



## Full wwPDB EM Validation Report ⓘ

May 27, 2024 – 07:29 AM EDT

PDB ID : 7SSW  
EMDB ID : EMD-25415  
Title : Late translocation intermediate with EF-G dissociated (Structure VI)  
Authors : Carbone, C.E.; Korostelev, A.A.  
Deposited on : 2021-11-11  
Resolution : 3.80 Å (reported)  
Based on initial model : 5U9F

This is a Full wwPDB EM Validation 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

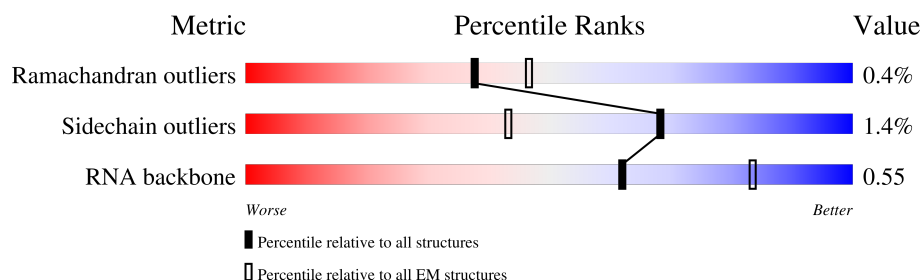
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.80 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.



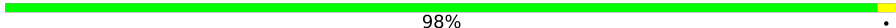


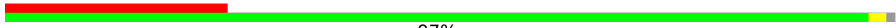
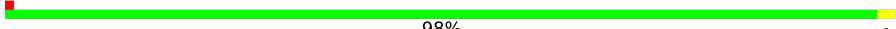
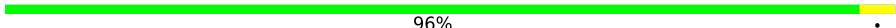

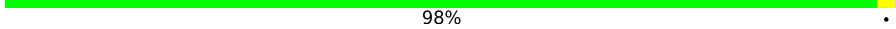
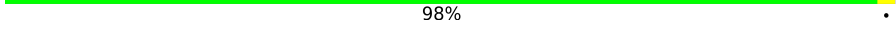
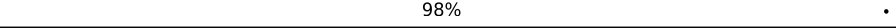
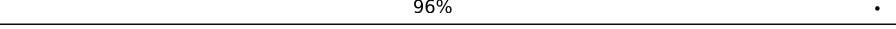
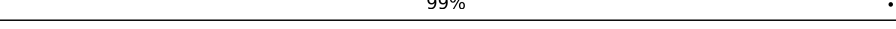
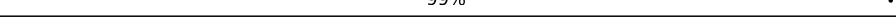
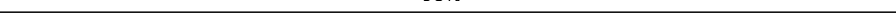







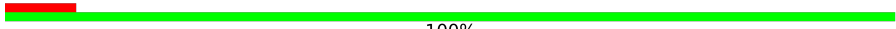

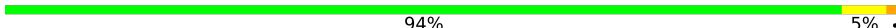

Metric	Whole archive (#Entries)	EM structures (#Entries)
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826
RNA backbone	4643	859

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	3	1539	
2	1	2903	
3	2	120	
4	6	77	
5	b	271	
6	c	209	
7	d	201	
8	e	177	

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Mol	Chain	Length	Quality of chain
9	f	176	 98%
10	g	149	 22% 99%
11	a	223	 60% 40%
12	i	142	 25% 97%
13	j	142	 98%
14	k	122	 96%
15	l	143	 94% 6%
16	m	136	 98%
17	n	120	 98%
18	o	116	 98%
19	p	114	 96%
20	q	117	 99%
21	r	103	 99%
22	s	110	 98%
23	t	93	 100%
24	u	102	 98%
25	v	94	 98%
26	w	75	 99%
27	x	77	 99%
28	y	63	 97%
29	z	58	 97%
30	B	56	 98%
31	C	50	 8% 100%
32	D	46	 100%
33	E	64	 94% 5%

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Mol	Chain	Length	Quality of chain
34	F	38	100%
35	4	39	5% 38% 13% 49%
36	5	77	81% 19%
37	G	225	8% 93% . . .
38	H	206	15% 99% .
39	I	205	. 100%
40	J	157	. 97% .
41	K	100	99% .
42	L	151	11% 99% .
43	M	129	99% .
44	N	127	. 98% .
45	O	98	7% 97% .
46	P	116	96% .
47	Q	123	95% . .
48	R	114	. 99% .
49	S	100	. 96% .
50	T	88	98% .
51	U	82	99% .
52	V	80	95% 5%
53	W	65	97% .
54	X	79	. 97% .
55	Y	85	100%
56	Z	65	. 92% 6% .

## 2 Entry composition [i](#)

There are 56 unique types of molecules in this entry. The entry contains 147596 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
1	3	1539	Total	C	N	O	P	0	0
			33012	14725	6052	10697	1538		

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

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

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 rRNA.

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

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 RNA chain called tRNA fMet.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	6	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 5 is a protein called 50S ribosomal protein L2.

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

- Molecule 6 is a protein called 50S ribosomal protein L3.

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

- Molecule 7 is a protein called 50S ribosomal protein L4.

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

- Molecule 8 is a protein called 50S ribosomal protein L5.

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

- Molecule 9 is a protein called 50S ribosomal protein L6.

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

- Molecule 10 is a protein called 50S ribosomal protein L9.

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

- Molecule 11 is a protein called 50S ribosomal protein L1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	a	134	Total	C	N	O	S	0	0
			1027	645	186	194	2		

- Molecule 12 is a protein called 50S ribosomal protein L11.

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

- Molecule 13 is a protein called 50S ribosomal protein L13.

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

- Molecule 14 is a protein called 50S ribosomal protein L14.

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

- Molecule 15 is a protein called 50S ribosomal protein L15.

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

- Molecule 16 is a protein called 50S ribosomal protein L16.

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

- Molecule 17 is a protein called 50S ribosomal protein L17.

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

- Molecule 18 is a protein called 50S ribosomal protein L18.

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

- Molecule 19 is a protein called 50S ribosomal protein L19.

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

- Molecule 20 is a protein called 50S ribosomal protein L20.

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

- Molecule 21 is a protein called 50S ribosomal protein L21.

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

- Molecule 22 is a protein called 50S ribosomal protein L22.

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

- Molecule 23 is a protein called 50S ribosomal protein L23.

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

- Molecule 24 is a protein called 50S ribosomal protein L24.

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

- Molecule 25 is a protein called 50S ribosomal protein L25.

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

- Molecule 26 is a protein called 50S ribosomal protein L27.



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

- Molecule 27 is a protein called 50S ribosomal protein L28.

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

- Molecule 28 is a protein called 50S ribosomal protein L29.

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

- Molecule 29 is a protein called 50S ribosomal protein L30.

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

- Molecule 30 is a protein called 50S ribosomal protein L32.

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

- Molecule 31 is a protein called 50S ribosomal protein L33.

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

- Molecule 32 is a protein called 50S ribosomal protein L34.

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

- Molecule 33 is a protein called 50S ribosomal protein L35.

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

- Molecule 34 is a protein called 50S ribosomal protein L36.

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

- Molecule 35 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
35	4	20	Total	C	N	O	P	0	0
			436	195	87	134	20		

- Molecule 36 is a RNA chain called tRNA Pro.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	5	77	Total	C	N	O	P	0	0
			1647	733	295	542	77		

- Molecule 37 is a protein called 30S ribosomal protein S2.

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

- Molecule 38 is a protein called 30S ribosomal protein S3.

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

- Molecule 39 is a protein called 30S ribosomal protein S4.

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

- Molecule 40 is a protein called 30S ribosomal protein S5.

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

- Molecule 41 is a protein called 30S ribosomal protein S6.

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

- Molecule 42 is a protein called 30S ribosomal protein S7.

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

- Molecule 43 is a protein called 30S ribosomal protein S8.

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

- Molecule 44 is a protein called 30S ribosomal protein S9.

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

- Molecule 45 is a protein called 30S ribosomal protein S10.

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

- Molecule 46 is a protein called 30S ribosomal protein S11.

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

- Molecule 47 is a protein called 30S ribosomal protein S12.

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

- Molecule 48 is a protein called 30S ribosomal protein S13.

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

- Molecule 49 is a protein called 30S ribosomal protein S14.

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

- Molecule 50 is a protein called 30S ribosomal protein S15.

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

- Molecule 51 is a protein called 30S ribosomal protein S16.

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

- Molecule 52 is a protein called 30S ribosomal protein S17.

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

- Molecule 53 is a protein called 30S ribosomal protein S18.

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

- Molecule 54 is a protein called 30S ribosomal protein S19.

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

- Molecule 55 is a protein called 30S ribosomal protein S20.

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

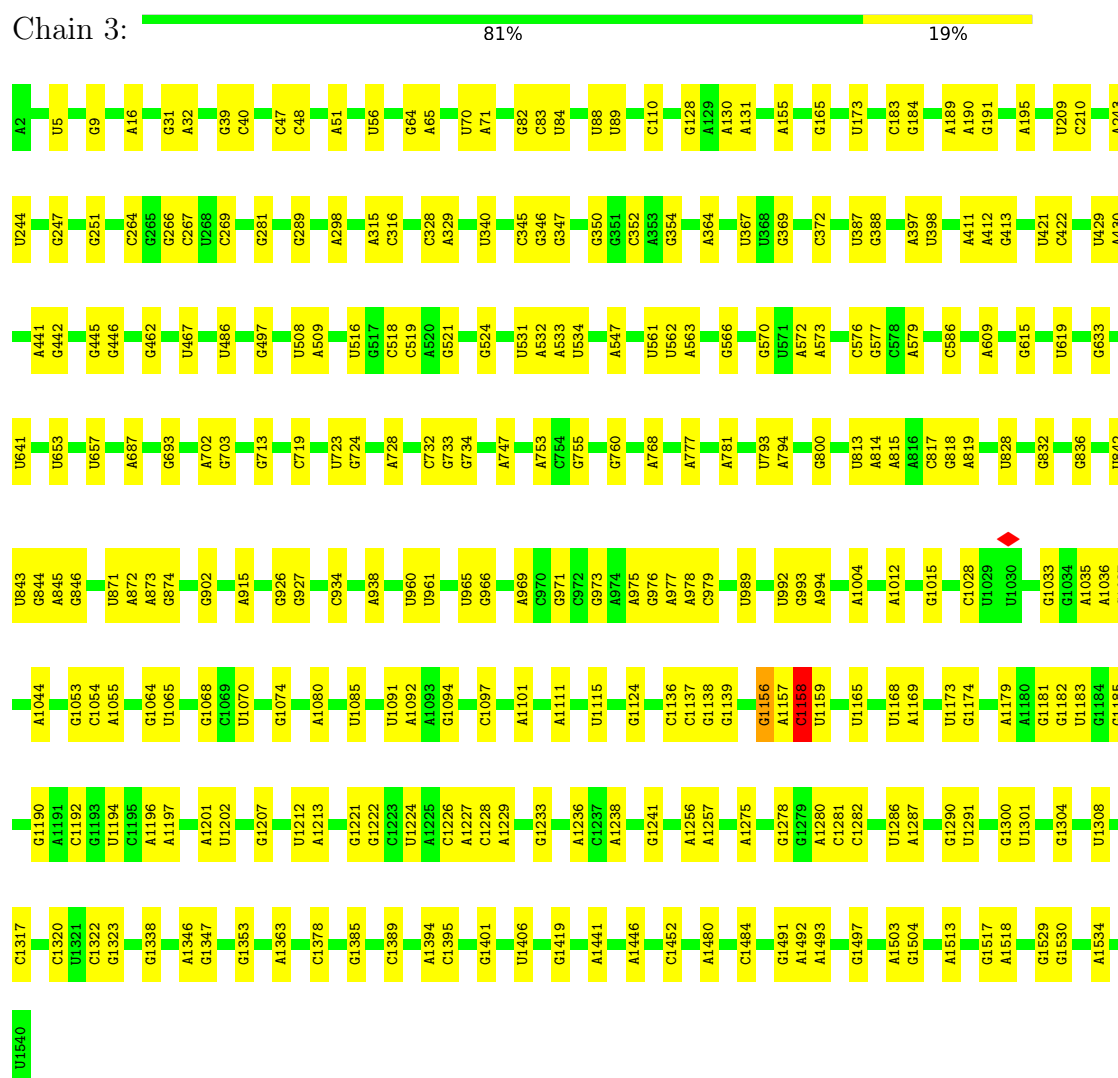
- Molecule 56 is a protein called 30S ribosomal protein S21.

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

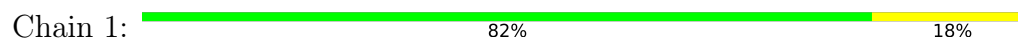
### 3 Residue-property plots

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




G1	G248	G481	G659	G858	C1013	U1176	C1414	A1626	A1791	C2001	G2162	G2361	G2535	C2755
C8	C249	G489	A666	G859	G1022	G1177	U1415	G1627	C1800	G2002	C2165	G2362	A2547	U2756
A10	A255	G491	A666	U860	U1033	G1179	G1416	G1627	A1801	U2022	U2166	G2383	G2549	G2759
U34	A265	A501	G684	C865	C1043	U1180	A1419	G1633	A1808	C2023	G2168	U2384	U2554	A2765
A42	G266	A502	A685	U868	G1044	U1199	C1428	G1643	G1811	A2030	A2170	C2385	U2555	C2771
G46	C267	A503	U686	A878	A1046	A1204	G1432	G1645	U1812	A2032	A2171	G2389	U2556	U2771
U50	U276	A504	G691	G883	G1206	G1206	G1450	C1646	C1816	A2033	A2172	G2390	C2558	A2776
G51	A294	A505	G696	U884	G1051	C1211	C1451	U1648	A1819	U2034	U2180	G2391	U2564	G2777
A63	A309	A508	G711	A886	G1055	G1212	G1452	A1654	U1820	C2036	A2198	A2392	A2565	A2778
A311	A310	C510	U877	C888	U1060	G1218	A1453	U1662	A1828	C2043	G2204	C2395	A2566	U2779
G70	G312	C527	U715	C889	U1061	A1247	C1454	G1663	A1829	G2046	G2207	U2402	A2567	G2791
A71	A322	A528	A714	C890	G1062	G1248	U1458	G1666	G1869	C2061	C2207	A2406	U2568	C2794
G93	C323	A529	A730	C891	U1065	G1253	C1461	G1669	G1869	A2062	A2207	A2406	A2572	A2799
C96	A324	A532	C747	A896	U1066	A1254	U1467	A1669	A1901	C2065	A2211	C2420	A2602	A2800
A103	G329	C544	A756	C898	A1067	U1255	U1467	G1674	C1902	C2066	A2225	G2421	G2801	G2801
U112	A330	A547	U773	C907	A1068	G1256	G1475	G1674	G1903	G2061	A2225	U2423	U2609	U2807
A119	G370	G555	G774	A910	A1069	A1272	G1482	C1694	G1906	A2062	G2228	C2424	U2613	U2818
U120	A371	G555	G775	C915	A1070	A1275	U1490	G1699	A1912	G2069	G2238	A2425	G2614	G2819
U120	G371	G555	G776	C915	A1071	A1275	U1490	G1700	A1913	G2072	G2239	C2427	U2615	A2820
A125	G372	U562	G776	C915	C1072	A1289	U1497	G1703	C1914	C2072	G2246	G2429	G2621	G2821
G134	G380	A563	A782	C915	U1083	A1300	A1515	U1713	G1929	U2075	G2250	C2440	U2629	A2823
U138	U387	A572	A783	U932	A1084	A1301	U1714	U1714	G1930	G2100	U2259	U2441	U2646	A2835
C140	U387	A574	G785	U933	A1085	A1302	G1519	G1715	A1937	U2109	A2268	G2447	U2656	U2866
G141	A404	A575	U803	U934	A1088	U1326	U1521	U1729	U1939	G2110	C2269	A2448	U2667	A2867
A142	U405	U588	A804	A941	A1089	A1327	G1524	C1730	U1940	U2111	G2283	U2449	G2663	A2868
C205	G406	U589	C806	C946	A1090	U1329	G1538	G1731	U1951	U2118	C2287	C2475	U2682	C2880
A162	G411	A590	U807	U959	C1104	U1329	G1538	C1732	U1955	A2119	A2287	A2476	U2685	U2884
C163	A412	U591	U811	C961	C1104	U1343	U1538	G1738	U1963	U2122	U2305	G2490	G2685	A2883
A161	C413	C595	C812	C961	A1111	U1344	U1555	U1757	U1963	U2126	C2306	C2498	U2689	U2883
A196	G424	A603	A819	C965	G1128	C1345	G1560	U1758	C1967	A2131	G2307	C2499	U2690	U2903
A204	U434	A614	U824	C974	U1132	G1361	A1566	C1764	G1968	U2132	A2309	U2500	C2691	
G205	A449	A616	U827	A975	A1133	G1377	G1567	U1765	A1969	G2133	A2311	G2502	G2714	
A216	U451	A627	U831	A983	A1134	U1378	C1585	G1773	A1970	G2134	A2311	U1971	C2716	
A222	A456	A637	G831	A990	C1135	U1379	U1585	A1773	U1971	A2134	A2322	U1971	G2717	
C228	U464	A646	A845	C995	A1142	G1380	A1598	G1776	A1981	C2145	G2325	U1982	A2727	
C229	G465	U646	U846	A996	A1143	U1386	A1608	A1780	U1982	A2147	A2327	U1982	A2733	
A233	A466	A654	U847	A996	A1169	U1396	A1616	A1784	G1992	A2154	G2331	C2521	A2744	
			G856	A1009	A1174	U1403	C1617	A1785	U1993	G2157	A2335	U2522	G2744	
			G857	U1012	A1175	A1403	A1618	A1786	C1997	A2158	A2336	G2529	A2748	

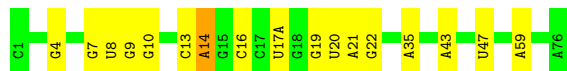
- Molecule 3: 5S rRNA

Chain 2:  90% 10%



- Molecule 4: tRNA fMet

Chain 6:  78% 21% .



- Molecule 5: 50S ribosomal protein L2

Chain b:  98% .



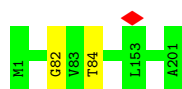
- Molecule 6: 50S ribosomal protein L3

Chain c:  96% .



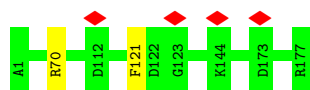
- Molecule 7: 50S ribosomal protein L4

Chain d:  99% .



- Molecule 8: 50S ribosomal protein L5

Chain e:  99% .



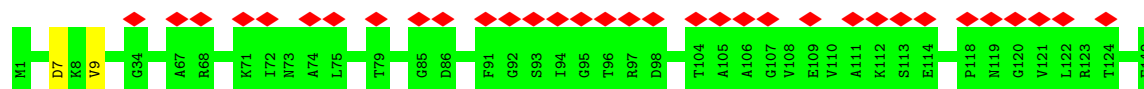
- Molecule 9: 50S ribosomal protein L6

Chain f:  98% .

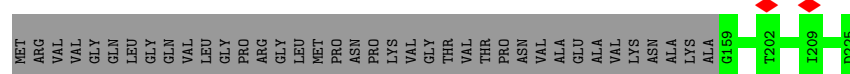
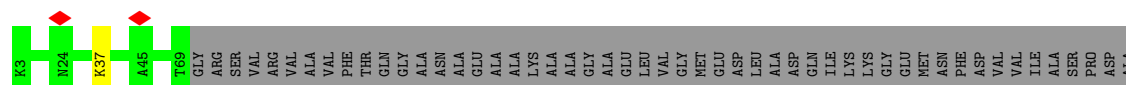




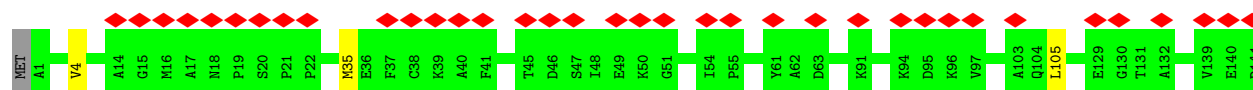
- Molecule 10: 50S ribosomal protein L9



- Molecule 11: 50S ribosomal protein L1



- Molecule 12: 50S ribosomal protein L11



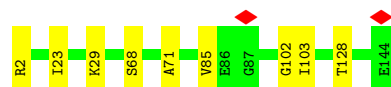
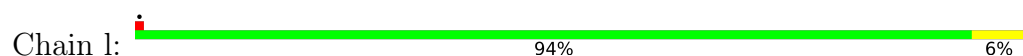
- Molecule 13: 50S ribosomal protein L13



- Molecule 14: 50S ribosomal protein L14



- Molecule 15: 50S ribosomal protein L15



- Molecule 16: 50S ribosomal protein L16

Chain m:  98%



- Molecule 17: 50S ribosomal protein L17

Chain n:  98%



- Molecule 18: 50S ribosomal protein L18

Chain o:  98%



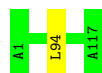
- Molecule 19: 50S ribosomal protein L19

Chain p:  96%



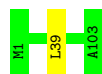
- Molecule 20: 50S ribosomal protein L20

Chain q:  99%



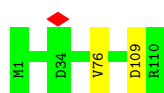
- Molecule 21: 50S ribosomal protein L21

Chain r:  99%



- Molecule 22: 50S ribosomal protein L22

Chain s:  98%



- Molecule 23: 50S ribosomal protein L23

Chain t:  100%

There are no outlier residues recorded for this chain.

- Molecule 24: 50S ribosomal protein L24

Chain u:  98%



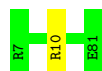
- Molecule 25: 50S ribosomal protein L25

Chain v:  98%



- Molecule 26: 50S ribosomal protein L27

Chain w:  99%



- Molecule 27: 50S ribosomal protein L28

Chain x:  99%



- Molecule 28: 50S ribosomal protein L29

Chain y:  97%



- Molecule 29: 50S ribosomal protein L30

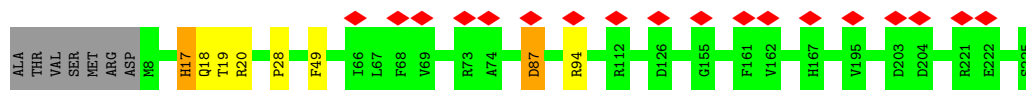
Chain z:  97%



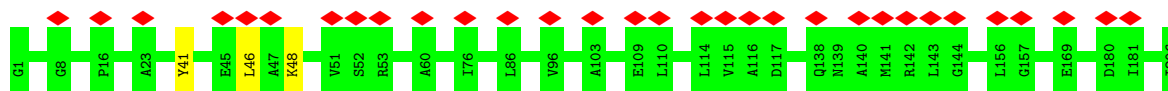
- Molecule 30: 50S ribosomal protein L32

Chain B:  98%

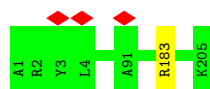




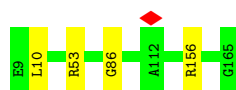
- Molecule 38: 30S ribosomal protein S3



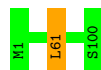
- Molecule 39: 30S ribosomal protein S4



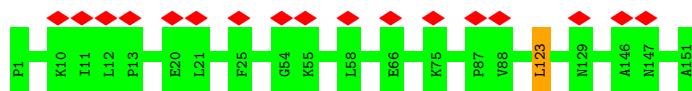
- Molecule 40: 30S ribosomal protein S5



- Molecule 41: 30S ribosomal protein S6



- Molecule 42: 30S ribosomal protein S7

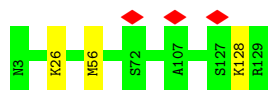


- Molecule 43: 30S ribosomal protein S8



- Molecule 44: 30S ribosomal protein S9

Chain N:  98%



- Molecule 45: 30S ribosomal protein S10

Chain O:  97%



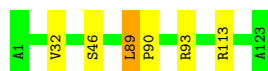
- Molecule 46: 30S ribosomal protein S11

Chain P:  96%



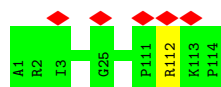
- Molecule 47: 30S ribosomal protein S12

Chain Q:  95%



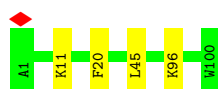
- Molecule 48: 30S ribosomal protein S13

Chain R:  99%



- Molecule 49: 30S ribosomal protein S14

Chain S:  96%



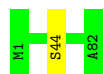
- Molecule 50: 30S ribosomal protein S15

Chain T:  98%



- Molecule 51: 30S ribosomal protein S16

Chain U:  99% .



- Molecule 52: 30S ribosomal protein S17

Chain V:  95% 5% .



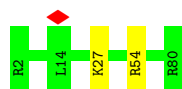
- Molecule 53: 30S ribosomal protein S18

Chain W:  97% .



- Molecule 54: 30S ribosomal protein S19

Chain X:  97% .




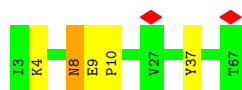
- Molecule 55: 30S ribosomal protein S20

Chain Y:  100% .

There are no outlier residues recorded for this chain.

- Molecule 56: 30S ribosomal protein S21

Chain Z:  92% 6% .



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	1163	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	20.281	Depositor
Minimum map value	-12.230	Depositor
Average map value	0.115	Depositor
Map value standard deviation	0.851	Depositor
Recommended contour level	0.5	Depositor
Map size (Å)	370.5408, 370.5408, 370.5408	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.8271, 0.8271, 0.8271	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	3	0.57	0/36963	0.68	4/57662 (0.0%)
2	1	0.56	0/69796	0.69	7/108888 (0.0%)
3	2	0.55	0/2872	0.68	0/4479
4	6	0.66	2/1832 (0.1%)	0.85	4/2855 (0.1%)
5	b	0.48	0/2122	0.72	1/2852 (0.0%)
6	c	0.43	0/1586	0.70	0/2134
7	d	0.37	0/1571	0.60	0/2113
8	e	0.37	0/1435	0.63	0/1926
9	f	0.34	0/1343	0.61	0/1816
10	g	0.34	0/1122	0.66	0/1515
11	a	0.28	0/1034	0.61	0/1387
12	i	0.33	0/1046	0.66	1/1410 (0.1%)
13	j	0.40	0/1152	0.64	0/1551
14	k	0.46	0/948	0.72	0/1268
15	l	0.40	0/1054	0.71	0/1403
16	m	0.44	0/1093	0.65	0/1460
17	n	0.43	0/974	0.68	0/1301
18	o	0.36	0/902	0.59	1/1209 (0.1%)
19	p	0.41	0/929	0.63	2/1242 (0.2%)
20	q	0.47	0/960	0.56	0/1278
21	r	0.43	0/829	0.68	1/1107 (0.1%)
22	s	0.38	0/864	0.59	0/1156
23	t	0.39	0/745	0.61	0/994
24	u	0.37	0/788	0.64	1/1051 (0.1%)
25	v	0.39	0/766	0.64	0/1025
26	w	0.42	0/582	0.64	0/769
27	x	0.43	0/635	0.64	0/848
28	y	0.29	0/510	0.66	0/677
29	z	0.35	0/453	0.62	1/605 (0.2%)
30	B	0.36	0/450	0.68	0/599
31	C	0.34	0/417	0.53	0/554
32	D	0.43	0/380	0.59	0/498
33	E	0.43	0/513	0.76	2/676 (0.3%)
34	F	0.38	0/303	0.68	0/397

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
35	4	0.68	0/490	0.75	0/763
36	5	0.64	0/1840	0.72	0/2868
37	G	0.35	0/1736	0.64	2/2338 (0.1%)
38	H	0.31	0/1652	0.58	0/2225
39	I	0.33	0/1665	0.58	0/2227
40	J	0.38	0/1170	0.69	1/1573 (0.1%)
41	K	0.39	0/836	0.64	1/1128 (0.1%)
42	L	0.30	0/1196	0.59	1/1602 (0.1%)
43	M	0.35	0/989	0.64	1/1326 (0.1%)
44	N	0.32	0/1034	0.64	0/1375
45	O	0.31	0/797	0.69	2/1077 (0.2%)
46	P	0.34	0/886	0.62	0/1195
47	Q	0.42	0/969	0.72	0/1300
48	R	0.31	0/893	0.65	0/1193
49	S	0.31	0/817	0.62	1/1088 (0.1%)
50	T	0.32	0/722	0.60	0/964
51	U	0.34	0/659	0.62	0/884
52	V	0.38	0/658	0.73	0/881
53	W	0.36	0/545	0.65	0/731
54	X	0.34	0/653	0.69	0/877
55	Y	0.30	0/671	0.53	0/888
56	Z	0.37	0/551	0.72	0/728
All	All	0.52	2/160398 (0.0%)	0.68	34/239936 (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
1	3	1	4
2	1	1	12
5	b	0	2
6	c	0	2
7	d	0	1
8	e	0	1
10	g	0	1
12	i	0	1
14	k	0	3
15	l	0	4
17	n	0	1
18	o	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
19	p	0	1
25	v	0	1
30	B	0	1
33	E	0	1
35	4	1	0
37	G	0	1
40	J	0	1
44	N	0	1
46	P	0	2
47	Q	0	2
51	U	0	1
52	V	0	2
56	Z	0	1
All	All	3	48

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	6	13	C	O3'-P	7.85	1.70	1.61
4	6	14	A	P-OP1	6.58	1.60	1.49

All (34) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	6	13	C	OP1-P-O3'	16.79	142.15	105.20
4	6	13	C	O3'-P-O5'	-15.05	75.40	104.00
4	6	13	C	P-O3'-C3'	9.45	131.04	119.70
4	6	14	A	O5'-P-OP1	-8.90	97.69	105.70
2	1	1828	G	N9-C1'-C2'	8.41	124.94	114.00
24	u	28	LEU	CA-CB-CG	7.26	132.00	115.30
18	o	26	LEU	CA-CB-CG	6.75	130.84	115.30
1	3	1156	G	N9-C1'-C2'	-6.43	104.93	112.00
33	E	32	LEU	CA-CB-CG	6.36	129.92	115.30
37	G	87	ASP	CB-CG-OD2	6.27	123.94	118.30
49	S	45	LEU	CA-CB-CG	6.12	129.38	115.30
1	3	1158	C	C3'-C2'-O2'	6.11	131.01	113.30
2	1	889	C	O4'-C1'-N1	5.88	112.90	108.20
33	E	28	LEU	CA-CB-CG	5.86	128.78	115.30
43	M	60	LEU	CA-CB-CG	5.74	128.50	115.30
19	p	54	LEU	CA-CB-CG	5.63	128.24	115.30
2	1	1669	A	N9-C1'-C2'	5.55	121.21	114.00
5	b	94	LEU	CA-CB-CG	5.53	128.01	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
40	J	10	LEU	CA-CB-CG	5.50	127.94	115.30
37	G	17	HIS	C-N-CA	5.47	135.38	121.70
2	1	847	U	N1-C1'-C2'	5.47	121.11	114.00
2	1	1328	A	N9-C1'-C2'	5.37	120.99	114.00
45	O	71	LEU	CA-CB-CG	5.37	127.65	115.30
29	z	47	ILE	CG1-CB-CG2	-5.35	99.63	111.40
12	i	105	LEU	CA-CB-CG	5.30	127.50	115.30
2	1	2109	U	N1-C1'-C2'	5.25	120.83	114.00
42	L	123	LEU	CA-CB-CG	5.25	127.37	115.30
19	p	83	ILE	CG1-CB-CG2	-5.19	99.98	111.40
41	K	61	LEU	CA-CB-CG	5.18	127.22	115.30
2	1	1970	A	C5'-C4'-O4'	5.18	115.31	109.10
45	O	35	GLN	CA-CB-CG	5.17	124.76	113.40
1	3	1158	C	C1'-C2'-O2'	5.09	125.89	110.60
1	3	563	A	N9-C1'-C2'	5.07	120.59	114.00
21	r	39	LEU	CA-CB-CG	5.07	126.96	115.30

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	3	1158	C	C2'
2	1	889	C	C2'
35	4	13	A	C4'

All (48) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	1328	A	Sidechain
2	1	1377	G	Sidechain
2	1	1432	G	Sidechain
2	1	1666	G	Sidechain
2	1	1828	G	Sidechain
2	1	1969	A	Sidechain
2	1	2109	U	Sidechain
2	1	2180	U	Sidechain
2	1	2447	G	Sidechain
2	1	370	G	Sidechain
2	1	775	G	Sidechain
2	1	889	C	Sidechain
1	3	1156	G	Sidechain
1	3	1158	C	Sidechain
1	3	1194	U	Sidechain

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Mol	Chain	Res	Type	Group
1	3	800	G	Sidechain
30	B	7	PRO	Peptide
33	E	30	HIS	Peptide
37	G	17	HIS	Peptide
40	J	86	GLY	Peptide
44	N	56	MET	Peptide
46	P	124	LYS	Peptide
46	P	125	LYS	Peptide
47	Q	46	SER	Peptide
47	Q	89	LEU	Peptide
51	U	44	SER	Peptide
52	V	42	LYS	Peptide
52	V	49	ASN	Peptide
56	Z	8	ASN	Peptide
5	b	46	GLY	Peptide
5	b	51	ARG	Peptide
6	c	149	ASN	Peptide
6	c	85	ALA	Peptide
7	d	82	GLY	Peptide
8	e	121	PHE	Peptide
10	g	7	ASP	Peptide
12	i	4	VAL	Peptide
14	k	13	ASN	Peptide
14	k	24	VAL	Peptide
14	k	29	HIS	Peptide
15	l	102	GLY	Peptide
15	l	23	ILE	Peptide
15	l	68	SER	Peptide
15	l	71	ALA	Peptide
17	n	43	GLU	Peptide
18	o	33	ARG	Peptide
19	p	112	ARG	Peptide
25	v	81	PRO	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	
5	b	269/271 (99%)	221 (82%)	48 (18%)	0	100	100
6	c	207/209 (99%)	172 (83%)	33 (16%)	2 (1%)	15	52
7	d	199/201 (99%)	167 (84%)	32 (16%)	0	100	100
8	e	175/177 (99%)	144 (82%)	31 (18%)	0	100	100
9	f	174/176 (99%)	154 (88%)	20 (12%)	0	100	100
10	g	147/149 (99%)	131 (89%)	15 (10%)	1 (1%)	22	60
11	a	130/223 (58%)	113 (87%)	17 (13%)	0	100	100
12	i	139/142 (98%)	117 (84%)	22 (16%)	0	100	100
13	j	140/142 (99%)	126 (90%)	13 (9%)	1 (1%)	22	60
14	k	120/122 (98%)	92 (77%)	28 (23%)	0	100	100
15	l	141/143 (99%)	106 (75%)	32 (23%)	3 (2%)	7	40
16	m	134/136 (98%)	109 (81%)	24 (18%)	1 (1%)	22	60
17	n	118/120 (98%)	96 (81%)	22 (19%)	0	100	100
18	o	114/116 (98%)	106 (93%)	8 (7%)	0	100	100
19	p	112/114 (98%)	95 (85%)	17 (15%)	0	100	100
20	q	115/117 (98%)	108 (94%)	7 (6%)	0	100	100
21	r	101/103 (98%)	84 (83%)	17 (17%)	0	100	100
22	s	108/110 (98%)	98 (91%)	10 (9%)	0	100	100
23	t	91/93 (98%)	75 (82%)	16 (18%)	0	100	100
24	u	100/102 (98%)	87 (87%)	13 (13%)	0	100	100
25	v	92/94 (98%)	82 (89%)	9 (10%)	1 (1%)	14	51
26	w	73/75 (97%)	61 (84%)	12 (16%)	0	100	100
27	x	75/77 (97%)	65 (87%)	10 (13%)	0	100	100
28	y	61/63 (97%)	55 (90%)	5 (8%)	1 (2%)	9	44
29	z	56/58 (97%)	49 (88%)	7 (12%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
30	B	54/56 (96%)	42 (78%)	12 (22%)	0	100	100
31	C	48/50 (96%)	46 (96%)	2 (4%)	0	100	100
32	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
33	E	62/64 (97%)	52 (84%)	8 (13%)	2 (3%)	4	32
34	F	36/38 (95%)	25 (69%)	11 (31%)	0	100	100
37	G	216/225 (96%)	187 (87%)	27 (12%)	2 (1%)	17	54
38	H	204/206 (99%)	184 (90%)	20 (10%)	0	100	100
39	I	203/205 (99%)	178 (88%)	25 (12%)	0	100	100
40	J	155/157 (99%)	130 (84%)	25 (16%)	0	100	100
41	K	98/100 (98%)	85 (87%)	13 (13%)	0	100	100
42	L	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
43	M	127/129 (98%)	113 (89%)	14 (11%)	0	100	100
44	N	125/127 (98%)	107 (86%)	18 (14%)	0	100	100
45	O	96/98 (98%)	81 (84%)	15 (16%)	0	100	100
46	P	114/116 (98%)	98 (86%)	16 (14%)	0	100	100
47	Q	121/123 (98%)	93 (77%)	26 (22%)	2 (2%)	9	43
48	R	112/114 (98%)	94 (84%)	18 (16%)	0	100	100
49	S	98/100 (98%)	87 (89%)	10 (10%)	1 (1%)	15	52
50	T	86/88 (98%)	77 (90%)	9 (10%)	0	100	100
51	U	80/82 (98%)	63 (79%)	17 (21%)	0	100	100
52	V	78/80 (98%)	51 (65%)	27 (35%)	0	100	100
53	W	63/65 (97%)	57 (90%)	6 (10%)	0	100	100
54	X	77/79 (98%)	62 (80%)	14 (18%)	1 (1%)	12	48
55	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
56	Z	63/65 (97%)	41 (65%)	18 (29%)	4 (6%)	1	20
All	All	5783/5982 (97%)	4926 (85%)	835 (14%)	22 (0%)	38	70

All (22) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
33	E	31	ILE
56	Z	37	TYR
10	g	9	VAL

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Mol	Chain	Res	Type
56	Z	10	PRO
15	l	103	ILE
15	l	128	THR
25	v	82	TYR
28	y	24	GLU
33	E	32	LEU
54	X	27	LYS
6	c	150	GLN
16	m	69	PRO
47	Q	90	PRO
56	Z	8	ASN
37	G	18	GLN
49	S	20	PHE
56	Z	9	GLU
6	c	129	THR
13	j	81	ILE
37	G	28	PRO
15	l	85	VAL
47	Q	32	VAL

### 5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
5	b	216/216 (100%)	214 (99%)	2 (1%)	78	88
6	c	164/164 (100%)	160 (98%)	4 (2%)	49	71
7	d	165/165 (100%)	164 (99%)	1 (1%)	86	92
8	e	148/148 (100%)	147 (99%)	1 (1%)	84	91
9	f	137/137 (100%)	133 (97%)	4 (3%)	42	67
10	g	114/114 (100%)	114 (100%)	0	100	100
11	a	110/174 (63%)	109 (99%)	1 (1%)	78	88
12	i	109/110 (99%)	108 (99%)	1 (1%)	78	88
13	j	116/116 (100%)	114 (98%)	2 (2%)	60	78

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
14	k	103/103 (100%)	101 (98%)	2 (2%)	57	76
15	l	102/102 (100%)	100 (98%)	2 (2%)	55	75
16	m	109/109 (100%)	107 (98%)	2 (2%)	59	77
17	n	100/100 (100%)	99 (99%)	1 (1%)	76	86
18	o	86/86 (100%)	86 (100%)	0	100	100
19	p	99/99 (100%)	98 (99%)	1 (1%)	76	86
20	q	89/89 (100%)	88 (99%)	1 (1%)	73	85
21	r	84/84 (100%)	84 (100%)	0	100	100
22	s	93/93 (100%)	91 (98%)	2 (2%)	52	72
23	t	80/80 (100%)	80 (100%)	0	100	100
24	u	83/83 (100%)	82 (99%)	1 (1%)	71	84
25	v	78/78 (100%)	78 (100%)	0	100	100
26	w	57/57 (100%)	56 (98%)	1 (2%)	59	77
27	x	67/67 (100%)	66 (98%)	1 (2%)	65	81
28	y	55/55 (100%)	54 (98%)	1 (2%)	59	77
29	z	48/48 (100%)	47 (98%)	1 (2%)	53	74
30	B	47/47 (100%)	47 (100%)	0	100	100
31	C	45/45 (100%)	45 (100%)	0	100	100
32	D	38/38 (100%)	38 (100%)	0	100	100
33	E	51/51 (100%)	51 (100%)	0	100	100
34	F	34/34 (100%)	34 (100%)	0	100	100
37	G	180/186 (97%)	175 (97%)	5 (3%)	43	68
38	H	170/170 (100%)	167 (98%)	3 (2%)	59	77
39	I	172/172 (100%)	171 (99%)	1 (1%)	86	92
40	J	119/119 (100%)	117 (98%)	2 (2%)	60	78
41	K	87/87 (100%)	86 (99%)	1 (1%)	73	85
42	L	124/124 (100%)	123 (99%)	1 (1%)	81	89
43	M	104/104 (100%)	104 (100%)	0	100	100
44	N	105/105 (100%)	103 (98%)	2 (2%)	57	76
45	O	86/86 (100%)	85 (99%)	1 (1%)	71	84
46	P	89/89 (100%)	86 (97%)	3 (3%)	37	64

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
47	Q	103/103 (100%)	100 (97%)	3 (3%)	42	67
48	R	92/92 (100%)	91 (99%)	1 (1%)	73	85
49	S	83/83 (100%)	81 (98%)	2 (2%)	49	71
50	T	76/76 (100%)	74 (97%)	2 (3%)	46	69
51	U	65/65 (100%)	65 (100%)	0	100	100
52	V	74/74 (100%)	72 (97%)	2 (3%)	44	69
53	W	56/56 (100%)	54 (96%)	2 (4%)	35	63
54	X	70/70 (100%)	69 (99%)	1 (1%)	67	81
55	Y	65/65 (100%)	65 (100%)	0	100	100
56	Z	55/55 (100%)	54 (98%)	1 (2%)	59	77
All	All	4802/4873 (98%)	4737 (99%)	65 (1%)	68	81

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
5	b	256	THR
5	b	257	ARG
6	c	33	ARG
6	c	108	ASP
6	c	179	ARG
6	c	197	THR
7	d	84	THR
8	e	70	ARG
9	f	28	LYS
9	f	68	ARG
9	f	103	ASN
9	f	176	LYS
11	a	37	LYS
12	i	35	MET
13	j	65	THR
13	j	111	LYS
14	k	32	TYR
14	k	49	ARG
15	l	2	ARG
15	l	29	LYS
16	m	44	ARG
16	m	59	ARG
17	n	57	THR

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Mol	Chain	Res	Type
19	p	86	LYS
20	q	94	LEU
22	s	76	VAL
22	s	109	ASP
24	u	81	ARG
26	w	10	ARG
27	x	32	LEU
28	y	7	ARG
29	z	30	ARG
37	G	19	THR
37	G	20	ARG
37	G	49	PHE
37	G	87	ASP
37	G	94	ARG
38	H	41	TYR
38	H	46	LEU
38	H	48	LYS
39	I	183	ARG
40	J	53	ARG
40	J	156	ARG
41	K	61	LEU
42	L	123	LEU
44	N	26	LYS
44	N	128	LYS
45	O	89	ARG
46	P	12	ARG
46	P	105	ARG
46	P	121	ARG
47	Q	89	LEU
47	Q	93	ARG
47	Q	113	ARG
48	R	112	ARG
49	S	11	LYS
49	S	96	LYS
50	T	16	ARG
50	T	88	ARG
52	V	5	ARG
52	V	26	ARG
53	W	11	ARG
53	W	69	TYR
54	X	54	ARG
56	Z	4	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (76) such sidechains are listed below:

Mol	Chain	Res	Type
5	b	20	ASN
5	b	24	HIS
5	b	44	ASN
5	b	116	GLN
5	b	238	ASN
6	c	36	GLN
8	e	20	ASN
9	f	63	GLN
9	f	103	ASN
10	g	2	GLN
10	g	43	ASN
10	g	133	GLN
12	i	5	GLN
13	j	130	HIS
13	j	132	HIS
14	k	9	ASN
15	l	35	HIS
15	l	38	GLN
15	l	99	ASN
16	m	22	GLN
17	n	9	GLN
17	n	11	ASN
18	o	38	GLN
19	p	2	ASN
19	p	65	ASN
20	q	55	GLN
20	q	58	GLN
21	r	11	GLN
21	r	91	GLN
23	t	59	ASN
24	u	73	ASN
24	u	98	ASN
25	v	44	HIS
25	v	49	ASN
26	w	42	HIS
26	w	72	ASN
28	y	15	ASN
29	z	48	ASN
32	D	16	HIS
32	D	29	GLN
33	E	25	HIS

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Mol	Chain	Res	Type
34	F	33	HIS
37	G	121	GLN
37	G	176	ASN
37	G	177	ASN
38	H	7	ASN
38	H	31	ASN
38	H	139	ASN
39	I	58	GLN
39	I	88	ASN
40	J	72	ASN
40	J	82	HIS
40	J	96	GLN
40	J	131	ASN
41	K	11	HIS
41	K	17	GLN
42	L	67	ASN
42	L	141	HIS
43	M	3	GLN
43	M	17	GLN
43	M	75	GLN
44	N	31	GLN
45	O	20	GLN
46	P	63	GLN
47	Q	58	ASN
48	R	13	HIS
49	S	3	GLN
49	S	59	GLN
50	T	34	GLN
51	U	63	GLN
52	V	30	HIS
53	W	51	GLN
54	X	52	ASN
54	X	55	GLN
55	Y	12	GLN
55	Y	60	GLN

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	282 (18%)	4 (0%)
2	1	2902/2903 (99%)	511 (17%)	10 (0%)

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	2	119/120 (99%)	12 (10%)	0
35	4	19/39 (48%)	5 (26%)	1 (5%)
36	5	76/77 (98%)	15 (19%)	0
4	6	76/77 (98%)	16 (21%)	0
All	All	4730/4755 (99%)	841 (17%)	15 (0%)

All (841) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	5	U
1	3	9	G
1	3	16	A
1	3	31	G
1	3	32	A
1	3	39	G
1	3	40	C
1	3	47	C
1	3	48	C
1	3	51	A
1	3	56	U
1	3	64	G
1	3	65	A
1	3	71	A
1	3	82	G
1	3	83	C
1	3	84	U
1	3	88	U
1	3	89	U
1	3	110	C
1	3	128	G
1	3	130	A
1	3	131	A
1	3	155	A
1	3	165	G
1	3	173	U
1	3	183	C
1	3	184	G
1	3	189	A
1	3	190	A
1	3	191	G
1	3	195	A
1	3	209	U

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Mol	Chain	Res	Type
1	3	210	C
1	3	243	A
1	3	244	U
1	3	247	G
1	3	251	G
1	3	264	C
1	3	266	G
1	3	267	C
1	3	269	C
1	3	281	G
1	3	289	G
1	3	298	A
1	3	315	A
1	3	316	C
1	3	328	C
1	3	329	A
1	3	340	U
1	3	345	C
1	3	346	G
1	3	347	G
1	3	350	G
1	3	352	C
1	3	354	G
1	3	364	A
1	3	367	U
1	3	369	G
1	3	372	C
1	3	387	U
1	3	388	G
1	3	397	A
1	3	398	U
1	3	411	A
1	3	412	A
1	3	413	G
1	3	421	U
1	3	422	C
1	3	429	U
1	3	430	A
1	3	441	A
1	3	442	G
1	3	445	G
1	3	446	G

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Mol	Chain	Res	Type
1	3	462	G
1	3	467	U
1	3	486	U
1	3	497	G
1	3	508	U
1	3	509	A
1	3	516	U
1	3	518	C
1	3	519	C
1	3	521	G
1	3	524	G
1	3	531	U
1	3	532	A
1	3	533	A
1	3	534	U
1	3	547	A
1	3	561	U
1	3	562	U
1	3	566	G
1	3	570	G
1	3	572	A
1	3	573	A
1	3	576	C
1	3	577	G
1	3	579	A
1	3	586	C
1	3	609	A
1	3	615	G
1	3	619	U
1	3	633	G
1	3	641	U
1	3	653	U
1	3	657	U
1	3	687	A
1	3	693	G
1	3	702	A
1	3	703	G
1	3	713	G
1	3	719	C
1	3	723	U
1	3	724	G
1	3	728	A

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Mol	Chain	Res	Type
1	3	732	C
1	3	733	G
1	3	734	G
1	3	747	A
1	3	753	A
1	3	755	G
1	3	760	G
1	3	768	A
1	3	777	A
1	3	781	A
1	3	793	U
1	3	794	A
1	3	813	U
1	3	814	A
1	3	815	A
1	3	817	C
1	3	818	G
1	3	819	A
1	3	828	U
1	3	832	G
1	3	836	G
1	3	842	U
1	3	843	U
1	3	844	G
1	3	845	A
1	3	846	G
1	3	871	U
1	3	872	A
1	3	873	A
1	3	874	G
1	3	902	G
1	3	915	A
1	3	926	G
1	3	927	G
1	3	934	C
1	3	938	A
1	3	960	U
1	3	961	U
1	3	965	U
1	3	966	G
1	3	969	A
1	3	971	G

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Mol	Chain	Res	Type
1	3	973	G
1	3	975	A
1	3	976	G
1	3	977	A
1	3	978	A
1	3	979	C
1	3	989	U
1	3	992	U
1	3	993	G
1	3	994	A
1	3	1004	A
1	3	1012	A
1	3	1015	G
1	3	1028	C
1	3	1033	G
1	3	1035	A
1	3	1036	A
1	3	1037	C
1	3	1044	A
1	3	1053	G
1	3	1054	C
1	3	1055	A
1	3	1064	G
1	3	1065	U
1	3	1068	G
1	3	1070	U
1	3	1074	G
1	3	1080	A
1	3	1085	U
1	3	1091	U
1	3	1092	A
1	3	1094	G
1	3	1097	C
1	3	1101	A
1	3	1111	A
1	3	1115	U
1	3	1124	G
1	3	1136	C
1	3	1137	C
1	3	1138	G
1	3	1139	G
1	3	1157	A

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Mol	Chain	Res	Type
1	3	1158	C
1	3	1159	U
1	3	1165	U
1	3	1168	U
1	3	1169	A
1	3	1173	U
1	3	1174	G
1	3	1179	A
1	3	1181	G
1	3	1182	G
1	3	1183	U
1	3	1185	G
1	3	1190	G
1	3	1192	C
1	3	1196	A
1	3	1197	A
1	3	1201	A
1	3	1202	U
1	3	1207	G
1	3	1212	U
1	3	1213	A
1	3	1221	G
1	3	1222	G
1	3	1224	U
1	3	1226	C
1	3	1227	A
1	3	1228	C
1	3	1229	A
1	3	1233	G
1	3	1236	A
1	3	1238	A
1	3	1241	G
1	3	1256	A
1	3	1257	A
1	3	1275	A
1	3	1278	G
1	3	1280	A
1	3	1281	C
1	3	1282	C
1	3	1286	U
1	3	1287	A
1	3	1290	G

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Mol	Chain	Res	Type
1	3	1291	U
1	3	1300	G
1	3	1301	U
1	3	1304	G
1	3	1308	U
1	3	1317	C
1	3	1320	C
1	3	1322	C
1	3	1323	G
1	3	1338	G
1	3	1346	A
1	3	1347	G
1	3	1353	G
1	3	1363	A
1	3	1378	C
1	3	1385	G
1	3	1389	C
1	3	1394	A
1	3	1395	C
1	3	1401	G
1	3	1406	U
1	3	1419	G
1	3	1441	A
1	3	1446	A
1	3	1452	C
1	3	1480	A
1	3	1484	C
1	3	1491	G
1	3	1492	A
1	3	1493	A
1	3	1497	G
1	3	1503	A
1	3	1504	G
1	3	1513	A
1	3	1517	G
1	3	1518	A
1	3	1529	G
1	3	1530	G
1	3	1534	A
2	1	8	C
2	1	10	A
2	1	34	U

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Mol	Chain	Res	Type
2	1	42	A
2	1	46	G
2	1	50	U
2	1	51	G
2	1	63	A
2	1	70	G
2	1	71	A
2	1	93	G
2	1	96	C
2	1	103	A
2	1	112	U
2	1	119	A
2	1	120	U
2	1	125	A
2	1	134	G
2	1	138	U
2	1	140	C
2	1	141	G
2	1	142	A
2	1	162	U
2	1	163	C
2	1	181	A
2	1	196	A
2	1	204	A
2	1	205	G
2	1	216	A
2	1	222	A
2	1	228	C
2	1	229	C
2	1	233	A
2	1	248	G
2	1	249	C
2	1	255	A
2	1	265	A
2	1	266	G
2	1	267	C
2	1	276	U
2	1	294	A
2	1	309	A
2	1	311	A
2	1	312	G
2	1	322	A

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Mol	Chain	Res	Type
2	1	323	C
2	1	324	A
2	1	329	G
2	1	330	A
2	1	349	U
2	1	361	G
2	1	371	A
2	1	372	G
2	1	380	G
2	1	386	G
2	1	387	U
2	1	404	A
2	1	406	G
2	1	411	G
2	1	412	A
2	1	413	C
2	1	424	G
2	1	434	U
2	1	449	A
2	1	451	U
2	1	456	C
2	1	464	U
2	1	465	G
2	1	466	A
2	1	481	G
2	1	489	G
2	1	491	G
2	1	501	A
2	1	502	A
2	1	504	A
2	1	505	A
2	1	508	A
2	1	510	C
2	1	527	C
2	1	529	A
2	1	532	A
2	1	544	C
2	1	547	A
2	1	549	G
2	1	550	C
2	1	555	G
2	1	562	U

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Mol	Chain	Res	Type
2	1	563	A
2	1	572	A
2	1	573	U
2	1	574	A
2	1	575	A
2	1	588	U
2	1	589	U
2	1	591	U
2	1	595	C
2	1	603	A
2	1	614	A
2	1	616	A
2	1	627	A
2	1	637	A
2	1	646	U
2	1	654	A
2	1	655	A
2	1	659	G
2	1	666	A
2	1	684	G
2	1	686	U
2	1	690	G
2	1	691	C
2	1	696	G
2	1	711	G
2	1	714	U
2	1	715	A
2	1	730	A
2	1	747	C
2	1	756	A
2	1	773	U
2	1	776	G
2	1	782	A
2	1	784	G
2	1	785	G
2	1	789	A
2	1	803	U
2	1	804	A
2	1	805	G
2	1	806	C
2	1	807	U
2	1	811	U

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Mol	Chain	Res	Type
2	1	812	C
2	1	819	A
2	1	824	U
2	1	827	U
2	1	831	G
2	1	845	A
2	1	846	U
2	1	847	U
2	1	856	G
2	1	858	G
2	1	859	G
2	1	860	U
2	1	865	C
2	1	868	U
2	1	878	A
2	1	883	G
2	1	885	C
2	1	886	A
2	1	887	U
2	1	890	C
2	1	891	G
2	1	897	C
2	1	898	C
2	1	907	G
2	1	910	A
2	1	915	C
2	1	932	U
2	1	934	U
2	1	941	A
2	1	946	C
2	1	953	G
2	1	957	C
2	1	958	U
2	1	961	C
2	1	965	C
2	1	974	G
2	1	975	A
2	1	983	A
2	1	990	A
2	1	995	C
2	1	996	A
2	1	1009	A

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Mol	Chain	Res	Type
2	1	1012	U
2	1	1013	C
2	1	1022	G
2	1	1033	U
2	1	1043	C
2	1	1045	C
2	1	1046	A
2	1	1051	G
2	1	1055	G
2	1	1060	U
2	1	1062	G
2	1	1065	U
2	1	1066	U
2	1	1067	A
2	1	1068	G
2	1	1069	A
2	1	1070	A
2	1	1071	G
2	1	1072	C
2	1	1079	C
2	1	1083	U
2	1	1085	A
2	1	1088	A
2	1	1089	A
2	1	1090	A
2	1	1094	U
2	1	1102	C
2	1	1104	C
2	1	1111	A
2	1	1128	G
2	1	1132	U
2	1	1133	A
2	1	1135	C
2	1	1142	A
2	1	1143	A
2	1	1169	A
2	1	1174	U
2	1	1175	A
2	1	1176	U
2	1	1177	G
2	1	1178	C
2	1	1180	U

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Mol	Chain	Res	Type
2	1	1199	U
2	1	1204	A
2	1	1206	G
2	1	1211	C
2	1	1212	G
2	1	1218	G
2	1	1247	A
2	1	1248	G
2	1	1253	A
2	1	1255	U
2	1	1256	G
2	1	1272	A
2	1	1275	A
2	1	1289	C
2	1	1300	G
2	1	1301	A
2	1	1302	A
2	1	1321	A
2	1	1325	U
2	1	1326	U
2	1	1329	U
2	1	1344	U
2	1	1345	C
2	1	1361	G
2	1	1379	U
2	1	1380	G
2	1	1383	A
2	1	1396	U
2	1	1403	A
2	1	1414	C
2	1	1416	G
2	1	1419	A
2	1	1420	A
2	1	1428	C
2	1	1450	G
2	1	1452	G
2	1	1453	A
2	1	1454	C
2	1	1458	U
2	1	1461	C
2	1	1467	U
2	1	1475	G

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Mol	Chain	Res	Type
2	1	1482	G
2	1	1490	A
2	1	1497	U
2	1	1515	A
2	1	1519	G
2	1	1521	G
2	1	1524	G
2	1	1535	A
2	1	1536	C
2	1	1537	G
2	1	1538	G
2	1	1555	G
2	1	1560	G
2	1	1566	A
2	1	1567	G
2	1	1585	C
2	1	1598	A
2	1	1608	A
2	1	1616	A
2	1	1617	C
2	1	1618	A
2	1	1627	G
2	1	1633	G
2	1	1643	G
2	1	1644	C
2	1	1646	C
2	1	1647	U
2	1	1648	U
2	1	1654	A
2	1	1662	U
2	1	1663	G
2	1	1674	G
2	1	1694	C
2	1	1699	G
2	1	1700	A
2	1	1703	G
2	1	1713	A
2	1	1714	U
2	1	1715	G
2	1	1729	U
2	1	1730	C
2	1	1731	G

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Mol	Chain	Res	Type
2	1	1732	C
2	1	1733	G
2	1	1738	G
2	1	1757	A
2	1	1758	U
2	1	1764	C
2	1	1766	G
2	1	1773	A
2	1	1776	G
2	1	1780	A
2	1	1784	A
2	1	1785	A
2	1	1786	A
2	1	1791	A
2	1	1800	C
2	1	1801	A
2	1	1808	A
2	1	1811	G
2	1	1812	U
2	1	1816	C
2	1	1819	A
2	1	1820	U
2	1	1829	A
2	1	1869	G
2	1	1901	A
2	1	1903	G
2	1	1906	G
2	1	1907	G
2	1	1912	A
2	1	1913	A
2	1	1914	C
2	1	1929	G
2	1	1930	G
2	1	1937	A
2	1	1939	U
2	1	1940	U
2	1	1951	U
2	1	1955	U
2	1	1963	U
2	1	1967	C
2	1	1969	A
2	1	1970	A

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Mol	Chain	Res	Type
2	1	1971	U
2	1	1972	G
2	1	1981	A
2	1	1982	U
2	1	1991	U
2	1	1993	U
2	1	1997	C
2	1	2001	C
2	1	2002	G
2	1	2022	U
2	1	2023	C
2	1	2030	A
2	1	2031	A
2	1	2032	G
2	1	2033	A
2	1	2034	U
2	1	2036	C
2	1	2043	C
2	1	2046	G
2	1	2055	C
2	1	2056	G
2	1	2060	A
2	1	2061	G
2	1	2062	A
2	1	2069	G
2	1	2072	C
2	1	2075	U
2	1	2100	G
2	1	2111	U
2	1	2112	G
2	1	2118	U
2	1	2119	A
2	1	2122	U
2	1	2126	A
2	1	2131	U
2	1	2132	U
2	1	2133	G
2	1	2134	A
2	1	2145	C
2	1	2146	C
2	1	2147	A
2	1	2154	A

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Mol	Chain	Res	Type
2	1	2157	G
2	1	2158	A
2	1	2162	G
2	1	2165	C
2	1	2166	U
2	1	2167	U
2	1	2168	G
2	1	2169	A
2	1	2171	A
2	1	2172	U
2	1	2173	A
2	1	2198	A
2	1	2204	G
2	1	2207	C
2	1	2211	A
2	1	2225	A
2	1	2228	G
2	1	2238	G
2	1	2239	G
2	1	2246	G
2	1	2250	G
2	1	2259	U
2	1	2268	A
2	1	2269	G
2	1	2283	C
2	1	2287	A
2	1	2305	U
2	1	2307	G
2	1	2309	A
2	1	2311	A
2	1	2322	A
2	1	2325	G
2	1	2327	A
2	1	2331	G
2	1	2335	A
2	1	2336	A
2	1	2361	G
2	1	2382	G
2	1	2383	G
2	1	2385	C
2	1	2388	A
2	1	2390	U

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Mol	Chain	Res	Type
2	1	2392	A
2	1	2395	C
2	1	2402	U
2	1	2406	A
2	1	2420	C
2	1	2422	C
2	1	2423	U
2	1	2425	A
2	1	2427	C
2	1	2429	G
2	1	2440	C
2	1	2441	U
2	1	2447	G
2	1	2448	A
2	1	2449	U
2	1	2475	C
2	1	2476	A
2	1	2490	G
2	1	2498	C
2	1	2499	C
2	1	2501	C
2	1	2502	G
2	1	2504	U
2	1	2505	G
2	1	2518	A
2	1	2520	C
2	1	2522	U
2	1	2529	G
2	1	2535	G
2	1	2547	A
2	1	2549	G
2	1	2554	U
2	1	2555	U
2	1	2556	C
2	1	2558	C
2	1	2564	A
2	1	2566	A
2	1	2567	G
2	1	2568	U
2	1	2572	A
2	1	2602	A
2	1	2609	U

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Mol	Chain	Res	Type
2	1	2610	C
2	1	2613	U
2	1	2615	U
2	1	2621	G
2	1	2629	U
2	1	2646	C
2	1	2656	U
2	1	2663	G
2	1	2682	A
2	1	2685	G
2	1	2689	U
2	1	2690	U
2	1	2691	C
2	1	2714	G
2	1	2716	C
2	1	2718	G
2	1	2727	A
2	1	2733	A
2	1	2744	G
2	1	2748	A
2	1	2755	C
2	1	2756	U
2	1	2759	G
2	1	2765	A
2	1	2771	C
2	1	2776	A
2	1	2777	G
2	1	2778	A
2	1	2779	U
2	1	2791	G
2	1	2794	C
2	1	2799	A
2	1	2800	A
2	1	2801	G
2	1	2807	U
2	1	2818	U
2	1	2820	A
2	1	2821	A
2	1	2823	A
2	1	2835	A
2	1	2866	U
2	1	2867	G

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Mol	Chain	Res	Type
2	1	2868	A
2	1	2880	C
2	1	2884	U
2	1	2893	A
3	2	2	G
3	2	4	C
3	2	15	A
3	2	24	G
3	2	35	C
3	2	41	G
3	2	44	G
3	2	53	A
3	2	57	A
3	2	89	U
3	2	90	C
3	2	109	A
4	6	4	G
4	6	7	G
4	6	8	U
4	6	9	G
4	6	10	G
4	6	14	A
4	6	16	C
4	6	17(A)	U
4	6	19	G
4	6	20	U
4	6	21	A
4	6	22	G
4	6	35	A
4	6	43	A
4	6	47	U
4	6	59	A
35	4	12	A
35	4	13	A
35	4	14	A
35	4	15	A
35	4	16	A
36	5	2	G
36	5	3	G
36	5	5	G
36	5	6	A
36	5	8	U

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Mol	Chain	Res	Type
36	5	15	G
36	5	16	C
36	5	19	G
36	5	20	U
36	5	21	A
36	5	22	G
36	5	53	G
36	5	59	A
36	5	61	C
36	5	73	A

All (15) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
1	3	70	U
1	3	429	U
1	3	1157	A
1	3	1173	U
2	1	889	C
2	1	896	A
2	1	1343	G
2	1	1453	A
2	1	1626	A
2	1	1730	C
2	1	1970	A
2	1	2001	C
2	1	2061	G
2	1	2391	G
35	4	13	A

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

## 5.6 Ligand geometry

There are no ligands in this entry.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

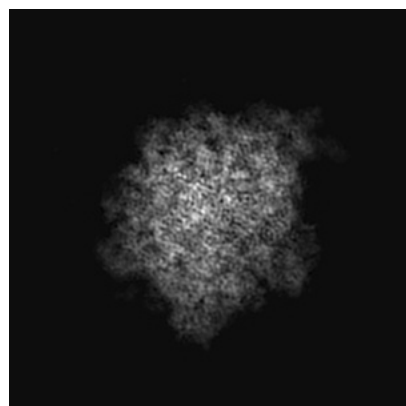
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25415. These allow visual inspection of the internal detail of the map and identification of artifacts.

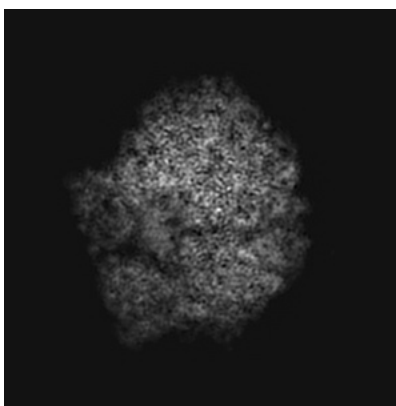
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

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

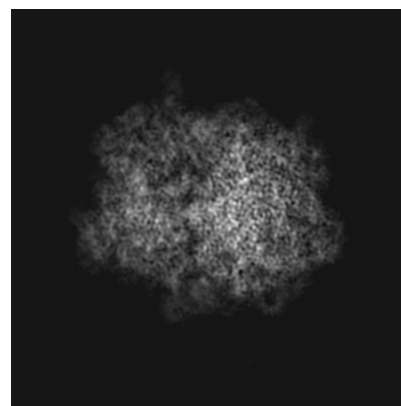
#### 6.1.1 Primary map



X

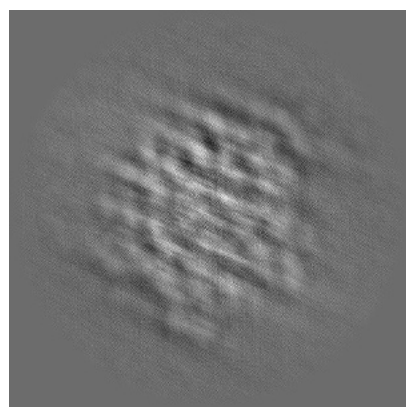


Y

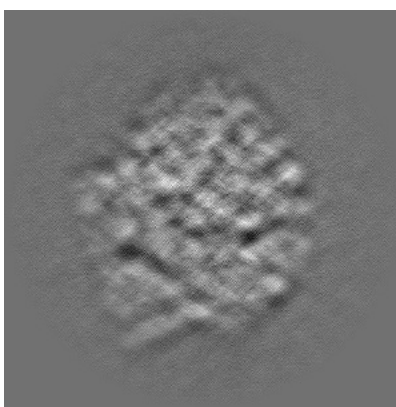


Z

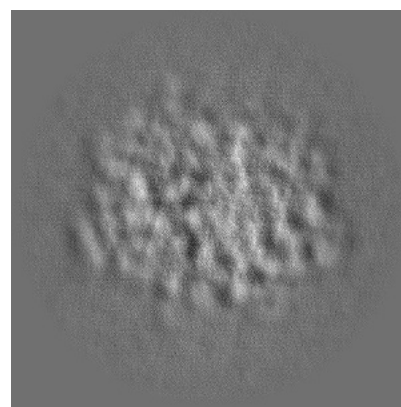
#### 6.1.2 Raw map



X



Y

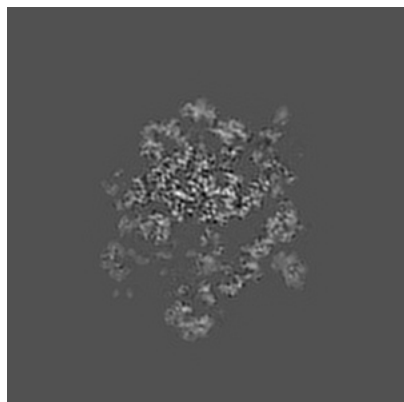


Z

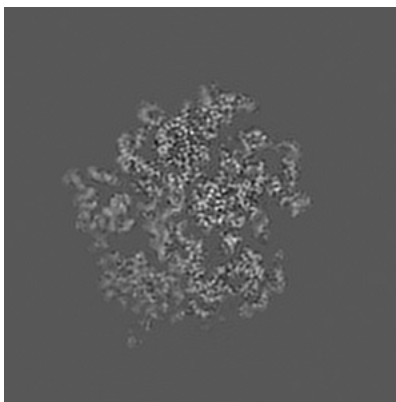
The images above show the map projected in three orthogonal directions.

## 6.2 Central slices [i](#)

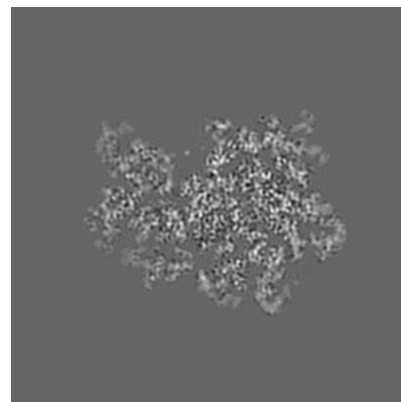
### 6.2.1 Primary map



X Index: 224

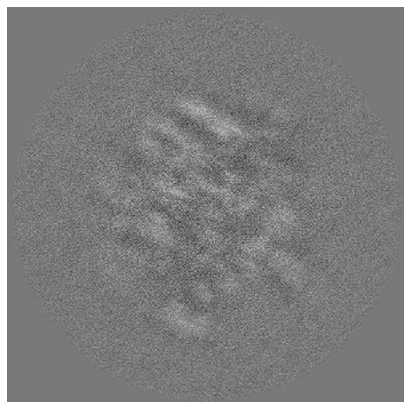


Y Index: 224

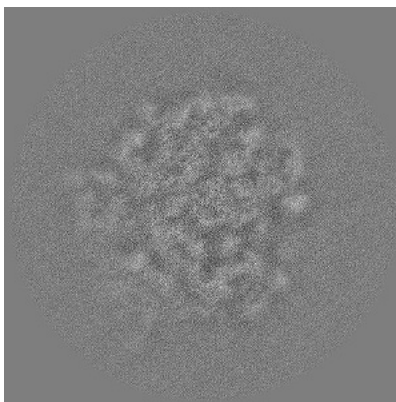


Z Index: 224

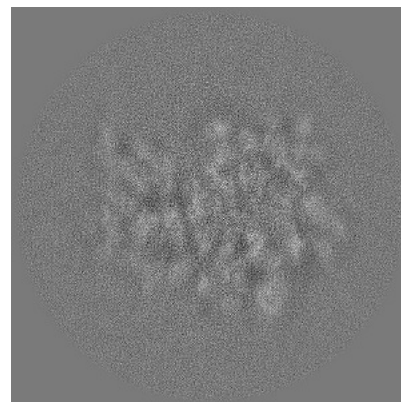
### 6.2.2 Raw map



X Index: 224



Y Index: 224

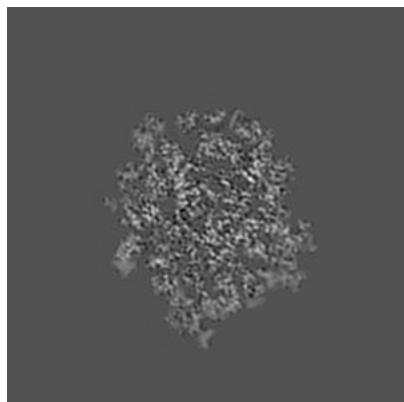


Z Index: 224

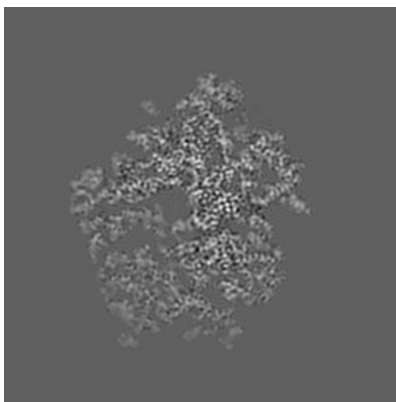
The images above show central slices of the map in three orthogonal directions.

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

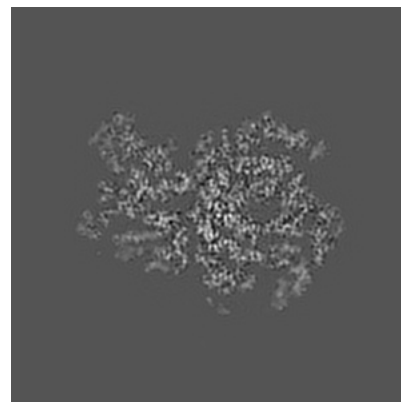
### 6.3.1 Primary map



X Index: 255

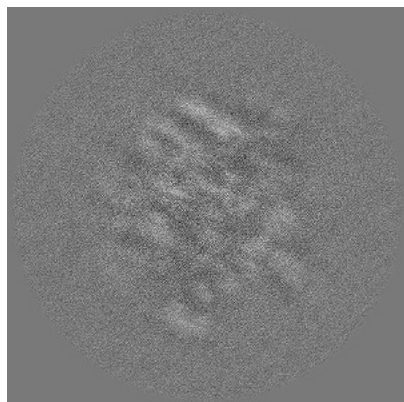


Y Index: 209

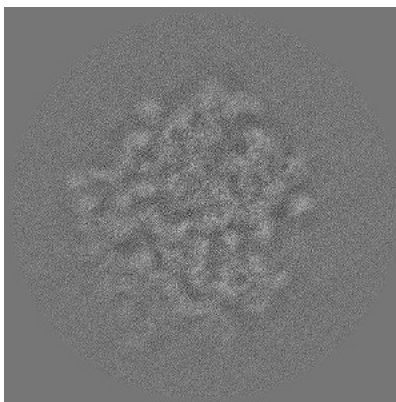


Z Index: 238

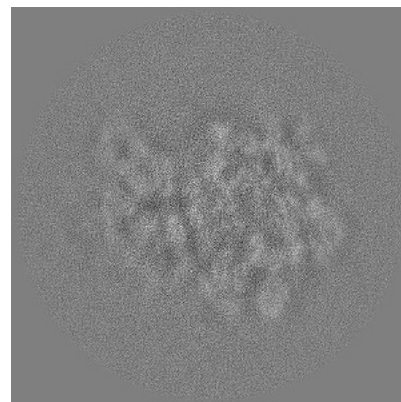
### 6.3.2 Raw map



X Index: 224



Y Index: 215



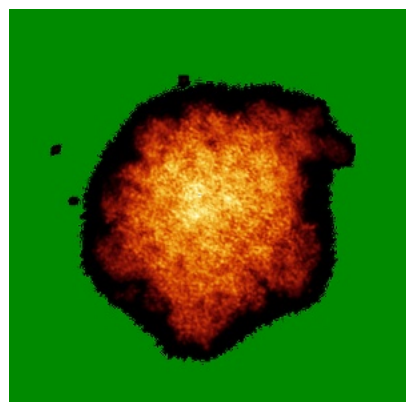
Z Index: 228

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

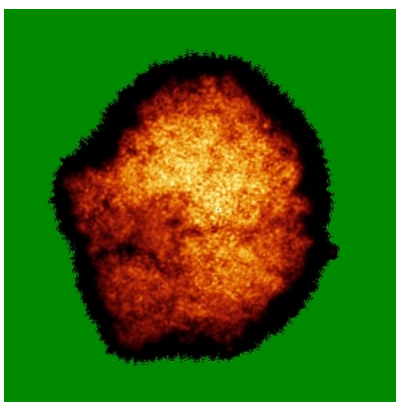


## 6.4 Orthogonal standard-deviation projections (False-color) [i](#)

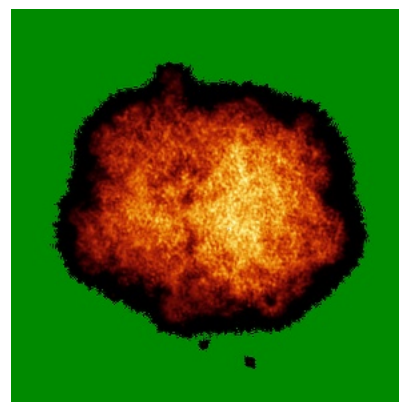
### 6.4.1 Primary map



X

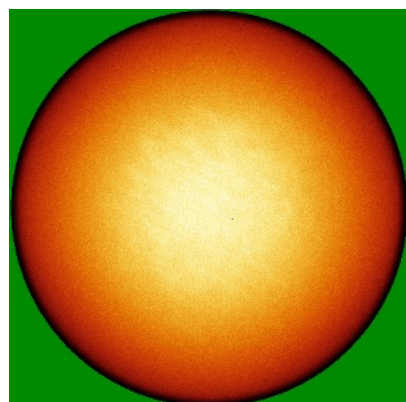


Y

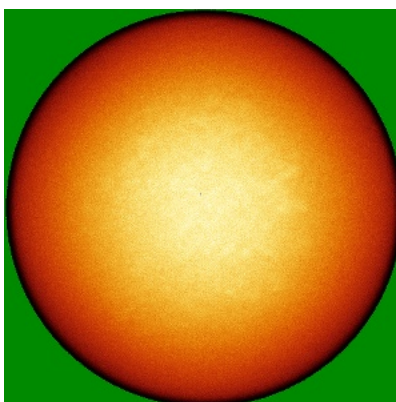


Z

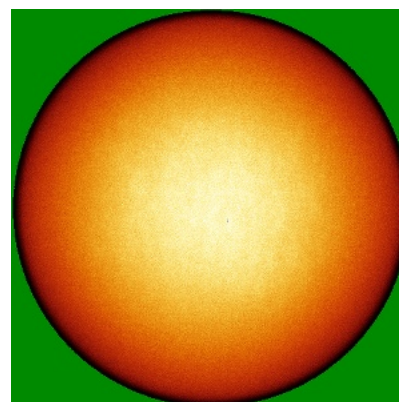
### 6.4.2 Raw map



X



Y

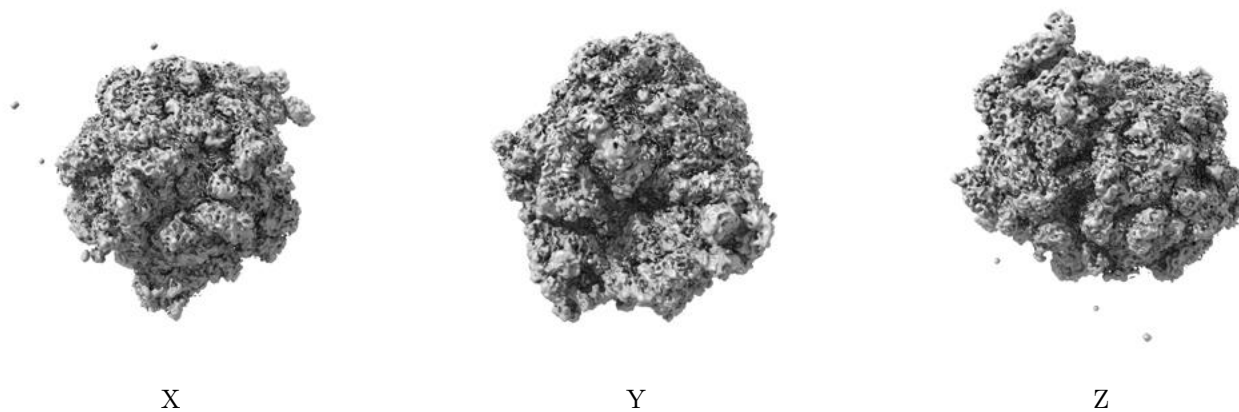


Z

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

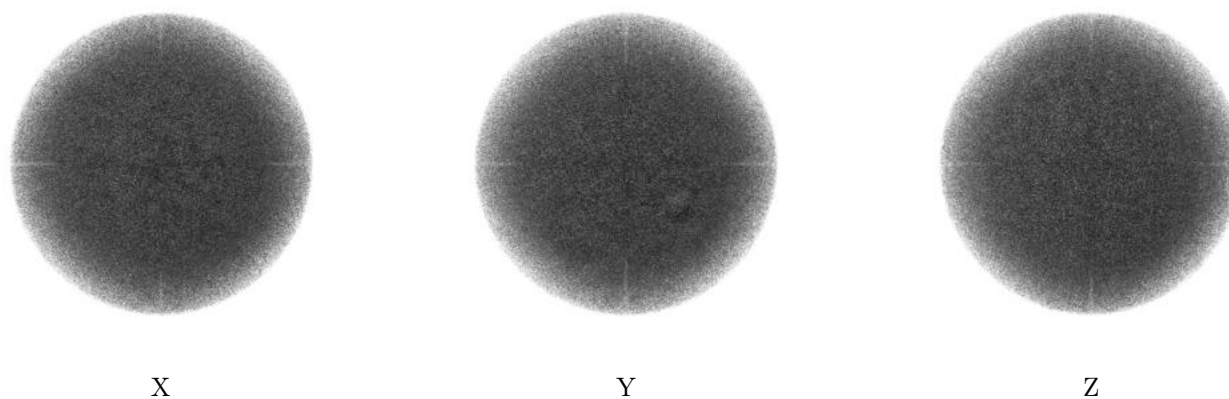
## 6.5 Orthogonal surface views [i](#)

### 6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

### 6.5.2 Raw map



These images show the 3D surface of the raw map. The raw map's contour level was selected so that its surface encloses the same volume as the primary map does at its recommended contour level.

## 6.6 Mask visualisation [i](#)

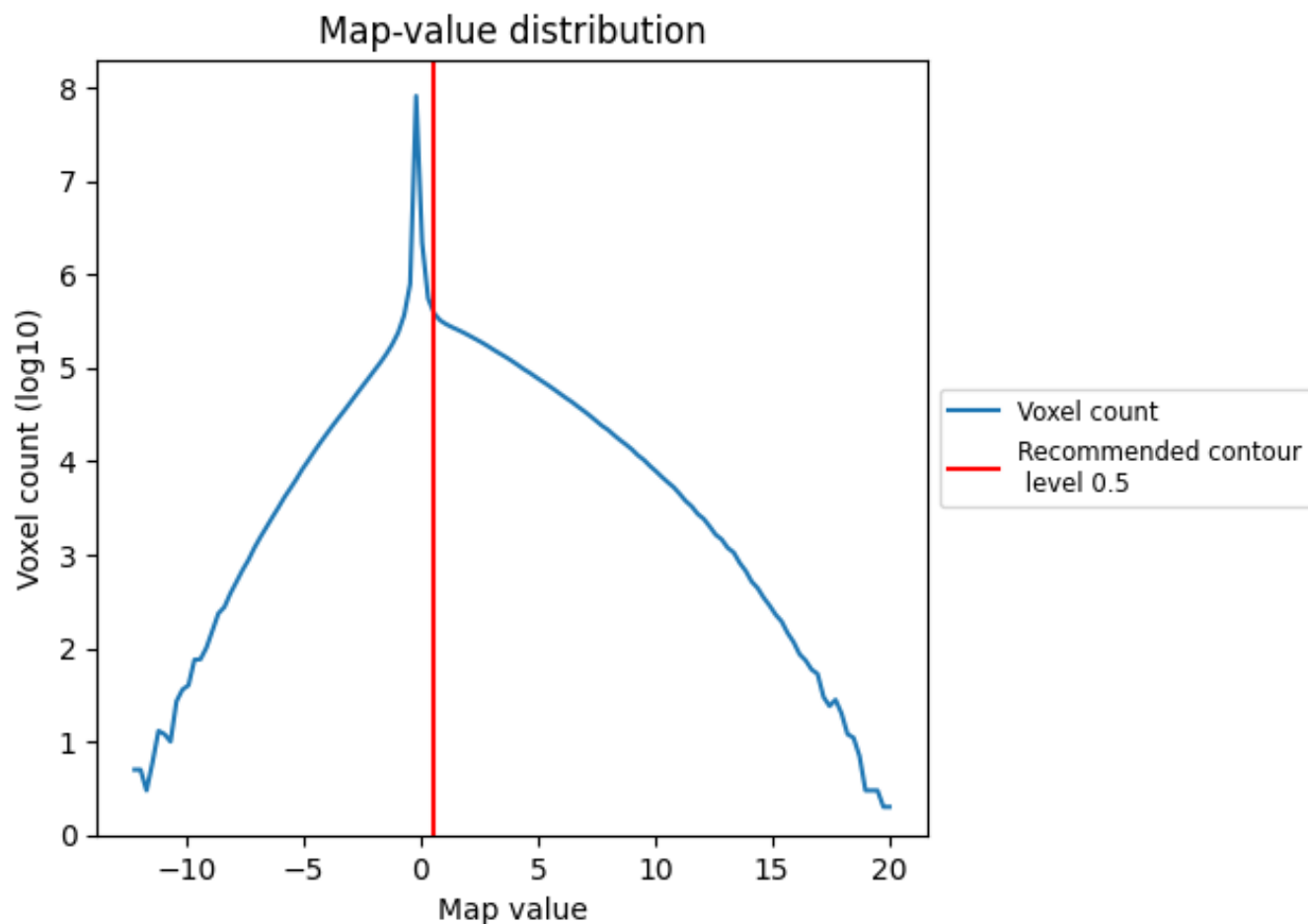
This section was not generated. No masks/segmentation were deposited.



## 7 Map analysis [i](#)

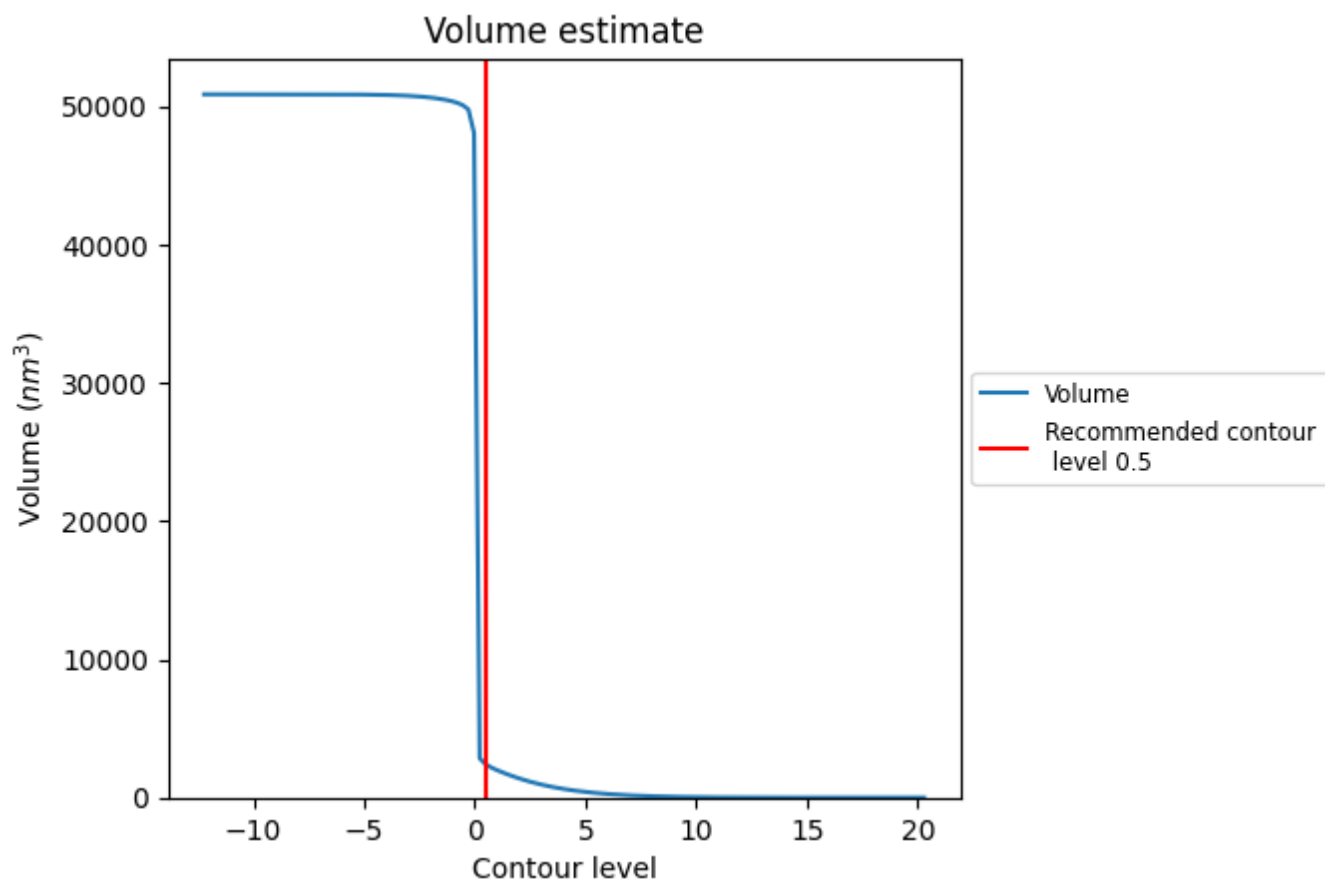
This section contains the results of statistical analysis of the map.

### 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.

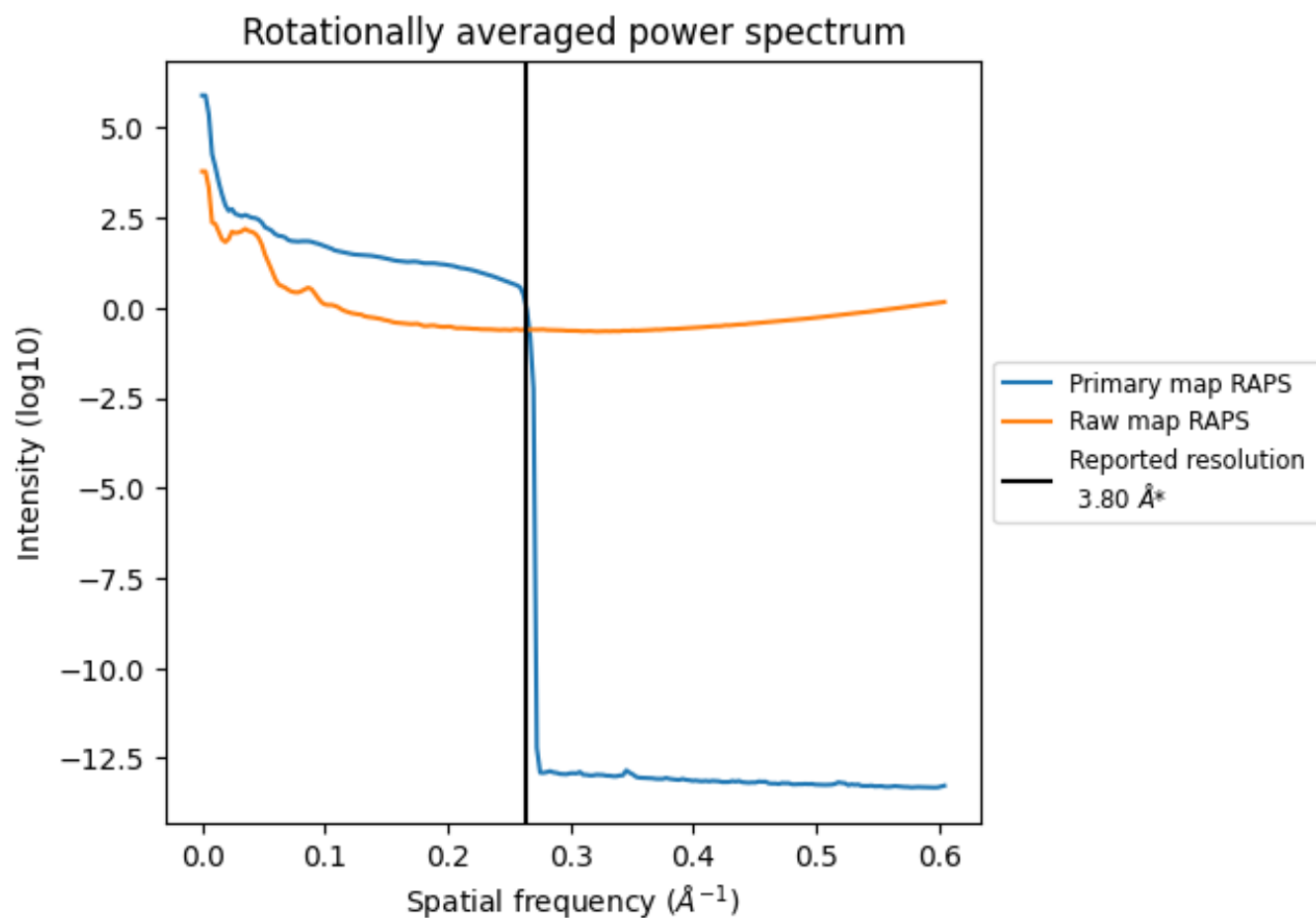
## 7.2 Volume estimate [i](#)



The volume at the recommended contour level is 2398 nm<sup>3</sup>; this corresponds to an approximate mass of 2166 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 ⓘ

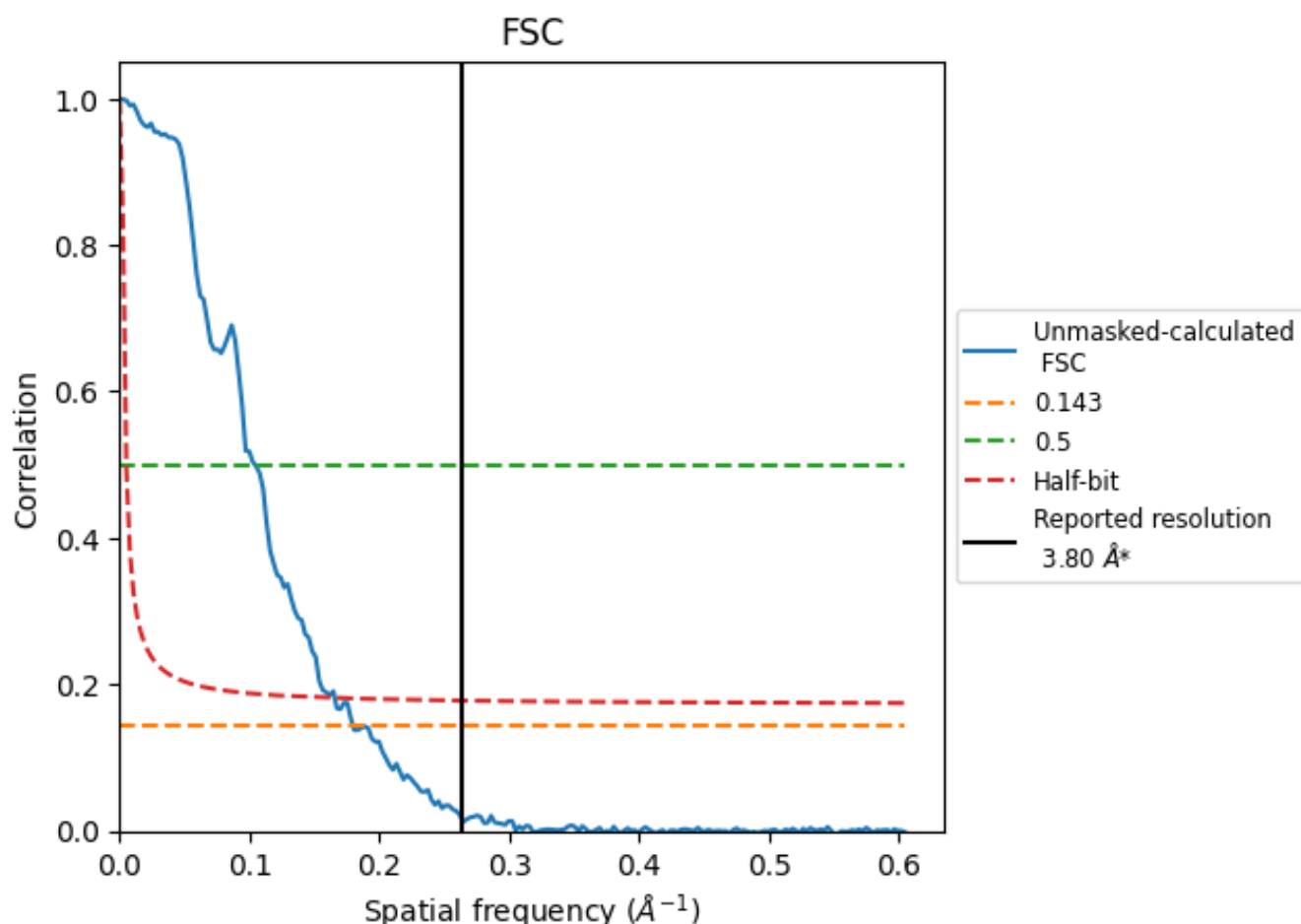


\*Reported resolution corresponds to spatial frequency of 0.263 Å<sup>-1</sup>

## 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 0.263  $\text{\AA}^{-1}$

## 8.2 Resolution estimates [i](#)

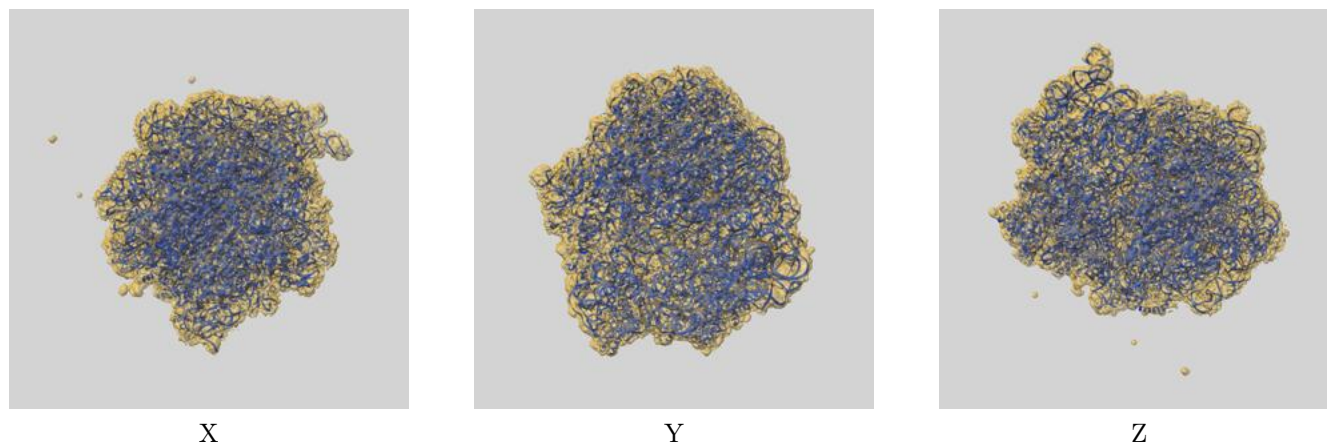
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	5.56	9.61	6.04

\*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 5.56 differs from the reported value 3.8 by more than 10 %

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

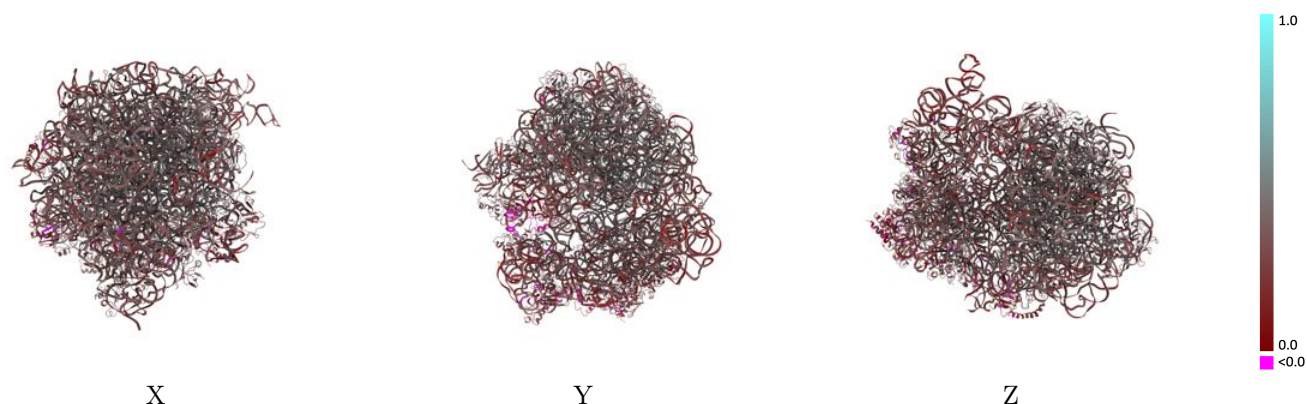
This section contains information regarding the fit between EMDB map EMD-25415 and PDB model 7SSW. Per-residue inclusion information can be found in section 3 on page 14.

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



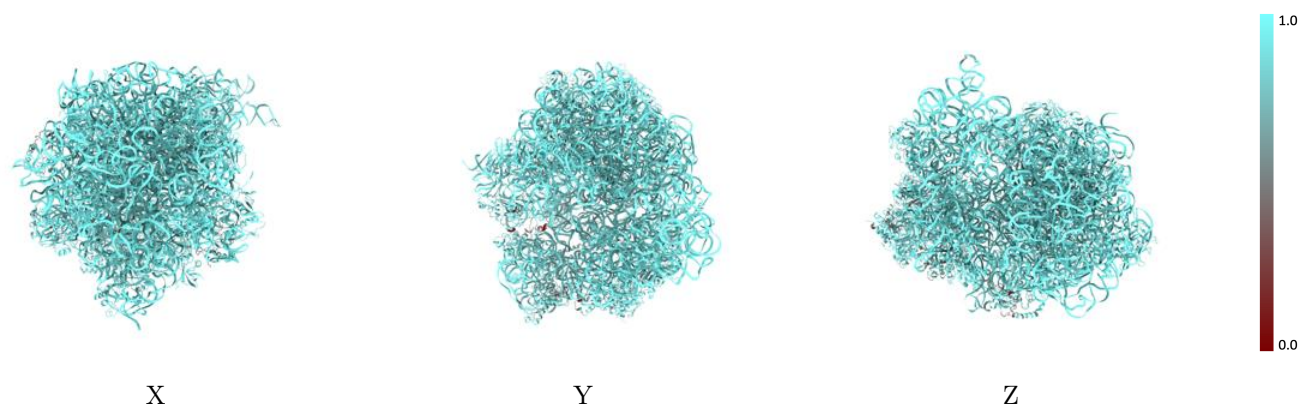
The images above show the 3D surface view of the map at the recommended contour level 0.5 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



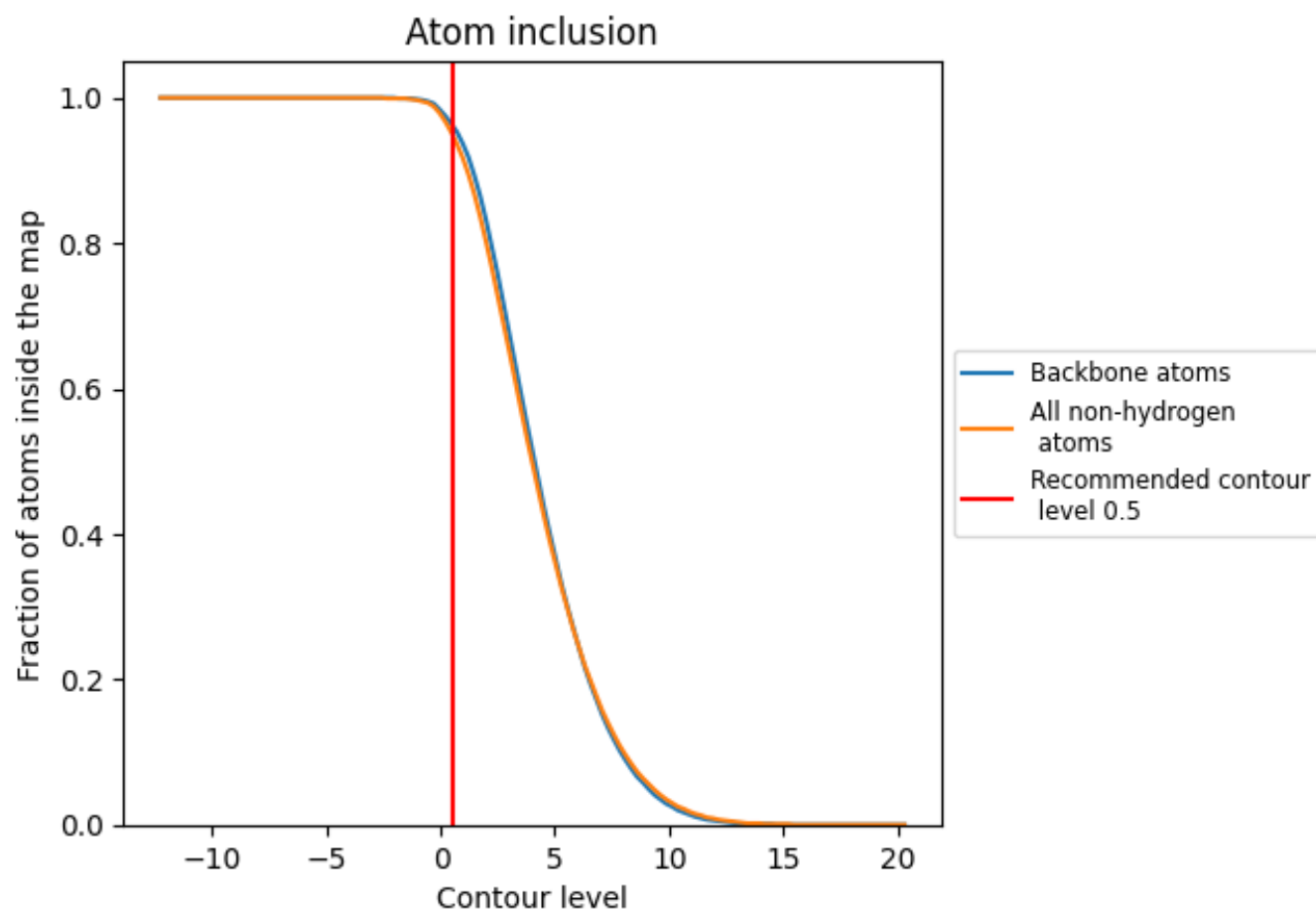
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.5).

## 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 (0.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9510	 0.3340
1	 0.9740	 0.3600
2	 0.9830	 0.3210
3	 0.9590	 0.2990
4	 0.8140	 0.1820
5	 0.9480	 0.2540
6	 0.9400	 0.2480
B	 0.9490	 0.4100
C	 0.8580	 0.3160
D	 0.9610	 0.4460
E	 0.9490	 0.4080
F	 0.9620	 0.4150
G	 0.7880	 0.1940
H	 0.7490	 0.2190
I	 0.9220	 0.2890
J	 0.9520	 0.3480
K	 0.9510	 0.3120
L	 0.8070	 0.2400
M	 0.9250	 0.3430
N	 0.8840	 0.2610
O	 0.8320	 0.2450
P	 0.9600	 0.3360
Q	 0.9250	 0.3340
R	 0.8740	 0.2500
S	 0.9250	 0.2820
T	 0.9590	 0.3580
U	 0.9390	 0.3280
V	 0.9180	 0.3250
W	 0.9670	 0.3470
X	 0.9230	 0.2950
Y	 0.9520	 0.3280
Z	 0.8820	 0.2900
a	 0.8750	 0.2070
b	 0.9600	 0.4350
c	 0.9660	 0.4080



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Chain	Atom inclusion	Q-score
d	 0.9430	 0.3930
e	 0.9180	 0.2780
f	 0.9550	 0.3190
g	 0.7000	 0.2240
i	 0.6610	 0.1890
j	 0.9680	 0.4160
k	 0.9570	 0.4030
l	 0.9510	 0.4070
m	 0.9560	 0.3900
n	 0.9640	 0.4230
o	 0.9690	 0.3580
p	 0.9620	 0.4060
q	 0.9570	 0.4060
r	 0.9570	 0.3720
s	 0.9510	 0.3980
t	 0.9490	 0.4030
u	 0.9520	 0.3620
v	 0.9610	 0.3370
w	 0.9480	 0.4200
x	 0.9480	 0.4110
y	 0.9720	 0.3610
z	 0.9540	 0.3900