



wwPDB EM Validation Summary Report ⓘ

Oct 14, 2021 – 11:04 pm BST

PDB ID : 7PJT
EMDB ID : EMD-13459
Title : Structure of the 70S ribosome with tRNAs in hybrid state 1 (H1)
Authors : Petrychenko, V.; Peng, B.Z.; Schwarzer, A.C.; Peske, F.; Rodnina, M.V.;
Fischer, N.
Deposited on : 2021-08-24
Resolution : 6.00 Å (reported)
Based on initial models : 4AQY, 6YSS, 5LZD

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

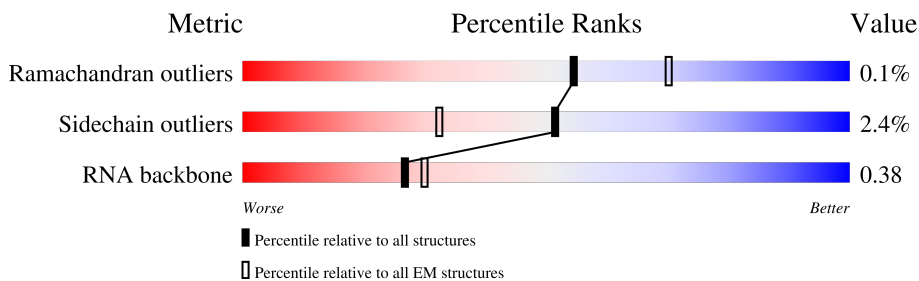
EMDB validation analysis : 0.0.0.dev97
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

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 6.00 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.




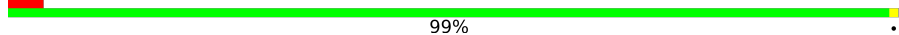
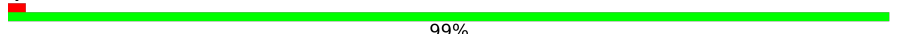
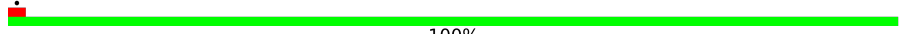




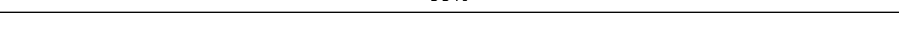
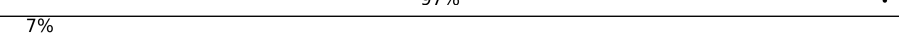
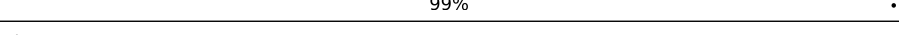
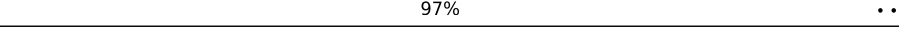
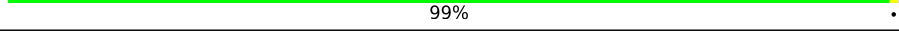
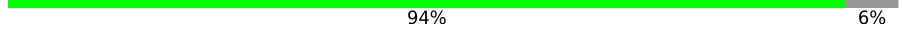
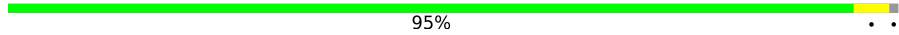
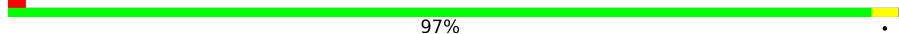
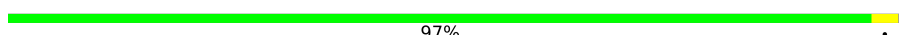
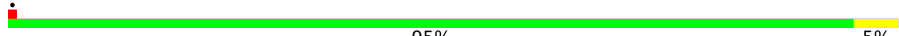






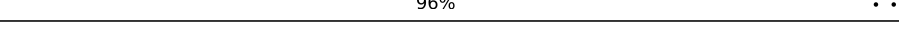
Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	57	
2	1	55	
3	2	46	
4	3	65	
5	4	38	
6	5	165	
7	6	70	
8	A	2903	

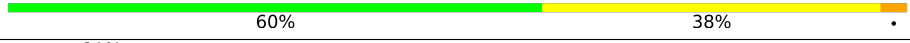


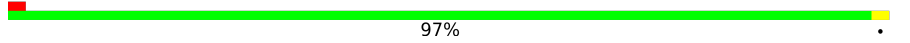
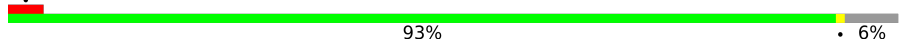


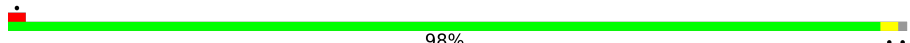
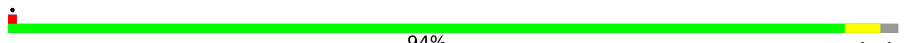
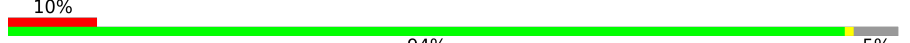

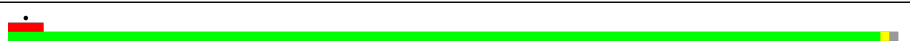



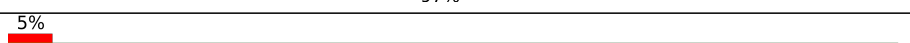
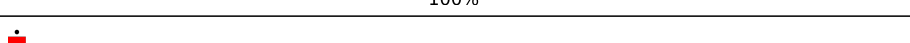
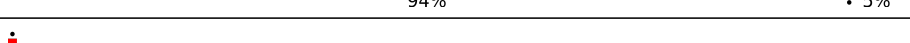


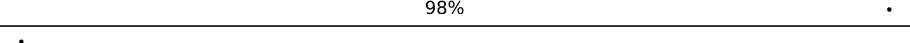
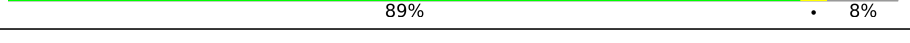


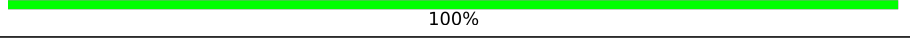
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Mol	Chain	Length	Quality of chain
9	B	120	 60% 39%
10	C	273	 99%
11	D	209	 99%
12	E	201	 100%
13	F	179	 95%
14	G	177	 98%
15	H	149	 51% 99%
16	I	142	 58% 99%
17	J	142	 97%
18	K	123	 7% 99%
19	L	144	 97%
20	M	136	 99%
21	N	127	 94% 6%
22	O	117	 95%
23	P	115	 97%
24	Q	118	 97%
25	R	103	 95% 5%
26	S	110	 95% 5%
27	T	100	 91% 7%
28	U	104	 96%
29	V	94	 100%
30	W	85	 87% 12%
31	X	78	 96%
32	Y	63	 92% 8%
33	Z	59	 98%

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Mol	Chain	Length	Quality of chain
34	a	1542	 60% 38%
35	b	240	 21% 90% 9%
36	c	233	 87% 12%
37	d	206	 97%
38	e	167	 93% 6%
39	f	135	 73% 26%
40	g	179	 9% 83% 16%
41	h	130	 98%
42	i	130	 94%
43	j	103	 10% 94% 5%
44	k	129	 88% 10%
45	l	124	 98%
46	m	118	 95%
47	n	102	 95%
48	o	89	 97%
49	p	82	 5% 100%
50	q	84	 94% 5%
51	r	75	 85% 13%
52	s	92	 83% 7% 11%
53	t	87	 98%
54	u	71	 89% 8%
55	v	77	 55% 38% 8%
56	w	76	 50% 45% 5%
57	y	2	 100%
58	z	33	 15% 18% 67%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 147222 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 L32.

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

- Molecule 2 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
2	1	50	409	263	75	71	0	0

- Molecule 3 is a protein called 50S ribosomal protein L34.

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

- Molecule 4 is a protein called 50S ribosomal protein L35.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	3	64	504	323	105	74	2	0	0

- Molecule 5 is a protein called 50S ribosomal protein L36.

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

- Molecule 6 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms				AltConf	Trace
			Total	C	N	O		
6	5	131	647	385	131	131	0	0

- Molecule 7 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
7	6	66	522	323	99	94	6	0	0

- Molecule 8 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
8	A	2902	62317	27806	11469	20140	2902	0	0

- Molecule 9 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
9	B	120	2570	1144	468	838	120	0	0

- Molecule 10 is a protein called 50S ribosomal protein L2.

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

- Molecule 11 is a protein called 50S ribosomal protein L3.

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

- Molecule 12 is a protein called 50S ribosomal protein L4.

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

- Molecule 13 is a protein called 50S ribosomal protein L5.

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

- Molecule 14 is a protein called 50S ribosomal protein L6.

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

- Molecule 15 is a protein called 50S ribosomal protein L9.

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

- Molecule 16 is a protein called 50S ribosomal protein L11.

Mol	Chain	Residues	Atoms				AltConf	Trace	
16	I	141	Total	C	N	O		0	0
			693	411	141	141			

- Molecule 17 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	142	Total	C	N	O	S	0	0
			1129	714	212	199	4		

- Molecule 18 is a protein called 50S ribosomal protein L14.

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

- Molecule 19 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	143	Total	C	N	O	S	0	0
			1045	649	206	189	1		

- Molecule 20 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	136	Total	C	N	O	S	0	0
			1074	686	205	177	6		

- Molecule 21 is a protein called 50S ribosomal protein L17.

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

- Molecule 22 is a protein called 50S ribosomal protein L18.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	O	116	Total	C	N	O	S	0	0
			892	552	178	162			

- Molecule 23 is a protein called 50S ribosomal protein L19.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	114	Total	C	N	O	S	0	0
			917	574	179	163	1		

- Molecule 24 is a protein called 50S ribosomal protein L20.

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

- Molecule 25 is a protein called 50S ribosomal protein L21.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	103	Total	C	N	O	S	0	0
			816	516	153	145	2		

- Molecule 26 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	110	Total	C	N	O	S	0	0
			857	532	166	156	3		

- Molecule 27 is a protein called 50S ribosomal protein L23.

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

- Molecule 28 is a protein called 50S ribosomal protein L24.

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

- Molecule 29 is a protein called 50S ribosomal protein L25.

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

- Molecule 30 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	W	75	Total	C	N	O	S	0	0
			575	356	116	102	1		

- Molecule 31 is a protein called 50S ribosomal protein L28.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	X	77	Total	C	N	O	S	0	0
			625	388	129	106	2		

- Molecule 32 is a protein called 50S ribosomal protein L29.

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

- Molecule 33 is a protein called 50S ribosomal protein L30.

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

- Molecule 34 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
34	a	1540	Total	C	N	O	P	0	0
			33050	14748	6057	10705	1540		

- Molecule 35 is a protein called 30S ribosomal protein S2.

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

- Molecule 36 is a protein called 30S ribosomal protein S3.

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

- Molecule 37 is a protein called 30S ribosomal protein S4.

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

- Molecule 38 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	e	157	Total	C	N	O	S	0	0
			1141	709	218	208	6		

- Molecule 39 is a protein called 30S ribosomal protein S6.

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

- Molecule 40 is a protein called 30S ribosomal protein S7.

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

- Molecule 41 is a protein called 30S ribosomal protein S8.

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

- Molecule 42 is a protein called 30S ribosomal protein S9.

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

- Molecule 43 is a protein called 30S ribosomal protein S10.

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

- Molecule 44 is a protein called 30S ribosomal protein S11.

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

- Molecule 45 is a protein called 30S ribosomal protein S12.

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

- Molecule 46 is a protein called 30S ribosomal protein S13.

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

- Molecule 47 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
47	n	101	799	498	165	133	3	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
n	35	ALA	-	insertion	UNP C3SR07

- Molecule 48 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	o	88	Total	C	N	O	S	0	0
			714	439	144	130	1		

- Molecule 49 is a protein called 30S ribosomal protein S16.

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

- Molecule 50 is a protein called 30S ribosomal protein S17.

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

- Molecule 51 is a protein called 30S ribosomal protein S18.

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

- Molecule 52 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	s	82	Total	C	N	O	S	0	0
			658	421	125	110	2		

- Molecule 53 is a protein called 30S ribosomal protein S20.

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

- Molecule 54 is a protein called 30S ribosomal protein S21.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	u	65	Total	C	N	O	S	0	0
			506	313	105	87	1		

- Molecule 55 is a RNA chain called P-site tRNA(fMet).

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	N	O	P			S
55	v	77	1642	733	297	534	77	1	0	0

- Molecule 56 is a RNA chain called P-site fMet-Phe-tRNA(Phe).

Mol	Chain	Residues	Atoms					AltConf	Trace	
			Total	C	N	O	P			S
56	w	76	1631	731	291	531	76	2	0	0

- Molecule 57 is a protein called Dipeptide (FME-PHE).

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
57	y	2	21	15	2	3	1	0	0

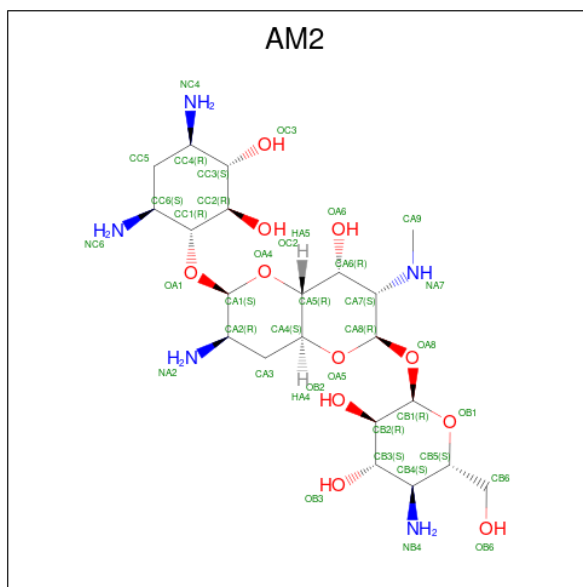
- Molecule 58 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
58	z	11	230	103	35	81	11	0	0

- Molecule 59 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
			Total	Zn	
59	4	1	1	1	0
59	6	1	1	1	0

- Molecule 60 is APRAMYCIN (three-letter code: AM2) (formula: C₂₁H₄₁N₅O₁₁).

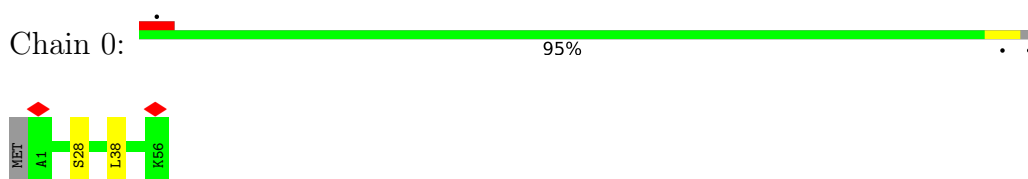


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
60	a	1	37	21	5	11	0

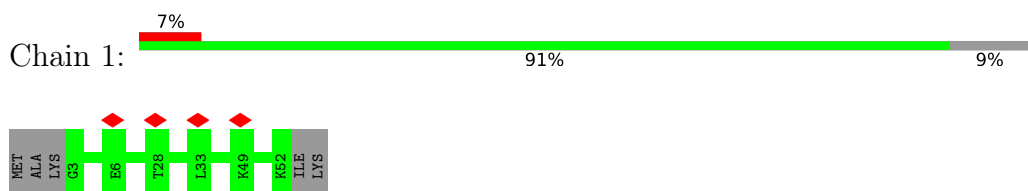
3 Residue-property plots [i](#)

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

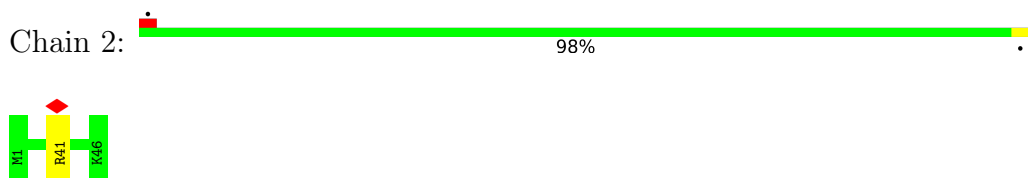
- Molecule 1: 50S ribosomal protein L32



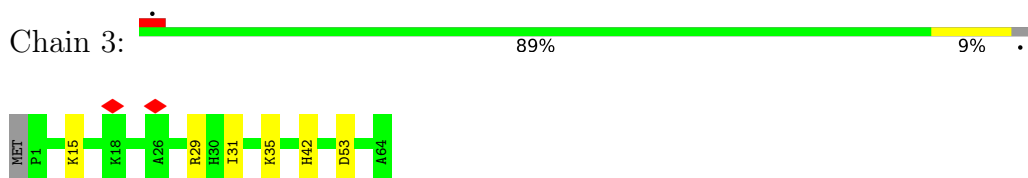
- Molecule 2: 50S ribosomal protein L33



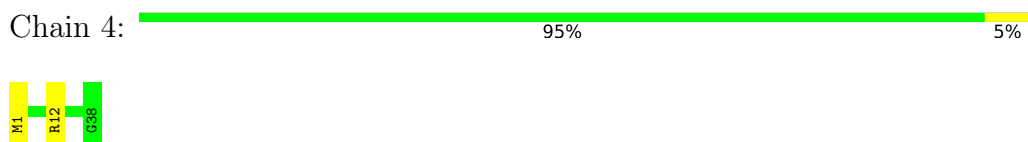
- Molecule 3: 50S ribosomal protein L34



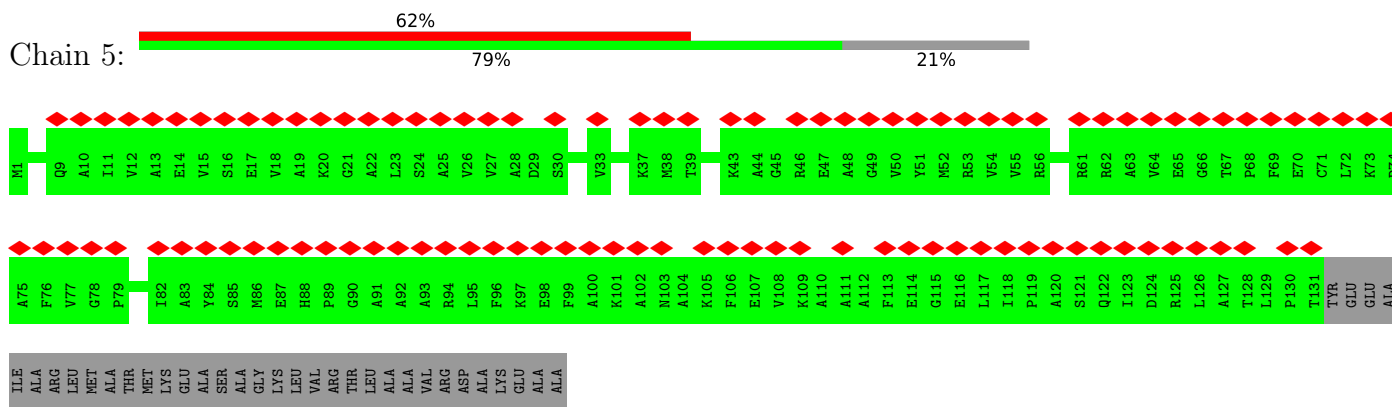
- Molecule 4: 50S ribosomal protein L35



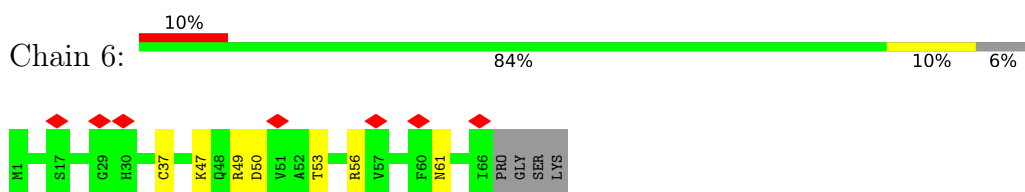
- Molecule 5: 50S ribosomal protein L36



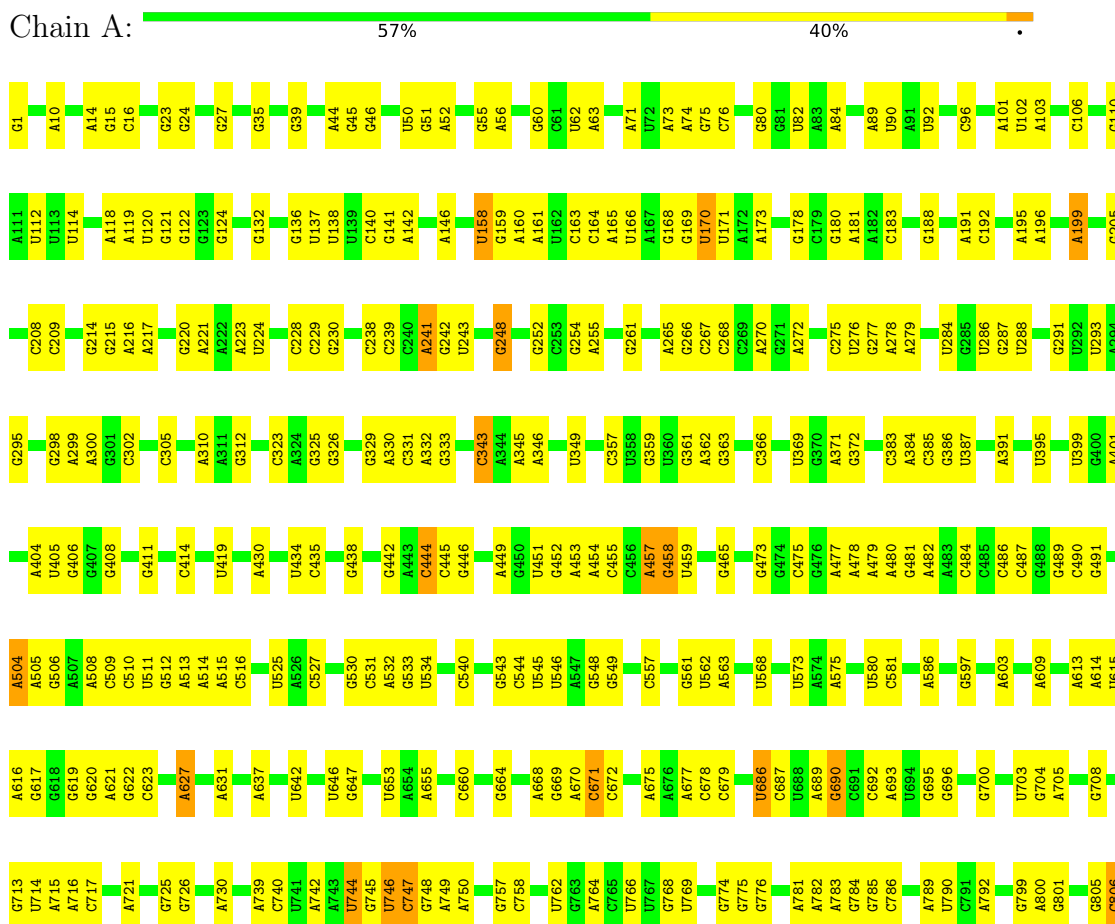
• Molecule 6: 50S ribosomal protein L10



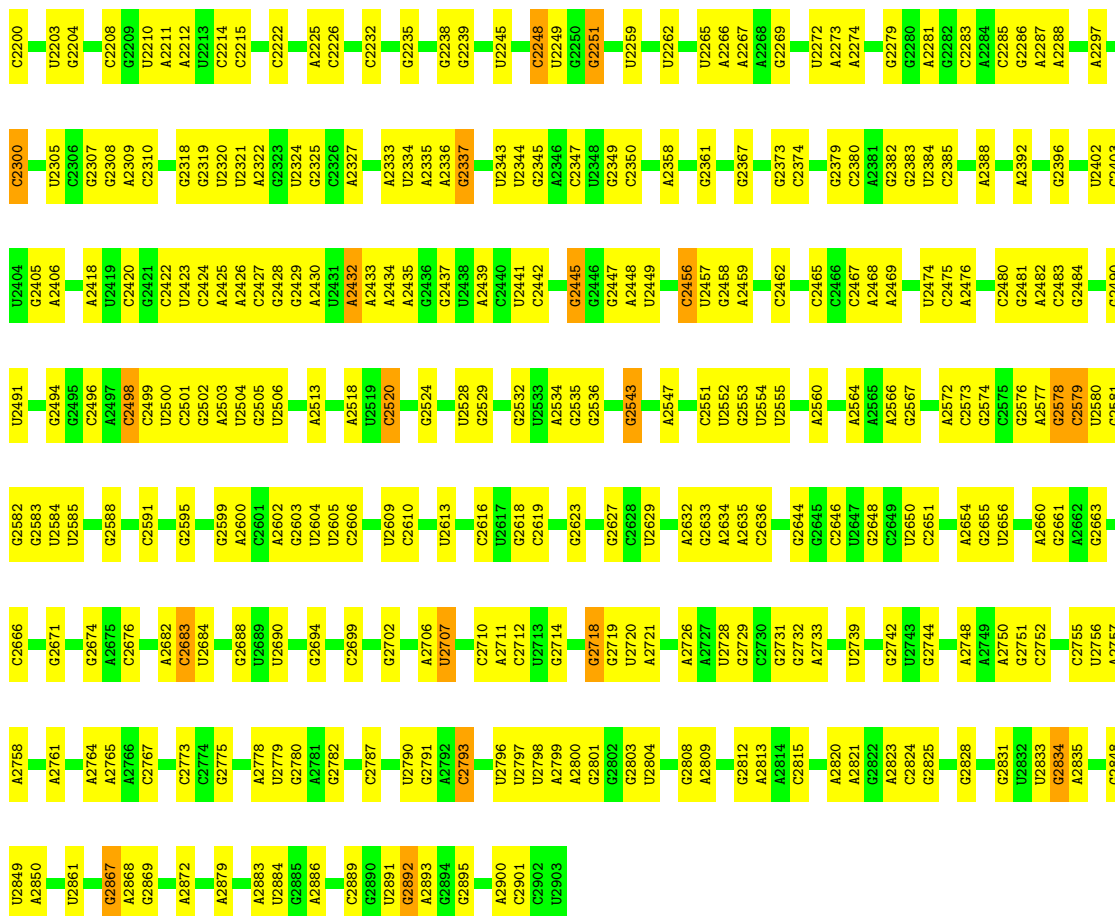
• Molecule 7: 50S ribosomal protein L31



• Molecule 8: 23S ribosomal RNA



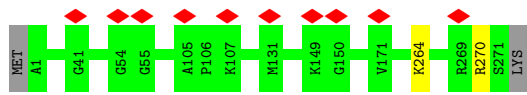
C2129	U1963	G1869	U1778	G1663	A1569	G1472	G1369	A1264	C1152	U1078	C995	A896	U807
U2130	G1964	G1873	U1779	A1664	A1570	G1473	C1370	U1255	A1152	C1079	A996	G808	G808
U2131	C1965	G1874	U1782	A1668	C1577	G1482	C1376	A1264	A1156	A1080	G1003	U811	U811
U2132	A1966	G1875	A1763	A1669	U1578	G1483	G1377	A1264	G1157	U1081	U1004	A899	A899
G2049	G1967	A1876	A1764	G1674	U1584	U1484	U1379	A1268	C1170	U1083	C1006	U1082	U1082
A2051	A1968	G1884	A1765	C1675	U1585	U1488	G1380	A1269	G1171	A1084	A1010	C901	C901
A2052	A1970	C1894	A1767	C1675	U1585	C1488	G1380	A1269	G1171	A1086	A1010	C902	C902
C2055	G1971	C1894	C1768	C1691	U1585	C1488	G1380	A1269	G1171	A1086	A1010	C903	C903
G2056	C1895	C1895	C1768	C1691	U1585	C1488	G1380	A1269	G1171	A1086	A1010	C903	C903
G2057	C1895	C1895	C1768	C1691	U1585	C1488	G1380	A1269	G1171	A1086	A1010	C903	C903
A2060	A1977	A1899	G1797	G1797	U1594	G1492	C1386	A1284	C1172	A1090	C1013	U826	U826
G2061	U1979	A1900	C1800	C1695	U1594	C1492	C1386	A1284	C1172	A1090	C1013	U826	U826
A2062	U1980	A1901	A1801	A1698	U1596	A1494	A1393	A1286	G1179	C1092	U1023	U828	U828
C2063	A1981	C1902	C1804	A1699	U1597	A1495	U1394	A1286	G1179	C1092	U1023	U828	U828
G2067	U1982	C1905	C1804	A1700	U1598	A1496	A1395	A1288	U1180	G1093	G1024	A829	A829
U2068	C1985	C1906	A1808	A1701	U1599	A1497	U1396	A1289	U1183	A1095	G1025	G831	G831
C2069	C1990	C1907	A1809	A1702	C1600	A1502	U1397	A1292	U1183	A1096	G1026	G834	G834
C2150	C1991	C1908	A1810	A1703	C1607	A1503	C1398	A1292	U1186	U1097	A1029	C835	C835
G2152	U1991	C1909	A1811	C1704	A1608	A1504	G1410	A1293	G1187	A1098	G926	G836	G836
C2153	U1992	C1910	U1812	A1505	A1609	A1505	U1411	A1293	G1187	A1098	G926	G836	G836
A2154	U1993	U1911	G1813	A1506	A1610	A1506	U1412	A1300	U1188	C1100	A927	C837	C837
U2155	C1997	C1914	G1814	U1506	A1610	U1506	U1412	A1301	G1193	U1101	U931	G841	G841
G2156	C1997	C1914	G1814	U1506	A1610	U1506	U1412	A1301	G1193	U1101	U931	G841	G841
G2157	C1997	C1914	G1814	U1506	A1610	U1506	U1412	A1301	G1193	U1101	U931	G841	G841
C2158	C2001	3TD	A1815	U1716	A1616	A1509	G1414	A1302	A1204	A1103	G1041	A845	A845
G2159	C2002	U1916	G1817	C1726	A1617	A1512	U1415	A1306	A1205	C1104	C1044	U846	U846
A2003	A2003	U1917	G1817	C1727	A1618	A1512	U1416	A1306	A1205	C1104	C1044	U846	U846
C2161	C2160	U1918	U1820	A1728	G1622	A1515	C1417	A1311	U2029	G1109	G1047	U850	U850
C2162	U2007	A1919	A1821	U1729	G1623	A1521	G1418	A1312	G1210	C1110	A048	G856	G856
A2163	U2009	C1920	G1824	C1730	G1623	G1521	A1419	A1313	C1211	C1111	C1049	G857	G857
C2164	C2009	C1921	G1824	C1731	A1626	G1524	A1420	A1314	G1212	A1111	A1050	G858	G858
C2165	A2009	U1922	G1828	C1732	G1627	G1524	G1421	A1315	G1213	G1112	C1051	G859	G859
C2166	C2012	U1923	A1829	G1733	G1628	A1528	G1425	A1322	G1218	G1114	C1053	C865	C865
U2166	A2013	C1924	C1830	A1735	G1631	A1532	C1428	A1323	G1218	G1115	A1054	C865	C865
A2101	A2014	U1926	C1833	G1738	G1631	A1532	G1429	A1324	U1224	G1122	G1055	U868	U868
C2102	A2015	A1927	U1834	C1750	A1635	C1533	G1432	A1325	G1225	A1129	G1056	U868	U868
C2103	U2016	U1928	G1835	U1750	A1635	U1534	G1433	A1328	A1226	C1123	A1057	G869	G869
C2104	U2016	G1929	G1835	U1751	C1638	A1535	A1433	A1328	G1227	G1128	U1058	U870	U870
U2109	A2019	U1930	G1845	C1752	C1638	C1536	A1434	A1331	G1228	A1128	U1059	A877	A877
C2110	C2021	A1932	G1846	G1753	C1639	G1537	G1435	A1332	G1228	A1128	U1060	A878	A878
U2111	U2022	U1932	G1847	A1754	G1643	A1544	G1448	A1332	G1228	A1128	U1061	A878	A878
G2112	C2023	G1935	A1848	A1754	C1644	A1544	G1448	A1332	G1228	A1128	U1061	A878	A878
A2118	G2027	A1938	U1852	A1757	G1645	C1547	C1451	A1336	U1234	A1130	G1062	G881	G881
G2114	U2028	U1939	U1758	U1758	G1645	C1547	C1451	A1336	U1234	A1130	G1062	G881	G881
G2115	G2029	U1940	A1759	U1759	C1646	A1551	G1452	A1340	G1237	G1131	C1063	G882	G882
G2116	G2029	U1940	A1759	U1759	C1646	A1551	G1452	A1340	G1237	G1131	C1063	G882	G882
A2117	A2030	C1941	G1857	C1764	U1648	A1552	C1454	A1342	U1241	A1133	U1065	G883	G883
U2118	A2030	C1941	G1858	C1764	U1649	A1553	G1455	A1342	U1241	A1133	U1065	G883	G883
A2119	U1944	U1944	A1859	G1767	A1650	U1554	U1455	A1344	A1244	G1139	A1069	A886	A886
G2123	G2032	G1945	G1860	C1768	A1651	C1345	U1458	A1346	A1244	A1142	A1070	A887	A887
G2124	U2034	U1946	G1862	U1769	A1654	C1346	U1460	A1346	A1245	A1142	A1071	C888	C888
G2125	C2036	U1955	U1865	U1773	A1657	U1562	U1461	U1352	G1248	A1143	C1072	C889	C889
A2126	U1956	U1956	A1866	U1774	C1658	U1563	U1466	A1365	U1249	A1144	A1073	C890	C890
G2127	C2040	C1962	G1867	U1775	U1662	U1563	U1466	A1365	U1249	A1144	A1073	C890	C890
G2128	U2041	C1962	C1868	U1775	U1662	U1563	U1466	A1365	U1249	A1144	A1073	C890	C890



• Molecule 9: 5S ribosomal RNA

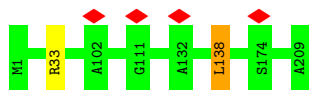


• Molecule 10: 50S ribosomal protein L2

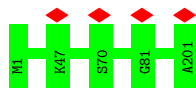


• Molecule 11: 50S ribosomal protein L3

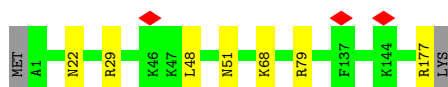




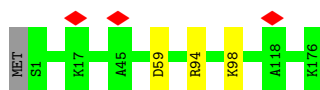
- Molecule 12: 50S ribosomal protein L4



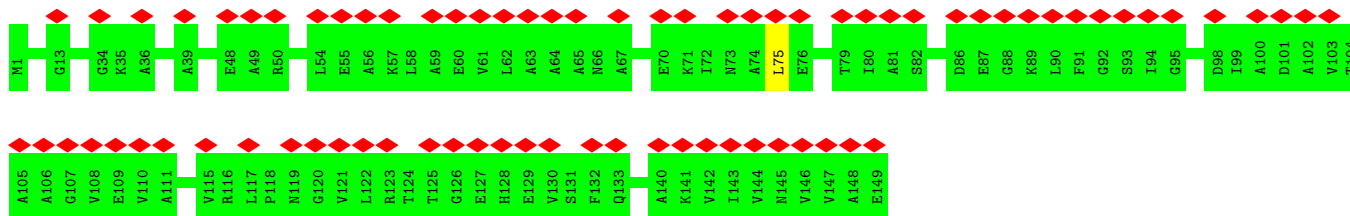
- Molecule 13: 50S ribosomal protein L5



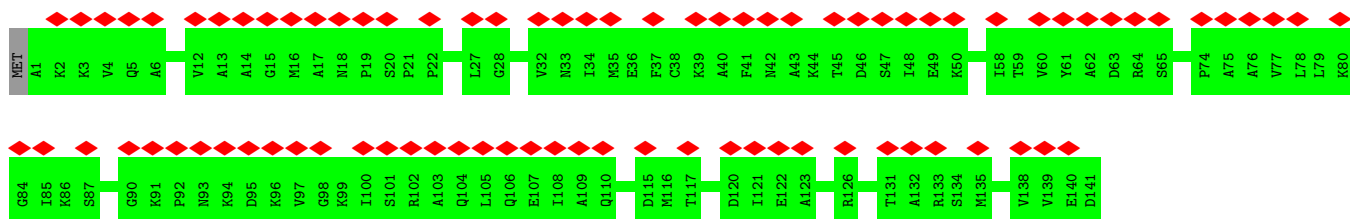
- Molecule 14: 50S ribosomal protein L6



- Molecule 15: 50S ribosomal protein L9

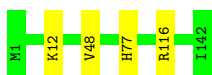


- Molecule 16: 50S ribosomal protein L11



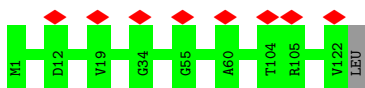
- Molecule 17: 50S ribosomal protein L13

Chain J:  97%



- Molecule 18: 50S ribosomal protein L14

Chain K:  99%



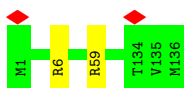
- Molecule 19: 50S ribosomal protein L15

Chain L:  97%



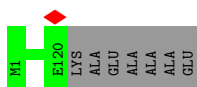
- Molecule 20: 50S ribosomal protein L16

Chain M:  99%



- Molecule 21: 50S ribosomal protein L17

Chain N:  94% 6%



- Molecule 22: 50S ribosomal protein L18

Chain O:  95%



- Molecule 23: 50S ribosomal protein L19

Chain P:  97%



- Molecule 24: 50S ribosomal protein L20

Chain Q:  97%



- Molecule 25: 50S ribosomal protein L21

Chain R:  95%




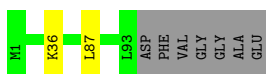
- Molecule 26: 50S ribosomal protein L22

Chain S:  95%



- Molecule 27: 50S ribosomal protein L23

Chain T:  91%



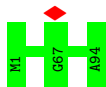
- Molecule 28: 50S ribosomal protein L24

Chain U:  96%




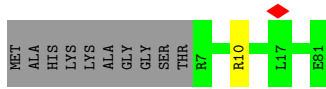
- Molecule 29: 50S ribosomal protein L25

Chain V:  100%

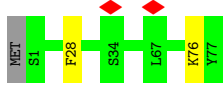


- Molecule 30: 50S ribosomal protein L27

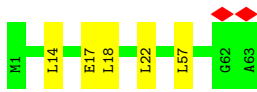
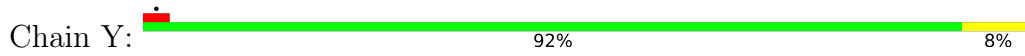
Chain W:  87%



- Molecule 31: 50S ribosomal protein L28



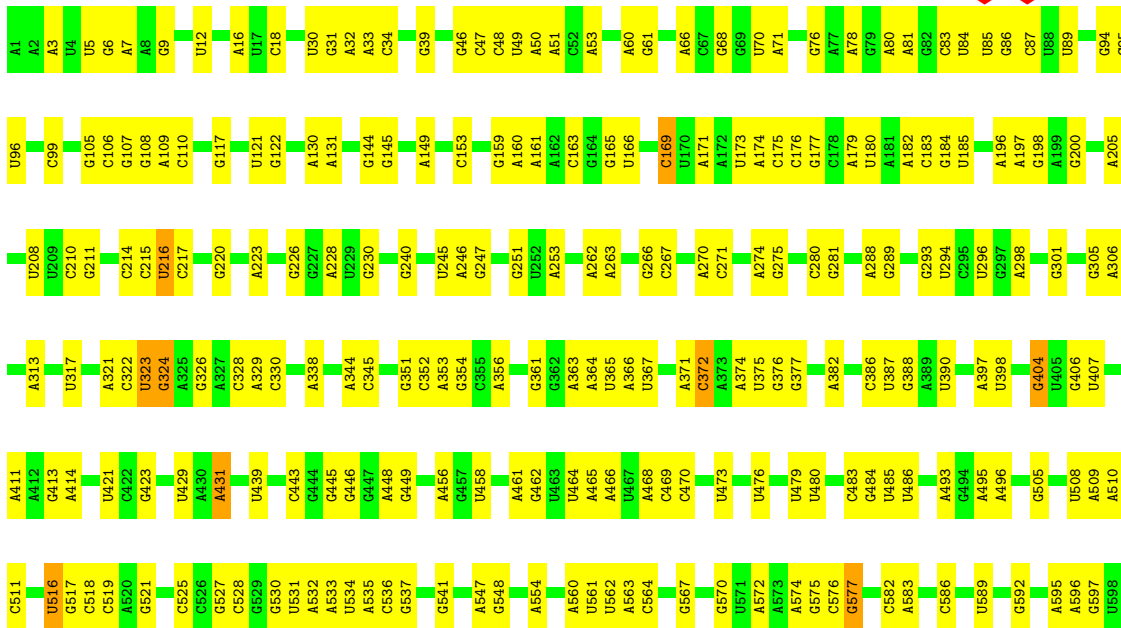
- Molecule 32: 50S ribosomal protein L29

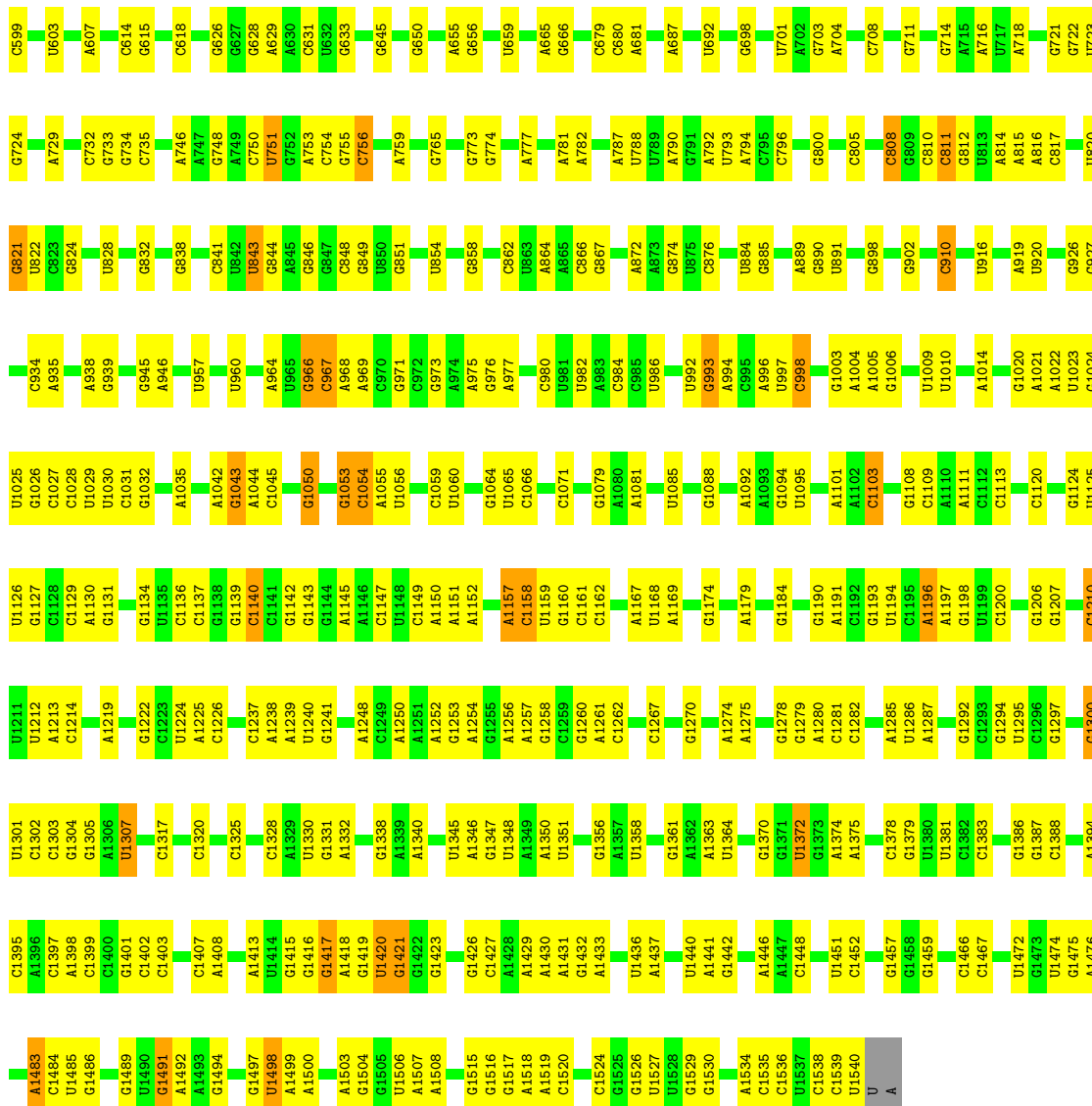


- Molecule 33: 50S ribosomal protein L30

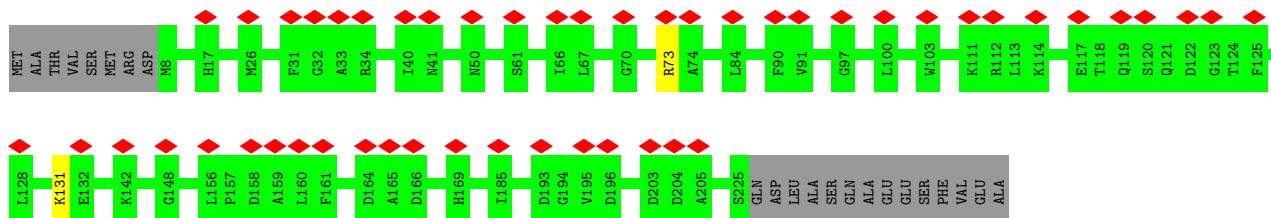
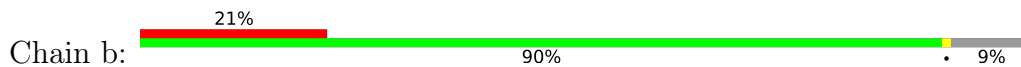


- Molecule 34: 16S ribosomal RNA

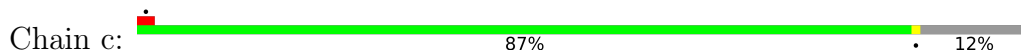


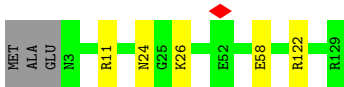


- Molecule 35: 30S ribosomal protein S2

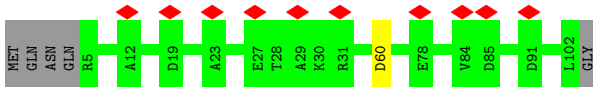
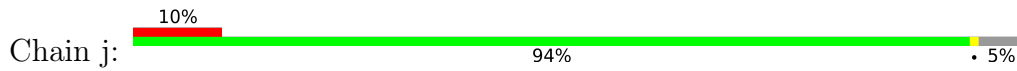


- Molecule 36: 30S ribosomal protein S3

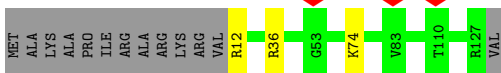
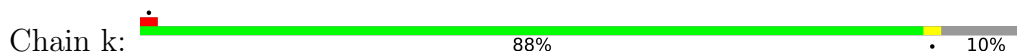




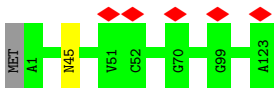
- Molecule 43: 30S ribosomal protein S10



- Molecule 44: 30S ribosomal protein S11



- Molecule 45: 30S ribosomal protein S12



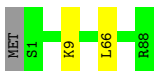
- Molecule 46: 30S ribosomal protein S13



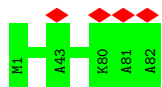
- Molecule 47: 30S ribosomal protein S14



- Molecule 48: 30S ribosomal protein S15



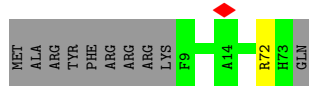
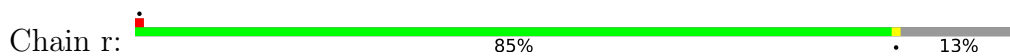
- Molecule 49: 30S ribosomal protein S16



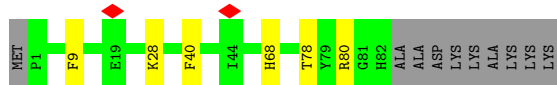
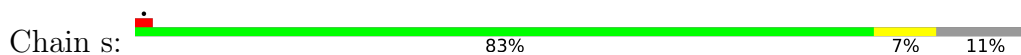
• Molecule 50: 30S ribosomal protein S17



• Molecule 51: 30S ribosomal protein S18



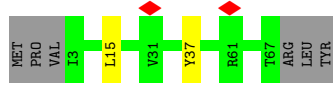
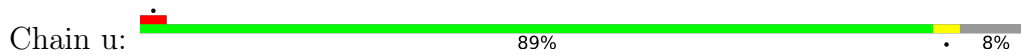
• Molecule 52: 30S ribosomal protein S19



• Molecule 53: 30S ribosomal protein S20



• Molecule 54: 30S ribosomal protein S21



• Molecule 55: P-site tRNA(fMet)



- Molecule 56: P-site fMet-Phe-tRNA(Phe)

Chain w:  50% 45% 5%



- Molecule 57: Dipeptide (FME-PHE)

Chain y:  100%

There are no outlier residues recorded for this chain.

- Molecule 58: mRNA

Chain z:  15% 18% 67%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	6937	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 ($e^-/\text{\AA}^2$)	30	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1200	Depositor
Magnification	59000	Depositor
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	11.607	Depositor
Minimum map value	-7.178	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	1.5	Depositor
Map size (\AA)	334.08, 334.08, 334.08	wwPDB
Map dimensions	288, 288, 288	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (\AA)	1.16, 1.16, 1.16	Depositor

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: FME, 1MG, ZN, H2U, MIA, 2MG, MA6, G7M, OMC, 6MZ, OMU, 2MA, UR3, PSU, 4OC, OMG, 5MC, 5MU, 4SU, AM2

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	0.53	0/450	0.60	0/599
2	1	0.39	0/416	0.52	0/554
3	2	0.46	0/380	0.66	0/498
4	3	0.50	0/513	0.69	0/676
5	4	0.43	0/303	0.60	0/397
6	5	0.26	0/646	0.51	0/898
7	6	0.49	0/531	0.73	0/709
8	A	1.04	22/69266 (0.0%)	1.20	242/108055 (0.2%)
9	B	0.87	2/2873 (0.1%)	1.10	1/4478 (0.0%)
10	C	0.48	0/2121	0.62	0/2852
11	D	0.47	0/1586	0.62	0/2134
12	E	0.46	0/1571	0.60	0/2113
13	F	0.43	0/1434	0.59	0/1926
14	G	0.40	0/1343	0.57	0/1816
15	H	0.38	0/1122	0.61	0/1515
16	I	0.26	0/692	0.50	0/960
17	J	0.50	0/1152	0.55	0/1551
18	K	0.43	0/947	0.61	0/1268
19	L	0.48	0/1054	0.69	1/1403 (0.1%)
20	M	0.46	0/1093	0.57	0/1460
21	N	0.42	0/973	0.62	0/1301
22	O	0.43	0/902	0.61	0/1209
23	P	0.47	0/929	0.63	2/1242 (0.2%)
24	Q	0.50	0/960	0.60	1/1278 (0.1%)
25	R	0.47	0/829	0.64	0/1107
26	S	0.44	0/864	0.61	0/1156
27	T	0.42	0/744	0.62	0/994
28	U	0.46	0/787	0.61	0/1051
29	V	0.46	0/766	0.57	0/1025
30	W	0.45	0/582	0.63	0/769
31	X	0.44	0/635	0.66	1/848 (0.1%)

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	Y	0.41	0/510	0.64	0/677
33	Z	0.40	0/453	0.55	0/605
34	a	0.91	3/36725 (0.0%)	1.17	121/57285 (0.2%)
35	b	0.37	0/1735	0.57	0/2338
36	c	0.43	0/1651	0.56	1/2225 (0.0%)
37	d	0.39	0/1665	0.59	0/2227
38	e	0.42	0/1154	0.58	0/1554
39	f	0.38	0/835	0.56	0/1128
40	g	0.37	0/1195	0.54	0/1602
41	h	0.41	0/989	0.59	0/1326
42	i	0.42	0/1034	0.60	0/1375
43	j	0.37	0/796	0.62	0/1077
44	k	0.43	0/885	0.61	0/1195
45	l	0.44	0/969	0.60	0/1300
46	m	0.37	0/892	0.60	0/1193
47	n	0.45	0/811	0.69	0/1081
48	o	0.40	0/722	0.63	1/964 (0.1%)
49	p	0.40	0/659	0.58	0/884
50	q	0.41	0/657	0.59	0/881
51	r	0.42	0/544	0.60	0/731
52	s	0.46	0/675	0.69	0/908
53	t	0.38	0/671	0.51	0/888
54	u	0.40	0/512	0.56	0/683
55	v	0.83	1/1745 (0.1%)	1.17	7/2716 (0.3%)
56	w	0.69	0/1650	1.17	5/2569 (0.2%)
57	y	0.63	0/11	0.43	0/13
58	z	0.53	0/255	0.95	0/394
All	All	0.86	28/158864 (0.0%)	1.07	383/237661 (0.2%)

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
55	v	1	C	OP3-P	-10.75	1.48	1.61
9	B	1	U	OP3-P	-10.74	1.48	1.61
8	A	1	G	OP3-P	-10.73	1.48	1.61
8	A	1786	A	N9-C4	-7.76	1.33	1.37
8	A	195	A	N9-C4	-6.71	1.33	1.37

The worst 5 of 383 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1054	C	O5'-P-OP1	14.14	127.67	110.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	1196	A	C2'-C3'-O3'	9.93	131.35	109.50
34	a	1053	G	O3'-P-O5'	-9.74	85.50	104.00
34	a	1421	G	N9-C4-C5	9.61	109.24	105.40
34	a	1421	G	C8-N9-C1'	9.46	139.30	127.00

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	54/57 (95%)	42 (78%)	12 (22%)	0	100	100
2	1	48/55 (87%)	38 (79%)	10 (21%)	0	100	100
3	2	44/46 (96%)	27 (61%)	17 (39%)	0	100	100
4	3	62/65 (95%)	48 (77%)	14 (23%)	0	100	100
5	4	36/38 (95%)	28 (78%)	8 (22%)	0	100	100
6	5	129/165 (78%)	100 (78%)	29 (22%)	0	100	100
7	6	64/70 (91%)	54 (84%)	10 (16%)	0	100	100
10	C	269/273 (98%)	213 (79%)	56 (21%)	0	100	100
11	D	207/209 (99%)	172 (83%)	34 (16%)	1 (0%)	29	69
12	E	199/201 (99%)	165 (83%)	34 (17%)	0	100	100
13	F	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
14	G	174/177 (98%)	149 (86%)	25 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	H	147/149 (99%)	117 (80%)	30 (20%)	0	100	100
16	I	139/142 (98%)	104 (75%)	35 (25%)	0	100	100
17	J	140/142 (99%)	109 (78%)	31 (22%)	0	100	100
18	K	120/123 (98%)	101 (84%)	19 (16%)	0	100	100
19	L	141/144 (98%)	108 (77%)	33 (23%)	0	100	100
20	M	134/136 (98%)	109 (81%)	24 (18%)	1 (1%)	22	62
21	N	118/127 (93%)	87 (74%)	31 (26%)	0	100	100
22	O	114/117 (97%)	101 (89%)	13 (11%)	0	100	100
23	P	112/115 (97%)	98 (88%)	14 (12%)	0	100	100
24	Q	115/118 (98%)	102 (89%)	13 (11%)	0	100	100
25	R	101/103 (98%)	87 (86%)	14 (14%)	0	100	100
26	S	108/110 (98%)	89 (82%)	19 (18%)	0	100	100
27	T	91/100 (91%)	74 (81%)	17 (19%)	0	100	100
28	U	100/104 (96%)	81 (81%)	19 (19%)	0	100	100
29	V	92/94 (98%)	79 (86%)	13 (14%)	0	100	100
30	W	73/85 (86%)	56 (77%)	17 (23%)	0	100	100
31	X	75/78 (96%)	63 (84%)	12 (16%)	0	100	100
32	Y	61/63 (97%)	49 (80%)	12 (20%)	0	100	100
33	Z	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
35	b	216/240 (90%)	184 (85%)	32 (15%)	0	100	100
36	c	204/233 (88%)	181 (89%)	23 (11%)	0	100	100
37	d	203/206 (98%)	160 (79%)	42 (21%)	1 (0%)	29	69
38	e	155/167 (93%)	119 (77%)	36 (23%)	0	100	100
39	f	98/135 (73%)	88 (90%)	10 (10%)	0	100	100
40	g	149/179 (83%)	130 (87%)	19 (13%)	0	100	100
41	h	127/130 (98%)	107 (84%)	20 (16%)	0	100	100
42	i	125/130 (96%)	98 (78%)	27 (22%)	0	100	100
43	j	96/103 (93%)	76 (79%)	19 (20%)	1 (1%)	15	54
44	k	114/129 (88%)	92 (81%)	22 (19%)	0	100	100
45	l	121/124 (98%)	96 (79%)	25 (21%)	0	100	100
46	m	112/118 (95%)	99 (88%)	13 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
47	n	99/102 (97%)	87 (88%)	12 (12%)	0	100	100
48	o	86/89 (97%)	74 (86%)	12 (14%)	0	100	100
49	p	80/82 (98%)	61 (76%)	19 (24%)	0	100	100
50	q	78/84 (93%)	68 (87%)	10 (13%)	0	100	100
51	r	63/75 (84%)	49 (78%)	14 (22%)	0	100	100
52	s	80/92 (87%)	70 (88%)	10 (12%)	0	100	100
53	t	83/87 (95%)	66 (80%)	17 (20%)	0	100	100
54	u	63/71 (89%)	50 (79%)	13 (21%)	0	100	100
All	All	5850/6220 (94%)	4809 (82%)	1037 (18%)	4 (0%)	54	85

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
43	j	60	ASP
37	d	144	ILE
11	D	138	LEU
20	M	59	ARG

5.3.2 Protein sidechains [i](#)

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	47/48 (98%)	45 (96%)	2 (4%)	29	54
2	1	45/49 (92%)	45 (100%)	0	100	100
3	2	38/38 (100%)	37 (97%)	1 (3%)	46	67
4	3	51/52 (98%)	45 (88%)	6 (12%)	5	21
5	4	34/34 (100%)	32 (94%)	2 (6%)	19	45
7	6	59/62 (95%)	52 (88%)	7 (12%)	5	20
10	C	216/218 (99%)	214 (99%)	2 (1%)	78	88
11	D	164/164 (100%)	162 (99%)	2 (1%)	71	84

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
12	E	165/165 (100%)	165 (100%)	0	100	100
13	F	148/150 (99%)	141 (95%)	7 (5%)	26	51
14	G	137/138 (99%)	134 (98%)	3 (2%)	52	71
15	H	114/114 (100%)	113 (99%)	1 (1%)	78	88
17	J	116/116 (100%)	112 (97%)	4 (3%)	37	60
18	K	103/104 (99%)	103 (100%)	0	100	100
19	L	102/103 (99%)	100 (98%)	2 (2%)	55	74
20	M	109/109 (100%)	108 (99%)	1 (1%)	78	88
21	N	100/103 (97%)	100 (100%)	0	100	100
22	O	86/87 (99%)	81 (94%)	5 (6%)	20	45
23	P	99/100 (99%)	98 (99%)	1 (1%)	76	86
24	Q	89/90 (99%)	87 (98%)	2 (2%)	52	71
25	R	84/84 (100%)	79 (94%)	5 (6%)	19	44
26	S	93/93 (100%)	88 (95%)	5 (5%)	22	47
27	T	80/84 (95%)	78 (98%)	2 (2%)	47	68
28	U	83/85 (98%)	81 (98%)	2 (2%)	49	69
29	V	78/78 (100%)	78 (100%)	0	100	100
30	W	57/63 (90%)	56 (98%)	1 (2%)	59	77
31	X	67/68 (98%)	66 (98%)	1 (2%)	65	80
32	Y	55/55 (100%)	50 (91%)	5 (9%)	9	30
33	Z	48/49 (98%)	48 (100%)	0	100	100
35	b	180/198 (91%)	178 (99%)	2 (1%)	73	84
36	c	170/190 (90%)	168 (99%)	2 (1%)	71	84
37	d	172/173 (99%)	168 (98%)	4 (2%)	50	71
38	e	114/126 (90%)	113 (99%)	1 (1%)	78	88
39	f	87/116 (75%)	85 (98%)	2 (2%)	50	71
40	g	124/147 (84%)	121 (98%)	3 (2%)	49	69
41	h	104/105 (99%)	102 (98%)	2 (2%)	57	75
42	i	105/107 (98%)	100 (95%)	5 (5%)	25	51
43	j	86/90 (96%)	86 (100%)	0	100	100
44	k	89/99 (90%)	86 (97%)	3 (3%)	37	60

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
45	l	103/104 (99%)	102 (99%)	1 (1%)	76	86
46	m	92/96 (96%)	90 (98%)	2 (2%)	52	71
47	n	79/84 (94%)	75 (95%)	4 (5%)	24	49
48	o	76/77 (99%)	75 (99%)	1 (1%)	69	82
49	p	65/65 (100%)	65 (100%)	0	100	100
50	q	74/78 (95%)	73 (99%)	1 (1%)	67	80
51	r	56/65 (86%)	55 (98%)	1 (2%)	59	77
52	s	72/79 (91%)	66 (92%)	6 (8%)	11	34
53	t	65/66 (98%)	65 (100%)	0	100	100
54	u	46/61 (75%)	44 (96%)	2 (4%)	29	54
57	y	1/1 (100%)	1 (100%)	0	100	100
All	All	4627/4830 (96%)	4516 (98%)	111 (2%)	51	69

5 of 111 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
26	S	104	THR
54	u	37	TYR
36	c	167	TYR
54	u	15	LEU
47	n	63	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 93 such sidechains are listed below:

Mol	Chain	Res	Type
32	Y	45	GLN
41	h	75	GLN
35	b	17	HIS
39	f	3	HIS
44	k	80	ASN

5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
34	a	1536/1542 (99%)	575 (37%)	0
55	v	76/77 (98%)	30 (39%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
56	w	74/76 (97%)	32 (43%)	0
58	z	10/33 (30%)	6 (60%)	0
8	A	2897/2903 (99%)	1092 (37%)	86 (2%)
9	B	119/120 (99%)	46 (38%)	2 (1%)
All	All	4712/4751 (99%)	1781 (37%)	88 (1%)

5 of 1781 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
8	A	10	A
8	A	14	A
8	A	15	G
8	A	16	C
8	A	23	G

5 of 88 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	1921	G
8	A	2405	G
8	A	2015	A
8	A	2192	U
8	A	2474	U

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

45 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	OMC	A	2498	8	15,22,23	1.04	2 (13%)	17,31,34	1.53	2 (11%)
34	MA6	a	1519	34	19,26,27	1.07	1 (5%)	18,38,41	2.72	2 (11%)
56	PSU	w	32	56	17,21,22	1.00	1 (5%)	20,30,33	3.28	7 (35%)
8	PSU	A	746	8	17,21,22	1.09	2 (11%)	20,30,33	3.08	6 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
55	4SU	v	8	55	14,21,22	3.18	5 (35%)	15,30,33	1.57	2 (13%)
8	G7M	A	2069	8	20,26,27	3.25	8 (40%)	20,39,42	3.03	6 (30%)
8	1MG	A	745	8	18,26,27	3.39	7 (38%)	19,39,42	2.44	3 (15%)
55	5MU	v	54	55	15,22,23	2.84	3 (20%)	16,32,35	2.70	2 (12%)
34	PSU	a	516	34	17,21,22	1.07	2 (11%)	20,30,33	3.37	7 (35%)
56	MIA	w	37	56	24,31,32	2.44	4 (16%)	26,44,47	3.10	9 (34%)
34	G7M	a	527	34	20,26,27	3.23	8 (40%)	20,39,42	2.06	3 (15%)
8	PSU	A	2604	8	17,21,22	1.11	2 (11%)	20,30,33	3.06	7 (35%)
8	6MZ	A	1618	8	18,25,26	4.09	8 (44%)	16,36,39	2.40	6 (37%)
8	OMU	A	2552	8	14,22,23	3.33	5 (35%)	14,31,34	0.78	0
34	2MG	a	1516	34	19,26,27	4.64	8 (42%)	21,38,41	2.28	7 (33%)
56	G7M	w	46	56	20,26,27	3.28	8 (40%)	20,39,42	2.33	5 (25%)
8	PSU	A	2605	8	17,21,22	0.95	1 (5%)	20,30,33	2.89	6 (30%)
8	5MU	A	1939	8	15,22,23	2.84	3 (20%)	16,32,35	2.71	2 (12%)
8	5MC	A	747	8	15,22,23	3.10	5 (33%)	19,32,35	1.33	1 (5%)
56	5MU	w	54	56	15,22,23	1.17	2 (13%)	16,32,35	2.15	3 (18%)
8	OMG	A	2251	56,8	18,26,27	3.50	7 (38%)	20,38,41	1.79	3 (15%)
34	5MC	a	967	34	15,22,23	3.18	5 (33%)	19,32,35	1.18	2 (10%)
8	PSU	A	2580	8	17,21,22	1.71	2 (11%)	20,30,33	3.24	9 (45%)
56	4SU	w	8	56	14,21,22	3.36	5 (35%)	15,30,33	1.18	2 (13%)
34	4OC	a	1402	34	16,23,24	3.02	6 (37%)	17,32,35	0.97	1 (5%)
55	PSU	v	55	55	17,21,22	0.97	1 (5%)	20,30,33	3.03	6 (30%)
8	PSU	A	1911	8	17,21,22	1.47	3 (17%)	20,30,33	3.12	6 (30%)
8	5MC	A	1962	8	15,22,23	3.05	5 (33%)	19,32,35	1.37	3 (15%)
34	MA6	a	1518	34	19,26,27	1.10	1 (5%)	18,38,41	1.94	2 (11%)
8	PSU	A	2457	8	17,21,22	1.19	3 (17%)	20,30,33	2.93	6 (30%)
8	2MG	A	2445	8	19,26,27	4.57	8 (42%)	21,38,41	2.20	7 (33%)
34	5MC	a	1407	34	15,22,23	2.87	5 (33%)	19,32,35	1.18	1 (5%)
8	PSU	A	955	8	17,21,22	1.43	2 (11%)	20,30,33	3.33	7 (35%)
8	2MG	A	1835	8	19,26,27	4.73	8 (42%)	21,38,41	2.37	6 (28%)
8	6MZ	A	2030	8	18,25,26	4.06	8 (44%)	16,36,39	2.60	4 (25%)
56	PSU	w	39	56	17,21,22	0.92	1 (5%)	20,30,33	3.11	7 (35%)
34	2MG	a	1207	34	19,26,27	4.47	8 (42%)	21,38,41	2.13	7 (33%)
34	UR3	a	1498	34	14,22,23	2.63	4 (28%)	15,32,35	0.77	0
8	PSU	A	1917	8	17,21,22	1.05	2 (11%)	20,30,33	2.85	6 (30%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
56	PSU	w	55	56	17,21,22	1.97	5 (29%)	20,30,33	3.38	6 (30%)
57	FME	y	101	57	8,9,10	0.90	0	7,9,11	1.14	0
8	2MA	A	2503	8	17,25,26	3.35	6 (35%)	19,37,40	1.97	5 (26%)
34	2MG	a	966	34	19,26,27	4.73	8 (42%)	21,38,41	2.29	6 (28%)
8	PSU	A	2504	8	17,21,22	1.59	3 (17%)	20,30,33	3.31	7 (35%)
55	H2U	v	20	55	18,21,22	2.95	5 (27%)	21,30,33	2.17	5 (23%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	OMC	A	2498	8	-	3/7/27/28	0/2/2/2
34	MA6	a	1519	34	-	4/7/29/30	0/3/3/3
56	PSU	w	32	56	-	2/7/25/26	0/2/2/2
8	PSU	A	746	8	-	4/7/25/26	0/2/2/2
55	4SU	v	8	55	-	1/5/25/26	0/2/2/2
8	G7M	A	2069	8	-	2/3/25/26	0/3/3/3
8	1MG	A	745	8	-	0/3/25/26	0/3/3/3
55	5MU	v	54	55	-	2/5/25/26	0/2/2/2
34	PSU	a	516	34	-	1/7/25/26	0/2/2/2
56	MIA	w	37	56	-	3/11/33/34	0/3/3/3
34	G7M	a	527	34	-	1/3/25/26	0/3/3/3
8	PSU	A	2604	8	-	0/7/25/26	0/2/2/2
8	6MZ	A	1618	8	-	5/5/27/28	0/3/3/3
8	OMU	A	2552	8	-	4/7/27/28	0/2/2/2
34	2MG	a	1516	34	-	0/5/27/28	0/3/3/3
56	G7M	w	46	56	-	3/3/25/26	0/3/3/3
8	PSU	A	2605	8	-	0/7/25/26	0/2/2/2
8	5MU	A	1939	8	-	1/5/25/26	0/2/2/2
8	5MC	A	747	8	-	2/5/25/26	0/2/2/2
56	5MU	w	54	56	-	5/5/25/26	0/2/2/2
8	OMG	A	2251	56,8	-	3/5/27/28	0/3/3/3
34	5MC	a	967	34	-	1/5/25/26	0/2/2/2
8	PSU	A	2580	8	-	0/7/25/26	0/2/2/2
56	4SU	w	8	56	-	4/5/25/26	0/2/2/2
34	4OC	a	1402	34	-	3/9/29/30	0/2/2/2

Continued on next page...

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
55	PSU	v	55	55	-	6/7/25/26	0/2/2/2
8	PSU	A	1911	8	-	1/7/25/26	0/2/2/2
8	5MC	A	1962	8	-	5/5/25/26	0/2/2/2
34	MA6	a	1518	34	-	3/7/29/30	0/3/3/3
8	PSU	A	2457	8	-	0/7/25/26	0/2/2/2
8	2MG	A	2445	8	-	2/5/27/28	0/3/3/3
34	5MC	a	1407	34	-	0/5/25/26	0/2/2/2
8	PSU	A	955	8	-	0/7/25/26	0/2/2/2
8	2MG	A	1835	8	-	2/5/27/28	0/3/3/3
8	6MZ	A	2030	8	-	2/5/27/28	0/3/3/3
56	PSU	w	39	56	-	4/7/25/26	0/2/2/2
34	2MG	a	1207	34	-	0/5/27/28	0/3/3/3
34	UR3	a	1498	34	-	2/5/25/26	0/2/2/2
8	PSU	A	1917	8	-	0/7/25/26	0/2/2/2
56	PSU	w	55	56	-	1/7/25/26	0/2/2/2
57	FME	y	101	57	-	6/7/9/11	-
8	2MA	A	2503	8	-	3/3/25/26	0/3/3/3
34	2MG	a	966	34	-	1/5/27/28	0/3/3/3
8	PSU	A	2504	8	-	0/7/25/26	0/2/2/2
55	H2U	v	20	55	-	5/7/38/39	0/2/2/2

The worst 5 of 196 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
34	a	1516	2MG	C2-N2	15.45	1.47	1.34
34	a	966	2MG	C2-N2	15.38	1.47	1.34
8	A	1835	2MG	C2-N2	15.31	1.47	1.34
8	A	2445	2MG	C2-N2	15.15	1.46	1.34
34	a	1207	2MG	C2-N2	14.80	1.46	1.34

The worst 5 of 200 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
34	a	516	PSU	N1-C2-N3	-11.42	119.35	128.43
56	w	32	PSU	N1-C2-N3	-11.34	119.41	128.43
8	A	2069	G7M	C1'-N9-C4	-10.93	107.44	126.64
56	w	55	PSU	N1-C2-N3	-10.65	119.97	128.43
8	A	746	PSU	N1-C2-N3	-10.34	120.21	128.43

There are no chirality outliers.

5 of 97 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
55	v	8	4SU	O4'-C1'-N1-C6
55	v	20	H2U	O4'-C1'-N1-C6
55	v	20	H2U	C2'-C1'-N1-C2
55	v	20	H2U	C2'-C1'-N1-C6
8	A	746	PSU	C2'-C1'-C5-C4

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
60	AM2	a	2001	-	40,40,40	1.66	10 (25%)	53,60,60	1.71	11 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
60	AM2	a	2001	-	-	8/12/84/84	0/4/4/4

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	a	2001	AM2	OA4-CA1	4.04	1.52	1.41
60	a	2001	AM2	CB3-CB4	-3.69	1.48	1.53
60	a	2001	AM2	OA5-CA8	3.20	1.50	1.41
60	a	2001	AM2	OA5-CA4	3.08	1.51	1.44
60	a	2001	AM2	OB1-CB1	2.89	1.49	1.41

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	a	2001	AM2	CA1-OA1-CC1	-5.36	104.71	117.96
60	a	2001	AM2	CA8-CA7-NA7	-3.99	103.86	111.00
60	a	2001	AM2	CB1-OA8-CA8	-3.84	107.56	114.42
60	a	2001	AM2	CA9-NA7-CA7	-3.31	109.57	114.38
60	a	2001	AM2	OA1-CA1-CA2	3.21	113.61	108.23

There are no chirality outliers.

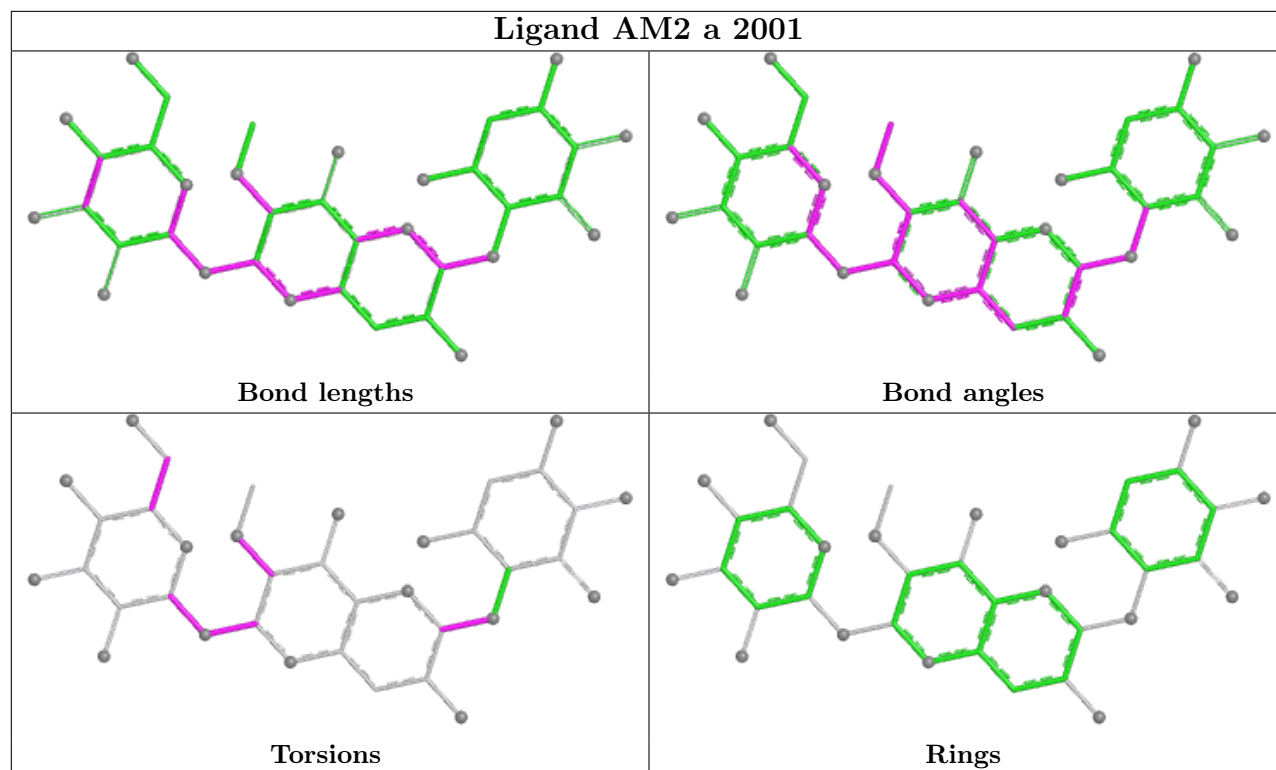
5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	a	2001	AM2	CA7-CA8-OA8-CB1
60	a	2001	AM2	OA5-CA8-OA8-CB1
60	a	2001	AM2	OB1-CB5-CB6-OB6
60	a	2001	AM2	CB4-CB5-CB6-OB6
60	a	2001	AM2	OB1-CB1-OA8-CA8

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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.

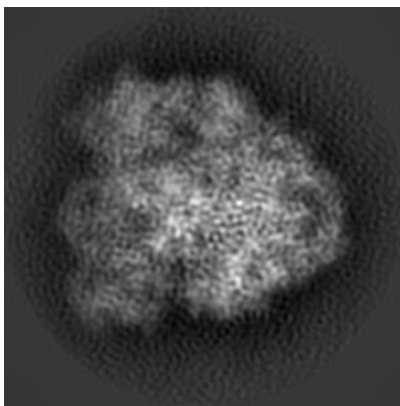
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13459. These allow visual inspection of the internal detail of the map and identification of artifacts.

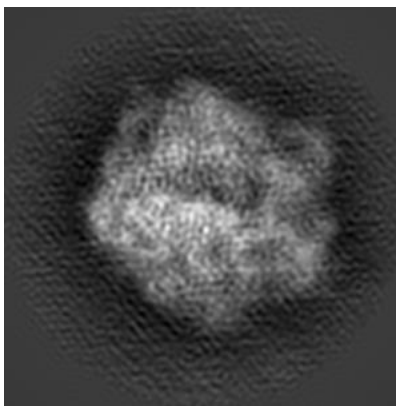
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

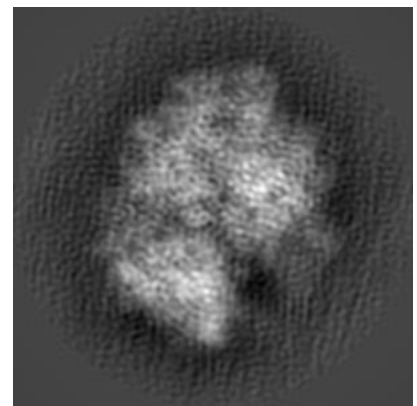
6.1.1 Primary map



X

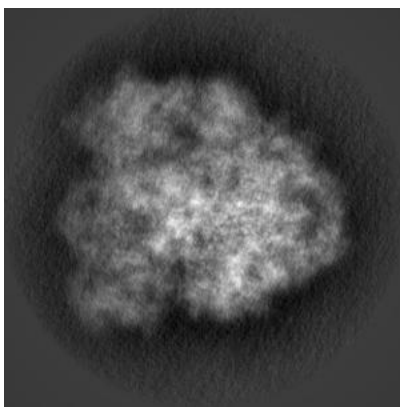


Y

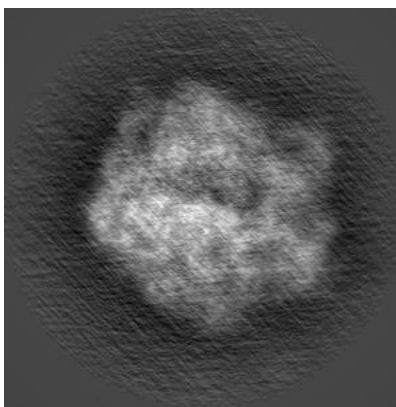


Z

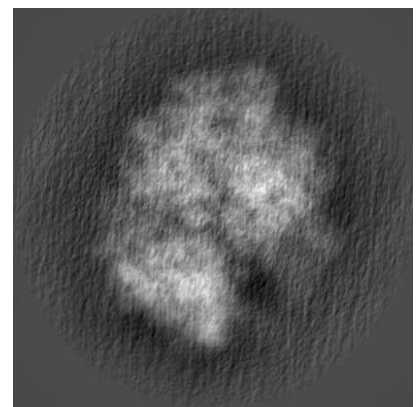
6.1.2 Raw map



X



Y

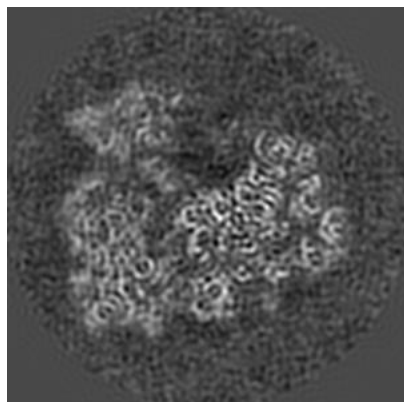


Z

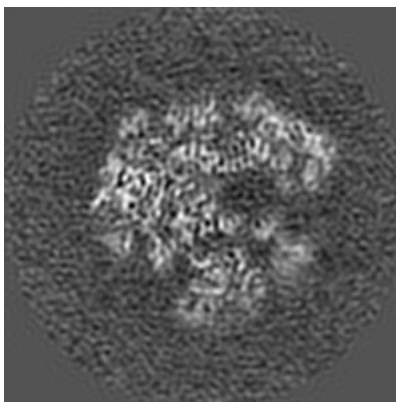
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

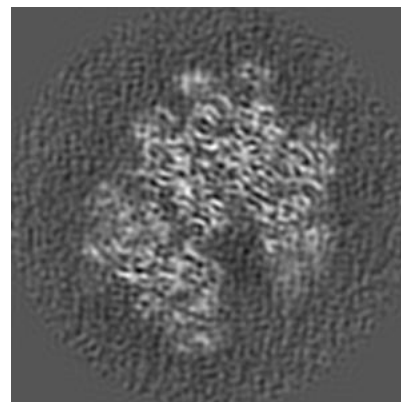
6.2.1 Primary map



X Index: 144

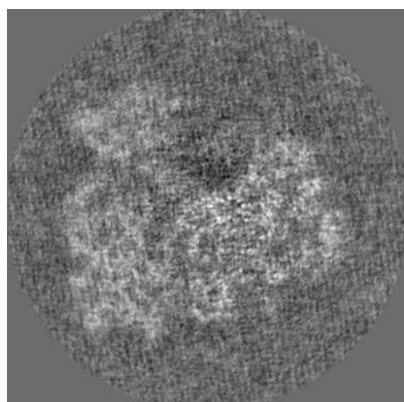


Y Index: 144

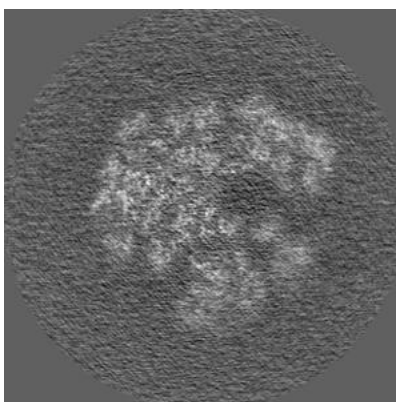


Z Index: 144

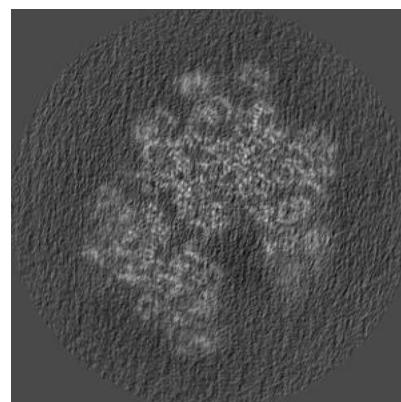
6.2.2 Raw map



X Index: 144



Y Index: 144

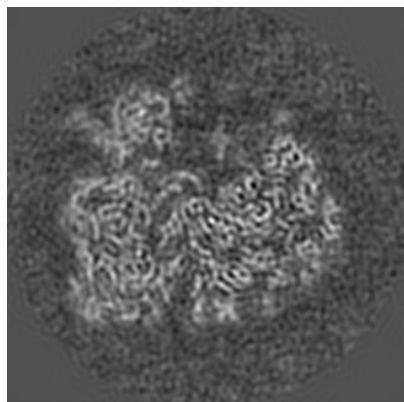


Z Index: 144

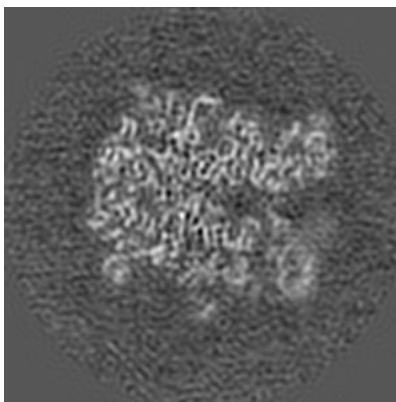
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

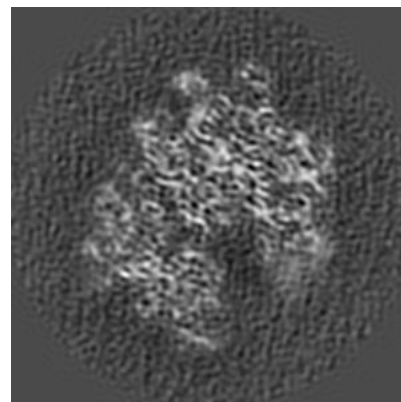
6.3.1 Primary map



X Index: 139

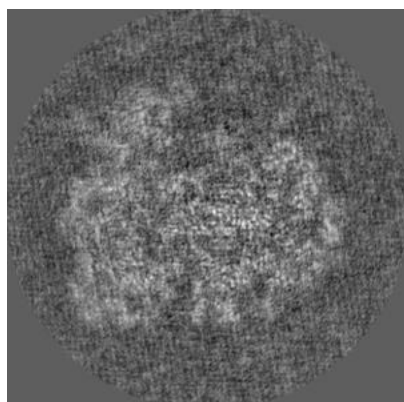


Y Index: 158

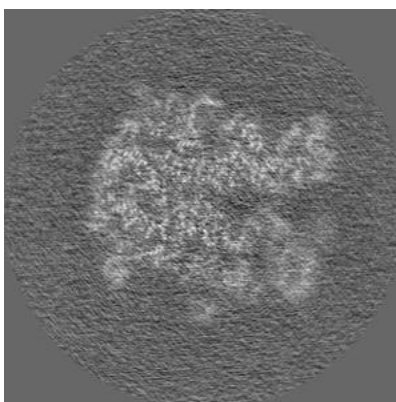


Z Index: 146

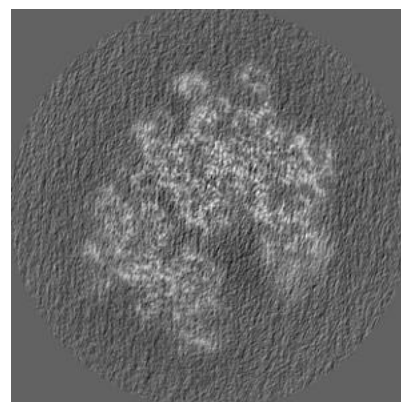
6.3.2 Raw map



X Index: 138



Y Index: 157

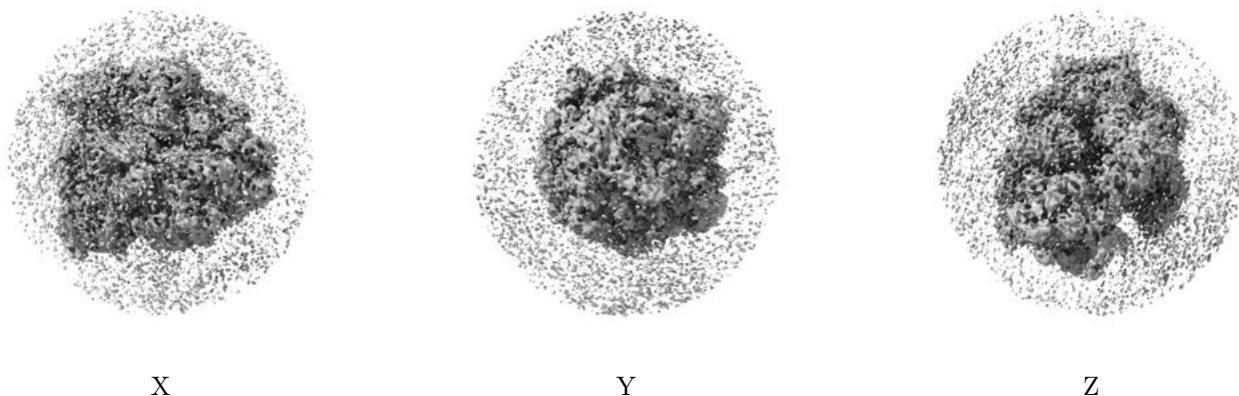


Z Index: 146

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

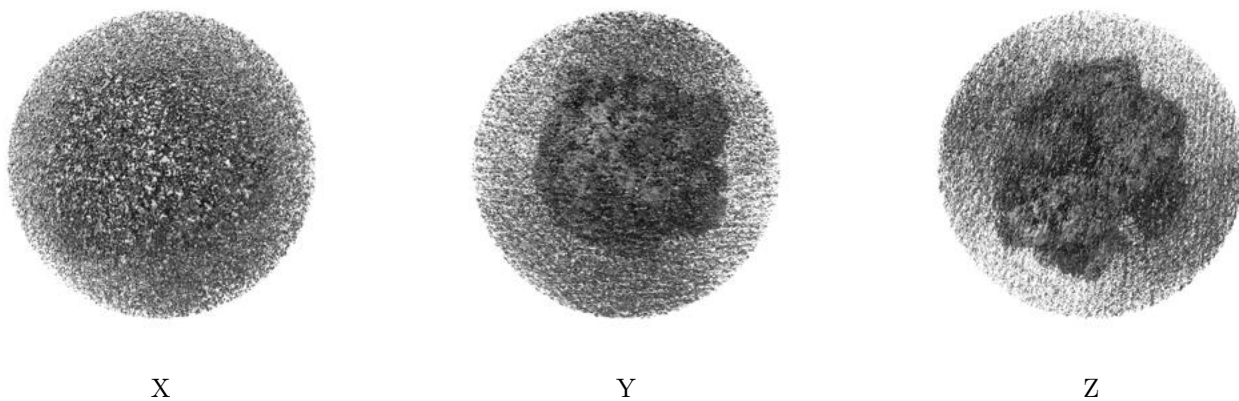
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 1.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 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.

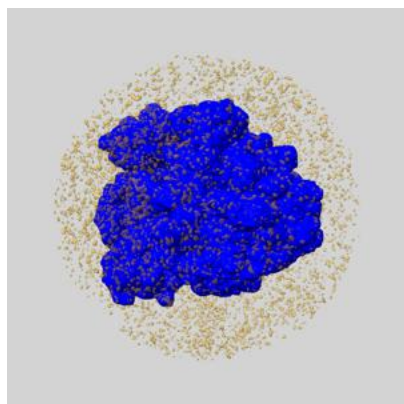
6.5 Mask visualisation [i](#)

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

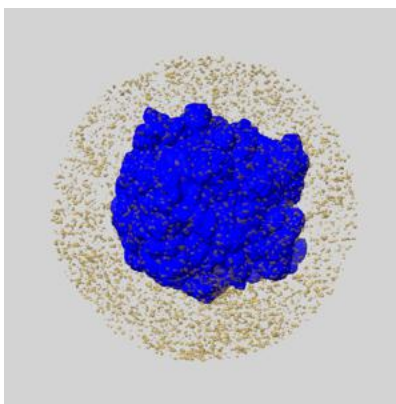
A mask typically either:

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

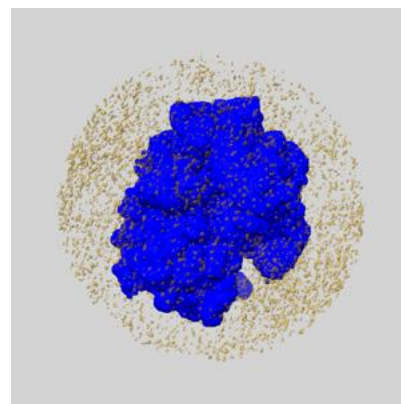
6.5.1 emd_13459_msk_1.map [i](#)



X



Y

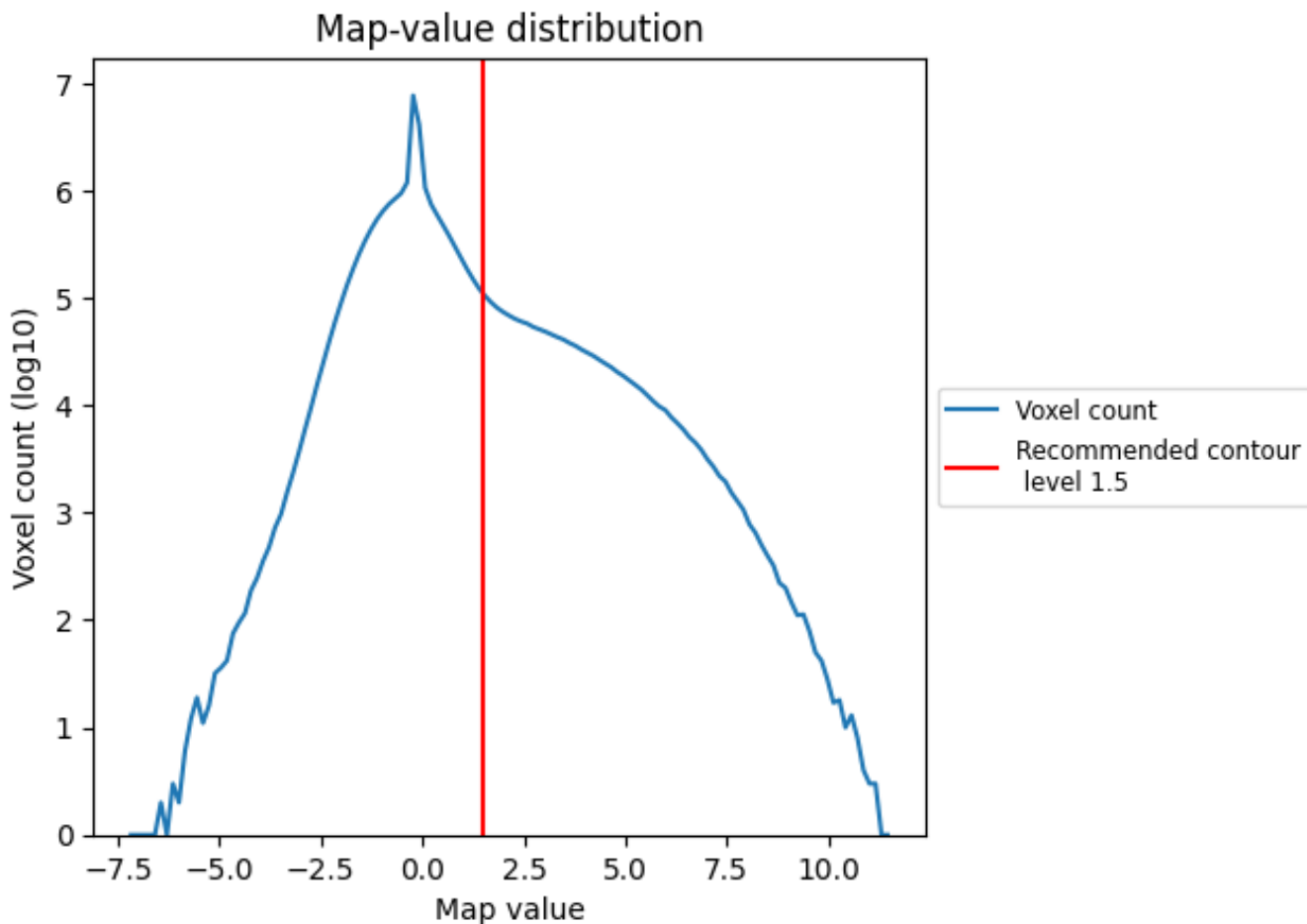


Z

7 Map analysis [i](#)

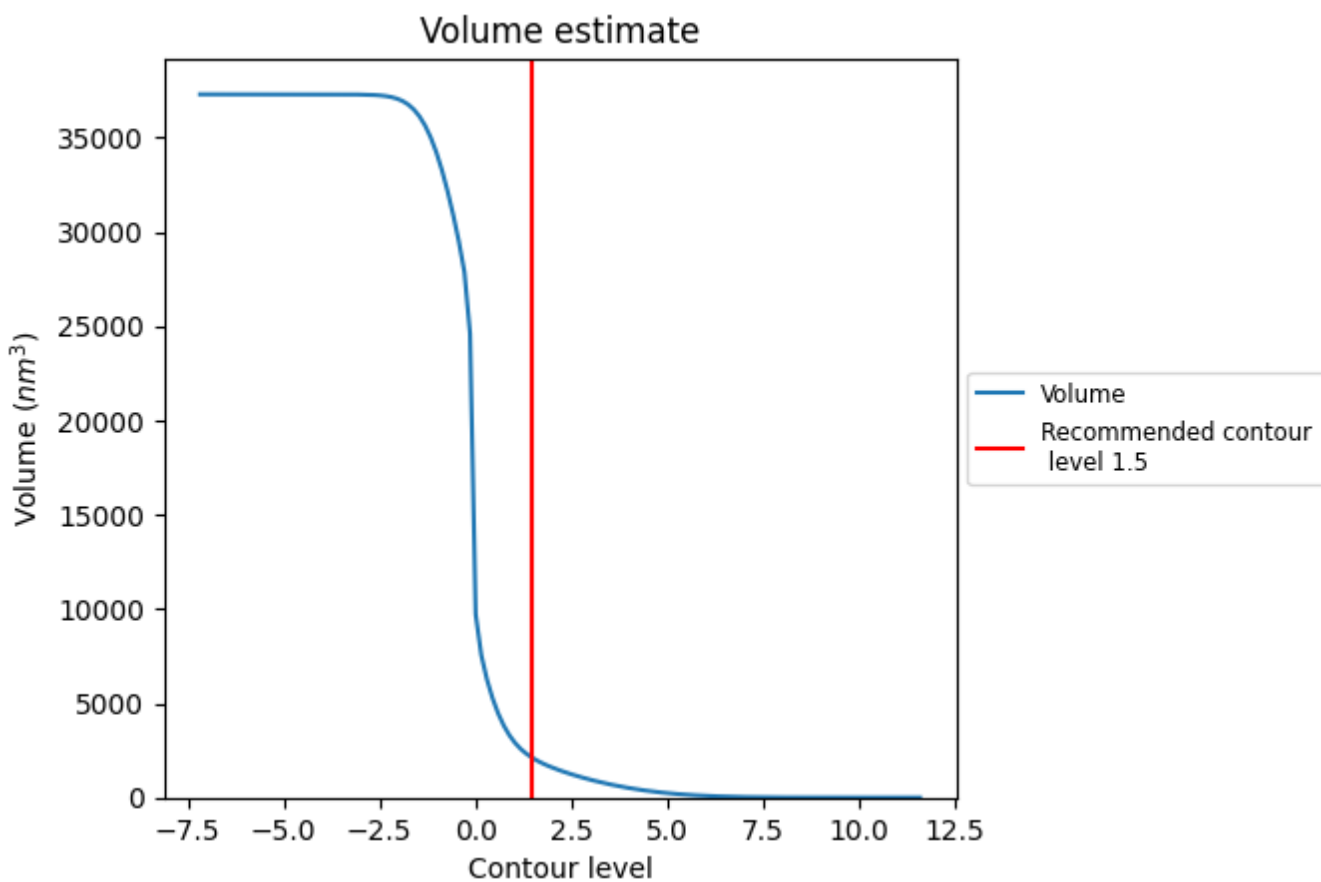
This section contains the results of statistical analysis of the map.

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.

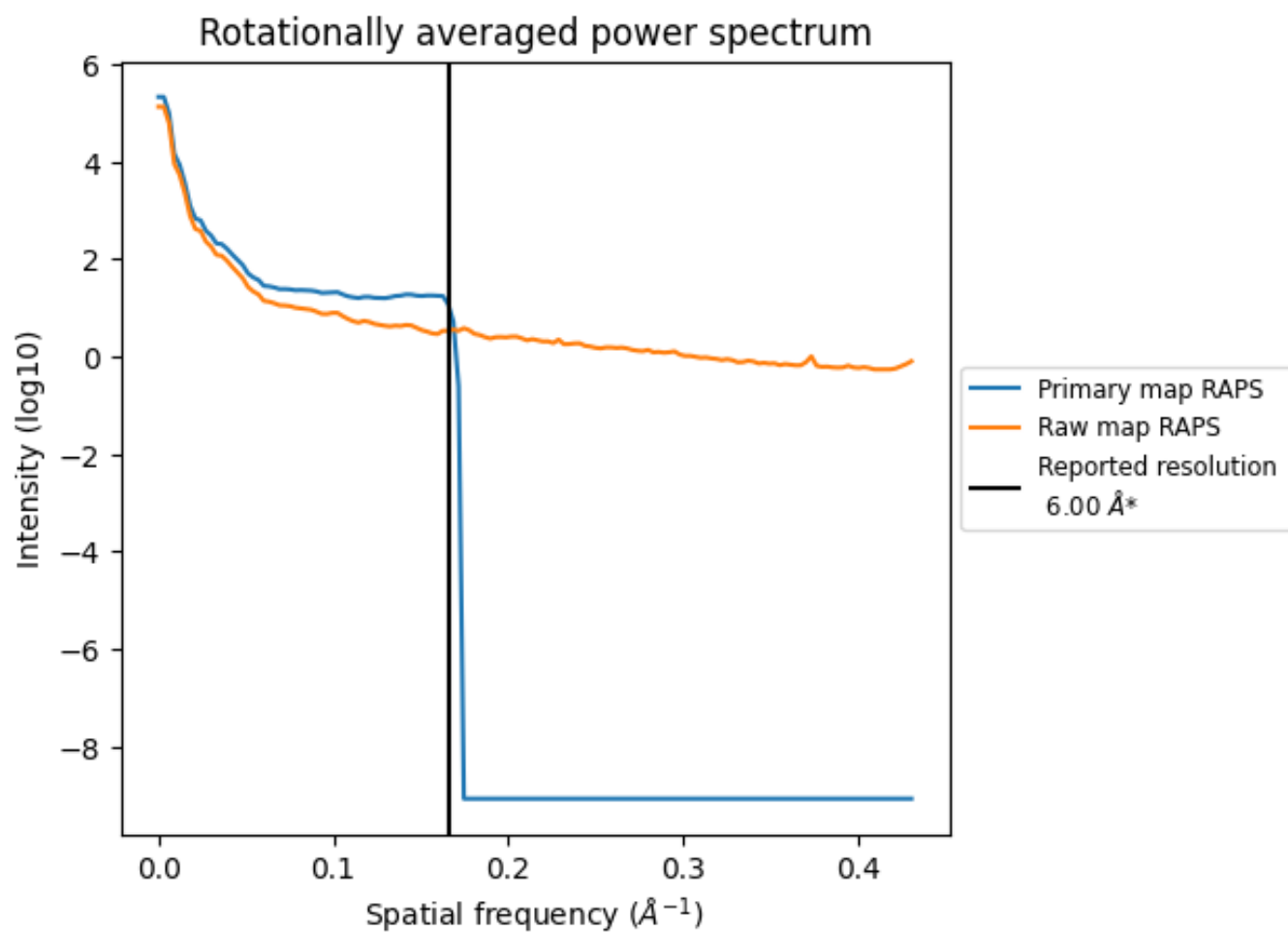
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2098 nm³; this corresponds to an approximate mass of 1895 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 i

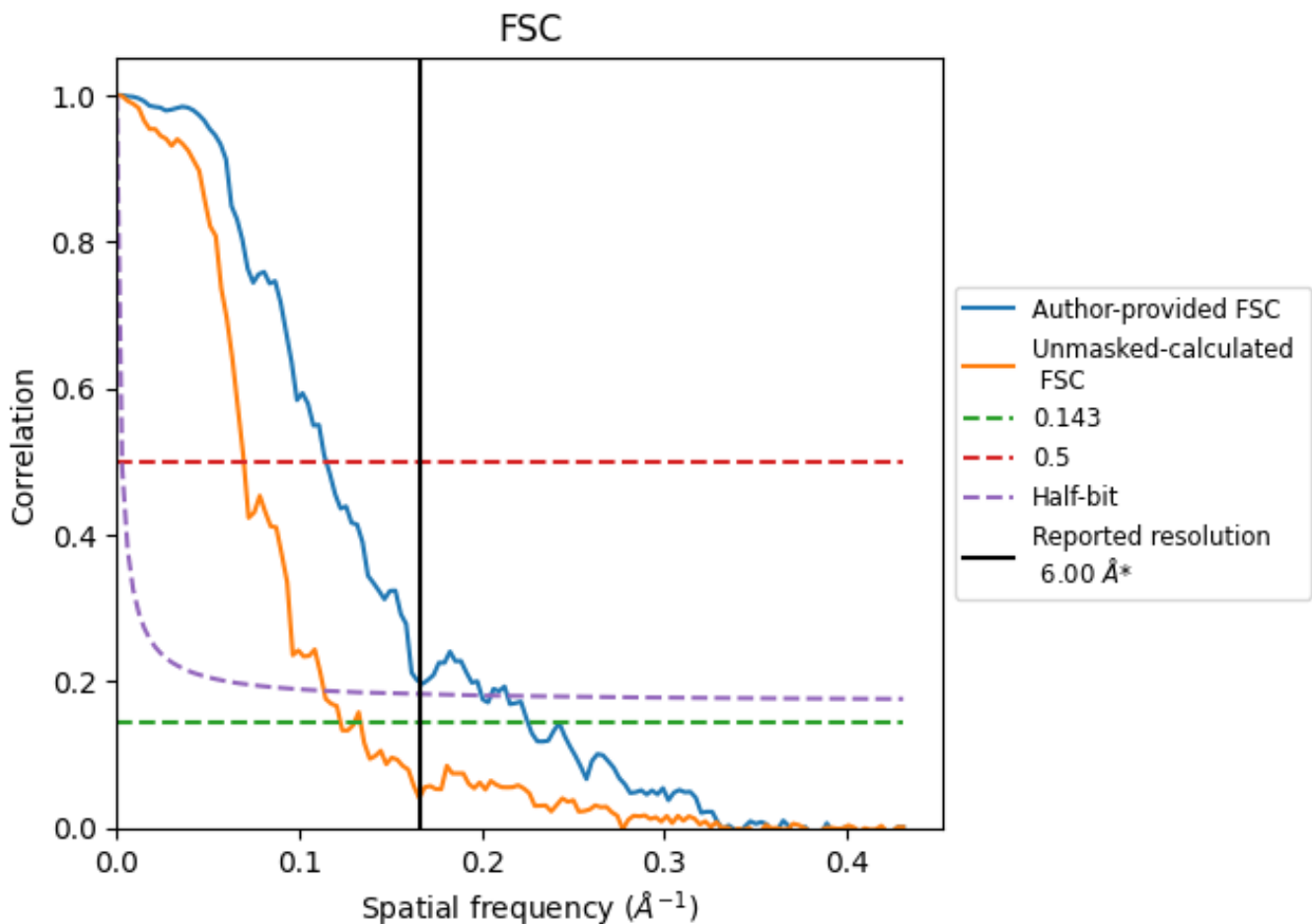


*Reported resolution corresponds to spatial frequency of 0.167 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.167\AA^{-1}

8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	6.00	-	-
Author-provided FSC curve	4.44	8.72	5.00
Unmasked-calculated*	8.15	14.37	8.80

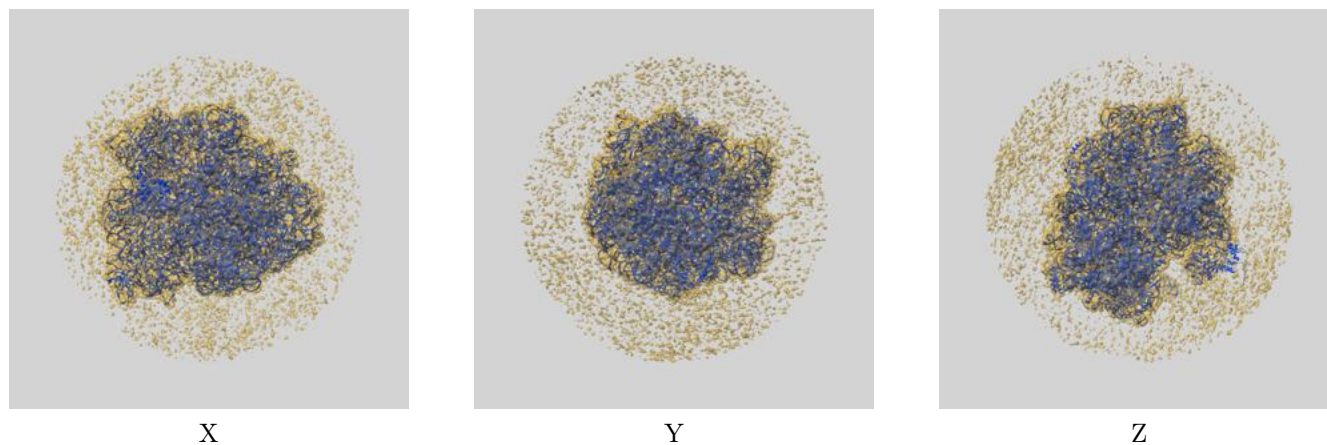
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 4.44 differs from the reported value 6.0 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 8.15 differs from the reported value 6.0 by more than 10 %

9 Map-model fit [i](#)

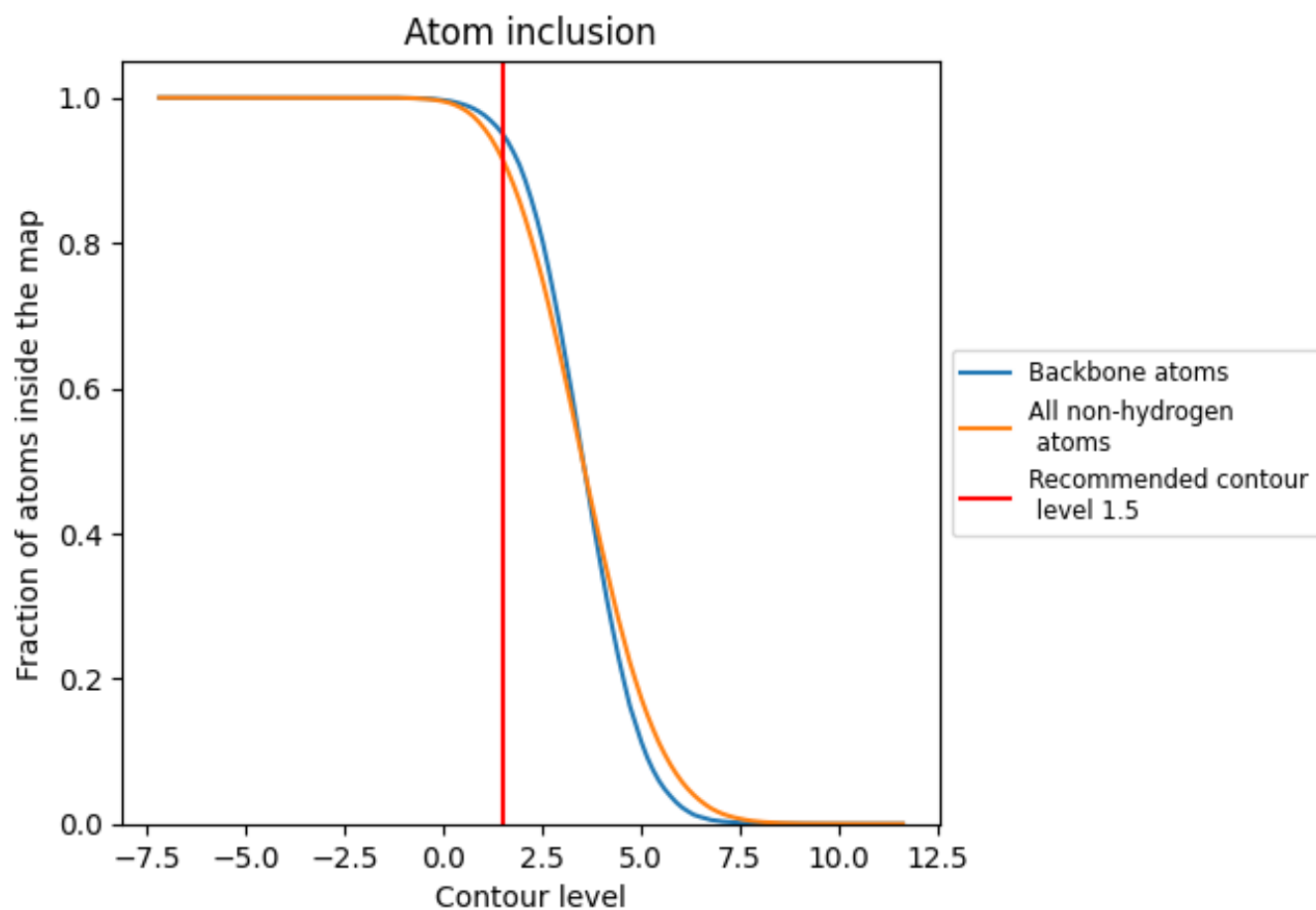
This section contains information regarding the fit between EMDB map EMD-13459 and PDB model 7PJT. Per-residue inclusion information can be found in section 3 on page 15.

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 1.5 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 Atom inclusion [i](#)



At the recommended contour level, 95% of all backbone atoms, 91% of all non-hydrogen atoms, are inside the map.