2 Entry composition

There are 52 unique types of molecules in this entry. The entry contains 143036 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 protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	b	271	Total	C	N	O	S	0	0
			2082	1288	423	364	7		

- Molecule 2 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	c	209	Total	C	N	O	S	0	0
			1564	979	288	293	4		

- Molecule 3 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	d	201	Total	C	N	O	S	0	0
			1551	974	283	289	5		

- Molecule 4 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	e	177	Total	C	N	O	S	0	0
			1410	899	249	256	6		

- Molecule 5 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	f	176	Total	C	N	O	S	0	0
			1322	832	243	245	2		

- Molecule 6 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	g	53	Total	C	N	O	S	0	0
			409	261	74	73	1		

- Molecule 7 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	h	131	Total	C	N	O	S	0	0
			988	625	175	183	5		

- Molecule 8 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	i	141	Total	C	N	O	S	0	0
			1031	651	179	195	6		

- Molecule 9 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	j	142	Total	C	N	O	S	0	0
			1128	714	212	198	4		

- Molecule 10 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	k	122	Total	C	N	O	S	0	0
			938	587	180	165	6		

- Molecule 11 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	l	143	Total	C	N	O	S	0	0
			1044	649	206	188	1		

- Molecule 12 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	n	120	Total	C	N	O	S	0	0
			960	593	196	166	5		

- Molecule 13 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms				AltConf	Trace
13	o	116	Total	C	N	O	0	0
			891	552	178	161		

- Molecule 14 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	p	114	Total	C	N	O	S	0	0
			916	574	179	162	1		

- Molecule 15 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	q	117	Total	C	N	O	S	0	0
			946	604	192	150			

- Molecule 16 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	r	103	Total	C	N	O	S	0	0
			815	516	153	144	2		

- Molecule 17 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	s	110	Total	C	N	O	S	0	0
			856	532	166	155	3		

- Molecule 18 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	t	93	Total	C	N	O	S	0	0
			738	466	139	131	2		

- Molecule 19 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	u	102	Total	C	N	O	S	0	0
			779	492	146	141			

- Molecule 20 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	v	94	Total	C	N	O	S	0	0
			752	479	137	133	3		

- Molecule 21 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	w	75	Total	C	N	O	S	0	0
			574	356	116	101	1		

- Molecule 22 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	x	77	Total	C	N	O	S	0	0
			624	388	129	105	2		

- Molecule 23 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	y	63	Total	C	N	O	S	0	0
			508	313	99	94	2		

- Molecule 24 is a protein called 50S ribosomal protein L30.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	z	58	Total	C	N	O	S	0	0
			448	281	87	78	2		

- Molecule 25 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	A	41	Total	C	N	O	S	0	0
			315	192	57	60	6		

- Molecule 26 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	B	56	Total	C	N	O	S	0	0
			443	269	94	79	1		

- Molecule 27 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	D	46	Total	C	N	O	S	0	0
			376	228	90	56	2		

- Molecule 28 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	E	64	Total	C	N	O	S	0	0
			503	323	105	73	2		

- Molecule 29 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	F	38	Total	C	N	O	S	0	0
			301	185	65	47	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
30	G	225	Total	C	N	O	S	0	0
			1756	1111	315	322	8		

- Molecule 31 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	H	206	Total	C	N	O	S	0	0
			1624	1028	305	288	3		

- Molecule 32 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	I	205	Total	C	N	O	S	0	0
			1642	1026	315	297	4		

- Molecule 33 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	J	157	Total	C	N	O	S	0	0
			1156	719	218	213	6		

- Molecule 34 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	K	100	Total	C	N	O	S	0	0
			817	515	148	148	6		

- Molecule 35 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	L	151	Total	C	N	O	S	0	0
			1181	735	227	215	4		

- Molecule 36 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	M	129	Total	C	N	O	S	0	0
			978	616	173	183	6		

- Molecule 37 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	N	127	Total	C	N	O	S	0	0
			1021	634	206	178	3		

- Molecule 38 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	O	98	Total	C	N	O	S	0	0
			786	493	150	142	1		

- Molecule 39 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	P	116	Total	C	N	O	S	0	0
			869	535	173	158	3		

- Molecule 40 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	Q	123	Total	C	N	O	S	0	0
			954	590	196	164	4		

- Molecule 41 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	R	114	Total	C	N	O	S	0	0
			883	546	178	156	3		

- Molecule 42 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	S	100	Total	C	N	O	S	0	0
			804	499	164	138	3		

- Molecule 43 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	T	88	Total	C	N	O	S	0	0
			713	439	144	129	1		

- Molecule 44 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	U	82	Total	C	N	O	S	0	0
			648	406	128	113	1		

- Molecule 45 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	V	80	Total	C	N	O	S	0	0
			648	411	121	113	3		

- Molecule 46 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	W	65	Total	C	N	O	S	0	0
			535	339	100	95	1		

- Molecule 47 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	X	79	Total	C	N	O	S	0	0
			637	408	120	107	2		

- Molecule 48 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	Y	85	Total	C	N	O	S	0	0
			664	411	137	113	3		

- Molecule 49 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	Z	65	Total	C	N	O	S	0	0
			545	335	117	92	1		

- Molecule 50 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	a	134	Total	C	N	O	S	0	0
			1026	645	186	193	2		

- Molecule 51 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

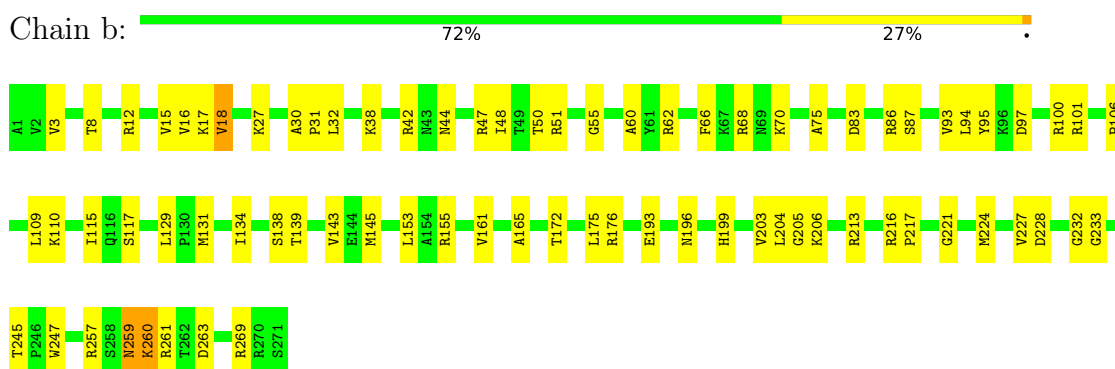
- Molecule 52 is a RNA chain called 23s-5s joint ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	3025	Total	C	N	O	P	0	0
			64925	28962	11938	21001	3024		

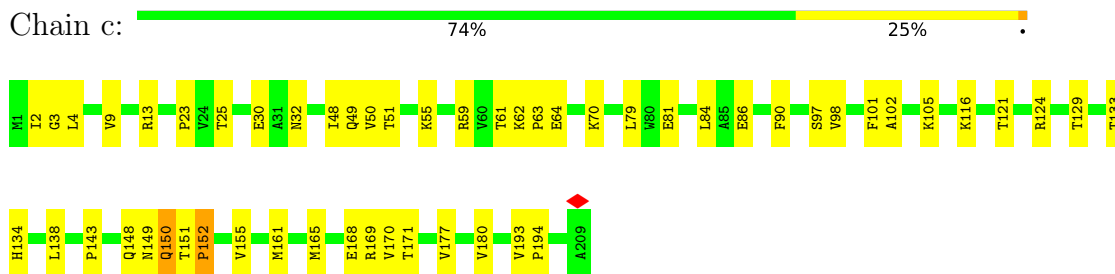
3 Residue-property plots [i](#)

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

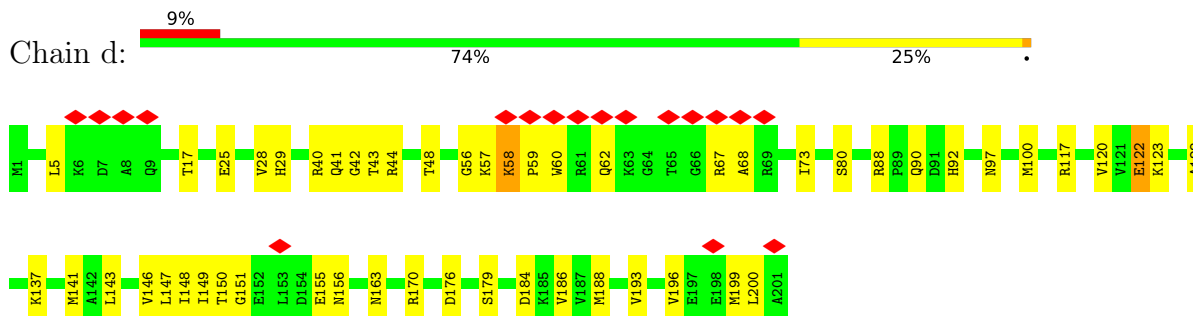
- Molecule 1: 50S ribosomal protein L2



- Molecule 2: 50S ribosomal protein L3

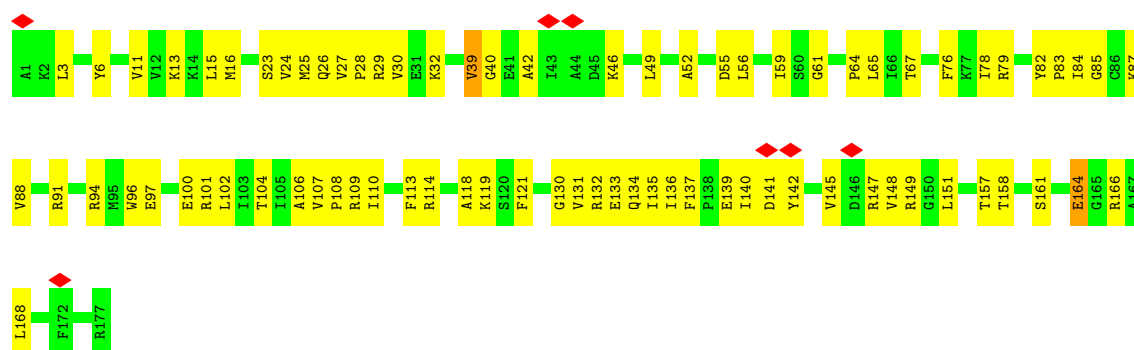


- Molecule 3: 50S ribosomal protein L4



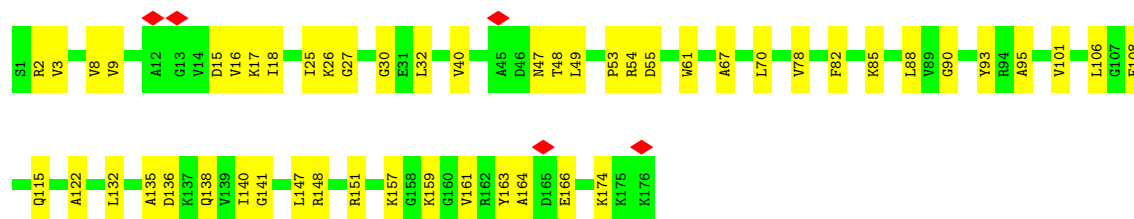
- Molecule 4: 50S ribosomal protein L5

Chain e:  56% 43%



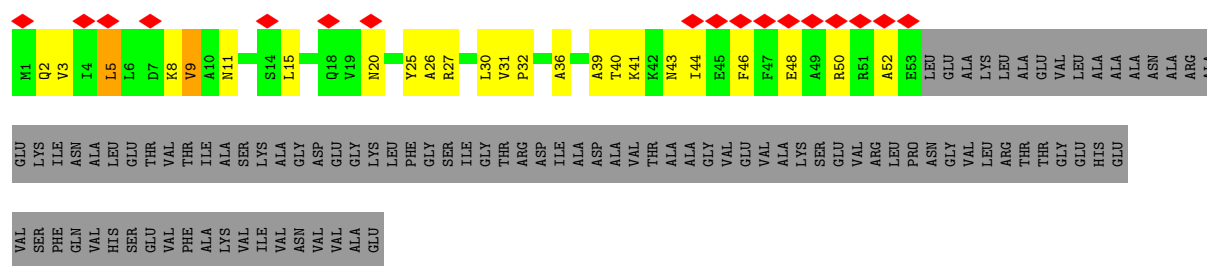
- Molecule 5: 50S ribosomal protein L6

Chain f:  71% 29%



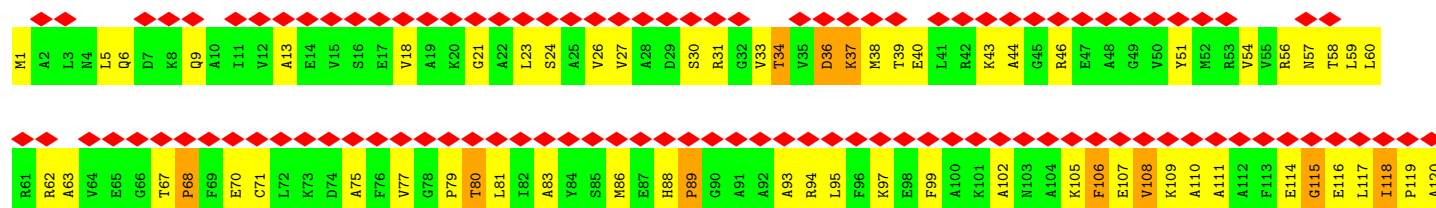
- Molecule 6: 50S ribosomal protein L9

Chain g:  11% 19% 15% 64%



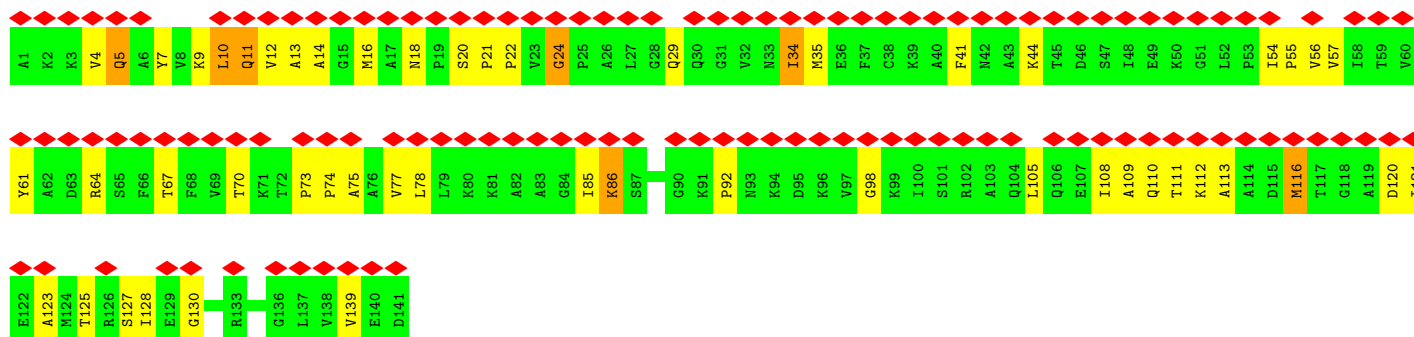
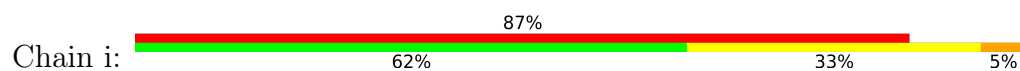
- Molecule 7: 50S ribosomal protein L10

Chain h:  89% 48% 44% 8%

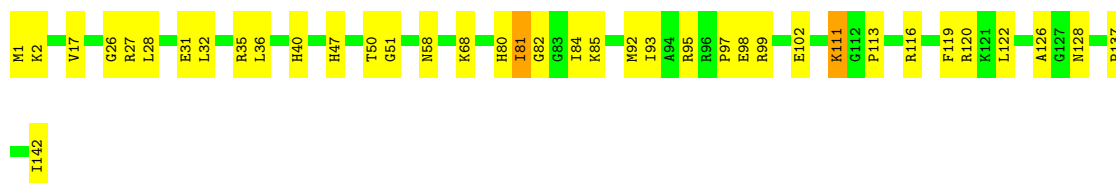




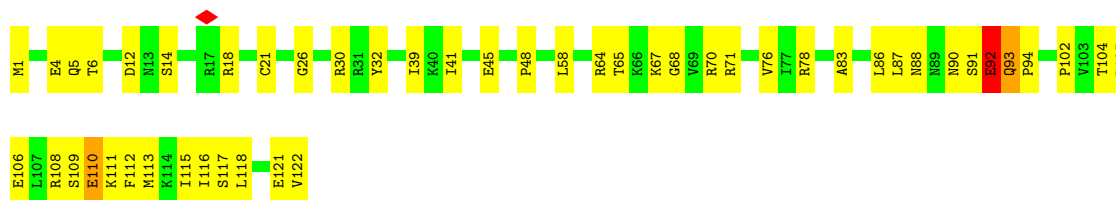
• Molecule 8: 50S ribosomal protein L11



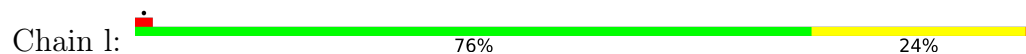
• Molecule 9: 50S ribosomal protein L13



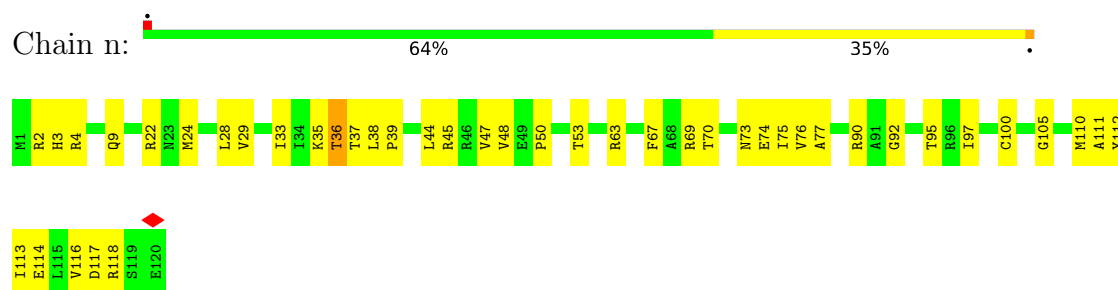
• Molecule 10: 50S ribosomal protein L14



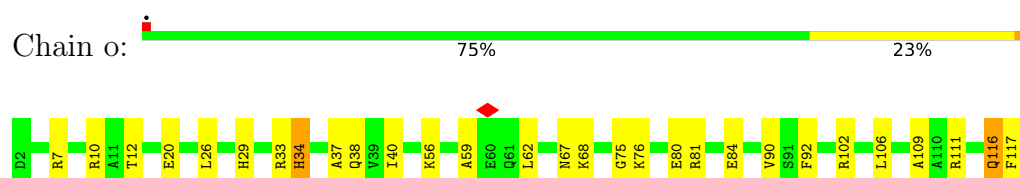
• Molecule 11: 50S ribosomal protein L15



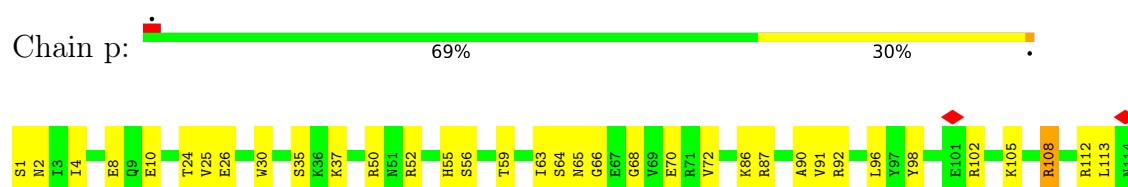
- Molecule 12: 50S ribosomal protein L17



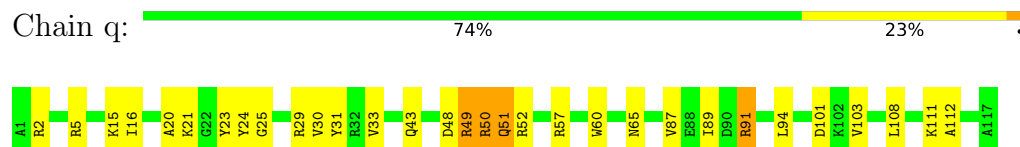
- Molecule 13: 50S ribosomal protein L18



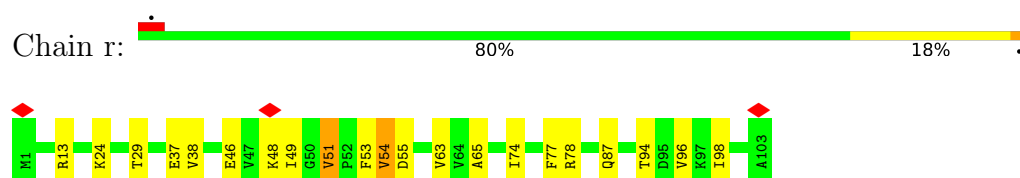
- Molecule 14: 50S ribosomal protein L19



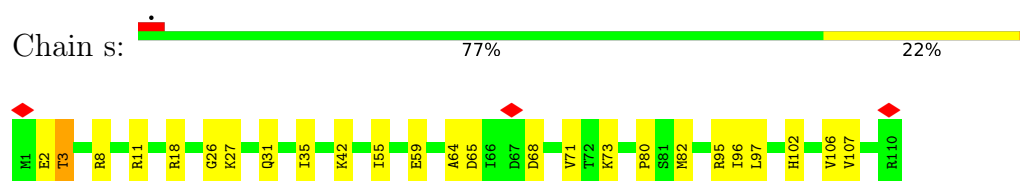
- Molecule 15: 50S ribosomal protein L20



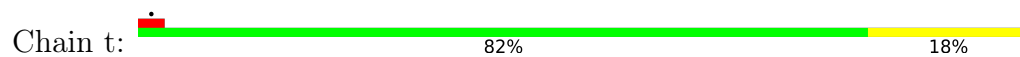
- Molecule 16: 50S ribosomal protein L21



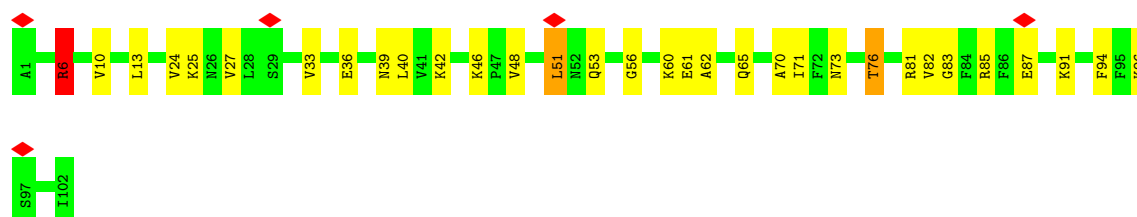
- Molecule 17: 50S ribosomal protein L22



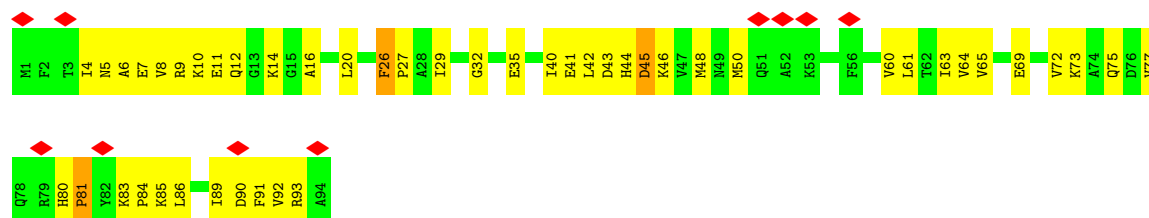
- Molecule 18: 50S ribosomal protein L23



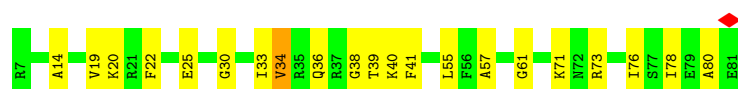
- Molecule 19: 50S ribosomal protein L24



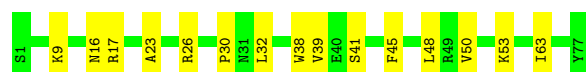
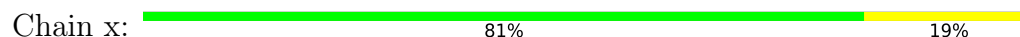
- Molecule 20: 50S ribosomal protein L25



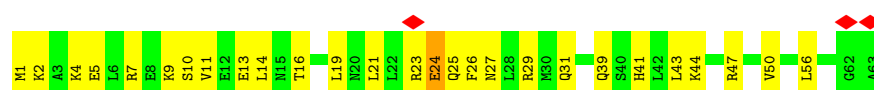
- Molecule 21: 50S ribosomal protein L27



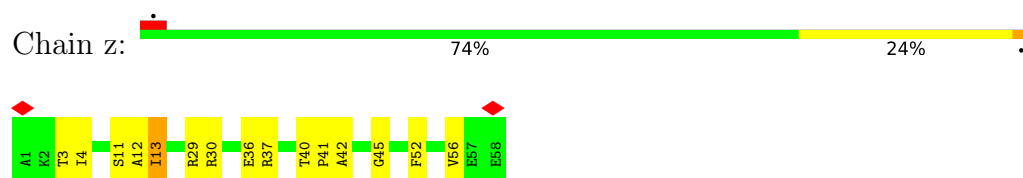
- Molecule 22: 50S ribosomal protein L28



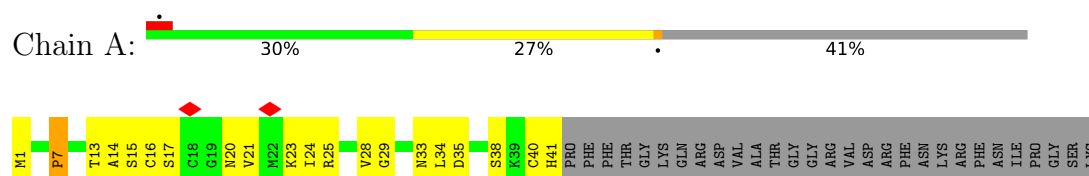
- Molecule 23: 50S ribosomal protein L29



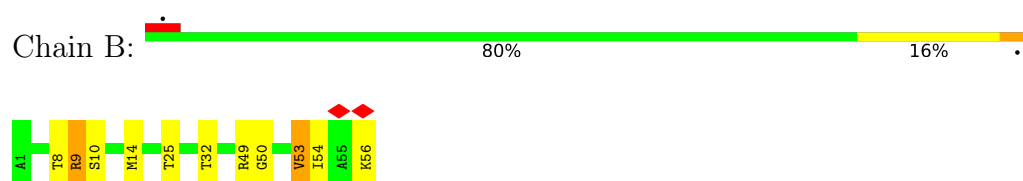
- Molecule 24: 50S ribosomal protein L30



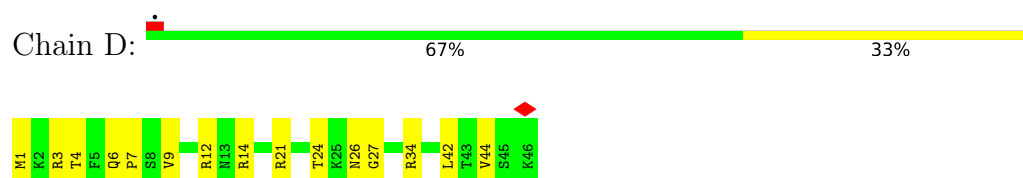
- Molecule 25: 50S ribosomal protein L31



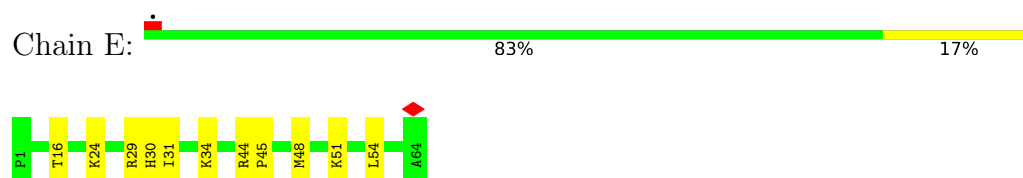
- Molecule 26: 50S ribosomal protein L32



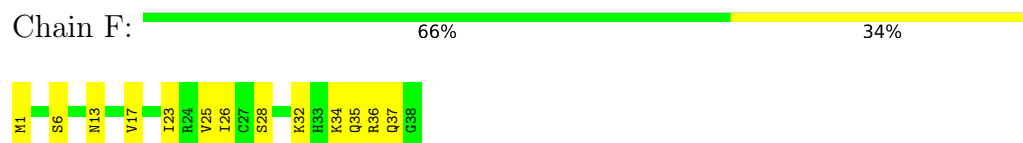
- Molecule 27: 50S ribosomal protein L34



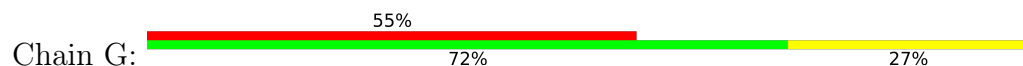
- Molecule 28: 50S ribosomal protein L35

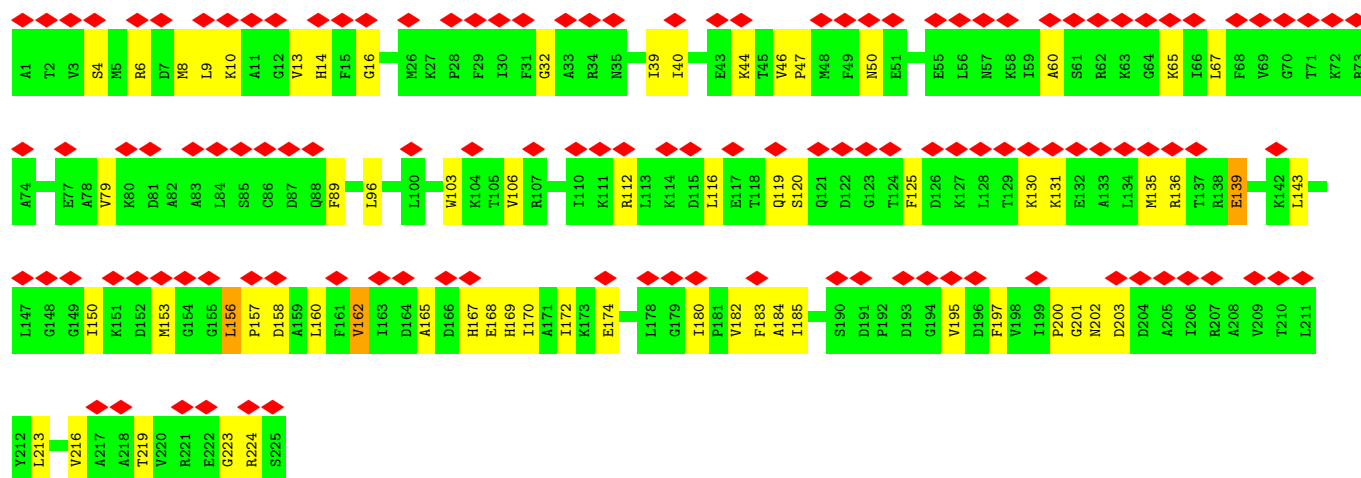


- Molecule 29: 50S ribosomal protein L36

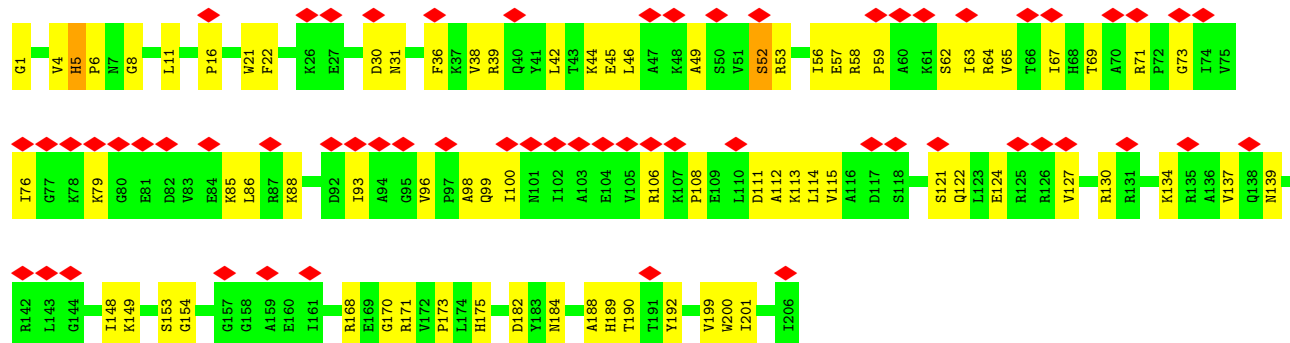


- Molecule 30: 30S ribosomal protein S2

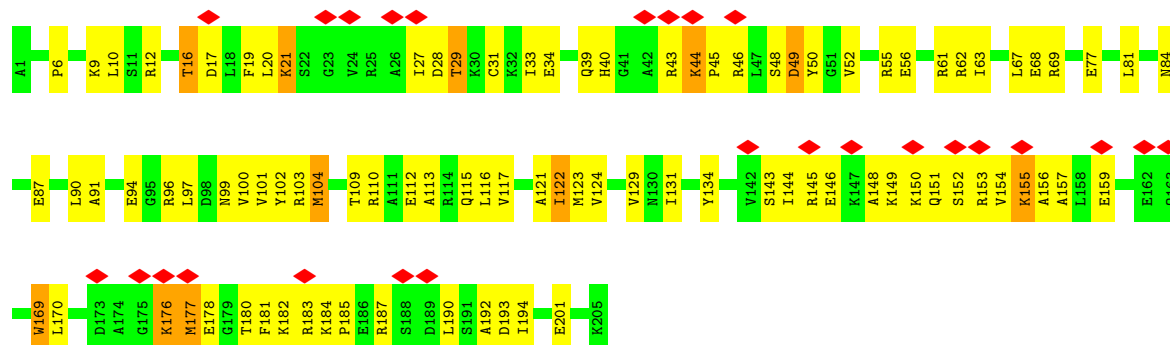




• Molecule 31: 30S ribosomal protein S3

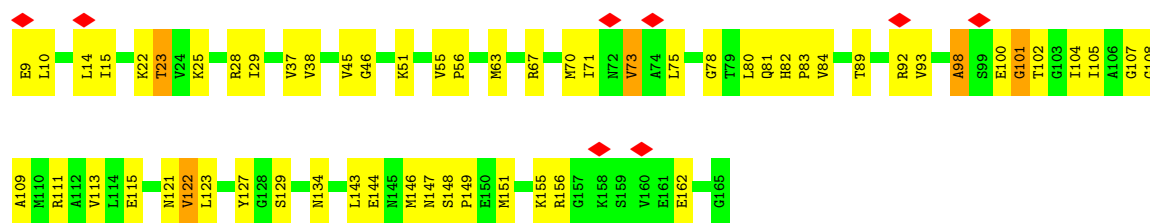


• Molecule 32: 30S ribosomal protein S4

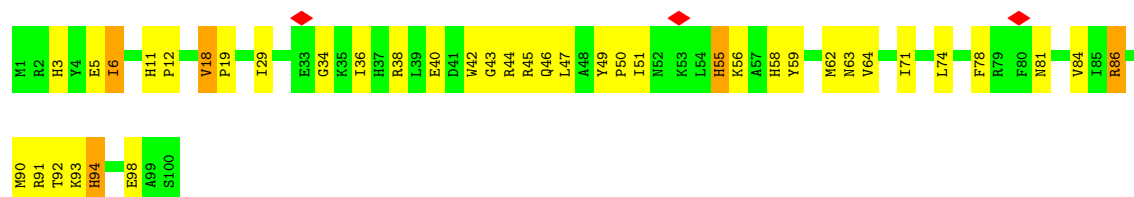


• Molecule 33: 30S ribosomal protein S5

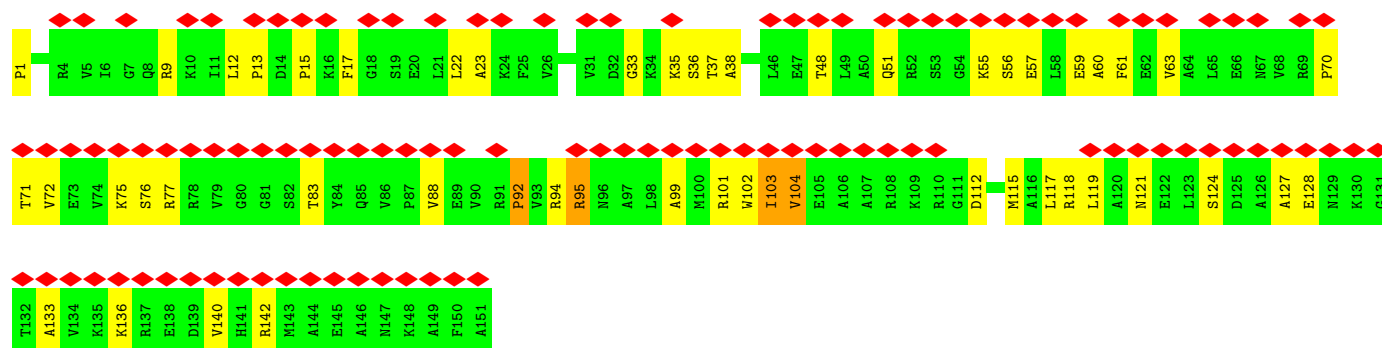




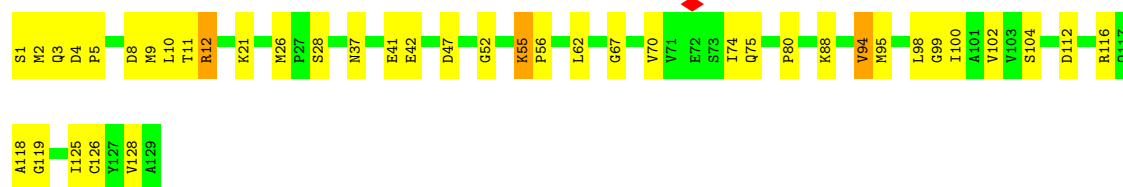
• Molecule 34: 30S ribosomal protein S6



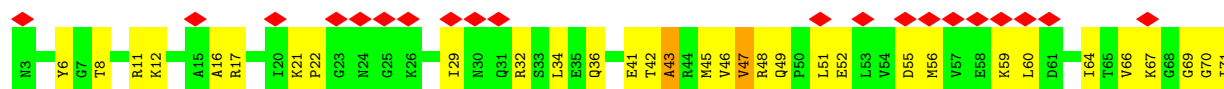
• Molecule 35: 30S ribosomal protein S7

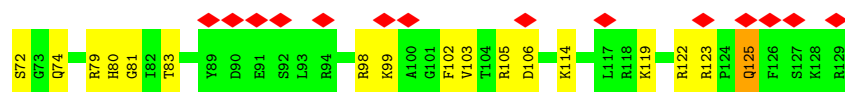


• Molecule 36: 30S ribosomal protein S8

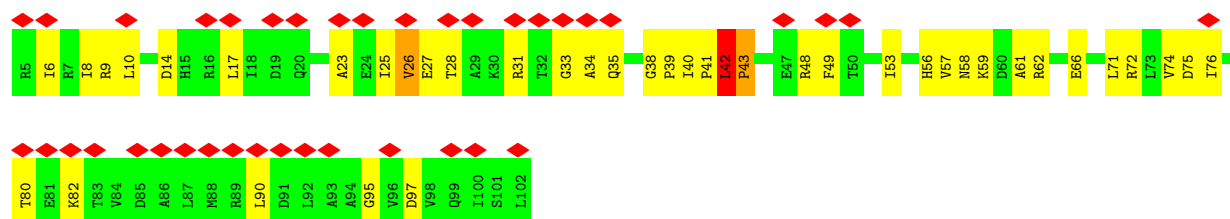
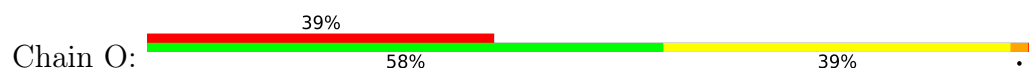


• Molecule 37: 30S ribosomal protein S9

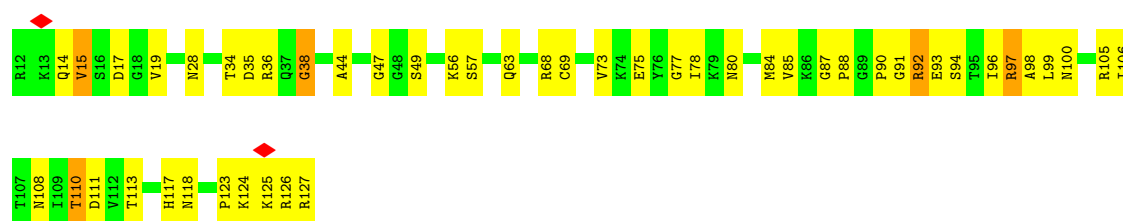




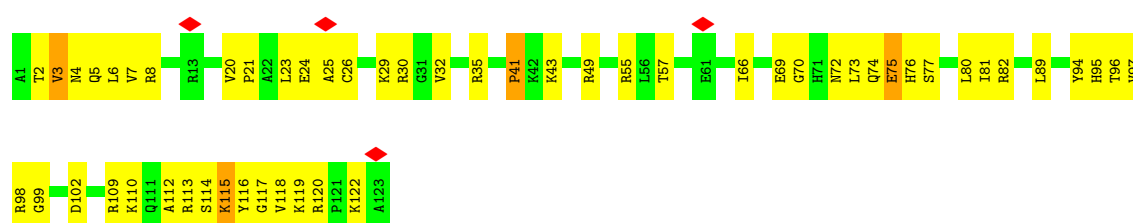
- Molecule 38: 30S ribosomal protein S10



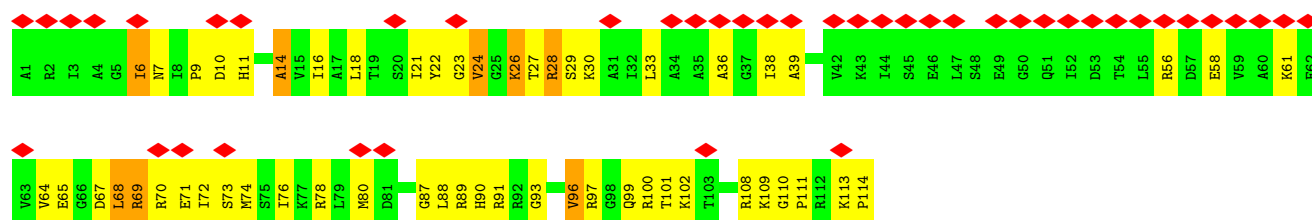
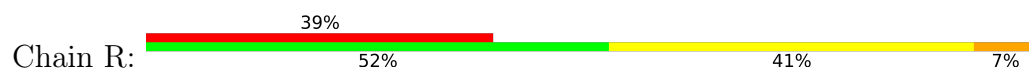
- Molecule 39: 30S ribosomal protein S11



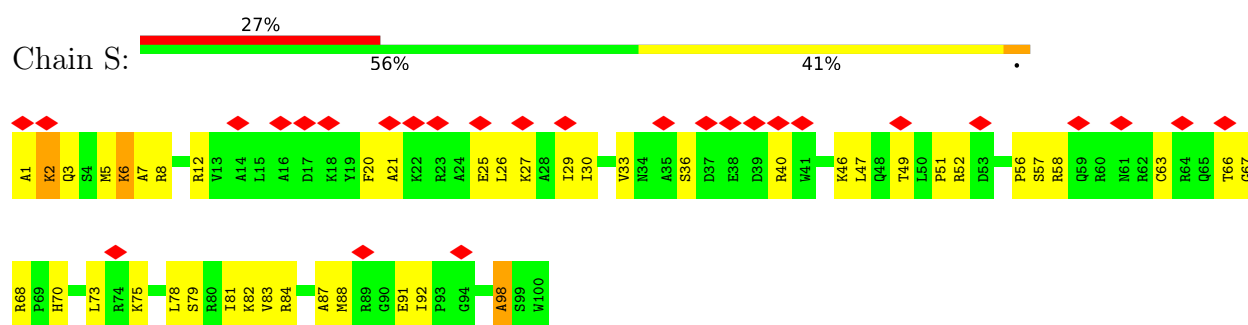
- Molecule 40: 30S ribosomal protein S12



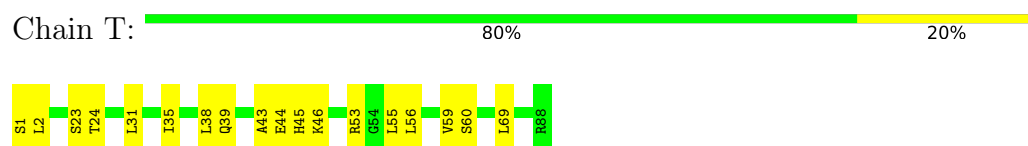
- Molecule 41: 30S ribosomal protein S13



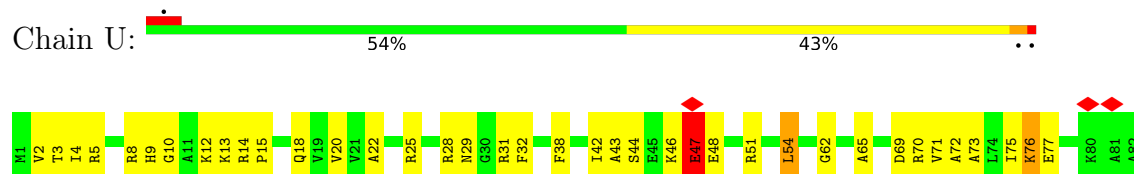
- Molecule 42: 30S ribosomal protein S14



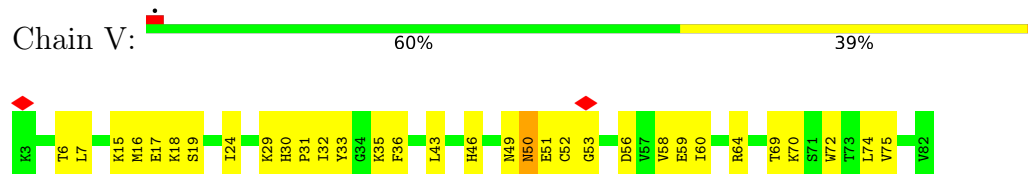
- Molecule 43: 30S ribosomal protein S15



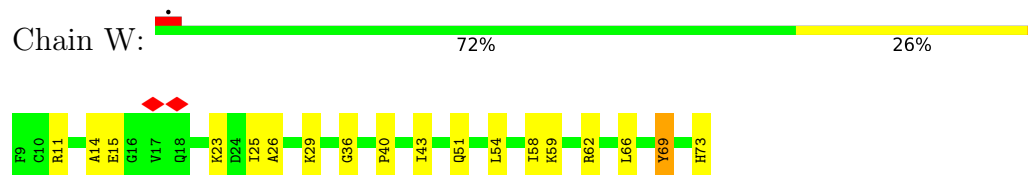
- Molecule 44: 30S ribosomal protein S16



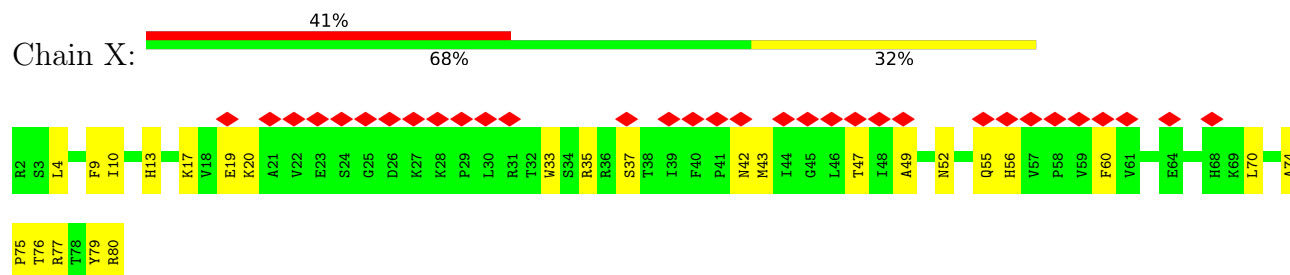
- Molecule 45: 30S ribosomal protein S17



- Molecule 46: 30S ribosomal protein S18



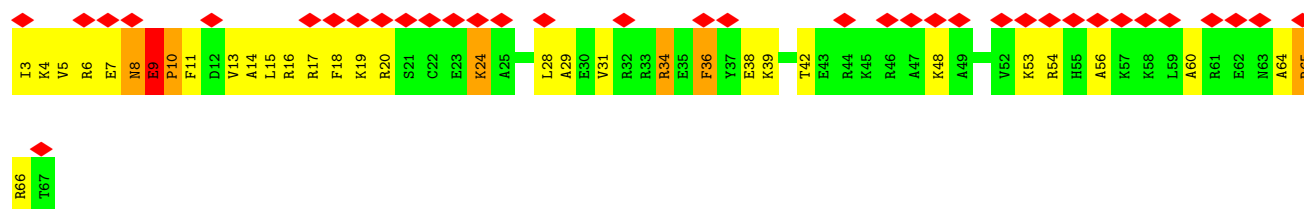
- Molecule 47: 30S ribosomal protein S19



- Molecule 48: 30S ribosomal protein S20



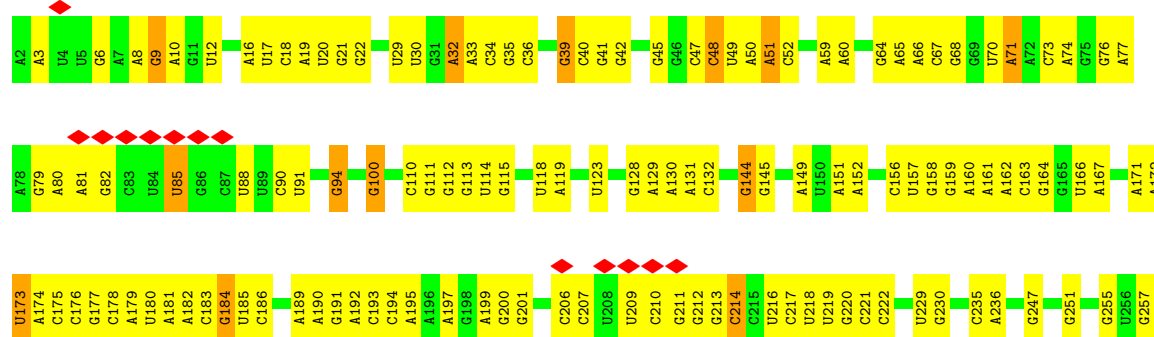
Chain Z: 55% 48% 42% 9%

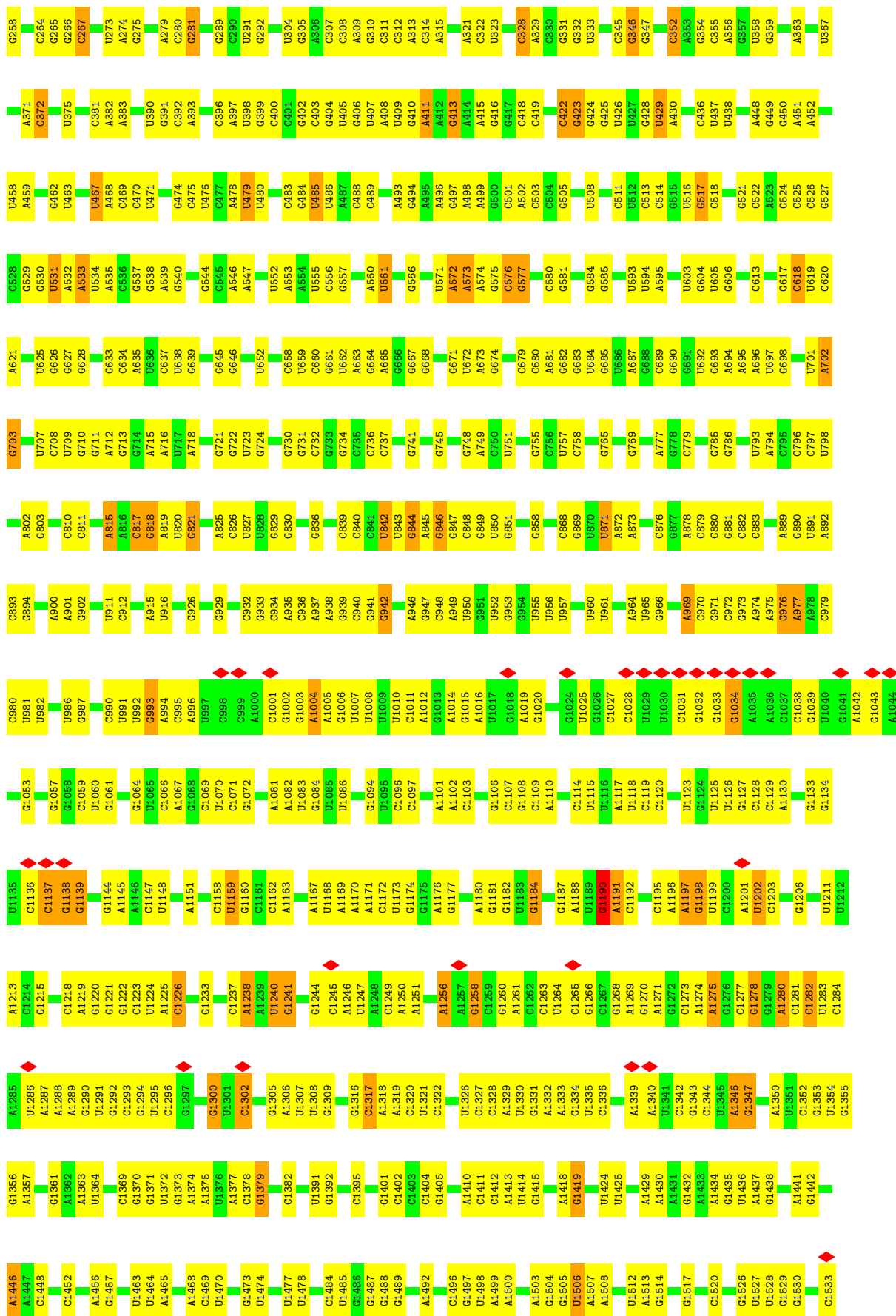


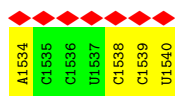
Chain a:



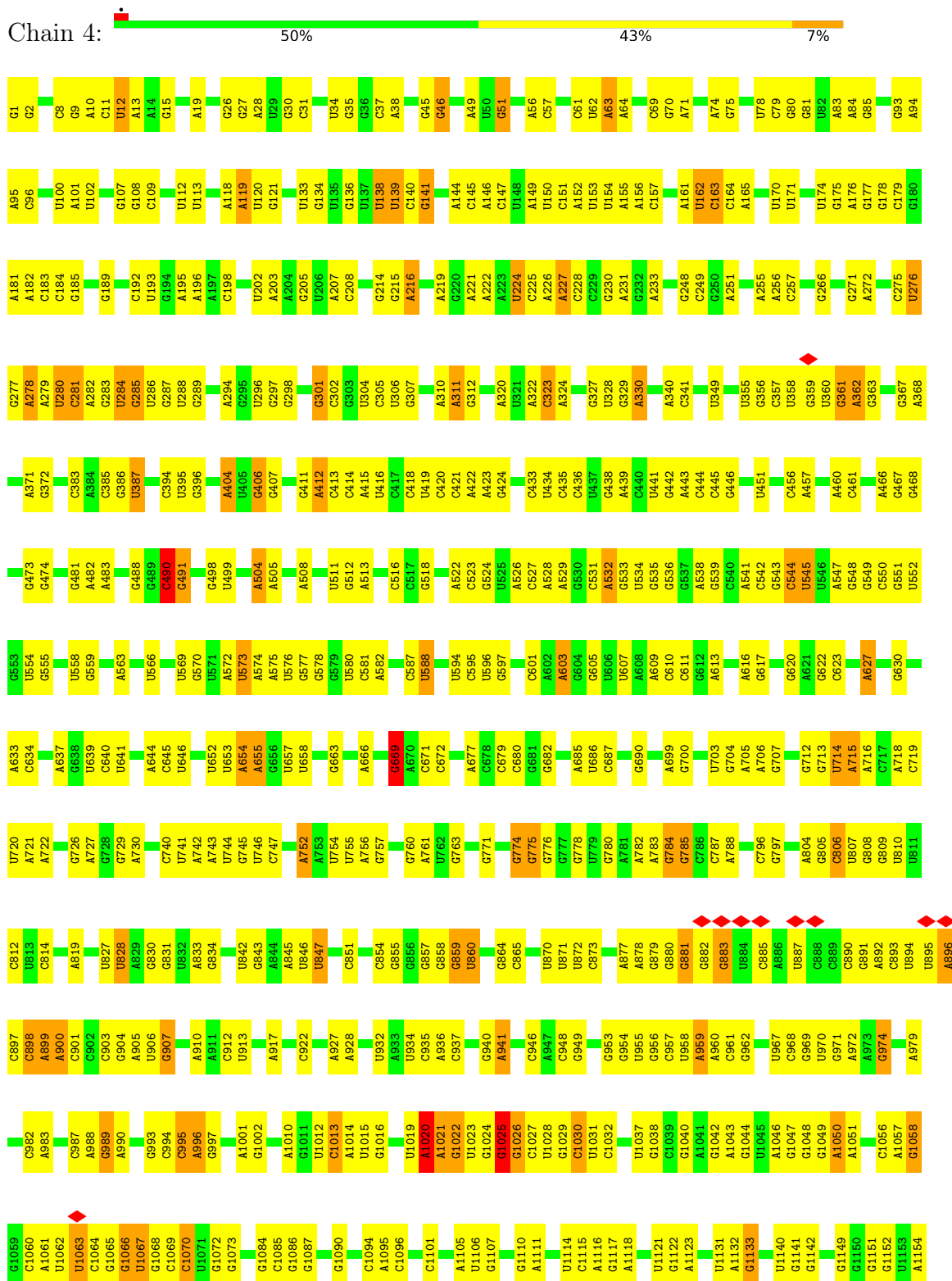
Chain 3: 48% 47% 5%







● Molecule 52: 23s-5s joint ribosomal RNA



U2313	G2181	U2091	A1986	C1892	G1802	G1701	U1613	C1514	C1406	A1303	G1219	A1155
G2314	A2182	C2095	G1991	A1901	A1806	C1702	U1614	A1515	G1407	U1304	C1220	A1156
U2315	C2183	G2096	U1992	C1902	A1807	C1703	A1618	U1522	A1413	G1305	G1221	A1157
G2318	G2185	A2097	G1997	G1903	U1808	C1705	A1624	U1533	A1414	C1306	A1222	A1160
A2319	A2186	A2098	G1998	G1904	G1809	U1706	U1625	U1534	G1425	U1307	A1223	U1161
U2320	A2187	U2099	A1999	U1905	G1810	A1707	U1626	U1534	G1426	U1308	A1224	G1166
G2321	A2188	G2100	A1999	U1906	U1811	A1708	G1626	U1537	G1428	U1309	U1225	A1167
G2265	G2189	G2100	A2000	U1907	U1812	A1709	U1629	U1538	G1429	U1310	A1226	A1168
C2257	A2190	U2110	C2002	A1908	C1813	U1712	G1629	U1539	A1429	U1311	G1227	G1169
C2258	C2191	U2119	G2003	A1912	G1815	C1713	A1632	U1540	G1437	G1313	C1228	G1170
U2259	C2192	U2120	A2004	A1913	G1816	A1718	A1633	U1541	G1438	G1314	U1229	C1171
U2260	C2193	U2121	G2009	A1914	G1823	A1719	A1634	U1542	U1444	U1315	C1230	G1172
G2261	C2194	C2124	U2010	A1917	G1824	A1720	U1635	U1543	U1445	U1316	A1231	C1173
A2262	U2196	G2125	U2011	C1918	U1828	U1722	A1636	U1544	U1446	U1317	A1174	A1173
A2263	G2197	A2126	G2012	C1919	A1829	C1723	A1637	U1547	U1447	G1325	U1233	G1175
G2264	A2198	C2127	A2013	A1919	A1829	A1725	G1638	A1547	G1447	U1326	G1234	A1176
U2265	A2199	C2128	G2022	C1922	C1834	A1726	G1639	G1552	A1448	U1327	G1235	C1177
C2200	C2200	G2138	A2029	G1927	G1843	A1744	G1688	G1553	A1449	C1328	C1237	A1178
C2201	C2201	U2139	G2033	C1935	U1848	A1737	A1651	U1556	A1450	C1329	G1238	C1180
C2202	C2202	G2140	G2034	G1936	A1850	A1738	G1652	U1557	U1454	A1333	A1239	C1181
G2206	G2206	A2141	C2035	A1937	A1851	A1739	G1653	U1558	A1455	U1337	G1240	A1182
U2207	G2211	G2142	G2036	C1938	G1852	A1744	G1654	U1559	A1456	G1338	U1241	A1183
G2210	G2211	A2143	C2037	G1939	U1853	A1744	G1655	U1560	U1457	G1339	C1242	G1184
U2214	U2214	U2144	G2038	G1942	A1854	A1764	G1656	U1561	G1461	G1340	G1243	A1185
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A2216	A2216	G2146	A2040	C1944	U1857	U1764	G1658	U1563	G1463	G1353	A1254	U1188
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A2222	A2222	A2150	A2043	C1946	U1864	A1773	G1661	U1566	U1472	G1357	G1259	C1192
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G2230	G2230	A2161	G2051	G1956	A1873	G1779	G1674	U1586	G1489	C1379	A1271	A1202
C2231	C2231	U2162	G2052	A1957	A1874	G1780	G1675	G1587	A1493	G1380	A1272	C1203
C2232	C2232	G2163	A2060	U1969	U1875	G1781	A1677	U1588	A1494	A1381	C1273	C1204
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G2244	G2244	G2181	C2087	G1986	G1891	U1799	A1700	G1613	G1514	U1401	U1301	A1218
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G2255	G2255	G2100	A1999	U1906	G1810	U1799	A1700	G1621	G1522	U1415	U1309	
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U2259	U2259	U2120	G2003	A1912	G1815	U1799	A1700	G1624	G1525	U1418	U1312	
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G2225	G2225	C2153	A2047	G1951	U1868	U1799	A1700	G1646	G1547	U1440	U1334	
U2226	U2226	A2157	A2048	C1952	G1869	U1799	A1700	G1647	G1548	U1441	U1335	
G2227	G2227	G2158	C2049	G1953	U1870	U1799	A1700	G1648	G1549	U1442	U1336	
G2228	G2228	A2159	G2050	U1955	A1872	U1799	A1700	G1649	G1550	U1443	U1337	
A2229	A2229	G2160	U2051	G1956	A1873	U1799	A1700	G1650	G1551	U1444	U1338	
G2230	G2230	A2161	G2052	A1957	A1874	U1799	A1700	G1651	G1552	U1445	U1339	
C2231	C2231	U2162	A2060	U1969	U1875	U1799	A1700	G1652	G1553	U1446	U1340	
C2232	C2232	G2163	G2061	U1970	C1876	U1799	A1700	G1653	G1554	U1447	U1341	
U2233	U2233	G2164	A2062	C1971	A1877	U1799	A1700	G1654	G1555	U1448	U1342	
U2234	U2234	U2167	A2063	G1972	G1881	U1799	A1700	G1655	G1556	U1449	U1343	
G2235	G2235	G2168	A2064	G1973	A1882	U1799	A1700	G1656	G1557	U1450	U1344	
A2236	A2236	U2169	A2065	G1974	U1883	U1799	A1700	G1657	G1558	U1451	U1345	
U2237	U2237	A2170	U2071	A1975	G1884	U1799	A1700	G1658	G1559	U1452	U1346	
G2238	G2238	C2171	U2072	A1976	U1885	U1799	A1700	G1659	G1560	U1453	U1347	
U2239	U2239	G2176	U2073	A1982	U1886	U1799	A1700	G1660	G1561	U1454	U1348	
A2240	A2240	C2177	U2084	U1983	C1888	U1799	A1700	G1661	G1562	U1455	U1349	
G2241	G2241	G2178	C2085	U1984	G1889	U1799	A1700	G1662	G1563	U1456	U1350	
U2242</												



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	9620	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING ONLY	Depositor
Microscope	TFS TALOS	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	16.217	Depositor
Minimum map value	-5.852	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.783	Depositor
Recommended contour level	3	Depositor
Map size (Å)	528.96, 528.96, 528.96	wwPDB
Map dimensions	608, 608, 608	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87000006, 0.87000006, 0.87000006	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	b	0.33	0/2121	0.88	5/2852 (0.2%)
2	c	0.34	0/1585	0.83	2/2134 (0.1%)
3	d	0.39	0/1570	0.89	5/2113 (0.2%)
4	e	0.42	0/1434	0.94	3/1926 (0.2%)
5	f	0.40	0/1342	0.87	3/1816 (0.2%)
6	g	0.44	0/414	1.03	2/556 (0.4%)
7	h	0.55	0/1001	1.15	14/1350 (1.0%)
8	i	0.54	0/1045	1.11	7/1410 (0.5%)
9	j	0.34	0/1151	0.84	1/1551 (0.1%)
10	k	0.34	0/947	0.92	2/1268 (0.2%)
11	l	0.36	0/1053	0.96	2/1403 (0.1%)
12	n	0.34	0/973	0.93	3/1301 (0.2%)
13	o	0.35	0/901	0.94	2/1209 (0.2%)
14	p	0.33	0/928	0.83	2/1242 (0.2%)
15	q	0.31	0/959	0.92	5/1278 (0.4%)
16	r	0.35	0/828	0.85	4/1107 (0.4%)
17	s	0.32	0/863	0.86	1/1156 (0.1%)
18	t	0.35	0/744	0.80	0/994
19	u	0.35	0/787	0.85	1/1051 (0.1%)
20	v	0.44	0/765	0.94	3/1025 (0.3%)
21	w	0.31	0/581	0.83	1/769 (0.1%)
22	x	0.33	0/634	0.80	0/848
23	y	0.34	0/509	0.90	1/677 (0.1%)
24	z	0.35	0/452	0.77	0/605
25	A	0.43	0/319	0.93	1/426 (0.2%)
26	B	0.32	0/449	0.82	3/599 (0.5%)
27	D	0.35	0/379	0.88	1/498 (0.2%)
28	E	0.32	0/512	0.89	1/676 (0.1%)
29	F	0.34	0/302	0.94	0/397
30	G	0.43	0/1787	0.91	3/2408 (0.1%)
31	H	0.43	0/1651	0.94	9/2225 (0.4%)
32	I	0.39	0/1664	0.99	10/2227 (0.4%)
33	J	0.41	0/1169	0.94	3/1573 (0.2%)
34	K	0.41	0/835	0.92	1/1128 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	L	0.50	0/1195	1.06	6/1602 (0.4%)
36	M	0.35	0/988	0.93	6/1326 (0.5%)
37	N	0.46	0/1033	0.94	4/1375 (0.3%)
38	O	0.47	0/796	1.00	5/1077 (0.5%)
39	P	0.42	0/885	0.96	3/1195 (0.3%)
40	Q	0.35	0/968	0.92	7/1300 (0.5%)
41	R	0.48	0/892	1.07	11/1193 (0.9%)
42	S	0.45	0/816	0.95	3/1088 (0.3%)
43	T	0.33	0/721	0.88	3/964 (0.3%)
44	U	0.35	0/658	1.02	7/884 (0.8%)
45	V	0.39	0/657	0.93	0/881
46	W	0.40	0/544	0.94	3/731 (0.4%)
47	X	0.51	0/652	0.82	1/877 (0.1%)
48	Y	0.36	0/670	0.95	4/888 (0.5%)
49	Z	0.50	0/551	1.08	6/728 (0.8%)
50	a	0.53	0/1033	0.97	6/1387 (0.4%)
51	3	0.47	0/36963	0.49	2/57662 (0.0%)
52	4	0.45	0/72710	0.50	4/113431 (0.0%)
All	All	0.44	0/155386	0.64	182/232387 (0.1%)

There are no bond length outliers.

The worst 5 of 182 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
41	R	96	VAL	N-CA-C	10.07	120.09	110.42
37	N	52	GLU	N-CA-C	-8.98	101.89	113.12
31	H	76	ILE	N-CA-C	-8.85	103.22	111.45
41	R	11	HIS	N-CA-C	8.55	123.28	111.74
7	h	89	PRO	N-CA-C	-8.36	103.98	114.68

There are no chirality outliers.

There are no planarity outliers.

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	b	2082	0	2157	56	0
2	c	1564	0	1616	42	0
3	d	1551	0	1619	34	0
4	e	1410	0	1447	71	0
5	f	1322	0	1374	41	0
6	g	409	0	429	17	0
7	h	988	0	1025	60	0
8	i	1031	0	1088	52	0
9	j	1128	0	1162	31	0
10	k	938	0	1012	38	0
11	l	1044	0	1117	26	0
12	n	960	0	1000	32	0
13	o	891	0	923	23	0
14	p	916	0	965	23	0
15	q	946	0	1022	26	0
16	r	815	0	839	18	0
17	s	856	0	922	19	0
18	t	738	0	807	16	0
19	u	779	0	834	22	0
20	v	752	0	780	43	0
21	w	574	0	592	16	0
22	x	624	0	655	9	0
23	y	508	0	543	23	0
24	z	448	0	491	13	0
25	A	315	0	318	16	0
26	B	443	0	461	10	0
27	D	376	0	418	16	0
28	E	503	0	574	8	0
29	F	301	0	343	10	0
30	G	1756	0	1787	54	0
31	H	1624	0	1699	54	0
32	I	1642	0	1710	74	0
33	J	1156	0	1199	46	0
34	K	817	0	808	34	0
35	L	1181	0	1240	34	0
36	M	978	0	1034	29	0
37	N	1021	0	1070	48	0
38	O	786	0	828	37	0
39	P	869	0	878	39	0
40	Q	954	0	1019	37	0
41	R	883	0	944	47	0
42	S	804	0	847	44	0
43	T	713	0	737	10	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
44	U	648	0	666	28	0
45	V	648	0	691	26	0
46	W	535	0	552	12	0
47	X	637	0	665	25	0
48	Y	664	0	714	15	0
49	Z	545	0	579	32	0
50	a	1026	0	1092	34	0
51	3	33012	0	16618	676	0
52	4	64925	0	32667	1192	0
All	All	143036	0	96577	3019	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 13.

The worst 5 of 3019 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)
52:4:45:G:H5''	52:4:46:G:H5'	1.26	1.16
52:4:138:U:H2'	52:4:139:U:H4'	1.31	1.12
52:4:1024:G:H3'	52:4:1025:G:H2'	1.17	1.12
52:4:283:G:H3'	52:4:284:U:H5''	1.30	1.06
51:3:1378:C:H3'	51:3:1379:G:H5''	1.32	1.05

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	
1	b	269/271 (99%)	230 (86%)	35 (13%)	4 (2%)	8	37
2	c	207/209 (99%)	185 (89%)	21 (10%)	1 (0%)	24	57

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
3	d	199/201 (99%)	173 (87%)	23 (12%)	3 (2%)	8	37
4	e	175/177 (99%)	155 (89%)	20 (11%)	0	100	100
5	f	174/176 (99%)	158 (91%)	16 (9%)	0	100	100
6	g	51/149 (34%)	38 (74%)	11 (22%)	2 (4%)	2	20
7	h	129/131 (98%)	95 (74%)	28 (22%)	6 (5%)	2	17
8	i	139/141 (99%)	118 (85%)	17 (12%)	4 (3%)	3	26
9	j	140/142 (99%)	129 (92%)	9 (6%)	2 (1%)	9	38
10	k	120/122 (98%)	99 (82%)	17 (14%)	4 (3%)	3	23
11	l	141/143 (99%)	118 (84%)	20 (14%)	3 (2%)	5	31
12	n	118/120 (98%)	99 (84%)	17 (14%)	2 (2%)	7	35
13	o	114/116 (98%)	106 (93%)	7 (6%)	1 (1%)	14	47
14	p	112/114 (98%)	99 (88%)	12 (11%)	1 (1%)	14	47
15	q	115/117 (98%)	109 (95%)	6 (5%)	0	100	100
16	r	101/103 (98%)	92 (91%)	7 (7%)	2 (2%)	6	32
17	s	108/110 (98%)	96 (89%)	11 (10%)	1 (1%)	14	47
18	t	91/93 (98%)	81 (89%)	10 (11%)	0	100	100
19	u	100/102 (98%)	84 (84%)	14 (14%)	2 (2%)	6	32
20	v	92/94 (98%)	75 (82%)	16 (17%)	1 (1%)	11	43
21	w	73/75 (97%)	67 (92%)	6 (8%)	0	100	100
22	x	75/77 (97%)	70 (93%)	5 (7%)	0	100	100
23	y	61/63 (97%)	57 (93%)	3 (5%)	1 (2%)	7	36
24	z	56/58 (97%)	49 (88%)	6 (11%)	1 (2%)	6	34
25	A	39/70 (56%)	26 (67%)	12 (31%)	1 (3%)	4	27
26	B	54/56 (96%)	48 (89%)	6 (11%)	0	100	100
27	D	44/46 (96%)	38 (86%)	6 (14%)	0	100	100
28	E	62/64 (97%)	56 (90%)	6 (10%)	0	100	100
29	F	36/38 (95%)	28 (78%)	7 (19%)	1 (3%)	4	26
30	G	223/225 (99%)	199 (89%)	24 (11%)	0	100	100
31	H	204/206 (99%)	182 (89%)	21 (10%)	1 (0%)	24	57
32	I	203/205 (99%)	172 (85%)	27 (13%)	4 (2%)	6	32
33	J	155/157 (99%)	123 (79%)	27 (17%)	5 (3%)	3	24

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
34	K	98/100 (98%)	85 (87%)	11 (11%)	2 (2%)	6	32
35	L	149/151 (99%)	129 (87%)	18 (12%)	2 (1%)	9	39
36	M	127/129 (98%)	116 (91%)	10 (8%)	1 (1%)	16	49
37	N	125/127 (98%)	90 (72%)	32 (26%)	3 (2%)	4	29
38	O	96/98 (98%)	74 (77%)	16 (17%)	6 (6%)	1	12
39	P	114/116 (98%)	99 (87%)	11 (10%)	4 (4%)	3	23
40	Q	121/123 (98%)	89 (74%)	28 (23%)	4 (3%)	3	23
41	R	112/114 (98%)	79 (70%)	30 (27%)	3 (3%)	4	27
42	S	98/100 (98%)	80 (82%)	16 (16%)	2 (2%)	6	32
43	T	86/88 (98%)	77 (90%)	8 (9%)	1 (1%)	10	41
44	U	80/82 (98%)	63 (79%)	16 (20%)	1 (1%)	9	39
45	V	78/80 (98%)	65 (83%)	10 (13%)	3 (4%)	2	20
46	W	63/65 (97%)	55 (87%)	8 (13%)	0	100	100
47	X	77/79 (98%)	58 (75%)	19 (25%)	0	100	100
48	Y	83/85 (98%)	80 (96%)	3 (4%)	0	100	100
49	Z	63/65 (97%)	38 (60%)	19 (30%)	6 (10%)	0	6
50	a	130/223 (58%)	121 (93%)	9 (7%)	0	100	100
All	All	5680/5996 (95%)	4852 (85%)	737 (13%)	91 (2%)	10	36

5 of 91 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	b	232	GLY
7	h	80	THR
7	h	108	VAL
7	h	111	ALA
8	i	11	GLN

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	b	216/216 (100%)	214 (99%)	2 (1%)	70	76
2	c	164/164 (100%)	162 (99%)	2 (1%)	63	73
3	d	165/165 (100%)	164 (99%)	1 (1%)	78	79
4	e	148/148 (100%)	148 (100%)	0	100	100
5	f	137/137 (100%)	136 (99%)	1 (1%)	76	78
6	g	42/114 (37%)	41 (98%)	1 (2%)	43	64
7	h	100/100 (100%)	97 (97%)	3 (3%)	36	60
8	i	109/109 (100%)	109 (100%)	0	100	100
9	j	116/116 (100%)	115 (99%)	1 (1%)	70	76
10	k	103/103 (100%)	102 (99%)	1 (1%)	68	75
11	l	102/102 (100%)	102 (100%)	0	100	100
12	n	100/100 (100%)	99 (99%)	1 (1%)	68	75
13	o	86/86 (100%)	86 (100%)	0	100	100
14	p	99/99 (100%)	98 (99%)	1 (1%)	68	75
15	q	89/89 (100%)	88 (99%)	1 (1%)	65	74
16	r	84/84 (100%)	84 (100%)	0	100	100
17	s	93/93 (100%)	92 (99%)	1 (1%)	65	74
18	t	80/80 (100%)	80 (100%)	0	100	100
19	u	83/83 (100%)	82 (99%)	1 (1%)	63	73
20	v	78/78 (100%)	78 (100%)	0	100	100
21	w	57/57 (100%)	57 (100%)	0	100	100
22	x	67/67 (100%)	67 (100%)	0	100	100
23	y	55/55 (100%)	55 (100%)	0	100	100
24	z	48/48 (100%)	48 (100%)	0	100	100
25	A	38/62 (61%)	38 (100%)	0	100	100
26	B	47/47 (100%)	47 (100%)	0	100	100
27	D	38/38 (100%)	38 (100%)	0	100	100
28	E	51/51 (100%)	51 (100%)	0	100	100
29	F	34/34 (100%)	34 (100%)	0	100	100
30	G	186/186 (100%)	183 (98%)	3 (2%)	55	70
31	H	170/170 (100%)	170 (100%)	0	100	100
32	I	172/172 (100%)	169 (98%)	3 (2%)	53	70

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
33	J	119/119 (100%)	118 (99%)	1 (1%)	73	77
34	K	87/87 (100%)	84 (97%)	3 (3%)	32	57
35	L	124/124 (100%)	123 (99%)	1 (1%)	73	77
36	M	104/104 (100%)	104 (100%)	0	100	100
37	N	105/105 (100%)	103 (98%)	2 (2%)	50	68
38	O	86/86 (100%)	84 (98%)	2 (2%)	44	64
39	P	89/89 (100%)	87 (98%)	2 (2%)	45	65
40	Q	103/103 (100%)	102 (99%)	1 (1%)	68	75
41	R	92/92 (100%)	89 (97%)	3 (3%)	33	58
42	S	83/83 (100%)	83 (100%)	0	100	100
43	T	76/76 (100%)	76 (100%)	0	100	100
44	U	65/65 (100%)	64 (98%)	1 (2%)	57	71
45	V	74/74 (100%)	73 (99%)	1 (1%)	59	71
46	W	56/56 (100%)	56 (100%)	0	100	100
47	X	70/70 (100%)	70 (100%)	0	100	100
48	Y	65/65 (100%)	65 (100%)	0	100	100
49	Z	55/55 (100%)	54 (98%)	1 (2%)	51	69
50	a	110/174 (63%)	109 (99%)	1 (1%)	70	76
All	All	4720/4880 (97%)	4678 (99%)	42 (1%)	68	76

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
37	N	34	LEU
41	R	24	VAL
37	N	47	VAL
39	P	15	VAL
41	R	88	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 100 such sidechains are listed below:

Mol	Chain	Res	Type
31	H	184	ASN
35	L	147	ASN
50	a	160	GLN

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Mol	Chain	Res	Type
32	I	73	ASN
33	J	121	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	1538/1539 (99%)	154 (10%)	1 (0%)
52	4	3023/3031 (99%)	377 (12%)	10 (0%)
All	All	4561/4570 (99%)	531 (11%)	11 (0%)

5 of 531 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	6	G
51	3	9	G
51	3	22	G
51	3	32	A
51	3	39	G

5 of 11 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
52	4	2424	U
52	4	2430	U
52	4	2632	U
52	4	2454	C
52	4	1020	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](#)

There are no chain breaks in this entry.

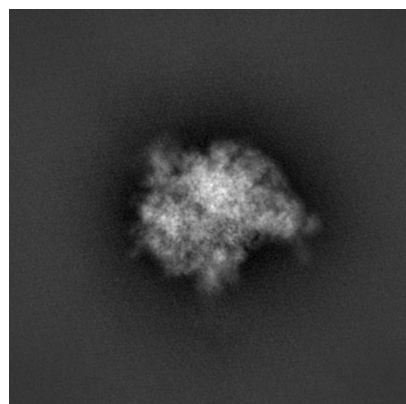
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21857. These allow visual inspection of the internal detail of the map and identification of artifacts.

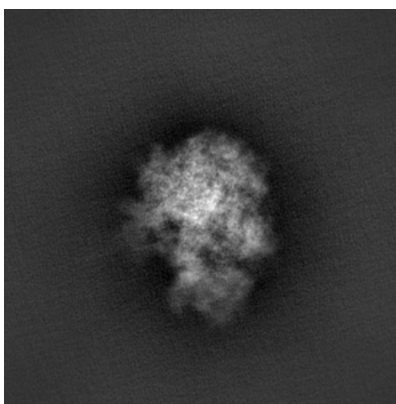
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

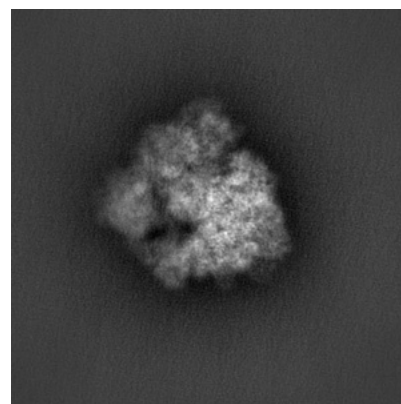
6.1.1 Primary map



X

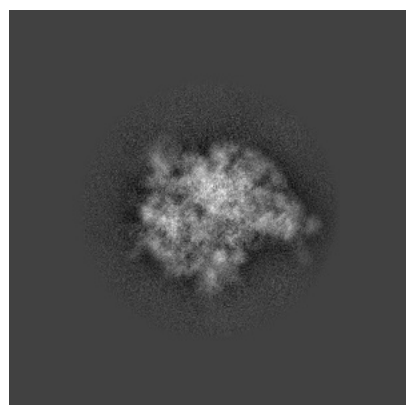


Y

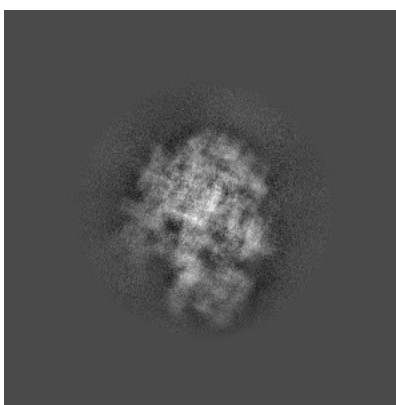


Z

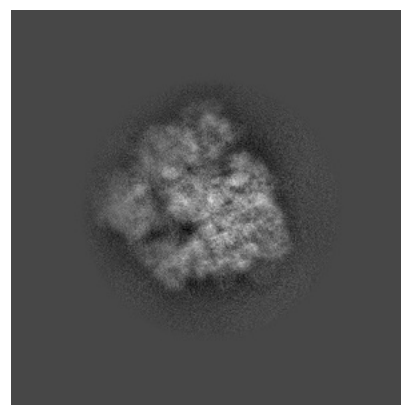
6.1.2 Raw map



X



Y

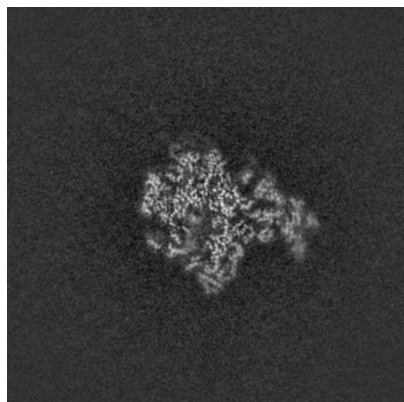


Z

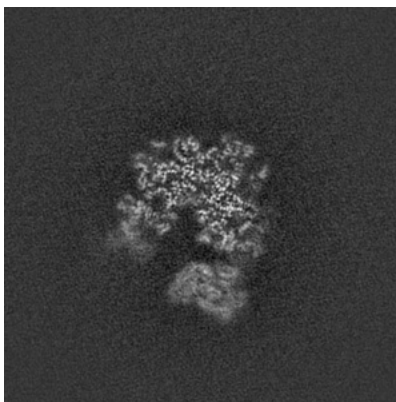
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

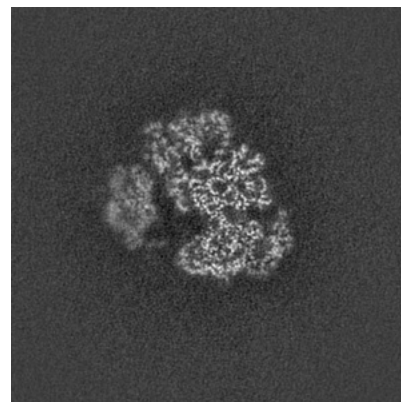
6.2.1 Primary map



X Index: 304

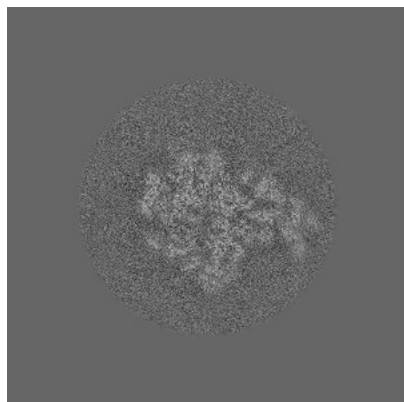


Y Index: 304

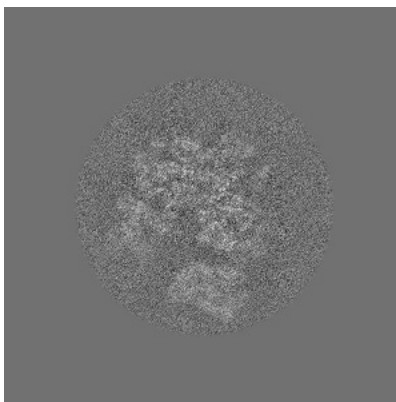


Z Index: 304

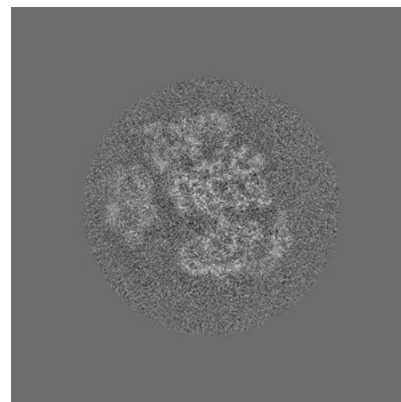
6.2.2 Raw map



X Index: 304



Y Index: 304

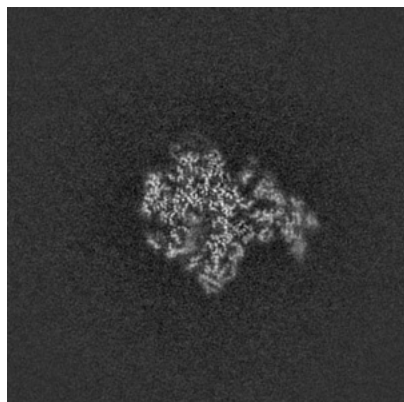


Z Index: 304

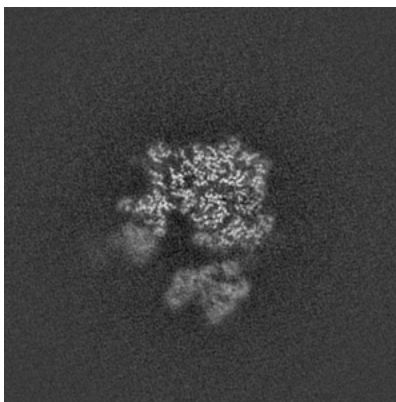
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

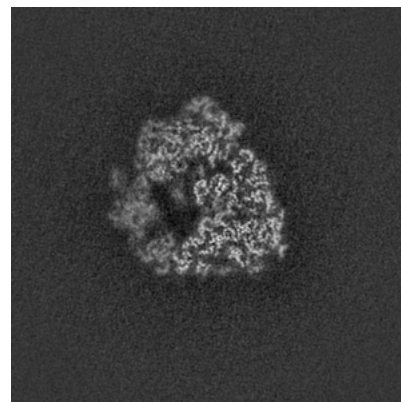
6.3.1 Primary map



X Index: 303

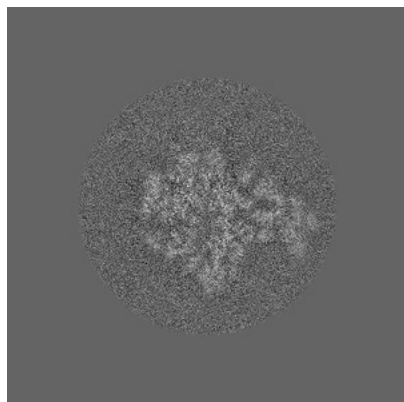


Y Index: 317

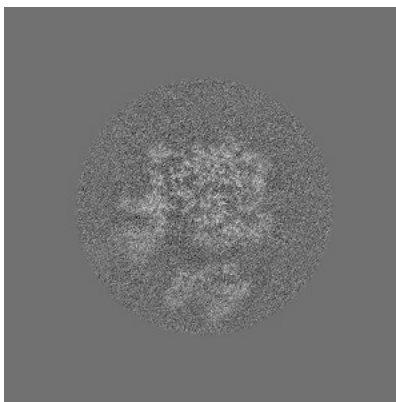


Z Index: 290

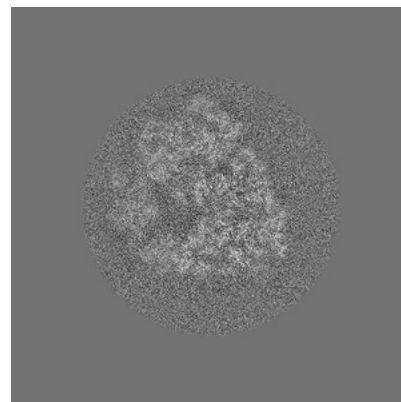
6.3.2 Raw map



X Index: 303



Y Index: 318

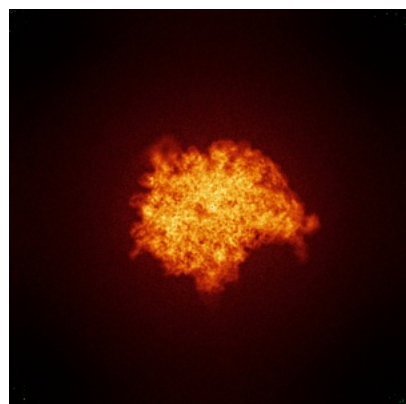


Z Index: 291

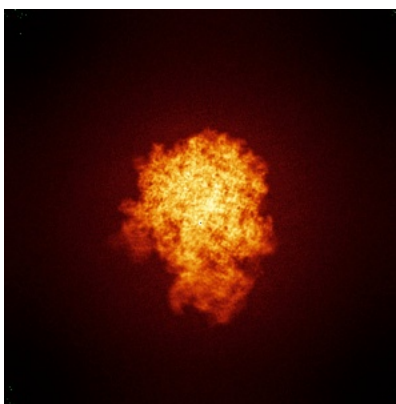
The images above show the largest variance slices of the map in three orthogonal directions.

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

6.4.1 Primary map



X

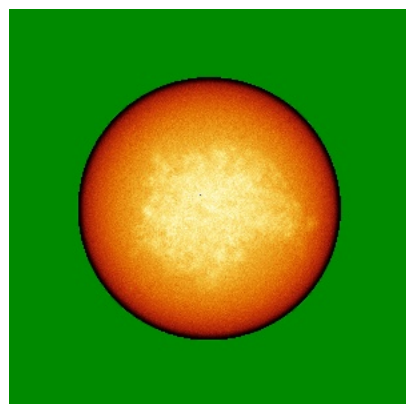


Y

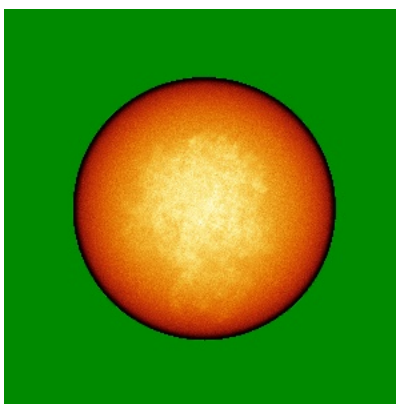


Z

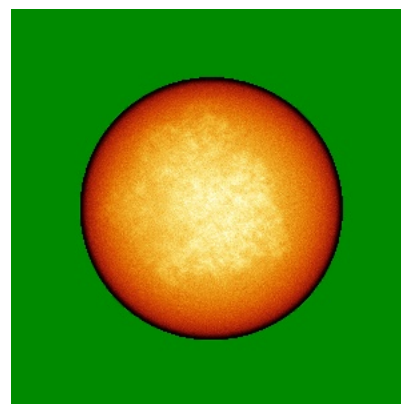
6.4.2 Raw map



X



Y

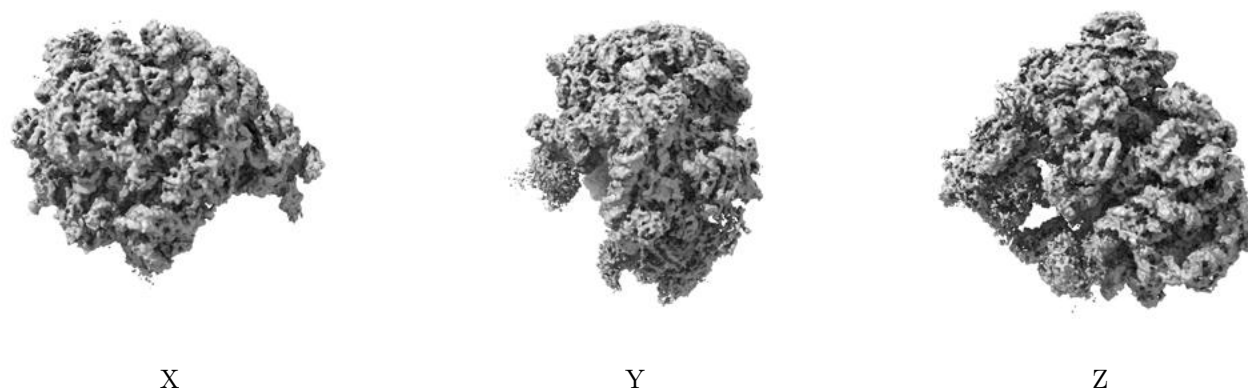


Z

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.

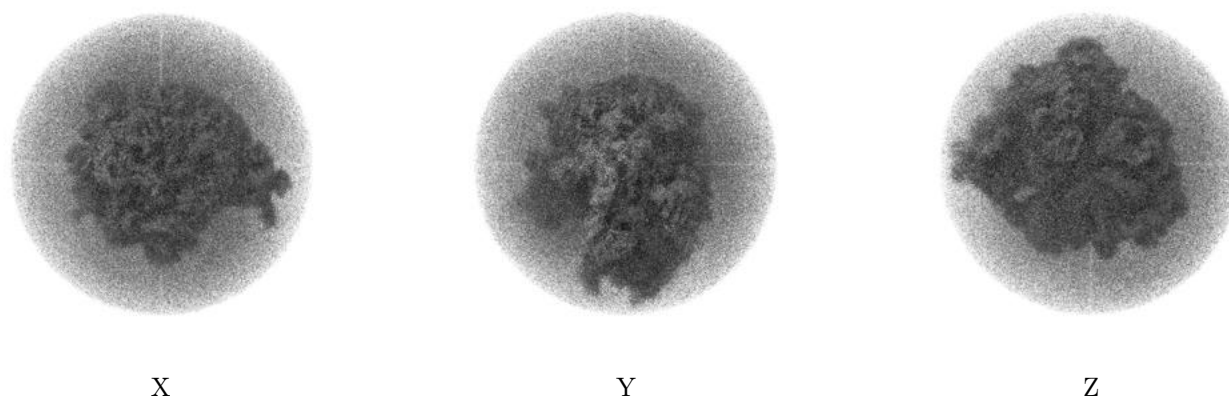
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 3.0. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

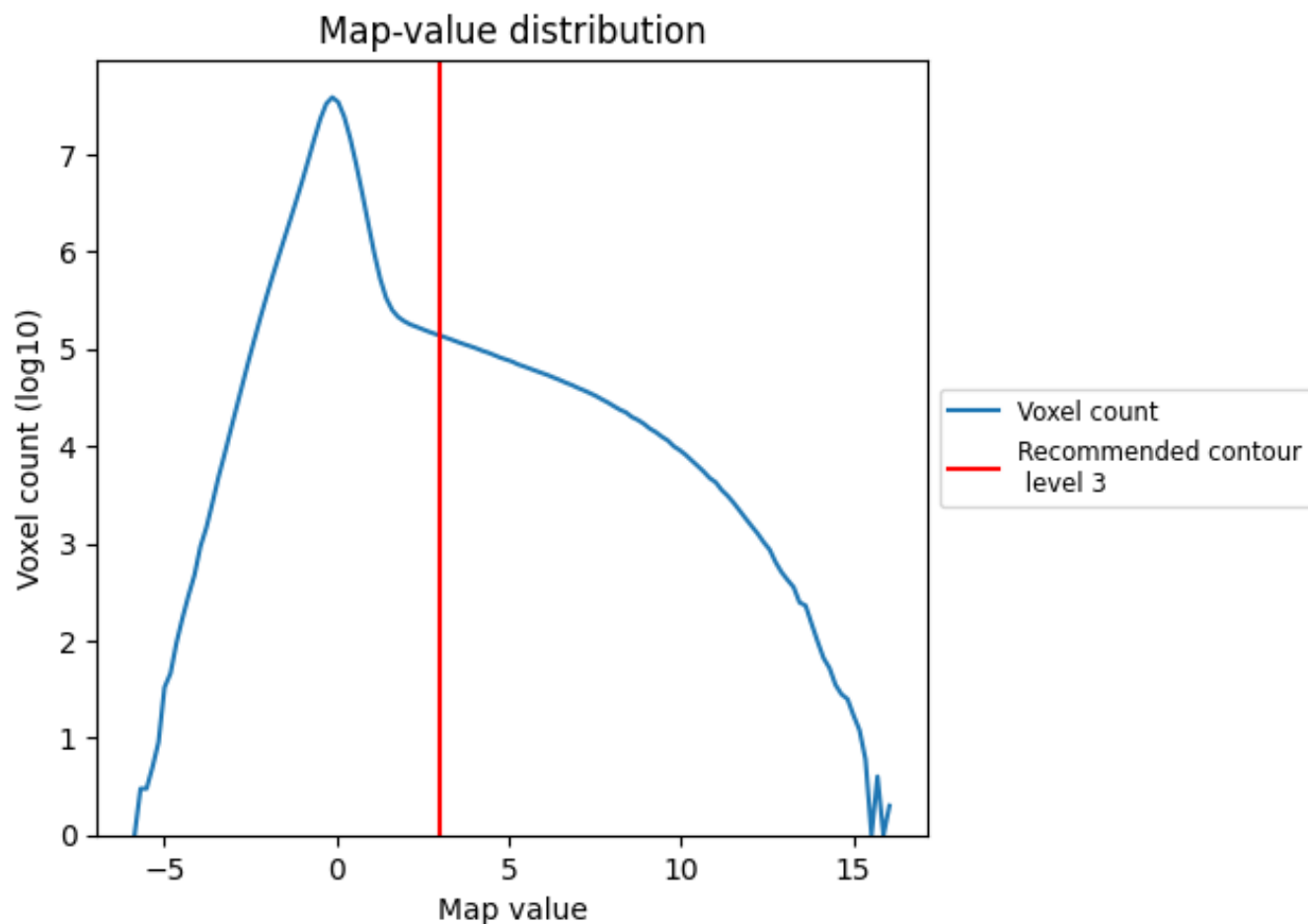
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

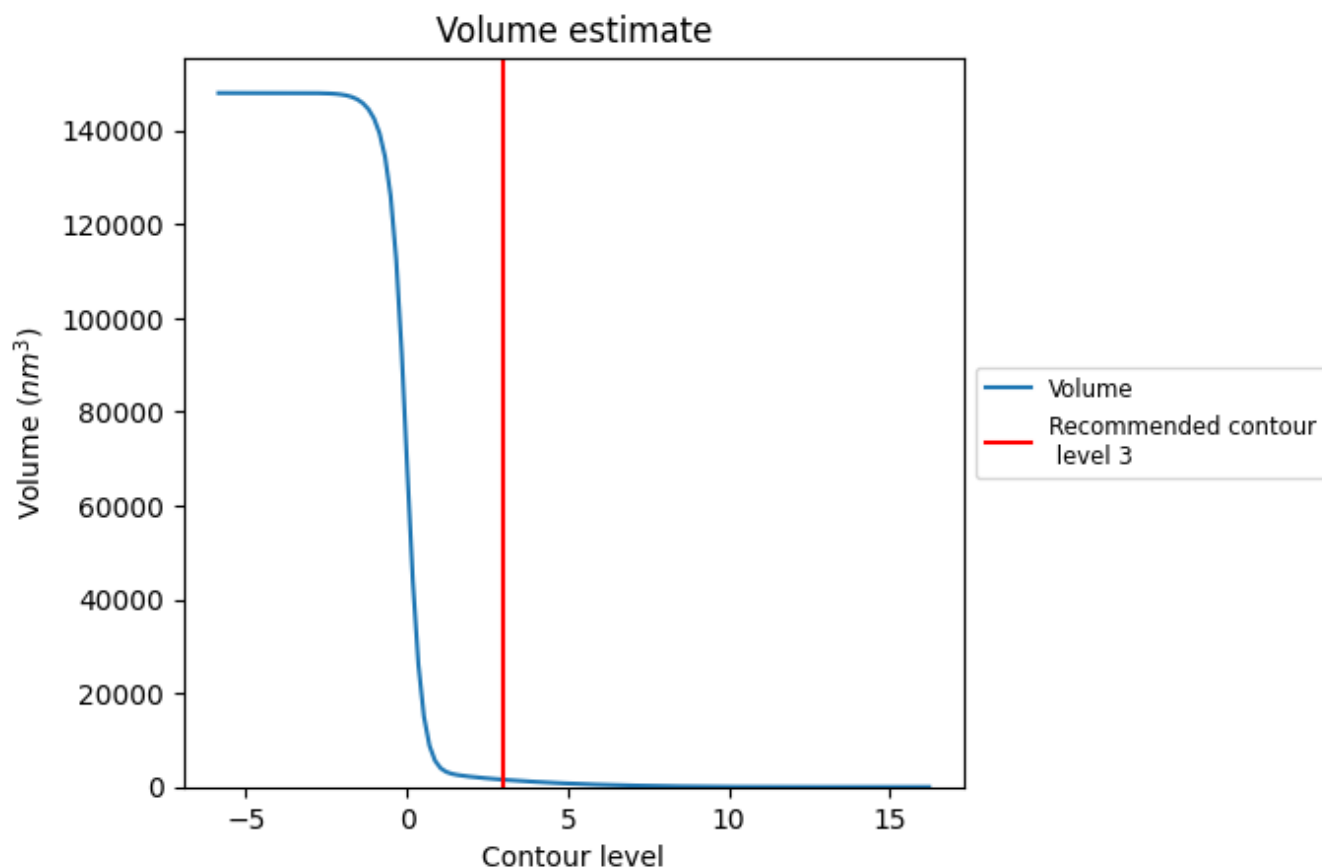
This section contains the results of statistical analysis of the map.

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.

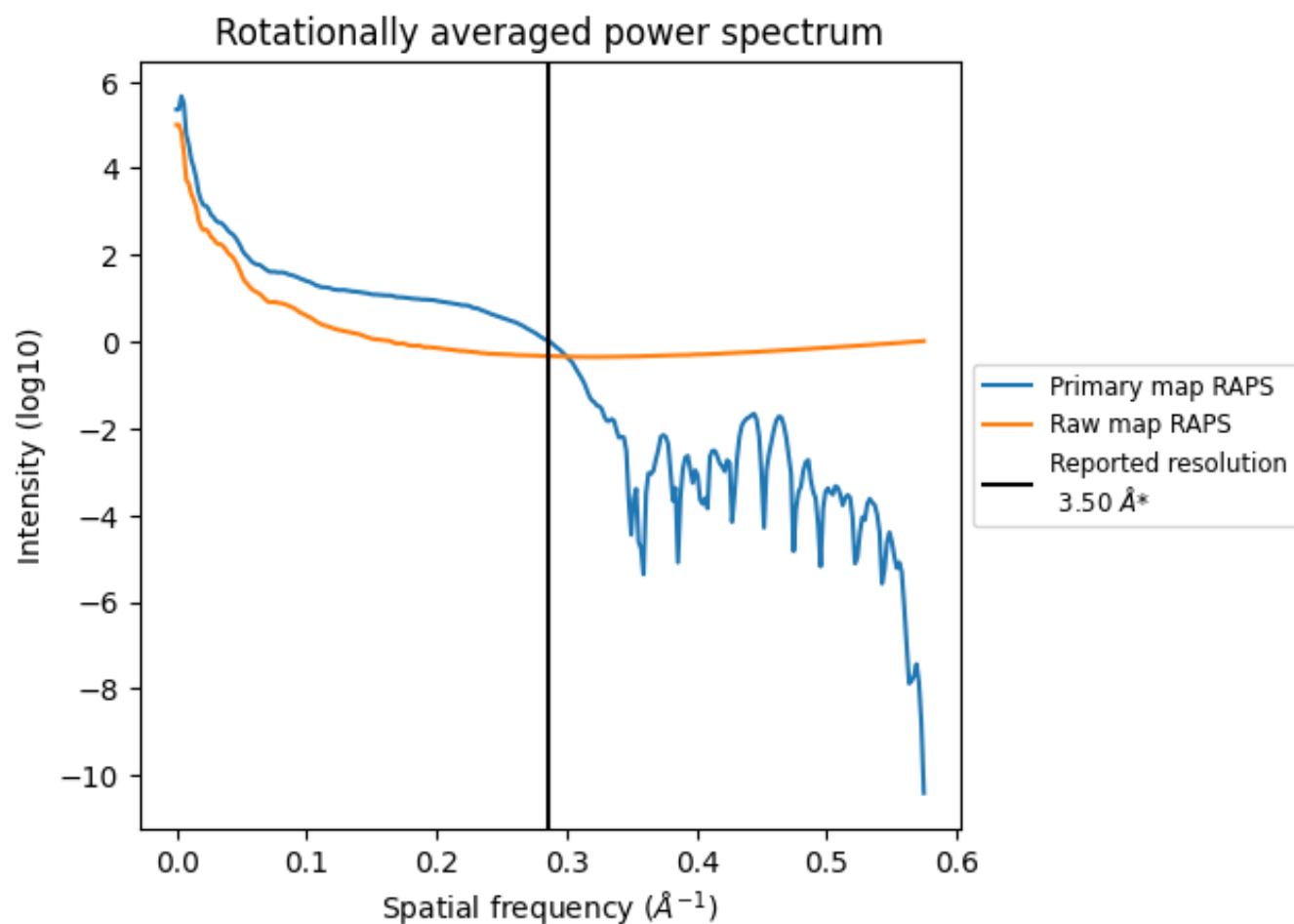
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1548 nm^3 ; this corresponds to an approximate mass of 1398 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ

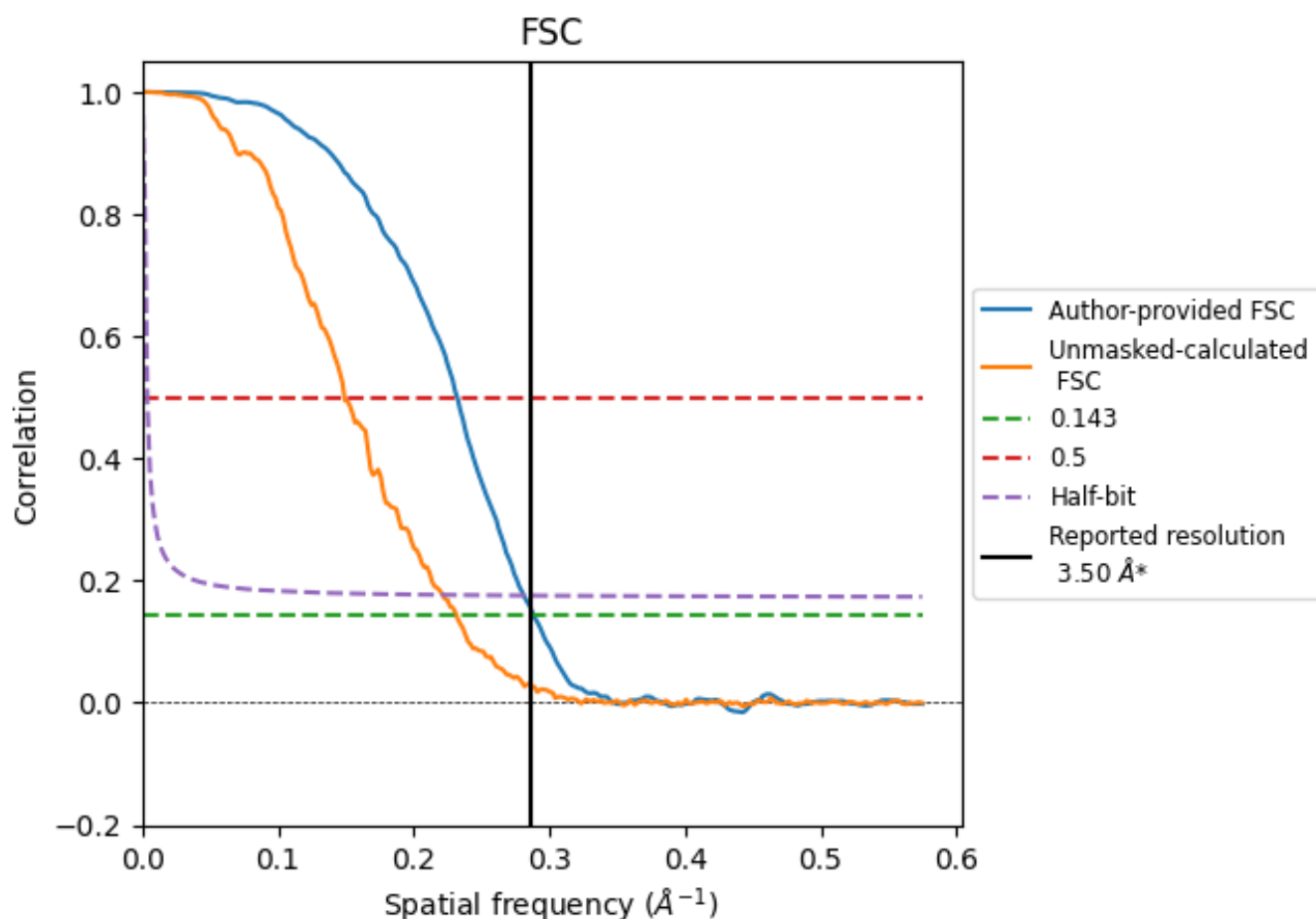


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

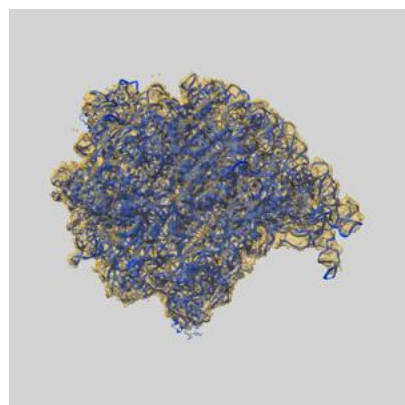
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.47	4.31	3.56
Unmasked-calculated*	4.32	6.71	4.52

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.32 differs from the reported value 3.5 by more than 10 %

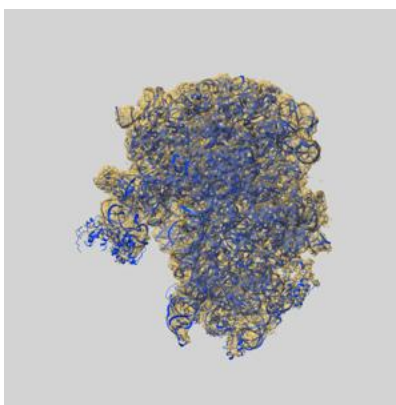
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-21857 and PDB model 6WNV. Per-residue inclusion information can be found in section [3](#) on page [13](#).

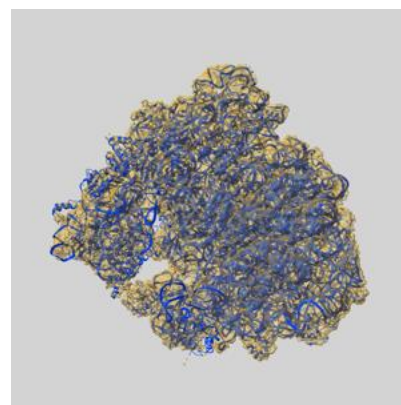
9.1 Map-model overlay [i](#)



X



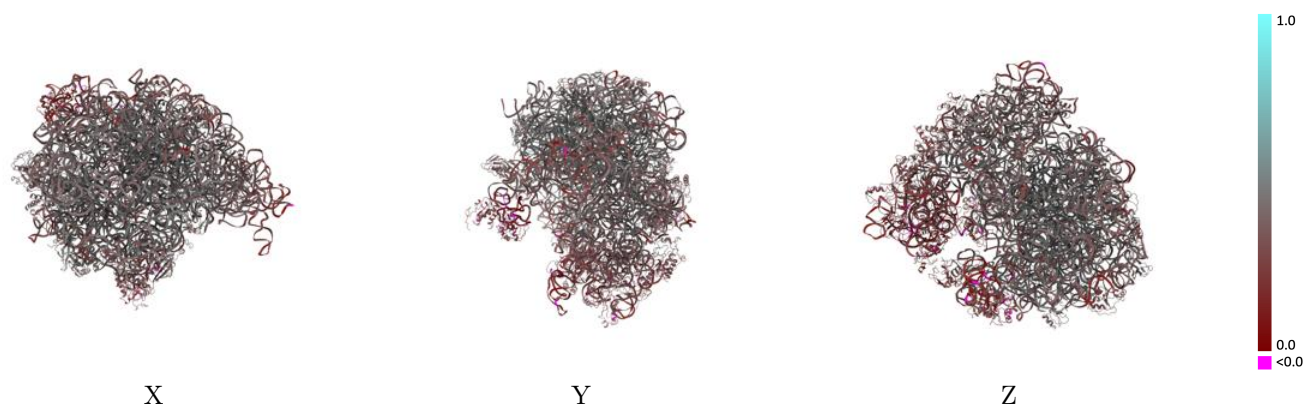
Y



Z

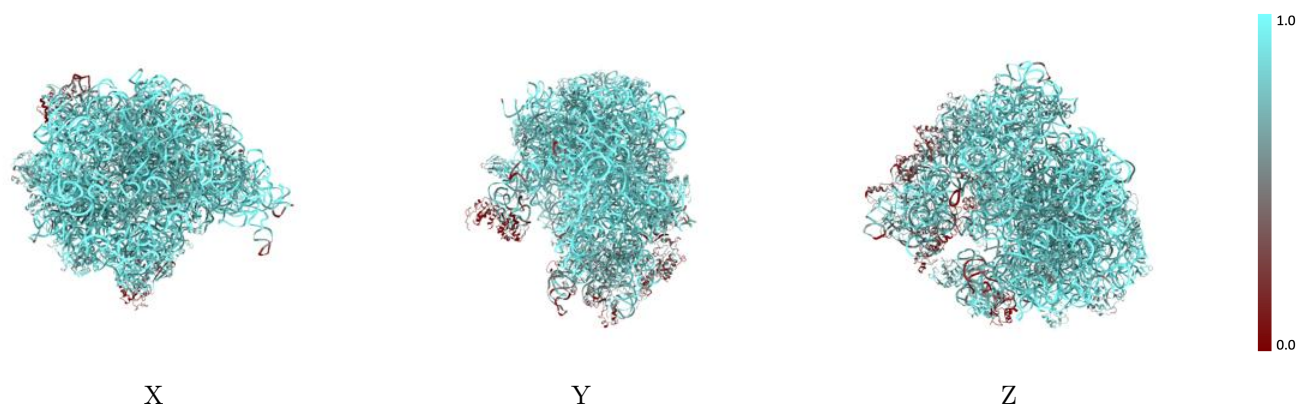
The images above show the 3D surface view of the map at the recommended contour level 3.0 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



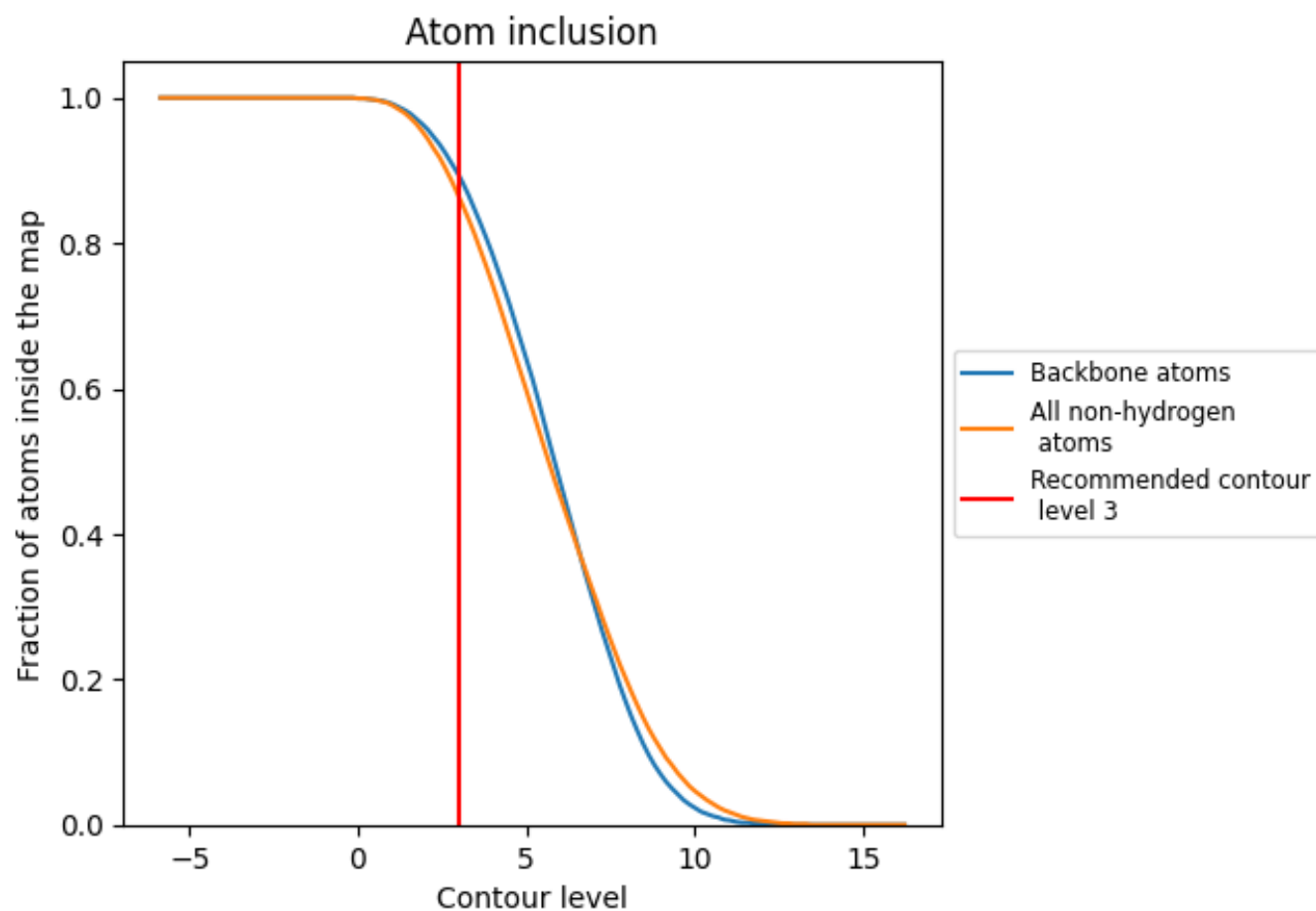
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (3).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 86% 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 (3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8640	 0.3830
3	 0.9140	 0.3500
4	 0.9550	 0.4050
A	 0.7690	 0.3250
B	 0.8500	 0.4490
D	 0.8760	 0.4610
E	 0.8960	 0.4640
F	 0.8110	 0.4470
G	 0.3750	 0.3510
H	 0.5510	 0.3320
I	 0.6920	 0.3470
J	 0.7330	 0.3930
K	 0.8090	 0.3760
L	 0.2620	 0.2700
M	 0.7870	 0.4140
N	 0.5860	 0.2560
O	 0.4650	 0.2900
P	 0.8300	 0.3610
Q	 0.8160	 0.4260
R	 0.5050	 0.2380
S	 0.5670	 0.2710
T	 0.8550	 0.3870
U	 0.8100	 0.4080
V	 0.8100	 0.4000
W	 0.8350	 0.3970
X	 0.5460	 0.2330
Y	 0.7810	 0.3560
Z	 0.4190	 0.3280
a	 0.1440	 0.2320
b	 0.8740	 0.4690
c	 0.8520	 0.4580
d	 0.7240	 0.4020
e	 0.7560	 0.3120
f	 0.8030	 0.3780
g	 0.4900	 0.3450



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Chain	Atom inclusion	Q-score
h	 0.1260	 0.2270
i	 0.1470	 0.2210
j	 0.8290	 0.4450
k	 0.8140	 0.4650
l	 0.8410	 0.4420
n	 0.8760	 0.4470
o	 0.8560	 0.3820
p	 0.8140	 0.4500
q	 0.8660	 0.4400
r	 0.8190	 0.4420
s	 0.8110	 0.4410
t	 0.8190	 0.4170
u	 0.8280	 0.4130
v	 0.7040	 0.3090
w	 0.8510	 0.4610
x	 0.8400	 0.4400
y	 0.8080	 0.3580
z	 0.8140	 0.4310