



Full wwPDB EM Validation Report ⓘ

Nov 2, 2024 – 11:34 pm GMT

PDB ID : 7PIP
EMDB ID : EMD-13446
Title : 70S ribosome with EF-Tu-tRNA and P-site tRNA in pseudouridimycin-treated Mycoplasma pneumoniae cells
Authors : Xue, L.; Lenz, S.; Rappsilber, J.; Mahamid, J.
Deposited on : 2021-08-23
Resolution : 9.30 Å (reported)
Based on initial models : 7OOD, 4V7C, 4V5L, 7OOC

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

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

A user guide is available at

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

The types of validation reports are described at

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

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

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

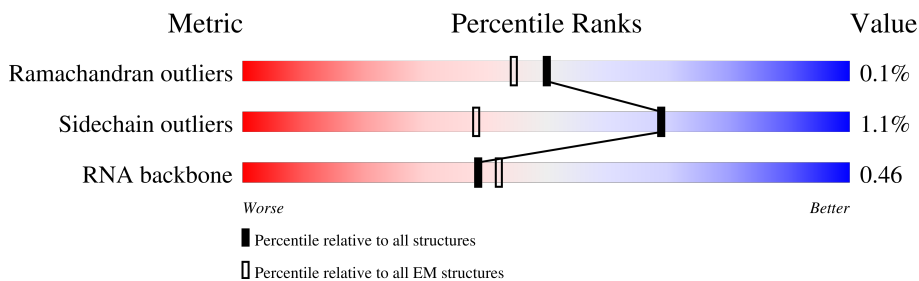
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 9.30 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	0	48	<div> <div>8%</div> <div>98%</div> <div>.</div> </div>
2	1	59	<div> <div>15%</div> <div>100%</div> </div>
3	2	37	<div> <div>14%</div> <div>100%</div> </div>
4	9	394	<div> <div>44%</div> <div>99%</div> <div>.</div> </div>
5	A	294	<div> <div>23%</div> <div>82%</div> <div>18%</div> </div>
6	B	273	<div> <div>21%</div> <div>78%</div> <div>.</div> <div>21%</div> </div>
7	C	205	<div> <div>14%</div> <div>99%</div> <div>.</div> </div>
8	D	219	<div> <div>18%</div> <div>67%</div> <div>.</div> <div>30%</div> </div>

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Mol	Chain	Length	Quality of chain
9	E	215	
10	F	155	
11	G	142	
12	H	132	
13	I	108	
14	J	121	
15	K	139	
16	L	124	
17	M	61	
18	N	86	
19	O	94	
20	P	85	
21	Q	104	
22	R	87	
23	S	87	
24	T	60	
25	a	287	
26	b	287	
27	c	212	
28	d	180	
29	e	184	
30	f	149	
31	g	161	
32	h	137	
33	i	146	

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Mol	Chain	Length	Quality of chain
34	j	122	
35	k	151	
36	l	139	
37	m	124	
38	n	116	
39	o	119	
40	p	127	
41	q	100	
42	r	159	
43	s	237	
44	t	111	
45	u	104	
46	v	65	
47	w	111	
48	x	97	
49	y	57	
50	z	53	
51	3	2907	
52	4	108	
53	5	1520	
54	6	76	
54	7	76	

2 Entry composition

There are 54 unique types of molecules in this entry. The entry contains 149091 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 L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	47	Total	C	N	O	S	0	0
			380	236	81	61	2		

- Molecule 2 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	59	Total	C	N	O	S	0	0
			477	300	99	77	1		

- Molecule 3 is a protein called 50S ribosomal protein L36.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	37	Total	C	N	O	S	0	0
			304	189	65	46	4		

- Molecule 4 is a protein called Elongation factor Tu.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	9	393	Total	C	N	O	S	0	0
			3021	1892	533	583	13		

- Molecule 5 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	A	240	Total	C	N	O	S	0	0
			1921	1226	334	352	9		

- Molecule 6 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	B	215	Total	C	N	O	S	0	0
			1698	1073	313	307	5		

- Molecule 7 is a protein called 30S ribosomal protein S4.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	C	203	Total	C	N	O	S	0	0
			1660	1051	314	290	5		

- Molecule 8 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	D	153	Total	C	N	O	S	0	0
			1173	742	226	202	3		

- Molecule 9 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	E	167	Total	C	N	O	S	0	0
			1362	857	240	263	2		

- Molecule 10 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	F	154	Total	C	N	O	S	0	0
			1246	785	239	216	6		

- Molecule 11 is a protein called 30S ribosomal protein S8.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	G	141	Total	C	N	O	S	0	0
			1110	723	193	192	2		

- Molecule 12 is a protein called 30S ribosomal protein S9.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	H	128	Total	C	N	O	S	0	0
			1028	655	191	181	1		

- Molecule 13 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	I	101	Total	C	N	O	S	0	0
			809	523	142	143	1		

- Molecule 14 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	J	114	Total	C	N	O	S	0	0
			829	514	153	156	6		

- Molecule 15 is a protein called 30S ribosomal protein S12.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	K	136	Total	C	N	O	S	0	0
			1076	680	213	181	2		

- Molecule 16 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	L	118	Total	C	N	O		0	0
			951	594	191	166			

- Molecule 17 is a protein called 30S ribosomal protein S14 type Z.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	M	60	Total	C	N	O	S	0	0
			474	302	96	72	4		

- Molecule 18 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	N	83	Total	C	N	O		0	0
			673	428	125	120			

- Molecule 19 is a protein called 30S ribosomal protein S16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	O	80	Total	C	N	O	S	0	0
			646	414	119	111	2		

- Molecule 20 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	P	83	Total	C	N	O		0	0
			675	425	135	115			

- Molecule 21 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	Q	65	Total	C	N	O	S	0	0
			535	342	103	86	4		

- Molecule 22 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	R	84	Total	C	N	O	S	0	0
			682	435	127	118	2		

- Molecule 23 is a protein called 30S ribosomal protein S20.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	S	77	Total	C	N	O		0	0
			629	383	135	111			

- Molecule 24 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	T	53	Total	C	N	O	S	0	0
			471	295	103	72	1		

- Molecule 25 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	a	285	Total	C	N	O	S	0	0
			2225	1385	437	397	6		

- Molecule 26 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	b	229	Total	C	N	O	S	0	0
			1762	1119	318	318	7		

- Molecule 27 is a protein called 50S ribosomal protein L4.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	c	210	Total	C	N	O	S	0	0
			1644	1047	297	297	3		

- Molecule 28 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	d	175	Total	C	N	O	S	0	0
			1388	893	245	246	4		

- Molecule 29 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	e	176	Total	C	N	O	S	0	0
			1396	899	247	250			

- Molecule 30 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	f	145	Total	C	N	O	S	0	0
			1160	746	204	207	3		

- Molecule 31 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	g	121	Total	C	N	O	S	0	0
			910	580	158	169	3		

- Molecule 32 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	h	128	Total	C	N	O	S	0	0
			959	616	160	177	6		

- Molecule 33 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	i	144	Total	C	N	O	S	0	0
			1164	737	213	209	5		

- Molecule 34 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	j	122	Total	C	N	O	S	0	0
			944	595	178	167	4		

- Molecule 35 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	k	148	Total	C	N	O		
			1153	731	226	196	0	0

- Molecule 36 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	l	136	Total	C	N	O	S		
			1079	694	196	182	7	0	0

- Molecule 37 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	m	119	Total	C	N	O	S		
			958	609	175	171	3	0	0

- Molecule 38 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	n	112	Total	C	N	O	S		
			889	557	175	155	2	0	0

- Molecule 39 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	o	115	Total	C	N	O	S		
			938	592	180	165	1	0	0

- Molecule 40 is a protein called 50S ribosomal protein L20.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	p	114	Total	C	N	O	S		
			947	603	188	154	2	0	0

- Molecule 41 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	q	99	Total	C	N	O	S		
			811	525	148	134	4	0	0

- Molecule 42 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	r	139	Total	C	N	O	S	0	0
			1068	663	207	191	7		

- Molecule 43 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	s	92	Total	C	N	O	S	0	0
			720	475	122	122	1		

- Molecule 44 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	t	111	Total	C	N	O	S	0	0
			872	550	166	153	3		

- Molecule 45 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
45	u	86	Total	C	N	O	S	0	0
			657	409	130	117	1		

- Molecule 46 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
46	v	63	Total	C	N	O	S	0	0
			513	317	108	87	1		

- Molecule 47 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	w	100	Total	C	N	O	S	0	0
			818	517	153	148			

- Molecule 48 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	x	44	Total	C	N	O	S	0	0
			344	221	55	64	4		

- Molecule 49 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	y	56	Total	C	N	O	S	0	0
			452	274	98	75	5		

- Molecule 50 is a protein called 50S ribosomal protein L33 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	z	50	Total	C	N	O	S	0	0
			408	255	81	68	4		

- Molecule 51 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	3	2878	Total	C	N	O	P	0	0
			61664	27558	11236	19995	2875		

- Molecule 52 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	4	105	Total	C	N	O	P	0	0
			2239	1003	409	724	103		

- Molecule 53 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	5	1493	Total	C	N	O	P	0	0
			31943	14279	5792	10382	1490		

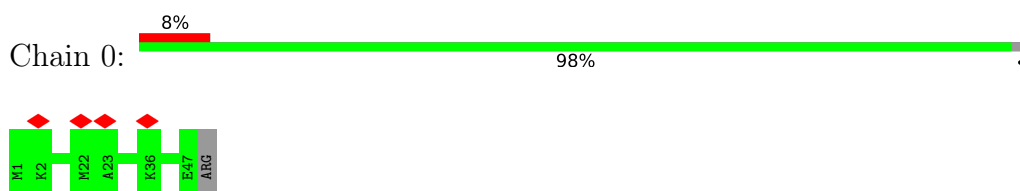
- Molecule 54 is a RNA chain called tRNA-Phe.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	6	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		
54	7	76	Total	C	N	O	P	0	0
			1618	723	289	531	75		

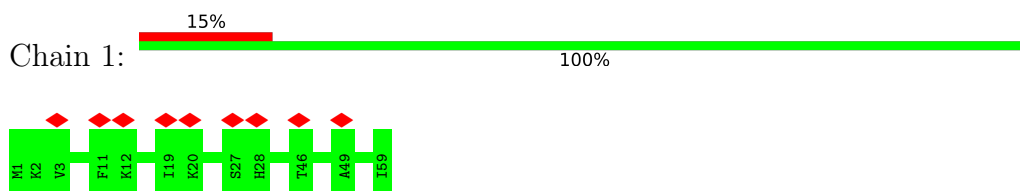
3 Residue-property plots

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.

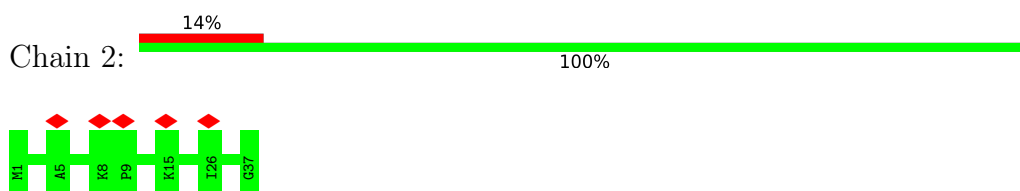
- Molecule 1: 50S ribosomal protein L34



- Molecule 2: 50S ribosomal protein L35

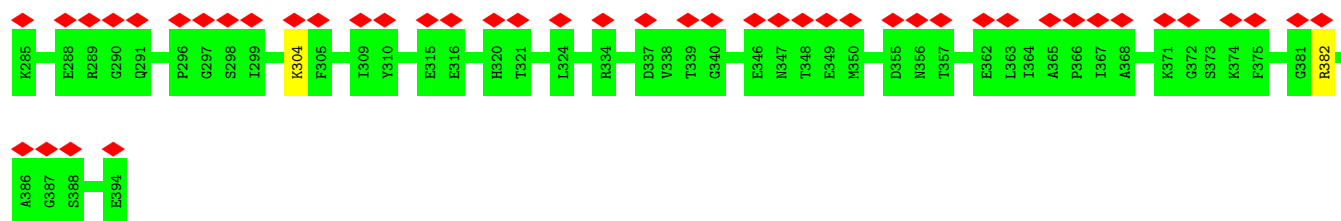


- Molecule 3: 50S ribosomal protein L36

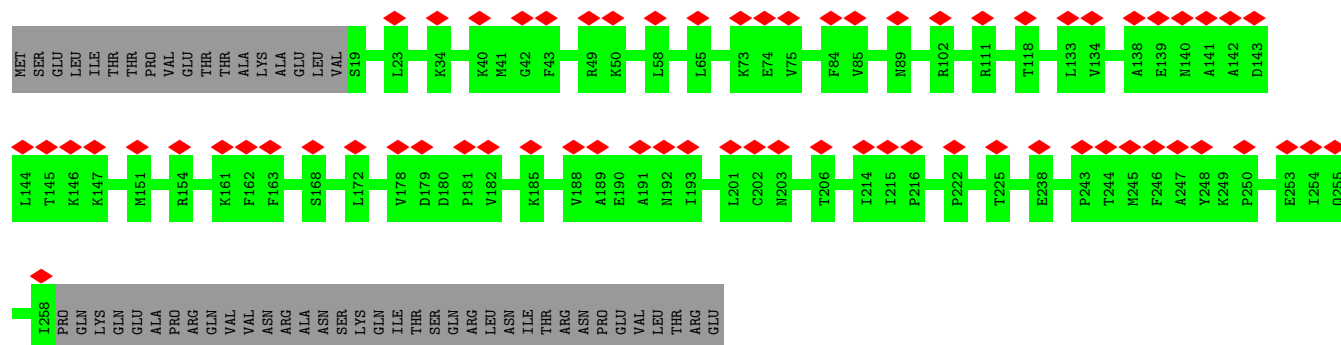
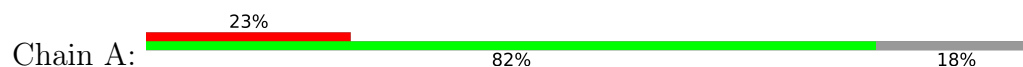


- Molecule 4: Elongation factor Tu

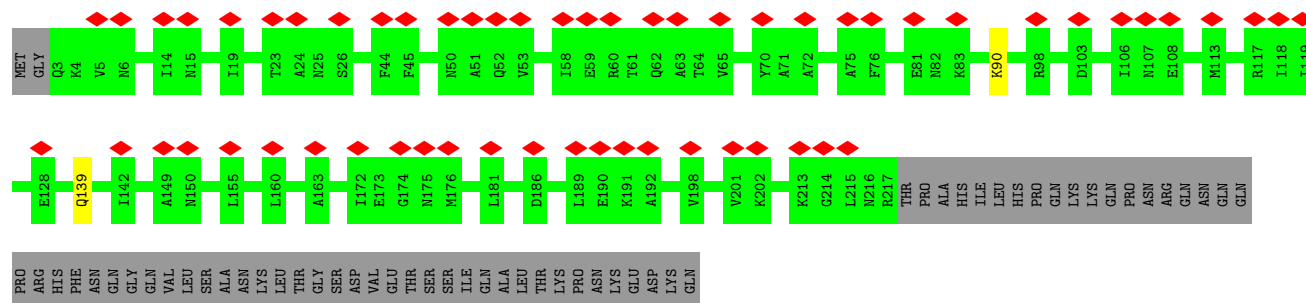
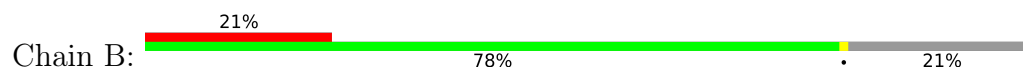




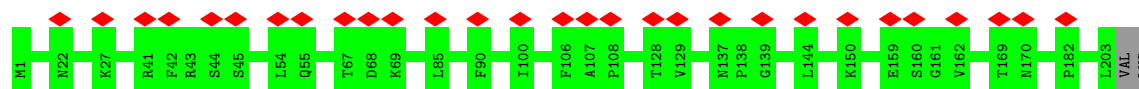
• Molecule 5: 30S ribosomal protein S2



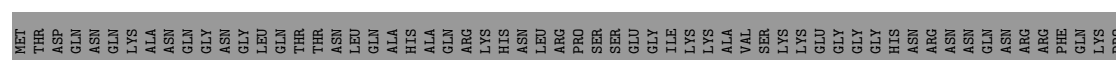
• Molecule 6: 30S ribosomal protein S3

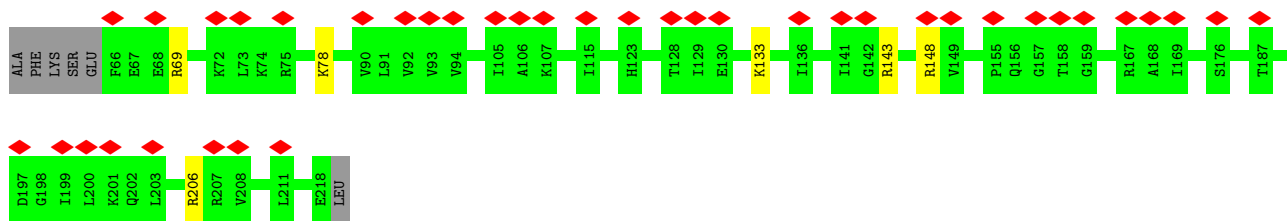


• Molecule 7: 30S ribosomal protein S4

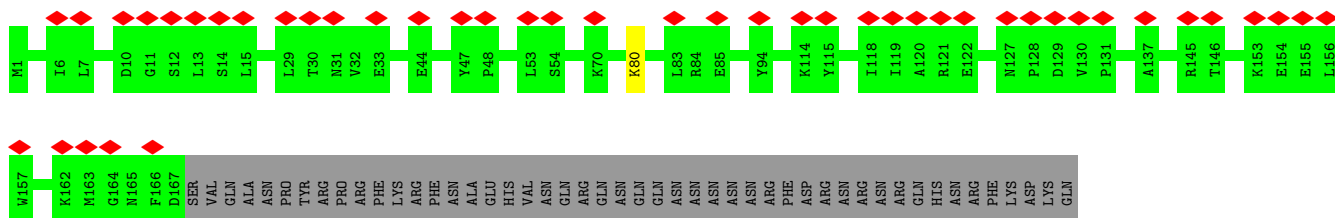
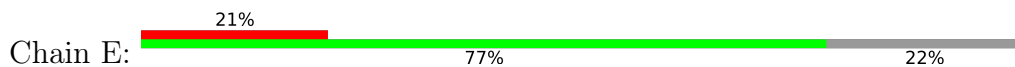


• Molecule 8: 30S ribosomal protein S5

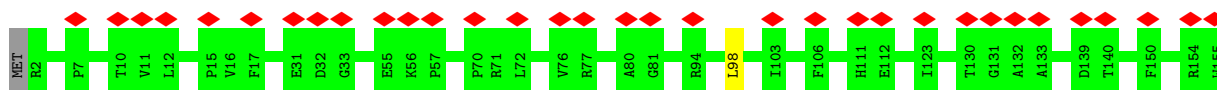




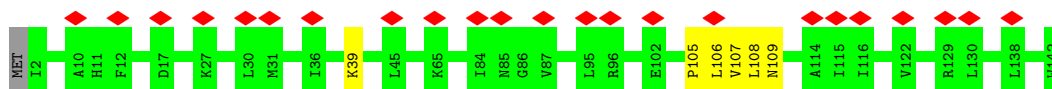
• Molecule 9: 30S ribosomal protein S6



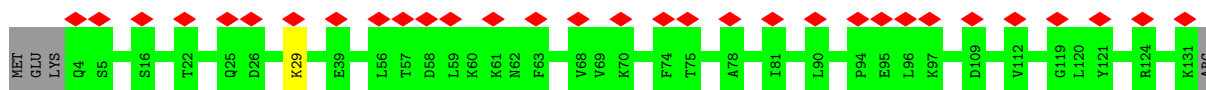
• Molecule 10: 30S ribosomal protein S7



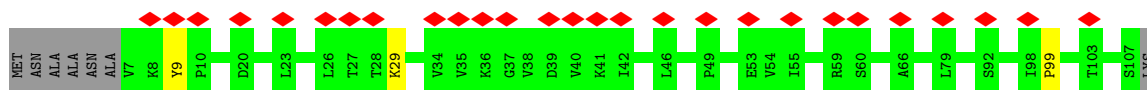
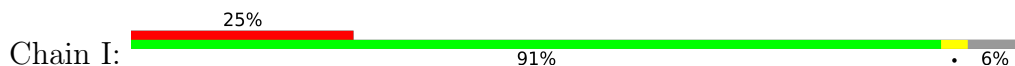
• Molecule 11: 30S ribosomal protein S8



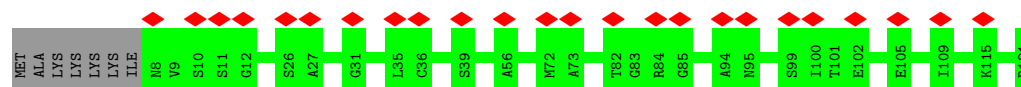
• Molecule 12: 30S ribosomal protein S9



• Molecule 13: 30S ribosomal protein S10



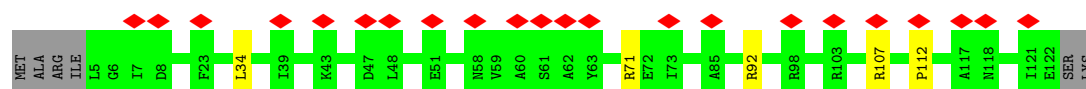
• Molecule 14: 30S ribosomal protein S11



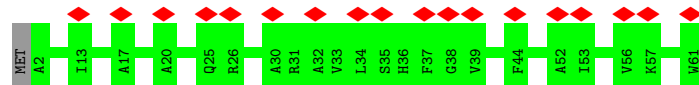
- Molecule 15: 30S ribosomal protein S12



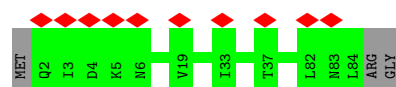
- Molecule 16: 30S ribosomal protein S13



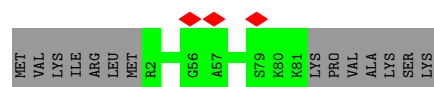
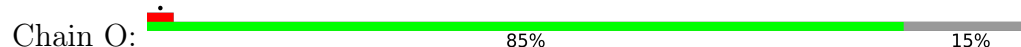
- Molecule 17: 30S ribosomal protein S14 type Z



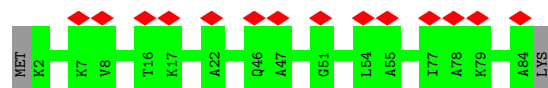
- Molecule 18: 30S ribosomal protein S15



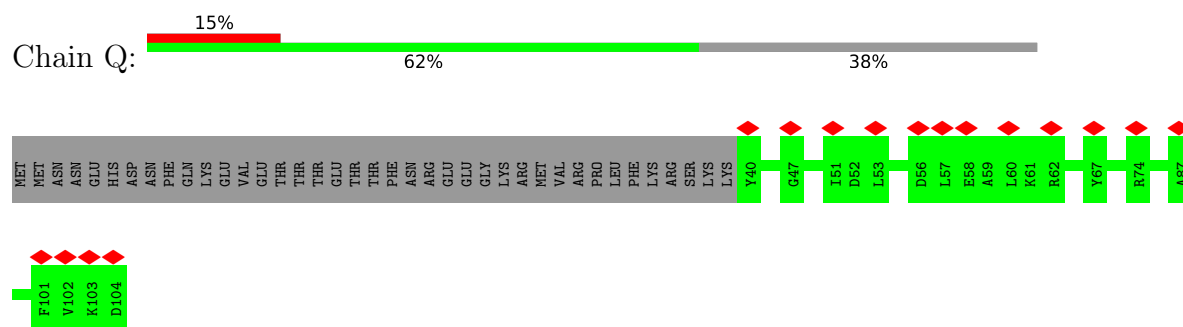
- Molecule 19: 30S ribosomal protein S16



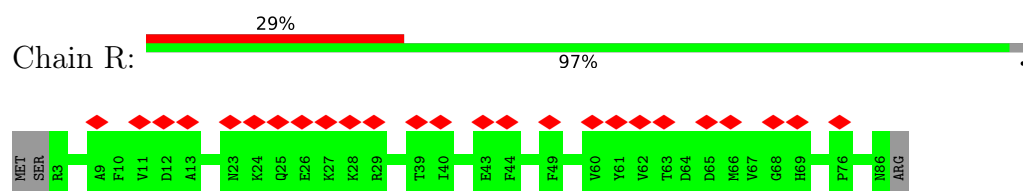
- Molecule 20: 30S ribosomal protein S17



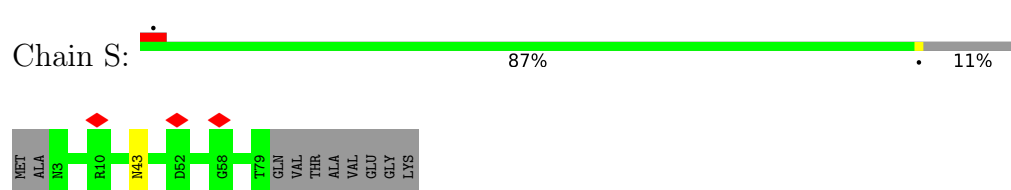
- Molecule 21: 30S ribosomal protein S18



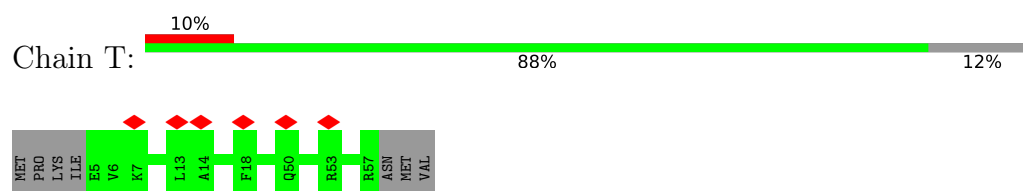
- Molecule 22: 30S ribosomal protein S19



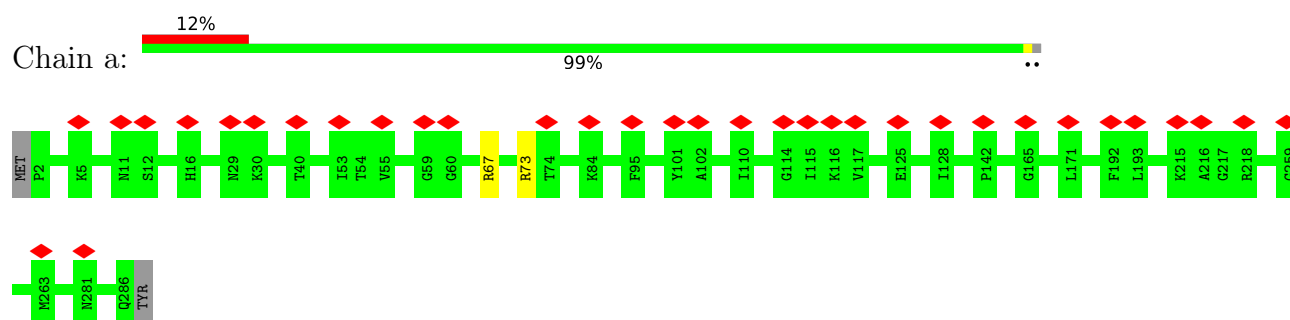
- Molecule 23: 30S ribosomal protein S20



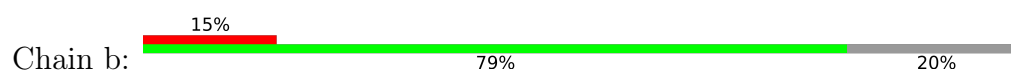
- Molecule 24: 30S ribosomal protein S21

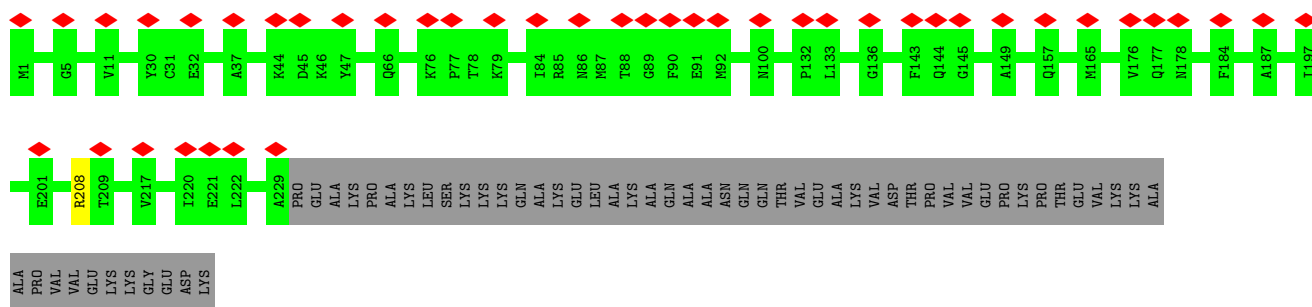


- Molecule 25: 50S ribosomal protein L2

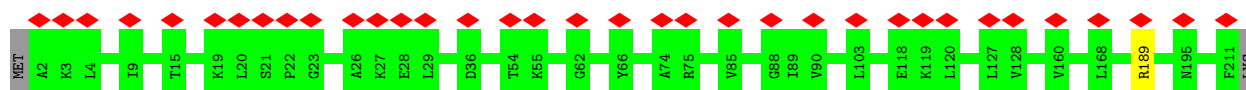


- Molecule 26: 50S ribosomal protein L3

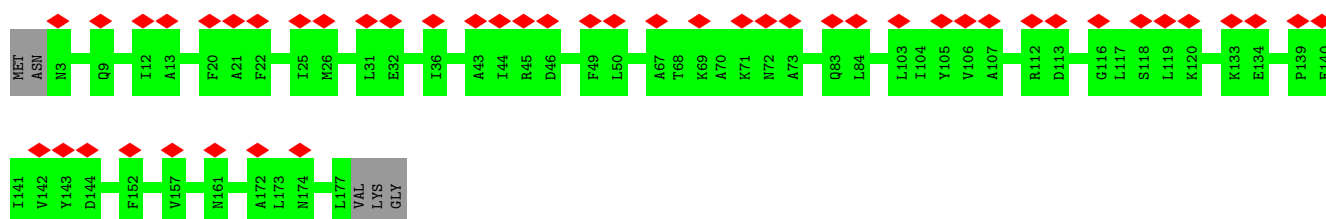




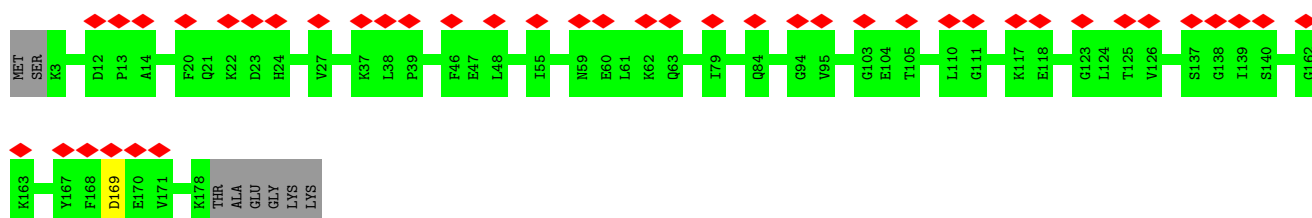
• Molecule 27: 50S ribosomal protein L4



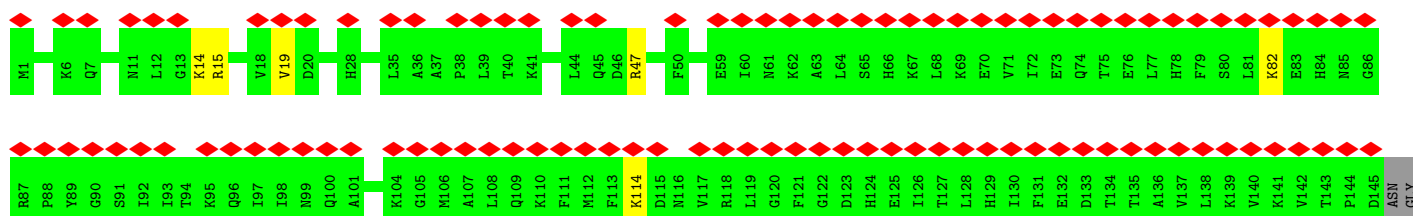
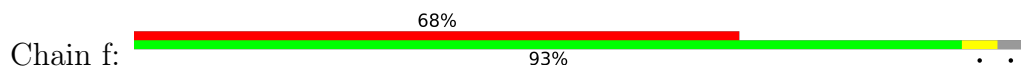
• Molecule 28: 50S ribosomal protein L5



• Molecule 29: 50S ribosomal protein L6



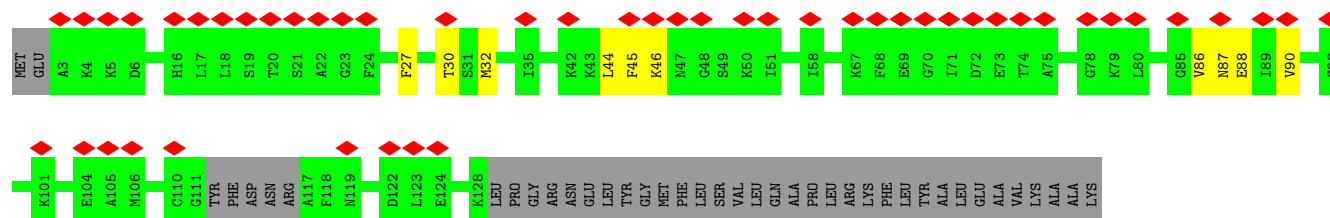
• Molecule 30: 50S ribosomal protein L9




VAL
LYS

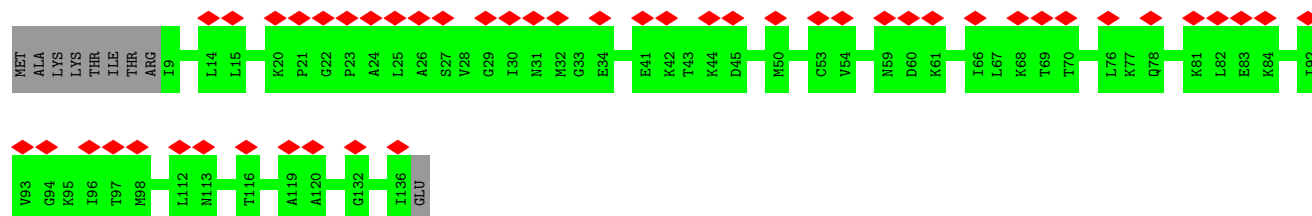
- Molecule 31: 50S ribosomal protein L10

Chain g: 



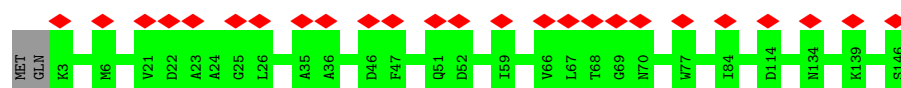
- Molecule 32: 50S ribosomal protein L11

Chain h: 



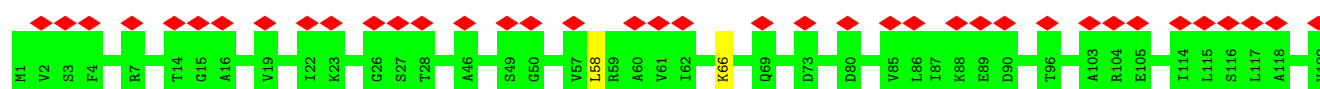
- Molecule 33: 50S ribosomal protein L13

Chain i: 



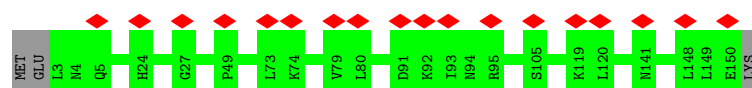
- Molecule 34: 50S ribosomal protein L14

Chain j: 

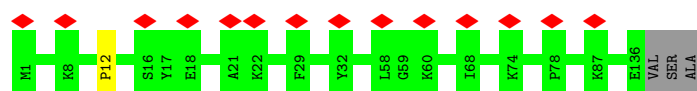


- Molecule 35: 50S ribosomal protein L15

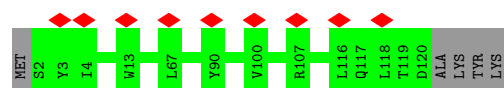
Chain k: 



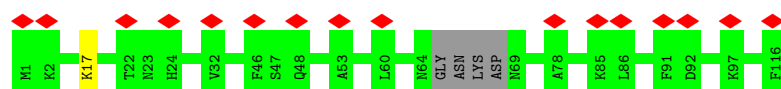
- Molecule 36: 50S ribosomal protein L16



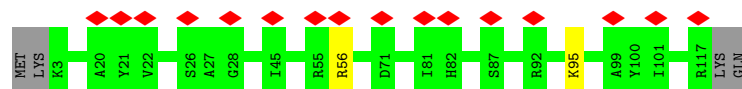
- Molecule 37: 50S ribosomal protein L17



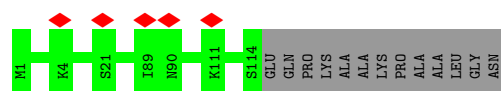
- Molecule 38: 50S ribosomal protein L18



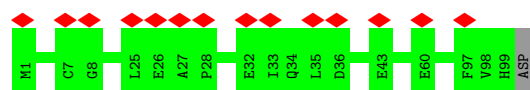
- Molecule 39: 50S ribosomal protein L19



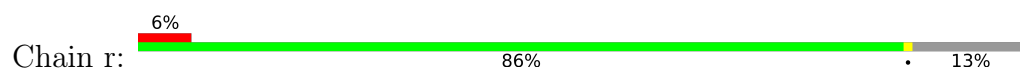
- Molecule 40: 50S ribosomal protein L20



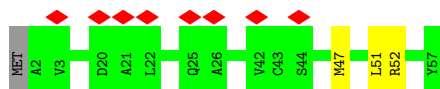
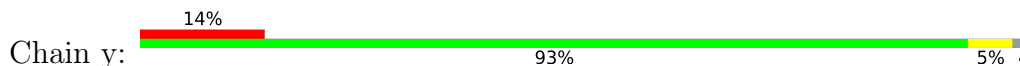
- Molecule 41: 50S ribosomal protein L21



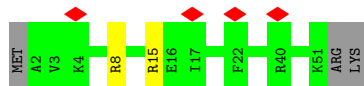
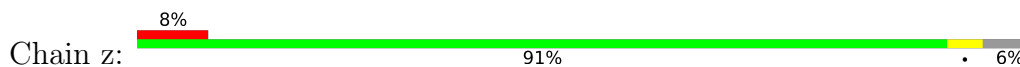
- Molecule 42: 50S ribosomal protein L22



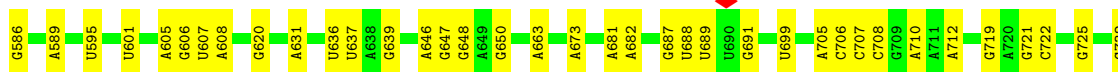
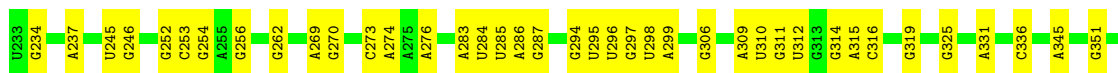
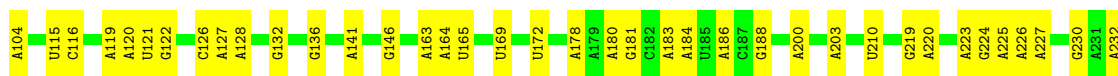
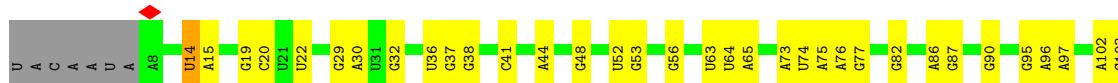
- Molecule 49: 50S ribosomal protein L32



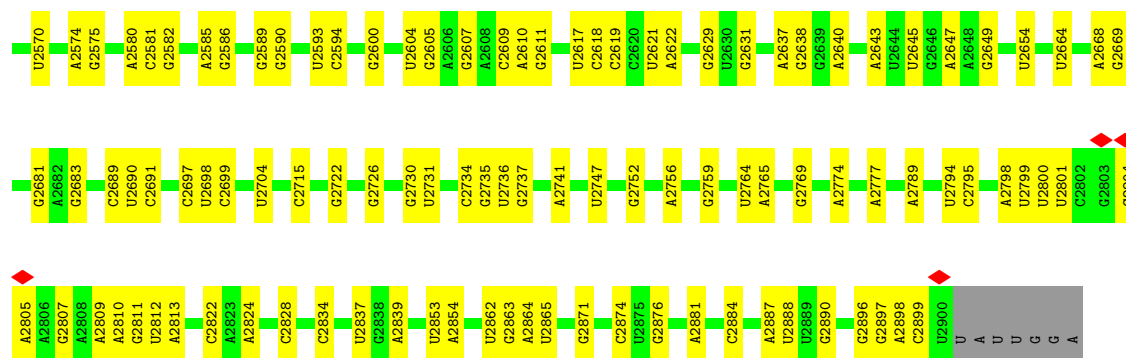
- Molecule 50: 50S ribosomal protein L33 1



- Molecule 51: 23S ribosomal RNA

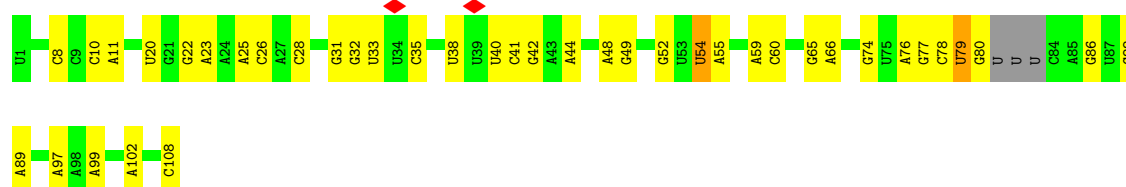


A2442	G2297	U1961	U1828	U1693	A	U1448	U1316	G1903	G1090	A977	U963
A2443	C2305	U1962	A1836	A1694	A1570	U1456	C1317	A1204	G1091	A978	A864
G2444	U2312	C1965	A1839	C1697	G1571	C1456	A1322	A1208	U1095	G982	A865
U2449	U2313	C1970	G1842	A1699	A1577	A1457	C1325	U1209	U1096	G983	G866
G2455	G2315	C1971	C1845	G1701	G1582	G1463	A1328	U1210	C1099	G984	C880
A2456	A2317	A1977	C1850	A1702	G1583	U1466	U1329	C1212	A1102	G989	A881
A2457	U2327	U1978	A1855	C1717	U1584	U1467	U1330	G1215	A1103	U994	C882
A2458	U2327	G1979	A1855	C1718	A1585	U1481	G1331	U1216	A1104	U994	A884
A2459	G2327	G1979	A1855	C1718	U1586	U1482	G1338	G1217	A1105	G997	U886
C2460	G2327	G1979	A1855	C1718	U1587	U1483	U1341	U1218	C1106	C998	A887
U2468	G2333	G1982	A1866	U1727	U1588	G1483	U1341	U1219	C1107	C1001	G895
C2475	U2335	U1998	G1866	U1728	G1594	U1486	G1353	A1225	A1108	A1002	U902
U2484	G2341	G1999	U1871	G1729	G1594	U1487	G1353	U1234	C1111	G1005	A903
U2485	U2342	C2003	A1873	G1733	A1600	A1497	G1356	U1235	G1115	U1006	C904
A2486	U2343	U2009	A1883	A1734	A1603	A1502	U1357	A1250	C1007	C1007	U905
U2487	U2351	G2010	C1886	G1736	G1607	A1506	U1360	G1251	A1123	A1008	G906
G2492	U2352	G2011	U1890	G1747	U1612	U1507	U1368	G1252	G1124	A1009	G914
A2495	C2355	A2020	A1891	U1748	G1615	G1508	A1370	G1257	A1130	A1016	G917
G2498	U2358	G2027	A1892	U1748	G1616	U1509	G1371	G1265	A1131	A1019	C921
U2499	U2362	C2028	C1893	A1751	U1617	A1510	U1374	G1266	C1132	A1026	C922
G2502	U2362	U2029	C1902	U1764	A1619	A1513	G1375	G1267	U1141	U1027	A
C2503	U2365	A2037	A1903	G1765	A1630	U1514	G1376	U1268	G1145	C1028	C
A2505	A2366	A2038	G1906	G1766	A1631	U1515	A1377	U1268	A1146	A1029	U
C2506	C2367	G2039	A1907	A1767	C1632	C1518	G1378	A1274	G1147	U1035	A
C2507	U2380	A2040	G1913	A1769	A1633	A1519	U1380	A1277	U1151	C1041	G928
G2510	U2387	C2041	C1916	C1771	A1641	C1523	A1387	G1278	U1154	C1044	G929
G2513	U2391	C2042	C1916	G1772	G1642	G1528	G1388	U1279	U1154	A1045	C930
U2514	U2392	C2043	A1920	A1780	A1643	A1534	A1393	G1280	A1045	A1046	G931
A2521	C2393	C2044	A1921	U1784	C1645	A1537	A1406	G1281	A1047	A1047	U932
C2525	A2396	C2045	A1934	C1788	A1651	A1541	U1407	G1282	A1048	A1048	A933
A2527	G2397	A2055	A1934	C1789	C1653	U1546	G1408	U1285	A1166	U1049	U935
C2528	U2414	A2056	A1938	A1792	A1661	U1546	A1412	G1286	C1170	A1052	G936
A2538	A2415	C2062	A1943	G1806	A1669	G1550	A1420	A1292	U1176	A1055	A940
A2539	G2422	G2063	A1944	C1807	A1669	G1550	A1421	U1297	A1177	A1061	U944
U2431	U2431	G2064	A1945	A1809	G1681	U1559	U1422	A1298	A1178	A1062	A947
C2432	C2432	U2067	A1945	C1808	C1682	U	U1423	C1300	C1187	U1068	A948
A2433	A2433	G2068	A1950	A1809	G1683	G	U1425	G1301	C1188	G1075	C949
A2434	A2434	C2070	U1950	C1813	A1684	A	A1431	C1302	G1189	G1075	U952
C2435	C2435	C2071	A1951	C1813	G1685	G	U1431	U1303	A1190	A1080	G953
G2436	U2291	C2071	G1952	A1816	U1686	U	U1434	U1304	A1191	A1081	A964
U2437	A2294	G2076	U1953	A1817	G1687	G	U1444	G1305	U1192	A1082	U968
A2438	A2295	G2077	G1955	A1817	A1688	A	C1444	A1314	U1193	A1089	A969
C2439	A2296	A2078	G1955	U1823	A1692	C	U1445	A1315	A1202	A1089	U970
G2173	G2173	G2173	G2173	G2173	G2173	G2173	G2173	G2173	G2173	G2173	G2173



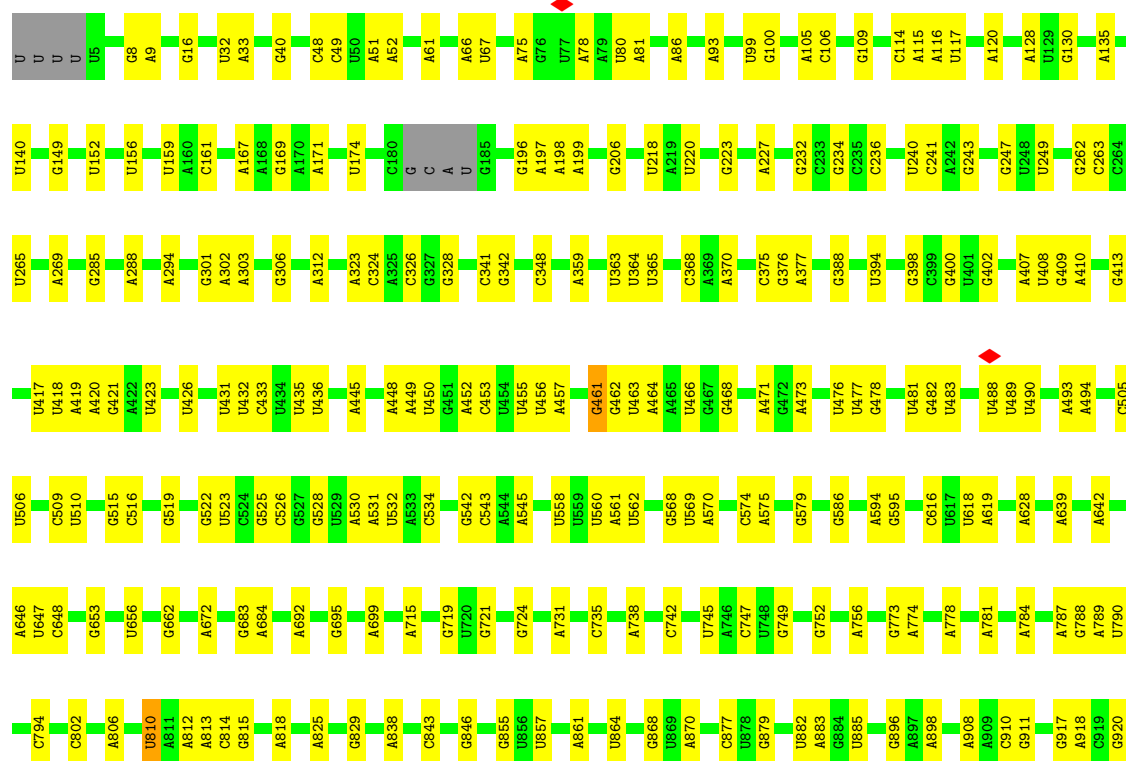
• Molecule 52: 5S ribosomal RNA

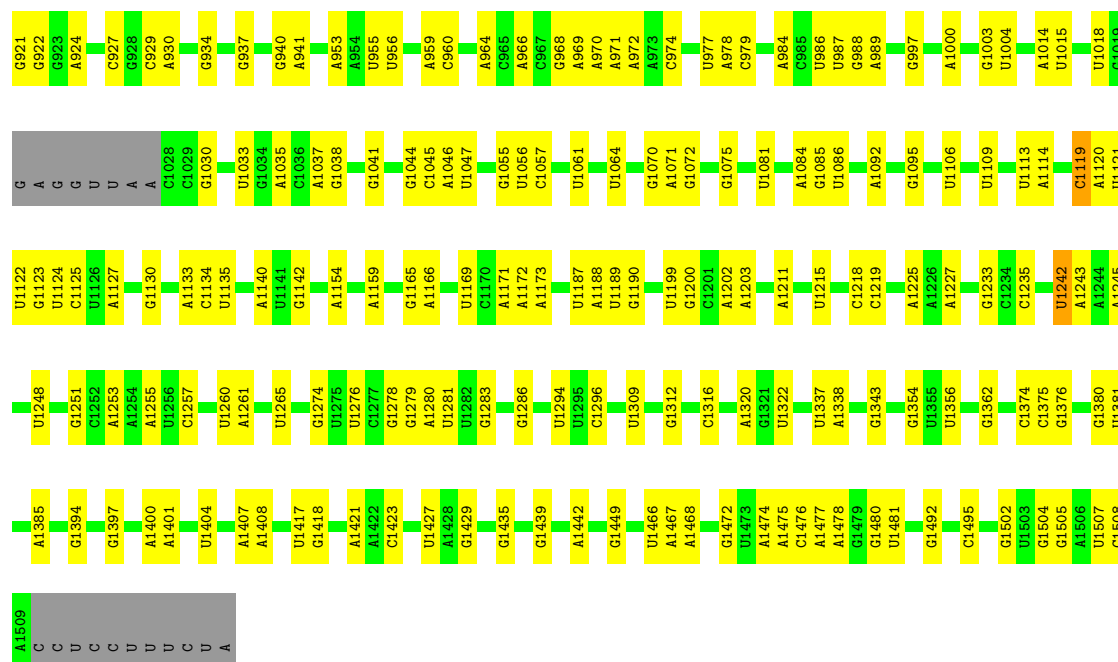
Chain 4: 60% 35%



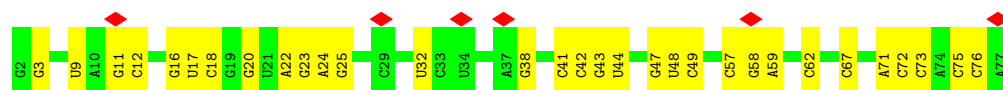
• Molecule 53: 16S ribosomal RNA

Chain 5: 71% 27%





• Molecule 54: tRNA-Phe



• Molecule 54: tRNA-Phe



4 Experimental information

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of subtomograms used	1128	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	3.2	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3750	Depositor
Magnification	81000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	1.595	Depositor
Minimum map value	-0.633	Depositor
Average map value	0.020	Depositor
Map value standard deviation	0.113	Depositor
Recommended contour level	0.39	Depositor
Map size (Å)	435.328, 435.328, 435.328	wwPDB
Map dimensions	256, 256, 256	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.7005, 1.7005, 1.7005	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	0	0.24	0/383	0.51	0/504
2	1	0.23	0/484	0.46	0/637
3	2	0.22	0/306	0.48	0/401
4	9	0.25	0/3071	0.49	0/4147
5	A	0.25	0/1954	0.48	0/2642
6	B	0.25	0/1721	0.50	0/2323
7	C	0.26	0/1691	0.47	0/2267
8	D	0.25	0/1188	0.52	0/1593
9	E	0.26	0/1384	0.51	0/1867
10	F	0.26	0/1266	0.51	1/1700 (0.1%)
11	G	0.28	0/1126	0.58	0/1517
12	H	0.25	0/1044	0.46	0/1395
13	I	0.31	0/820	0.65	2/1103 (0.2%)
14	J	0.26	0/844	0.49	0/1136
15	K	0.28	0/1094	0.56	0/1468
16	L	0.27	0/962	0.54	1/1289 (0.1%)
17	M	0.24	0/483	0.47	0/643
18	N	0.26	0/679	0.47	0/907
19	O	0.26	0/659	0.53	0/885
20	P	0.24	0/684	0.46	0/913
21	Q	0.25	0/545	0.52	0/730
22	R	0.25	0/698	0.54	0/936
23	S	0.23	0/631	0.37	0/838
24	T	0.29	0/475	0.60	0/621
25	a	0.23	0/2267	0.46	0/3044
26	b	0.29	0/1795	0.55	0/2412
27	c	0.25	0/1671	0.50	0/2246
28	d	0.28	0/1409	0.52	0/1894
29	e	0.28	0/1420	0.55	0/1912
30	f	0.26	0/1183	0.56	0/1587
31	g	0.36	0/916	0.57	0/1222
32	h	0.27	0/968	0.50	0/1298
33	i	0.25	0/1186	0.50	0/1592
34	j	0.24	0/953	0.54	1/1275 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	k	0.25	0/1170	0.49	0/1559
36	l	0.27	0/1104	0.52	0/1481
37	m	0.24	0/973	0.52	0/1309
38	n	0.26	0/897	0.49	0/1198
39	o	0.24	0/948	0.49	0/1262
40	p	0.24	0/961	0.44	0/1278
41	q	0.26	0/828	0.56	0/1111
42	r	0.24	0/1077	0.48	0/1441
43	s	0.26	0/732	0.51	0/988
44	t	0.25	0/879	0.52	0/1165
45	u	0.25	0/665	0.52	0/884
46	v	0.30	0/519	0.56	0/695
47	w	0.24	0/826	0.49	0/1104
48	x	0.38	0/353	0.51	0/474
49	y	0.31	0/457	0.52	0/601
50	z	0.25	0/412	0.53	0/547
51	3	0.21	0/69073	0.81	31/107710 (0.0%)
52	4	0.24	0/2505	0.87	4/3902 (0.1%)
53	5	0.20	0/35768	0.79	15/55764 (0.0%)
54	6	0.23	0/1808	0.88	0/2817
54	7	0.23	0/1808	0.88	0/2817
All	All	0.22	0/161723	0.74	55/241051 (0.0%)

There are no bond length outliers.

All (55) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	I	99	PRO	CA-N-CD	-8.78	99.21	111.50
53	5	843	C	N3-C2-O2	-8.42	116.01	121.90
51	3	559	C	N3-C2-O2	-7.66	116.54	121.90
52	4	79	U	C2-N1-C1'	7.49	126.69	117.70
51	3	1916	C	N3-C2-O2	-7.18	116.87	121.90
52	4	79	U	N1-C2-O2	7.01	127.71	122.80
51	3	1718	C	N3-C2-O2	-6.83	117.12	121.90
51	3	1697	C	N3-C2-O2	-6.75	117.17	121.90
51	3	1341	U	C2-N1-C1'	6.66	125.69	117.70
51	3	708	C	N3-C2-O2	-6.64	117.25	121.90
52	4	79	U	N3-C2-O2	-6.61	117.57	122.20
34	j	58	LEU	CA-CB-CG	6.57	130.41	115.30
53	5	810	U	N1-C2-O2	6.50	127.35	122.80
51	3	1341	U	N1-C2-O2	6.47	127.33	122.80
53	5	648	C	N1-C2-O2	6.44	122.76	118.90

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
53	5	648	C	N3-C2-O2	-6.27	117.51	121.90
53	5	810	U	N3-C2-O2	-6.20	117.86	122.20
53	5	463	U	C2-N1-C1'	6.10	125.02	117.70
53	5	1219	C	N3-C2-O2	-6.09	117.64	121.90
51	3	2070	C	C2-N1-C1'	5.99	125.38	118.80
51	3	426	U	C2-N1-C1'	5.95	124.83	117.70
51	3	1341	U	N3-C2-O2	-5.93	118.05	122.20
53	5	810	U	C2-N1-C1'	5.87	124.74	117.70
51	3	1902	C	N3-C2-O2	-5.85	117.81	121.90
51	3	1507	G	O4'-C1'-N9	5.84	112.87	108.20
53	5	974	C	N1-C2-O2	5.83	122.40	118.90
51	3	1717	C	N1-C2-O2	5.79	122.38	118.90
53	5	1242	U	O4'-C1'-N1	5.76	112.80	108.20
53	5	461	G	O4'-C1'-N9	5.65	112.72	108.20
51	3	708	C	C6-N1-C2	-5.57	118.07	120.30
51	3	707	C	N1-C2-O2	5.54	122.22	118.90
53	5	1119	C	N1-C2-O2	5.52	122.21	118.90
51	3	904	C	C2-N1-C1'	5.49	124.83	118.80
51	3	2070	C	N1-C2-O2	5.37	122.12	118.90
51	3	739	G	O4'-C1'-N9	5.25	112.40	108.20
16	L	34	LEU	CA-CB-CG	5.25	127.37	115.30
53	5	974	C	C2-N1-C1'	5.24	124.56	118.80
53	5	463	U	N1-C2-O2	5.21	126.44	122.80
51	3	1507	G	C8-N9-C1'	5.19	133.75	127.00
51	3	1316	U	N1-C2-O2	5.19	126.43	122.80
51	3	1507	G	C4-N9-C1'	-5.18	119.77	126.50
51	3	1893	C	N1-C2-O2	5.17	122.00	118.90
13	I	99	PRO	N-CD-CG	-5.13	95.50	103.20
51	3	440	C	C2-N1-C1'	5.10	124.41	118.80
51	3	2199	C	N3-C2-O2	-5.09	118.34	121.90
10	F	98	LEU	CA-CB-CG	5.08	126.97	115.30
51	3	2691	C	N1-C2-O2	5.07	121.94	118.90
51	3	2874	C	N3-C2-O2	-5.06	118.36	121.90
51	3	1316	U	C2-N1-C1'	5.05	123.76	117.70
51	3	19	G	C5-C6-O6	5.05	131.63	128.60
51	3	14	U	C2-N1-C1'	5.04	123.75	117.70
52	4	54	U	P-O3'-C3'	5.02	125.72	119.70
53	5	843	C	N1-C2-O2	5.01	121.91	118.90
51	3	394	C	N3-C2-O2	-5.01	118.39	121.90
51	3	881	A	P-O3'-C3'	5.01	125.71	119.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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

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	0	45/48 (94%)	43 (96%)	2 (4%)	0	100	100
2	1	57/59 (97%)	53 (93%)	4 (7%)	0	100	100
3	2	35/37 (95%)	31 (89%)	4 (11%)	0	100	100
4	9	391/394 (99%)	360 (92%)	31 (8%)	0	100	100
5	A	238/294 (81%)	212 (89%)	26 (11%)	0	100	100
6	B	213/273 (78%)	200 (94%)	13 (6%)	0	100	100
7	C	201/205 (98%)	191 (95%)	10 (5%)	0	100	100
8	D	151/219 (69%)	143 (95%)	8 (5%)	0	100	100
9	E	165/215 (77%)	143 (87%)	22 (13%)	0	100	100
10	F	152/155 (98%)	137 (90%)	15 (10%)	0	100	100
11	G	139/142 (98%)	123 (88%)	15 (11%)	1 (1%)	19	57
12	H	126/132 (96%)	121 (96%)	5 (4%)	0	100	100
13	I	99/108 (92%)	84 (85%)	15 (15%)	0	100	100
14	J	112/121 (93%)	106 (95%)	6 (5%)	0	100	100
15	K	134/139 (96%)	117 (87%)	17 (13%)	0	100	100
16	L	116/124 (94%)	104 (90%)	11 (10%)	1 (1%)	14	52
17	M	58/61 (95%)	55 (95%)	3 (5%)	0	100	100
18	N	81/86 (94%)	80 (99%)	1 (1%)	0	100	100
19	O	78/94 (83%)	70 (90%)	8 (10%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
20	P	81/85 (95%)	79 (98%)	2 (2%)	0	100	100
21	Q	63/104 (61%)	54 (86%)	9 (14%)	0	100	100
22	R	82/87 (94%)	72 (88%)	10 (12%)	0	100	100
23	S	75/87 (86%)	75 (100%)	0	0	100	100
24	T	51/60 (85%)	49 (96%)	2 (4%)	0	100	100
25	a	283/287 (99%)	261 (92%)	22 (8%)	0	100	100
26	b	227/287 (79%)	209 (92%)	18 (8%)	0	100	100
27	c	208/212 (98%)	196 (94%)	12 (6%)	0	100	100
28	d	173/180 (96%)	160 (92%)	13 (8%)	0	100	100
29	e	174/184 (95%)	165 (95%)	8 (5%)	1 (1%)	22	60
30	f	143/149 (96%)	128 (90%)	14 (10%)	1 (1%)	19	57
31	g	117/161 (73%)	107 (92%)	7 (6%)	3 (3%)	4	26
32	h	126/137 (92%)	115 (91%)	11 (9%)	0	100	100
33	i	142/146 (97%)	128 (90%)	14 (10%)	0	100	100
34	j	120/122 (98%)	114 (95%)	6 (5%)	0	100	100
35	k	146/151 (97%)	137 (94%)	9 (6%)	0	100	100
36	l	134/139 (96%)	125 (93%)	8 (6%)	1 (1%)	19	57
37	m	117/124 (94%)	114 (97%)	3 (3%)	0	100	100
38	n	108/116 (93%)	98 (91%)	10 (9%)	0	100	100
39	o	113/119 (95%)	102 (90%)	11 (10%)	0	100	100
40	p	112/127 (88%)	109 (97%)	3 (3%)	0	100	100
41	q	97/100 (97%)	85 (88%)	12 (12%)	0	100	100
42	r	137/159 (86%)	124 (90%)	13 (10%)	0	100	100
43	s	90/237 (38%)	86 (96%)	4 (4%)	0	100	100
44	t	109/111 (98%)	101 (93%)	8 (7%)	0	100	100
45	u	84/104 (81%)	81 (96%)	3 (4%)	0	100	100
46	v	61/65 (94%)	61 (100%)	0	0	100	100
47	w	96/111 (86%)	91 (95%)	5 (5%)	0	100	100
48	x	42/97 (43%)	35 (83%)	7 (17%)	0	100	100
49	y	54/57 (95%)	51 (94%)	3 (6%)	0	100	100
50	z	48/53 (91%)	47 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	6204/7064 (88%)	5732 (92%)	464 (8%)	8 (0%)	50 83

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
31	g	88	GLU
29	e	169	ASP
31	g	32	MET
31	g	30	THR
11	G	105	PRO
16	L	112	PRO
36	l	12	PRO
30	f	19	VAL

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	0	40/41 (98%)	40 (100%)	0	100	100
2	1	51/51 (100%)	51 (100%)	0	100	100
3	2	35/35 (100%)	35 (100%)	0	100	100
4	9	324/325 (100%)	322 (99%)	2 (1%)	84	88
5	A	212/262 (81%)	212 (100%)	0	100	100
6	B	180/232 (78%)	178 (99%)	2 (1%)	70	80
7	C	181/183 (99%)	181 (100%)	0	100	100
8	D	123/178 (69%)	117 (95%)	6 (5%)	21	42
9	E	150/196 (76%)	149 (99%)	1 (1%)	81	87
10	F	131/132 (99%)	131 (100%)	0	100	100
11	G	123/124 (99%)	118 (96%)	5 (4%)	26	47
12	H	111/115 (96%)	110 (99%)	1 (1%)	75	83
13	I	95/99 (96%)	93 (98%)	2 (2%)	48	66

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	J	91/97 (94%)	91 (100%)	0	100	100
15	K	117/120 (98%)	111 (95%)	6 (5%)	20	41
16	L	100/105 (95%)	97 (97%)	3 (3%)	36	55
17	M	47/48 (98%)	47 (100%)	0	100	100
18	N	76/78 (97%)	76 (100%)	0	100	100
19	O	69/82 (84%)	69 (100%)	0	100	100
20	P	73/75 (97%)	73 (100%)	0	100	100
21	Q	56/94 (60%)	56 (100%)	0	100	100
22	R	74/77 (96%)	74 (100%)	0	100	100
23	S	70/77 (91%)	69 (99%)	1 (1%)	62	75
24	T	49/56 (88%)	49 (100%)	0	100	100
25	a	241/243 (99%)	239 (99%)	2 (1%)	79	85
26	b	186/233 (80%)	185 (100%)	1 (0%)	86	89
27	c	182/184 (99%)	181 (100%)	1 (0%)	86	89
28	d	150/154 (97%)	150 (100%)	0	100	100
29	e	153/159 (96%)	153 (100%)	0	100	100
30	f	123/134 (92%)	118 (96%)	5 (4%)	26	47
31	g	96/129 (74%)	89 (93%)	7 (7%)	11	31
32	h	102/110 (93%)	102 (100%)	0	100	100
33	i	126/128 (98%)	126 (100%)	0	100	100
34	j	103/103 (100%)	102 (99%)	1 (1%)	73	82
35	k	123/126 (98%)	123 (100%)	0	100	100
36	l	113/115 (98%)	113 (100%)	0	100	100
37	m	105/109 (96%)	105 (100%)	0	100	100
38	n	96/99 (97%)	95 (99%)	1 (1%)	73	82
39	o	101/105 (96%)	99 (98%)	2 (2%)	50	68
40	p	100/108 (93%)	100 (100%)	0	100	100
41	q	90/91 (99%)	90 (100%)	0	100	100
42	r	116/132 (88%)	114 (98%)	2 (2%)	56	72
43	s	82/208 (39%)	81 (99%)	1 (1%)	67	78
44	t	96/96 (100%)	95 (99%)	1 (1%)	73	82

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	u	69/85 (81%)	68 (99%)	1 (1%)	62	75
46	v	58/60 (97%)	58 (100%)	0	100	100
47	w	87/98 (89%)	87 (100%)	0	100	100
48	x	41/86 (48%)	39 (95%)	2 (5%)	21	42
49	y	48/49 (98%)	45 (94%)	3 (6%)	15	36
50	z	47/50 (94%)	45 (96%)	2 (4%)	25	46
All	All	5412/6076 (89%)	5351 (99%)	61 (1%)	69	80

All (61) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
4	9	304	LYS
4	9	382	ARG
6	B	90	LYS
6	B	139	GLN
8	D	69	ARG
8	D	78	LYS
8	D	133	LYS
8	D	143	ARG
8	D	148	ARG
8	D	206	ARG
9	E	80	LYS
11	G	39	LYS
11	G	106	LEU
11	G	107	VAL
11	G	108	LEU
11	G	109	ASN
12	H	29	LYS
13	I	9	TYR
13	I	29	LYS
15	K	44	ARG
15	K	96	ARG
15	K	107	ARG
15	K	118	VAL
15	K	120	VAL
15	K	127	ARG
16	L	71	ARG
16	L	92	ARG
16	L	107	ARG
23	S	43	ASN

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Mol	Chain	Res	Type
25	a	67	ARG
25	a	73	ARG
26	b	208	ARG
27	c	189	ARG
30	f	14	LYS
30	f	15	ARG
30	f	47	ARG
30	f	82	LYS
30	f	114	LYS
31	g	27	PHE
31	g	44	LEU
31	g	45	PHE
31	g	46	LYS
31	g	86	VAL
31	g	87	ASN
31	g	90	VAL
34	j	66	LYS
38	n	17	LYS
39	o	56	ARG
39	o	95	LYS
42	r	9	ARG
42	r	128	ARG
43	s	5	ASN
44	t	96	LYS
45	u	18	LYS
48	x	30	LYS
48	x	41	LYS
49	y	47	MET
49	y	51	LEU
49	y	52	ARG
50	z	8	ARG
50	z	15	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
3	2	30	GLN
4	9	12	HIS
4	9	194	ASN
4	9	302	HIS
5	A	51	HIS
7	C	52	GLN

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Mol	Chain	Res	Type
7	C	81	GLN
11	G	58	GLN
15	K	25	HIS
15	K	125	GLN
18	N	2	GLN
18	N	35	GLN
20	P	5	GLN
20	P	42	HIS
22	R	53	ASN
23	S	63	ASN
26	b	171	HIS
27	c	50	HIS
27	c	81	ASN
29	e	77	ASN
30	f	124	HIS
33	i	126	HIS
34	j	56	GLN
35	k	39	GLN
35	k	83	ASN
36	l	13	HIS
36	l	108	ASN
42	r	7	GLN
42	r	38	ASN
44	t	17	ASN
47	w	64	ASN
50	z	28	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
51	3	2875/2907 (98%)	849 (29%)	29 (1%)
52	4	103/108 (95%)	38 (36%)	3 (2%)
53	5	1490/1520 (98%)	411 (27%)	7 (0%)
54	6	75/76 (98%)	30 (40%)	2 (2%)
54	7	75/76 (98%)	30 (40%)	2 (2%)
All	All	4618/4687 (98%)	1358 (29%)	43 (0%)

All (1358) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
51	3	14	U

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Mol	Chain	Res	Type
51	3	15	A
51	3	20	C
51	3	22	U
51	3	29	G
51	3	30	A
51	3	32	G
51	3	36	U
51	3	37	G
51	3	38	G
51	3	41	C
51	3	44	A
51	3	48	G
51	3	52	U
51	3	53	G
51	3	56	G
51	3	63	U
51	3	64	U
51	3	65	A
51	3	73	A
51	3	74	U
51	3	75	A
51	3	76	A
51	3	77	G
51	3	82	G
51	3	86	A
51	3	87	G
51	3	90	G
51	3	95	G
51	3	96	A
51	3	97	A
51	3	102	A
51	3	103	G
51	3	104	A
51	3	115	U
51	3	116	C
51	3	119	A
51	3	120	A
51	3	121	U
51	3	122	G
51	3	126	C
51	3	127	A
51	3	128	A

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Mol	Chain	Res	Type
51	3	132	G
51	3	136	G
51	3	141	A
51	3	146	G
51	3	163	A
51	3	164	A
51	3	165	U
51	3	169	U
51	3	172	U
51	3	178	A
51	3	180	A
51	3	181	G
51	3	183	A
51	3	184	A
51	3	186	A
51	3	188	G
51	3	200	A
51	3	203	A
51	3	210	U
51	3	219	G
51	3	220	A
51	3	223	A
51	3	224	G
51	3	225	A
51	3	226	A
51	3	227	A
51	3	230	G
51	3	232	A
51	3	234	G
51	3	237	A
51	3	245	U
51	3	246	G
51	3	252	G
51	3	253	C
51	3	254	G
51	3	256	G
51	3	262	G
51	3	269	A
51	3	270	G
51	3	273	C
51	3	274	A
51	3	276	A

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Mol	Chain	Res	Type
51	3	283	A
51	3	284	U
51	3	285	U
51	3	286	A
51	3	287	G
51	3	294	G
51	3	295	U
51	3	296	U
51	3	297	G
51	3	298	U
51	3	299	A
51	3	306	G
51	3	310	U
51	3	312	U
51	3	314	G
51	3	315	A
51	3	316	C
51	3	319	G
51	3	325	G
51	3	331	A
51	3	336	C
51	3	345	A
51	3	351	G
51	3	355	A
51	3	356	A
51	3	357	A
51	3	363	G
51	3	364	A
51	3	369	C
51	3	374	A
51	3	396	A
51	3	397	G
51	3	399	G
51	3	400	A
51	3	401	G
51	3	402	A
51	3	403	U
51	3	404	C
51	3	408	G
51	3	409	A
51	3	410	G
51	3	411	U

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Mol	Chain	Res	Type
51	3	417	G
51	3	422	A
51	3	424	G
51	3	425	U
51	3	426	U
51	3	428	U
51	3	432	G
51	3	434	G
51	3	437	A
51	3	441	U
51	3	442	G
51	3	447	G
51	3	448	A
51	3	460	G
51	3	464	A
51	3	465	A
51	3	466	A
51	3	471	A
51	3	482	G
51	3	483	A
51	3	484	U
51	3	485	A
51	3	487	C
51	3	490	A
51	3	491	A
51	3	494	G
51	3	495	U
51	3	500	U
51	3	501	G
51	3	502	A
51	3	507	A
51	3	509	G
51	3	511	U
51	3	514	A
51	3	515	A
51	3	516	A
51	3	517	G
51	3	519	A
51	3	520	C
51	3	523	A
51	3	529	G
51	3	530	G

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Mol	Chain	Res	Type
51	3	539	U
51	3	544	U
51	3	545	C
51	3	548	A
51	3	553	A
51	3	558	C
51	3	562	C
51	3	565	C
51	3	566	G
51	3	567	U
51	3	568	G
51	3	581	A
51	3	583	U
51	3	584	G
51	3	586	G
51	3	589	A
51	3	595	U
51	3	601	U
51	3	605	A
51	3	606	G
51	3	607	U
51	3	608	A
51	3	620	G
51	3	631	A
51	3	636	U
51	3	637	U
51	3	639	G
51	3	646	A
51	3	647	G
51	3	648	G
51	3	650	G
51	3	663	A
51	3	673	A
51	3	681	A
51	3	682	A
51	3	687	G
51	3	689	U
51	3	691	G
51	3	699	U
51	3	705	A
51	3	706	C
51	3	710	A

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Mol	Chain	Res	Type
51	3	712	A
51	3	719	G
51	3	721	G
51	3	722	C
51	3	725	G
51	3	732	G
51	3	737	U
51	3	739	G
51	3	740	A
51	3	743	G
51	3	752	C
51	3	761	G
51	3	762	A
51	3	764	G
51	3	765	A
51	3	769	A
51	3	774	A
51	3	782	U
51	3	792	G
51	3	797	U
51	3	798	G
51	3	799	A
51	3	810	G
51	3	811	G
51	3	812	G
51	3	816	A
51	3	817	A
51	3	819	U
51	3	820	U
51	3	824	A
51	3	825	U
51	3	827	G
51	3	828	A
51	3	829	A
51	3	835	U
51	3	837	A
51	3	840	G
51	3	842	U
51	3	847	C
51	3	854	A
51	3	860	C
51	3	862	U

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Mol	Chain	Res	Type
51	3	863	U
51	3	864	A
51	3	865	A
51	3	866	G
51	3	880	C
51	3	881	A
51	3	882	C
51	3	883	A
51	3	885	A
51	3	887	A
51	3	895	G
51	3	902	U
51	3	904	C
51	3	906	G
51	3	914	G
51	3	917	G
51	3	922	C
51	3	930	C
51	3	931	G
51	3	932	U
51	3	933	A
51	3	936	G
51	3	937	A
51	3	940	A
51	3	944	U
51	3	947	A
51	3	949	C
51	3	953	G
51	3	964	A
51	3	968	U
51	3	970	U
51	3	977	A
51	3	982	G
51	3	984	C
51	3	989	G
51	3	994	U
51	3	997	G
51	3	998	C
51	3	1001	C
51	3	1002	A
51	3	1005	G
51	3	1007	C

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Mol	Chain	Res	Type
51	3	1008	A
51	3	1009	A
51	3	1010	G
51	3	1016	A
51	3	1019	A
51	3	1026	A
51	3	1027	U
51	3	1029	A
51	3	1035	U
51	3	1041	C
51	3	1044	C
51	3	1046	A
51	3	1048	A
51	3	1049	U
51	3	1052	A
51	3	1055	A
51	3	1061	A
51	3	1062	A
51	3	1068	U
51	3	1075	G
51	3	1080	A
51	3	1081	A
51	3	1082	A
51	3	1089	A
51	3	1091	G
51	3	1095	U
51	3	1096	U
51	3	1099	C
51	3	1102	A
51	3	1103	G
51	3	1104	A
51	3	1105	A
51	3	1106	G
51	3	1107	C
51	3	1108	A
51	3	1111	C
51	3	1115	G
51	3	1123	A
51	3	1124	G
51	3	1125	U
51	3	1126	G
51	3	1130	A

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Mol	Chain	Res	Type
51	3	1132	C
51	3	1141	U
51	3	1145	G
51	3	1146	A
51	3	1147	G
51	3	1151	U
51	3	1154	U
51	3	1165	U
51	3	1166	G
51	3	1167	U
51	3	1168	A
51	3	1169	A
51	3	1170	C
51	3	1171	G
51	3	1176	U
51	3	1177	A
51	3	1178	A
51	3	1187	C
51	3	1189	G
51	3	1191	A
51	3	1193	U
51	3	1202	A
51	3	1204	A
51	3	1208	A
51	3	1209	U
51	3	1210	A
51	3	1212	C
51	3	1215	G
51	3	1216	U
51	3	1217	G
51	3	1219	U
51	3	1225	A
51	3	1234	U
51	3	1235	U
51	3	1250	A
51	3	1251	G
51	3	1253	G
51	3	1256	A
51	3	1257	G
51	3	1265	G
51	3	1266	G
51	3	1267	A

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Mol	Chain	Res	Type
51	3	1268	U
51	3	1274	A
51	3	1277	A
51	3	1279	U
51	3	1281	A
51	3	1283	A
51	3	1284	A
51	3	1285	U
51	3	1286	G
51	3	1292	A
51	3	1297	U
51	3	1298	A
51	3	1300	C
51	3	1301	G
51	3	1302	C
51	3	1304	U
51	3	1305	G
51	3	1314	A
51	3	1316	U
51	3	1317	C
51	3	1322	A
51	3	1325	C
51	3	1328	A
51	3	1329	U
51	3	1330	U
51	3	1331	G
51	3	1338	G
51	3	1353	G
51	3	1356	G
51	3	1357	U
51	3	1360	U
51	3	1368	U
51	3	1369	U
51	3	1371	G
51	3	1374	U
51	3	1376	G
51	3	1378	C
51	3	1380	U
51	3	1387	A
51	3	1388	G
51	3	1393	A
51	3	1406	A

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Mol	Chain	Res	Type
51	3	1407	U
51	3	1408	G
51	3	1412	A
51	3	1420	A
51	3	1422	U
51	3	1423	A
51	3	1424	U
51	3	1425	U
51	3	1431	A
51	3	1434	U
51	3	1444	C
51	3	1445	U
51	3	1448	U
51	3	1456	C
51	3	1457	A
51	3	1463	G
51	3	1466	U
51	3	1467	U
51	3	1480	A
51	3	1481	U
51	3	1482	U
51	3	1483	G
51	3	1486	U
51	3	1487	U
51	3	1497	A
51	3	1502	A
51	3	1506	U
51	3	1507	G
51	3	1508	G
51	3	1510	A
51	3	1513	A
51	3	1515	A
51	3	1518	C
51	3	1519	A
51	3	1523	C
51	3	1528	G
51	3	1534	A
51	3	1537	A
51	3	1541	A
51	3	1546	U
51	3	1550	G
51	3	1559	A

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Mol	Chain	Res	Type
51	3	1571	G
51	3	1577	A
51	3	1582	G
51	3	1584	U
51	3	1585	A
51	3	1586	U
51	3	1587	U
51	3	1588	A
51	3	1589	A
51	3	1593	U
51	3	1594	G
51	3	1600	A
51	3	1603	A
51	3	1607	G
51	3	1612	U
51	3	1615	G
51	3	1616	G
51	3	1617	U
51	3	1618	U
51	3	1619	A
51	3	1630	A
51	3	1632	C
51	3	1641	A
51	3	1642	G
51	3	1643	A
51	3	1644	A
51	3	1645	C
51	3	1651	C
51	3	1653	C
51	3	1661	A
51	3	1669	A
51	3	1681	G
51	3	1682	C
51	3	1683	G
51	3	1685	G
51	3	1687	G
51	3	1688	A
51	3	1692	A
51	3	1694	A
51	3	1698	A
51	3	1699	A
51	3	1701	G

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Mol	Chain	Res	Type
51	3	1702	A
51	3	1708	G
51	3	1727	U
51	3	1728	A
51	3	1729	G
51	3	1733	G
51	3	1734	A
51	3	1735	A
51	3	1737	G
51	3	1747	G
51	3	1748	U
51	3	1751	A
51	3	1764	U
51	3	1765	G
51	3	1766	A
51	3	1768	G
51	3	1769	A
51	3	1770	A
51	3	1771	C
51	3	1772	G
51	3	1780	A
51	3	1784	U
51	3	1788	A
51	3	1789	C
51	3	1792	A
51	3	1806	G
51	3	1807	C
51	3	1809	A
51	3	1813	C
51	3	1816	A
51	3	1817	A
51	3	1823	U
51	3	1828	A
51	3	1836	A
51	3	1839	C
51	3	1842	G
51	3	1845	C
51	3	1850	C
51	3	1855	A
51	3	1866	G
51	3	1871	U
51	3	1873	A

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Mol	Chain	Res	Type
51	3	1883	A
51	3	1886	C
51	3	1890	U
51	3	1891	A
51	3	1892	A
51	3	1903	A
51	3	1906	G
51	3	1907	A
51	3	1913	G
51	3	1920	A
51	3	1921	C
51	3	1923	A
51	3	1934	A
51	3	1938	U
51	3	1943	A
51	3	1944	A
51	3	1945	A
51	3	1950	U
51	3	1951	A
51	3	1952	G
51	3	1953	U
51	3	1955	G
51	3	1961	A
51	3	1962	U
51	3	1965	C
51	3	1970	C
51	3	1971	G
51	3	1972	C
51	3	1977	A
51	3	1978	U
51	3	1979	G
51	3	1982	G
51	3	1998	U
51	3	1999	G
51	3	2000	U
51	3	2003	C
51	3	2009	U
51	3	2011	G
51	3	2020	A
51	3	2027	G
51	3	2028	G
51	3	2030	A

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Mol	Chain	Res	Type
51	3	2037	A
51	3	2038	A
51	3	2039	G
51	3	2040	A
51	3	2041	C
51	3	2043	C
51	3	2045	C
51	3	2050	G
51	3	2055	A
51	3	2056	A
51	3	2062	C
51	3	2063	G
51	3	2064	G
51	3	2067	A
51	3	2068	G
51	3	2069	A
51	3	2070	C
51	3	2071	C
51	3	2076	G
51	3	2078	A
51	3	2083	U
51	3	2084	A
51	3	2087	G
51	3	2095	A
51	3	2099	U
51	3	2100	G
51	3	2106	G
51	3	2107	A
51	3	2109	A
51	3	2111	U
51	3	2112	A
51	3	2114	C
51	3	2115	A
51	3	2117	G
51	3	2123	A
51	3	2124	A
51	3	2125	U
51	3	2127	G
51	3	2130	A
51	3	2131	G
51	3	2133	A
51	3	2135	C

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Mol	Chain	Res	Type
51	3	2139	C
51	3	2140	G
51	3	2152	C
51	3	2153	U
51	3	2154	A
51	3	2155	G
51	3	2165	A
51	3	2166	U
51	3	2171	A
51	3	2173	G
51	3	2180	U
51	3	2182	C
51	3	2193	U
51	3	2194	G
51	3	2195	U
51	3	2198	G
51	3	2200	U
51	3	2201	G
51	3	2202	U
51	3	2203	U
51	3	2204	C
51	3	2206	A
51	3	2211	G
51	3	2218	U
51	3	2220	A
51	3	2221	U
51	3	2222	C
51	3	2226	U
51	3	2227	U
51	3	2228	U
51	3	2231	A
51	3	2233	A
51	3	2246	G
51	3	2247	G
51	3	2258	G
51	3	2267	G
51	3	2274	A
51	3	2275	A
51	3	2276	A
51	3	2280	U
51	3	2284	G
51	3	2286	A

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Mol	Chain	Res	Type
51	3	2291	U
51	3	2294	A
51	3	2295	A
51	3	2296	A
51	3	2297	G
51	3	2305	C
51	3	2312	G
51	3	2313	U
51	3	2315	G
51	3	2316	G
51	3	2317	A
51	3	2327	U
51	3	2333	G
51	3	2335	A
51	3	2340	U
51	3	2341	G
51	3	2342	U
51	3	2343	A
51	3	2351	U
51	3	2352	U
51	3	2355	C
51	3	2358	U
51	3	2362	A
51	3	2365	U
51	3	2367	C
51	3	2380	U
51	3	2387	U
51	3	2391	G
51	3	2393	C
51	3	2396	A
51	3	2397	G
51	3	2414	U
51	3	2415	A
51	3	2422	G
51	3	2431	U
51	3	2433	A
51	3	2435	C
51	3	2436	G
51	3	2437	G
51	3	2438	A
51	3	2439	U
51	3	2442	A

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Mol	Chain	Res	Type
51	3	2444	G
51	3	2449	U
51	3	2455	G
51	3	2457	U
51	3	2458	A
51	3	2460	C
51	3	2468	U
51	3	2475	C
51	3	2484	A
51	3	2486	A
51	3	2487	U
51	3	2492	G
51	3	2495	A
51	3	2498	G
51	3	2499	U
51	3	2502	G
51	3	2504	C
51	3	2505	A
51	3	2506	C
51	3	2507	C
51	3	2510	G
51	3	2513	G
51	3	2514	U
51	3	2521	A
51	3	2525	C
51	3	2526	A
51	3	2528	C
51	3	2538	A
51	3	2539	A
51	3	2543	G
51	3	2544	G
51	3	2551	G
51	3	2555	U
51	3	2557	G
51	3	2570	U
51	3	2574	A
51	3	2575	G
51	3	2580	A
51	3	2581	C
51	3	2582	G
51	3	2585	A
51	3	2586	G

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Mol	Chain	Res	Type
51	3	2589	G
51	3	2590	G
51	3	2593	U
51	3	2594	C
51	3	2600	G
51	3	2604	U
51	3	2605	G
51	3	2607	G
51	3	2609	C
51	3	2610	A
51	3	2611	G
51	3	2617	U
51	3	2618	C
51	3	2619	C
51	3	2621	U
51	3	2622	A
51	3	2629	G
51	3	2631	G
51	3	2637	A
51	3	2638	G
51	3	2640	A
51	3	2643	A
51	3	2645	U
51	3	2647	A
51	3	2649	G
51	3	2654	U
51	3	2664	U
51	3	2669	G
51	3	2681	G
51	3	2683	G
51	3	2689	C
51	3	2690	U
51	3	2697	C
51	3	2698	U
51	3	2699	C
51	3	2704	U
51	3	2715	C
51	3	2722	G
51	3	2726	G
51	3	2730	G
51	3	2731	U
51	3	2734	C

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Mol	Chain	Res	Type
51	3	2735	G
51	3	2736	U
51	3	2737	G
51	3	2741	A
51	3	2747	U
51	3	2752	G
51	3	2756	A
51	3	2759	G
51	3	2764	U
51	3	2765	A
51	3	2769	G
51	3	2774	A
51	3	2777	A
51	3	2789	A
51	3	2794	U
51	3	2795	C
51	3	2798	A
51	3	2799	U
51	3	2800	U
51	3	2801	U
51	3	2804	C
51	3	2805	A
51	3	2807	G
51	3	2809	A
51	3	2810	A
51	3	2811	G
51	3	2812	U
51	3	2813	A
51	3	2822	C
51	3	2824	A
51	3	2828	C
51	3	2834	C
51	3	2837	U
51	3	2839	A
51	3	2853	U
51	3	2854	A
51	3	2863	G
51	3	2864	A
51	3	2865	U
51	3	2871	G
51	3	2876	G
51	3	2881	A

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Mol	Chain	Res	Type
51	3	2884	C
51	3	2887	A
51	3	2888	U
51	3	2890	G
51	3	2896	G
51	3	2897	G
51	3	2898	A
51	3	2899	C
52	4	8	C
52	4	10	C
52	4	11	A
52	4	20	U
52	4	22	G
52	4	23	A
52	4	25	A
52	4	26	C
52	4	28	C
52	4	31	G
52	4	32	G
52	4	33	U
52	4	35	C
52	4	38	U
52	4	40	U
52	4	41	C
52	4	42	G
52	4	44	A
52	4	48	A
52	4	49	G
52	4	52	G
52	4	55	A
52	4	60	C
52	4	65	G
52	4	66	A
52	4	74	G
52	4	76	A
52	4	77	G
52	4	78	C
52	4	79	U
52	4	80	G
52	4	86	G
52	4	88	G
52	4	89	A

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Mol	Chain	Res	Type
52	4	97	A
52	4	99	A
52	4	102	A
52	4	108	C
53	5	8	G
53	5	9	A
53	5	16	G
53	5	32	U
53	5	33	A
53	5	40	G
53	5	48	C
53	5	49	C
53	5	51	A
53	5	52	A
53	5	61	A
53	5	66	A
53	5	67	U
53	5	75	A
53	5	78	A
53	5	80	U
53	5	81	A
53	5	86	A
53	5	93	A
53	5	99	U
53	5	100	G
53	5	105	A
53	5	106	C
53	5	109	G
53	5	114	C
53	5	115	A
53	5	116	A
53	5	117	U
53	5	120	A
53	5	128	A
53	5	130	G
53	5	135	A
53	5	140	U
53	5	149	G
53	5	152	U
53	5	156	U
53	5	159	U
53	5	161	C

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Mol	Chain	Res	Type
53	5	167	A
53	5	169	G
53	5	171	A
53	5	174	U
53	5	197	A
53	5	198	A
53	5	199	A
53	5	206	G
53	5	218	U
53	5	220	U
53	5	223	G
53	5	227	A
53	5	232	G
53	5	234	G
53	5	236	C
53	5	240	U
53	5	241	C
53	5	243	G
53	5	247	G
53	5	249	U
53	5	262	G
53	5	263	C
53	5	265	U
53	5	269	A
53	5	285	G
53	5	288	A
53	5	294	A
53	5	301	G
53	5	302	A
53	5	303	A
53	5	306	G
53	5	312	A
53	5	323	A
53	5	324	C
53	5	326	C
53	5	328	G
53	5	341	C
53	5	342	G
53	5	348	C
53	5	359	A
53	5	363	U
53	5	364	U

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Mol	Chain	Res	Type
53	5	365	U
53	5	368	C
53	5	370	A
53	5	375	C
53	5	376	G
53	5	377	A
53	5	388	G
53	5	394	U
53	5	398	G
53	5	400	G
53	5	402	G
53	5	407	A
53	5	408	U
53	5	409	G
53	5	410	A
53	5	413	G
53	5	417	U
53	5	418	U
53	5	419	A
53	5	420	A
53	5	421	G
53	5	423	U
53	5	426	U
53	5	431	U
53	5	432	U
53	5	433	C
53	5	435	U
53	5	436	U
53	5	445	A
53	5	449	A
53	5	450	U
53	5	452	A
53	5	453	C
53	5	455	U
53	5	456	U
53	5	457	A
53	5	461	G
53	5	462	G
53	5	464	A
53	5	466	U
53	5	468	G
53	5	471	A

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Mol	Chain	Res	Type
53	5	473	A
53	5	476	U
53	5	477	U
53	5	478	G
53	5	481	U
53	5	482	G
53	5	483	U
53	5	488	U
53	5	489	U
53	5	490	U
53	5	493	A
53	5	494	A
53	5	505	C
53	5	506	U
53	5	509	C
53	5	510	U
53	5	515	G
53	5	516	C
53	5	519	G
53	5	522	G
53	5	523	U
53	5	525	G
53	5	526	C
53	5	528	G
53	5	530	A
53	5	531	A
53	5	532	U
53	5	534	C
53	5	542	G
53	5	543	C
53	5	545	A
53	5	558	U
53	5	560	U
53	5	561	A
53	5	562	U
53	5	568	G
53	5	569	U
53	5	570	A
53	5	574	C
53	5	575	A
53	5	579	G
53	5	586	G

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Mol	Chain	Res	Type
53	5	594	A
53	5	595	G
53	5	616	C
53	5	618	U
53	5	619	A
53	5	628	A
53	5	639	A
53	5	642	A
53	5	646	A
53	5	647	U
53	5	653	G
53	5	656	U
53	5	662	G
53	5	672	A
53	5	683	G
53	5	684	A
53	5	692	A
53	5	695	G
53	5	699	A
53	5	715	A
53	5	719	G
53	5	721	G
53	5	724	G
53	5	731	A
53	5	735	C
53	5	738	A
53	5	742	C
53	5	745	U
53	5	747	C
53	5	749	G
53	5	752	G
53	5	756	A
53	5	773	G
53	5	774	A
53	5	778	A
53	5	781	A
53	5	784	A
53	5	787	A
53	5	788	G
53	5	789	A
53	5	790	U
53	5	794	C

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Mol	Chain	Res	Type
53	5	802	C
53	5	806	A
53	5	810	U
53	5	812	A
53	5	813	A
53	5	814	C
53	5	815	G
53	5	818	A
53	5	825	A
53	5	829	G
53	5	838	A
53	5	846	G
53	5	855	G
53	5	857	U
53	5	861	A
53	5	864	U
53	5	868	G
53	5	870	A
53	5	877	C
53	5	879	G
53	5	882	U
53	5	883	A
53	5	885	U
53	5	896	G
53	5	898	A
53	5	908	A
53	5	910	C
53	5	911	G
53	5	917	G
53	5	918	A
53	5	921	G
53	5	922	G
53	5	924	A
53	5	927	C
53	5	929	C
53	5	930	A
53	5	934	G
53	5	937	G
53	5	940	G
53	5	941	A
53	5	953	A
53	5	955	U

Continued on next page...

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Mol	Chain	Res	Type
53	5	956	U
53	5	959	A
53	5	960	C
53	5	964	A
53	5	966	A
53	5	968	G
53	5	969	A
53	5	970	A
53	5	971	A
53	5	972	A
53	5	977	U
53	5	978	A
53	5	979	C
53	5	984	A
53	5	986	U
53	5	987	U
53	5	988	G
53	5	989	A
53	5	997	G
53	5	1000	A
53	5	1003	G
53	5	1004	U
53	5	1014	A
53	5	1015	U
53	5	1018	U
53	5	1030	G
53	5	1033	U
53	5	1035	A
53	5	1037	A
53	5	1038	G
53	5	1041	G
53	5	1044	G
53	5	1045	C
53	5	1046	A
53	5	1047	U
53	5	1055	G
53	5	1056	U
53	5	1057	C
53	5	1061	U
53	5	1064	U
53	5	1070	G
53	5	1071	A

Continued on next page...

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Mol	Chain	Res	Type
53	5	1072	G
53	5	1075	G
53	5	1081	U
53	5	1084	A
53	5	1085	G
53	5	1086	U
53	5	1092	A
53	5	1095	G
53	5	1106	U
53	5	1109	U
53	5	1113	U
53	5	1114	A
53	5	1119	C
53	5	1120	A
53	5	1121	U
53	5	1122	U
53	5	1123	G
53	5	1124	U
53	5	1125	C
53	5	1127	A
53	5	1130	G
53	5	1134	C
53	5	1135	U
53	5	1140	A
53	5	1142	G
53	5	1154	A
53	5	1159	A
53	5	1165	G
53	5	1166	A
53	5	1169	U
53	5	1171	A
53	5	1172	A
53	5	1173	A
53	5	1187	U
53	5	1188	A
53	5	1189	U
53	5	1190	G
53	5	1199	U
53	5	1200	G
53	5	1202	A
53	5	1203	A
53	5	1211	A

Continued on next page...

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Mol	Chain	Res	Type
53	5	1215	U
53	5	1218	C
53	5	1225	A
53	5	1227	A
53	5	1233	G
53	5	1235	C
53	5	1242	U
53	5	1243	A
53	5	1245	A
53	5	1248	U
53	5	1251	G
53	5	1253	A
53	5	1255	A
53	5	1257	C
53	5	1260	U
53	5	1261	A
53	5	1265	U
53	5	1274	G
53	5	1276	U
53	5	1278	G
53	5	1279	G
53	5	1280	A
53	5	1281	U
53	5	1283	G
53	5	1286	G
53	5	1294	U
53	5	1296	C
53	5	1309	U
53	5	1312	G
53	5	1316	C
53	5	1320	A
53	5	1322	U
53	5	1337	U
53	5	1338	A
53	5	1343	G
53	5	1354	G
53	5	1356	U
53	5	1362	G
53	5	1374	C
53	5	1375	C
53	5	1376	G
53	5	1380	G

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Mol	Chain	Res	Type
53	5	1381	U
53	5	1385	A
53	5	1394	G
53	5	1397	G
53	5	1400	A
53	5	1401	A
53	5	1404	U
53	5	1407	A
53	5	1408	A
53	5	1417	U
53	5	1418	G
53	5	1421	A
53	5	1423	C
53	5	1427	U
53	5	1429	G
53	5	1435	G
53	5	1439	G
53	5	1442	A
53	5	1449	G
53	5	1466	U
53	5	1467	A
53	5	1468	A
53	5	1472	G
53	5	1474	A
53	5	1475	A
53	5	1476	C
53	5	1477	A
53	5	1478	A
53	5	1480	G
53	5	1481	U
53	5	1492	G
53	5	1495	C
53	5	1502	G
53	5	1504	G
53	5	1505	G
53	5	1507	U
53	5	1508	C
54	6	3	G
54	6	9	U
54	6	11	G
54	6	12	C
54	6	17	U

Continued on next page...

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Mol	Chain	Res	Type
54	6	18	C
54	6	20	G
54	6	22	A
54	6	23	G
54	6	24	A
54	6	25	G
54	6	32	U
54	6	38	G
54	6	41	C
54	6	42	C
54	6	43	G
54	6	44	U
54	6	47	G
54	6	48	U
54	6	49	C
54	6	57	C
54	6	58	G
54	6	59	A
54	6	62	C
54	6	67	C
54	6	71	A
54	6	72	C
54	6	73	C
54	6	75	C
54	6	76	C
54	7	3	G
54	7	9	U
54	7	11	G
54	7	12	C
54	7	17	U
54	7	18	C
54	7	20	G
54	7	22	A
54	7	23	G
54	7	24	A
54	7	25	G
54	7	32	U
54	7	38	G
54	7	41	C
54	7	42	C
54	7	43	G
54	7	44	U

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Mol	Chain	Res	Type
54	7	47	G
54	7	48	U
54	7	49	C
54	7	57	C
54	7	58	G
54	7	59	A
54	7	62	C
54	7	67	C
54	7	71	A
54	7	72	C
54	7	73	C
54	7	75	C
54	7	76	C

All (43) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
51	3	309	A
51	3	311	G
51	3	315	A
51	3	410	G
51	3	425	U
51	3	500	U
51	3	513	A
51	3	688	U
51	3	881	A
51	3	935	U
51	3	936	G
51	3	952	U
51	3	1048	A
51	3	1124	G
51	3	1209	U
51	3	1216	U
51	3	1297	U
51	3	1507	G
51	3	1583	G
51	3	1587	U
51	3	1588	A
51	3	2124	A
51	3	2219	U
51	3	2504	C
51	3	2604	U

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Mol	Chain	Res	Type
51	3	2668	A
51	3	2764	U
51	3	2862	U
51	3	2897	G
52	4	10	C
52	4	54	U
52	4	59	A
53	5	8	G
53	5	196	G
53	5	448	A
53	5	618	U
53	5	787	A
53	5	920	G
53	5	1133	A
54	6	16	G
54	6	48	U
54	7	16	G
54	7	48	U

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

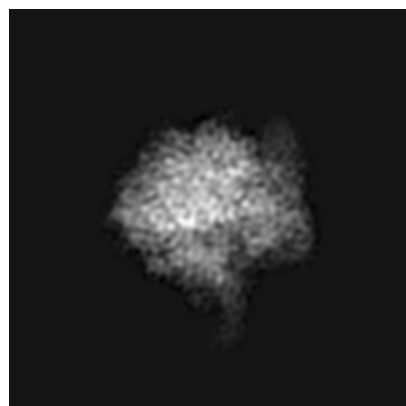
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13446. These allow visual inspection of the internal detail of the map and identification of artifacts.

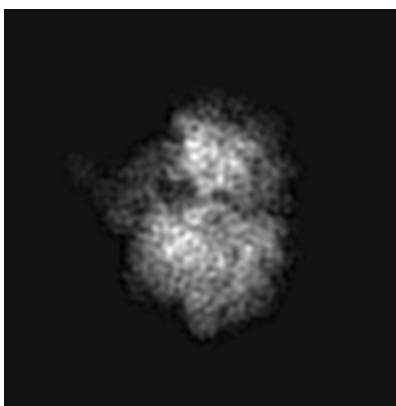
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

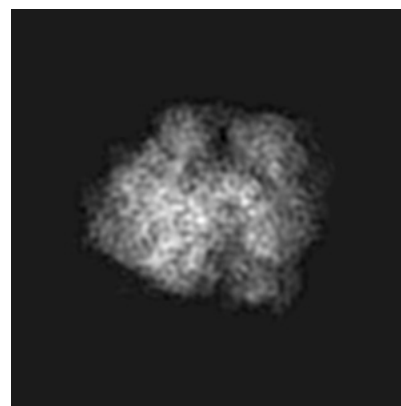
6.1.1 Primary map



X

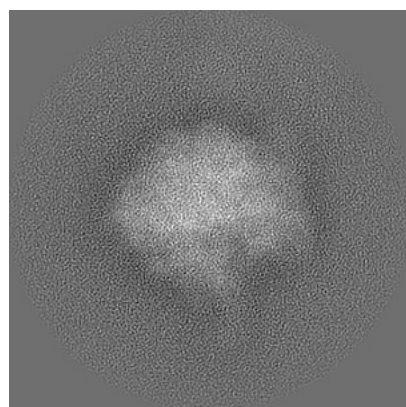


Y

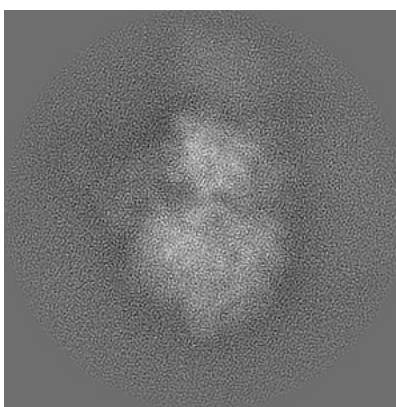


Z

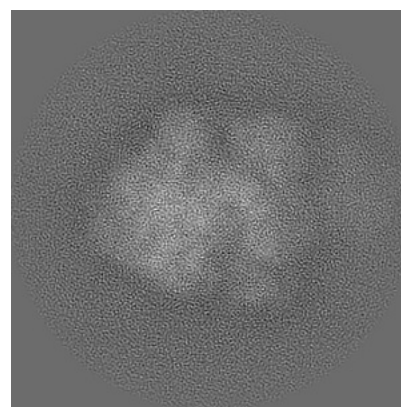
6.1.2 Raw map



X



Y

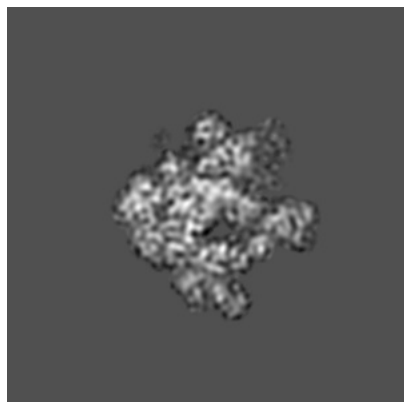


Z

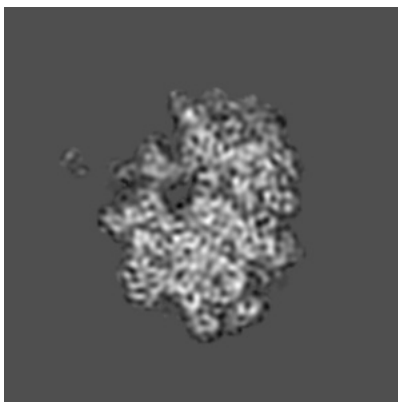
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

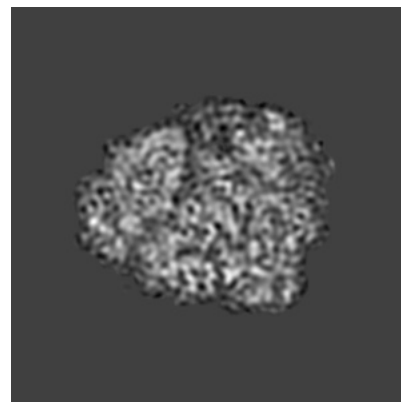
6.2.1 Primary map



X Index: 128

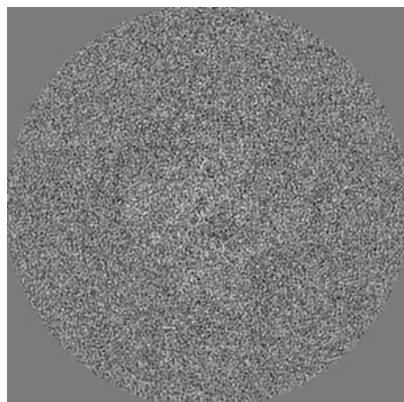


Y Index: 128

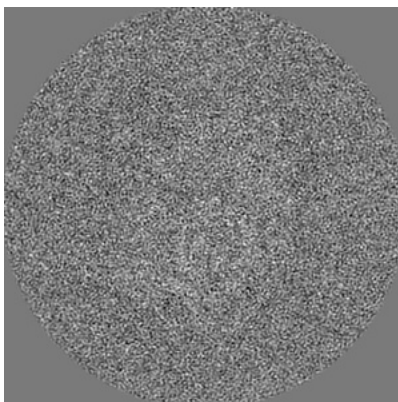


Z Index: 128

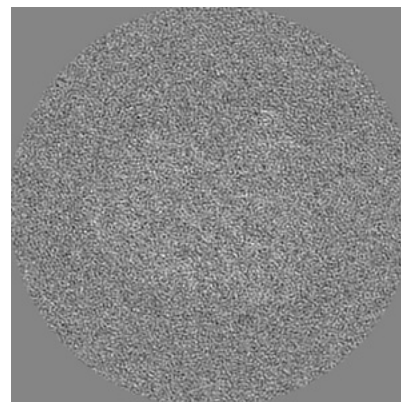
6.2.2 Raw map



X Index: 128



Y Index: 128

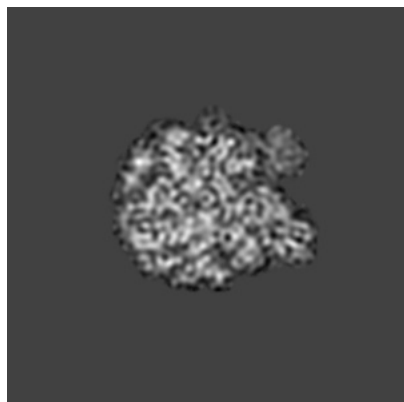


Z Index: 128

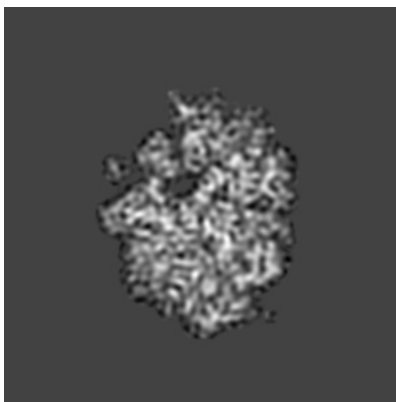
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

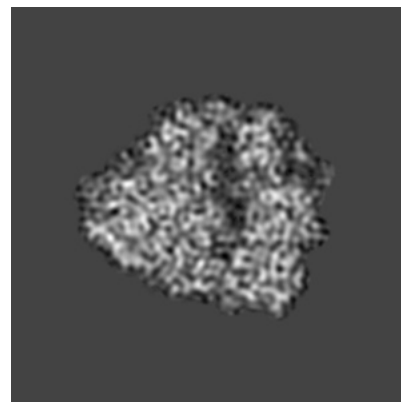
6.3.1 Primary map



X Index: 103

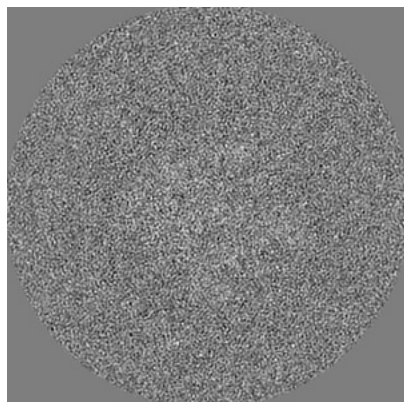


Y Index: 121

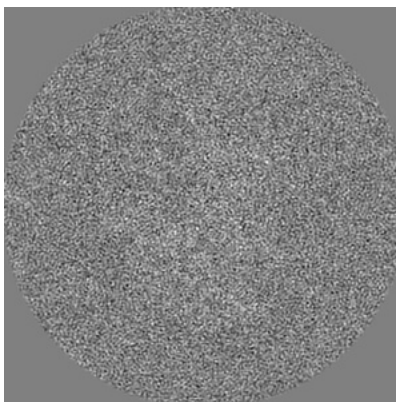


Z Index: 121

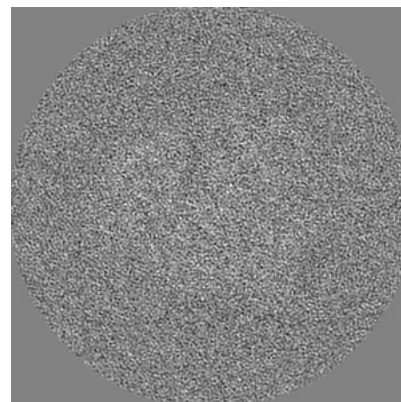
6.3.2 Raw map



X Index: 125



Y Index: 127

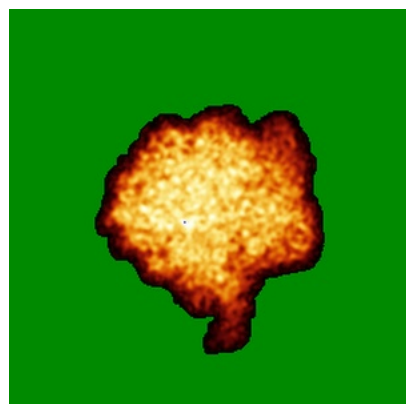


Z Index: 129

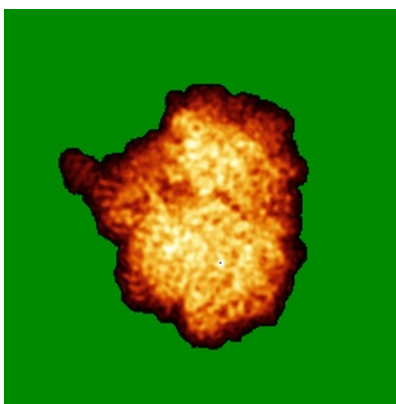
The images above show the largest variance slices of the map in three orthogonal directions.

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

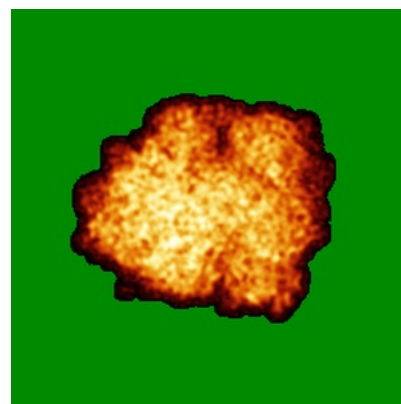
6.4.1 Primary map



X

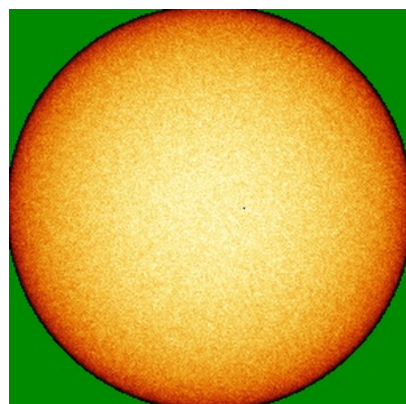


Y

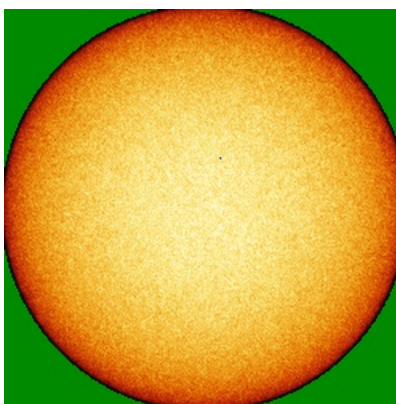


Z

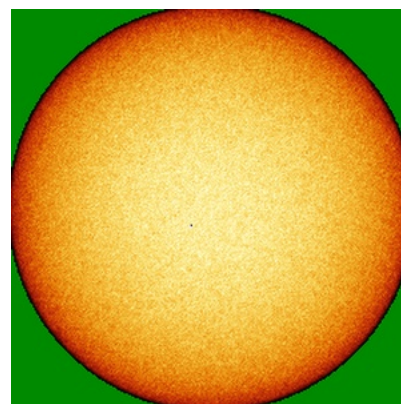
6.4.2 Raw map



X



Y

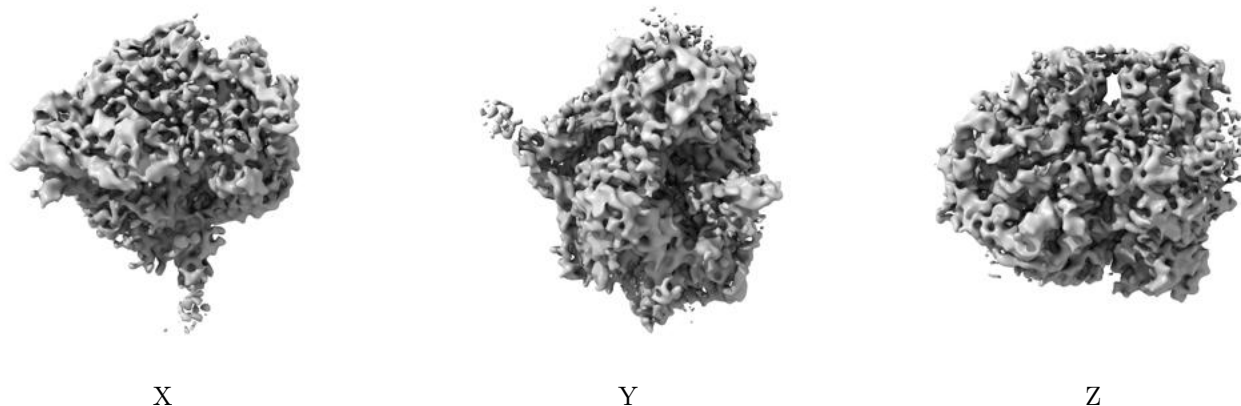


Z

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.

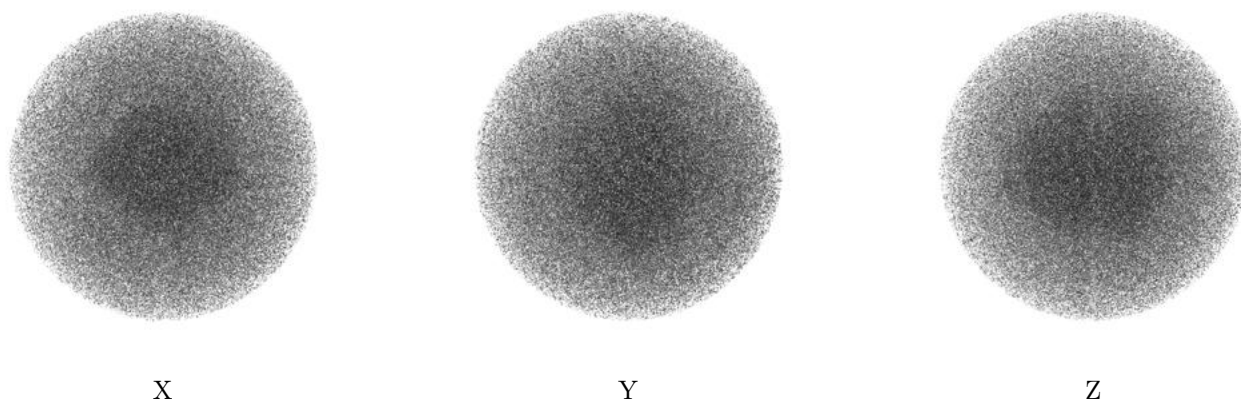
6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.39. 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.

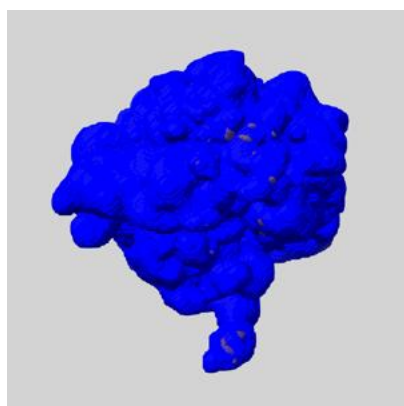
6.6 Mask visualisation [i](#)

This section shows the 3D surface view of the primary map at 50% transparency overlaid with the specified mask at 0% transparency

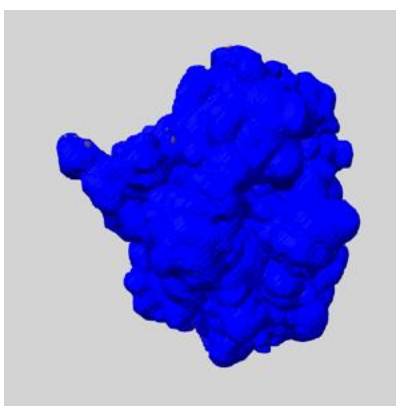
A mask typically either:

- Encompasses the whole structure
- Separates out a domain, a functional unit, a monomer or an area of interest from a larger structure

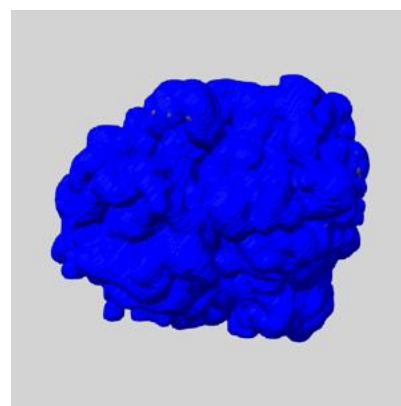
6.6.1 emd_13446_msk_1.map [i](#)



X



Y

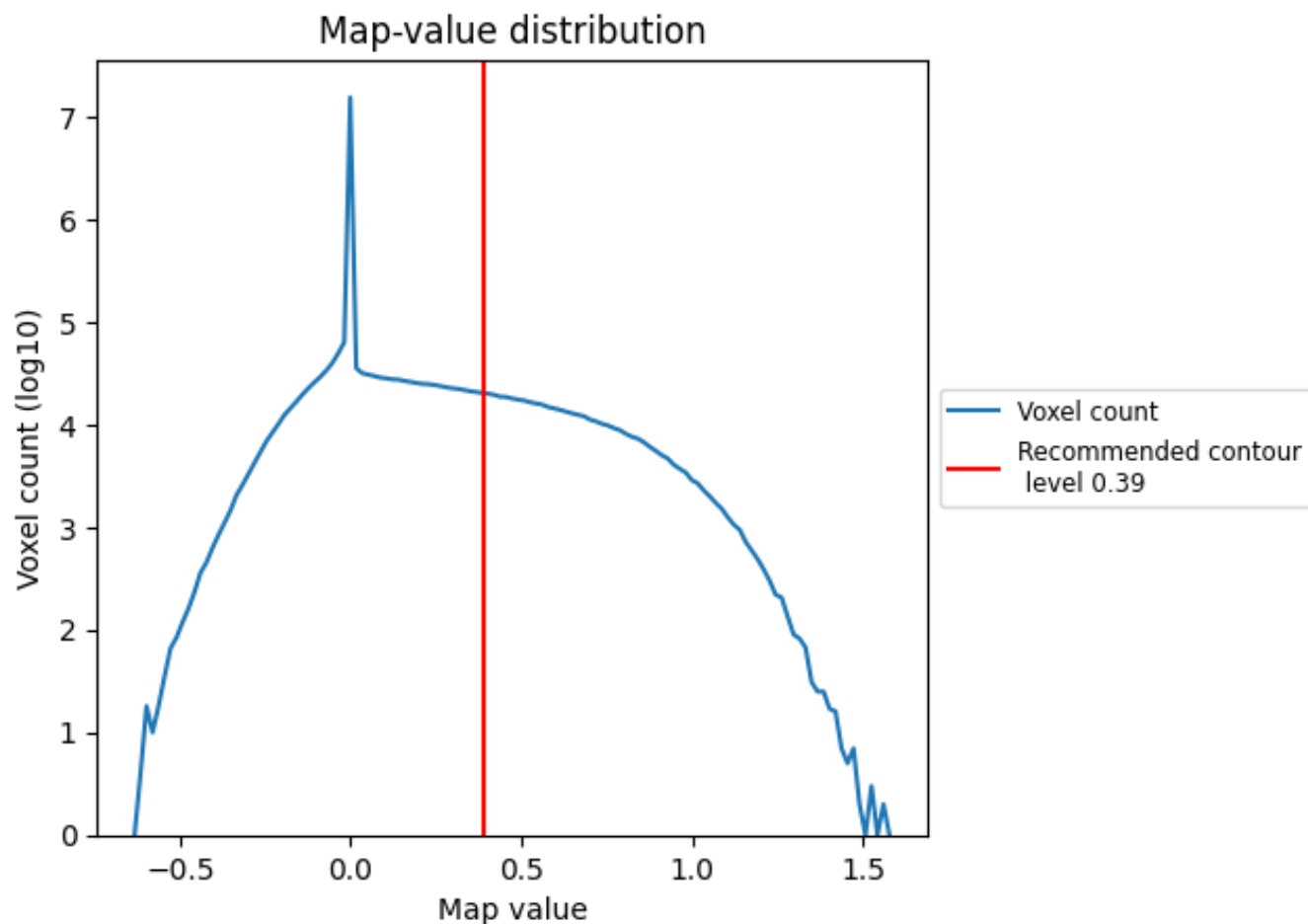


Z

7 Map analysis [i](#)

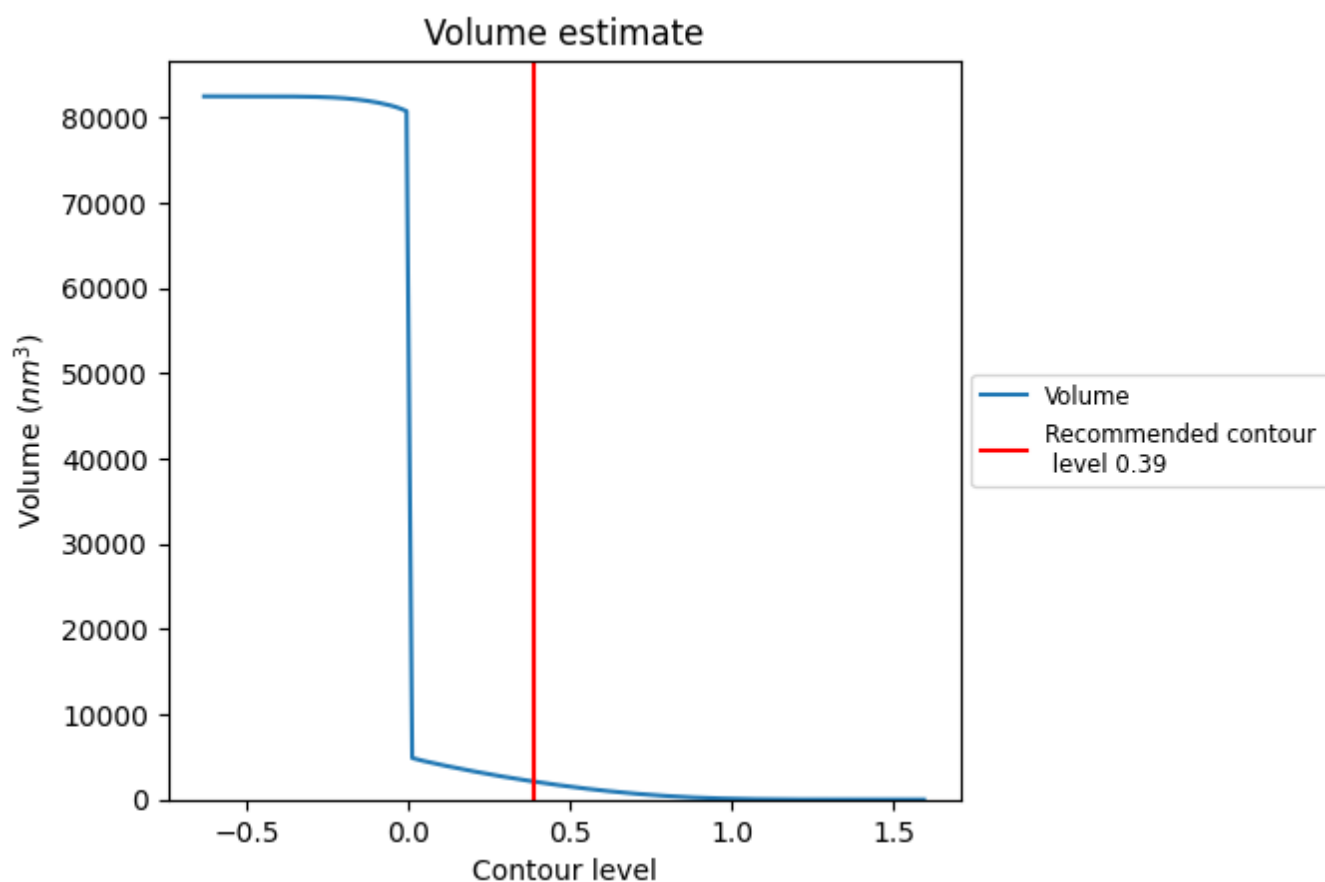
This section contains the results of statistical analysis of the map.

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.

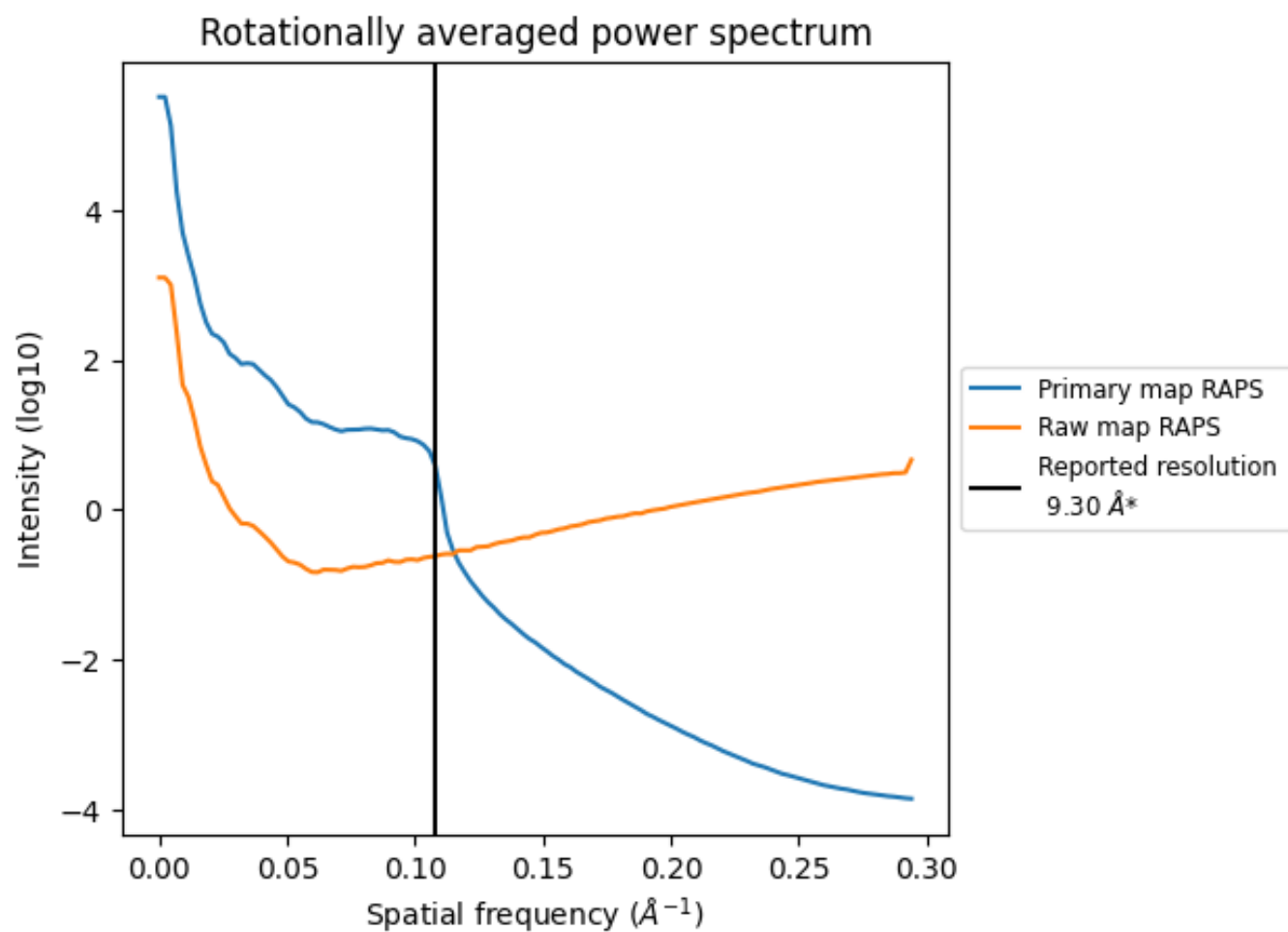
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2100 nm³; this corresponds to an approximate mass of 1897 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 ⓘ

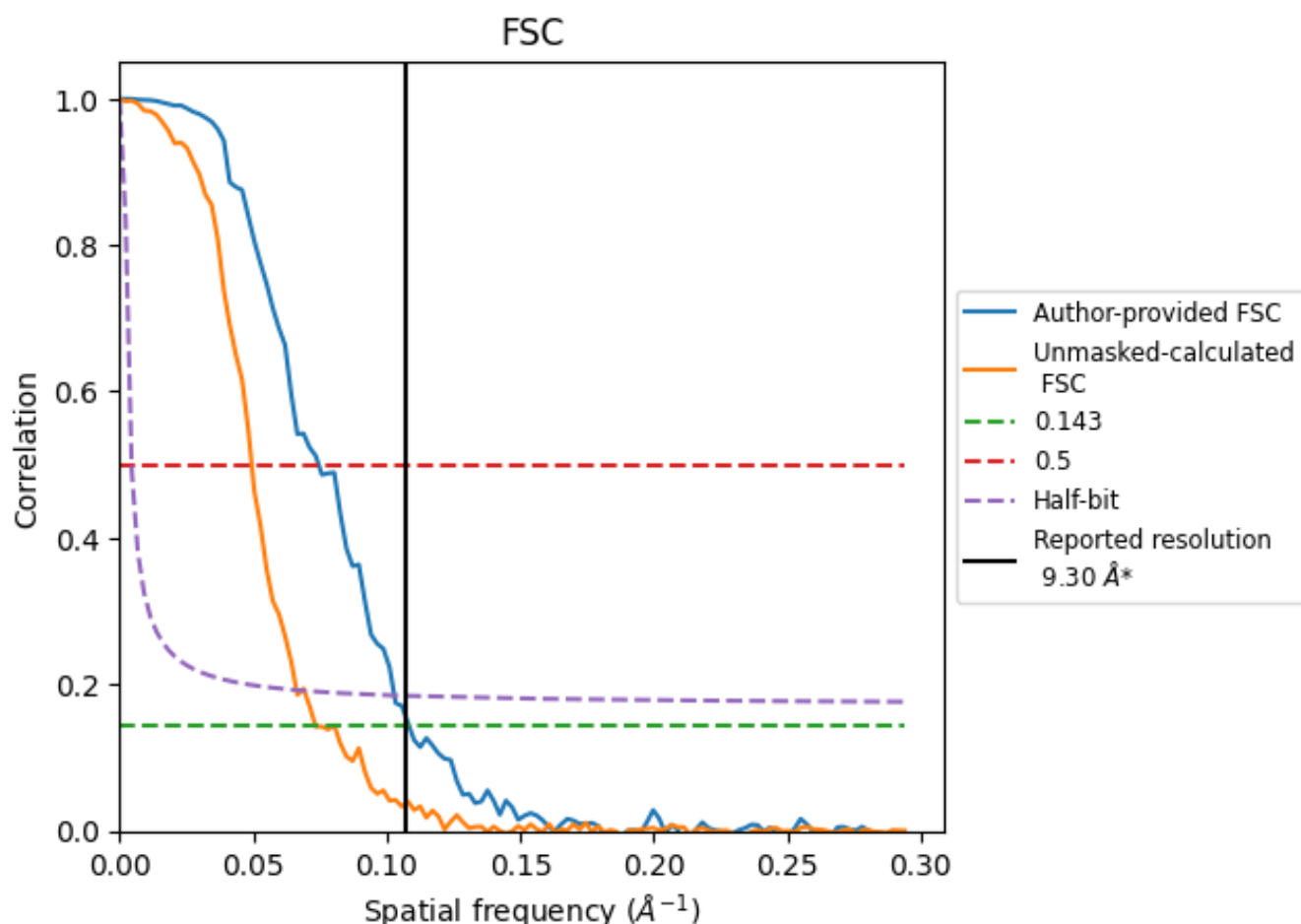


*Reported resolution corresponds to spatial frequency of 0.108 \AA^{-1}

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 0.108 Å⁻¹

8.2 Resolution estimates [i](#)

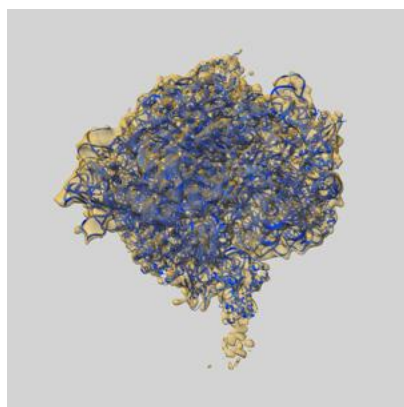
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	9.30	-	-
Author-provided FSC curve	9.23	13.40	9.72
Unmasked-calculated*	13.62	20.16	15.08

*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 13.62 differs from the reported value 9.3 by more than 10 %

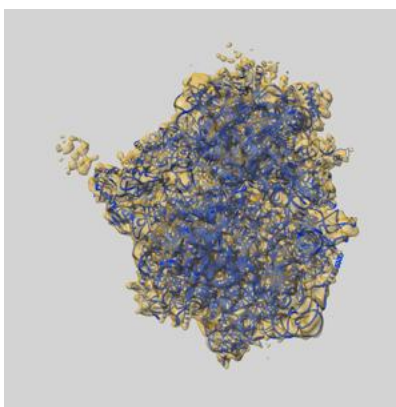
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13446 and PDB model 7PIP. Per-residue inclusion information can be found in section [3](#) on page [13](#).

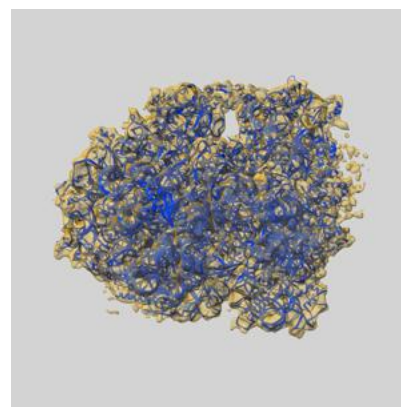
9.1 Map-model overlay [i](#)



X



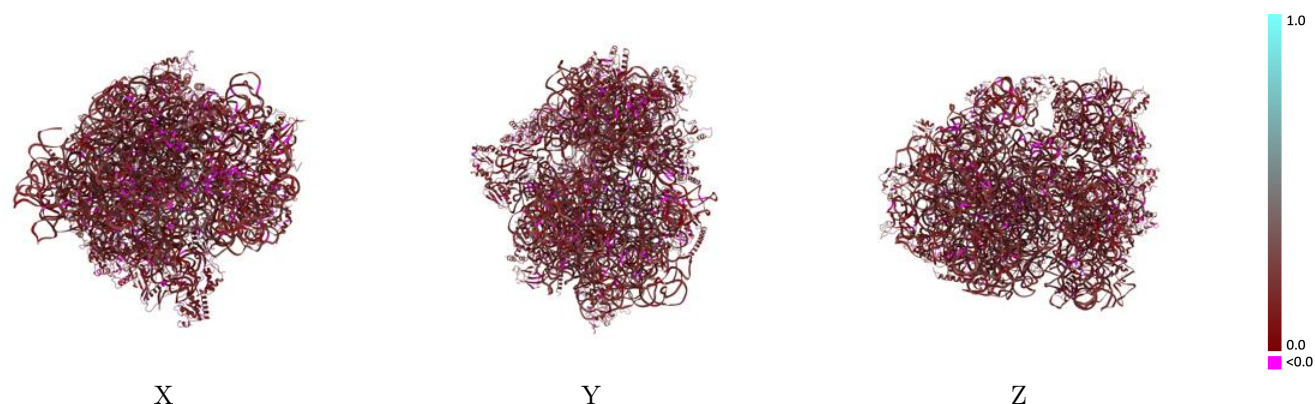
Y



Z

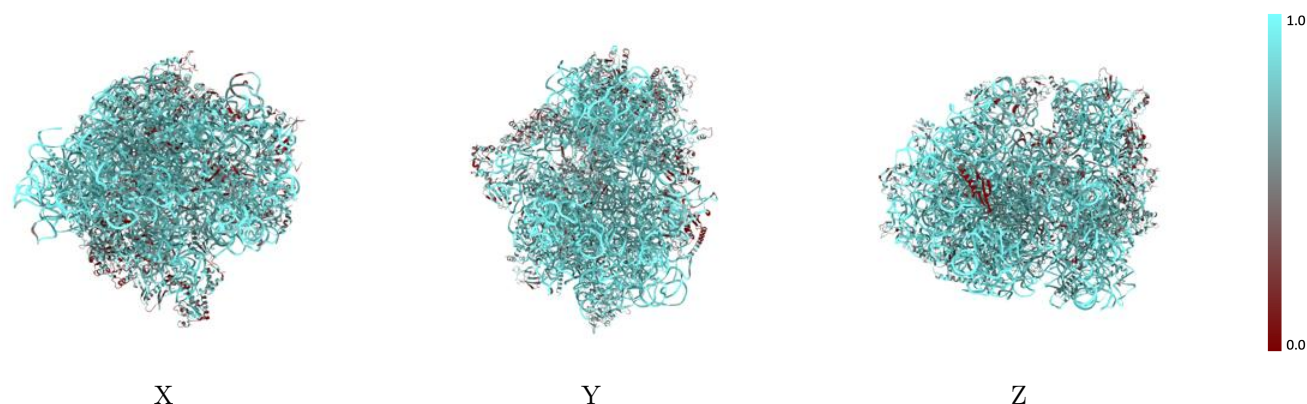
The images above show the 3D surface view of the map at the recommended contour level 0.39 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



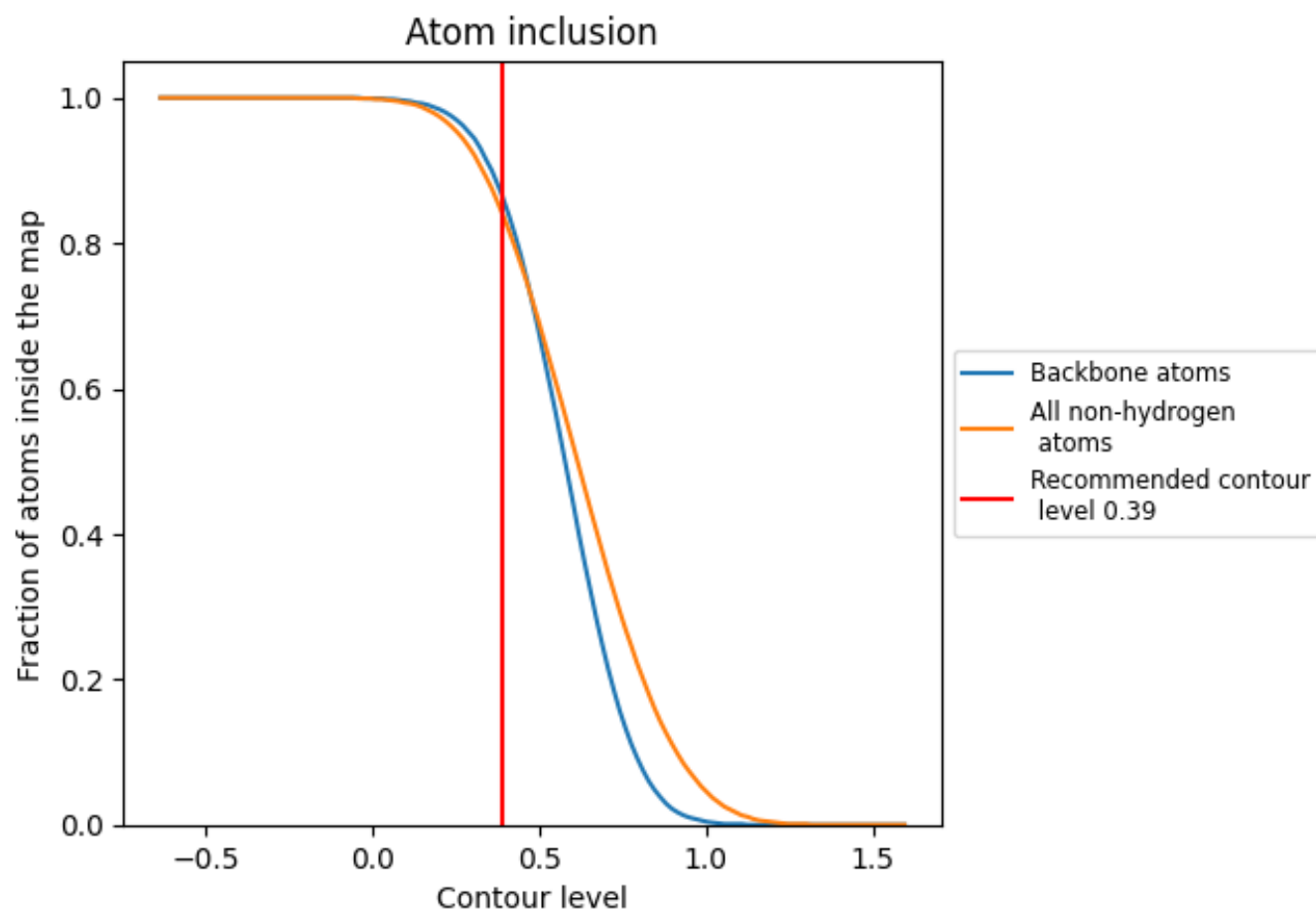
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.39).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 87% 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 (0.39) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8420	 0.1590
0	 0.7940	 0.1400
1	 0.7620	 0.1410
2	 0.7470	 0.1130
3	 0.9410	 0.1680
4	 0.9420	 0.1790
5	 0.9440	 0.1710
6	 0.7850	 0.1530
7	 0.7500	 0.1100
9	 0.4820	 0.1290
A	 0.5770	 0.1580
B	 0.5900	 0.1450
C	 0.6760	 0.1420
D	 0.6320	 0.1390
E	 0.6040	 0.1620
F	 0.6310	 0.1450
G	 0.6580	 0.1360
H	 0.6260	 0.1110
I	 0.6080	 0.1400
J	 0.6400	 0.1270
K	 0.7010	 0.1410
L	 0.6570	 0.1480
M	 0.6240	 0.1050
N	 0.7020	 0.1720
O	 0.8190	 0.1670
P	 0.7310	 0.1640
Q	 0.6200	 0.1360
R	 0.6180	 0.0970
S	 0.7790	 0.1640
T	 0.7190	 0.1880
a	 0.7320	 0.1280
b	 0.6840	 0.1320
c	 0.6900	 0.1490
d	 0.6190	 0.1470
e	 0.6300	 0.1530



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Chain	Atom inclusion	Q-score
f	 0.2460	 0.1380
g	 0.5150	 0.1540
h	 0.5220	 0.1410
i	 0.7030	 0.1310
j	 0.5900	 0.1290
k	 0.7410	 0.1430
l	 0.7280	 0.1410
m	 0.7420	 0.1370
n	 0.6770	 0.1450
o	 0.6820	 0.1550
p	 0.7720	 0.1390
q	 0.6850	 0.1400
r	 0.7960	 0.1710
s	 0.6700	 0.1370
t	 0.6270	 0.1510
u	 0.7640	 0.1170
v	 0.7510	 0.1520
w	 0.7550	 0.1870
x	 0.5390	 0.1620
y	 0.7470	 0.1270
z	 0.7930	 0.1300