



## wwPDB EM Validation Summary Report ⓘ

May 20, 2024 – 12:00 AM JST

PDB ID : 7D80  
EMDB ID : EMD-30611  
Title : Molecular model of the cryo-EM structure of 70S ribosome in complex with peptide deformylase, trigger factor, and methionine aminopeptidase  
Authors : Akbar, S.; Bhakta, S.; Sengupta, J.  
Deposited on : 2020-10-06  
Resolution : 4.10 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:

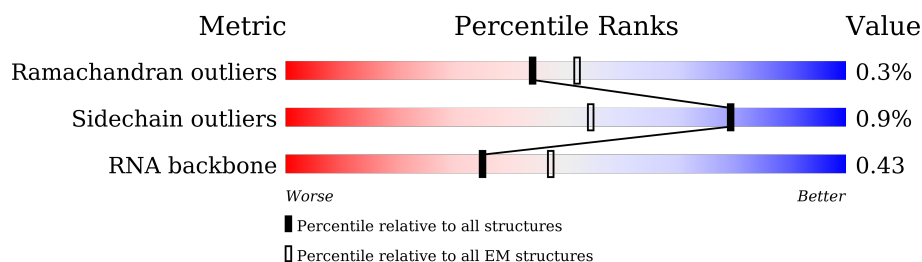
EMDB validation analysis : 0.0.1.dev92  
MolProbity : 4.02b-467  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
MapQ : 1.9.13  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

# 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 4.10 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.





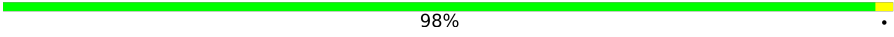



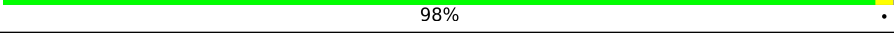
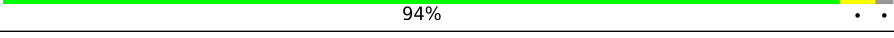
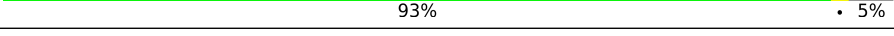

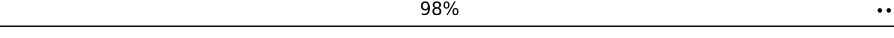
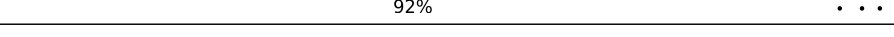
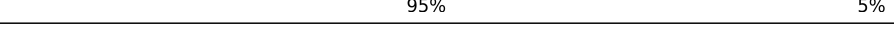
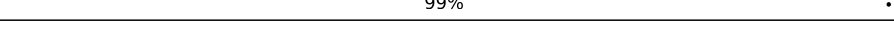
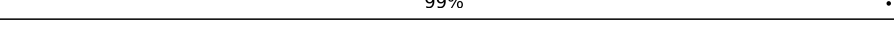

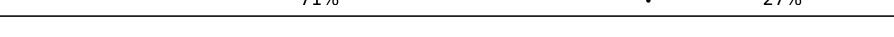

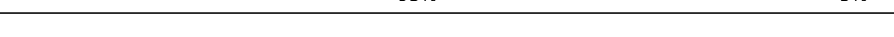






Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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  $\geq 3$ , 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	0	46	
2	1	65	
3	2	38	
4	3	169	
5	5	432	
6	6	57	
7	A	2903	
8	B	1539	

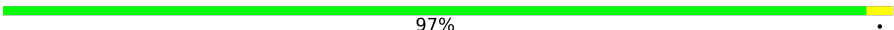
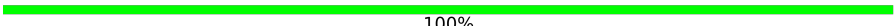
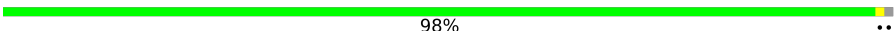
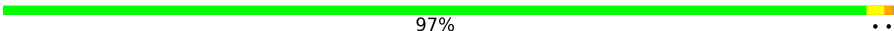

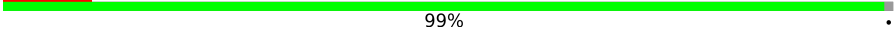
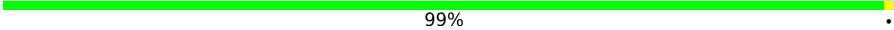
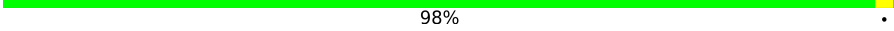
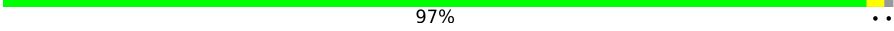
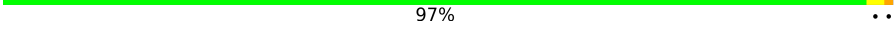

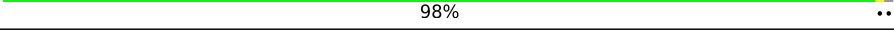
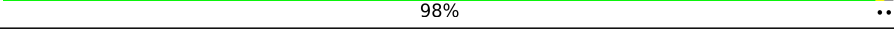
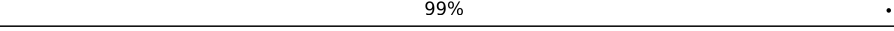
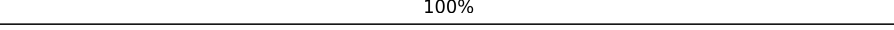
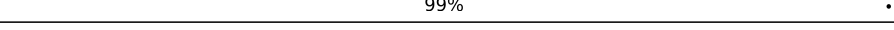
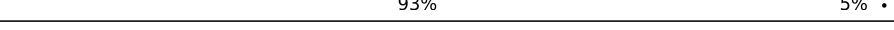
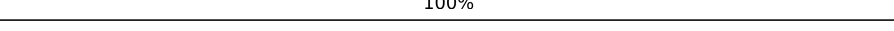

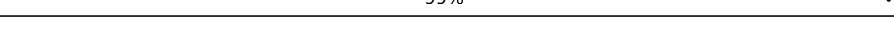
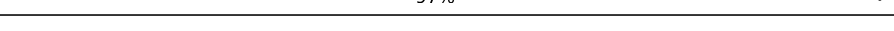
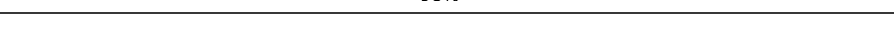


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Mol	Chain	Length	Quality of chain
9	C	241	
10	D	233	
11	E	206	
12	F	167	
13	G	135	
14	H	179	
15	I	130	
16	J	130	
17	K	103	
18	L	129	
19	M	124	
20	N	118	
21	O	101	
22	P	89	
23	Q	82	
24	R	84	
25	S	75	
26	T	92	
27	U	87	
28	V	71	
29	W	100	
30	X	73	
31	Z	76	
32	a	118	
33	b	273	

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Mol	Chain	Length	Quality of chain
34	c	209	 97% .
35	d	201	 100%
36	e	179	 98% ..
37	f	177	 97% ...
38	g	149	 32% 68%
39	h	142	 10% 99% .
40	i	142	 99% .
41	j	123	 98% ..
42	k	144	 97% ..
43	l	136	 97% ..
44	m	127	 91% . . 6%
45	n	117	 98% ..
46	o	115	 98% ..
47	p	118	 99% .
48	q	103	 100%
49	r	110	 99% .
50	s	104	 93% 5% .
51	t	94	 100%
52	u	85	 88% 12%
53	v	78	 99% .
54	w	63	 97% .
55	x	59	 98% .
56	y	77	 64% 27% 9%
57	z	55	 87% . 9%

## 2 Entry composition

There are 57 unique types of molecules in this entry. The entry contains 150808 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	0	46	Total	C	N	O	S	0	0
			377	228	90	57	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	64	Total	C	N	O	S	0	0
			504	323	105	74	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
3	2	38	Total	C	N	O	S	0	0
			302	185	65	48	4		

- Molecule 4 is a protein called Peptide deformylase.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	3	168	Total	C	N	O	S	0	0
			1346	844	241	255	6		

- Molecule 5 is a protein called Trigger factor.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	5	432	Total	C	N	O	S	0	0
			3386	2119	582	674	11		

- Molecule 6 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	6	56	Total	C	N	O	S	0	0
			444	269	94	80	1		

- Molecule 7 is a RNA chain called 23S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	A	2903	Total	C	N	O	P	0	0
			62317	27801	11467	20147	2902		

- Molecule 8 is a RNA chain called 16S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	B	1539	Total	C	N	O	P	0	0
			33015	14725	6052	10699	1539		

- Molecule 9 is a protein called 30S ribosomal protein S2.

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

- Molecule 10 is a protein called 30S ribosomal protein S3.

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

- Molecule 11 is a protein called 30S ribosomal protein S4.

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

- Molecule 12 is a protein called 30S ribosomal protein S5.

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

- Molecule 13 is a protein called 30S ribosomal protein S6, fully modified isoform.

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

- Molecule 14 is a protein called 30S ribosomal protein S7.

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

- Molecule 15 is a protein called 30S ribosomal protein S8.

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

- Molecule 16 is a protein called 30S ribosomal protein S9.

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

- Molecule 17 is a protein called 30S ribosomal protein S10.

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

- Molecule 18 is a protein called 30S ribosomal protein S11.

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

- Molecule 19 is a protein called 30S ribosomal protein S12.

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

- Molecule 20 is a protein called 30S ribosomal protein S13.

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

- Molecule 21 is a protein called 30S ribosomal protein S14.

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

- Molecule 22 is a protein called 30S ribosomal protein S15.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	P	88	Total	C	N	O	S	0	0
			710	437	143	129	1		

- Molecule 23 is a protein called 30S ribosomal protein S16.

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

- Molecule 24 is a protein called 30S ribosomal protein S17.

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

- Molecule 25 is a protein called 30S ribosomal protein S18.

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

- Molecule 26 is a protein called 30S ribosomal protein S19.

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

- Molecule 27 is a protein called 30S ribosomal protein S20.

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

- Molecule 28 is a protein called 30S ribosomal protein S21.

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

- Molecule 29 is a protein called 50S ribosomal protein L23.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	96	Total	C	N	O	S	0	0
			764	484	142	136	2		

- Molecule 30 is a RNA chain called E-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	X	65	Total	C	N	O	P	0	0
			1392	621	258	449	64		

- Molecule 31 is a RNA chain called A-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	Z	66	Total	C	N	O	P	0	0
			1406	629	255	457	65		

- Molecule 32 is a RNA chain called 5S ribosomal RNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	a	118	Total	C	N	O	P	0	0
			2529	1126	464	821	118		

- Molecule 33 is a protein called 50S ribosomal protein L2.

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

- Molecule 34 is a protein called 50S ribosomal protein L3.

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

- Molecule 35 is a protein called 50S ribosomal protein L4.

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

- Molecule 36 is a protein called 50S ribosomal protein L5.

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

- Molecule 37 is a protein called 50S ribosomal protein L6.

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

- Molecule 38 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	g	47	Total	C	N	O	S	0	0
			359	233	62	63	1		

- Molecule 39 is a protein called 50S ribosomal protein L11.

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

- Molecule 40 is a protein called 50S ribosomal protein L13.

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

- Molecule 41 is a protein called 50S ribosomal protein L14.

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

- Molecule 42 is a protein called 50S ribosomal protein L15.

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

- Molecule 43 is a protein called 50S ribosomal protein L16.

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

- Molecule 44 is a protein called 50S ribosomal protein L17.

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

- Molecule 45 is a protein called 50S ribosomal protein L18.

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

- Molecule 46 is a protein called 50S ribosomal protein L19.

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

- Molecule 47 is a protein called 50S ribosomal protein L20.

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

- Molecule 48 is a protein called 50S ribosomal protein L21.

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

- Molecule 49 is a protein called 50S ribosomal protein L22.

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

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

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

- Molecule 51 is a protein called 50S ribosomal protein L25.

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

- Molecule 52 is a protein called 50S ribosomal protein L27.

Mol	Chain	Residues	Atoms					AltConf	Trace
52	u	75	Total	C	N	O	S	0	0
			569	353	113	102	1		

- Molecule 53 is a protein called 50S ribosomal protein L28.

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

- Molecule 54 is a protein called 50S ribosomal protein L29.

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

- Molecule 55 is a protein called 50S ribosomal protein L30.

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

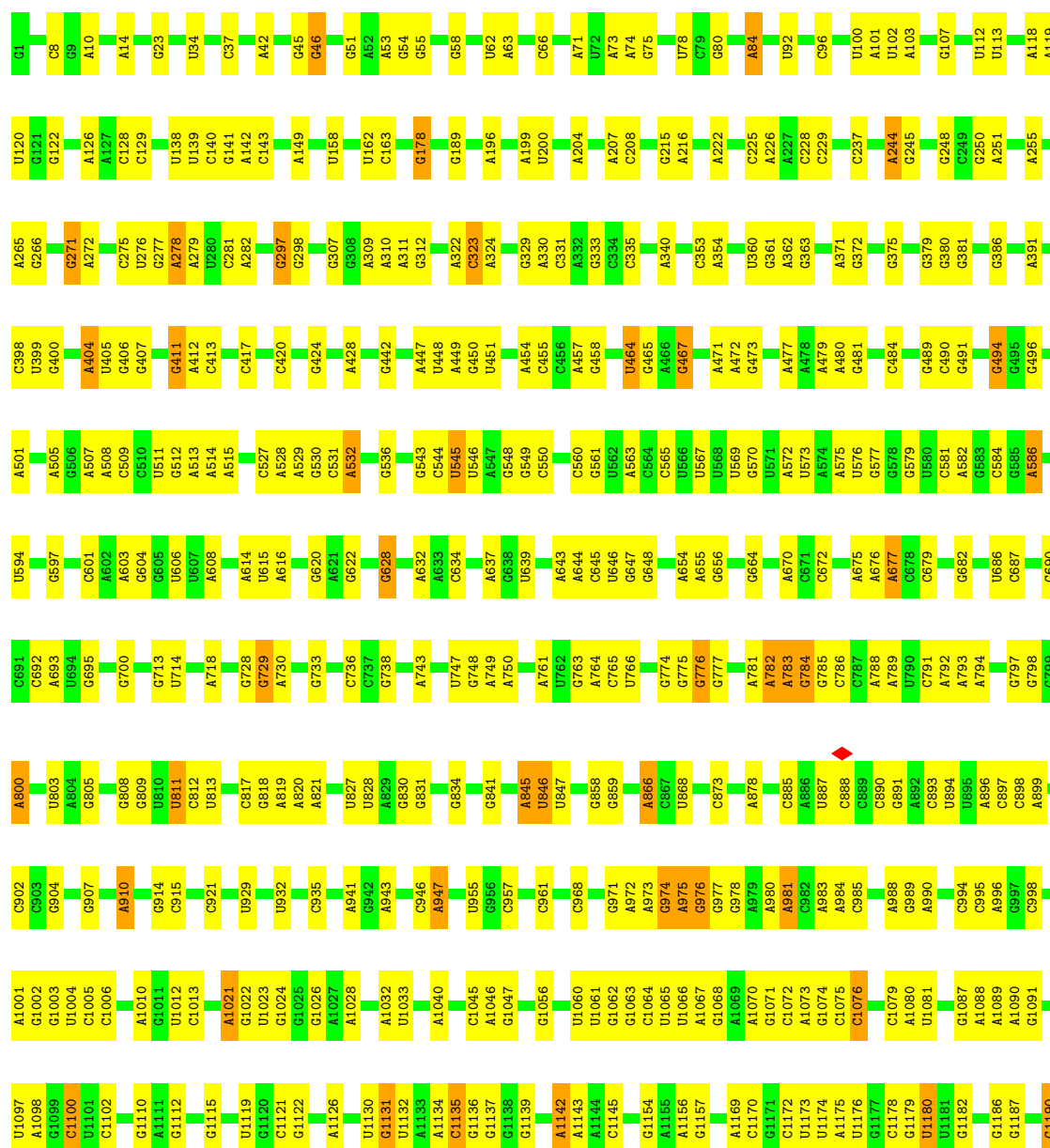
- Molecule 56 is a RNA chain called P-site tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
56	y	70	Total	C	N	O	P	0	0
			1496	665	267	494	70		

- Molecule 57 is a protein called 50S ribosomal protein L33.

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

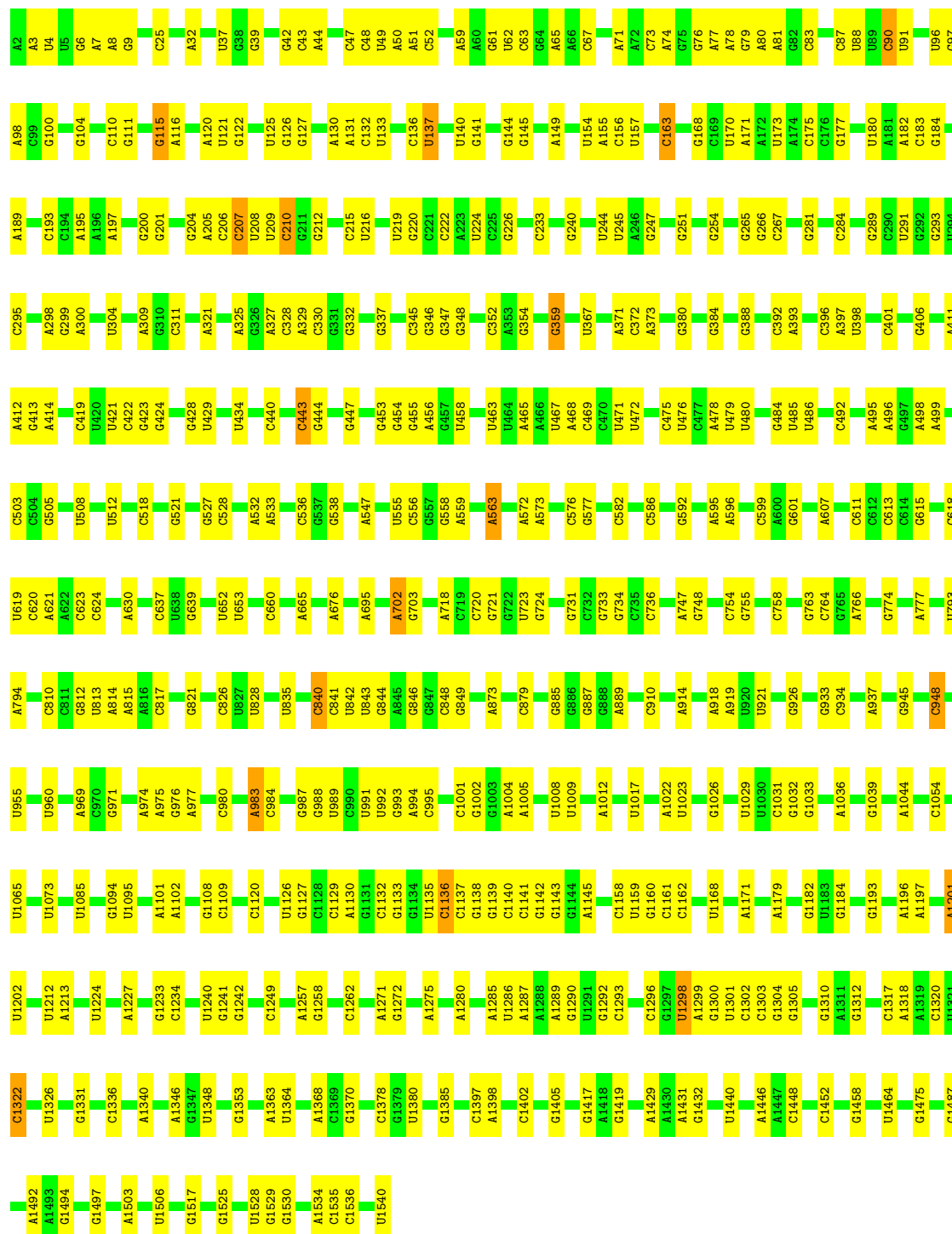





A2882	A2566	G2464	C2338	G2228	U2131	C2043	A1953	G1824	G1743	A1635	G1510	U1375	G1191
G2586	C2567	A2469	U2344	C2232	U2132	A2052	G1954	U1825	C1752	A1635	G1510	C1376	G1195
C2572	A2572	C2470	C2345	C2232	A2135	A2052	U1955	G1826	C1752	G1642	A1515	C1377	C1196
U2689	C2575	U2474	A2346	G2238	G2136	G2053	G2253	U1827	A1754	U1379	A1515	U1378	U1999
C2691	C2576	C2475	C2347	C2239	U2137	C2055	A1960	A1829	A1755	C1646	A1522	G1293	C1200
U2696	C2581	A2476	C2354	G2242	G2140	A2059	G1964	C1833	G1756	U1647	U1523	G1299	
C2710	C2582	U2477	U2243	U2244	G2141	A2060	A1965	U1834	U1757	C1386	U1524	G1300	
C2714	U2585	A2478	G2357	U2244	C2145	A2061	A1966	G1835	U1758	A1650	G1529	A1302	A1204
	U2586	C2480	A2358	A2247	C2146	A2062	C1967	C1836	C1761	G1651	G1529	A1602	
	U2586		G2361		A2147	C2063	A1970		C1764	A1655	C1533	A1304	U1209
	A2587	G2484		G2250	A2150	C2064	U1971	U1841	C1764	A1655	U1534	C1304	G1210
	C2588	C2486	A2376	G2251	C2150		U1972	A1947	A1772	A1656	A1535	A1307	G1212
U2724	U2596		C2383	G2255	G2151	U2068	A1977	A1853	C1774	G1660	G1537	G1309	
A2725	C2597	U2384	U2385	G2256	G2152	C2069		A1852	C1774	U1402	U1537	G1310	
A2726		C2385		U2257	G2157	U2075	G1984	U1855	G1776	A1403	G1540	G1311	
	A2600		U2390	C2258	A2158			U1855	U1777	U1404		U1312	
A2733	C2601	C2496	U2390	C2258		C2078	G1989	G1869	U1778	G1667	C1568	U1313	U1219
A2738	A2602	C2498	C2394	U2259	G2162	A2082	U1991	A1871	U1779	A1668	A1566	C1314	
	C2607	C2499		A2266	A2163		U1991	A1871	G1780	A1669	G1567	A1237	
G2744	C2608	U2500	U2402	G2271	C2165	G2087	U1993	G1873	U1781	C1670	G1568	A1237	G1238
	U2609	C2501	C2403	G2271	U2166		U1993	G1873	U1781		A1569		
A2748	C2610	C2502	U2404	A2274	U2167	G2093	U1995	C1874	A1783	G1674	A1570	U1325	C1243
	U2613	A2503	A2405	C2274	C2168	A2094	C1996	U1882	A1785	A1676	C1675	U1326	
U2756		U2504	A2406	A2279	A2169	A2095	C1997	U1887	A1786	A1677	G1432	A1327	A1246
A2757	U2617	G2505	A2407	C2279	A2170	A2095	A1998	G1887	A1787	A1678	C1574	A1328	A1247
	C2618	U2506			A2171	U2098	C2001	G1888	U1788	A1679	C1577	A1329	G1248
C2772	C2619	C2508	C2420	C2283	U2172	U2099	G2002	A1889	A1789	A1679	U1578	C1330	
C2773	C2619			C2283	A2173	G2100	G2002	A1889	C1790	C1685	U1578	G1331	G1252
			U2423	A2287	C2174	A2101	A1959	A1959	A1791	C1685	G1581	G1332	A1253
A2776	G2624	C2512	A2424	A2288	C2175	G2102	A2005	C1904	C1795	A1690	C1582	G1332	A1253
C2777	C2625	G2513	A2425	C2289			C2006	C1905	U1795	A1452	C1582	G1333	G1256
A2778	C2626	U2514	A2426	G2289	C2178	G2107		C1905	U1796	A1453	C1583	G1338	C1257
U2779			C2427	A2297	U2182	A2108	A2013	G1906	U1797	U1268	U1584	G1339	U1258
	U2629	A2518	G2428	A2297	U2183	U2109	A2014	G1907	U1798	G1455	C1585	G1340	G1259
C2783	C2630	U2519	C2429	U2305	A2183	G2110	A2015	A1913	G1799	U1456	U1602	A1341	A1260
		C2520	A2430	A2309	U2189	U2111	A2015	A1913	C1800	U1457	A1603	A1342	C1261
C2793	A2635	C2527	U2431	A2309	U2189	C2112	A2019	C1914	A1801	U1458	A1603	G1343	A1262
	C2636		A2432	A2309	U2189	U2113	A2020	C1914	A1801	G1459	C1604	G1343	U1263
A2799	U2528	U2528	A2432	A2317	A2198	A2113	C2021	A1919	A1803	U1460	C1604	C1349	
	C2645	G2529	A2435	G2318	A2199	G2115	U2022	A1919	A1803	C1606	C1606	C1362	A1264
U2907	C2646		U2436	G2319	C2200	G2116	C2023	U1926	C1804	C1607	C1606	U1352	A1265
C2908		A2542	G2437	G2319		G2117	C2024	U1926	A1805	A1705	A1608	A1353	G1267
	A2654			A2322	U2203	A2118	G2025	G1929	A1808	U1467	A1609	A1354	A1268
		A2547	U2441	A2322	G2204	U2119	C2025	G1930	A1809	U1468	A1610	G1355	A1269
	C2658			G2325	G2204	A2119	C2026	U1930	A1809	G1715	C1611	G1270	C1270
G2819		G2550	G2444	G2325	A2211	G2120	G2029	A1936	A1810	U1716	A1614	A1359	A1271
A2821	C2661	C2552	G2445	C2326	A2211	G2120	G2029	A1936	A1810	U1716	A1614	A1359	A1272
C2822	U2552	C2552	G2446	A2327	U2212	U2122	A2030	A1936	A1811	G1478	C1362	U1271	U1273
A2823	C2663	G2447	G2447	A2327	U2213	G2123	A2031	C1941	A1815	G1482	C1362		
C2824	U2554	A2448	G2447	G2330	C2214	G2124	C2032	C1941	C1816	A1490	A1365	A1276	
	U2555	A2448	G2447	C2331	C2214	G2124	C2032	U1944	C1816	A1366	A1366	A1277	
C2825	C2668	G2455	G2455	C2332	C2222	A2126	U2034	G1944	A1819	C1493	A1366	A1277	
A2826	G2669	C2556	A2333	C2332	G2223	G2127	G2035	G1944	A1819	C1493	A1366	A1277	
		C2557	U2334	C2332	G2224	G2128	C2036	U1946	U1820	C1493	A1366	A1277	
	U2680	C2558	C2456	U2334	G2224	G2128	C2036	U1946	U1820	C1493	A1366	A1277	
A2829	C2681	C2558	C2456	A2335	A2225	U2129	A2037	G1949	C1822	A1498	G1371	A1284	A1284

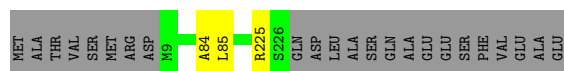
- Molecule 8: 16S ribosomal RNA

Chain B:  70% 29%




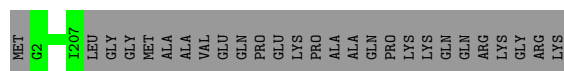
- Molecule 9: 30S ribosomal protein S2

Chain C:  89% • 10%



- Molecule 10: 30S ribosomal protein S3

Chain D:  88% 12%




- Molecule 11: 30S ribosomal protein S4

Chain E:  98% •



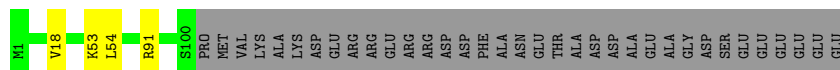
- Molecule 12: 30S ribosomal protein S5

Chain F:  89% • 10%




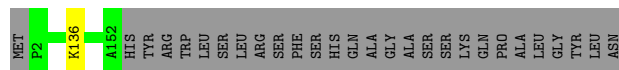
- Molecule 13: 30S ribosomal protein S6, fully modified isoform

Chain G:  71% • 26%



- Molecule 14: 30S ribosomal protein S7

Chain H:  84% • 16%



- Molecule 15: 30S ribosomal protein S8

Chain I:  98% • •



- Molecule 16: 30S ribosomal protein S9

Chain J:  94% . .




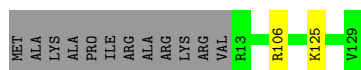
- Molecule 17: 30S ribosomal protein S10

Chain K:  93% . 5%



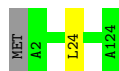
- Molecule 18: 30S ribosomal protein S11

Chain L:  89% . 9%



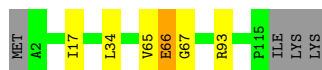
- Molecule 19: 30S ribosomal protein S12

Chain M:  98% ..



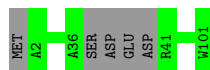
- Molecule 20: 30S ribosomal protein S13

Chain N:  92% . . .



- Molecule 21: 30S ribosomal protein S14

Chain O:  95% 5%



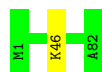
- Molecule 22: 30S ribosomal protein S15

Chain P:  99% .




- Molecule 23: 30S ribosomal protein S16

Chain Q:  99%



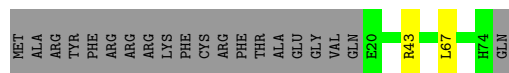
- Molecule 24: 30S ribosomal protein S17

Chain R:  90% 5% 5%




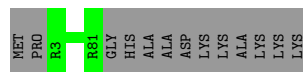
- Molecule 25: 30S ribosomal protein S18

Chain S:  71% 27%



- Molecule 26: 30S ribosomal protein S19

Chain T:  86% 14%



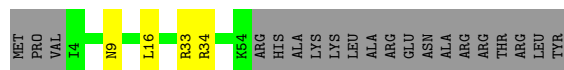
- Molecule 27: 30S ribosomal protein S20

Chain U:  93% 5%



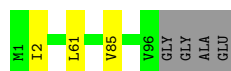
- Molecule 28: 30S ribosomal protein S21

Chain V:  66% 6% 28%



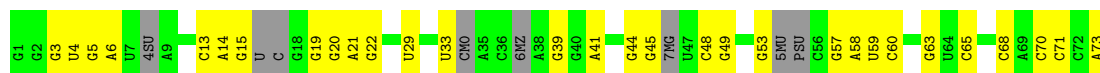
- Molecule 29: 50S ribosomal protein L23

Chain W:  93%



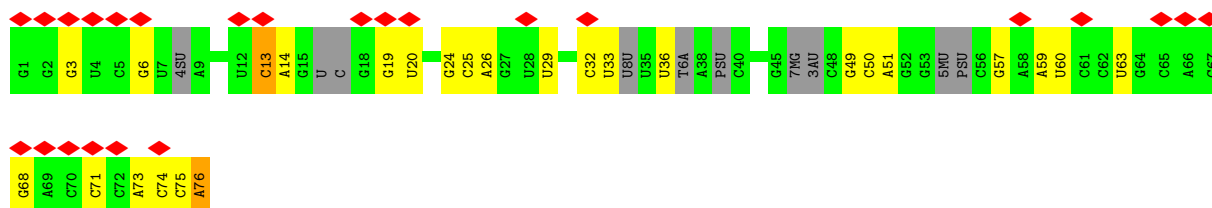
- Molecule 30: E-site tRNA

Chain X:  48% 41% 11%




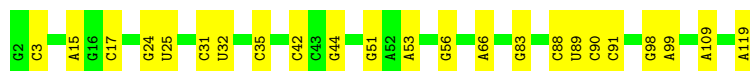
• Molecule 31: A-site tRNA

Chain Z:  32% 53% 32% 13%



• Molecule 32: 5S ribosomal RNA

Chain a:  81% 19%



• Molecule 33: 50S ribosomal protein L2

Chain b:  98% ..



• Molecule 34: 50S ribosomal protein L3

Chain c:  97% .



• Molecule 35: 50S ribosomal protein L4

Chain d:  100%

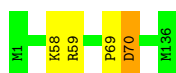


• Molecule 36: 50S ribosomal protein L5

Chain e:  98% ..



- Chain 1:  97% ..



- Molecule 44: 50S ribosomal protein L17

Chain m: 91% .. 6%



- Molecule 45: 50S ribosomal protein L18

Chain n: 98% ..



- Molecule 46: 50S ribosomal protein L19

Chain o: 98% ..



- Molecule 47: 50S ribosomal protein L20

Chain p: 99% .



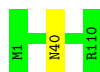
- Molecule 48: 50S ribosomal protein L21

Chain q: 100%

There are no outlier residues recorded for this chain.

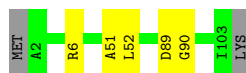
- Molecule 49: 50S ribosomal protein L22

Chain r: 99% .



- Molecule 50: 50S ribosomal protein L24

Chain s: 93% 5% .





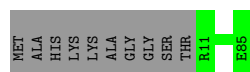
- Molecule 51: 50S ribosomal protein L25

Chain t:  100%

There are no outlier residues recorded for this chain.

- Molecule 52: 50S ribosomal protein L27

Chain u:  88%  12%



- Molecule 53: 50S ribosomal protein L28

Chain v:  99%



- Molecule 54: 50S ribosomal protein L29

Chain w:  97%



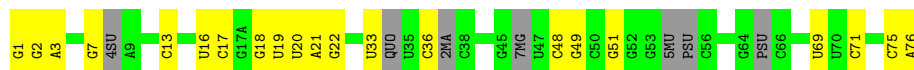
- Molecule 55: 50S ribosomal protein L30

Chain x:  98%



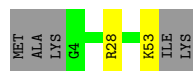
- Molecule 56: P-site tRNA

Chain y:  64%  27%  9%



- Molecule 57: 50S ribosomal protein L33

Chain z:  87%  9%



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	54875	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 ( $e^-/\text{\AA}^2$ )	32.57	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	FEI FALCON III (4k x 4k)	Depositor
Maximum map value	0.093	Depositor
Minimum map value	-0.024	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.005	Depositor
Map size (Å)	441.6, 441.6, 441.6	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.38, 1.38, 1.38	Depositor

## 5 Model quality ⓘ

### 5.1 Standard geometry ⓘ

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z  > 5$	RMSZ	$\# Z  > 5$
1	0	0.72	0/380	0.69	0/498
2	1	0.66	0/513	0.76	0/676
3	2	0.63	0/303	0.64	0/397
4	3	0.30	0/1361	0.61	0/1830
5	5	0.30	0/3426	0.58	0/4605
6	6	0.63	0/450	0.68	0/599
7	A	1.54	229/69796 (0.3%)	1.28	438/108888 (0.4%)
8	B	0.76	0/36966	1.07	76/57666 (0.1%)
9	C	0.38	0/1735	0.58	1/2338 (0.0%)
10	D	0.33	0/1651	0.58	0/2225
11	E	0.33	0/1665	0.57	0/2227
12	F	0.40	0/1118	0.63	0/1504
13	G	0.35	0/835	0.63	1/1128 (0.1%)
14	H	0.29	0/1195	0.52	0/1602
15	I	0.39	0/989	0.57	0/1326
16	J	0.29	0/1034	0.56	0/1375
17	K	0.30	0/796	0.61	0/1077
18	L	0.36	0/893	0.58	0/1205
19	M	0.41	0/969	0.64	0/1300
20	N	0.29	0/892	0.62	1/1193 (0.1%)
21	O	0.30	0/785	0.56	0/1043
22	P	0.37	0/718	0.58	0/959
23	Q	0.37	0/659	0.63	0/884
24	R	0.38	0/657	0.61	0/881
25	S	0.35	0/462	0.59	1/621 (0.2%)
26	T	0.30	0/652	0.54	0/877
27	U	0.32	0/671	0.56	0/888
28	V	0.38	0/430	0.77	1/570 (0.2%)
29	W	0.67	0/771	0.70	0/1031
30	X	0.39	0/1551	1.04	0/2404
31	Z	0.44	1/1565 (0.1%)	1.01	5/2421 (0.2%)
32	a	1.10	0/2828	1.09	5/4410 (0.1%)
33	b	0.71	0/2121	0.67	0/2852
34	c	0.70	0/1586	0.67	0/2134

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	d	0.70	0/1571	0.63	0/2113
36	e	0.37	0/1434	0.58	0/1926
37	f	0.48	0/1343	0.59	1/1816 (0.1%)
38	g	0.44	0/364	0.66	0/490
39	h	0.32	0/1046	0.61	0/1410
40	i	0.75	0/1152	0.64	0/1551
41	j	0.67	0/947	0.70	0/1268
42	k	0.63	0/1054	0.73	0/1403
43	l	0.63	0/1093	0.69	1/1460 (0.1%)
44	m	0.69	0/973	0.78	1/1301 (0.1%)
45	n	0.48	0/902	0.56	0/1209
46	o	0.67	0/929	0.65	1/1242 (0.1%)
47	p	0.85	0/960	0.65	0/1278
48	q	0.72	0/829	0.67	0/1107
49	r	0.71	0/864	0.64	0/1156
50	s	0.60	0/787	0.62	0/1051
51	t	0.57	0/766	0.57	0/1025
52	u	0.66	0/576	0.60	0/762
53	v	0.69	0/635	0.63	0/848
54	w	0.59	0/510	0.66	1/677 (0.1%)
55	x	0.63	0/453	0.69	0/605
56	y	0.51	1/1664 (0.1%)	1.02	2/2577 (0.1%)
57	z	0.47	0/416	0.54	0/554
All	All	1.12	231/163691 (0.1%)	1.08	536/244463 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
2	1	0	1
3	2	0	1
9	C	0	1
11	E	0	2
12	F	0	2
13	G	0	1
16	J	0	2
17	K	0	1
19	M	0	1
20	N	0	1
23	Q	0	1

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	#Chirality outliers	#Planarity outliers
24	R	0	2
28	V	0	2
29	W	0	1
34	c	0	1
37	f	0	2
41	j	0	1
42	k	0	1
43	l	0	1
50	s	0	3
All	All	0	28

The worst 5 of 231 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
56	y	1	G	OP3-P	-10.67	1.48	1.61
7	A	783	A	N9-C4	-8.57	1.32	1.37
7	A	1142	A	N9-C4	-8.35	1.32	1.37
7	A	984	A	N9-C4	-8.20	1.32	1.37
7	A	447	A	N9-C4	-8.01	1.33	1.37

The worst 5 of 536 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	761	A	N1-C6-N6	11.81	125.69	118.60
7	A	545	U	C2-N1-C1'	11.52	131.53	117.70
7	A	761	A	C5-N7-C8	-11.09	98.35	103.90
7	A	545	U	N3-C2-O2	-10.48	114.86	122.20
7	A	545	U	N1-C2-O2	10.40	130.08	122.80

There are no chirality outliers.

5 of 28 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	31	HIS	Peptide
3	2	20	ASP	Peptide
9	C	84	ALA	Peptide
11	E	173	VAL	Peptide
11	E	20	PHE	Peptide

## 5.2 Too-close contacts ⓘ

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

## 5.3 Torsion angles ⓘ

### 5.3.1 Protein backbone ⓘ

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	44/46 (96%)	41 (93%)	3 (7%)	0	100	100
2	1	62/65 (95%)	51 (82%)	9 (14%)	2 (3%)	4	30
3	2	36/38 (95%)	30 (83%)	5 (14%)	1 (3%)	5	32
4	3	166/169 (98%)	145 (87%)	21 (13%)	0	100	100
5	5	430/432 (100%)	387 (90%)	43 (10%)	0	100	100
6	6	54/57 (95%)	45 (83%)	8 (15%)	1 (2%)	8	39
9	C	216/241 (90%)	178 (82%)	38 (18%)	0	100	100
10	D	204/233 (88%)	176 (86%)	28 (14%)	0	100	100
11	E	203/206 (98%)	179 (88%)	24 (12%)	0	100	100
12	F	148/167 (89%)	114 (77%)	34 (23%)	0	100	100
13	G	98/135 (73%)	84 (86%)	14 (14%)	0	100	100
14	H	149/179 (83%)	138 (93%)	11 (7%)	0	100	100
15	I	127/130 (98%)	119 (94%)	8 (6%)	0	100	100
16	J	125/130 (96%)	111 (89%)	14 (11%)	0	100	100
17	K	96/103 (93%)	84 (88%)	12 (12%)	0	100	100
18	L	115/129 (89%)	92 (80%)	23 (20%)	0	100	100
19	M	121/124 (98%)	95 (78%)	26 (22%)	0	100	100
20	N	112/118 (95%)	97 (87%)	13 (12%)	2 (2%)	8	40
21	O	92/101 (91%)	81 (88%)	11 (12%)	0	100	100
22	P	86/89 (97%)	78 (91%)	8 (9%)	0	100	100
23	Q	80/82 (98%)	66 (82%)	14 (18%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
24	R	78/84 (93%)	58 (74%)	19 (24%)	1 (1%)	12	47
25	S	53/75 (71%)	51 (96%)	2 (4%)	0	100	100
26	T	77/92 (84%)	69 (90%)	8 (10%)	0	100	100
27	U	83/87 (95%)	78 (94%)	4 (5%)	1 (1%)	13	48
28	V	49/71 (69%)	37 (76%)	12 (24%)	0	100	100
29	W	94/100 (94%)	80 (85%)	14 (15%)	0	100	100
33	b	269/273 (98%)	230 (86%)	39 (14%)	0	100	100
34	c	207/209 (99%)	187 (90%)	18 (9%)	2 (1%)	15	52
35	d	199/201 (99%)	185 (93%)	14 (7%)	0	100	100
36	e	175/179 (98%)	153 (87%)	22 (13%)	0	100	100
37	f	174/177 (98%)	159 (91%)	13 (8%)	2 (1%)	14	50
38	g	45/149 (30%)	34 (76%)	11 (24%)	0	100	100
39	h	139/142 (98%)	115 (83%)	24 (17%)	0	100	100
40	i	140/142 (99%)	126 (90%)	14 (10%)	0	100	100
41	j	120/123 (98%)	89 (74%)	30 (25%)	1 (1%)	19	58
42	k	141/144 (98%)	121 (86%)	19 (14%)	1 (1%)	22	60
43	l	134/136 (98%)	118 (88%)	13 (10%)	3 (2%)	6	37
44	m	118/127 (93%)	99 (84%)	17 (14%)	2 (2%)	9	42
45	n	114/117 (97%)	103 (90%)	11 (10%)	0	100	100
46	o	112/115 (97%)	97 (87%)	15 (13%)	0	100	100
47	p	115/118 (98%)	109 (95%)	6 (5%)	0	100	100
48	q	101/103 (98%)	85 (84%)	16 (16%)	0	100	100
49	r	108/110 (98%)	99 (92%)	9 (8%)	0	100	100
50	s	100/104 (96%)	81 (81%)	17 (17%)	2 (2%)	7	39
51	t	92/94 (98%)	87 (95%)	5 (5%)	0	100	100
52	u	73/85 (86%)	62 (85%)	11 (15%)	0	100	100
53	v	75/78 (96%)	64 (85%)	11 (15%)	0	100	100
54	w	61/63 (97%)	54 (88%)	7 (12%)	0	100	100
55	x	56/59 (95%)	51 (91%)	5 (9%)	0	100	100
57	z	48/55 (87%)	42 (88%)	6 (12%)	0	100	100
All	All	6114/6586 (93%)	5314 (87%)	779 (13%)	21 (0%)	44	75

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	1	32	ILE
20	N	67	GLY
37	f	48	ASN
2	1	33	LEU
3	2	21	GLY

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	0	38/38 (100%)	38 (100%)	0	100	100
2	1	51/52 (98%)	51 (100%)	0	100	100
3	2	34/34 (100%)	34 (100%)	0	100	100
4	3	148/149 (99%)	147 (99%)	1 (1%)	84	90
5	5	359/359 (100%)	358 (100%)	1 (0%)	92	95
6	6	47/48 (98%)	47 (100%)	0	100	100
9	C	180/199 (90%)	179 (99%)	1 (1%)	86	92
10	D	170/190 (90%)	170 (100%)	0	100	100
11	E	172/173 (99%)	170 (99%)	2 (1%)	71	83
12	F	113/126 (90%)	113 (100%)	0	100	100
13	G	87/116 (75%)	85 (98%)	2 (2%)	50	70
14	H	124/147 (84%)	123 (99%)	1 (1%)	81	88
15	I	104/105 (99%)	102 (98%)	2 (2%)	57	75
16	J	105/107 (98%)	102 (97%)	3 (3%)	42	64
17	K	86/90 (96%)	85 (99%)	1 (1%)	71	83
18	L	90/99 (91%)	88 (98%)	2 (2%)	52	71
19	M	103/104 (99%)	103 (100%)	0	100	100
20	N	92/96 (96%)	89 (97%)	3 (3%)	38	62
21	O	79/84 (94%)	79 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
22	P	75/77 (97%)	75 (100%)	0	100	100
23	Q	65/65 (100%)	65 (100%)	0	100	100
24	R	74/78 (95%)	73 (99%)	1 (1%)	67	80
25	S	48/65 (74%)	47 (98%)	1 (2%)	53	72
26	T	70/79 (89%)	70 (100%)	0	100	100
27	U	65/66 (98%)	62 (95%)	3 (5%)	27	54
28	V	44/61 (72%)	43 (98%)	1 (2%)	50	70
29	W	83/84 (99%)	81 (98%)	2 (2%)	49	69
33	b	216/218 (99%)	212 (98%)	4 (2%)	57	75
34	c	164/164 (100%)	161 (98%)	3 (2%)	59	77
35	d	165/165 (100%)	164 (99%)	1 (1%)	86	92
36	e	148/150 (99%)	147 (99%)	1 (1%)	84	90
37	f	137/138 (99%)	136 (99%)	1 (1%)	84	90
38	g	38/114 (33%)	38 (100%)	0	100	100
39	h	109/110 (99%)	109 (100%)	0	100	100
40	i	116/116 (100%)	115 (99%)	1 (1%)	78	87
41	j	103/104 (99%)	103 (100%)	0	100	100
42	k	102/103 (99%)	101 (99%)	1 (1%)	76	85
43	l	109/109 (100%)	109 (100%)	0	100	100
44	m	100/103 (97%)	97 (97%)	3 (3%)	41	64
45	n	86/87 (99%)	85 (99%)	1 (1%)	71	83
46	o	99/100 (99%)	99 (100%)	0	100	100
47	p	89/90 (99%)	89 (100%)	0	100	100
48	q	84/84 (100%)	84 (100%)	0	100	100
49	r	93/93 (100%)	92 (99%)	1 (1%)	73	84
50	s	83/85 (98%)	83 (100%)	0	100	100
51	t	78/78 (100%)	78 (100%)	0	100	100
52	u	56/63 (89%)	56 (100%)	0	100	100
53	v	67/68 (98%)	67 (100%)	0	100	100
54	w	55/55 (100%)	54 (98%)	1 (2%)	59	77
55	x	48/49 (98%)	48 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
57	z	45/49 (92%)	43 (96%)	2 (4%)	28 55
All	All	5096/5386 (95%)	5049 (99%)	47 (1%)	79 87

5 of 47 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
33	b	114	ASP
36	e	125	ARG
33	b	171	TYR
34	c	142	VAL
40	i	17	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 50 such sidechains are listed below:

Mol	Chain	Res	Type
34	c	130	GLN
37	f	143	GLN
51	t	49	ASN
35	d	9	GLN
37	f	88	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	X	58/73 (79%)	30 (51%)	0
31	Z	58/76 (76%)	24 (41%)	1 (1%)
32	a	117/118 (99%)	21 (17%)	0
56	y	63/77 (81%)	19 (30%)	0
7	A	2902/2903 (99%)	740 (25%)	13 (0%)
8	B	1538/1539 (99%)	426 (27%)	3 (0%)
All	All	4736/4786 (98%)	1260 (26%)	17 (0%)

5 of 1260 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
7	A	10	A
7	A	14	A
7	A	23	G
7	A	34	U
7	A	42	A

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	B	428	G
31	Z	13	C
7	A	1730	C
7	A	1904	G
7	A	1913	A

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

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

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

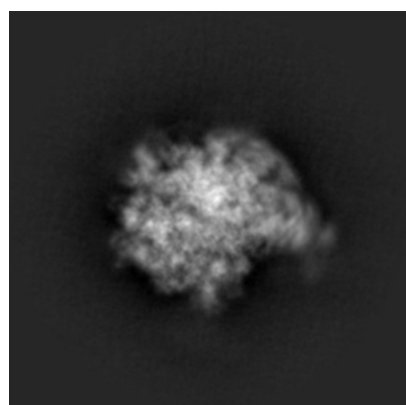
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-30611. These allow visual inspection of the internal detail of the map and identification of artifacts.

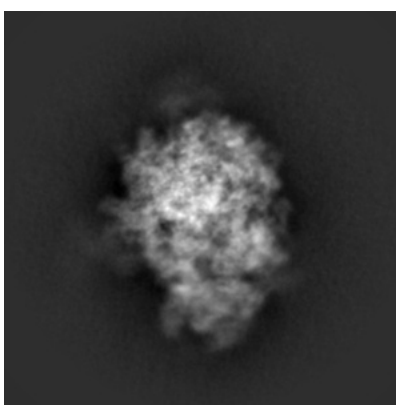
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

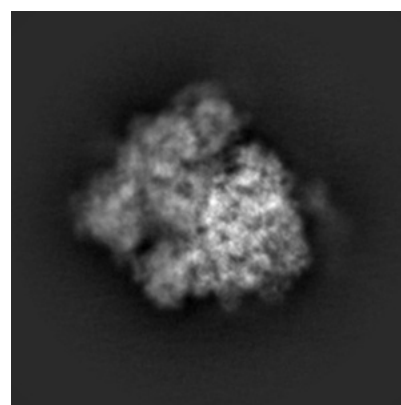
#### 6.1.1 Primary map



X



Y

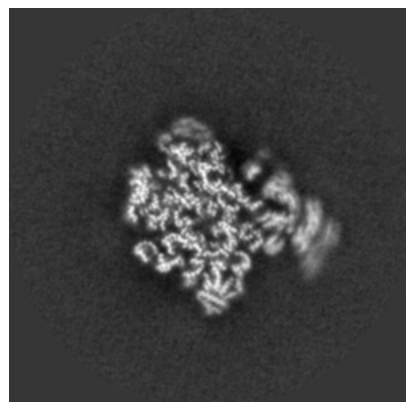


Z

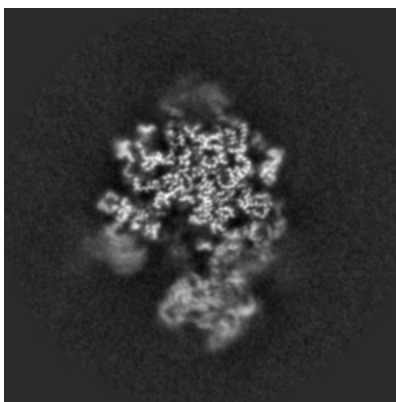
The images above show the map projected in three orthogonal directions.

### 6.2 Central slices [i](#)

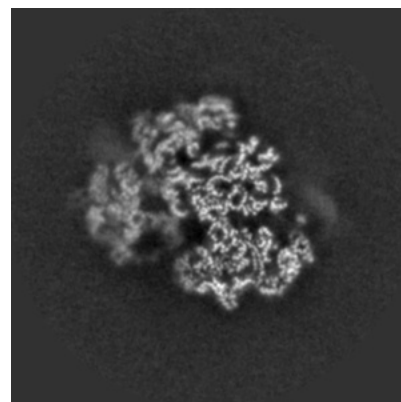
#### 6.2.1 Primary map



X Index: 160



Y Index: 160

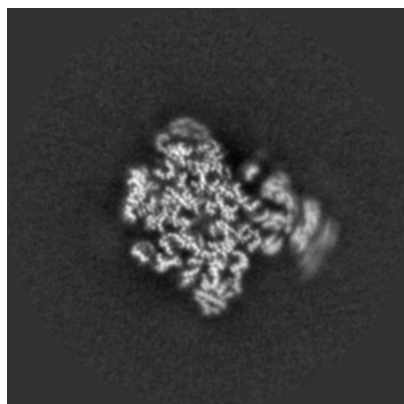


Z Index: 160

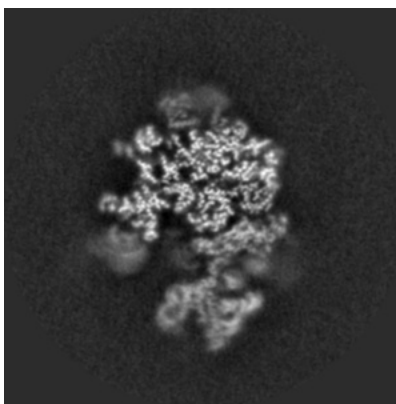
The images above show central slices of the map in three orthogonal directions.

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

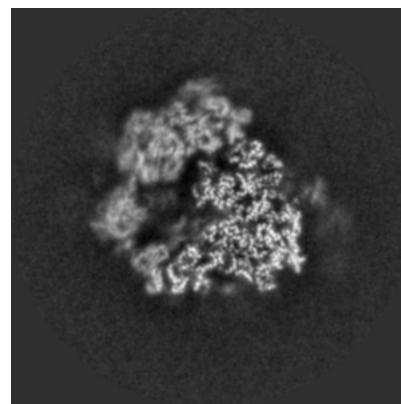
### 6.3.1 Primary map



X Index: 161



Y Index: 165

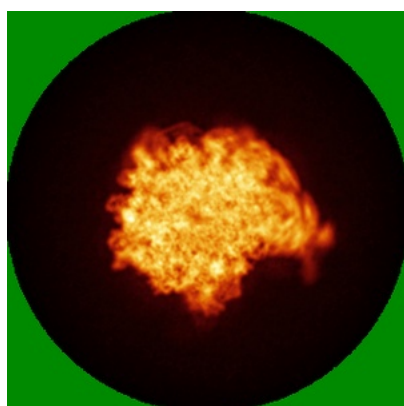


Z Index: 147

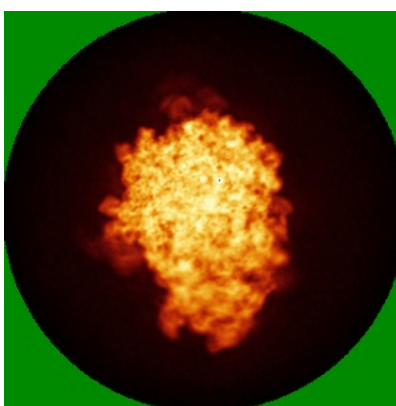
The images above show the largest variance slices of the map in three orthogonal directions.

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

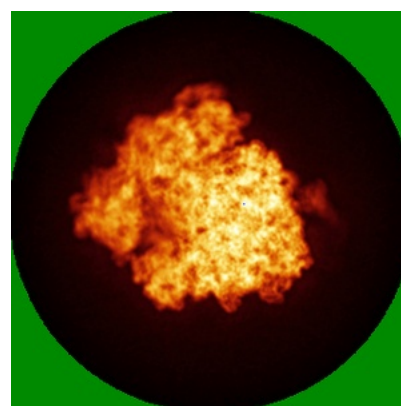
### 6.4.1 Primary map



X



Y



Z

The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.005. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

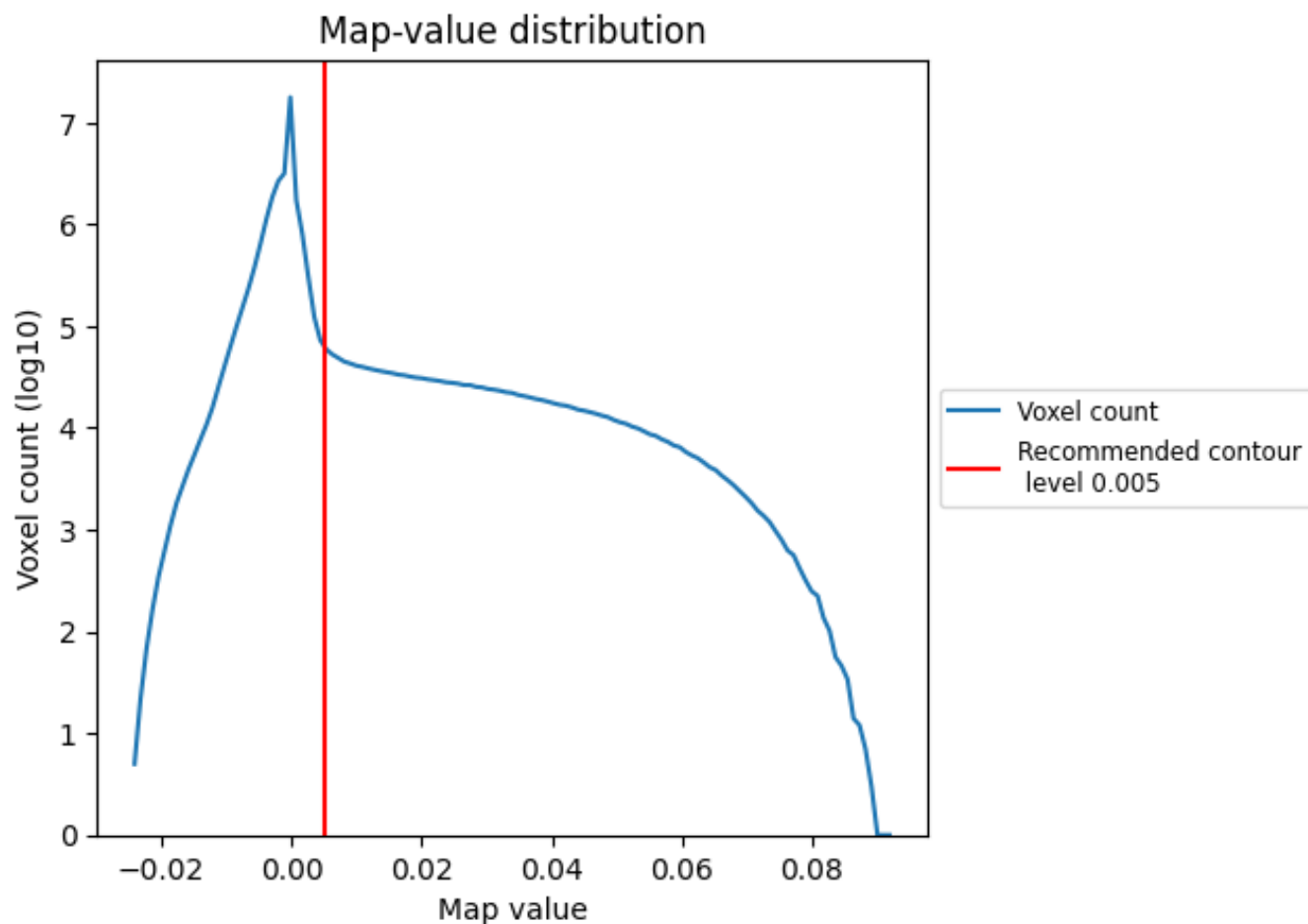
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

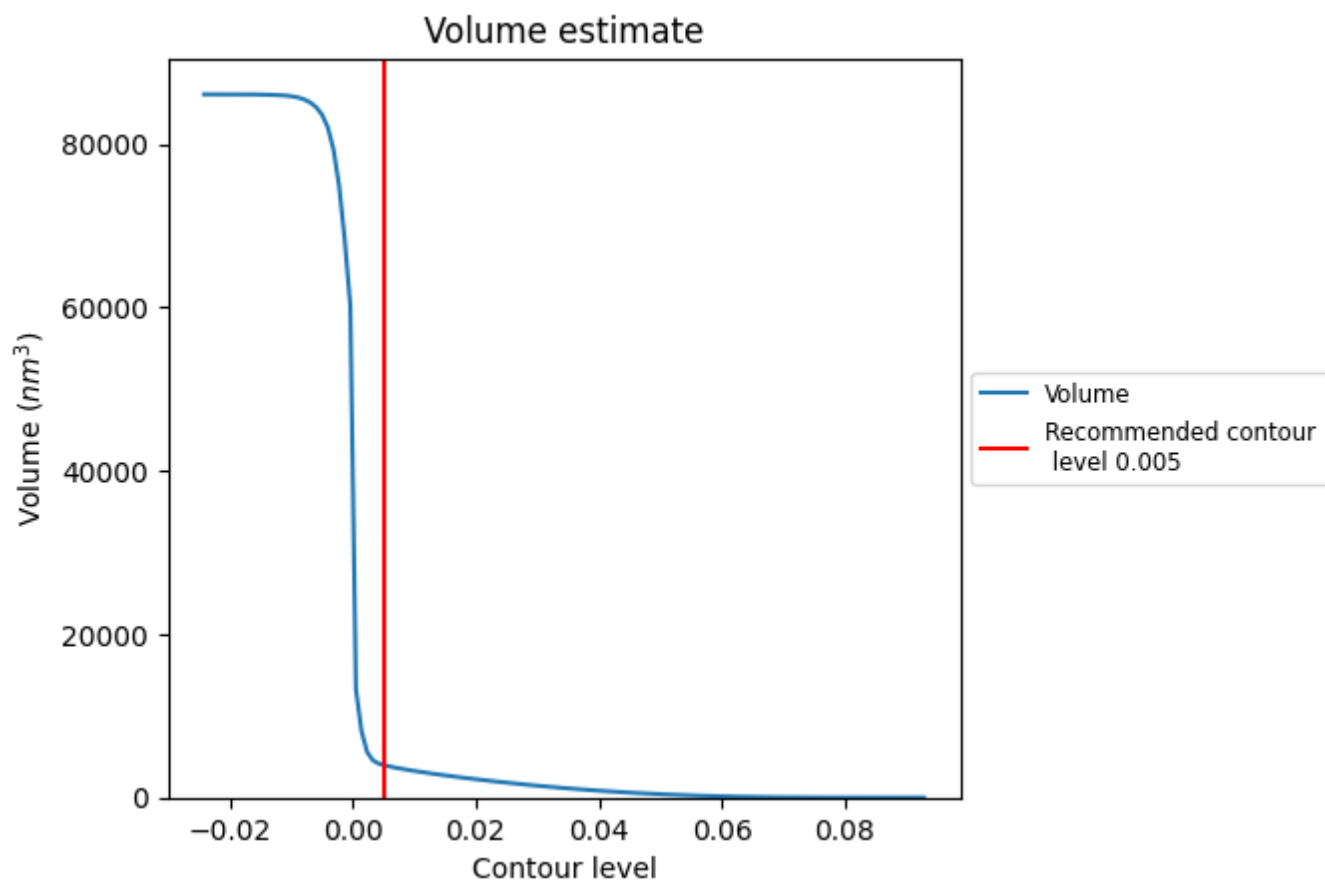
This section contains the results of statistical analysis of the map.

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



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

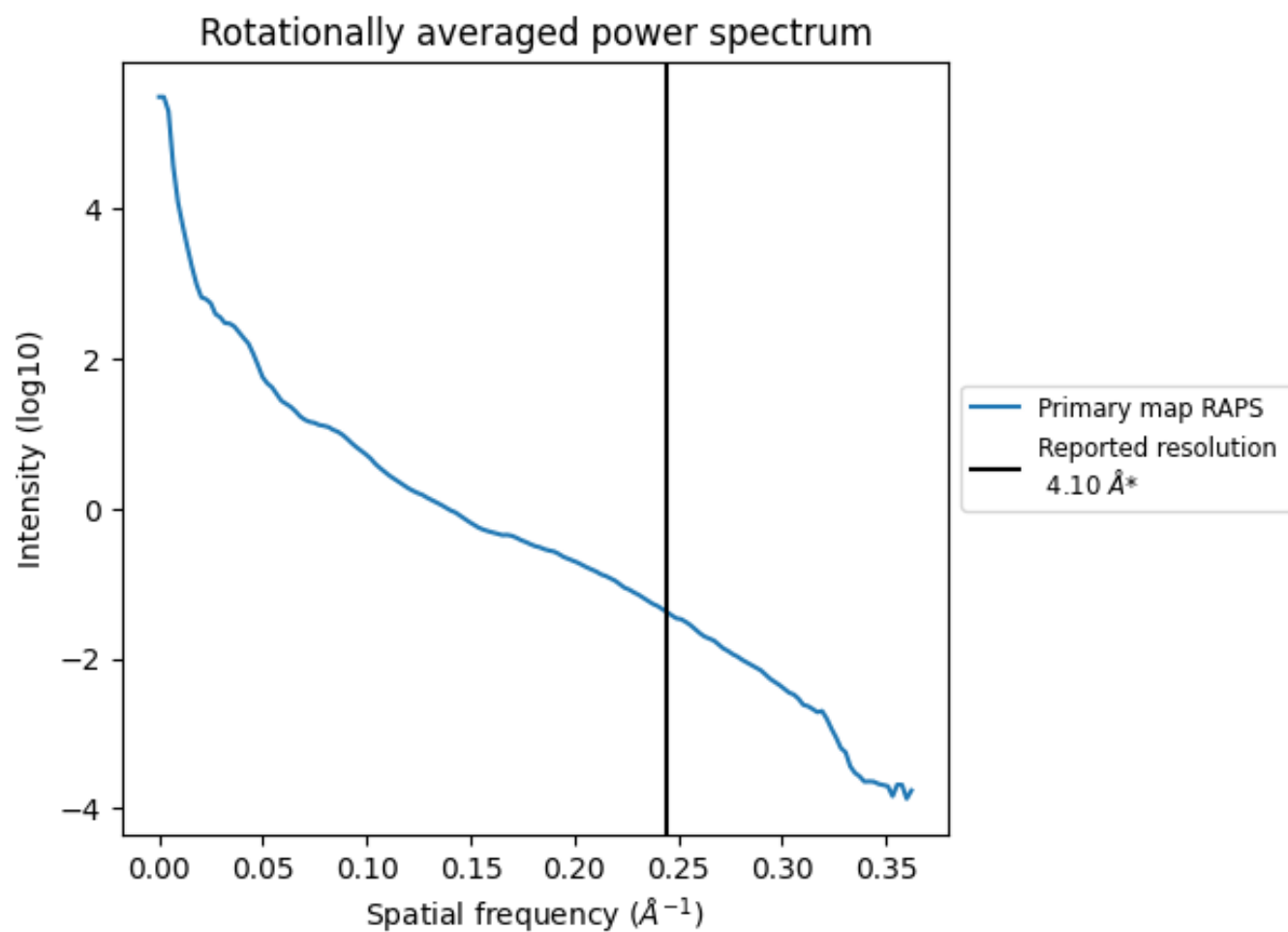
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 3991 nm<sup>3</sup>; this corresponds to an approximate mass of 3605 kDa.

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

### 7.3 Rotationally averaged power spectrum ⓘ

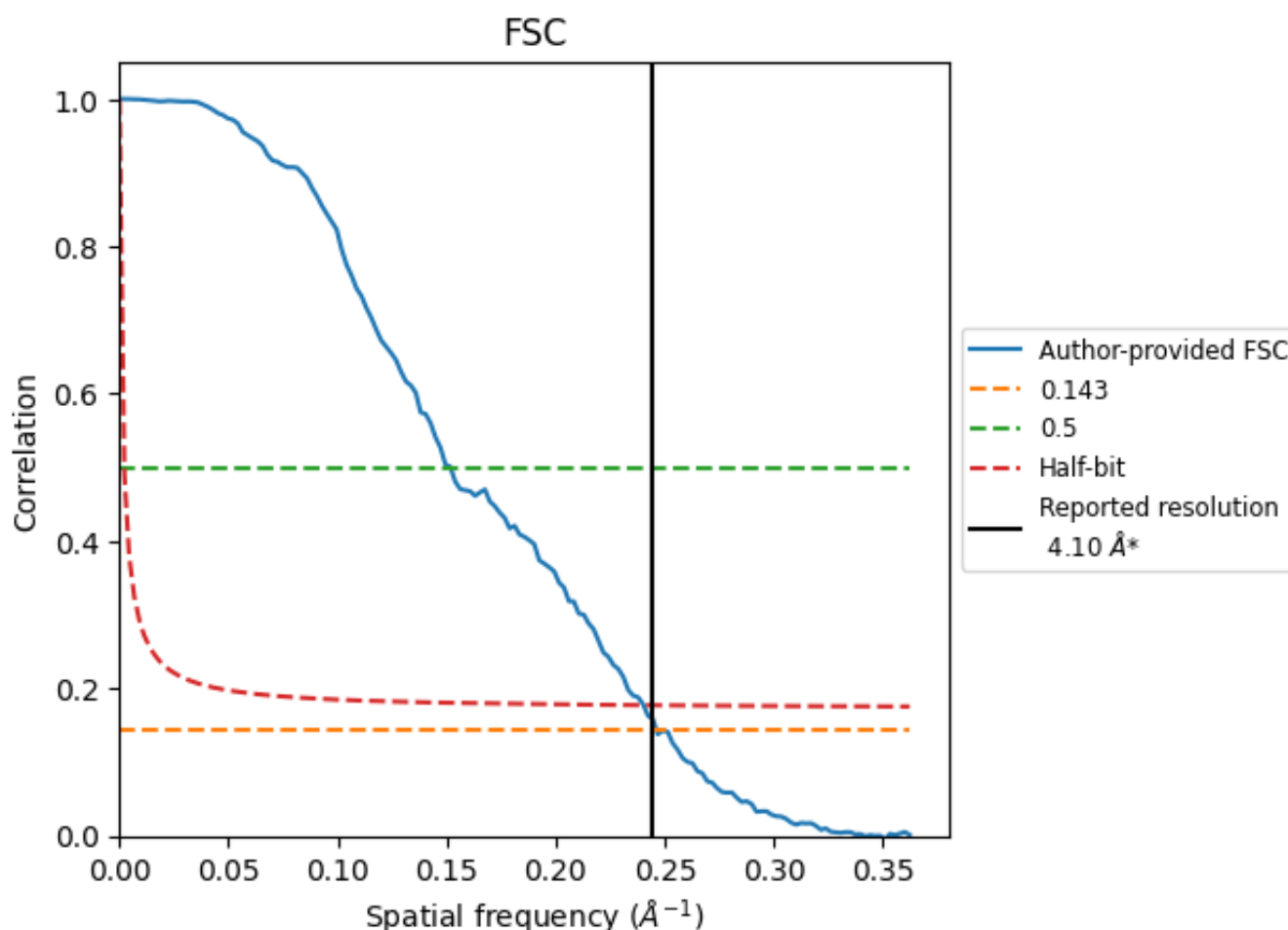


\*Reported resolution corresponds to spatial frequency of 0.244 Å<sup>-1</sup>

## 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 0.244 Å<sup>-1</sup>

## 8.2 Resolution estimates [i](#)

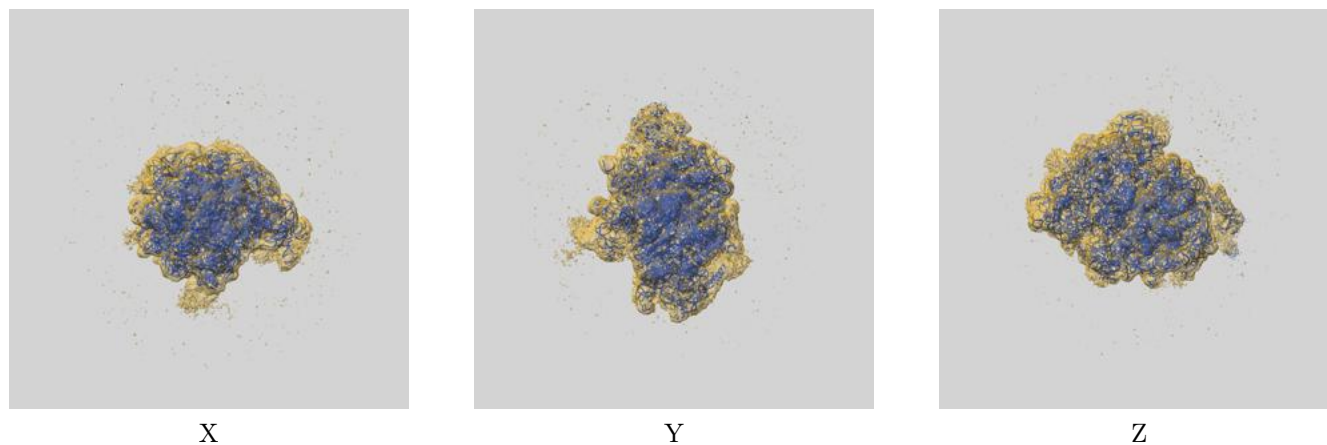
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	4.10	-	-
Author-provided FSC curve	4.06	6.59	4.16
Unmasked-calculated*	-	-	-

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

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

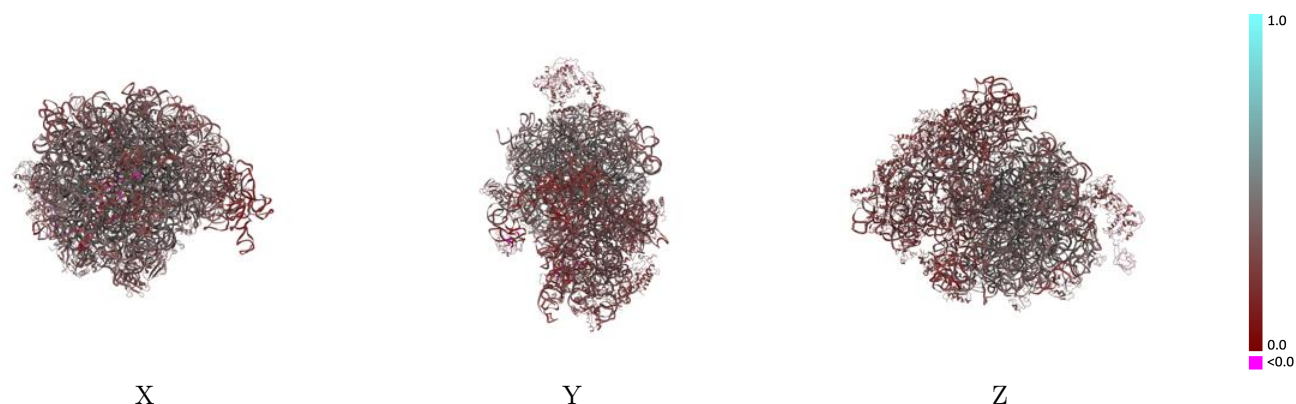
This section contains information regarding the fit between EMDB map EMD-30611 and PDB model 7D80. Per-residue inclusion information can be found in [section 3](#) on [page 14](#).

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



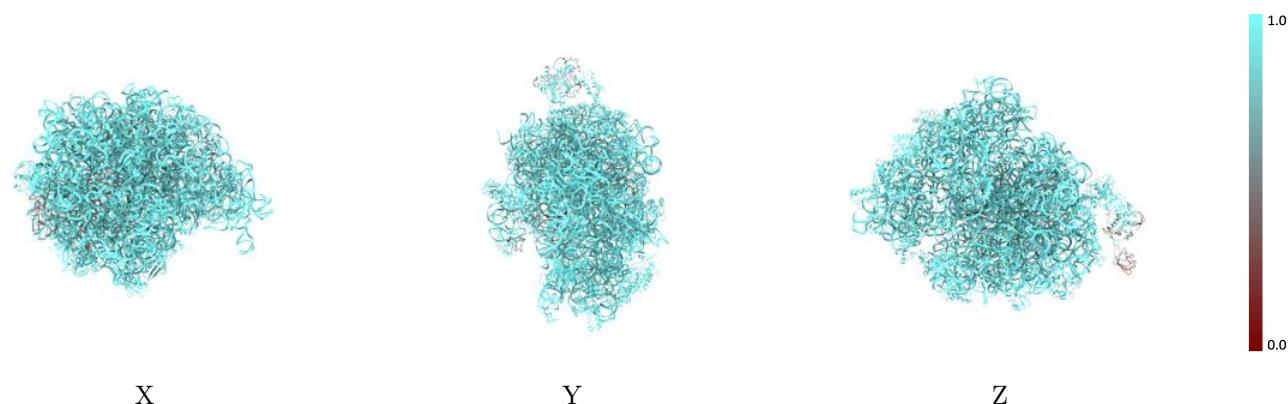
The images above show the 3D surface view of the map at the recommended contour level 0.005 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



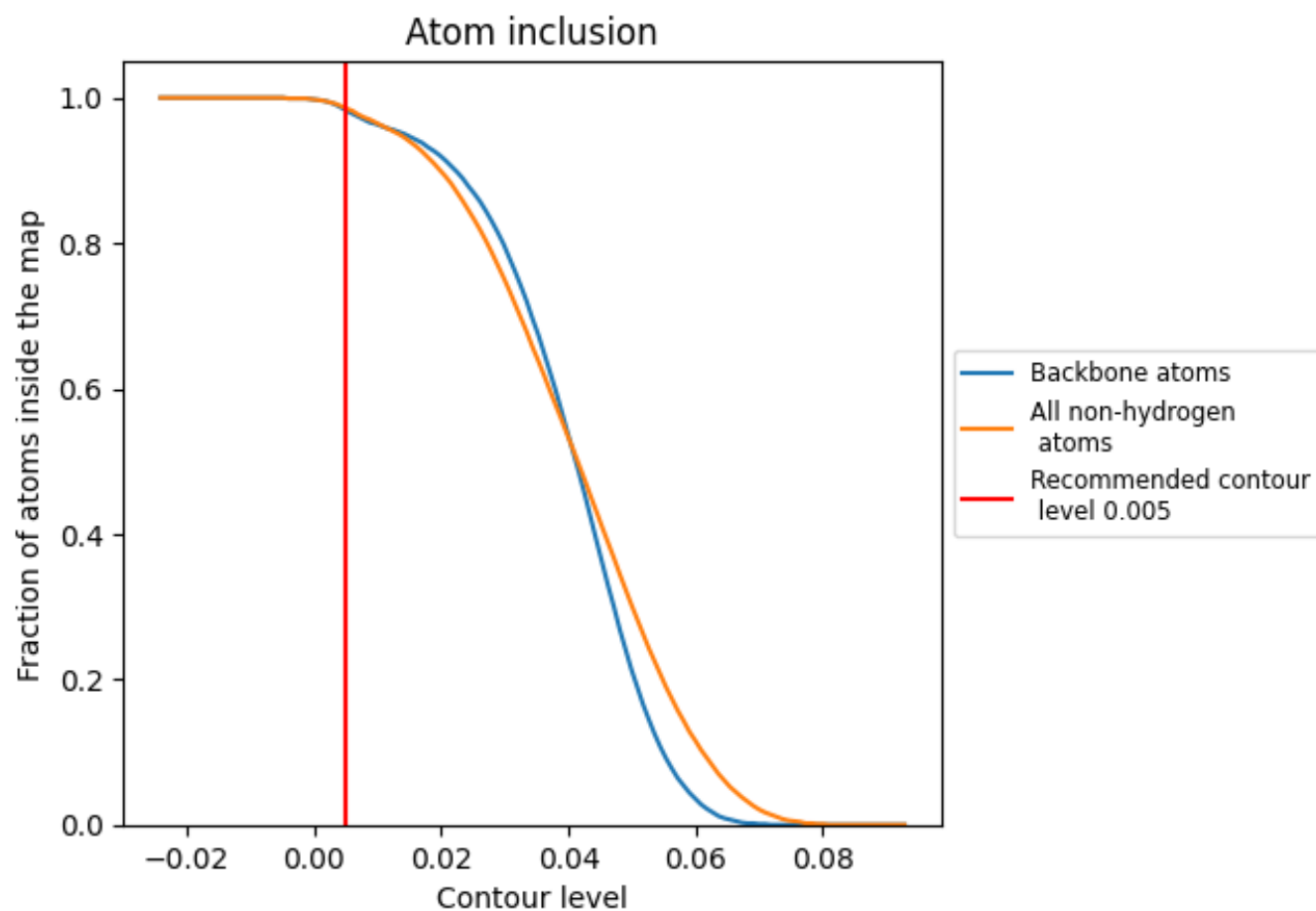
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.005).







































































## 9.4 Atom inclusion [i](#)



At the recommended contour level, 98% of all backbone atoms, 99% 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 (0.005) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9860	 0.3390
0	 0.9750	 0.3790
1	 0.9940	 0.3960
2	 1.0000	 0.3610
3	 0.9890	 0.2710
5	 0.6750	 0.2400
6	 1.0000	 0.3920
A	 0.9990	 0.3870
B	 1.0000	 0.3000
C	 1.0000	 0.2690
D	 0.9980	 0.2850
E	 1.0000	 0.2120
F	 0.9980	 0.3040
G	 0.9940	 0.2860
H	 0.9990	 0.2410
I	 0.9990	 0.2790
J	 1.0000	 0.2260
K	 0.9970	 0.2560
L	 0.9970	 0.2910
M	 0.9940	 0.2620
N	 0.9980	 0.2210
O	 1.0000	 0.2350
P	 0.9960	 0.2560
Q	 0.9980	 0.2510
R	 1.0000	 0.2680
S	 1.0000	 0.3140
T	 0.9980	 0.2050
U	 0.9970	 0.2250
V	 0.9930	 0.2600
W	 0.9950	 0.3610
X	 0.9980	 0.2180
Z	 0.5280	 0.2640
a	 1.0000	 0.3520
b	 0.9910	 0.4030
c	 0.9940	 0.4000



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Chain	Atom inclusion	Q-score
d	 0.9970	 0.3740
e	 0.9990	 0.2550
f	 1.0000	 0.3330
g	 1.0000	 0.3360
h	 0.8800	 0.1720
i	 0.9960	 0.3910
j	 0.9910	 0.4010
k	 0.9950	 0.3920
l	 0.9970	 0.3940
m	 0.9980	 0.3800
n	 1.0000	 0.3220
o	 0.9930	 0.3830
p	 0.9990	 0.3670
q	 0.9960	 0.4020
r	 0.9920	 0.3850
s	 0.9960	 0.3580
t	 1.0000	 0.3620
u	 0.9980	 0.4010
v	 0.9970	 0.3730
w	 1.0000	 0.2840
x	 0.9950	 0.3850
y	 0.9700	 0.2890
z	 0.9880	 0.3580