



wwPDB EM Validation Summary Report ⓘ

Mar 5, 2026 – 07:50 PM UTC

PDB ID : 6O9J / pdb_00006o9j
EMDB ID : EMD-0661
Title : 70S Elongation Competent Ribosome
Authors : Frank, J.; Gonzalez Jr., R.L.; Kaledhonkar, S.; Fu, Z.; Caban, K.; Li, W.;
Chen, B.; Sun, M.
Deposited on : 2019-03-14
Resolution : 3.90 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

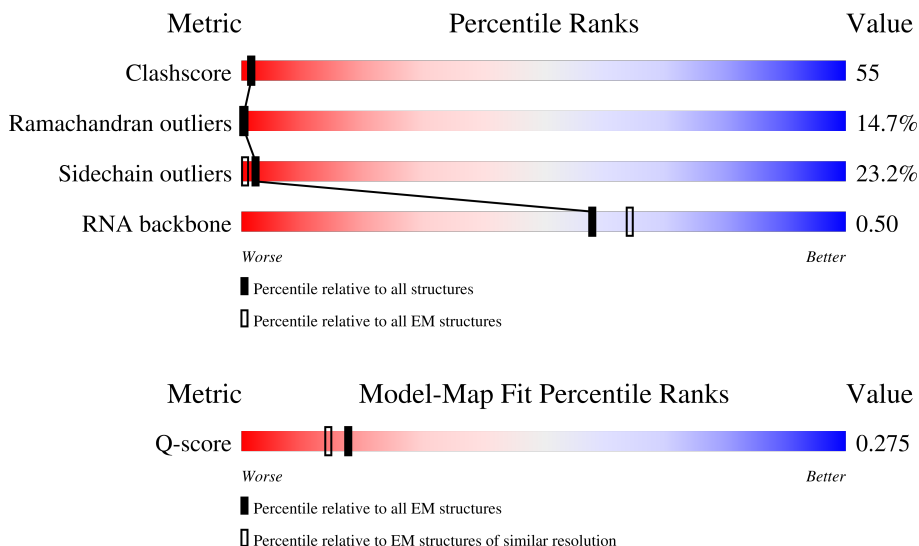
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.90 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	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	8855 (3.40 - 4.40)

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	117	
2	B	2841	
3	V	94	

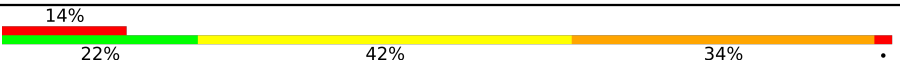
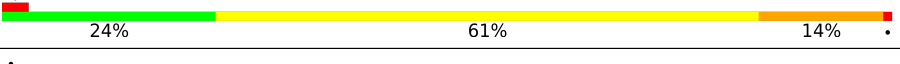
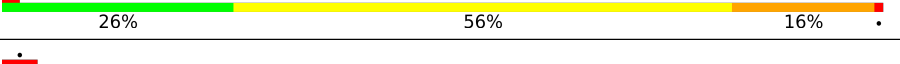
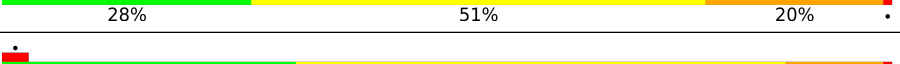
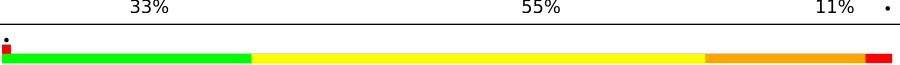
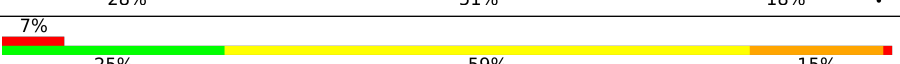
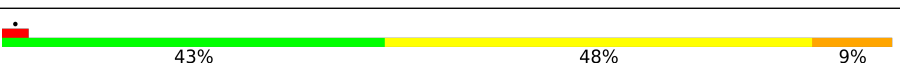
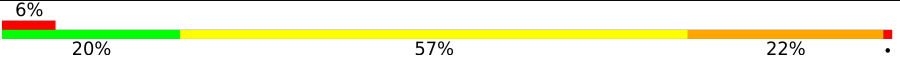
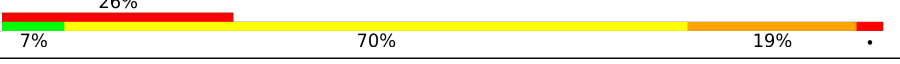
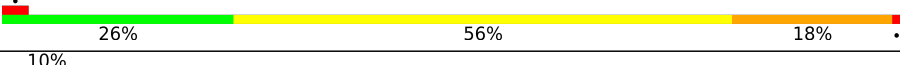
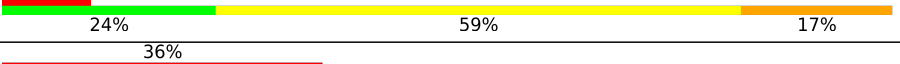
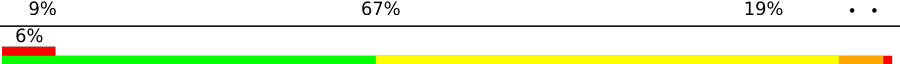
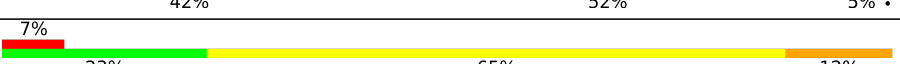
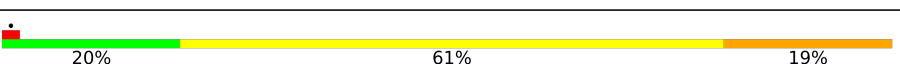
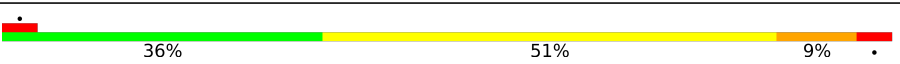
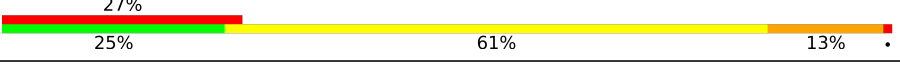
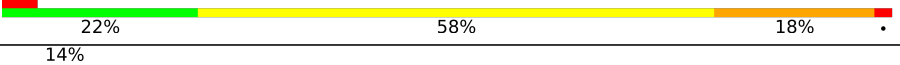
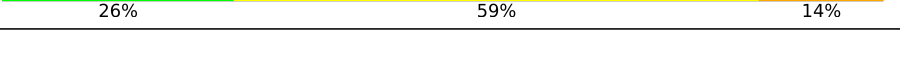
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Mol	Chain	Length	Quality of chain
4	C	267	
5	D	209	
6	E	201	
7	F	178	
8	G	176	
9	H	149	
10	J	140	
11	K	121	
12	L	144	
13	M	136	
14	N	127	
15	O	117	
16	P	114	
17	Q	117	
18	R	103	
19	S	110	
20	T	99	
21	U	102	
22	W	84	
23	X	63	
24	Y	58	
25	Z	70	
26	1	56	
27	2	54	
28	3	46	

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Mol	Chain	Length	Quality of chain
29	4	64	
30	5	38	
31	6	141	
32	a	1530	
33	c	206	
34	d	205	
35	e	150	
36	f	100	
37	g	150	
38	h	129	
39	i	127	
40	j	98	
41	k	117	
42	l	123	
43	m	114	
44	n	100	
45	o	88	
46	p	82	
47	q	80	
48	r	55	
49	s	79	
50	t	85	
51	7	218	
52	u	51	
53	v	76	

2 Entry composition

There are 53 unique types of molecules in this entry. The entry contains 142682 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 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	117	Total	C	N	O	P	0	0
			2507	1116	459	815	117		

- Molecule 2 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	2841	Total	C	N	O	P	0	0
			60995	27210	11229	19715	2841		

- Molecule 3 is a protein called 50S ribosomal protein L25.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	V	94	Total	C	N	O	S	0	0
			753	479	137	134	3		

- Molecule 4 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	C	267	Total	C	N	O	S	0	0
			2053	1271	416	359	7		

- Molecule 5 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	D	209	Total	C	N	O	S	0	0
			1565	979	288	294	4		

- Molecule 6 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	E	201	Total	C	N	O	S	0	0
			1552	974	283	290	5		

- Molecule 7 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	F	178	Total	C	N	O	S	0	0
			1420	905	251	258	6		

- Molecule 8 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	G	176	Total	C	N	O	S	0	0
			1323	832	243	246	2		

- Molecule 9 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	H	149	Total	C	N	O	S	0	0
			1111	699	197	214	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
10	J	140	Total	C	N	O	S	0	0
			1112	704	210	194	4		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
11	K	121	Total	C	N	O	S	0	0
			930	582	179	164	5		

- 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
			1053	654	207	190	2		

- 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
			1074	686	205	177	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	N	127	Total	C	N	O	S	0	0
			1008	621	204	178	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
15	O	117	Total	C	N	O	S	0	0
			900	557	179	163	1		

- 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
			917	574	179	163	1		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
17	Q	117	Total	C	N	O		
			947	604	192	151	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
18	R	103	Total	C	N	O	S	0	0
			816	516	153	145	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
			857	532	166	156	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	T	99	Total	C	N	O	S	0	0
			777	491	145	139	2		

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

Mol	Chain	Residues	Atoms				AltConf	Trace
21	U	102	Total	C	N	O		
			779	492	146	141	0	0

- Molecule 22 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms				AltConf	Trace
22	W	84	Total	C	N	O	S	
			634	391	129	113	1	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
23	X	63	Total	C	N	O	S	
			509	313	99	95	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
24	Y	58	Total	C	N	O	S	
			449	281	87	79	2	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
25	Z	70	Total	C	N	O	S	
			549	339	104	100	6	0

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

Mol	Chain	Residues	Atoms				AltConf	Trace
26	1	56	Total	C	N	O	S	
			444	269	94	80	1	0

- Molecule 27 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
27	2	54	Total	C	N	O		
			441	284	81	76	0	0

- Molecule 28 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	3	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

- Molecule 29 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	4	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

- Molecule 30 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	5	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 31 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	6	141	Total	C	N	O	S	0	0
			1032	651	179	196	6		

- Molecule 32 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	1530	Total	C	N	O	P	0	0
			32831	14642	6024	10635	1530		

- Molecule 33 is a protein called 30S ribosomal protein S3.

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

- Molecule 34 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	d	205	Total	C	N	O	S	0	0
			1643	1026	315	298	4		

- Molecule 35 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	e	150	Total	C	N	O	S	0	0
			1105	687	211	201	6		

- Molecule 36 is a protein called 30S ribosomal protein S6.

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

- Molecule 37 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	g	150	Total	C	N	O	S	0	0
			1174	730	226	214	4		

- Molecule 38 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	h	129	Total	C	N	O	S	0	0
			979	616	173	184	6		

- Molecule 39 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	i	127	Total	C	N	O	S	0	0
			1022	634	206	179	3		

- Molecule 40 is a protein called 30S ribosomal protein S10.

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

- Molecule 41 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	k	117	Total	C	N	O	S	0	0
			877	540	174	160	3		

- Molecule 42 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	l	123	Total	C	N	O	S	0	0
			955	590	196	165	4		

- Molecule 43 is a protein called 30S ribosomal protein S13.

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

- Molecule 44 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	n	96	Total	C	N	O	S	0	0
			774	483	160	128	3		

- Molecule 45 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	o	88	Total	C	N	O	S	0	0
			716	440	146	129	1		

- Molecule 46 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	p	82	Total	C	N	O	S	0	0
			649	406	128	114	1		

- Molecule 47 is a protein called 30S ribosomal protein S17.

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

- Molecule 48 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms				AltConf	Trace
48	r	55	Total	C	N	O	0	0
			455	288	86	81		

- Molecule 49 is a protein called 30S ribosomal protein S19.

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

- Molecule 50 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	t	85	Total	C	N	O	S	0	0
			665	411	137	114	3		

- Molecule 51 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	7	218	Total	C	N	O	S	0	0
			1704	1081	305	311	7		

- Molecule 52 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	51	Total	C	N	O	S	0	0
			425	265	86	73	1		

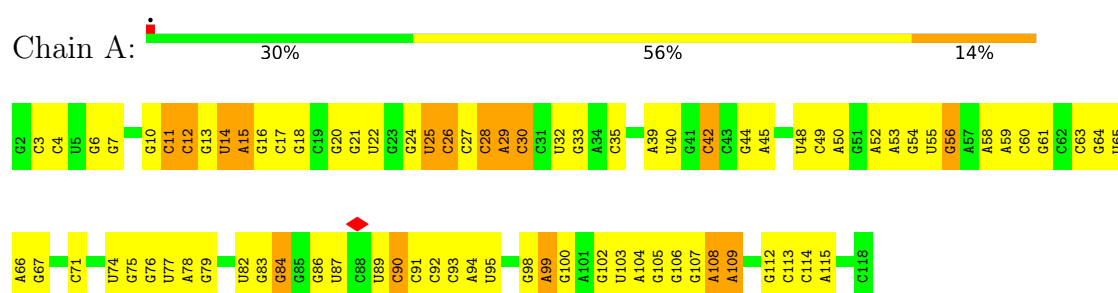
- Molecule 53 is a RNA chain called P-tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	v	76	Total	C	N	O	P	0	0
			1623	723	290	534	76		

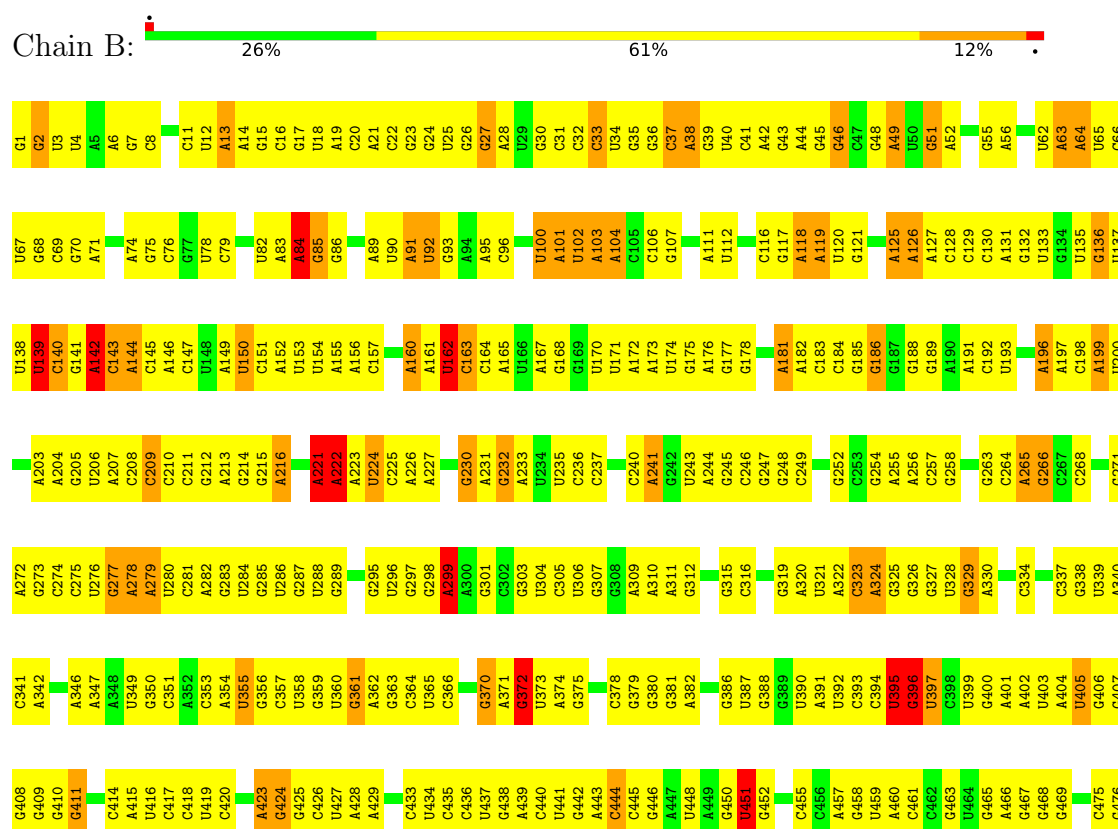
3 Residue-property plots

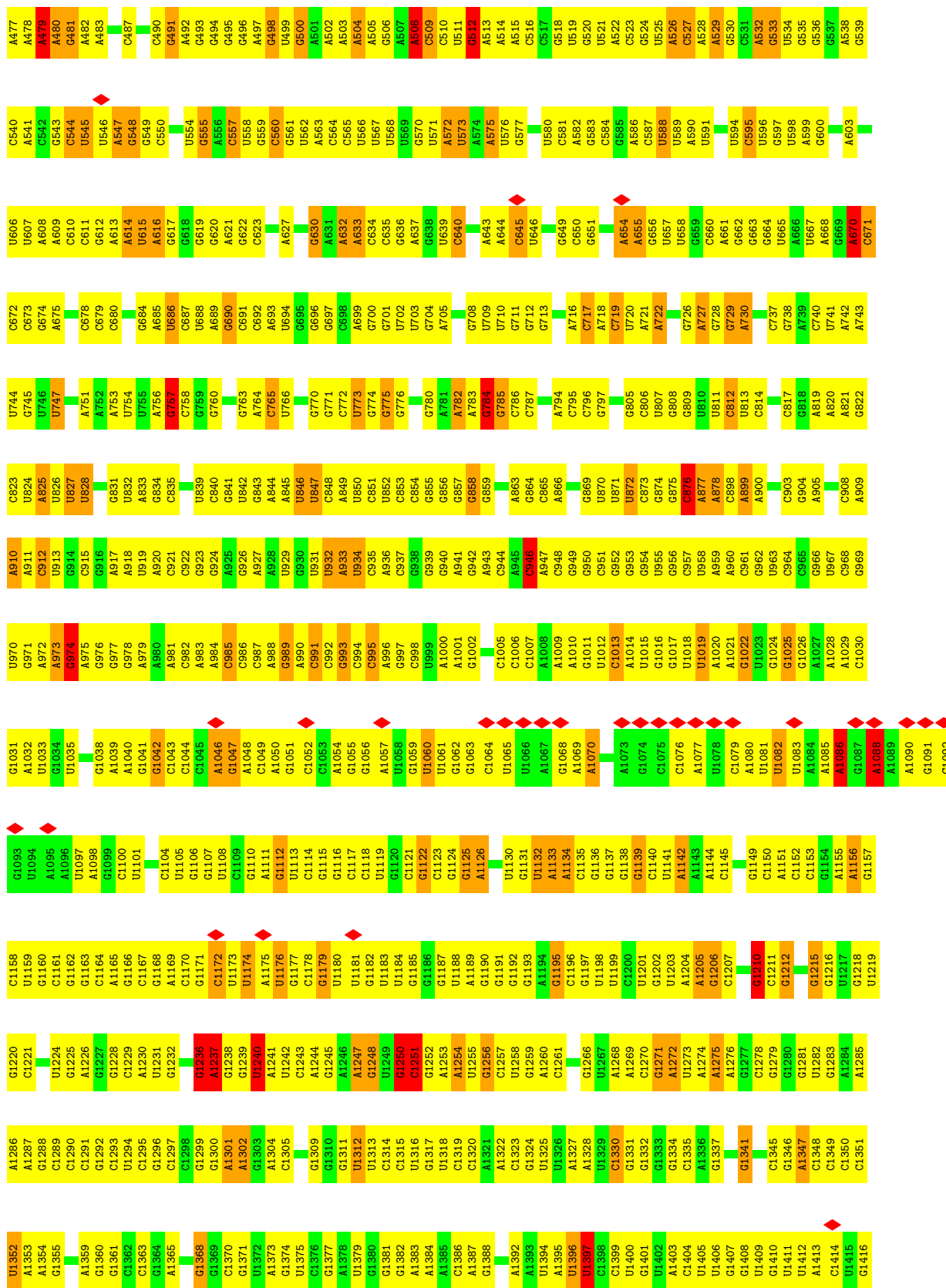
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

• Molecule 1: 5S rRNA

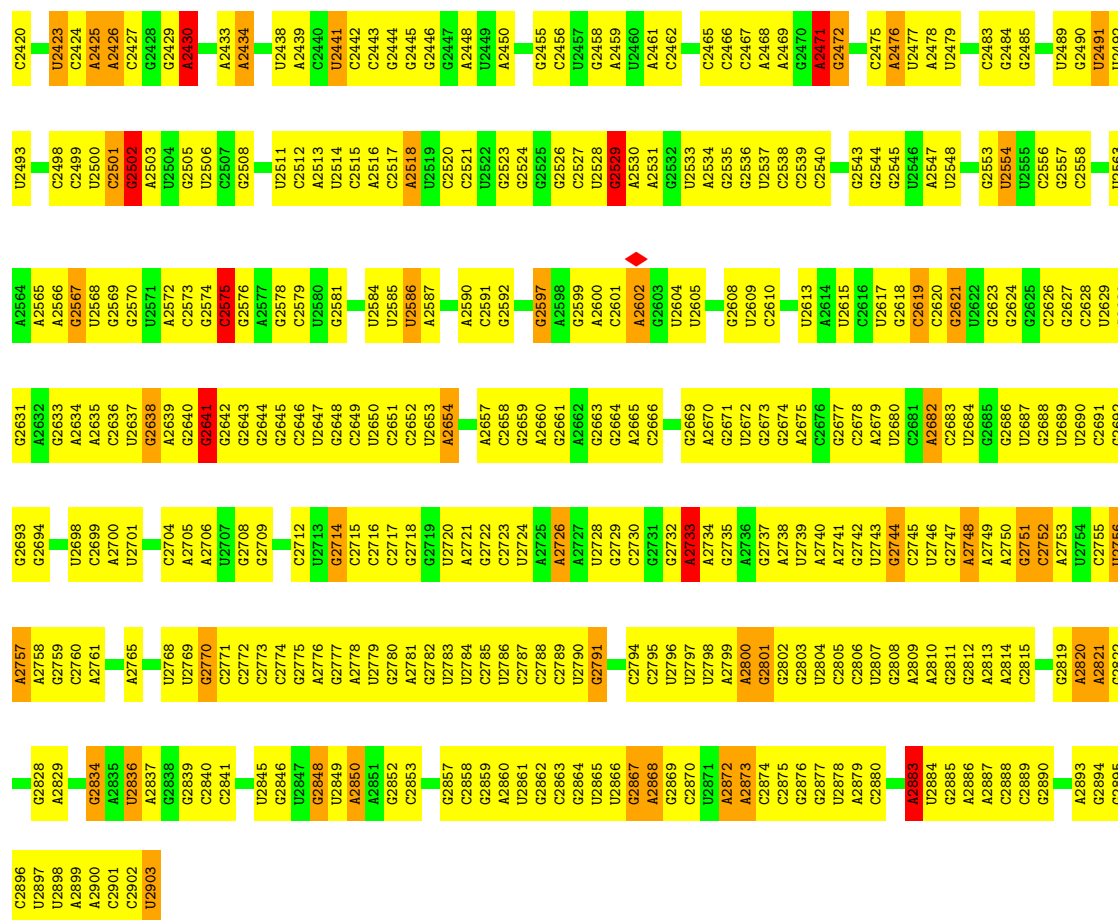


• Molecule 2: 23S rRNA

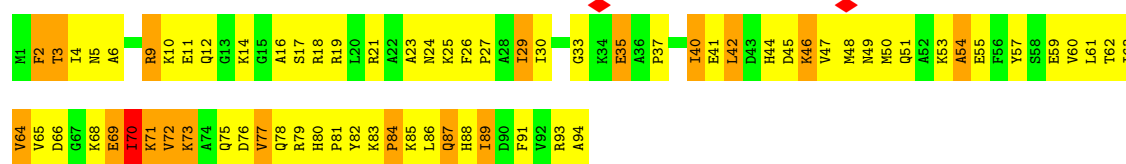




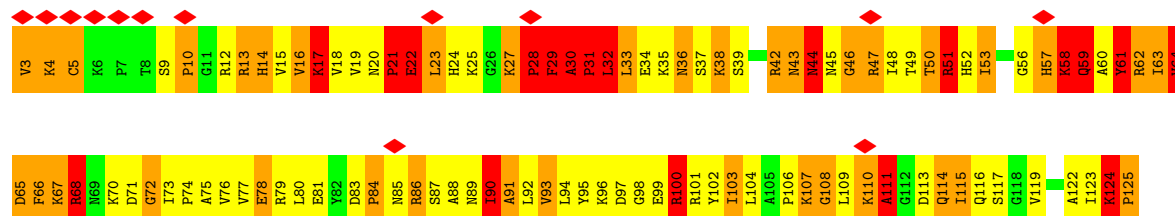
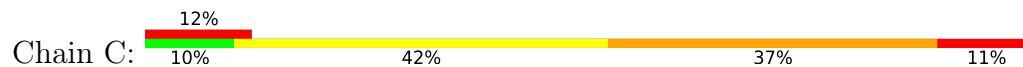
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A2340	G2277	G2210	G2100	G1964		U1818	G1750	U1688	C1617	A1549	U1485	A1419
G2341	A2278	U2210	A2101	C1966	U1898	U1819	U1751	A1689	A1618	C1550	U1486	A1420
		A2211	G2102	A1966		U1820	C1752	A1690	G1619	A1551	U1487	
U2344	G2282	C2283	C2103	C1967	A1901	A1821	G1753	C1691	G1622	A1552	C1488	G1424
G2345	C2283	U2213	C2104		C1902	C1822	A1754	U1692	G1623	A1553	C1489	G1425
A2346	A2284	C2214	U2105	U1970	C1903	G1823	A1755	U1693	U1624	U1554	A1490	G1426
C2347	G2285	G2215	U2106	U1971	G1904	G1824	G1756	C1694		G1555		A1427
U2348	G2286	G2216		U1972	C1905	U1825	A1757	G1695	U1629	C1556	C1493	C1428
G2349	G2287	G2217	G2133	G1973	G1906	G1826	U1758	G1696		C1557	A1494	G1429
C2350	A2288	G2218		C1974		U1827	A1759			C1558	A1495	A1430
G2351	G2289	U2219	U2137	U1979	C1909	G1828	G1760	A1701	G1633	U1559	U1496	A1431
A2352	G2290	U2220	G2138	G1980	G1910	A1829	C1761	A1701	A1634	G1560	A1497	A1432
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	G2304	U2236	U2151	C1996	A1927	U1851	A1780	G1715		U1586		G1448
G2379	U2305	G2237	G2152	C1997	A1928	U1852	U1781	U1716	A1652	U1578	U1513	G1449
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U2265	U2194	A2088	U2026	U2026	G1950	G1878	A1803	G1738	C1675	U1602	G1537	U1474
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G2271		A2094	G2032	G2032	U1956	G1884	G1813	A1745	U1683	A1609	G1543	C1480
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A2273	C2206	G2096	U2034	U2034	G1958		A1815	U1747	C1686	G1613	G1546	U1482
A2274	G2204	A2097	G2035	G2035	G1959	G1888	G1816	C1816				G1483
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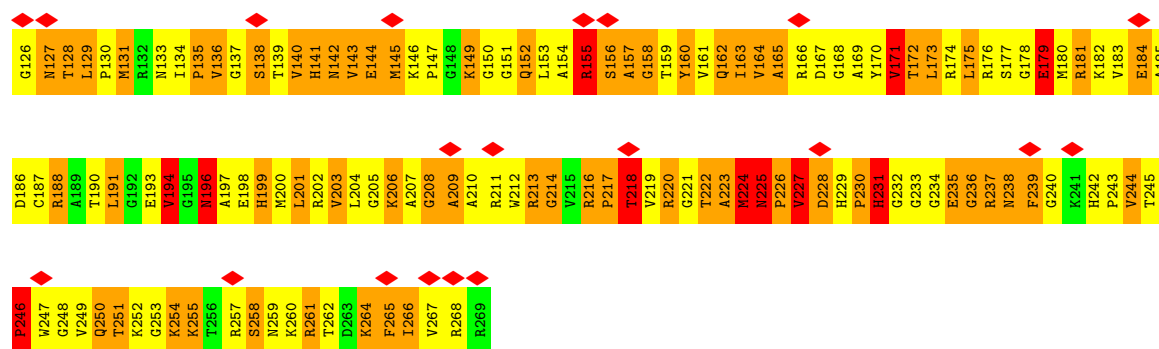


• Molecule 3: 50S ribosomal protein L25

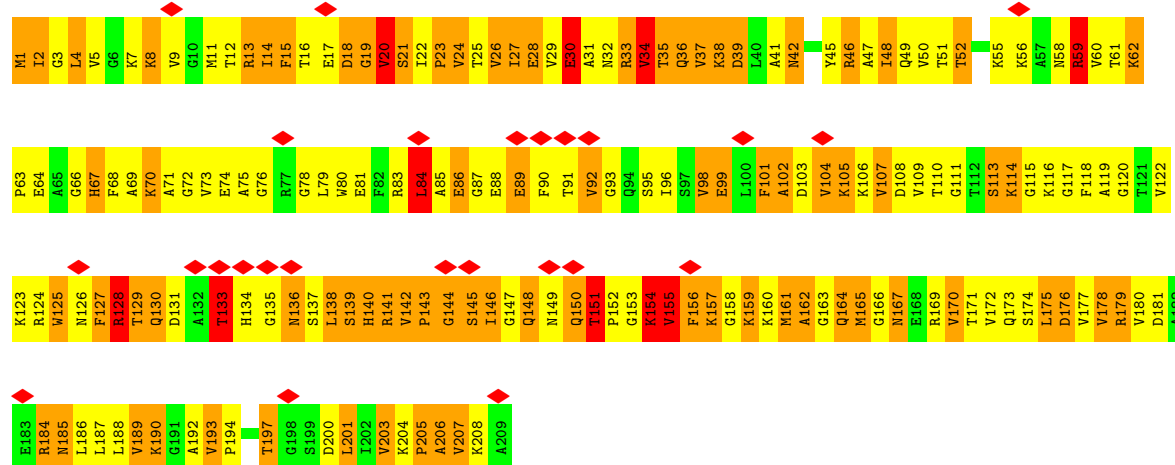


• Molecule 4: 50S ribosomal protein L2

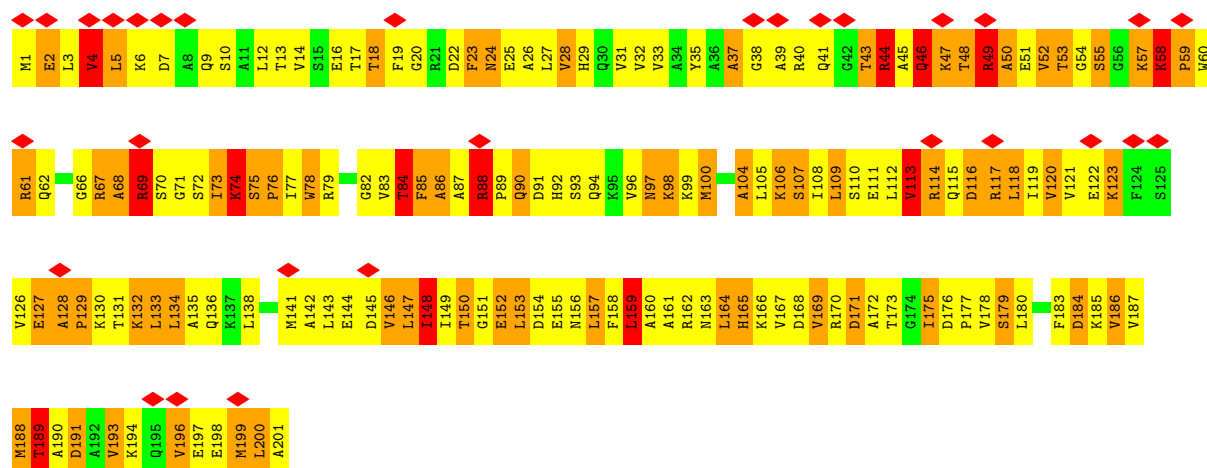
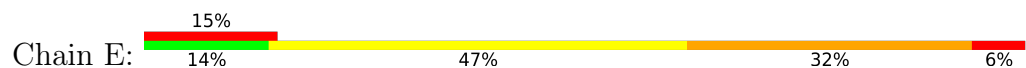




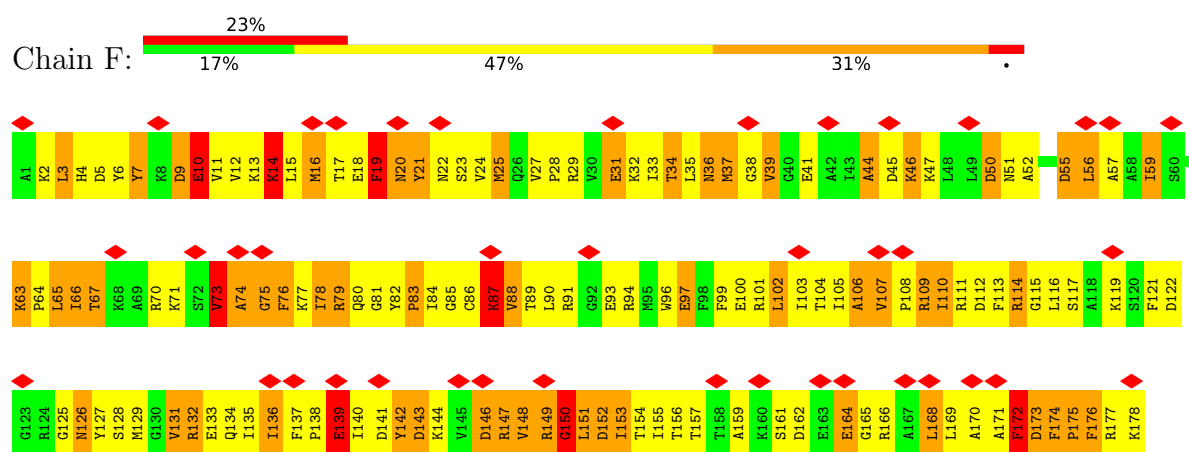
• Molecule 5: 50S ribosomal protein L3



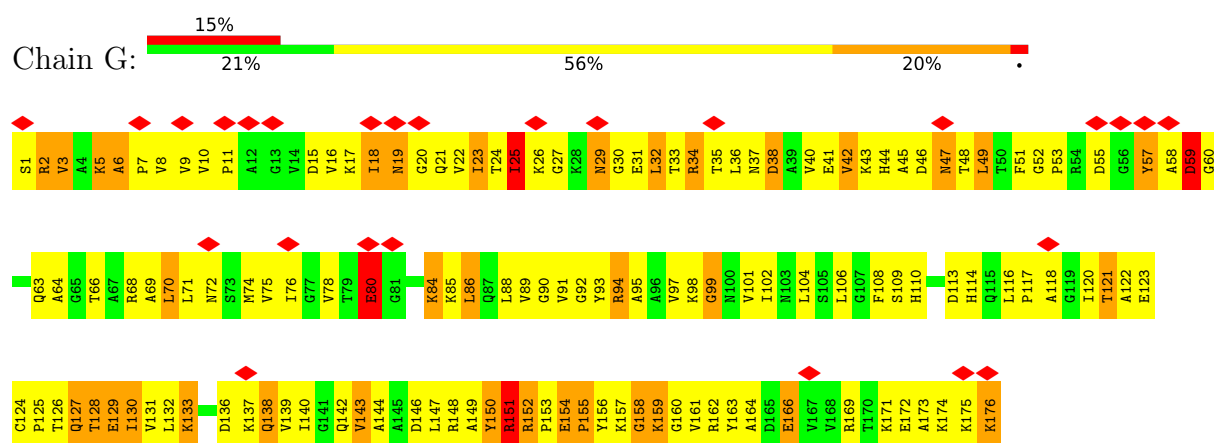
• Molecule 6: 50S ribosomal protein L4



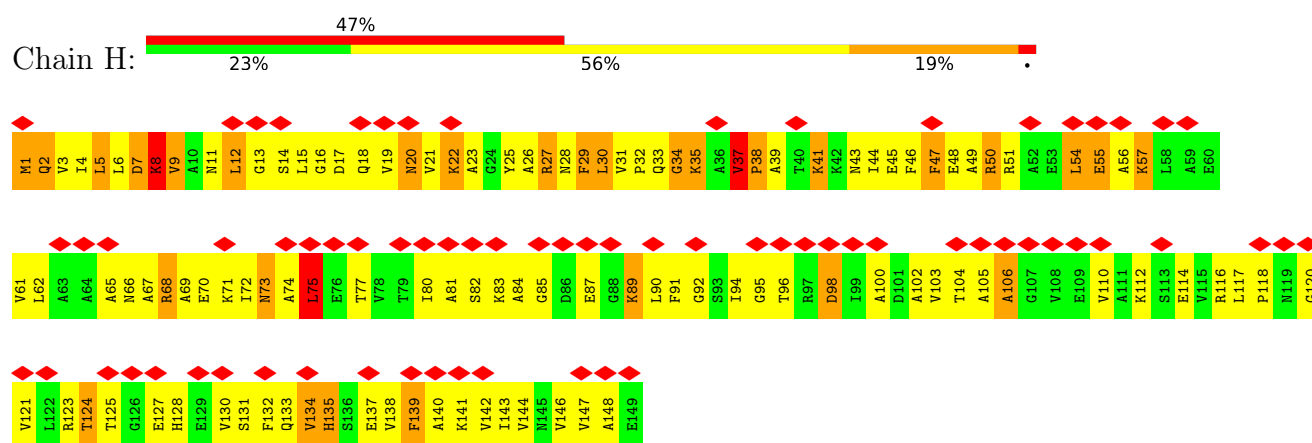
• Molecule 7: 50S ribosomal protein L5



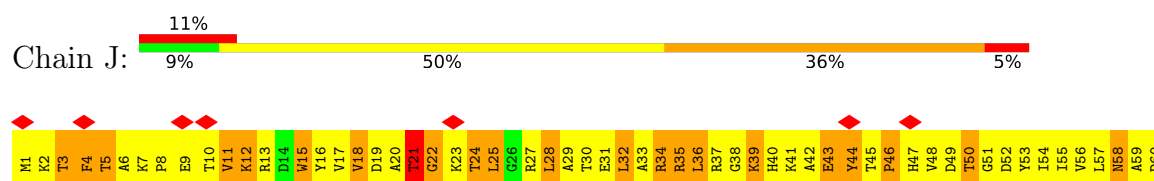
• Molecule 8: 50S ribosomal protein L6



• Molecule 9: 50S ribosomal protein L9

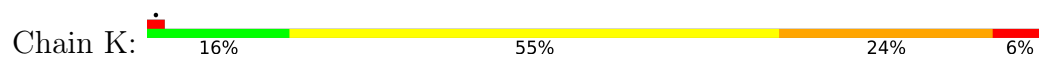


• Molecule 10: 50S ribosomal protein L13

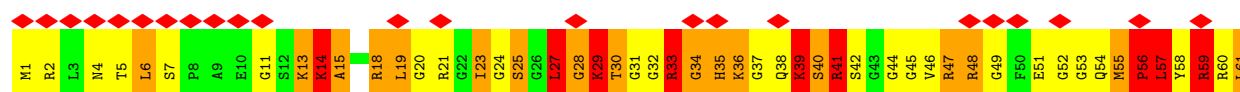




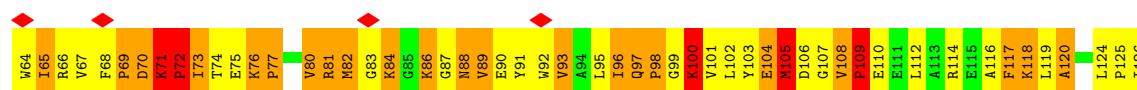
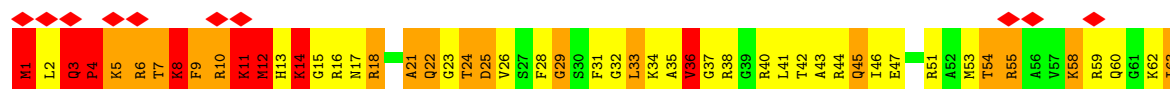
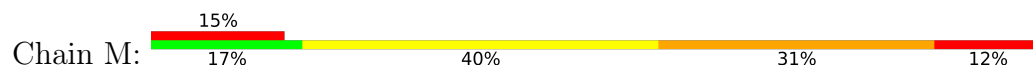
• Molecule 11: 50S ribosomal protein L14



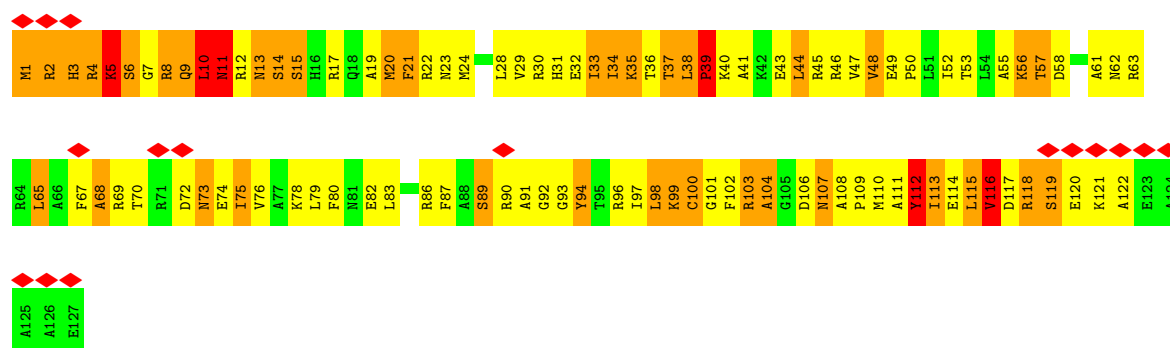
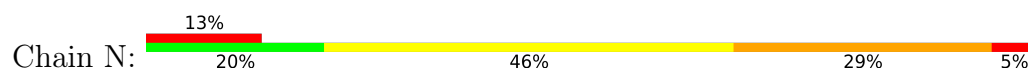
• Molecule 12: 50S ribosomal protein L15



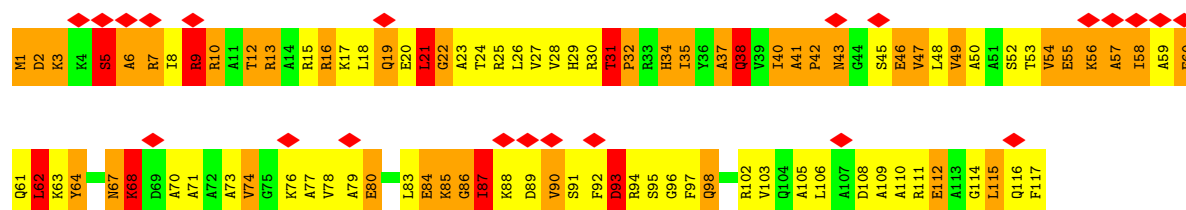
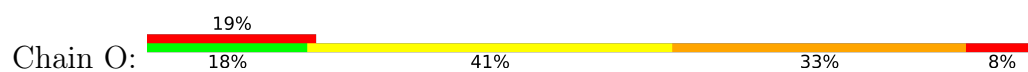
• Molecule 13: 50S ribosomal protein L16



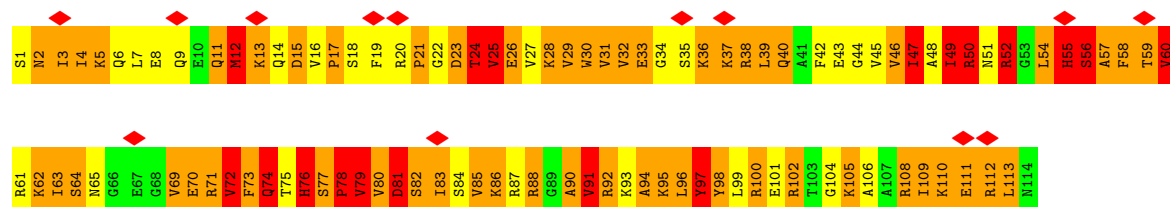
• Molecule 14: 50S ribosomal protein L17



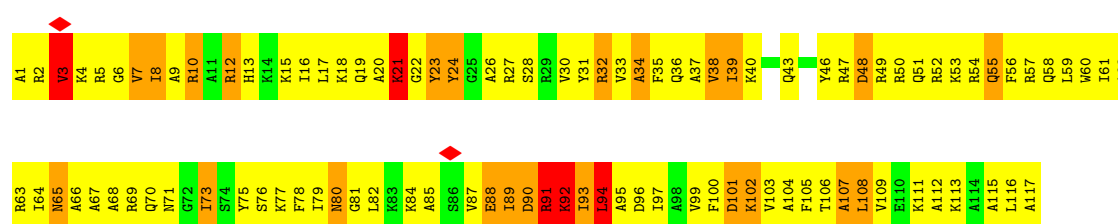
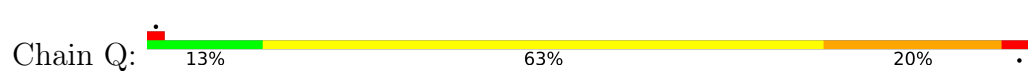
• Molecule 15: 50S ribosomal protein L18



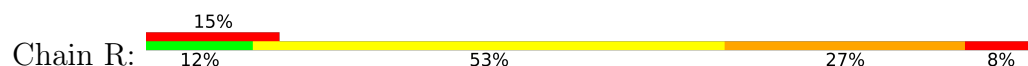
• Molecule 16: 50S ribosomal protein L19

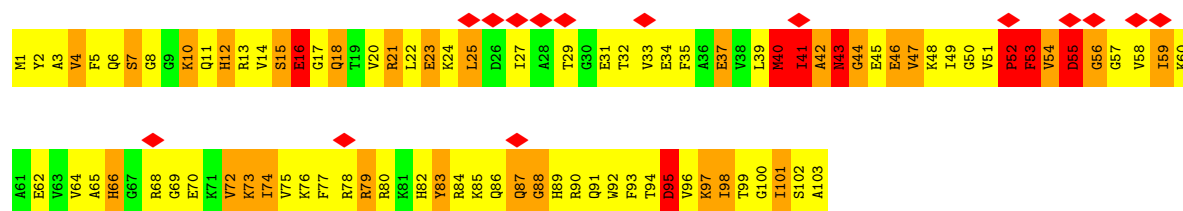


• Molecule 17: 50S ribosomal protein L20

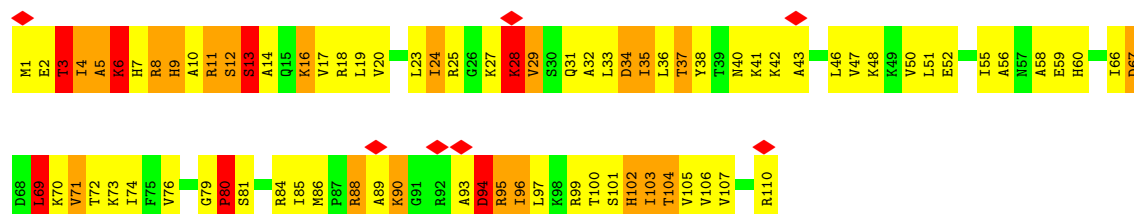


• Molecule 18: 50S ribosomal protein L21

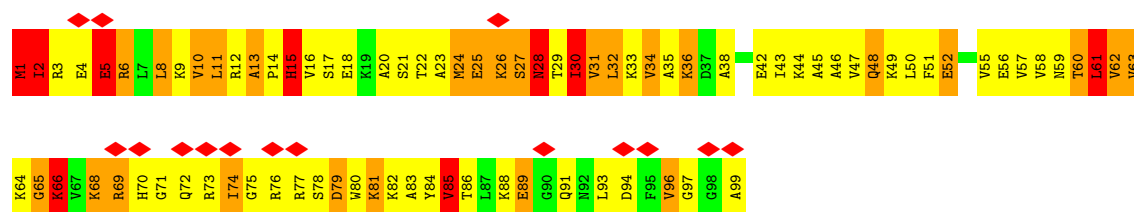
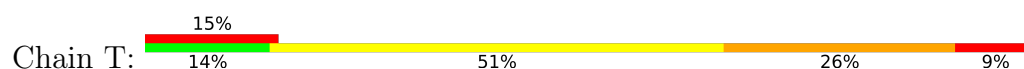




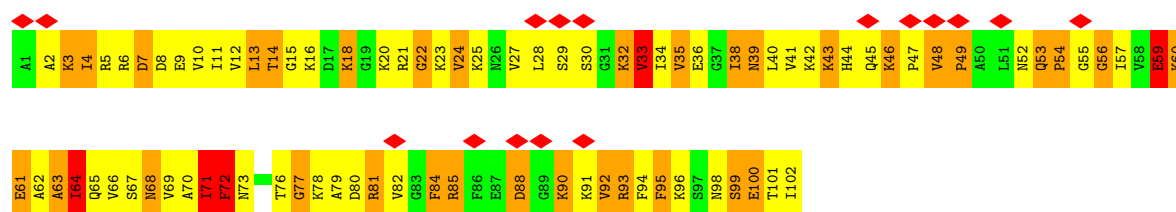
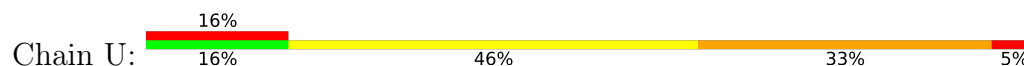
• Molecule 19: 50S ribosomal protein L22



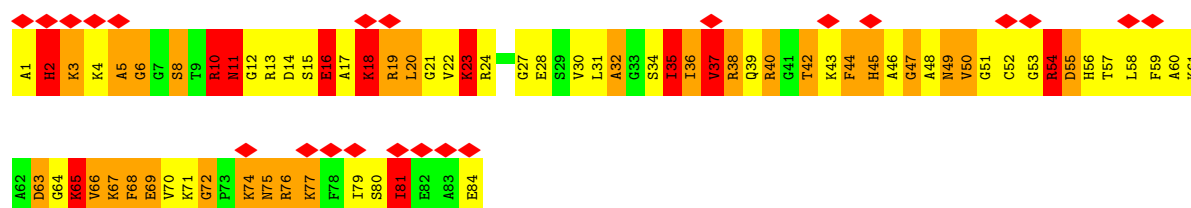
• Molecule 20: 50S ribosomal protein L23



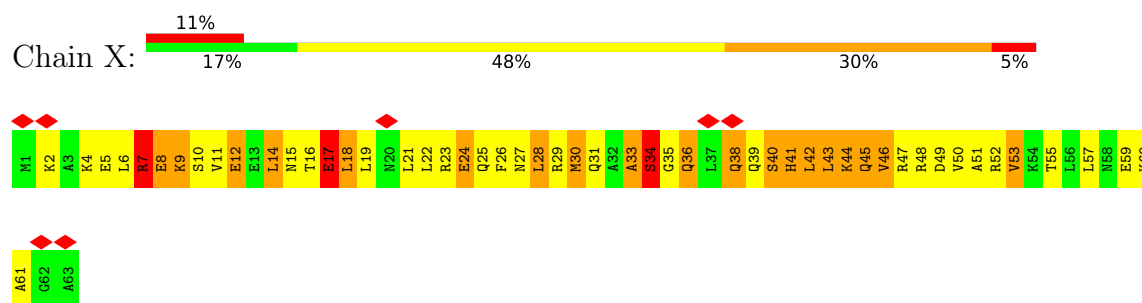
• Molecule 21: 50S ribosomal protein L24



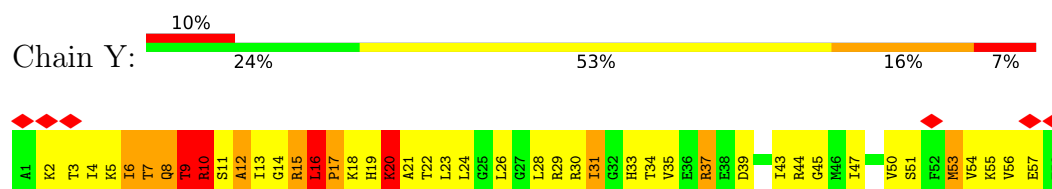
• Molecule 22: 50S ribosomal protein L27



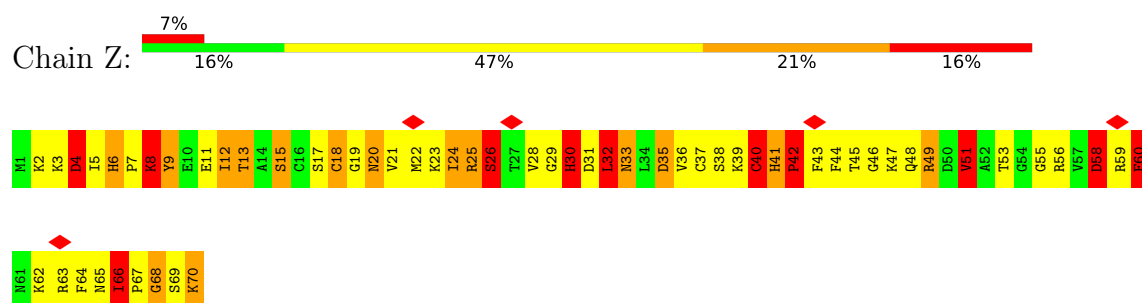
- Molecule 23: 50S ribosomal protein L29



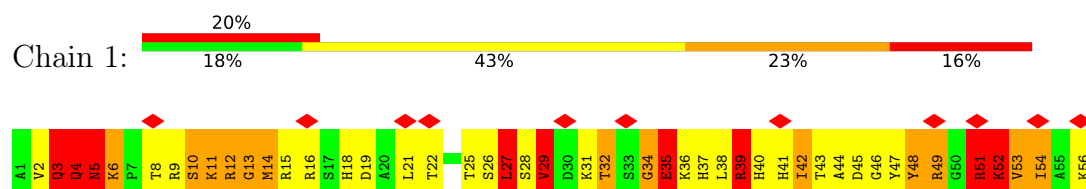
- Molecule 24: 50S ribosomal protein L30



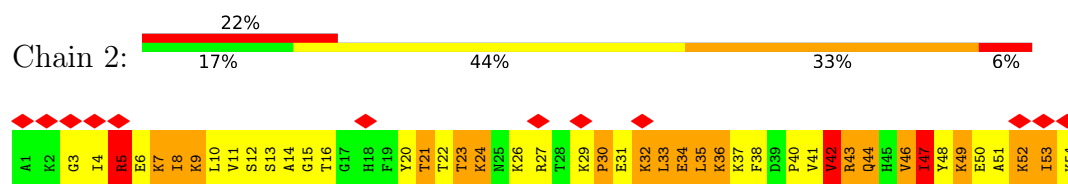
- Molecule 25: 50S ribosomal protein L31



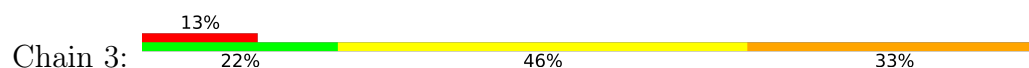
- Molecule 26: 50S ribosomal protein L32

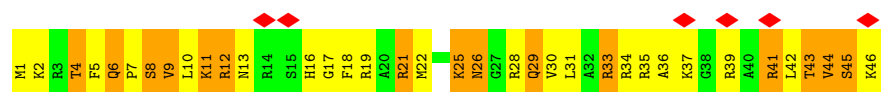


- Molecule 27: 50S ribosomal protein L33

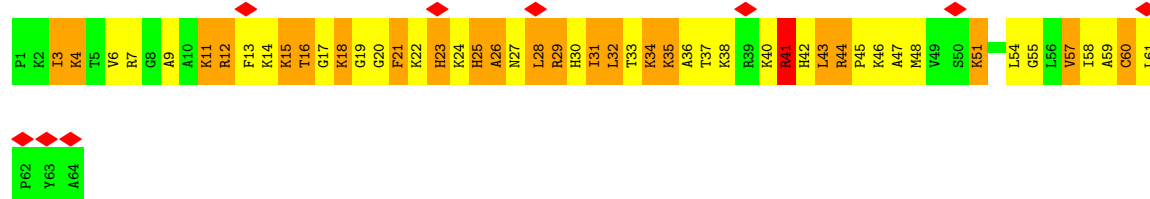
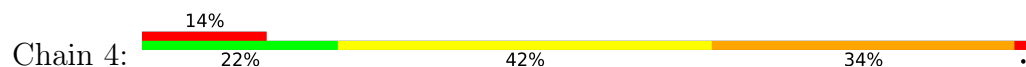


- Molecule 28: 50S ribosomal protein L34

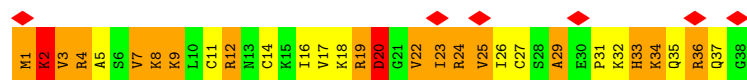
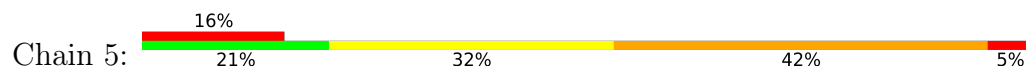




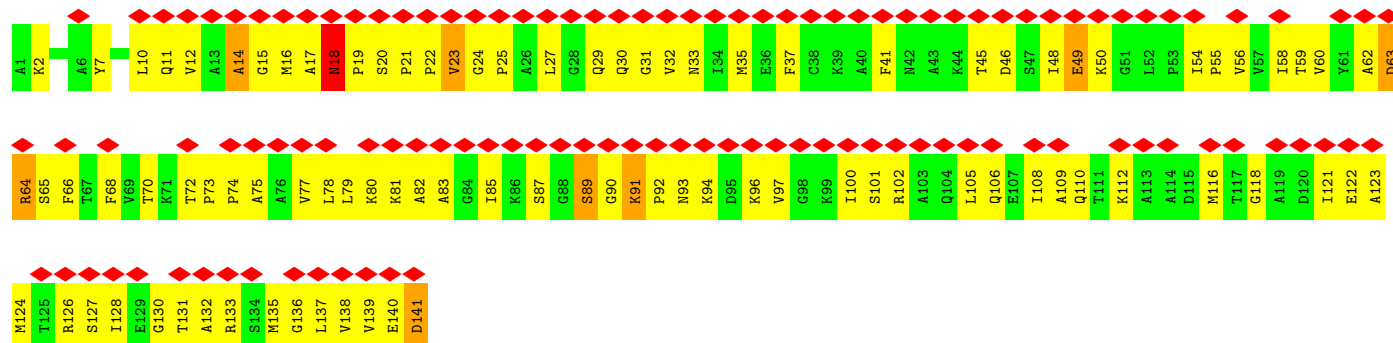
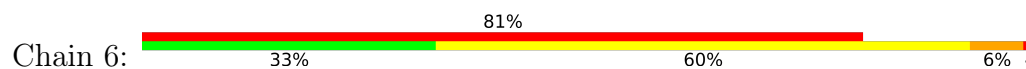
• Molecule 29: 50S ribosomal protein L35



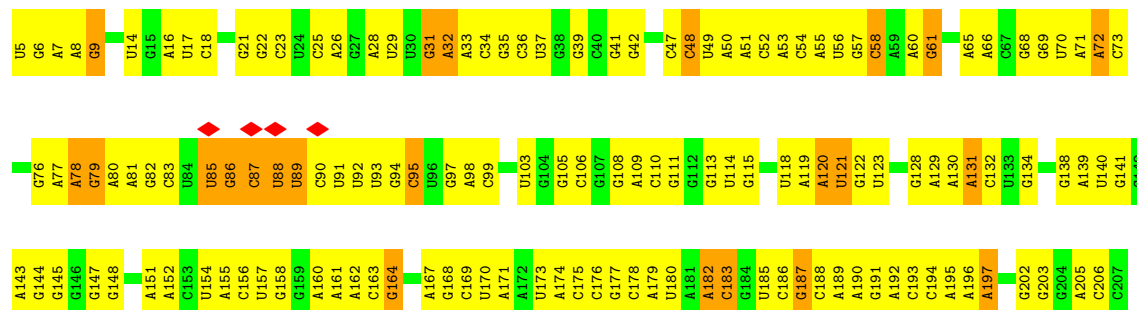
• Molecule 30: 50S ribosomal protein L36



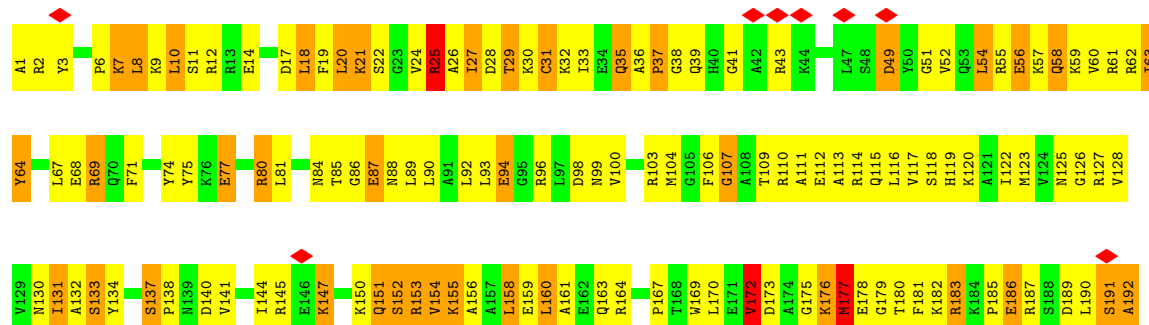
• Molecule 31: 50S ribosomal protein L11



• Molecule 32: 16S rRNA

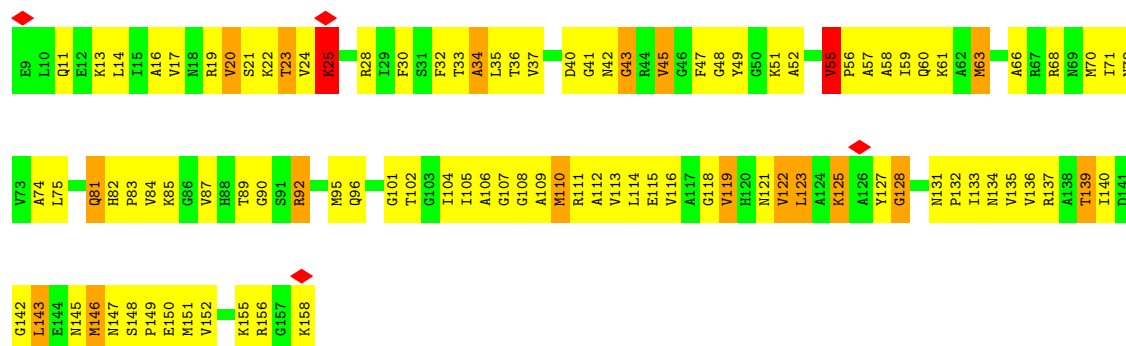
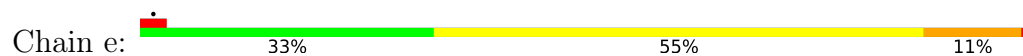


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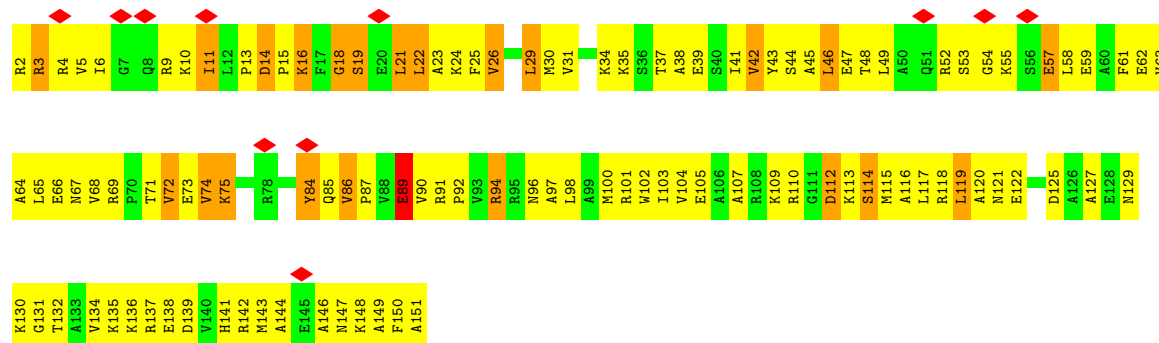
• Molecule 35: 30S ribosomal protein S5



• Molecule 36: 30S ribosomal protein S6

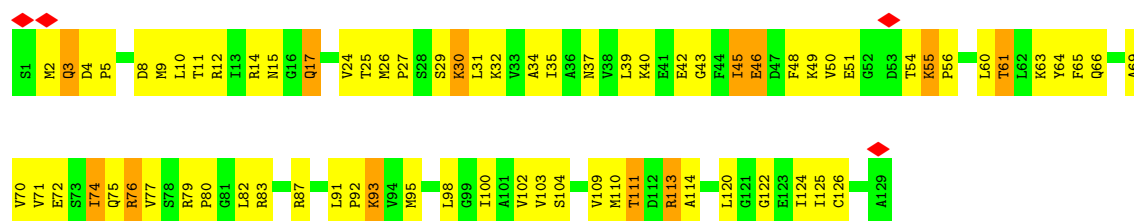


• Molecule 37: 30S ribosomal protein S7

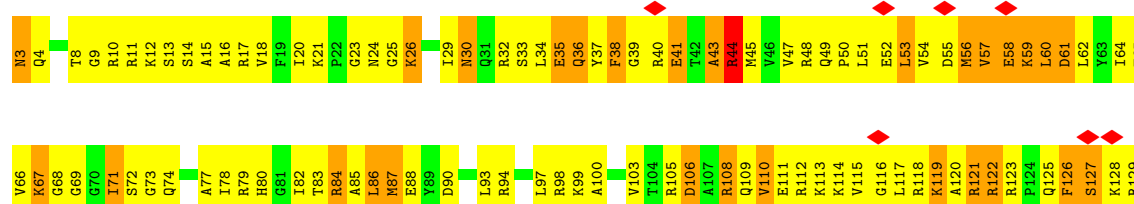


• Molecule 38: 30S ribosomal protein S8

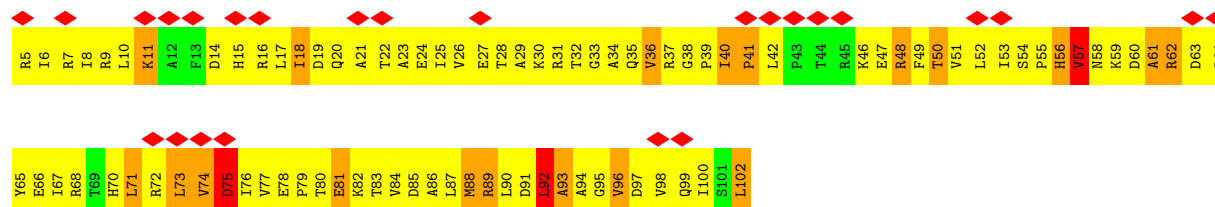
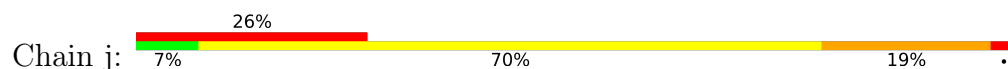




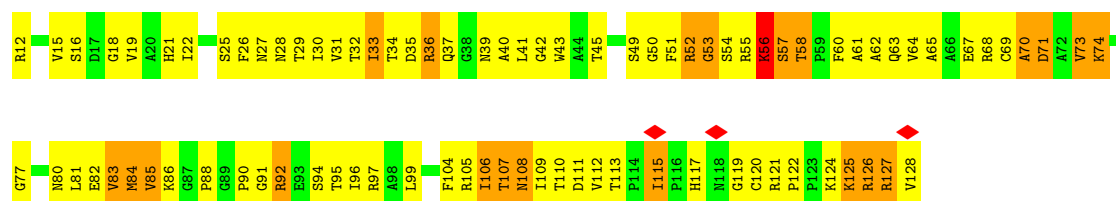
• Molecule 39: 30S ribosomal protein S9



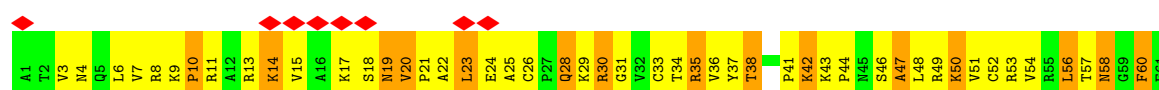
• Molecule 40: 30S ribosomal protein S10

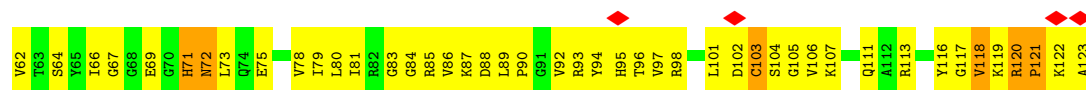


• Molecule 41: 30S ribosomal protein S11

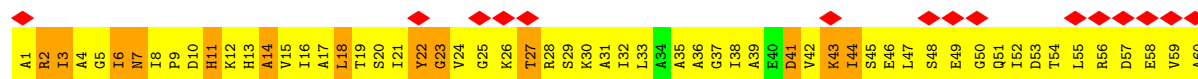
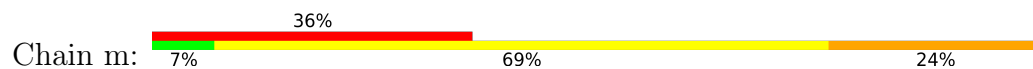


• Molecule 42: 30S ribosomal protein S12

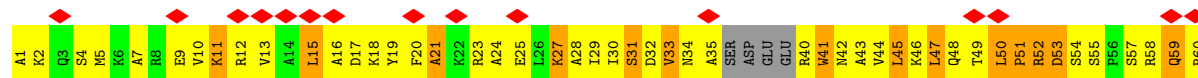
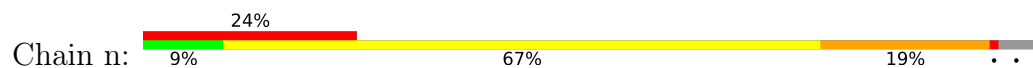




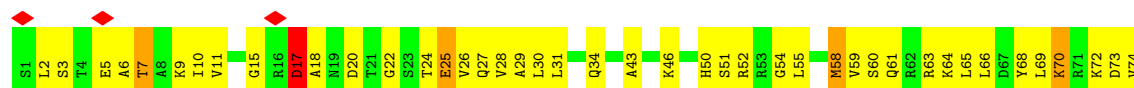
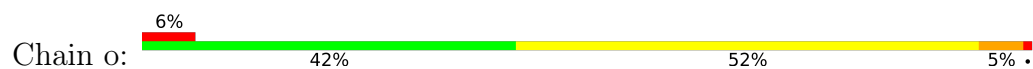
• Molecule 43: 30S ribosomal protein S13



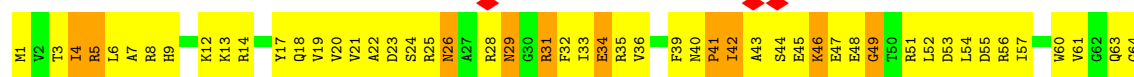
• Molecule 44: 30S ribosomal protein S14



• Molecule 45: 30S ribosomal protein S15

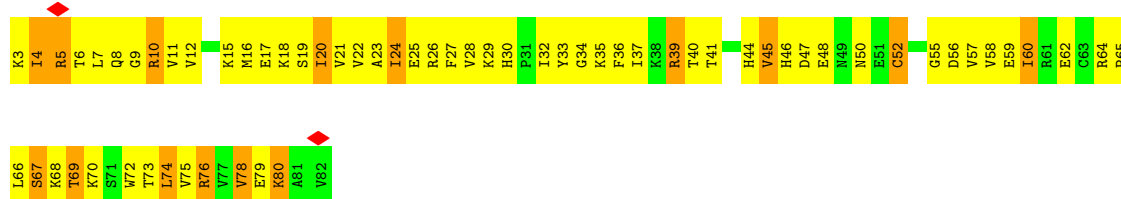


• Molecule 46: 30S ribosomal protein S16

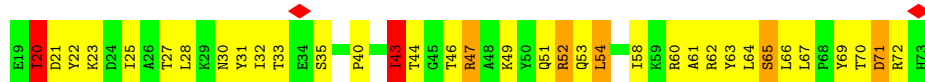


• Molecule 47: 30S ribosomal protein S17

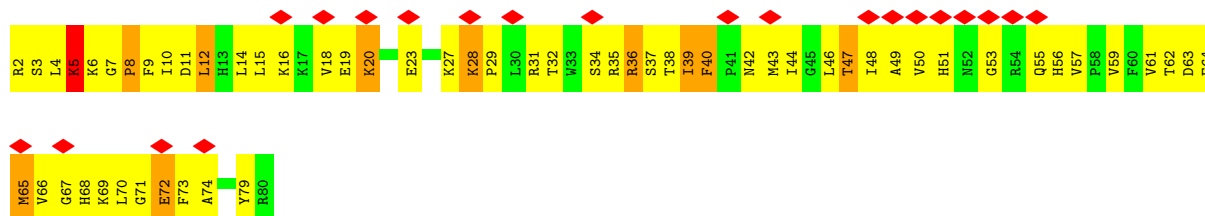




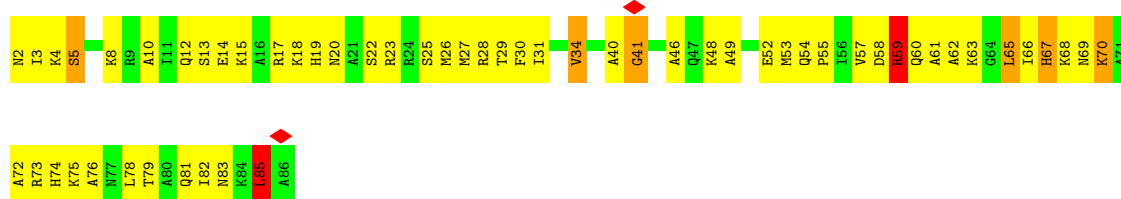
- Molecule 48: 30S ribosomal protein S18



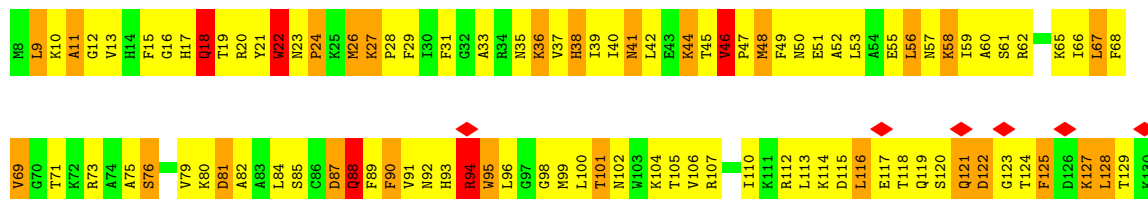
- Molecule 49: 30S ribosomal protein S19

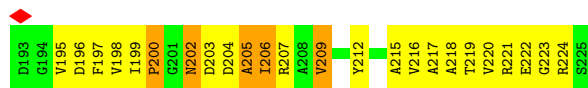


- Molecule 50: 30S ribosomal protein S20

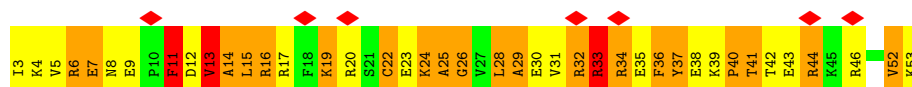
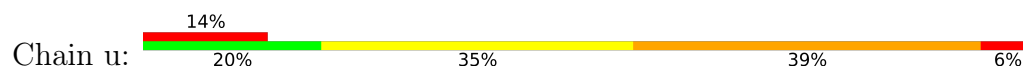


- Molecule 51: 30S ribosomal protein S2

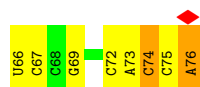
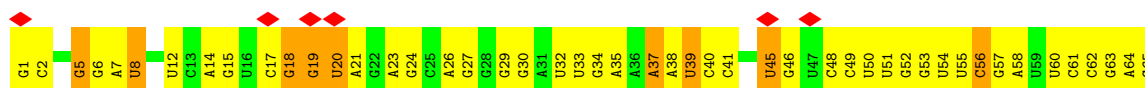




• Molecule 52: 30S ribosomal protein S21



• Molecule 53: P-tRNA



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	46042	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TECNAI F30	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	8	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.302	Depositor
Minimum map value	-0.149	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.013	Depositor
Recommended contour level	0.03	Depositor
Map size (Å)	424.96, 424.96, 424.96	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.66, 1.66, 1.66	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	0.28	0/2803	0.62	0/4371
2	B	0.30	5/68314 (0.0%)	0.66	96/106569 (0.1%)
3	V	0.38	0/766	0.82	1/1025 (0.1%)
4	C	0.51	0/2092	1.24	25/2813 (0.9%)
5	D	0.52	0/1586	1.17	16/2134 (0.7%)
6	E	0.55	2/1571 (0.1%)	1.40	24/2113 (1.1%)
7	F	0.41	0/1444	1.36	31/1937 (1.6%)
8	G	0.39	0/1343	1.00	9/1816 (0.5%)
9	H	0.33	0/1122	0.90	4/1515 (0.3%)
10	J	0.43	0/1135	1.06	11/1529 (0.7%)
11	K	0.44	0/939	1.46	21/1258 (1.7%)
12	L	0.96	5/1062 (0.5%)	2.35	65/1413 (4.6%)
13	M	0.68	2/1093 (0.2%)	1.43	24/1460 (1.6%)
14	N	0.46	0/1021	1.17	16/1364 (1.2%)
15	O	0.36	0/910	1.08	11/1219 (0.9%)
16	P	0.78	1/929 (0.1%)	2.02	43/1242 (3.5%)
17	Q	0.53	1/960 (0.1%)	1.24	9/1278 (0.7%)
18	R	1.37	7/829 (0.8%)	1.75	24/1107 (2.2%)
19	S	0.35	0/864	0.93	4/1156 (0.3%)
20	T	0.54	1/784 (0.1%)	1.05	9/1048 (0.9%)
21	U	0.41	0/787	1.09	9/1051 (0.9%)
22	W	0.43	0/642	1.34	15/848 (1.8%)
23	X	0.36	0/510	1.10	4/677 (0.6%)
24	Y	0.41	0/453	0.84	1/605 (0.2%)
25	Z	0.57	0/559	1.51	10/745 (1.3%)
26	1	0.79	1/450 (0.2%)	1.63	17/599 (2.8%)
27	2	0.42	0/448	0.92	2/594 (0.3%)
28	3	0.40	0/380	0.97	2/498 (0.4%)
29	4	0.57	0/513	1.15	4/676 (0.6%)
30	5	0.55	1/303 (0.3%)	1.11	3/397 (0.8%)
31	6	0.34	0/1046	1.00	9/1410 (0.6%)
32	a	0.27	1/36762 (0.0%)	0.63	27/57350 (0.0%)
33	c	0.28	0/1651	0.74	1/2225 (0.0%)
34	d	0.27	0/1665	0.72	1/2227 (0.0%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	e	0.30	0/1118	0.76	1/1504 (0.1%)
36	f	0.30	0/835	0.81	2/1128 (0.2%)
37	g	0.27	0/1187	0.74	0/1591
38	h	0.28	0/989	0.79	0/1326
39	i	0.28	0/1034	0.75	0/1375
40	j	0.29	0/796	0.71	0/1077
41	k	0.30	0/893	0.80	2/1205 (0.2%)
42	l	0.28	0/969	0.72	0/1300
43	m	0.27	0/892	0.77	0/1193
44	n	0.28	0/785	0.74	0/1043
45	o	0.27	0/724	0.73	1/966 (0.1%)
46	p	0.29	0/659	0.76	0/884
47	q	0.26	0/657	0.63	0/881
48	r	0.31	0/462	0.71	0/621
49	s	0.29	0/652	0.72	0/877
50	t	0.28	0/671	0.79	1/888 (0.1%)
51	7	0.31	1/1735 (0.1%)	0.77	1/2338 (0.0%)
52	u	1.53	5/430 (1.2%)	1.15	7/570 (1.2%)
53	v	0.41	0/1813	0.51	0/2823
All	All	0.36	33/155037 (0.0%)	0.80	563/231859 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	B	0	61
4	C	0	3
9	H	0	1
10	J	0	2
12	L	0	1
16	P	0	1
17	Q	0	1
18	R	0	1
32	a	0	16
52	u	0	1
All	All	0	88

The worst 5 of 33 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
52	u	15	LEU	C-N	-23.68	0.99	1.33
18	R	54	VAL	N-CA	-18.64	1.23	1.46
18	R	54	VAL	CA-CB	17.35	1.78	1.54
18	R	54	VAL	CA-C	14.95	1.71	1.52
18	R	53	PHE	CB-CG	13.51	1.81	1.50

The worst 5 of 563 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	E	73	ILE	N-CA-C	20.95	131.70	112.43
6	E	74	LYS	N-CA-C	-19.18	90.85	112.72
18	R	54	VAL	CB-CA-C	17.59	140.13	111.29
12	L	6	LEU	N-CA-C	16.94	134.26	111.90
16	P	40	GLN	N-CA-C	-16.82	89.08	112.13

There are no chirality outliers.

5 of 88 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	136	G	Sidechain
2	B	139	U	Sidechain
2	B	142	A	Sidechain
2	B	143	C	Sidechain
2	B	51	G	Sidechain

5.2 Too-close contacts [i](#)

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	A	2507	0	1270	87	0
2	B	60995	0	30679	2441	0
3	V	753	0	780	107	0
4	C	2053	0	2122	456	0
5	D	1565	0	1616	392	0
6	E	1552	0	1619	269	0
7	F	1420	0	1448	511	0
8	G	1323	0	1374	189	0
9	H	1111	0	1148	224	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	J	1112	0	1147	225	0
11	K	930	0	1000	135	0
12	L	1053	0	1129	293	0
13	M	1074	0	1157	251	0
14	N	1008	0	1045	160	0
15	O	900	0	935	142	0
16	P	917	0	965	219	0
17	Q	947	0	1022	183	0
18	R	816	0	839	175	0
19	S	857	0	922	121	0
20	T	777	0	840	148	0
21	U	779	0	834	161	0
22	W	634	0	656	162	0
23	X	509	0	543	73	0
24	Y	449	0	491	63	0
25	Z	549	0	552	116	0
26	1	444	0	461	78	0
27	2	441	0	485	67	0
28	3	377	0	418	56	0
29	4	504	0	574	111	0
30	5	302	0	343	44	0
31	6	1032	0	1088	131	0
32	a	32831	0	16416	3918	0
33	c	1624	0	1680	660	0
34	d	1643	0	1710	217	0
35	e	1105	0	1148	120	0
36	f	817	0	807	95	0
37	g	1174	0	1225	206	0
38	h	979	0	1034	80	0
39	i	1022	0	1068	254	0
40	j	786	0	782	1068	0
41	k	877	0	887	127	0
42	l	955	0	1019	112	0
43	m	883	0	892	1117	0
44	n	774	0	791	897	0
45	o	716	0	742	64	0
46	p	649	0	666	100	0
47	q	648	0	691	85	0
48	r	455	0	478	54	0
49	s	637	0	660	292	0
50	t	665	0	713	100	0
51	7	1704	0	1732	203	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
52	u	425	0	448	103	0
53	v	1623	0	816	182	0
All	All	142682	0	95907	13185	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 55.

The worst 5 of 13185 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)
32:a:1335:U:C6	43:m:11:HIS:CG	1.78	1.68
32:a:988:G:C6	44:n:46:LYS:HG2	1.23	1.67
32:a:1016:A:C8	44:n:31:SER:HA	1.17	1.67
32:a:1233:G:P	39:i:125:GLN:HG2	1.24	1.65
32:a:1330:U:C5	43:m:64:VAL:CG1	1.80	1.64

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	
3	V	92/94 (98%)	62 (67%)	22 (24%)	8 (9%)	0	10
4	C	265/267 (99%)	103 (39%)	82 (31%)	80 (30%)	0	0
5	D	207/209 (99%)	90 (44%)	69 (33%)	48 (23%)	0	1
6	E	199/201 (99%)	98 (49%)	60 (30%)	41 (21%)	0	1
7	F	176/178 (99%)	95 (54%)	48 (27%)	33 (19%)	0	2
8	G	174/176 (99%)	118 (68%)	39 (22%)	17 (10%)	0	8
9	H	147/149 (99%)	88 (60%)	46 (31%)	13 (9%)	0	10
10	J	138/140 (99%)	68 (49%)	41 (30%)	29 (21%)	0	1

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
11	K	119/121 (98%)	71 (60%)	32 (27%)	16 (13%)	0	3
12	L	142/144 (99%)	60 (42%)	40 (28%)	42 (30%)	0	0
13	M	134/136 (98%)	69 (52%)	37 (28%)	28 (21%)	0	1
14	N	125/127 (98%)	73 (58%)	35 (28%)	17 (14%)	0	3
15	O	115/117 (98%)	64 (56%)	26 (23%)	25 (22%)	0	1
16	P	112/114 (98%)	39 (35%)	36 (32%)	37 (33%)	0	0
17	Q	115/117 (98%)	81 (70%)	23 (20%)	11 (10%)	0	8
18	R	101/103 (98%)	43 (43%)	32 (32%)	26 (26%)	0	1
19	S	108/110 (98%)	63 (58%)	27 (25%)	18 (17%)	0	2
20	T	97/99 (98%)	42 (43%)	40 (41%)	15 (16%)	0	2
21	U	100/102 (98%)	33 (33%)	46 (46%)	21 (21%)	0	1
22	W	82/84 (98%)	29 (35%)	26 (32%)	27 (33%)	0	0
23	X	61/63 (97%)	28 (46%)	21 (34%)	12 (20%)	0	1
24	Y	56/58 (97%)	29 (52%)	17 (30%)	10 (18%)	0	2
25	Z	68/70 (97%)	29 (43%)	26 (38%)	13 (19%)	0	2
26	1	54/56 (96%)	30 (56%)	15 (28%)	9 (17%)	0	2
27	2	52/54 (96%)	19 (36%)	23 (44%)	10 (19%)	0	2
28	3	44/46 (96%)	23 (52%)	14 (32%)	7 (16%)	0	2
29	4	62/64 (97%)	30 (48%)	25 (40%)	7 (11%)	0	5
30	5	36/38 (95%)	18 (50%)	9 (25%)	9 (25%)	0	1
31	6	139/141 (99%)	124 (89%)	11 (8%)	4 (3%)	3	26
33	c	204/206 (99%)	135 (66%)	49 (24%)	20 (10%)	0	8
34	d	203/205 (99%)	130 (64%)	55 (27%)	18 (9%)	0	10
35	e	148/150 (99%)	107 (72%)	34 (23%)	7 (5%)	2	19
36	f	98/100 (98%)	69 (70%)	23 (24%)	6 (6%)	1	15
37	g	148/150 (99%)	102 (69%)	38 (26%)	8 (5%)	1	17
38	h	127/129 (98%)	105 (83%)	19 (15%)	3 (2%)	4	29
39	i	125/127 (98%)	87 (70%)	27 (22%)	11 (9%)	0	10
40	j	96/98 (98%)	63 (66%)	21 (22%)	12 (12%)	0	4
41	k	115/117 (98%)	75 (65%)	27 (24%)	13 (11%)	0	5
42	l	121/123 (98%)	74 (61%)	30 (25%)	17 (14%)	0	3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
43	m	112/114 (98%)	87 (78%)	14 (12%)	11 (10%)	0	8
44	n	92/100 (92%)	59 (64%)	24 (26%)	9 (10%)	0	8
45	o	86/88 (98%)	66 (77%)	18 (21%)	2 (2%)	5	30
46	p	80/82 (98%)	59 (74%)	17 (21%)	4 (5%)	1	18
47	q	78/80 (98%)	48 (62%)	26 (33%)	4 (5%)	1	17
48	r	53/55 (96%)	27 (51%)	19 (36%)	7 (13%)	0	3
49	s	77/79 (98%)	57 (74%)	14 (18%)	6 (8%)	1	12
50	t	83/85 (98%)	69 (83%)	8 (10%)	6 (7%)	1	13
51	7	216/218 (99%)	145 (67%)	53 (24%)	18 (8%)	0	10
52	u	49/51 (96%)	22 (45%)	12 (24%)	15 (31%)	0	0
All	All	5631/5735 (98%)	3305 (59%)	1496 (27%)	830 (15%)	0	3

5 of 830 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	C	21	PRO
4	C	22	GLU
4	C	28	PRO
4	C	29	PHE
4	C	31	PRO

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	V	78/78 (100%)	63 (81%)	15 (19%)	1	9
4	C	213/213 (100%)	137 (64%)	76 (36%)	0	1
5	D	164/164 (100%)	108 (66%)	56 (34%)	0	1
6	E	165/165 (100%)	116 (70%)	49 (30%)	0	2
7	F	149/149 (100%)	123 (83%)	26 (17%)	2	12
8	G	137/137 (100%)	106 (77%)	31 (23%)	1	5

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
9	H	114/114 (100%)	85 (75%)	29 (25%)	0	4
10	J	114/114 (100%)	84 (74%)	30 (26%)	0	3
11	K	102/102 (100%)	78 (76%)	24 (24%)	1	5
12	L	103/103 (100%)	57 (55%)	46 (45%)	0	0
13	M	109/109 (100%)	78 (72%)	31 (28%)	0	3
14	N	103/103 (100%)	80 (78%)	23 (22%)	1	6
15	O	87/87 (100%)	56 (64%)	31 (36%)	0	1
16	P	99/99 (100%)	76 (77%)	23 (23%)	1	5
17	Q	89/89 (100%)	67 (75%)	22 (25%)	1	4
18	R	84/84 (100%)	68 (81%)	16 (19%)	1	10
19	S	93/93 (100%)	72 (77%)	21 (23%)	1	5
20	T	83/83 (100%)	54 (65%)	29 (35%)	0	1
21	U	83/83 (100%)	62 (75%)	21 (25%)	0	4
22	W	62/62 (100%)	44 (71%)	18 (29%)	0	3
23	X	55/55 (100%)	36 (66%)	19 (34%)	0	1
24	Y	48/48 (100%)	37 (77%)	11 (23%)	1	5
25	Z	62/62 (100%)	43 (69%)	19 (31%)	0	2
26	1	47/47 (100%)	31 (66%)	16 (34%)	0	1
27	2	48/48 (100%)	30 (62%)	18 (38%)	0	1
28	3	38/38 (100%)	28 (74%)	10 (26%)	0	3
29	4	51/51 (100%)	34 (67%)	17 (33%)	0	2
30	5	34/34 (100%)	22 (65%)	12 (35%)	0	1
31	6	109/109 (100%)	106 (97%)	3 (3%)	38	59
33	c	170/170 (100%)	145 (85%)	25 (15%)	3	16
34	d	172/172 (100%)	137 (80%)	35 (20%)	1	8
35	e	113/113 (100%)	93 (82%)	20 (18%)	2	12
36	f	87/87 (100%)	68 (78%)	19 (22%)	1	6
37	g	123/123 (100%)	101 (82%)	22 (18%)	2	12
38	h	104/104 (100%)	87 (84%)	17 (16%)	2	14
39	i	105/105 (100%)	83 (79%)	22 (21%)	1	7
40	j	86/86 (100%)	70 (81%)	16 (19%)	1	11

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
41	k	90/90 (100%)	74 (82%)	16 (18%)	2	12
42	l	103/103 (100%)	89 (86%)	14 (14%)	3	18
43	m	92/92 (100%)	72 (78%)	20 (22%)	1	6
44	n	79/83 (95%)	66 (84%)	13 (16%)	2	13
45	o	76/76 (100%)	70 (92%)	6 (8%)	11	36
46	p	65/65 (100%)	54 (83%)	11 (17%)	2	13
47	q	74/74 (100%)	59 (80%)	15 (20%)	1	8
48	r	48/48 (100%)	42 (88%)	6 (12%)	4	20
49	s	70/70 (100%)	60 (86%)	10 (14%)	3	17
50	t	65/65 (100%)	57 (88%)	8 (12%)	4	20
51	7	180/180 (100%)	144 (80%)	36 (20%)	1	9
52	u	44/44 (100%)	36 (82%)	8 (18%)	2	11
All	All	4669/4673 (100%)	3588 (77%)	1081 (23%)	2	5

5 of 1081 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
41	k	83	VAL
43	m	43	LYS
41	k	74	LYS
51	7	26	MET
13	M	14	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 177 such sidechains are listed below:

Mol	Chain	Res	Type
33	c	139	ASN
39	i	36	GLN
34	d	99	ASN
36	f	14	GLN
42	l	58	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	116/117 (99%)	23 (19%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	2837/2841 (99%)	450 (15%)	18 (0%)
32	a	1529/1530 (99%)	279 (18%)	0
53	v	75/76 (98%)	15 (20%)	0
All	All	4557/4564 (99%)	767 (16%)	18 (0%)

5 of 767 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	11	C
1	A	12	C
1	A	13	G
1	A	14	U
1	A	15	A

5 of 18 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	B	2282	G
2	B	2756	U
2	B	2425	A
2	B	1236	G
2	B	2258	C

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	B	3
52	u	2

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	B	2157:G	O3'	2179:C	P	42.86
1	B	2110:G	O3'	2133:G	P	29.82
1	B	878:A	O3'	898:C	P	11.30
1	u	25:ALA	C	26:GLY	N	1.16
1	u	15:LEU	C	16:ARG	N	0.99

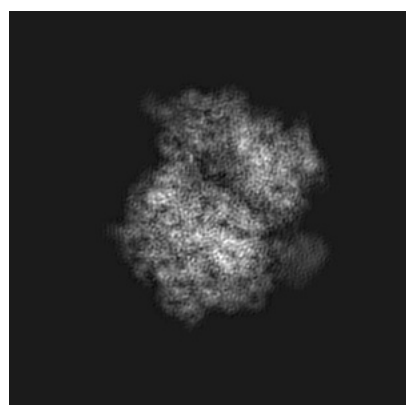
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-0661. These allow visual inspection of the internal detail of the map and identification of artifacts.

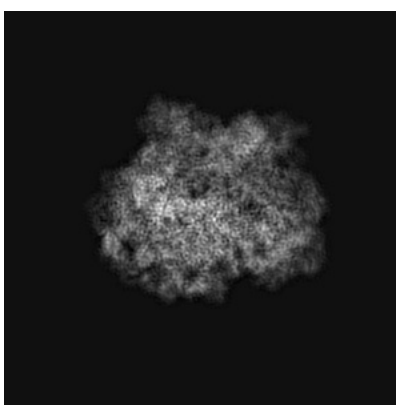
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

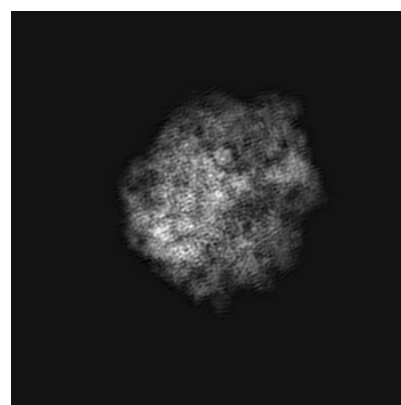
6.1.1 Primary map



X



Y

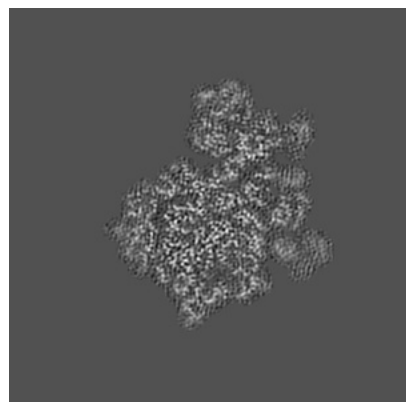


Z

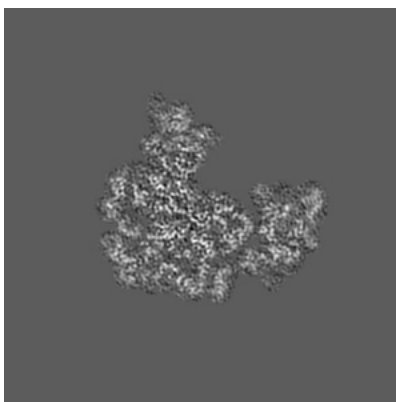
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

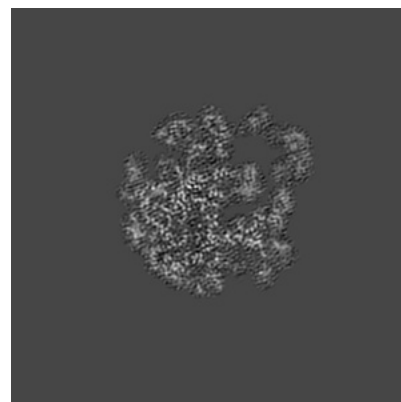
6.2.1 Primary map



X Index: 128



Y Index: 128

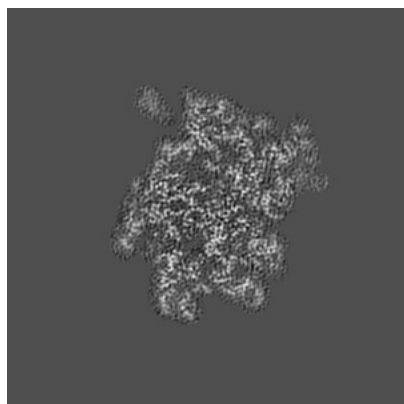


Z Index: 128

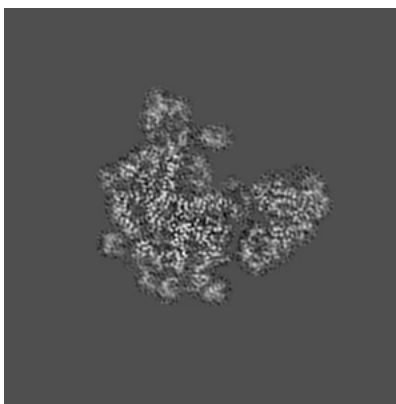
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

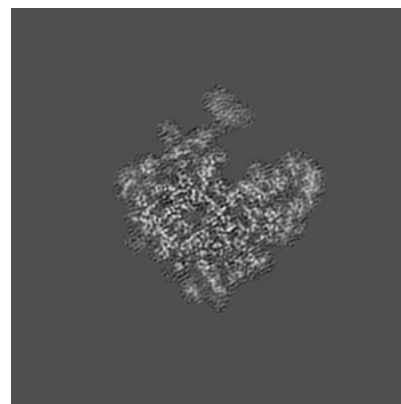
6.3.1 Primary map



X Index: 116



Y Index: 137

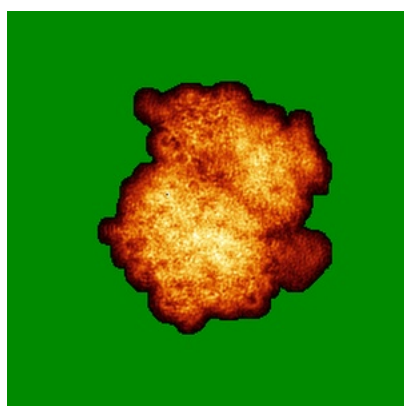


Z Index: 108

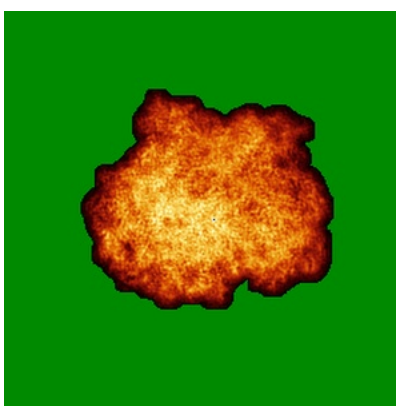
The images above show the largest variance slices of the map in three orthogonal directions.

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

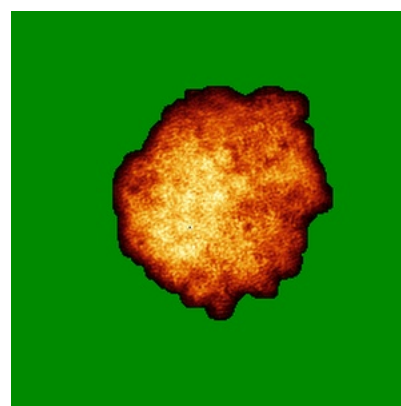
6.4.1 Primary map



X



Y

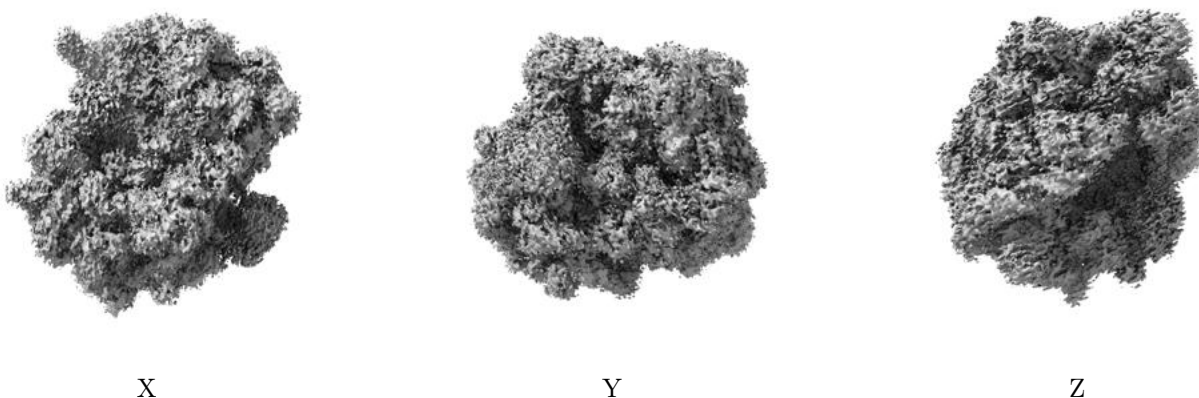


Z

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

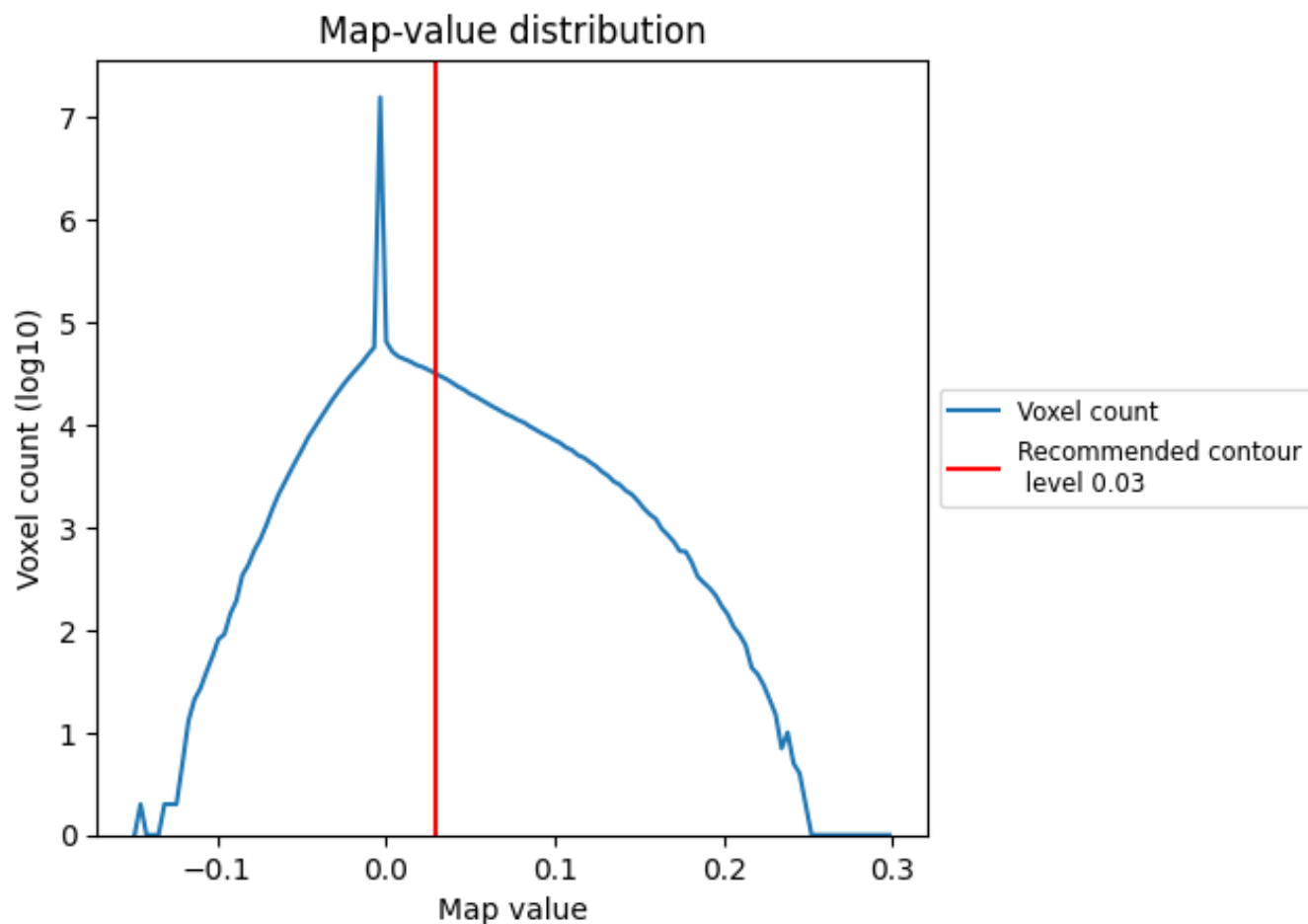
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

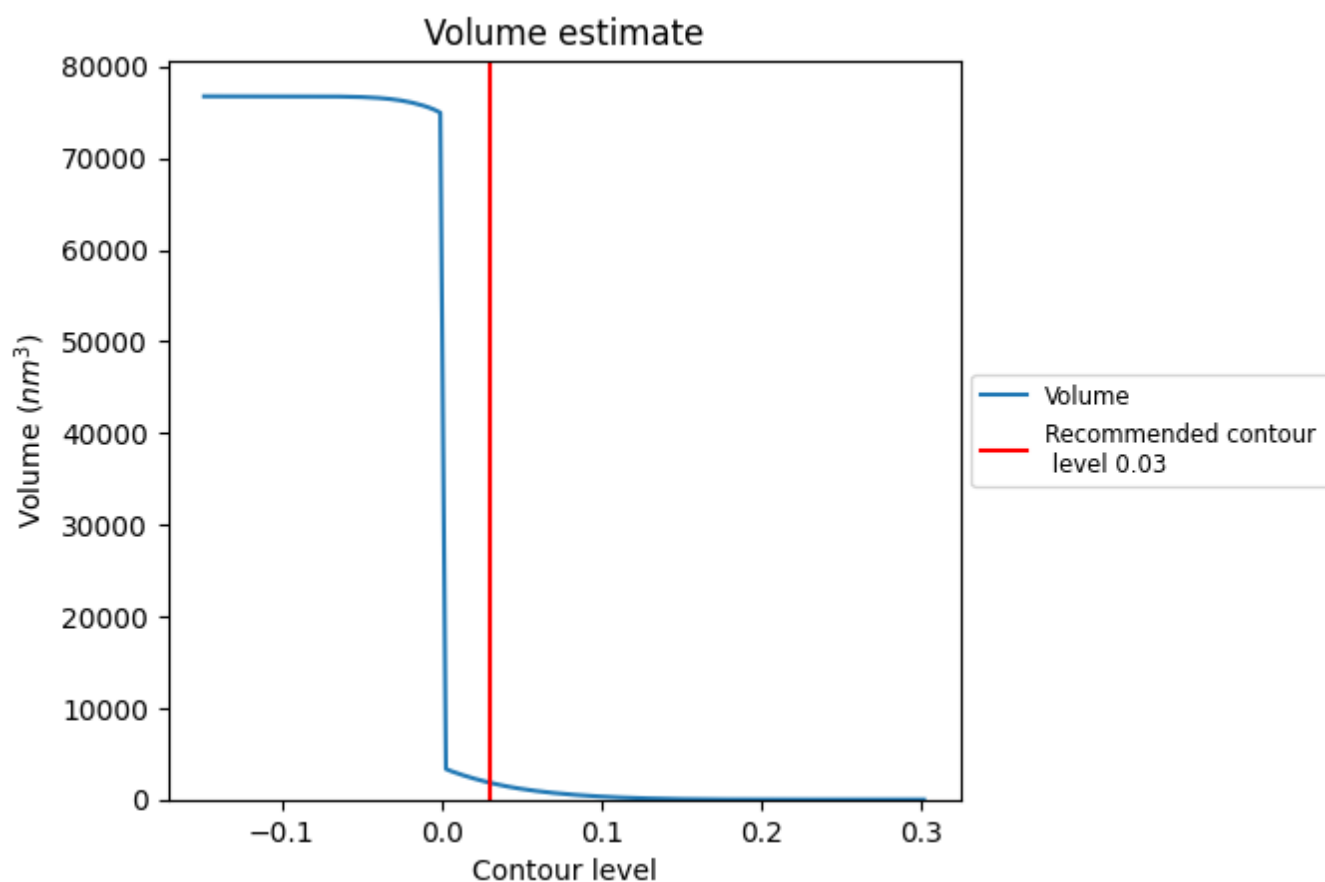
This section contains the results of statistical analysis of the map.

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.

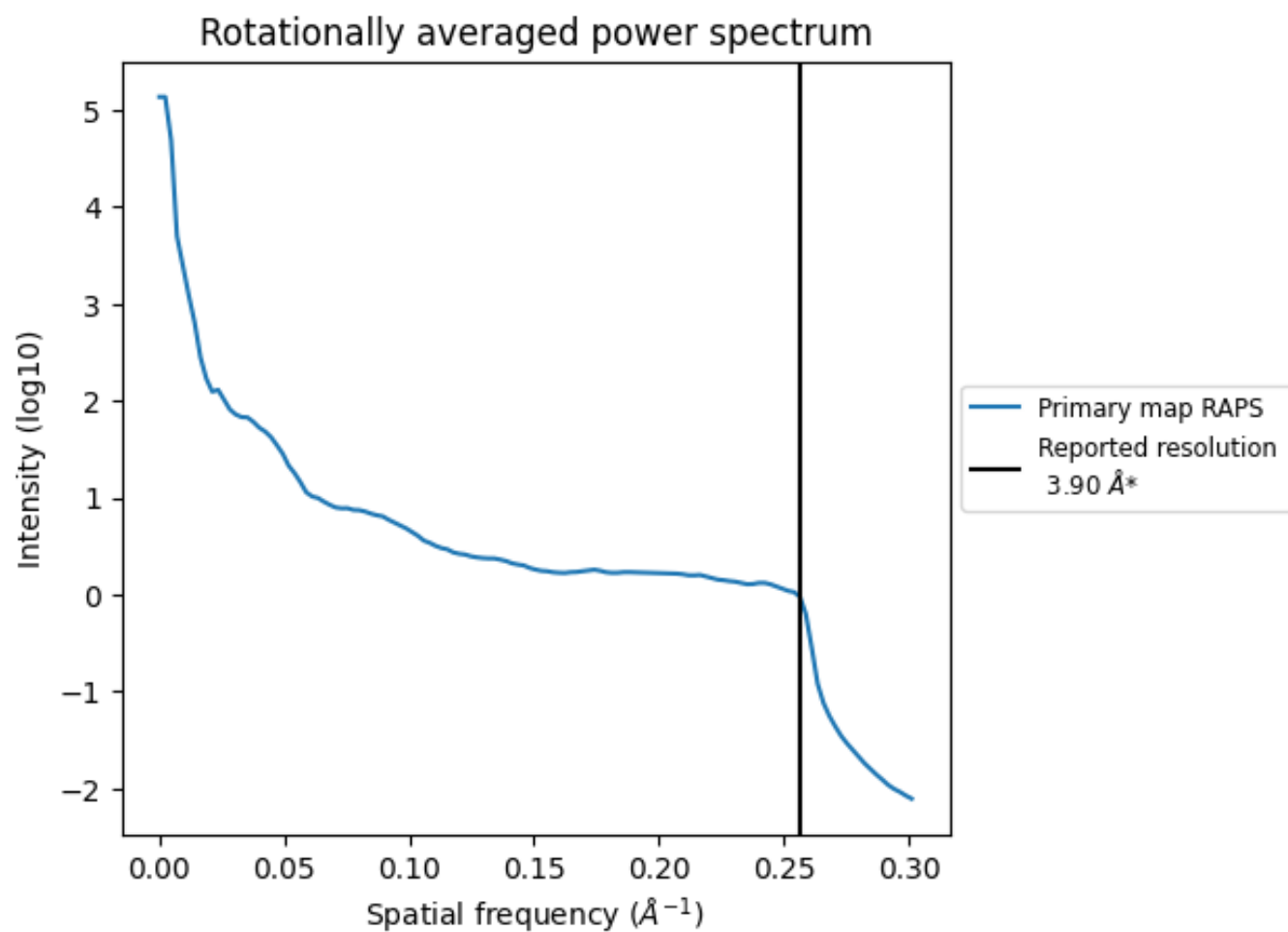
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1845 nm³; this corresponds to an approximate mass of 1667 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ

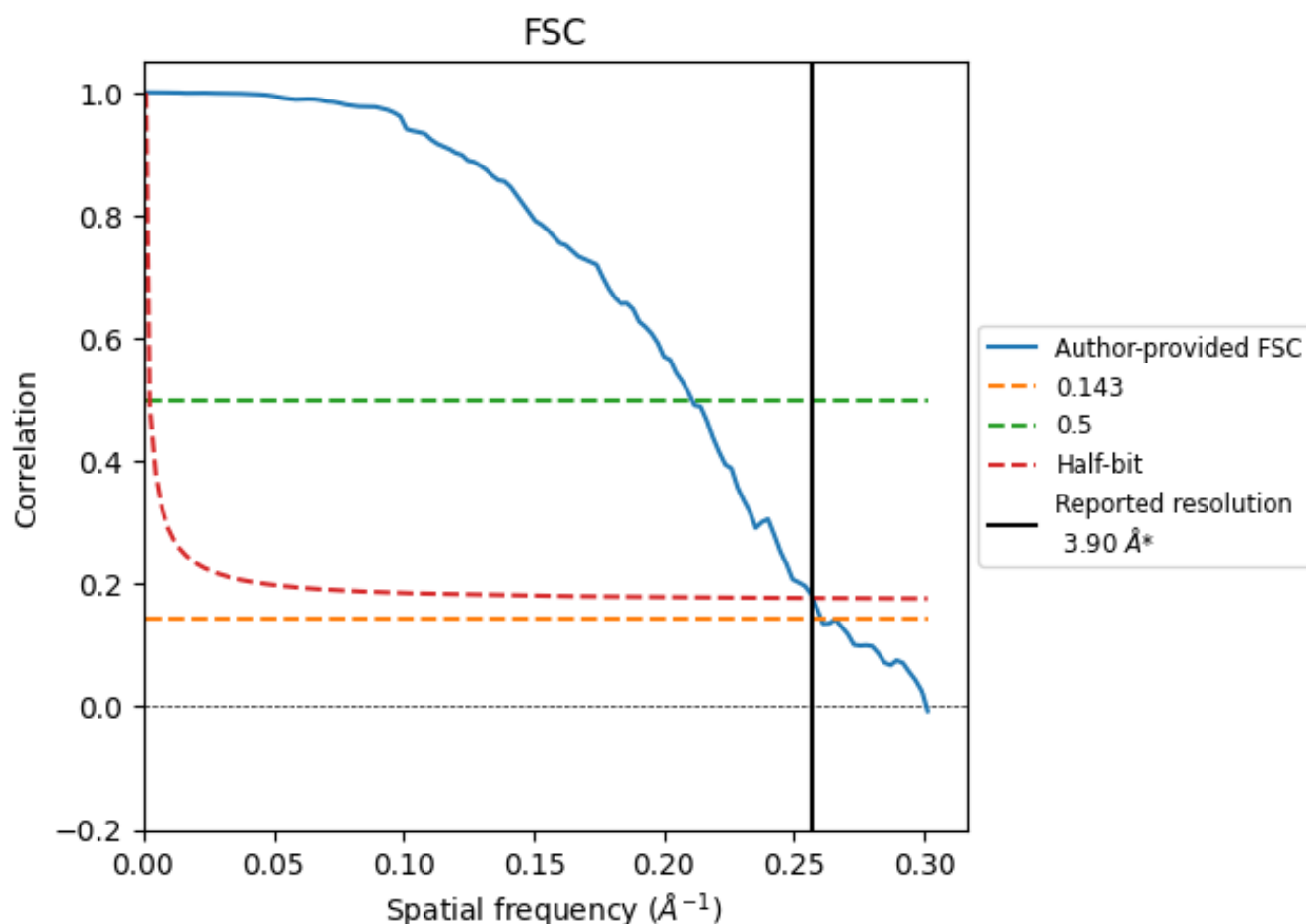


*Reported resolution corresponds to spatial frequency of 0.256 $\text{\AA}^{-1}$

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 0.256 Å⁻¹

8.2 Resolution estimates [i](#)

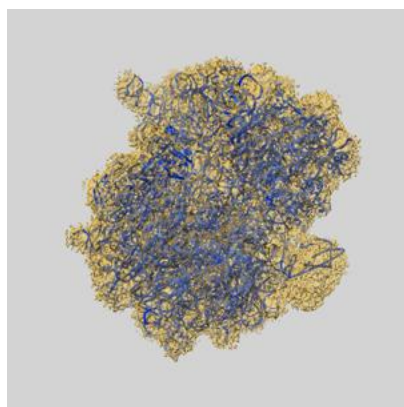
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.90	-	-
Author-provided FSC curve	3.84	4.74	3.89
Unmasked-calculated*	-	-	-

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

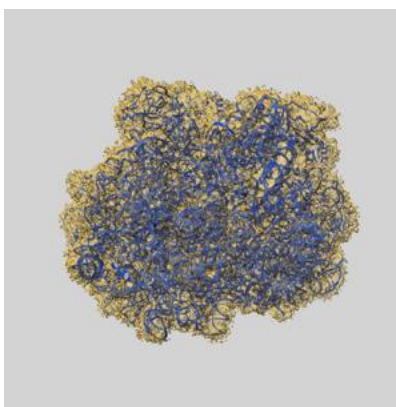
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-0661 and PDB model 6O9J. Per-residue inclusion information can be found in [section 3](#) on [page 13](#).

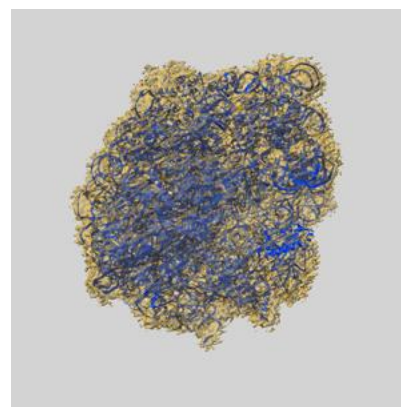
9.1 Map-model overlay [i](#)



X



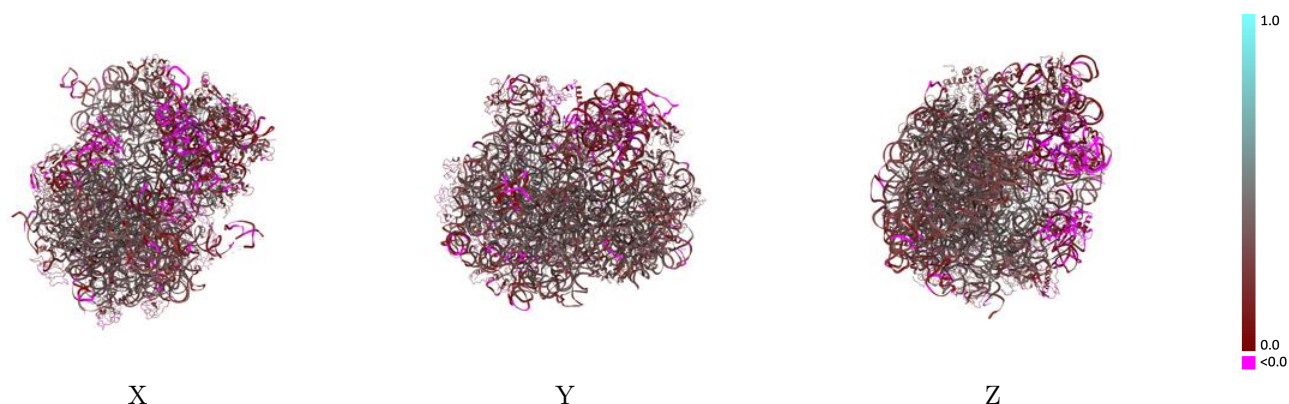
Y



Z

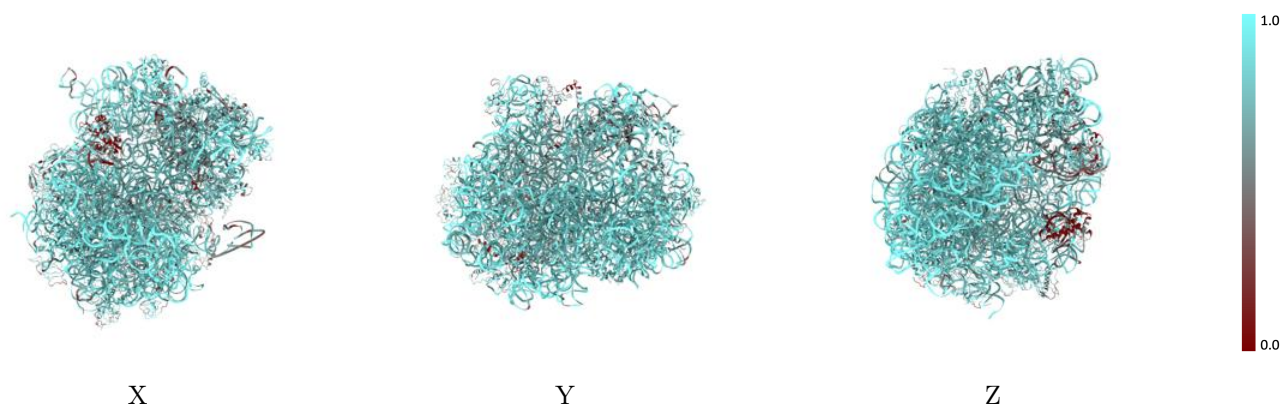
The images above show the 3D surface view of the map at the recommended contour level 0.03 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



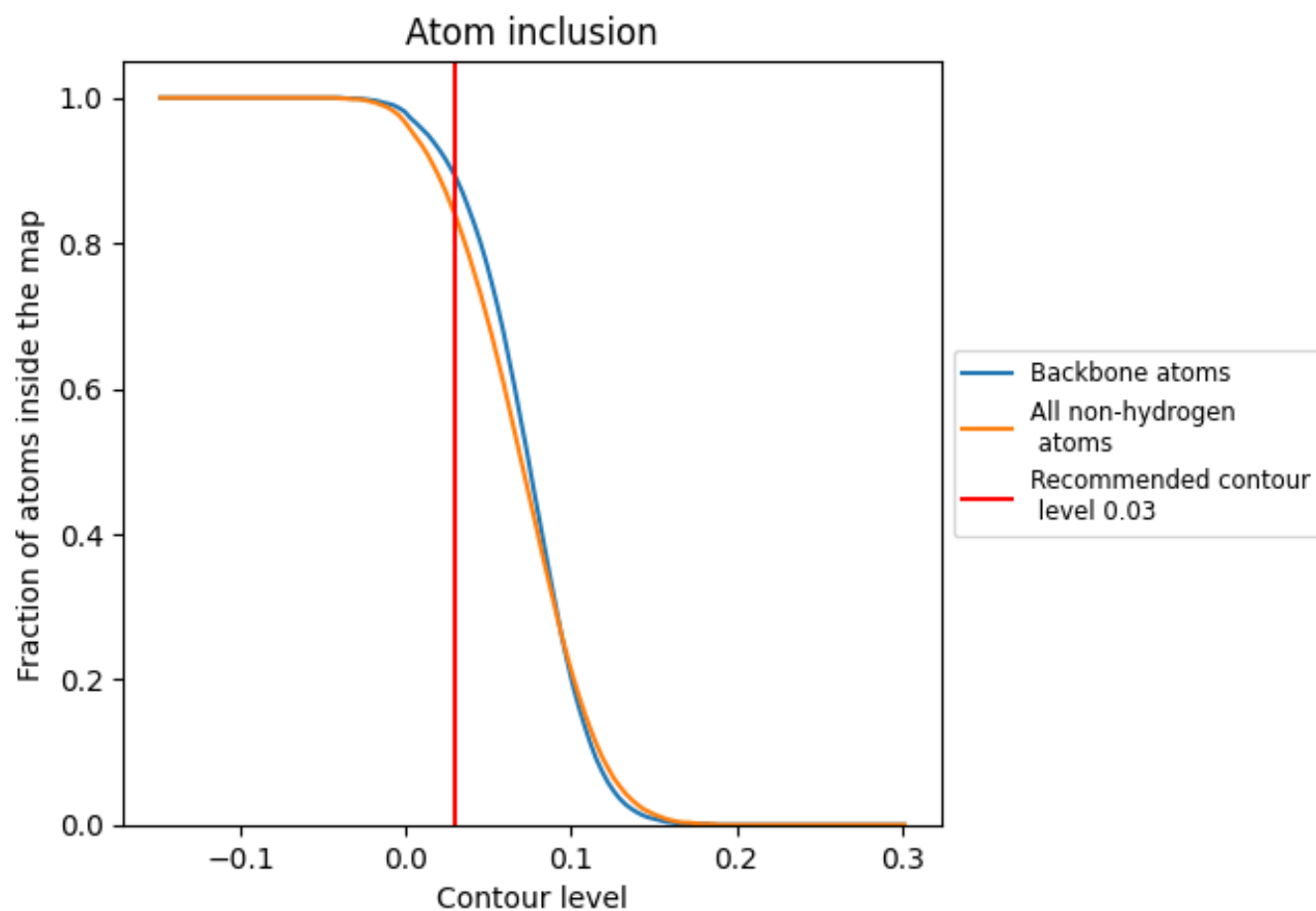
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.03).

9.4 Atom inclusion [i](#)



At the recommended contour level, 89% of all backbone atoms, 84% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.03) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8370	 0.2750
1	 0.6170	 0.1870
2	 0.6050	 0.1960
3	 0.7010	 0.2750
4	 0.6290	 0.2290
5	 0.6850	 0.1590
6	 0.1850	 -0.0110
7	 0.7620	 0.2650
A	 0.9230	 0.2570
B	 0.9140	 0.3270
C	 0.7010	 0.2810
D	 0.7060	 0.2420
E	 0.6860	 0.2150
F	 0.6060	 0.0750
G	 0.6750	 0.1580
H	 0.4670	 0.0970
J	 0.7270	 0.2490
K	 0.7490	 0.3210
L	 0.6160	 0.1750
M	 0.6710	 0.2220
N	 0.7030	 0.2540
O	 0.6970	 0.1820
P	 0.6680	 0.2130
Q	 0.7790	 0.2960
R	 0.6810	 0.2040
S	 0.7320	 0.2860
T	 0.6810	 0.2240
U	 0.6700	 0.1620
V	 0.7780	 0.2670
W	 0.5920	 0.1690
X	 0.7000	 0.1870
Y	 0.7000	 0.2310
Z	 0.6880	 0.2420
a	 0.8790	 0.2530
c	 0.7900	 0.3010



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Chain	Atom inclusion	Q-score
d	 0.7890	 0.2820
e	 0.7930	 0.3240
f	 0.7960	 0.3000
g	 0.7410	 0.2420
h	 0.8050	 0.3350
i	 0.8190	 0.2830
j	 0.6220	 0.0450
k	 0.7760	 0.2970
l	 0.7390	 0.3080
m	 0.5480	 0.0590
n	 0.6530	 0.0540
o	 0.7770	 0.2970
p	 0.7730	 0.3010
q	 0.7560	 0.2920
r	 0.7890	 0.3150
s	 0.6070	 0.0470
t	 0.7860	 0.2700
u	 0.6920	 0.2530
v	 0.7810	 0.2140