



## wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 01:04 AM UTC

PDB ID : 7SSD / pdb\_00007ssd  
EMDB ID : EMD-25407  
Title : Mid translocation intermediate with EF-G bound with GDP (Structure IV)  
Authors : Carbone, C.E.; Korostelev, A.A.  
Deposited on : 2021-11-10  
Resolution : 3.30 Å (reported)

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

We welcome your comments at [validation@mail.wwpdb.org](mailto: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>.

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

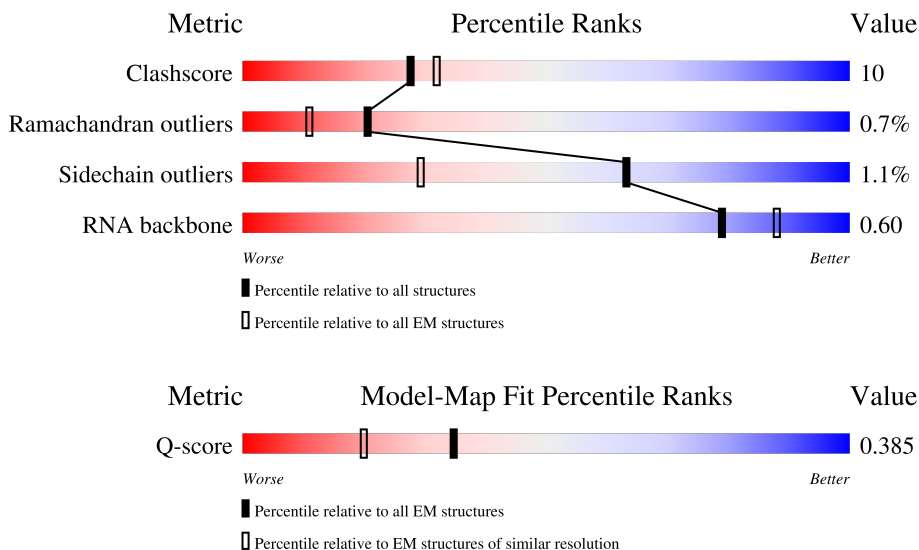
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Buster-report : wwPDB partial adaption of 1.1.7 (2018)  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

# 1 Overall quality at a glance i

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

The reported resolution of this entry is 3.30 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.



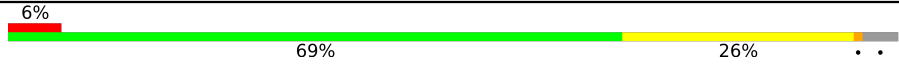




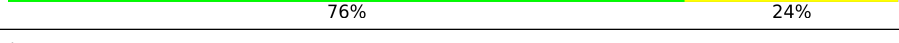
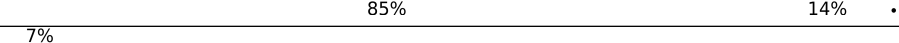
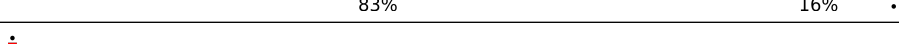
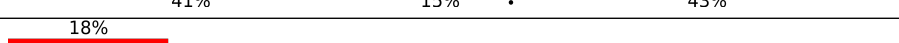
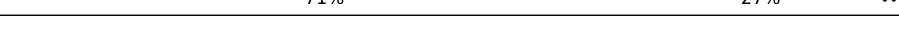


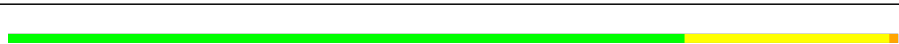












Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	15087 ( 2.80 - 3.80 )

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  $\geq 3$ , 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	3	1539	54% (Green), 39% (Yellow), 6% (Orange)
2	1	2903	56% (Green), 39% (Yellow), 5% (Orange)
3	2	120	57% (Green), 38% (Yellow), 5% (Orange)

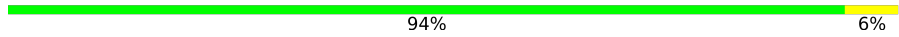







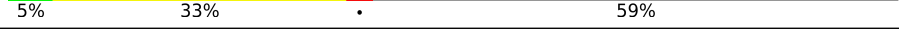

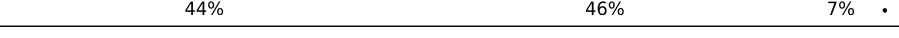
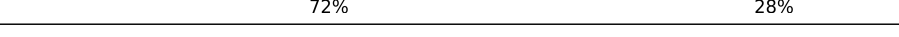

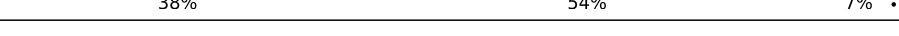


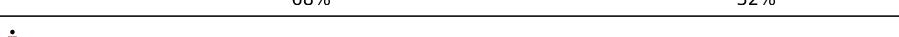

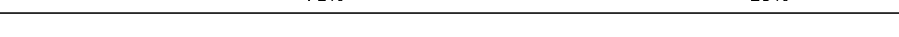






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Mol	Chain	Length	Quality of chain
4	8	697	
5	6	77	
6	b	271	
7	c	209	
8	d	201	
9	e	177	
10	f	176	
11	g	149	
12	a	234	
13	i	142	
14	j	142	
15	k	122	
16	l	143	
17	m	136	
18	n	120	
19	o	116	
20	p	114	
21	q	117	
22	r	103	
23	s	110	
24	t	93	
25	u	102	
26	v	94	
27	w	75	
28	x	77	




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Mol	Chain	Length	Quality of chain
29	y	63	 94% 6%
30	z	58	 76% 22%
31	A	66	 65% 5% 30%
32	B	56	 80% 18%
33	C	50	 76% 24%
34	D	46	 85% 15%
35	E	64	 83% 11% 5%
36	F	38	 79% 21%
37	4	39	 5% 33% 59%
38	5	77	 40% 45% 14%
39	G	225	 44% 46% 7%
40	H	206	 72% 28%
41	I	205	 74% 25%
42	J	157	 38% 54% 7%
43	K	100	 70% 28%
44	L	151	 84% 16%
45	M	129	 68% 32%
46	N	127	 68% 30%
47	O	98	 71% 29%
48	P	116	 72% 28%
49	Q	123	 63% 32% 5%
50	R	114	 76% 21%
51	S	100	 80% 20%
52	T	88	 68% 32%
53	U	82	 80% 18%

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Mol	Chain	Length	Quality of chain
54	V	80	 79% 21%
55	W	65	 83% 17%
56	X	79	 80% 20%
57	Y	85	 78% 22%
58	Z	65	 65% 34% .

## 2 Entry composition

There are 59 unique types of molecules in this entry. The entry contains 153049 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a RNA chain called 16S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
1	3	1539	33012	14725	6052	10697	1538	0	0

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

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
2	1	2903	62317	27801	11468	20146	2902	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	747	C	U	conflict	GB 802133627

- Molecule 3 is a RNA chain called 5S RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	P		
3	2	120	2568	1145	471	833	119	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
2	120	A	-	insertion	GB 1266961702

- Molecule 4 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
4	8	666	5157	3256	886	992	23	0	0

- Molecule 5 is a RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 6 is a protein called 50S ribosomal protein L2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	b	271	Total	C	N	O	S	0	0
			2083	1288	423	365	7		

- Molecule 7 is a protein called 50S ribosomal protein L3.

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

- Molecule 8 is a protein called 50S ribosomal protein L4.

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

- Molecule 9 is a protein called 50S ribosomal protein L5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	e	177	Total	C	N	O	S	0	0
			1411	899	249	257	6		

- Molecule 10 is a protein called 50S ribosomal protein L6.

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

- Molecule 11 is a protein called 50S ribosomal protein L9.

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

- Molecule 12 is a protein called 50S ribosomal protein L1.

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

- Molecule 13 is a protein called 50S ribosomal protein L11.

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

- Molecule 14 is a protein called 50S ribosomal protein L13.

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

- Molecule 15 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	k	122	Total	C	N	O	S	0	0
			939	587	180	166	6		

- Molecule 16 is a protein called 50S ribosomal protein L15.

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

- Molecule 17 is a protein called 50S ribosomal protein L16.

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

- Molecule 18 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	n	120	Total	C	N	O	S	0	0
			961	593	196	167	5		

- Molecule 19 is a protein called 50S ribosomal protein L18.

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

- Molecule 20 is a protein called 50S ribosomal protein L19.

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

- Molecule 21 is a protein called 50S ribosomal protein L20.

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

- Molecule 22 is a protein called 50S ribosomal protein L21.

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

- Molecule 23 is a protein called 50S ribosomal protein L22.

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

- Molecule 24 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	t	93	Total	C	N	O	S	0	0
			739	466	139	132	2		

- Molecule 25 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms				AltConf	Trace
25	u	102	Total	C	N	O	0	0
			780	492	146	142		

- Molecule 26 is a protein called 50S ribosomal protein L25.

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

- Molecule 27 is a protein called 50S ribosomal protein L27.

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

- Molecule 28 is a protein called 50S ribosomal protein L28.

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

- Molecule 29 is a protein called 50S ribosomal protein L29.

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

- Molecule 30 is a protein called 50S ribosomal protein L30.

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

- Molecule 31 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	46	Total	C	N	O	S	0	0
			355	221	62	66	6		

- Molecule 32 is a protein called 50S ribosomal protein L32.

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

- Molecule 33 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
33	C	50	Total	C	N	O	0	0
			410	263	75	72		

- Molecule 34 is a protein called 50S ribosomal protein L34.

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

- Molecule 35 is a protein called 50S ribosomal protein L35.

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

- Molecule 36 is a protein called 50S ribosomal protein L36.

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

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	4	16	Total	C	N	O	P	0	0
			350	156	70	108	16		

- Molecule 38 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 39 is a protein called 30S ribosomal protein S2.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	G	218	Total	C	N	O	S	0	0
			1705	1081	305	312	7		

- Molecule 40 is a protein called 30S ribosomal protein S3.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	H	206	Total	C	N	O	S	0	0
			1625	1028	305	289	3		

- Molecule 41 is a protein called 30S ribosomal protein S4.

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

- Molecule 42 is a protein called 30S ribosomal protein S5.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	J	157	Total	C	N	O	S	0	0
			1157	719	218	214	6		

- Molecule 43 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
43	K	100	Total	C	N	O	S	0	0
			818	515	148	149	6		

- Molecule 44 is a protein called 30S ribosomal protein S7.

Mol	Chain	Residues	Atoms					AltConf	Trace
44	L	151	Total	C	N	O	S	0	0
			1182	735	227	216	4		

- Molecule 45 is a protein called 30S ribosomal protein S8.

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

- Molecule 46 is a protein called 30S ribosomal protein S9.

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

- Molecule 47 is a protein called 30S ribosomal protein S10.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	O	98	Total	C	N	O	S	0	0
			787	493	150	143	1		

- Molecule 48 is a protein called 30S ribosomal protein S11.

Mol	Chain	Residues	Atoms					AltConf	Trace
48	P	116	Total	C	N	O	S	0	0
			870	535	173	159	3		

- Molecule 49 is a protein called 30S ribosomal protein S12.

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

- Molecule 50 is a protein called 30S ribosomal protein S13.

Mol	Chain	Residues	Atoms					AltConf	Trace
50	R	114	Total	C	N	O	S	0	0
			884	546	178	157	3		

- Molecule 51 is a protein called 30S ribosomal protein S14.

Mol	Chain	Residues	Atoms					AltConf	Trace
51	S	100	Total	C	N	O	S	0	0
			805	499	164	139	3		

- Molecule 52 is a protein called 30S ribosomal protein S15.

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

- Molecule 53 is a protein called 30S ribosomal protein S16.

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

- Molecule 54 is a protein called 30S ribosomal protein S17.

Mol	Chain	Residues	Atoms					AltConf	Trace
54	V	80	Total	C	N	O	S	0	0
			649	411	121	114	3		

- Molecule 55 is a protein called 30S ribosomal protein S18.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	W	65	Total	C	N	O	S	0	0
			536	339	100	96	1		

- Molecule 56 is a protein called 30S ribosomal protein S19.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	X	79	Total	C	N	O	S	0	0
			638	408	120	108	2		

- Molecule 57 is a protein called 30S ribosomal protein S20.

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

- Molecule 58 is a protein called 30S ribosomal protein S21.

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

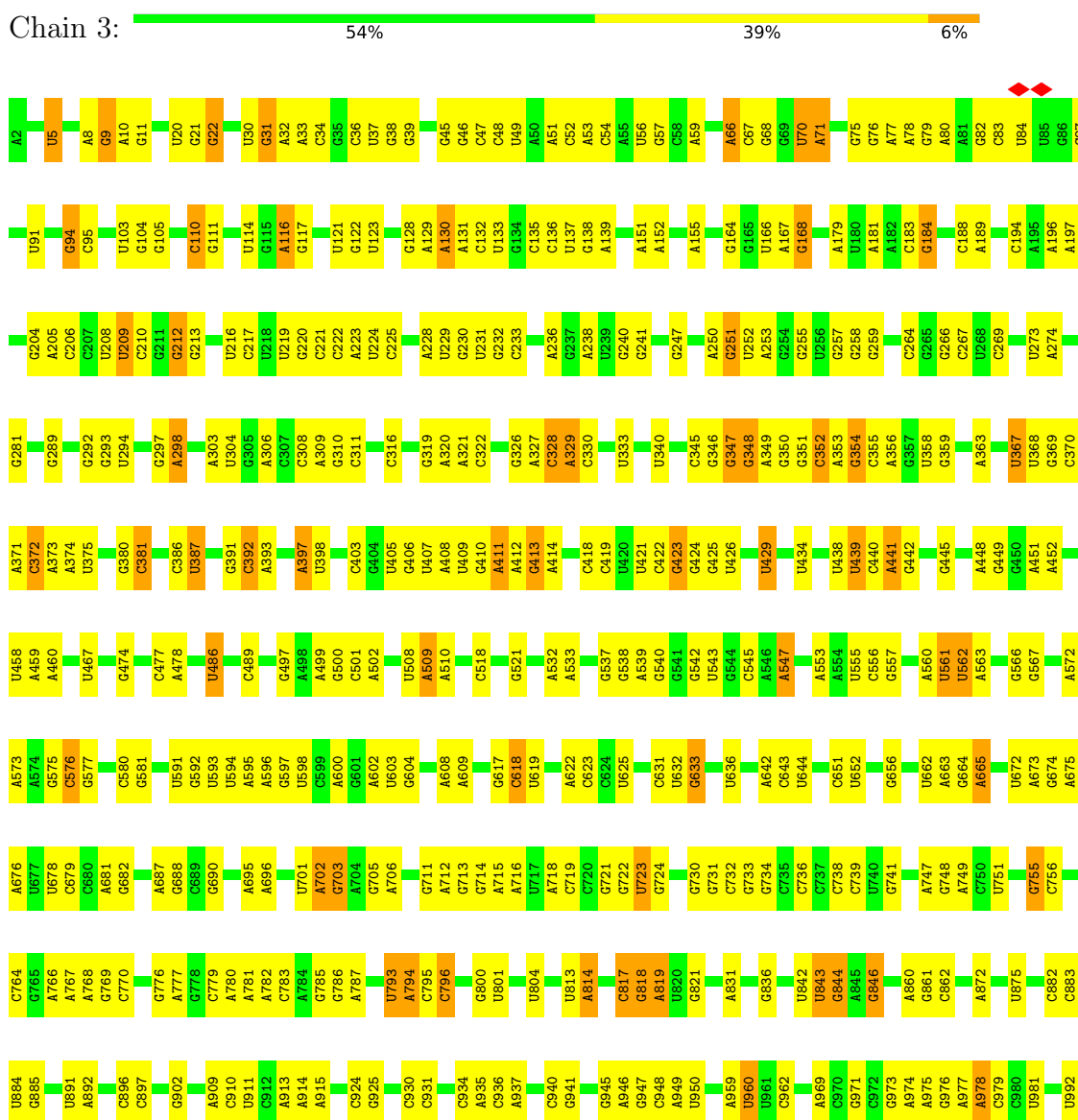
- Molecule 59 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: C<sub>10</sub>H<sub>15</sub>N<sub>5</sub>O<sub>11</sub>P<sub>2</sub>) (labeled as "Ligand of Interest" by depositor).

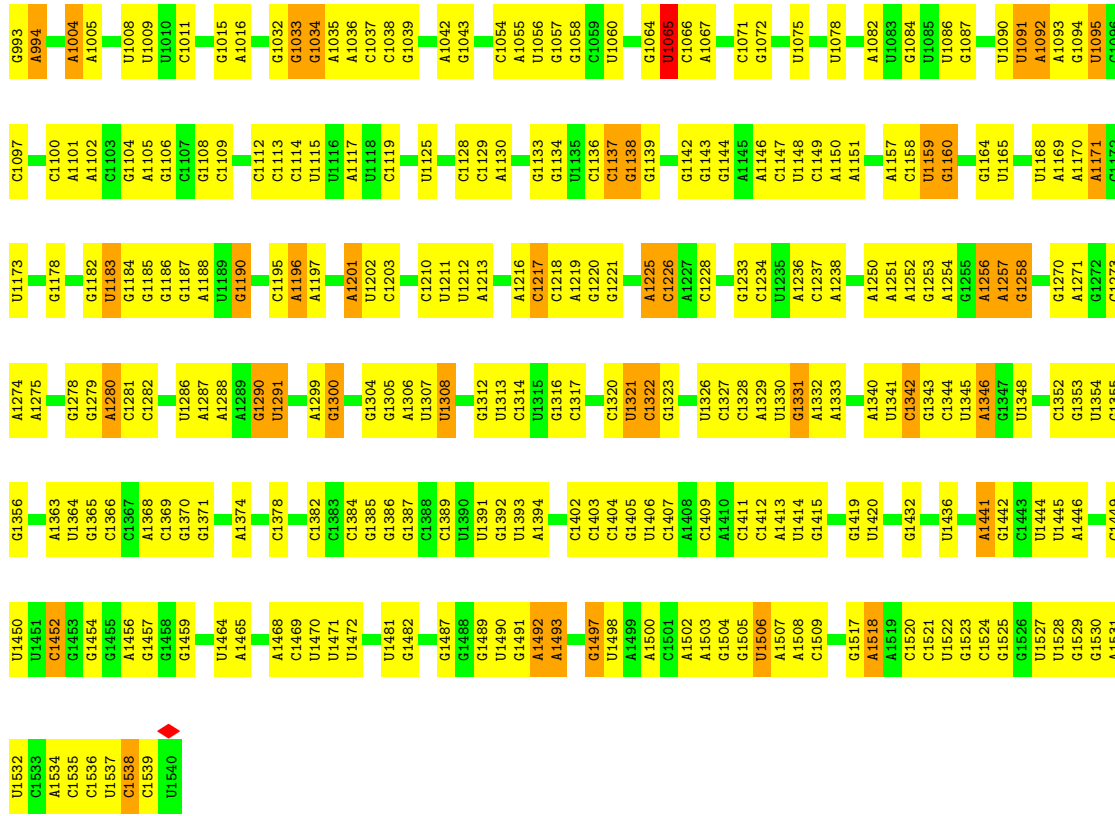


### 3 Residue-property plots

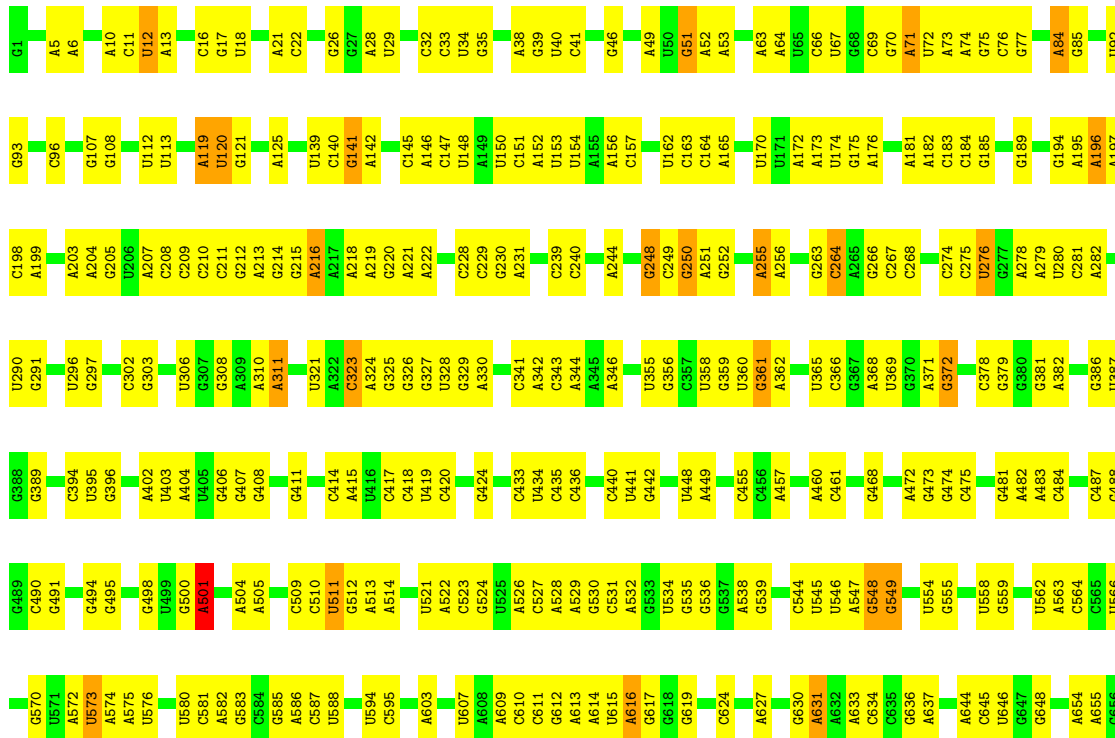
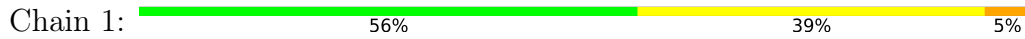
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: 16S rRNA

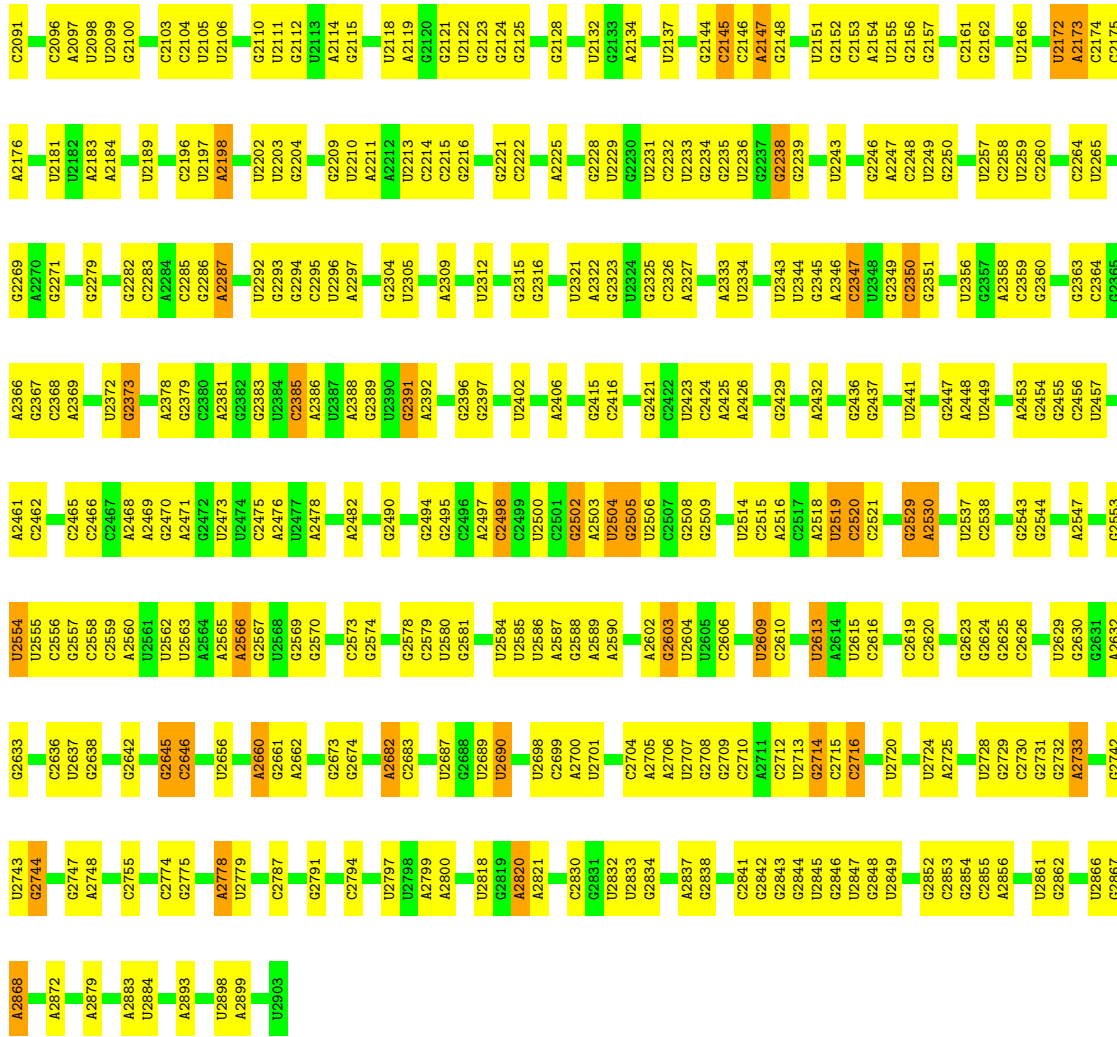




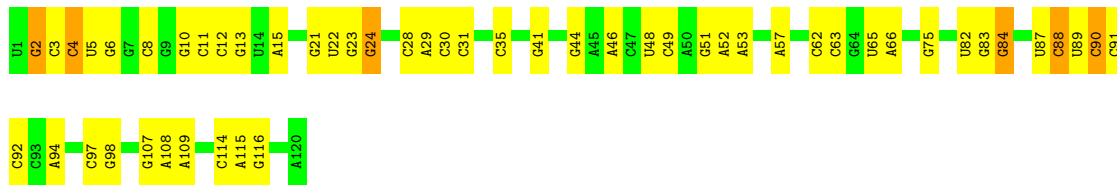
• Molecule 2: 23S rRNA



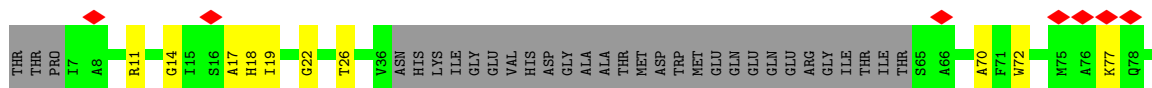
U2011	G1929	U1818	C1726	U1624	G1527	A1143	G1062	U1970	C873	U767	U657
G2012	A1937	A1819	C1727	C1625	A1528	A1144	G1063	G971	G874	G768	C660
A2013	U1938	G1824	U1728	A1626	G1529	C1145	U1065	A972	G875	U769	
A2014	U1939	G1825	C1729	G1627	U1530	G1149	U1066	A973	C876	G770	G669
U2015	A1932	U1826	C1730	G1628	A1535	C1150	A1070	G974	A877	G771	G674
U2016	G1933	U1827	C1731	A1634	C1536	G1153	G1071	A975	A878	C772	
U2017	U1937	G1828	C1732	A1635	G1537	C1154	A1071	C982	G879	U773	A676
U2022	A1938	A1829	U1736	U1636	U1542	G1155	C1076	A983	G883	G776	A675
G2023	U1939	C1830	G1737	A1637	G1543	A1156	A1077	A984	U884	G777	U686
G2024	U1940	G1831	C1738	G1435	U1340	A1155	U1078	C985	C885	G778	
U2025	U1941	C1832	G1739	G1441	U1341	G1162	A1080	C986	A886	U779	G690
U2026	G1942	U1833	C1740	G1442	A1342	C1163	U1081	G989	U887	G780	C691
A2030	U1943	G1834	A1744	G1443	U1343	A1165	G1082	A990	G891	A781	U694
A2031	C1947	G1835	A1745	G1444	U1344	G1166	A992	C991	A892	A782	G695
G2032	G1948	U1836	U1748	G1445	C1345	C1167	U1083	C992	C893	G783	
A2033	U1949	G1837	A1749	G1446	U1346	C1168	A1084	G993	U894	A784	
U2034	U1951	C1838	U1758	C1447	C1351	G1169	A1085	C994	U895	G785	A699
U2039	A1952	U1839	U1759	G1448	U1352	A1170	A1086	C995	A896	G786	G700
G2040	A1953	G1840	C1760	G1451	A1353	C1171	A1087	G996	C897	A788	G701
G2041	G1954	U1841	U1761	G1452	A1354	U1171	A1088	A997	A898	A789	A705
U2043	U1955	G1842	U1765	G1454	G1356	U1172	C1089	A1000	C898	G799	A706
G2044	C1958	U1843	G1770	C1454	G1360	U1173	G1092	A1001	A910	A800	G707
C2045	G1959	G1844	A1773	G1461	G1361	A1175	G1093	G1002	A911	G801	G708
G2046	U1963	C1867	C1774	G1462	C1362	U1176	U1097	C1005	C912	A802	U709
C2047	G1964	G1868	U1774	G1463	U1363	C1177	A1098	U1012	U913	U803	U710
G2048	C1965	C1869	U1775	G1464	C1364	G1179	U1101	U1013	A918	A804	A716
G2049	U1966	U1870	G1776	G1465	A1365	U1180	C1102	U1019	G923	G809	C717
A2052	C1967	A1871	U1777	U1468	U1376	U1181	C1103	U1022	G924	A718	A718
C2055	G1968	A1872	U1778	A1468	G1377	G1182	A1103	G1023	U929	U810	C719
U2056	A1969	G1873	U1779	A1469	U1378	U1183	C1104	U1024	U929	U811	U720
G2056	U1970	U1874	U1779	G1471	U1379	U1184	U1105	G1024	U929	C812	A721
U2060	C1971	G1875	U1782	U1475	A1383	G1186	G1110	U832	U932	A819	G725
C2061	G1972	U1876	A1783	A1476	A1384	G1187	A1111	A933	U934	A820	G726
A2062	U1973	G1877	A1784	A1477	A1385	U1188	G1112	A1029	C935	A821	A727
C2065	C1974	C1878	U1785	G1482	A1386	A1189	U1113	C1030	A936	G728	G729
G2066	U1975	U1879	A1786	G1482	A1387	G1190	U1114	U1033	A937	U827	A730
U2067	G1976	C1881	A1791	A1490	U1388	G1191	G1115	G1034	U937	U828	A730
G2068	U1977	A1885	U1796	A1494	U1390	C1196	G1124	U1035	G940	A833	U741
U2076	A1982	A1889	G1797	A1503	U1394	G1197	G1125	G1036	A941	G834	A742
C2077	G1983	G1890	U1798	A1503	A1395	U1198	A1126	U1037	G942	U845	A743
U2079	U1984	A1901	C1799	A1504	U1396	U1199	U1127	G1038	A943	A846	U744
U2081	C1985	U1709	U1800	A1505	U1397	C1200	G1128	C1043	A944	U847	G745
A2082	U1986	G1710	G1601	A1506	G1300	U1203	U1130	C1044	C946	U847	U746
U2085	C1987	U1713	U1602	A1508	A1301	A1204	G1131	C1045	A947	C747	C747
U2086	U1988	A1713	A1603	A1509	A1302	A1205	U1132	A1046	C948	C851	G748
G2087	U1989	U1714	A1608	G1510	U1406	G1212	U1133	G1047	G952	U852	
	C1990	G1715	G1613	A1515	U1409	G1212	A1134	G1055	G953	G857	A753
	U1991	U1719	G1613	A1515	G1410	U1219	C1135	G1056	A953	U754	U754
	A1992	U1720	A1616	A1522	G1416	G1220	G1138	A1057	C961	G859	G760
	U1993	G1723	C1617	A1523	G1416	G1220	U1139	U1058	G962	G864	A761
	C1994	U1724	A1618	A1524	A1419	G1225	C1140	U1059	C968	U762	G763
	U1995	U1725	C1526	C1526	A1420	C1229	A1141	U1060	C968	G865	A764

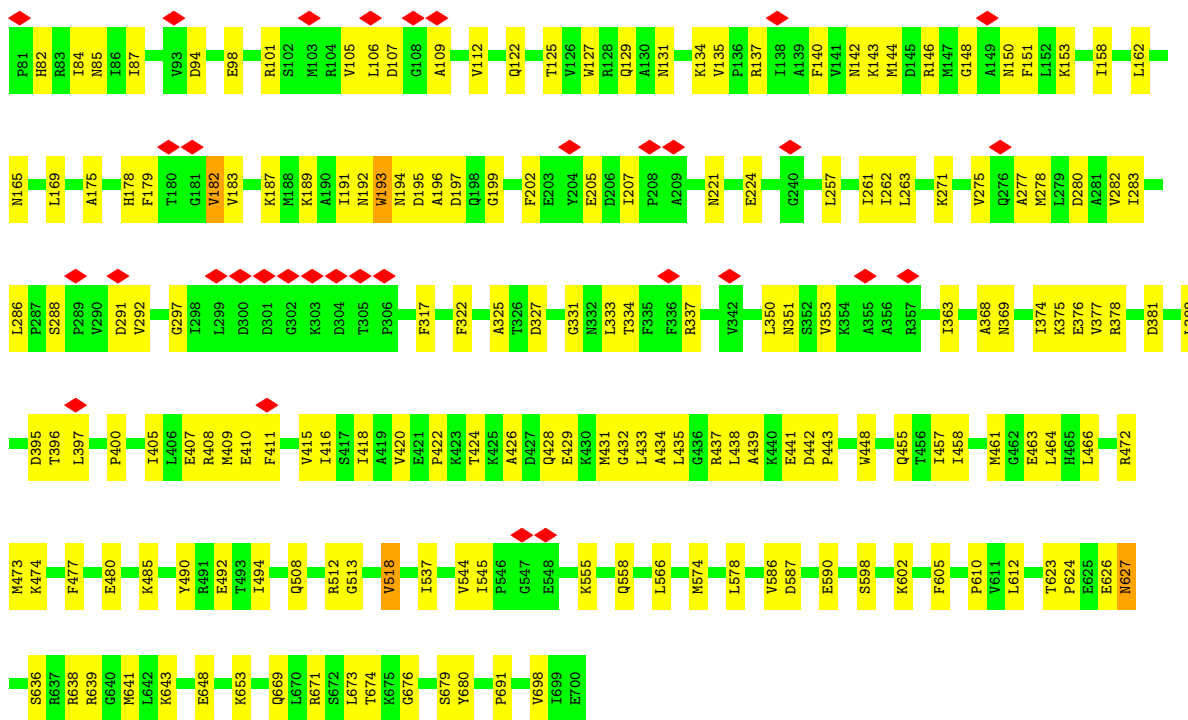


• Molecule 3: 5S RNA

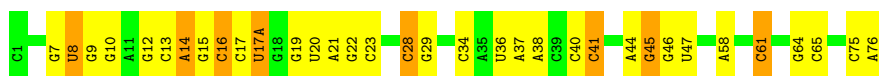


• Molecule 4: Elongation factor G

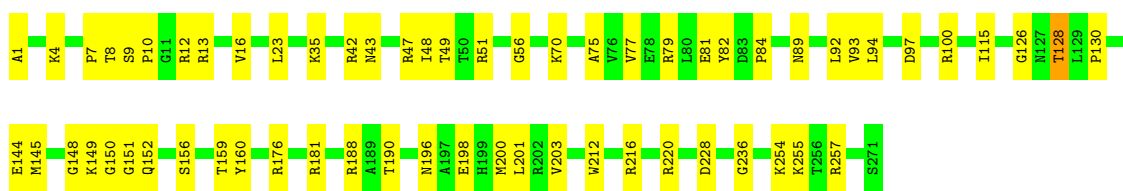
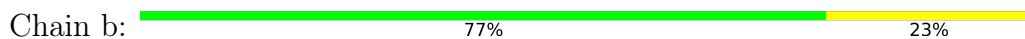




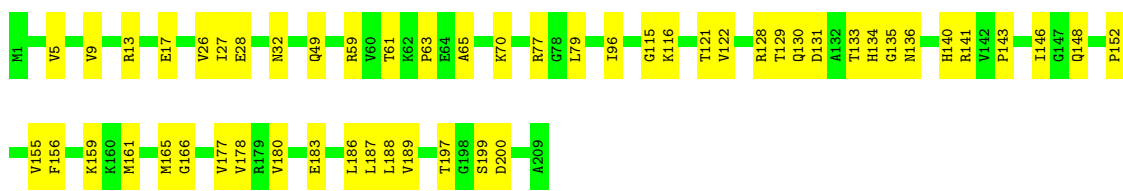
• Molecule 5: tRNA fMet



• Molecule 6: 50S ribosomal protein L2

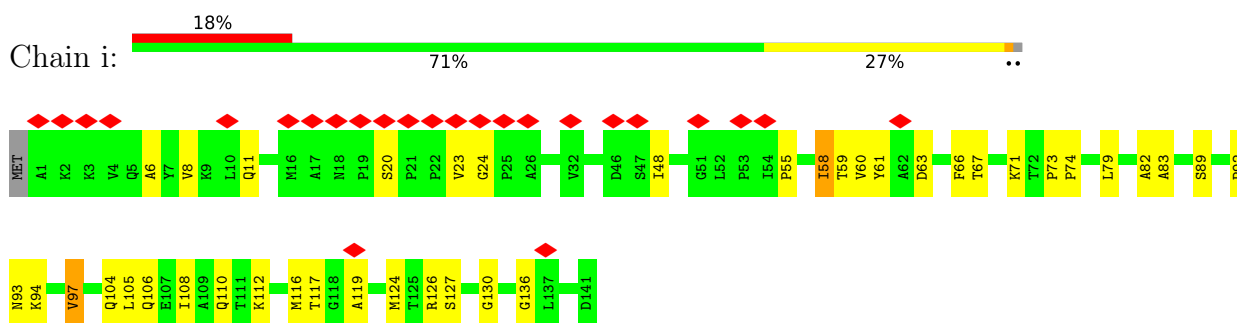


• Molecule 7: 50S ribosomal protein L3

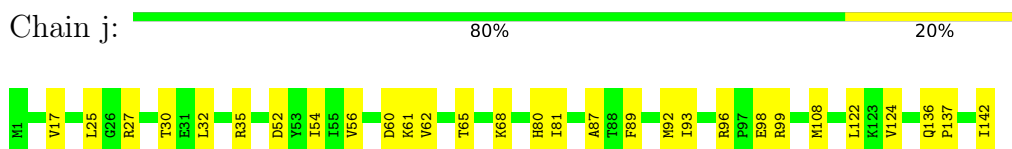


• Molecule 8: 50S ribosomal protein L4

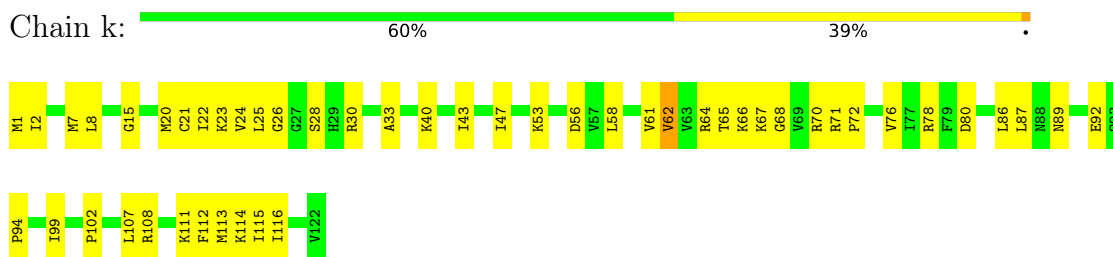




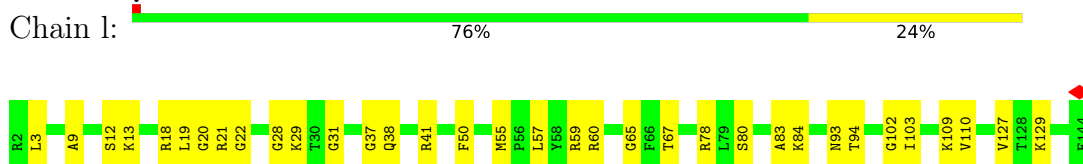
- Molecule 14: 50S ribosomal protein L13



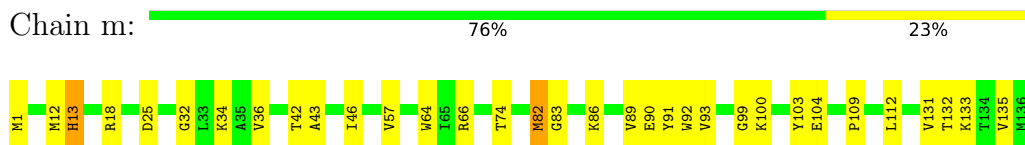
- Molecule 15: 50S ribosomal protein L14



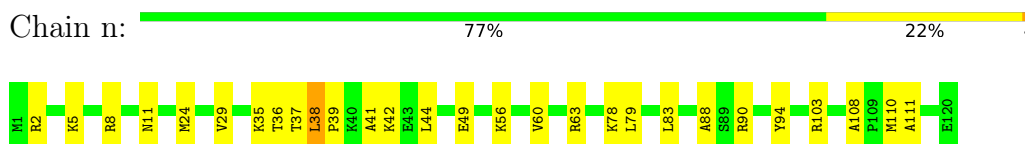
- Molecule 16: 50S ribosomal protein L15




- Molecule 17: 50S ribosomal protein L16



- Molecule 18: 50S ribosomal protein L17




- Molecule 19: 50S ribosomal protein L18

Chain o:  84% 16%




- Molecule 20: 50S ribosomal protein L19

Chain p:  77% 23%



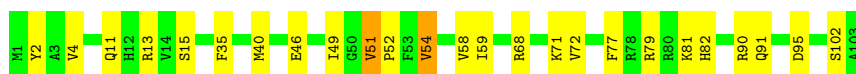
- Molecule 21: 50S ribosomal protein L20

Chain q:  81% 18%



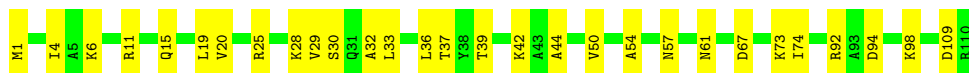
- Molecule 22: 50S ribosomal protein L21

Chain r:  76% 22%




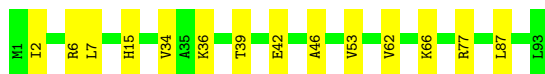
- Molecule 23: 50S ribosomal protein L22

Chain s:  74% 26%




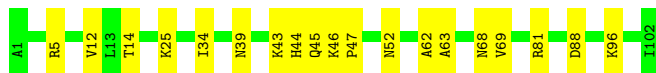
- Molecule 24: 50S ribosomal protein L23

Chain t:  85% 15%



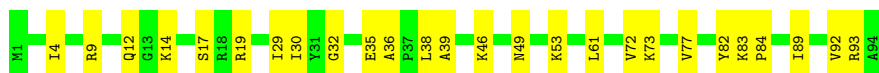
- Molecule 25: 50S ribosomal protein L24

Chain u:  81% 19%




- Molecule 26: 50S ribosomal protein L25

Chain v:  72% 28%




- Molecule 27: 50S ribosomal protein L27

Chain w:  83% 17%



- Molecule 28: 50S ribosomal protein L28

Chain x:  82% 18%



- Molecule 29: 50S ribosomal protein L29

Chain y:  94% 6%



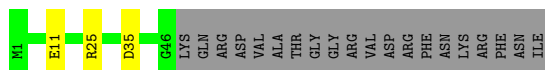
- Molecule 30: 50S ribosomal protein L30

Chain z:  76% 22%




- Molecule 31: 50S ribosomal protein L31

Chain A:  65% 5% 30%

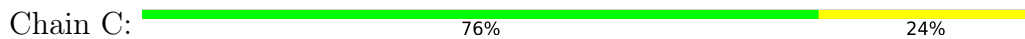


- Molecule 32: 50S ribosomal protein L32

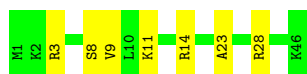
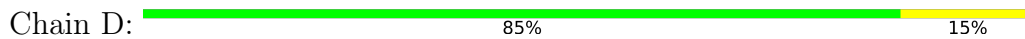
Chain B:  80% 18%



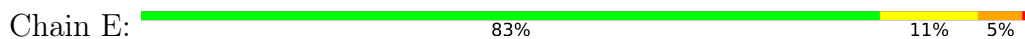
- Molecule 33: 50S ribosomal protein L33



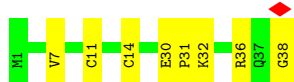
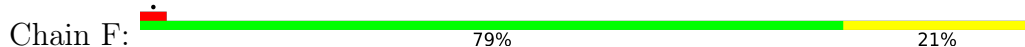
● Molecule 34: 50S ribosomal protein L34



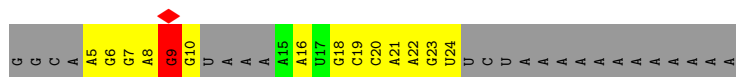
● Molecule 35: 50S ribosomal protein L35



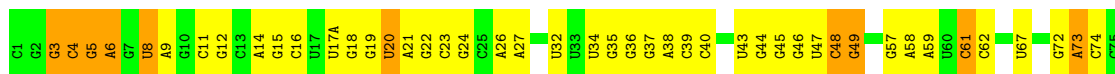
● Molecule 36: 50S ribosomal protein L36



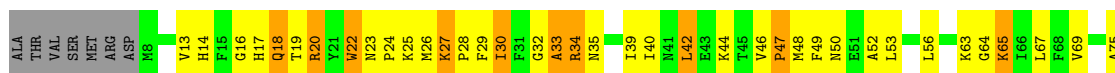
● Molecule 37: mRNA

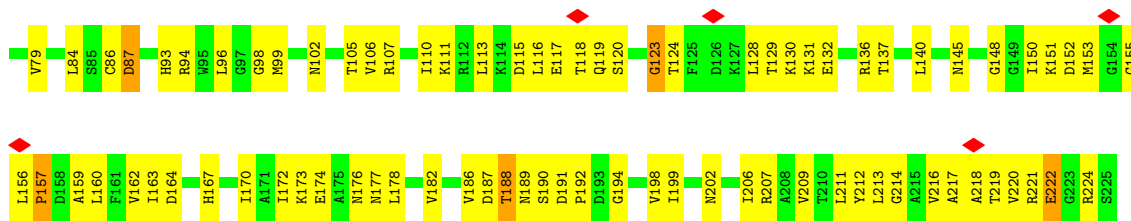


● Molecule 38: tRNA Pro

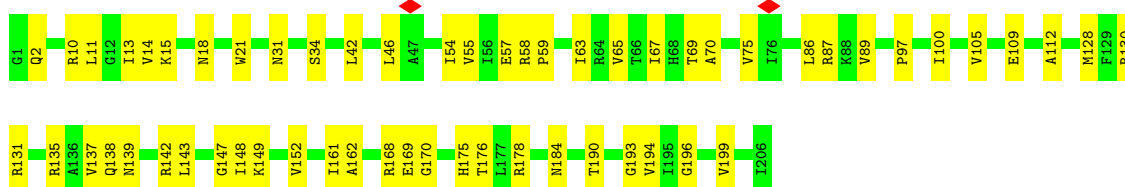


● Molecule 39: 30S ribosomal protein S2

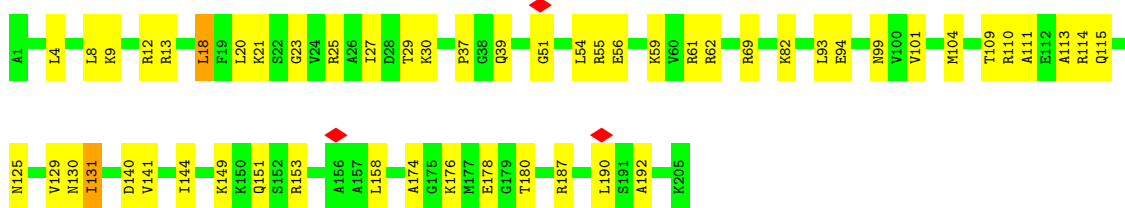




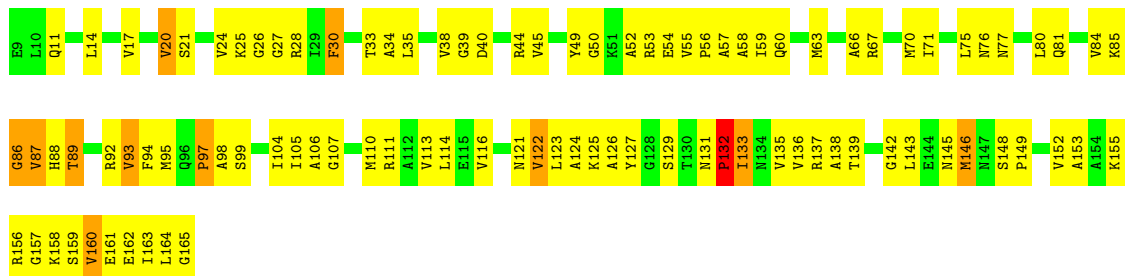
• Molecule 40: 30S ribosomal protein S3



• Molecule 41: 30S ribosomal protein S4




• Molecule 42: 30S ribosomal protein S5

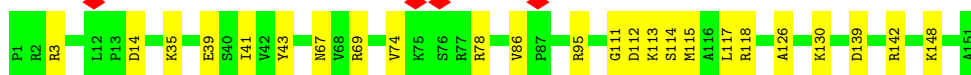


• Molecule 43: 30S ribosomal protein S6



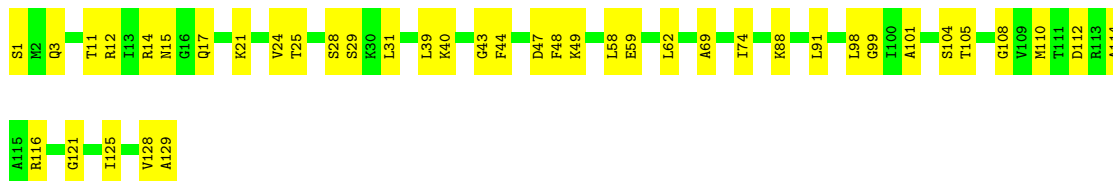
• Molecule 44: 30S ribosomal protein S7

Chain L:  84% 16%



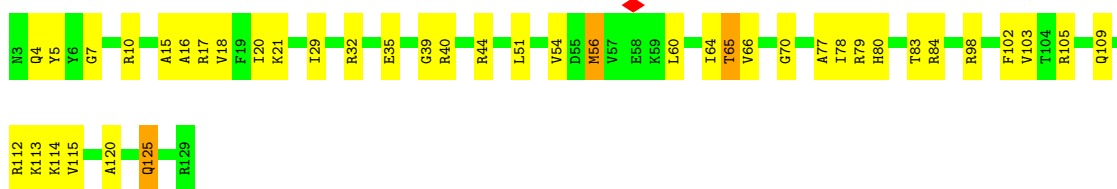
- Molecule 45: 30S ribosomal protein S8

Chain M:  68% 32%



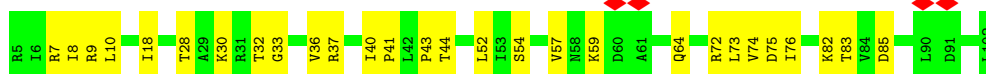
- Molecule 46: 30S ribosomal protein S9

Chain N:  68% 30%



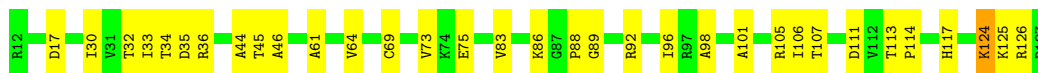
- Molecule 47: 30S ribosomal protein S10

Chain O:  71% 29%



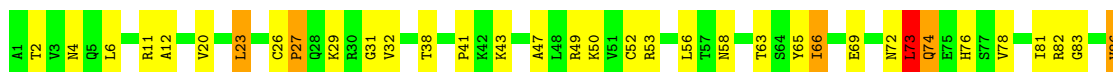
- Molecule 48: 30S ribosomal protein S11

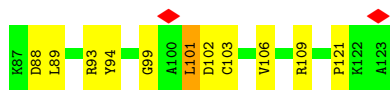
Chain P:  72% 28%



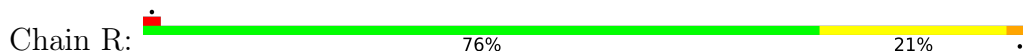
- Molecule 49: 30S ribosomal protein S12

Chain Q:  63% 32% 5%

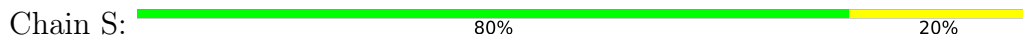




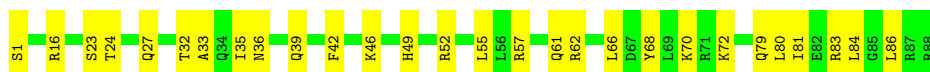
- Molecule 50: 30S ribosomal protein S13



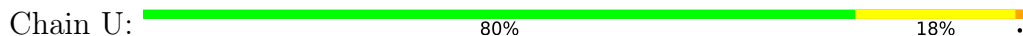
- Molecule 51: 30S ribosomal protein S14



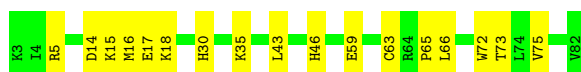
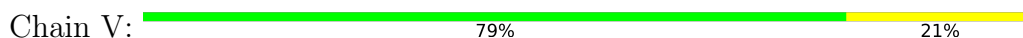
- Molecule 52: 30S ribosomal protein S15



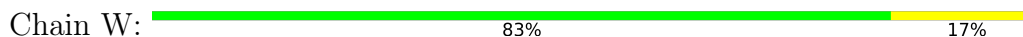
- Molecule 53: 30S ribosomal protein S16



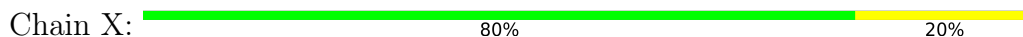
- Molecule 54: 30S ribosomal protein S17



- Molecule 55: 30S ribosomal protein S18

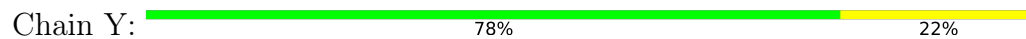


- Molecule 56: 30S ribosomal protein S19





- Molecule 57: 30S ribosomal protein S20



- Molecule 58: 30S ribosomal protein S21



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	3778	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 ( $e^-/\text{\AA}^2$ )	47.6	Depositor
Minimum defocus (nm)	800	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	27.032	Depositor
Minimum map value	-14.235	Depositor
Average map value	0.111	Depositor
Map value standard deviation	0.944	Depositor
Recommended contour level	0.7	Depositor
Map size ( $\text{\AA}$ )	370.5408, 370.5408, 370.5408	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.8271, 0.8271, 0.8271	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: GDP

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	3	0.43	0/36963	0.50	2/57662 (0.0%)
2	1	0.44	0/69796	0.51	4/108888 (0.0%)
3	2	0.44	0/2872	0.49	0/4479
4	8	0.30	0/5253	0.80	9/7106 (0.1%)
5	6	0.44	0/1832	0.50	0/2855
6	b	0.48	0/2122	0.74	0/2852
7	c	0.40	0/1586	0.70	0/2134
8	d	0.35	0/1571	0.65	0/2113
9	e	0.30	0/1435	0.69	0/1926
10	f	0.26	0/1343	0.56	0/1816
11	g	0.26	0/1122	0.68	2/1515 (0.1%)
12	a	0.22	0/1033	0.52	0/1387
13	i	0.27	0/1046	0.66	0/1410
14	j	0.38	0/1152	0.57	0/1551
15	k	0.43	0/948	0.77	2/1268 (0.2%)
16	l	0.39	0/1054	0.83	2/1403 (0.1%)
17	m	0.40	0/1093	0.67	0/1460
18	n	0.42	0/974	0.77	0/1301
19	o	0.28	0/902	0.57	0/1209
20	p	0.35	0/929	0.61	0/1242
21	q	0.41	0/960	0.59	0/1278
22	r	0.34	0/829	0.66	0/1107
23	s	0.37	0/864	0.67	0/1156
24	t	0.32	0/745	0.59	0/994
25	u	0.31	0/788	0.64	2/1051 (0.2%)
26	v	0.31	0/766	0.58	0/1025
27	w	0.36	0/582	0.66	0/769
28	x	0.41	0/635	0.57	0/848
29	y	0.28	0/510	0.51	0/677
30	z	0.34	0/453	0.71	0/605
31	A	0.24	0/362	0.62	0/485
32	B	0.38	0/450	0.69	0/599

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
33	C	0.29	0/417	0.55	0/554
34	D	0.46	0/380	0.77	0/498
35	E	0.43	0/513	0.91	4/676 (0.6%)
36	F	0.42	0/303	0.87	0/397
37	4	0.56	0/392	0.64	0/608
38	5	0.45	0/1840	0.54	0/2868
39	G	0.38	0/1736	0.88	4/2338 (0.2%)
40	H	0.27	0/1652	0.63	0/2225
41	I	0.27	0/1665	0.66	0/2227
42	J	0.38	0/1170	0.82	0/1573
43	K	0.34	0/836	0.83	5/1128 (0.4%)
44	L	0.23	0/1196	0.58	0/1602
45	M	0.29	0/989	0.58	0/1326
46	N	0.31	0/1034	0.76	1/1375 (0.1%)
47	O	0.29	0/797	0.71	0/1077
48	P	0.32	0/886	0.71	2/1195 (0.2%)
49	Q	0.33	0/969	0.81	3/1300 (0.2%)
50	R	0.29	0/893	0.70	1/1193 (0.1%)
51	S	0.23	0/817	0.52	0/1088
52	T	0.32	0/722	0.63	0/964
53	U	0.29	0/659	0.80	0/884
54	V	0.33	0/658	0.69	0/881
55	W	0.29	0/545	0.65	0/731
56	X	0.28	0/653	0.76	2/877 (0.2%)
57	Y	0.27	0/671	0.62	0/888
58	Z	0.33	0/551	0.88	2/728 (0.3%)
All	All	0.41	0/165914	0.57	47/247372 (0.0%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1	0	3
4	8	0	5
7	c	0	1
8	d	0	2
9	e	0	1
10	f	0	1
11	g	0	1
16	l	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
17	m	0	2
22	r	0	1
30	z	0	1
35	E	0	1
37	4	0	1
41	I	0	1
43	K	0	1
44	L	0	1
46	N	0	1
49	Q	0	4
50	R	0	2
54	V	0	2
55	W	0	1
56	X	0	1
58	Z	0	3
All	All	0	38

There are no bond length outliers.

The worst 5 of 47 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
4	8	194	ASN	CA-C-N	7.76	136.35	121.54
4	8	194	ASN	C-N-CA	7.76	136.35	121.54
43	K	51	ILE	CA-C-N	7.01	134.93	121.54
43	K	51	ILE	C-N-CA	7.01	134.93	121.54
35	E	30	HIS	CA-C-N	6.72	134.06	121.97

There are no chirality outliers.

5 of 38 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	1779	U	Sidechain
2	1	1964	G	Sidechain
2	1	511	U	Sidechain
4	8	193	TRP	Peptide
4	8	368	ALA	Peptide

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	3	33012	0	16618	524	0
2	1	62317	0	31346	867	0
3	2	2568	0	1303	46	0
4	8	5157	0	5137	138	0
5	6	1640	0	837	23	0
6	b	2083	0	2157	50	0
7	c	1565	0	1616	35	0
8	d	1552	0	1619	33	0
9	e	1411	0	1447	28	0
10	f	1323	0	1374	15	0
11	g	1111	0	1148	15	0
12	a	1026	0	1092	25	0
13	i	1032	0	1088	27	0
14	j	1129	0	1162	21	0
15	k	939	0	1012	27	0
16	l	1045	0	1117	27	0
17	m	1074	0	1157	21	0
18	n	961	0	1000	21	0
19	o	892	0	923	14	0
20	p	917	0	965	15	0
21	q	947	0	1022	17	0
22	r	816	0	839	18	0
23	s	857	0	922	23	0
24	t	739	0	807	7	0
25	u	780	0	834	13	0
26	v	753	0	780	18	0
27	w	575	0	592	12	0
28	x	625	0	655	9	0
29	y	509	0	543	3	0
30	z	449	0	491	10	0
31	A	355	0	353	2	0
32	B	444	0	461	10	0
33	C	410	0	440	9	0
34	D	377	0	418	5	0
35	E	504	0	574	8	0
36	F	302	0	341	6	0
37	4	350	0	176	57	0
38	5	1647	0	832	40	0
39	G	1705	0	1732	120	0
40	H	1625	0	1699	35	0
41	I	1643	0	1710	38	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
42	J	1157	0	1199	102	0
43	K	818	0	808	18	0
44	L	1182	0	1240	14	0
45	M	979	0	1034	26	0
46	N	1022	0	1070	32	0
47	O	787	0	828	22	0
48	P	870	0	878	23	0
49	Q	955	0	1019	30	0
50	R	884	0	944	26	0
51	S	805	0	847	16	0
52	T	714	0	737	18	0
53	U	649	0	666	17	0
54	V	649	0	691	12	0
55	W	536	0	552	18	0
56	X	638	0	665	13	0
57	Y	665	0	714	14	0
58	Z	545	0	579	17	0
59	8	28	0	12	2	0
All	All	153049	0	104822	2492	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 2492 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:8:512:ARG:HD2	37:4:22:A:OP2	1.30	1.23
1:3:813:U:H2'	1:3:814:A:H5''	1.28	1.12
4:8:512:ARG:HD3	37:4:22:A:O5'	1.49	1.10
2:1:1175:A:H3'	2:1:1176:U:H5'	1.29	1.09
3:2:83:G:H2'	3:2:84:G:H5''	1.35	1.08

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
4	8	662/697 (95%)	595 (90%)	65 (10%)	2 (0%)	36	65
6	b	269/271 (99%)	234 (87%)	33 (12%)	2 (1%)	18	49
7	c	207/209 (99%)	190 (92%)	16 (8%)	1 (0%)	24	55
8	d	199/201 (99%)	173 (87%)	25 (13%)	1 (0%)	24	55
9	e	175/177 (99%)	152 (87%)	23 (13%)	0	100	100
10	f	174/176 (99%)	152 (87%)	22 (13%)	0	100	100
11	g	147/149 (99%)	128 (87%)	19 (13%)	0	100	100
12	a	130/234 (56%)	118 (91%)	12 (9%)	0	100	100
13	i	139/142 (98%)	115 (83%)	24 (17%)	0	100	100
14	j	140/142 (99%)	128 (91%)	12 (9%)	0	100	100
15	k	120/122 (98%)	106 (88%)	13 (11%)	1 (1%)	16	45
16	l	141/143 (99%)	120 (85%)	20 (14%)	1 (1%)	18	49
17	m	134/136 (98%)	114 (85%)	18 (13%)	2 (2%)	8	32
18	n	118/120 (98%)	102 (86%)	16 (14%)	0	100	100
19	o	114/116 (98%)	111 (97%)	3 (3%)	0	100	100
20	p	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
21	q	115/117 (98%)	113 (98%)	2 (2%)	0	100	100
22	r	101/103 (98%)	88 (87%)	13 (13%)	0	100	100
23	s	108/110 (98%)	102 (94%)	6 (6%)	0	100	100
24	t	91/93 (98%)	80 (88%)	11 (12%)	0	100	100
25	u	100/102 (98%)	89 (89%)	11 (11%)	0	100	100
26	v	92/94 (98%)	81 (88%)	11 (12%)	0	100	100
27	w	73/75 (97%)	64 (88%)	9 (12%)	0	100	100
28	x	75/77 (97%)	67 (89%)	8 (11%)	0	100	100
29	y	61/63 (97%)	60 (98%)	1 (2%)	0	100	100
30	z	56/58 (97%)	49 (88%)	7 (12%)	0	100	100
31	A	44/66 (67%)	35 (80%)	9 (20%)	0	100	100
32	B	54/56 (96%)	49 (91%)	5 (9%)	0	100	100
33	C	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
34	D	44/46 (96%)	38 (86%)	6 (14%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
35	E	62/64 (97%)	51 (82%)	9 (14%)	2 (3%)	3	19
36	F	36/38 (95%)	30 (83%)	6 (17%)	0	100	100
39	G	216/225 (96%)	179 (83%)	28 (13%)	9 (4%)	2	14
40	H	204/206 (99%)	193 (95%)	11 (5%)	0	100	100
41	I	203/205 (99%)	180 (89%)	22 (11%)	1 (0%)	24	55
42	J	155/157 (99%)	108 (70%)	32 (21%)	15 (10%)	0	3
43	K	98/100 (98%)	79 (81%)	18 (18%)	1 (1%)	12	40
44	L	149/151 (99%)	132 (89%)	17 (11%)	0	100	100
45	M	127/129 (98%)	114 (90%)	13 (10%)	0	100	100
46	N	125/127 (98%)	107 (86%)	18 (14%)	0	100	100
47	O	96/98 (98%)	78 (81%)	18 (19%)	0	100	100
48	P	114/116 (98%)	99 (87%)	14 (12%)	1 (1%)	14	43
49	Q	121/123 (98%)	94 (78%)	23 (19%)	4 (3%)	3	19
50	R	112/114 (98%)	101 (90%)	11 (10%)	0	100	100
51	S	98/100 (98%)	91 (93%)	7 (7%)	0	100	100
52	T	86/88 (98%)	79 (92%)	7 (8%)	0	100	100
53	U	80/82 (98%)	64 (80%)	15 (19%)	1 (1%)	9	35
54	V	78/80 (98%)	68 (87%)	10 (13%)	0	100	100
55	W	63/65 (97%)	59 (94%)	4 (6%)	0	100	100
56	X	77/79 (98%)	64 (83%)	13 (17%)	0	100	100
57	Y	83/85 (98%)	77 (93%)	6 (7%)	0	100	100
58	Z	63/65 (97%)	48 (76%)	14 (22%)	1 (2%)	7	31
All	All	6489/6756 (96%)	5692 (88%)	752 (12%)	45 (1%)	20	49

5 of 45 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
35	E	31	ILE
39	G	18	GLN
39	G	34	ARG
42	J	87	VAL
42	J	160	VAL

### 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	
4	8	548/574 (96%)	545 (100%)	3 (0%)	81	83
6	b	216/216 (100%)	214 (99%)	2 (1%)	70	78
7	c	164/164 (100%)	163 (99%)	1 (1%)	78	81
8	d	165/165 (100%)	163 (99%)	2 (1%)	63	75
9	e	148/148 (100%)	147 (99%)	1 (1%)	76	80
10	f	137/137 (100%)	135 (98%)	2 (2%)	57	72
11	g	114/114 (100%)	114 (100%)	0	100	100
12	a	110/181 (61%)	107 (97%)	3 (3%)	39	63
13	i	109/110 (99%)	106 (97%)	3 (3%)	38	62
14	j	116/116 (100%)	116 (100%)	0	100	100
15	k	103/103 (100%)	100 (97%)	3 (3%)	37	62
16	l	102/102 (100%)	101 (99%)	1 (1%)	68	76
17	m	109/109 (100%)	107 (98%)	2 (2%)	51	70
18	n	100/100 (100%)	99 (99%)	1 (1%)	68	76
19	o	86/86 (100%)	84 (98%)	2 (2%)	44	66
20	p	99/99 (100%)	98 (99%)	1 (1%)	68	76
21	q	89/89 (100%)	88 (99%)	1 (1%)	65	76
22	r	84/84 (100%)	81 (96%)	3 (4%)	31	58
23	s	93/93 (100%)	93 (100%)	0	100	100
24	t	80/80 (100%)	78 (98%)	2 (2%)	42	64
25	u	83/83 (100%)	83 (100%)	0	100	100
26	v	78/78 (100%)	78 (100%)	0	100	100
27	w	57/57 (100%)	57 (100%)	0	100	100
28	x	67/67 (100%)	67 (100%)	0	100	100
29	y	55/55 (100%)	55 (100%)	0	100	100
30	z	48/48 (100%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
31	A	42/59 (71%)	42 (100%)	0	100	100
32	B	47/47 (100%)	46 (98%)	1 (2%)	47	67
33	C	45/45 (100%)	45 (100%)	0	100	100
34	D	38/38 (100%)	38 (100%)	0	100	100
35	E	51/51 (100%)	50 (98%)	1 (2%)	48	68
36	F	34/34 (100%)	34 (100%)	0	100	100
39	G	180/186 (97%)	176 (98%)	4 (2%)	45	66
40	H	170/170 (100%)	167 (98%)	3 (2%)	51	70
41	I	172/172 (100%)	171 (99%)	1 (1%)	78	81
42	J	119/119 (100%)	116 (98%)	3 (2%)	42	64
43	K	87/87 (100%)	86 (99%)	1 (1%)	65	76
44	L	124/124 (100%)	123 (99%)	1 (1%)	73	79
45	M	104/104 (100%)	104 (100%)	0	100	100
46	N	105/105 (100%)	103 (98%)	2 (2%)	50	68
47	O	86/86 (100%)	85 (99%)	1 (1%)	63	75
48	P	89/89 (100%)	88 (99%)	1 (1%)	65	76
49	Q	103/103 (100%)	100 (97%)	3 (3%)	37	62
50	R	92/92 (100%)	90 (98%)	2 (2%)	45	66
51	S	83/83 (100%)	83 (100%)	0	100	100
52	T	76/76 (100%)	76 (100%)	0	100	100
53	U	65/65 (100%)	65 (100%)	0	100	100
54	V	74/74 (100%)	74 (100%)	0	100	100
55	W	56/56 (100%)	56 (100%)	0	100	100
56	X	70/70 (100%)	69 (99%)	1 (1%)	59	73
57	Y	65/65 (100%)	65 (100%)	0	100	100
58	Z	55/55 (100%)	55 (100%)	0	100	100
All	All	5392/5513 (98%)	5334 (99%)	58 (1%)	63	76

5 of 58 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
22	r	51	VAL
50	R	24	VAL

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Mol	Chain	Res	Type
39	G	42	LEU
49	Q	86	VAL
46	N	65	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
24	t	48	GLN
57	Y	69	ASN
40	H	7	ASN
57	Y	67	HIS
51	S	59	GLN

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	201 (13%)	2 (0%)
2	1	2902/2903 (99%)	383 (13%)	9 (0%)
3	2	119/120 (99%)	12 (10%)	1 (0%)
37	4	14/39 (35%)	2 (14%)	0
38	5	76/77 (98%)	17 (22%)	0
5	6	76/77 (98%)	17 (22%)	0
All	All	4725/4755 (99%)	632 (13%)	12 (0%)

5 of 632 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	5	U
1	3	9	G
1	3	22	G
1	3	30	U
1	3	31	G

5 of 12 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	1	1930	G
2	1	2326	C
3	2	88	C
2	1	2391	G

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Mol	Chain	Res	Type
2	1	784	G

## 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](#)

1 ligand is 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
59	GDP	8	801	-	29,30,30	1.17	3 (10%)	45,47,47	1.82	7 (15%)

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
59	GDP	8	801	-	-	4/16/32/32	0/3/3/3

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
59	8	801	GDP	C5-C4	2.91	1.46	1.38
59	8	801	GDP	C6-N1	-2.78	1.33	1.38
59	8	801	GDP	C5-N7	-2.13	1.34	1.39

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
59	8	801	GDP	C5-C4-N3	-6.42	118.17	128.39
59	8	801	GDP	C2-N3-C4	5.35	121.51	112.30
59	8	801	GDP	N9-C4-N3	4.62	135.18	125.95
59	8	801	GDP	C6-C5-N7	3.09	135.91	130.29
59	8	801	GDP	C4-C5-N7	-2.53	106.67	110.67

There are no chirality outliers.

All (4) torsion outliers are listed below:

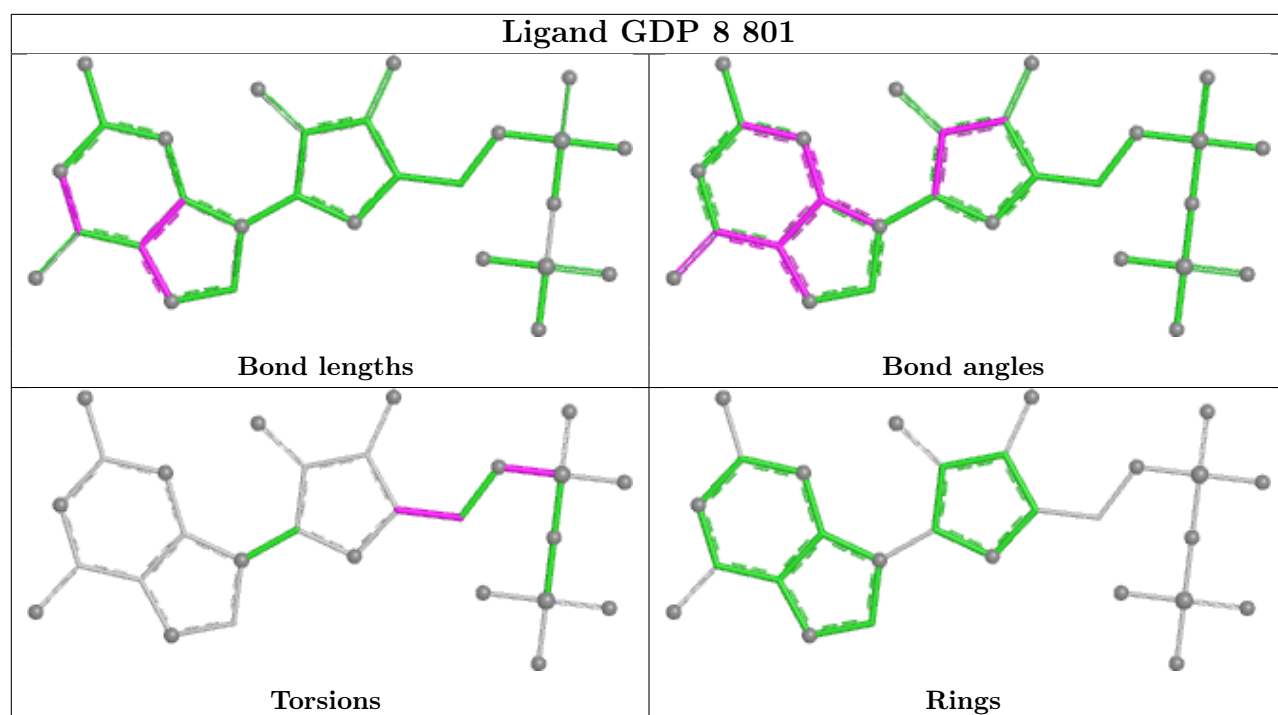
Mol	Chain	Res	Type	Atoms
59	8	801	GDP	C5'-O5'-PA-O1A
59	8	801	GDP	C5'-O5'-PA-O3A
59	8	801	GDP	C5'-O5'-PA-O2A
59	8	801	GDP	O4'-C4'-C5'-O5'

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
59	8	801	GDP	2	0

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.

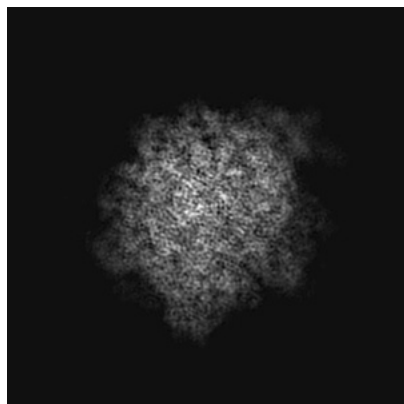
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25407. These allow visual inspection of the internal detail of the map and identification of artifacts.

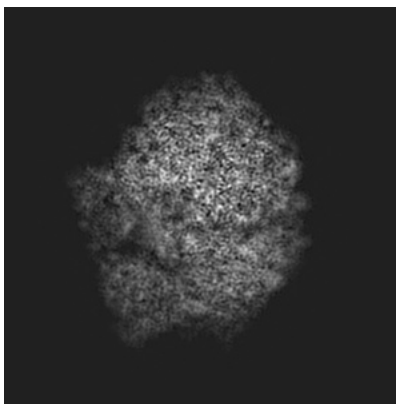
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

### 6.1 Orthogonal projections [i](#)

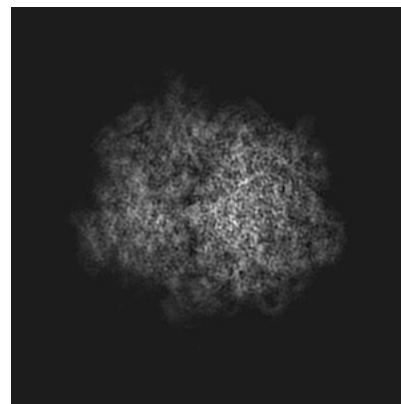
#### 6.1.1 Primary map



X

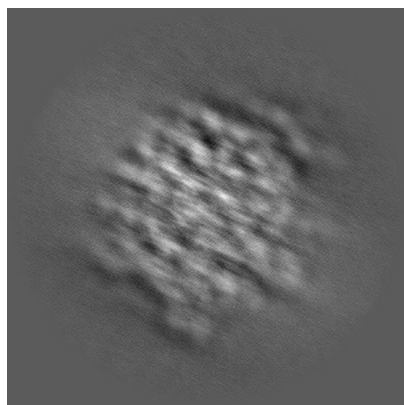


Y

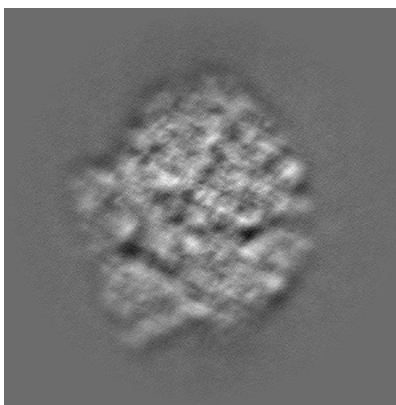


Z

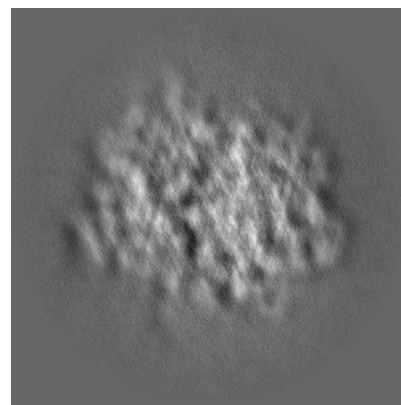
#### 6.1.2 Raw map



X



Y

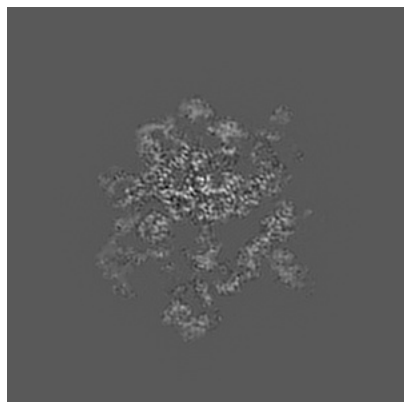


Z

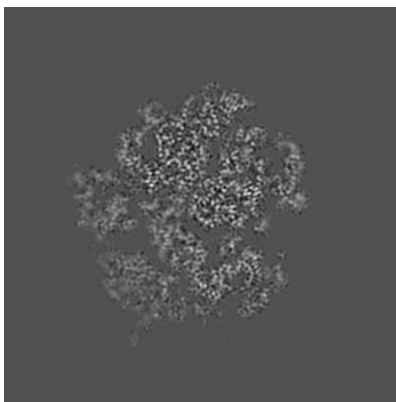
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

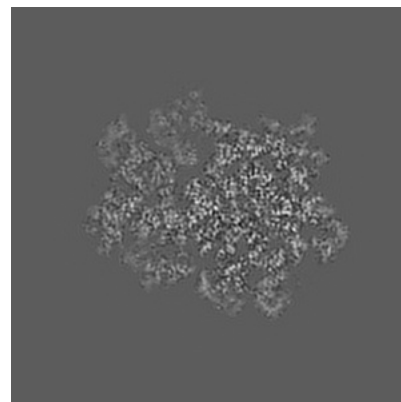
### 6.2.1 Primary map



X Index: 224

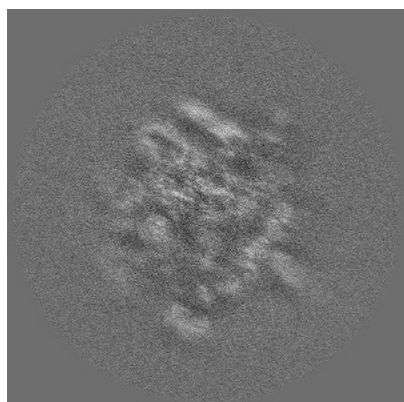


Y Index: 224

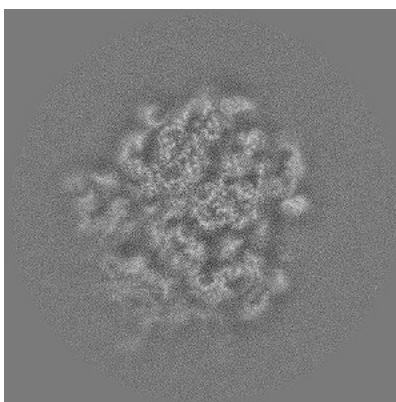


Z Index: 224

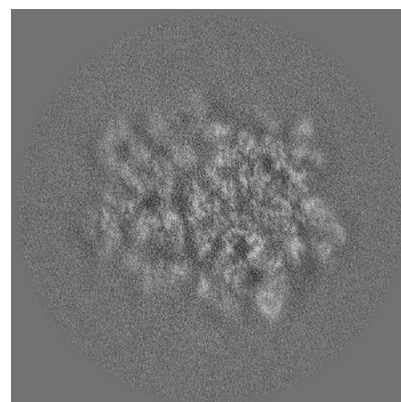
### 6.2.2 Raw map



X Index: 224



Y Index: 224

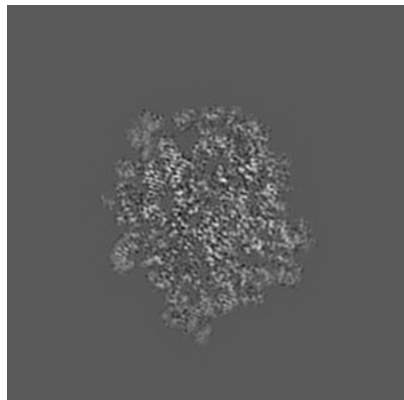


Z Index: 224

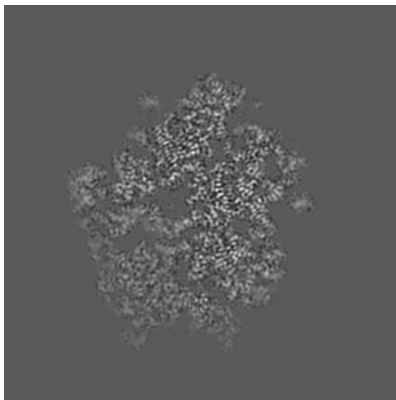
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

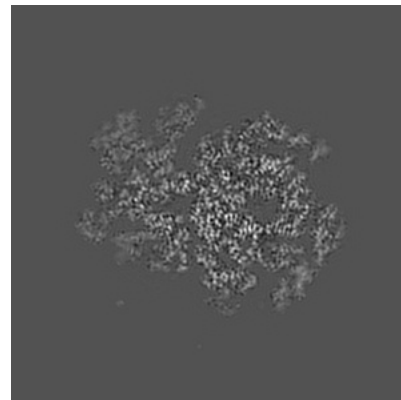
### 6.3.1 Primary map



X Index: 257

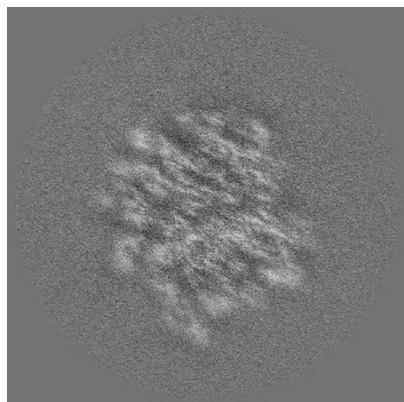


Y Index: 210

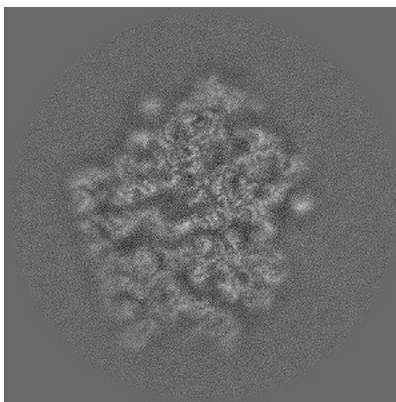


Z Index: 238

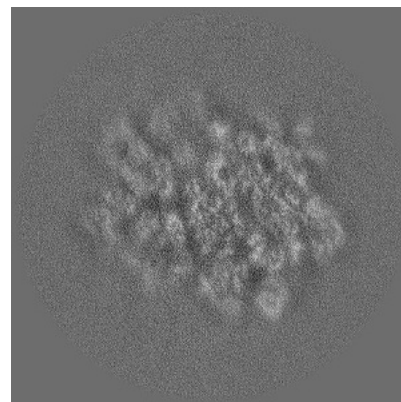
### 6.3.2 Raw map



X Index: 252



Y Index: 210

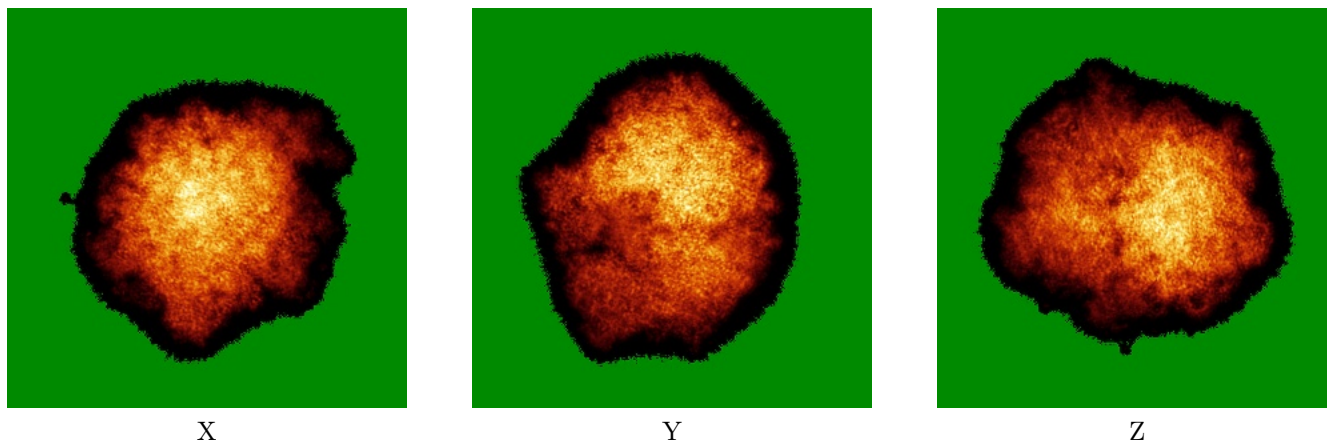


Z Index: 227

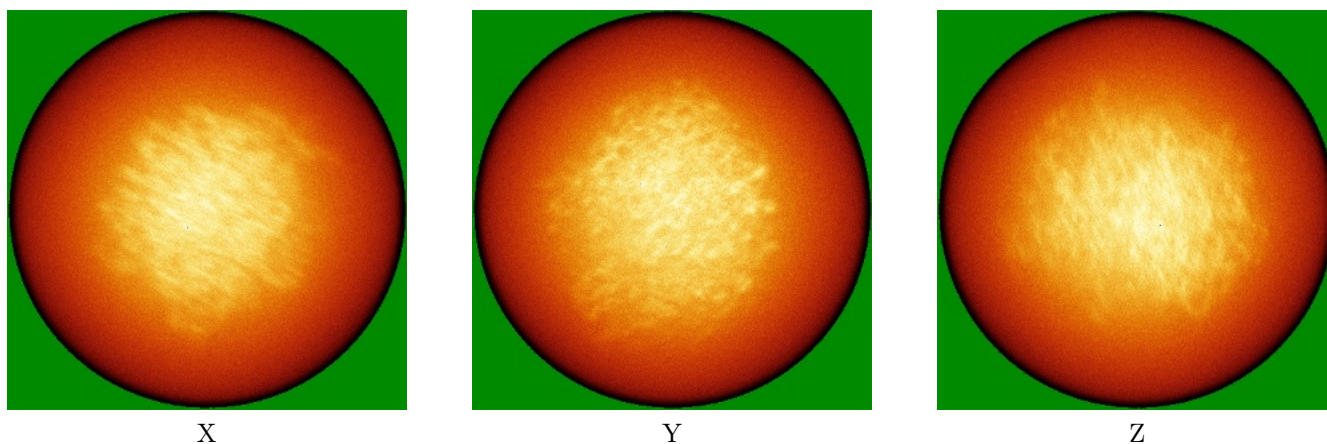
The images above show the largest variance slices of the map in three orthogonal directions.

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

### 6.4.1 Primary map



### 6.4.2 Raw map



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](#)

This section was not generated.

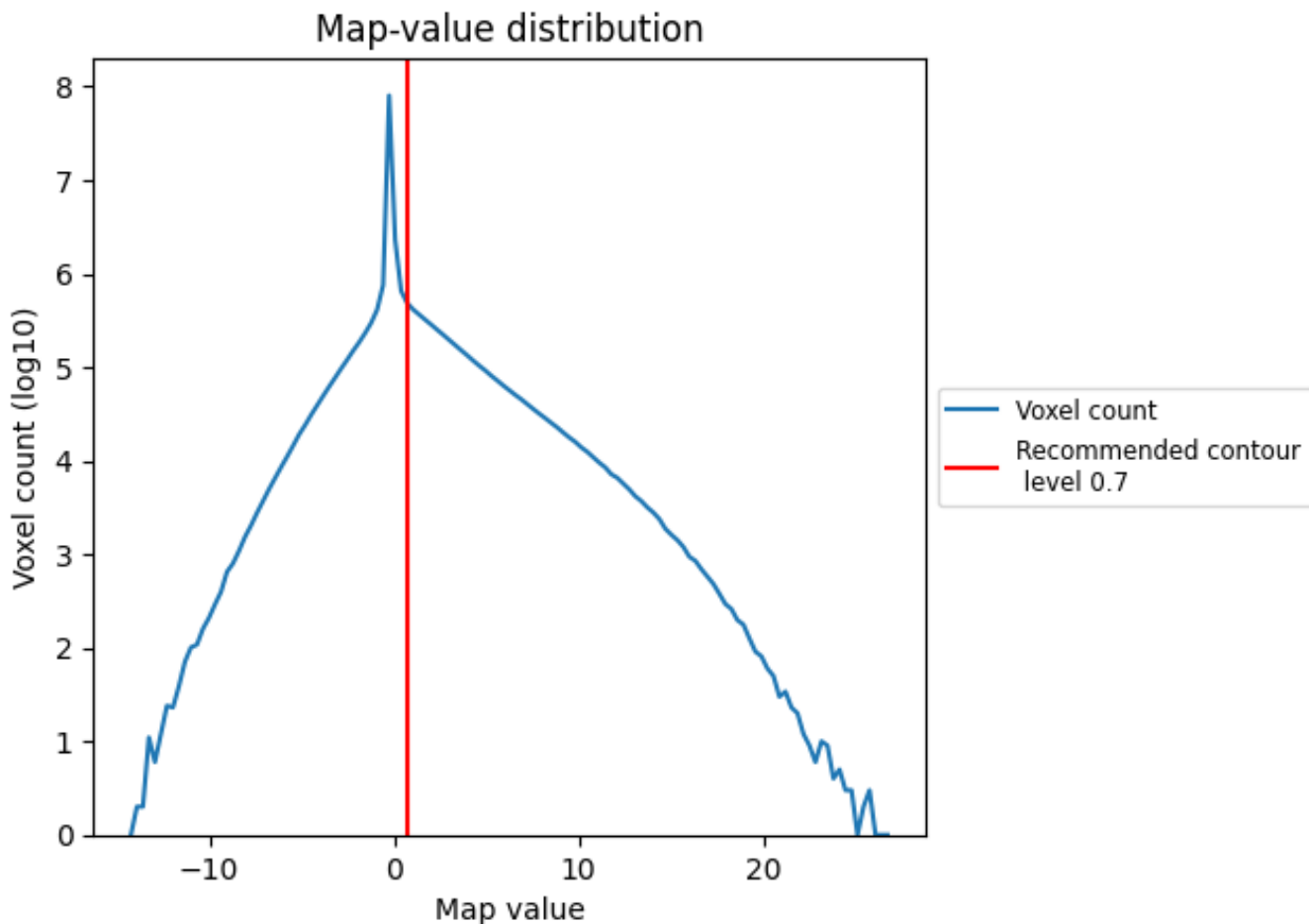
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

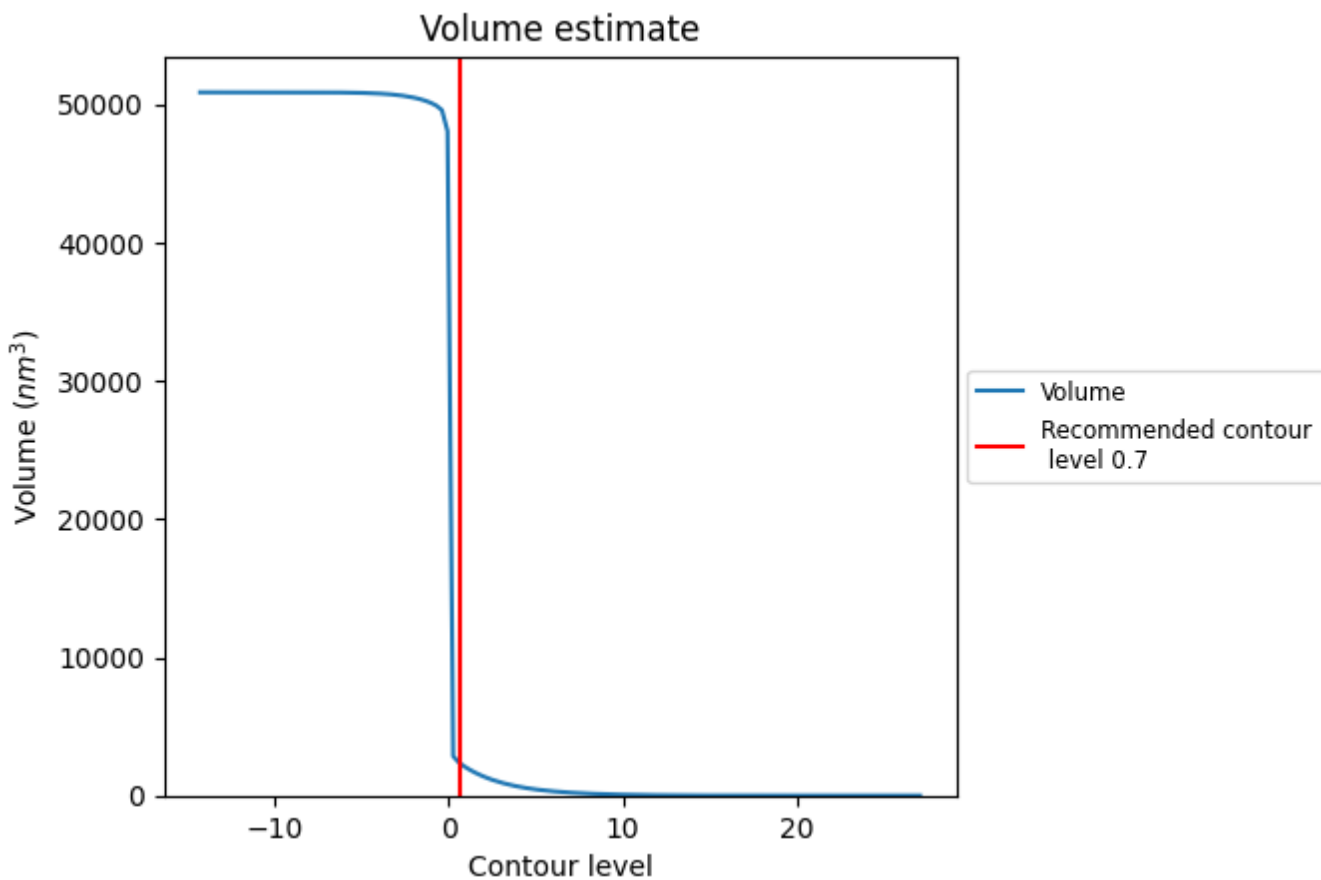
This section contains the results of statistical analysis of the map.

### 7.1 Map-value distribution [i](#)



The map-value distribution is plotted in 128 intervals along the x-axis. The y-axis is logarithmic. A spike in this graph at zero usually indicates that the volume has been masked.

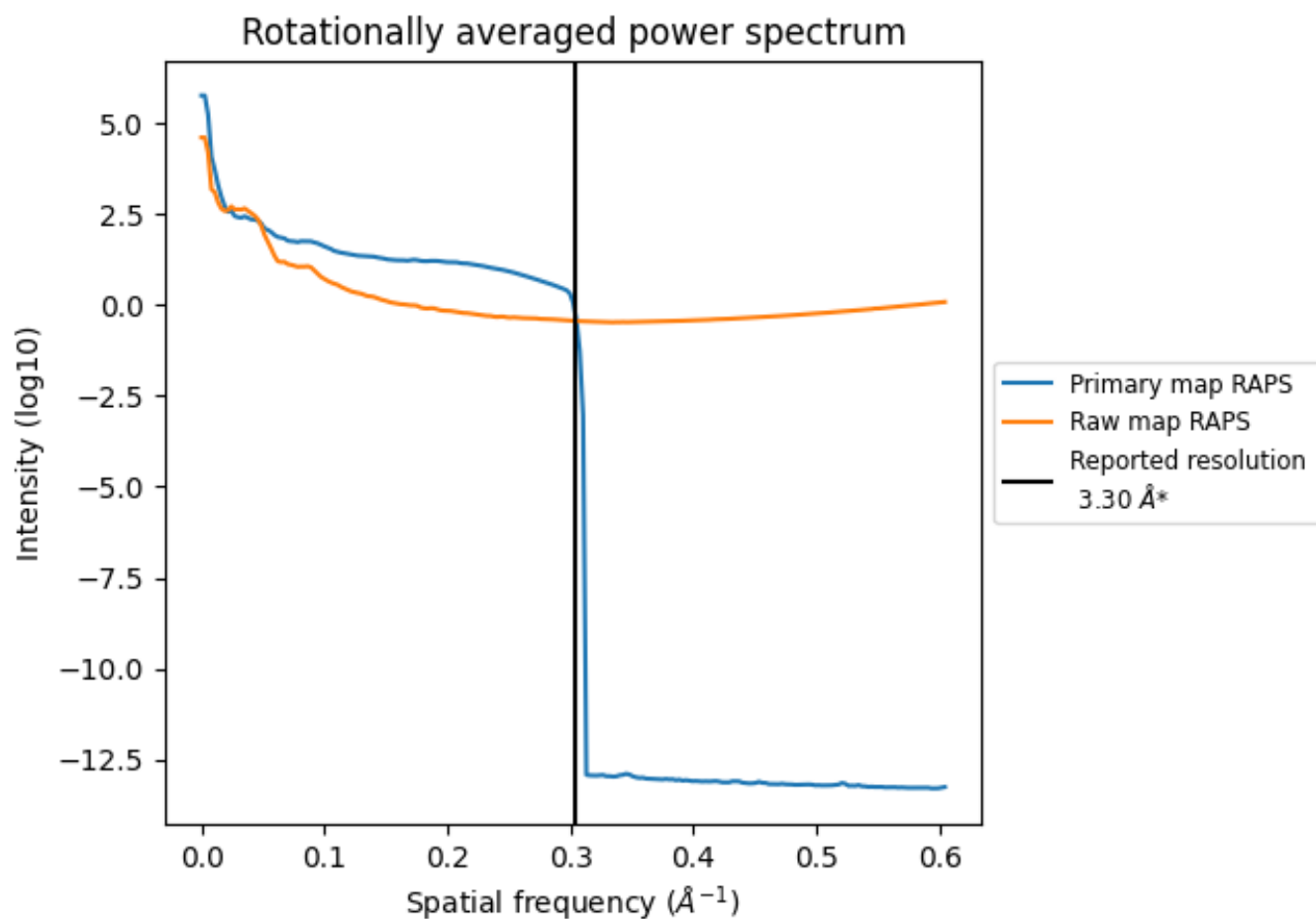
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2300 nm<sup>3</sup>; this corresponds to an approximate mass of 2078 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](#)

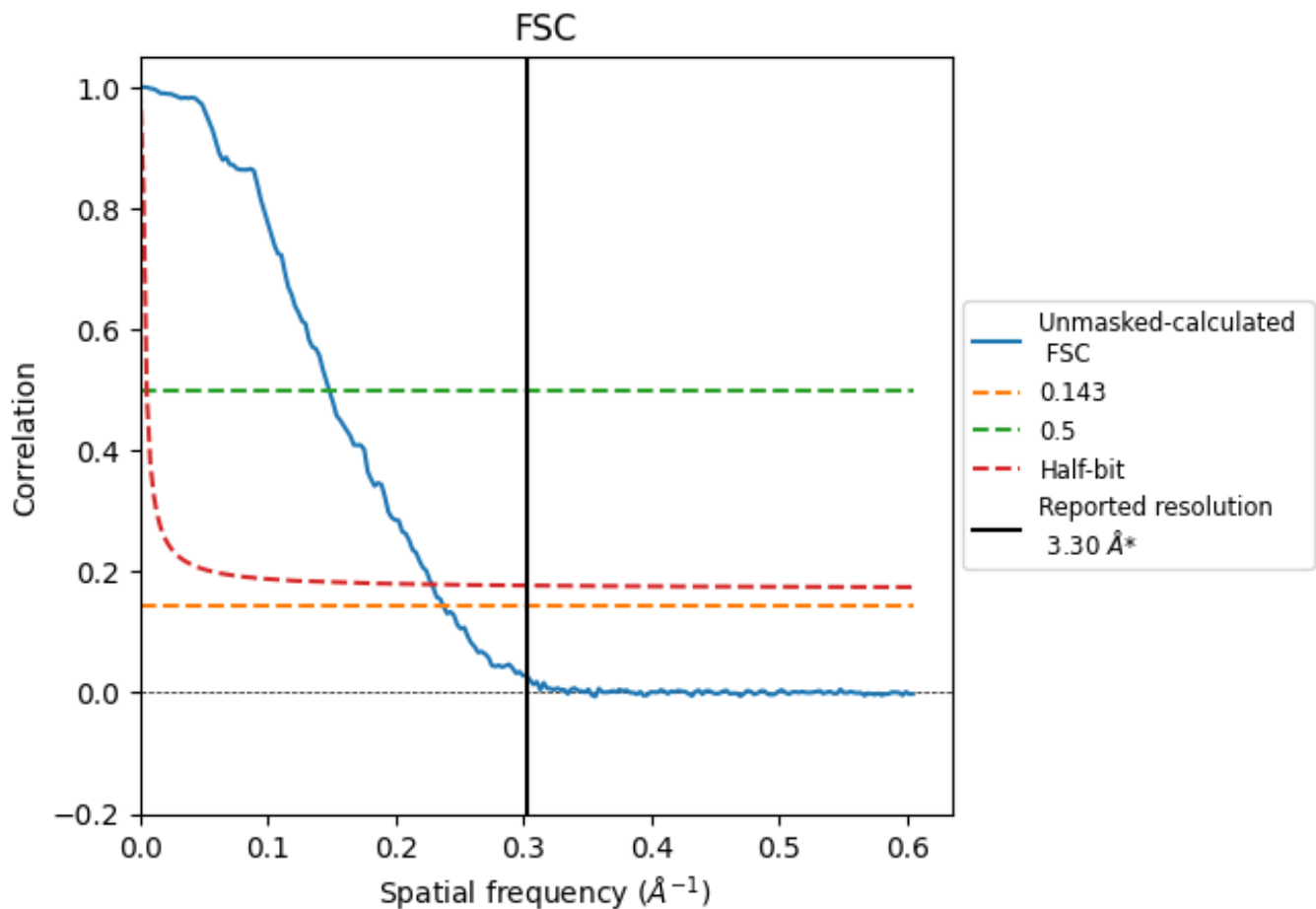


\*Reported resolution corresponds to spatial frequency of  $0.303 \text{ \AA}^{-1}$

## 8 Fourier-Shell correlation [i](#)

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

### 8.1 FSC [i](#)



\*Reported resolution corresponds to spatial frequency of 0.303 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.30	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.21	6.76	4.38

\*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 4.21 differs from the reported value 3.3 by more than 10 %

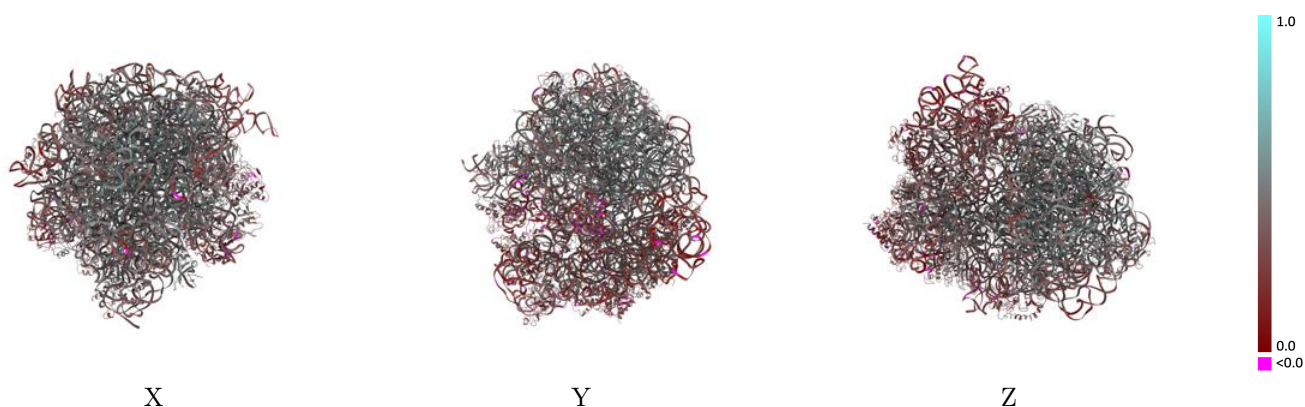
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-25407 and PDB model 7SSD. Per-residue inclusion information can be found in section 3 on page 16.

### 9.1 Map-model overlay [i](#)

This section was not generated.

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

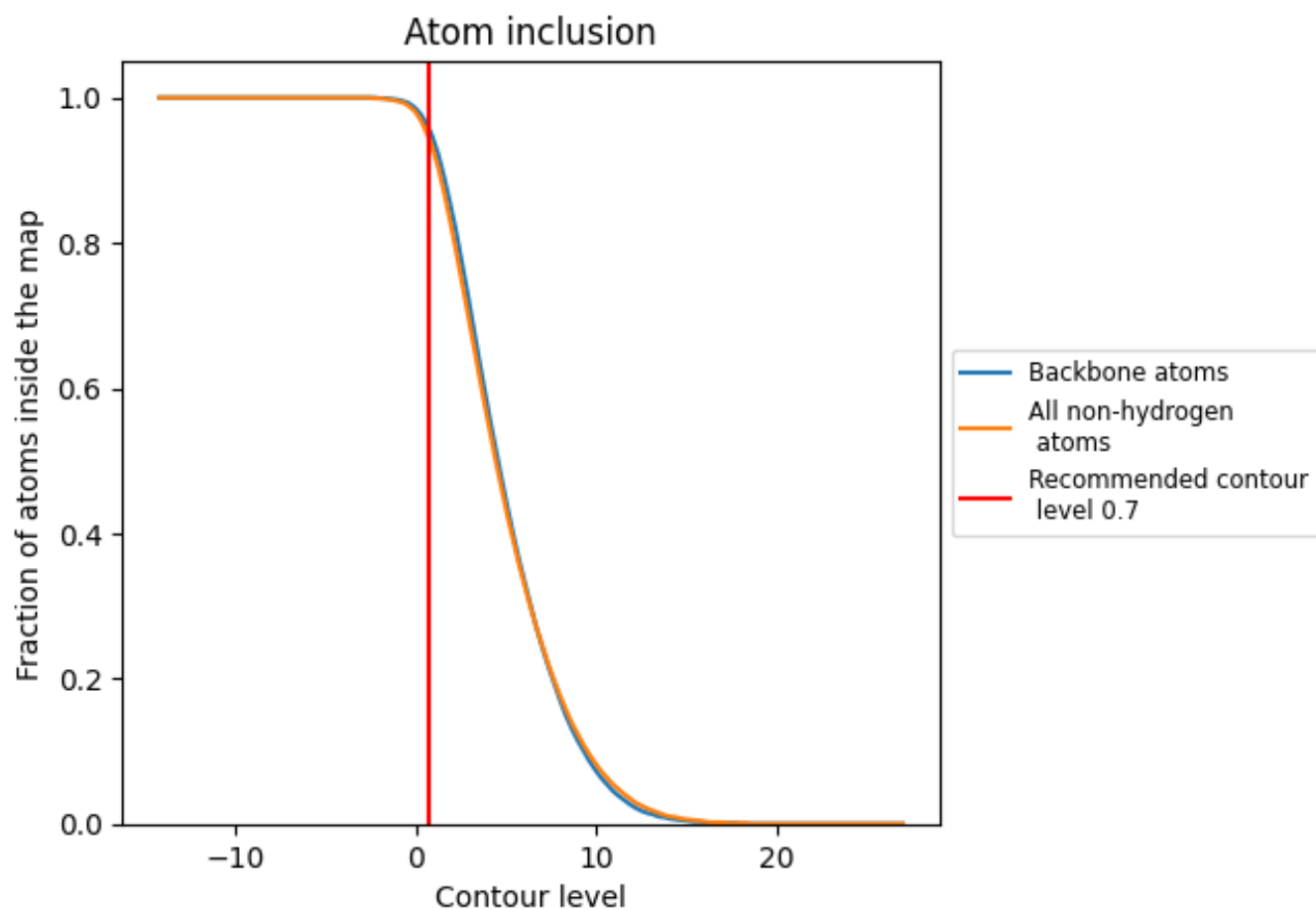


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions at which atoms can be resolved. Low Q-score values may therefore be expected for many entries.

### 9.3 Atom inclusion mapped to coordinate model [i](#)

This section was not generated.







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 95% 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 (0.7) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9460	 0.3850
1	 0.9740	 0.4280
2	 0.9770	 0.3950
3	 0.9420	 0.3230
4	 0.8170	 0.1920
5	 0.9450	 0.3160
6	 0.9450	 0.3080
8	 0.8230	 0.2730
A	 0.9260	 0.3310
B	 0.9740	 0.4740
C	 0.8860	 0.3930
D	 0.9580	 0.5160
E	 0.9720	 0.5020
F	 0.9450	 0.4570
G	 0.8510	 0.2790
H	 0.8920	 0.3170
I	 0.9040	 0.2880
J	 0.9370	 0.3710
K	 0.9490	 0.3490
L	 0.8520	 0.2810
M	 0.9500	 0.4130
N	 0.8800	 0.3240
O	 0.8400	 0.2630
P	 0.9490	 0.3980
Q	 0.9030	 0.3800
R	 0.8620	 0.2820
S	 0.9100	 0.3160
T	 0.9540	 0.3960
U	 0.9250	 0.3660
V	 0.9380	 0.3650
W	 0.9610	 0.4030
X	 0.8670	 0.2880
Y	 0.9420	 0.3570
Z	 0.9130	 0.3540
a	 0.8540	 0.2550



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Chain	Atom inclusion	Q-score
b	 0.9670	 0.4920
c	 0.9620	 0.4710
d	 0.9590	 0.4490
e	 0.9190	 0.3470
f	 0.9540	 0.4090
g	 0.7910	 0.2970
i	 0.7430	 0.2190
j	 0.9650	 0.4840
k	 0.9640	 0.4720
l	 0.9710	 0.4640
m	 0.9590	 0.4640
n	 0.9580	 0.4670
o	 0.9570	 0.4220
p	 0.9610	 0.4690
q	 0.9690	 0.4820
r	 0.9610	 0.4440
s	 0.9810	 0.4840
t	 0.9650	 0.4670
u	 0.9580	 0.4140
v	 0.9620	 0.4350
w	 0.9590	 0.4860
x	 0.9670	 0.4770
y	 0.9380	 0.4040
z	 0.9680	 0.4630