



wwPDB EM Validation Summary Report ⓘ

Sep 29, 2024 – 03:40 AM EDT

PDB ID : 7ST2
EMDB ID : EMD-25418
Title : Post translocation, non-rotated 70S ribosome with EF-G dissociated (Structure VII)
Authors : Carbone, C.E.; Korostelev, A.A.
Deposited on : 2021-11-11
Resolution : 2.90 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

A user guide is available at

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

The types of validation reports are described at

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

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

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

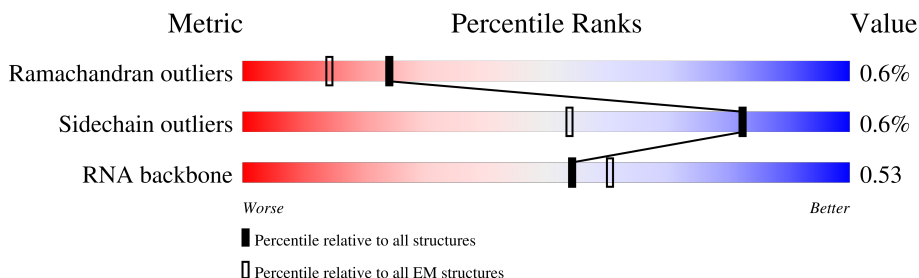
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 2.90 Å.

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



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

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

Mol	Chain	Length	Quality of chain
1	3	1539	84% 16% .
2	1	2903	81% 17% .
3	2	120	82% 13% .
4	6	77	75% 69% 29% .
5	b	271	99% .
6	c	209	99% .
7	d	201	100%
8	e	177	98% ..

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Mol	Chain	Length	Quality of chain
9	f	176	100%
10	g	149	44% 98% ..
11	a	234	29% 57% 43%
12	h	131	63% 95% . .
13	i	142	32% 96% . .
14	j	142	100%
15	k	122	97% .
16	l	143	99% ..
17	m	136	99% ..
18	n	120	98% .
19	o	116	99% .
20	p	114	99% .
21	q	117	100%
22	r	103	98% .
23	s	110	95% 5%
24	t	93	100%
25	u	102	99% .
26	v	94	99% .
27	w	75	99% .
28	x	77	100%
29	y	63	95% ..
30	z	58	100%
31	A	66	98% .
32	B	56	96% .
33	C	50	100%

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Mol	Chain	Length	Quality of chain
34	D	46	100%
35	E	64	97%
36	F	38	97%
37	4	35	31% 17% 6% 46%
38	5	77	71% 27%
39	G	225	93%
40	H	206	100%
41	I	205	98%
42	J	157	97%
43	K	100	99%
44	L	151	100%
45	M	129	100%
46	N	127	100%
47	O	98	97%
48	P	116	97%
49	Q	123	99%
50	R	114	98%
51	S	100	98%
52	T	88	98%
53	U	82	100%
54	V	80	98%
55	W	65	97%
56	X	79	100%
57	Y	85	100%
58	Z	65	88% 9%

2 Entry composition [i](#)

There are 58 unique types of molecules in this entry. The entry contains 149087 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
			1026	645	186	193	2		

- Molecule 12 is a protein called 50S ribosomal protein L10.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	h	131	Total	C	N	O	S	0	0
			989	625	175	184	5		

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
31	A	66	Total	C	N	O	S	0	0
			523	323	99	95	6		

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

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

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

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

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

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

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

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

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

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

- Molecule 37 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	4	19	Total	C	N	O	P	0	0
			416	186	85	126	19		

- Molecule 38 is a RNA chain called tRNA Pro.

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

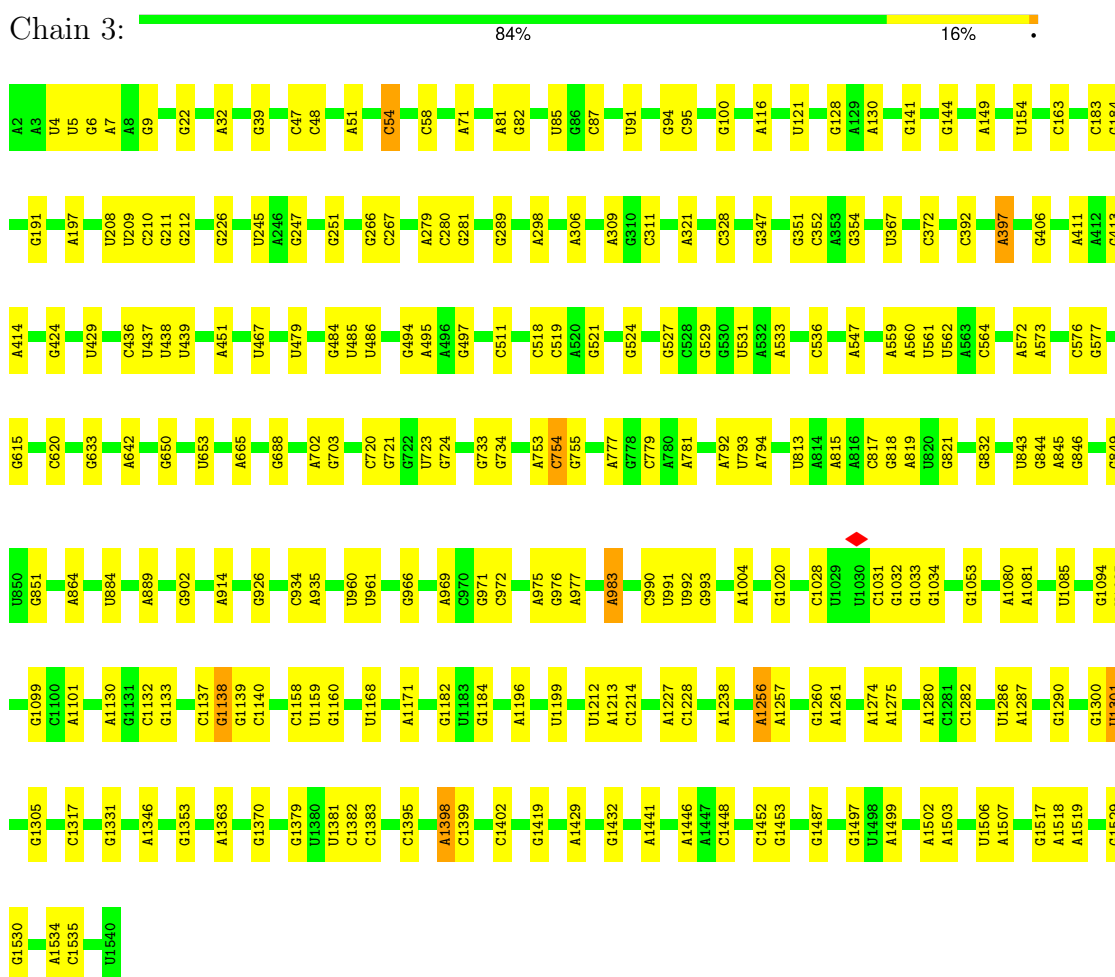
- Molecule 58 is a protein called 30S ribosomal protein S21.

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

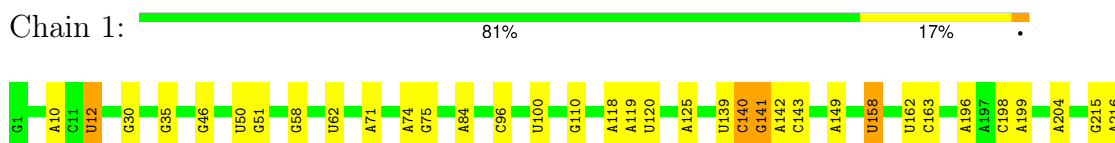
3 Residue-property plots

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




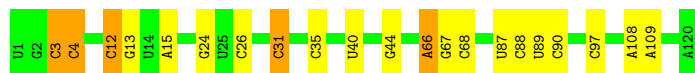
• Molecule 2: 23S rRNA




G2867	U2809	U2402	U2189	A2062	U1716	A1508	A1275	A1089	A983	A782	U546	U387	A219
A2868	U2613	C2403	U2192	G2069	U1729	A1515	G1300	A1090	A984	A783	A547	U395	G220
C2870	U2615	A2406	U2192	U1915	C1730	A1522	A1301	G1091	G989	G784	G548	G396	A221
U2871	U2629	A2407	A2198	C1920	G1738	U1523	U1313	U1101	C989	A788	U562	U403	A222
A2872	G2630	U2423	U2203	A1927	A1744	G1524	C1314	A1103	C995	A789	A563	A404	C225
A2873	C2646	A2430	G2204	A1928	A1757	U1532	C1345	C1102	A996	A800	U406	U405	C228
C2880	A2211	G2100	G1930	G1929	U1758	C1533	C1348	C1104	U999	G805	G411	U406	C229
U2884	U2441	G2110	A1936	U1944	C1764	U1534	U1348	A1112	U1004	C812	U573	A412	G230
A2887	G2445	U2111	A1937	U1944	A1773	C1536	U1352	U1130	G1003	A819	A575	G424	A241
U2891	A2448	G2112	A1938	U1939	A1774	G1537	U1352	G1131	G1005	U827	A603	A443	G248
C2902	G2470	G2116	U1939	U1943	U1775	U1554	A1359	A1132	U1012	U828	A614	A457	G252
U2903	U2474	A2117	U1944	U1944	G1776	C1555	A1365	A1134	C1013	A829	U615	A255	A255
A2726	C2475	G2118	U1955	U1955	A1780	C1557	G1368	G1139	A1020	G830	G622	U464	A265
C2715	A2476	A2119	U1966	U1966	U1781	C1558	C1376	A1142	A1021	A845	U846	G465	G266
C2716	C2480	G2123	C1967	C1967	U1782	U1559	U1379	A1155	G1023	U847	A627	G467	G266
A2732	C2283	G2128	A1970	U1971	A1786	C1566	U1383	C1172	G1025	G858	C634	G475	C275
A2733	A2287	C2129	U1971	U1971	A1786	A1569	A1383	U1173	G1026	G859	A637	G476	C277
G2744	A2288	U2130	G1972	U1972	C1800	U1578	A1395	U1174	U1033	C281	A477	A478	C281
A2748	A2297	U2131	G1980	U1981	A1801	U1584	C1414	U1175	A1040	A866	C645	A479	C281
A2764	U2305	G2132	A1981	U1991	A1808	U1584	U1415	U1176	A1046	G869	U646	A480	U284
A2765	A2309	U2137	U1991	U1992	C1816	A1608	G1416	C1177	G1047	A878	A654	G481	G285
A2766	C2313	G2141	U1993	U1993	A1819	A1614	A1419	G1179	G1059	U887	A655	C490	A294
A2778	G2325	C2145	C1997	C1997	C1822	G1627	G1421	U1180	U1061	U887	G656	G491	A294
G2791	A2326	C2146	A2020	A2020	A1829	A1634	A1427	U1186	G1062	G891	A670	G500	A311
C2794	A2327	A2147	C2021	C2021	U1847	C1639	C1428	A1204	G1063	A896	A685	A501	A322
U2797	G2331	G2148	U2022	U2022	A1848	U1647	A1434	G1206	C1064	C897	U686	A505	C323
U2798	C2332	U2149	C2023	C2023	G1857	U1648	C1437	C1211	U1065	G907	G695	A508	G329
U2799	A2333	A2154	A2030	A2030	C1870	G1649	G1452	G1212	A1067	A910	U714	C510	A330
A2800	U2334	G2157	G2032	G2032	G1873	A1654	C1454	C1221	A1069	C915	A730	U611	C334
G2808	A2336	C2160	A2033	A2033	U1880	A1669	U1458	G1236	C1072	U932	C737	C517	C345
A2809	G2345	G2161	C2043	C2043	G1884	A1672	C1461	A1247	G1073	A941	C747	A528	A345
U2818	C2350	G2162	G2049	G2049	U1901	G1673	G1478	G1248	C1075	C946	A752	A529	A346
G2819	C2354	C2163	A2052	A2052	C1902	G1674	G1482	A1253	C1076	A764	C765	A532	A346
A2820	C2361	U2166	C2055	C2055	G1903	C1675	G1490	U1255	U1077	C961	A764	A532	A371
A2823	U2172	A2173	G2060	G2060	U1906	C1694	G1491	G1256	U1078	A973	C765	A532	G372
U2833	C2174	C2174	A2060	A2060	G1906	A1698	G1491	A1265	A1083	A973	G775	A544	C383
G2834	C2178	C2178	G2061	G2061	G1906	G1715	A1504	A1272	A1086	A975	G775	U545	G386
A2835	C2179	C2179											

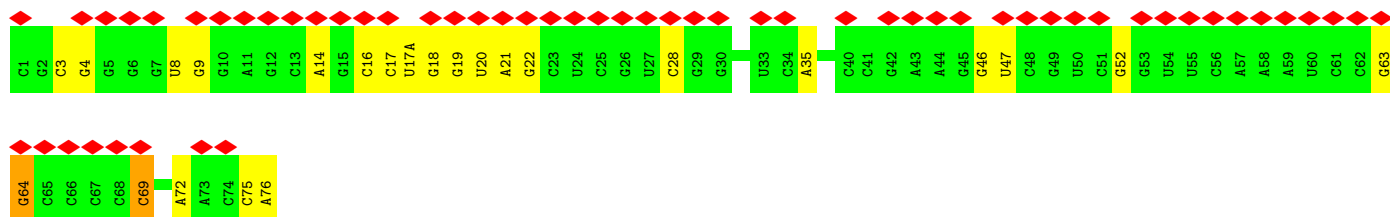
- Molecule 3: 5S rRNA

Chain 2:  82% 13% .



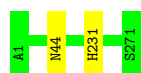
- Molecule 4: tRNA fMet

Chain 6:  75% 69% 29% .



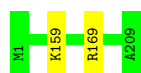
- Molecule 5: 50S ribosomal protein L2

Chain b:  99% .



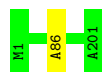
- Molecule 6: 50S ribosomal protein L3

Chain c:  99% .



- Molecule 7: 50S ribosomal protein L4

Chain d:  100% .



- Molecule 8: 50S ribosomal protein L5

Chain e:  98% ..



- Molecule 9: 50S ribosomal protein L6

Chain f:  100% .

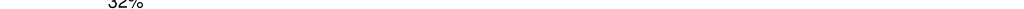
- Molecule 10: 50S ribosomal protein L9

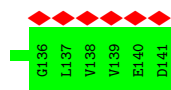
[illegible][illegible]

Chain h:

63%

95%

Chain i: 



- Molecule 14: 50S ribosomal protein L13

Chain j: 100%

There are no outlier residues recorded for this chain.

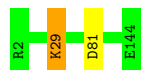
- Molecule 15: 50S ribosomal protein L14

Chain k: 97%



- Molecule 16: 50S ribosomal protein L15

Chain l: 99%



- Molecule 17: 50S ribosomal protein L16

Chain m: 99%



- Molecule 18: 50S ribosomal protein L17

Chain n: 98%



- Molecule 19: 50S ribosomal protein L18

Chain o: 99%



- Molecule 20: 50S ribosomal protein L19

Chain p: 99%



- Molecule 21: 50S ribosomal protein L20

Chain q:  100%

There are no outlier residues recorded for this chain.

- Molecule 22: 50S ribosomal protein L21

Chain r:  98%



- Molecule 23: 50S ribosomal protein L22

Chain s:  95%



- Molecule 24: 50S ribosomal protein L23

Chain t:  100%



- Molecule 25: 50S ribosomal protein L24

Chain u:  99%



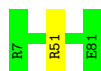
- Molecule 26: 50S ribosomal protein L25

Chain v:  99%



- Molecule 27: 50S ribosomal protein L27

Chain w:  99%



- Molecule 28: 50S ribosomal protein L28

Chain x:  100%

There are no outlier residues recorded for this chain.

- Molecule 29: 50S ribosomal protein L29

Chain y:  95%



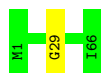
- Molecule 30: 50S ribosomal protein L30

Chain z:  100%

There are no outlier residues recorded for this chain.

- Molecule 31: 50S ribosomal protein L31

Chain A:  98%



- Molecule 32: 50S ribosomal protein L32

Chain B:  96%



- Molecule 33: 50S ribosomal protein L33

Chain C:  100%

There are no outlier residues recorded for this chain.

- Molecule 34: 50S ribosomal protein L34

Chain D:  100%

There are no outlier residues recorded for this chain.

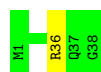
- Molecule 35: 50S ribosomal protein L35

Chain E:  97%



- Molecule 36: 50S ribosomal protein L36

Chain F: 97% .



- Molecule 37: mRNA

Chain 4: 31% 17% 6% 46%



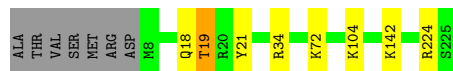
- Molecule 38: tRNA Pro

Chain 5: 71% 27% .



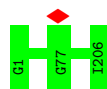
- Molecule 39: 30S ribosomal protein S2

Chain G: 93% . .



- Molecule 40: 30S ribosomal protein S3

Chain H: 100%



- Molecule 41: 30S ribosomal protein S4

Chain I: 98% .



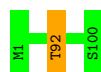
- Molecule 42: 30S ribosomal protein S5

Chain J: 97% .



- Molecule 43: 30S ribosomal protein S6

Chain K: 99%



- Molecule 44: 30S ribosomal protein S7

Chain L: 100%

There are no outlier residues recorded for this chain.

- Molecule 45: 30S ribosomal protein S8

Chain M: 100%

There are no outlier residues recorded for this chain.

- Molecule 46: 30S ribosomal protein S9

Chain N: 100%

There are no outlier residues recorded for this chain.

- Molecule 47: 30S ribosomal protein S10

Chain O: 97%



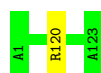
- Molecule 48: 30S ribosomal protein S11

Chain P: 97%



- Molecule 49: 30S ribosomal protein S12

Chain Q: 99%



- Molecule 50: 30S ribosomal protein S13

Chain R:  98% .



- Molecule 51: 30S ribosomal protein S14

Chain S:  98% .



- Molecule 52: 30S ribosomal protein S15

Chain T:  98% .



- Molecule 53: 30S ribosomal protein S16

Chain U:  100% .



- Molecule 54: 30S ribosomal protein S17

Chain V:  98% .



- Molecule 55: 30S ribosomal protein S18

Chain W:  97% .



- Molecule 56: 30S ribosomal protein S19

Chain X:  100%


There are no outlier residues recorded for this chain.

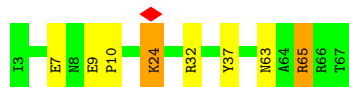
- Molecule 57: 30S ribosomal protein S20

Chain Y:  100%

There are no outlier residues recorded for this chain.

- Molecule 58: 30S ribosomal protein S21

Chain Z: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	55457	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TALOS ARCTICA	Depositor
Voltage (kV)	200	Depositor
Electron dose ($e^-/\text{\AA}^2$)	30.4	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	1500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	20.855	Depositor
Minimum map value	-7.489	Depositor
Average map value	0.009	Depositor
Map value standard deviation	1.005	Depositor
Recommended contour level	1.35	Depositor
Map size (Å)	389.76, 389.76, 389.76	wwPDB
Map dimensions	448, 448, 448	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.87, 0.87, 0.87	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	1.23	1/36963 (0.0%)	0.99	51/57662 (0.1%)
2	1	1.34	19/69796 (0.0%)	1.02	141/108888 (0.1%)
3	2	0.99	0/2872	1.02	11/4479 (0.2%)
4	6	0.41	0/1832	0.93	3/2855 (0.1%)
5	b	0.66	0/2122	0.63	1/2852 (0.0%)
6	c	0.61	0/1586	0.59	0/2134
7	d	0.47	0/1571	0.58	0/2113
8	e	0.45	0/1435	0.59	0/1926
9	f	0.41	0/1343	0.53	0/1816
10	g	0.35	0/1122	0.67	0/1515
11	a	0.29	0/1033	0.62	0/1387
12	h	0.34	0/1002	0.76	1/1350 (0.1%)
13	i	0.31	0/1046	0.63	1/1410 (0.1%)
14	j	0.55	0/1152	0.53	0/1551
15	k	0.61	0/948	0.66	0/1268
16	l	0.54	0/1054	0.63	1/1403 (0.1%)
17	m	0.59	0/1093	0.59	1/1460 (0.1%)
18	n	0.55	0/974	0.62	0/1301
19	o	0.44	0/902	0.50	0/1209
20	p	0.61	0/929	0.62	1/1242 (0.1%)
21	q	0.64	0/960	0.53	0/1278
22	r	0.53	0/829	0.59	0/1107
23	s	0.53	0/864	0.62	1/1156 (0.1%)
24	t	0.48	0/745	0.54	0/994
25	u	0.45	0/788	0.62	0/1051
26	v	0.49	0/766	0.53	0/1025
27	w	0.60	0/582	0.56	0/769
28	x	0.56	0/635	0.56	0/848
29	y	0.37	0/510	0.63	1/677 (0.1%)
30	z	0.48	0/453	0.53	0/605
31	A	0.37	0/532	0.58	0/709
32	B	0.53	0/450	0.59	0/599
33	C	0.37	0/417	0.52	0/554
34	D	0.59	0/380	0.58	0/498

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
35	E	0.58	0/513	0.59	0/676
36	F	0.56	0/303	0.59	0/397
37	4	0.81	0/468	1.47	8/729 (1.1%)
38	5	0.96	0/1840	1.06	7/2868 (0.2%)
39	G	0.42	0/1736	0.63	0/2338
40	H	0.46	0/1652	0.55	0/2225
41	I	0.46	0/1665	0.63	2/2227 (0.1%)
42	J	0.55	0/1170	0.62	0/1573
43	K	0.44	0/836	0.62	1/1128 (0.1%)
44	L	0.41	0/1196	0.58	0/1602
45	M	0.52	0/989	0.60	0/1326
46	N	0.44	0/1034	0.59	0/1375
47	O	0.45	0/797	0.67	0/1077
48	P	0.52	0/886	0.61	0/1195
49	Q	0.63	0/969	0.69	0/1300
50	R	0.45	0/893	0.62	1/1193 (0.1%)
51	S	0.46	0/817	0.54	0/1088
52	T	0.46	0/722	0.57	0/964
53	U	0.51	0/659	0.59	0/884
54	V	0.51	0/658	0.57	0/881
55	W	0.51	0/545	0.63	0/731
56	X	0.44	0/653	0.59	0/877
57	Y	0.40	0/671	0.49	0/888
58	Z	0.43	0/551	0.87	1/728 (0.1%)
All	All	1.10	20/161909 (0.0%)	0.92	234/241961 (0.1%)

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	l	0	1
6	c	0	1
8	e	0	2
10	g	0	2
12	h	0	4
15	k	0	2
18	n	0	1
22	r	0	1
23	s	0	1
29	y	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
31	A	0	1
35	E	0	1
36	F	0	1
39	G	0	2
41	I	0	2
42	J	0	2
47	O	0	1
48	P	0	2
50	R	0	1
51	S	0	1
54	V	0	2
55	W	0	1
58	Z	0	1
All	All	0	34

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	1	1936	A	N9-C4	-7.70	1.33	1.37
2	1	528	A	N9-C4	-7.28	1.33	1.37
2	1	984	A	N9-C4	-7.08	1.33	1.37
2	1	783	A	N9-C4	-6.98	1.33	1.37
2	1	1784	A	N7-C5	-6.10	1.35	1.39

The worst 5 of 234 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
37	4	13	A	O4'-C1'-N9	15.19	120.35	108.20
1	3	1301	U	C2-N1-C1'	10.97	130.86	117.70
1	3	1301	U	N1-C2-O2	10.82	130.37	122.80
2	1	62	U	N1-C2-O2	10.43	130.10	122.80
2	1	62	U	C2-N1-C1'	10.22	129.96	117.70

There are no chirality outliers.

5 of 34 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	1	2166	U	Sidechain
6	c	159	LYS	Peptide
8	e	174	PHE	Peptide
8	e	175	PRO	Peptide

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Mol	Chain	Res	Type	Group
10	g	8	LYS	Peptide

5.2 Too-close contacts [i](#)

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

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	b	269/271 (99%)	251 (93%)	18 (7%)	0	100	100
6	c	207/209 (99%)	190 (92%)	16 (8%)	1 (0%)	25	56
7	d	199/201 (99%)	181 (91%)	17 (8%)	1 (0%)	25	56
8	e	175/177 (99%)	158 (90%)	15 (9%)	2 (1%)	12	37
9	f	174/176 (99%)	160 (92%)	14 (8%)	0	100	100
10	g	147/149 (99%)	125 (85%)	20 (14%)	2 (1%)	9	31
11	a	130/234 (56%)	115 (88%)	15 (12%)	0	100	100
12	h	129/131 (98%)	95 (74%)	31 (24%)	3 (2%)	5	20
13	i	139/142 (98%)	119 (86%)	19 (14%)	1 (1%)	19	49
14	j	140/142 (99%)	132 (94%)	8 (6%)	0	100	100
15	k	120/122 (98%)	101 (84%)	18 (15%)	1 (1%)	16	45
16	l	141/143 (99%)	129 (92%)	11 (8%)	1 (1%)	19	49
17	m	134/136 (98%)	125 (93%)	7 (5%)	2 (2%)	8	29
18	n	118/120 (98%)	101 (86%)	15 (13%)	2 (2%)	7	27
19	o	114/116 (98%)	107 (94%)	7 (6%)	0	100	100
20	p	112/114 (98%)	107 (96%)	5 (4%)	0	100	100
21	q	115/117 (98%)	115 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
22	r	101/103 (98%)	90 (89%)	10 (10%)	1 (1%)	13	40
23	s	108/110 (98%)	100 (93%)	8 (7%)	0	100	100
24	t	91/93 (98%)	84 (92%)	7 (8%)	0	100	100
25	u	100/102 (98%)	87 (87%)	12 (12%)	1 (1%)	13	40
26	v	92/94 (98%)	89 (97%)	3 (3%)	0	100	100
27	w	73/75 (97%)	63 (86%)	10 (14%)	0	100	100
28	x	75/77 (97%)	71 (95%)	4 (5%)	0	100	100
29	y	61/63 (97%)	58 (95%)	2 (3%)	1 (2%)	8	28
30	z	56/58 (97%)	55 (98%)	1 (2%)	0	100	100
31	A	64/66 (97%)	57 (89%)	7 (11%)	0	100	100
32	B	54/56 (96%)	48 (89%)	4 (7%)	2 (4%)	2	11
33	C	48/50 (96%)	47 (98%)	1 (2%)	0	100	100
34	D	44/46 (96%)	42 (96%)	2 (4%)	0	100	100
35	E	62/64 (97%)	58 (94%)	3 (5%)	1 (2%)	8	28
36	F	36/38 (95%)	33 (92%)	3 (8%)	0	100	100
39	G	216/225 (96%)	193 (89%)	21 (10%)	2 (1%)	14	43
40	H	204/206 (99%)	190 (93%)	14 (7%)	0	100	100
41	I	203/205 (99%)	177 (87%)	26 (13%)	0	100	100
42	J	155/157 (99%)	136 (88%)	19 (12%)	0	100	100
43	K	98/100 (98%)	84 (86%)	13 (13%)	1 (1%)	13	40
44	L	149/151 (99%)	139 (93%)	10 (7%)	0	100	100
45	M	127/129 (98%)	119 (94%)	8 (6%)	0	100	100
46	N	125/127 (98%)	110 (88%)	15 (12%)	0	100	100
47	O	96/98 (98%)	81 (84%)	14 (15%)	1 (1%)	13	40
48	P	114/116 (98%)	105 (92%)	9 (8%)	0	100	100
49	Q	121/123 (98%)	100 (83%)	20 (16%)	1 (1%)	16	45
50	R	112/114 (98%)	97 (87%)	15 (13%)	0	100	100
51	S	98/100 (98%)	81 (83%)	17 (17%)	0	100	100
52	T	86/88 (98%)	78 (91%)	6 (7%)	2 (2%)	5	20
53	U	80/82 (98%)	74 (92%)	6 (8%)	0	100	100
54	V	78/80 (98%)	71 (91%)	7 (9%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
55	W	63/65 (97%)	56 (89%)	7 (11%)	0	100	100
56	X	77/79 (98%)	70 (91%)	7 (9%)	0	100	100
57	Y	83/85 (98%)	79 (95%)	4 (5%)	0	100	100
58	Z	63/65 (97%)	39 (62%)	19 (30%)	5 (8%)	1	2
All	All	5976/6190 (96%)	5372 (90%)	570 (10%)	34 (1%)	24	52

5 of 34 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
18	n	70	THR
8	e	175	PRO
8	e	176	PHE
10	g	9	VAL
16	l	29	LYS

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%)	215 (100%)	1 (0%)	86	96
6	c	164/164 (100%)	164 (100%)	0	100	100
7	d	165/165 (100%)	165 (100%)	0	100	100
8	e	148/148 (100%)	147 (99%)	1 (1%)	81	94
9	f	137/137 (100%)	137 (100%)	0	100	100
10	g	114/114 (100%)	114 (100%)	0	100	100
11	a	110/181 (61%)	109 (99%)	1 (1%)	75	92
12	h	100/100 (100%)	99 (99%)	1 (1%)	73	91
13	i	109/110 (99%)	106 (97%)	3 (3%)	38	73
14	j	116/116 (100%)	116 (100%)	0	100	100
15	k	103/103 (100%)	102 (99%)	1 (1%)	73	91
16	l	102/102 (100%)	101 (99%)	1 (1%)	73	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
17	m	109/109 (100%)	109 (100%)	0	100	100
18	n	100/100 (100%)	100 (100%)	0	100	100
19	o	86/86 (100%)	85 (99%)	1 (1%)	67	89
20	p	99/99 (100%)	99 (100%)	0	100	100
21	q	89/89 (100%)	89 (100%)	0	100	100
22	r	84/84 (100%)	84 (100%)	0	100	100
23	s	93/93 (100%)	90 (97%)	3 (3%)	34	69
24	t	80/80 (100%)	80 (100%)	0	100	100
25	u	83/83 (100%)	83 (100%)	0	100	100
26	v	78/78 (100%)	77 (99%)	1 (1%)	65	88
27	w	57/57 (100%)	56 (98%)	1 (2%)	54	82
28	x	67/67 (100%)	67 (100%)	0	100	100
29	y	55/55 (100%)	54 (98%)	1 (2%)	54	82
30	z	48/48 (100%)	48 (100%)	0	100	100
31	A	59/59 (100%)	59 (100%)	0	100	100
32	B	47/47 (100%)	47 (100%)	0	100	100
33	C	45/45 (100%)	45 (100%)	0	100	100
34	D	38/38 (100%)	38 (100%)	0	100	100
35	E	51/51 (100%)	51 (100%)	0	100	100
36	F	34/34 (100%)	34 (100%)	0	100	100
39	G	180/186 (97%)	175 (97%)	5 (3%)	38	73
40	H	170/170 (100%)	170 (100%)	0	100	100
41	I	172/172 (100%)	171 (99%)	1 (1%)	84	95
42	J	119/119 (100%)	117 (98%)	2 (2%)	56	83
43	K	87/87 (100%)	87 (100%)	0	100	100
44	L	124/124 (100%)	124 (100%)	0	100	100
45	M	104/104 (100%)	104 (100%)	0	100	100
46	N	105/105 (100%)	105 (100%)	0	100	100
47	O	86/86 (100%)	85 (99%)	1 (1%)	67	89
48	P	89/89 (100%)	88 (99%)	1 (1%)	70	90
49	Q	103/103 (100%)	103 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
50	R	92/92 (100%)	92 (100%)	0	100	100
51	S	83/83 (100%)	82 (99%)	1 (1%)	67	89
52	T	76/76 (100%)	76 (100%)	0	100	100
53	U	65/65 (100%)	65 (100%)	0	100	100
54	V	74/74 (100%)	74 (100%)	0	100	100
55	W	56/56 (100%)	55 (98%)	1 (2%)	54	82
56	X	70/70 (100%)	70 (100%)	0	100	100
57	Y	65/65 (100%)	65 (100%)	0	100	100
58	Z	55/55 (100%)	52 (94%)	3 (6%)	18	48
All	All	4961/5039 (98%)	4930 (99%)	31 (1%)	82	95

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
27	w	51	ARG
55	W	11	ARG
39	G	34	ARG
58	Z	32	ARG
47	O	30	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 64 such sidechains are listed below:

Mol	Chain	Res	Type
52	T	34	GLN
54	V	30	HIS
24	t	48	GLN
22	r	43	ASN
55	W	51	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	3	1538/1539 (99%)	234 (15%)	1 (0%)
2	1	2902/2903 (99%)	508 (17%)	11 (0%)
3	2	119/120 (99%)	17 (14%)	3 (2%)
37	4	18/35 (51%)	8 (44%)	2 (11%)
38	5	76/77 (98%)	19 (25%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
4	6	76/77 (98%)	23 (30%)	0
All	All	4729/4751 (99%)	809 (17%)	17 (0%)

5 of 809 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	3	4	U
1	3	5	U
1	3	6	G
1	3	7	A
1	3	9	G

5 of 17 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
3	2	88	C
37	4	13	A
2	1	1847	A
2	1	2326	C
2	1	2406	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

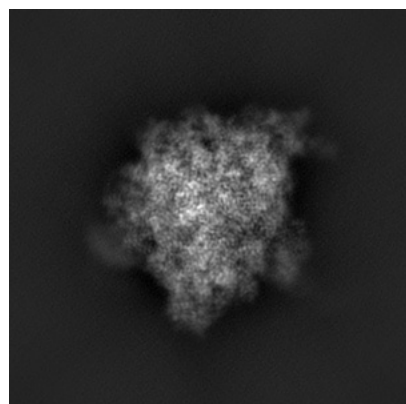
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-25418. These allow visual inspection of the internal detail of the map and identification of artifacts.

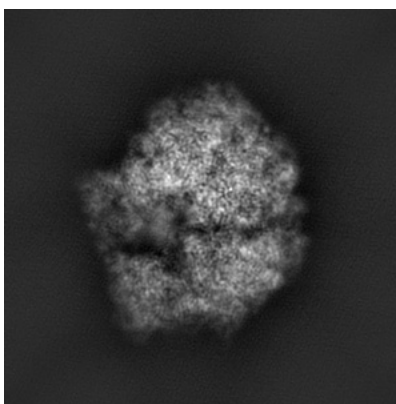
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

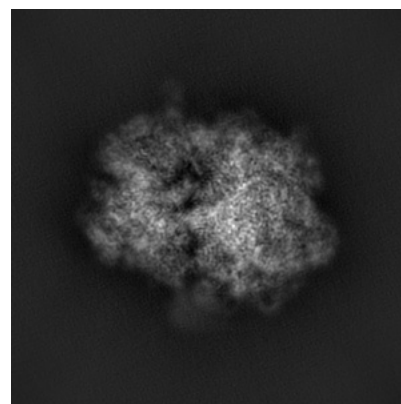
6.1.1 Primary map



X

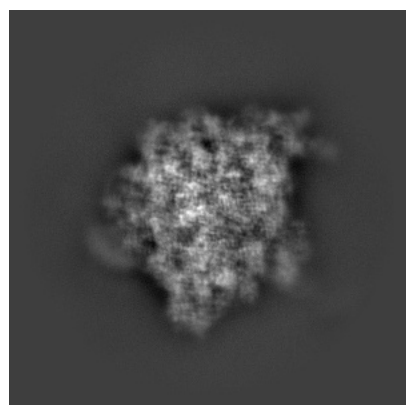


Y

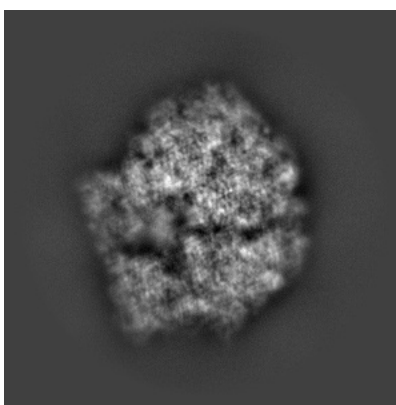


Z

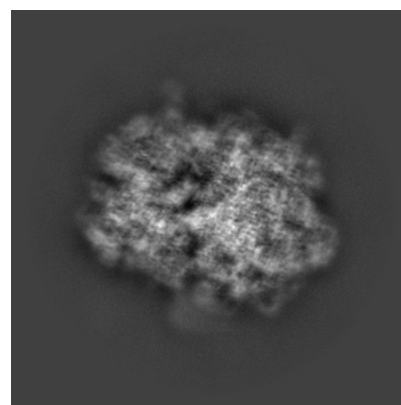
6.1.2 Raw map



X



Y

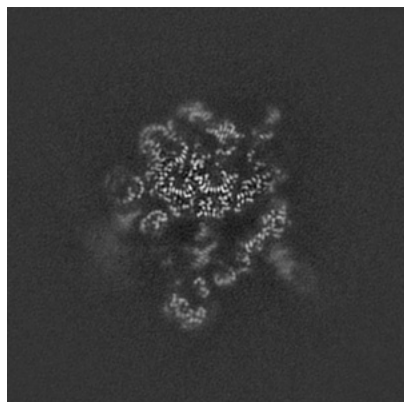


Z

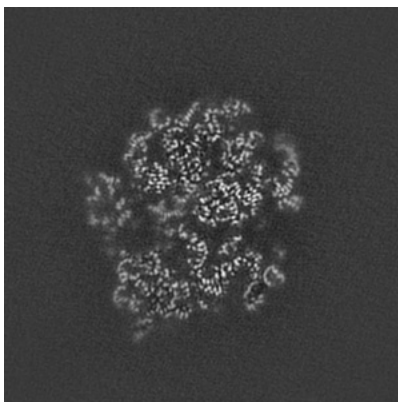
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

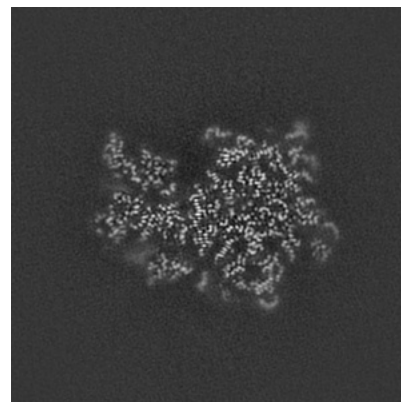
6.2.1 Primary map



X Index: 224

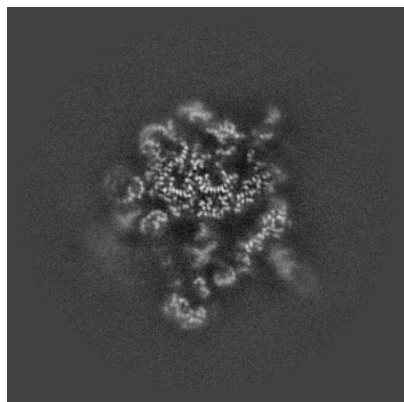


Y Index: 224

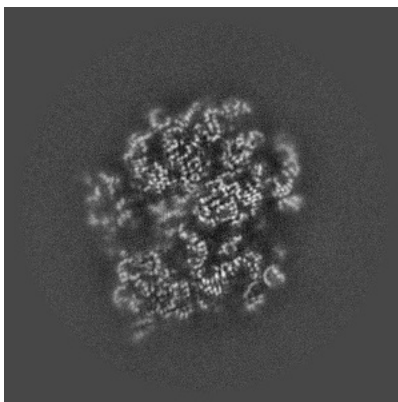


Z Index: 224

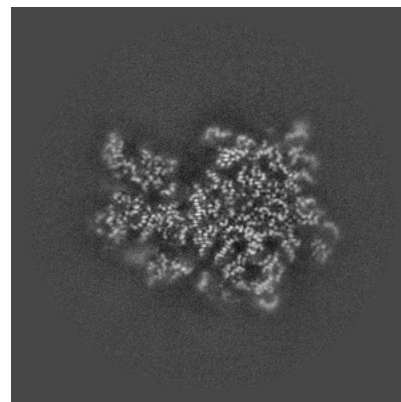
6.2.2 Raw map



X Index: 224



Y Index: 224

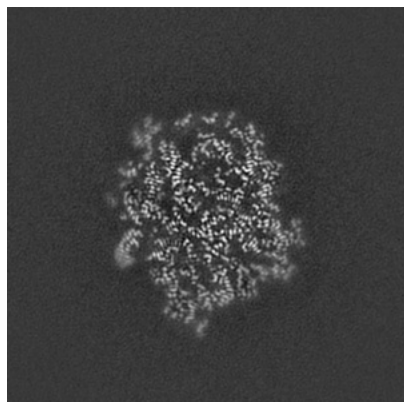


Z Index: 224

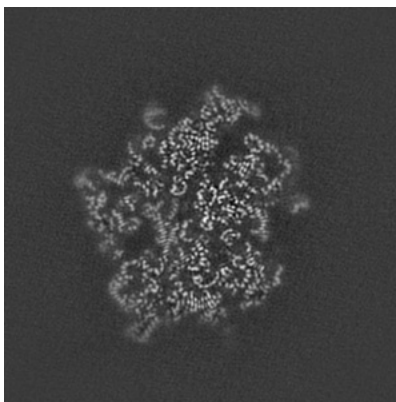
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

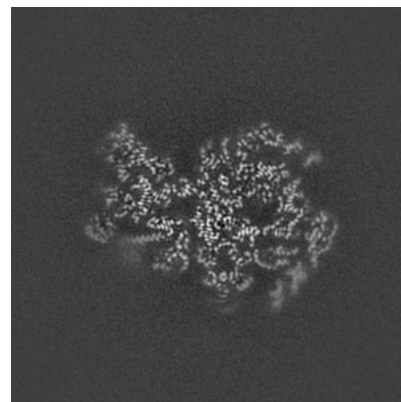
6.3.1 Primary map



X Index: 254

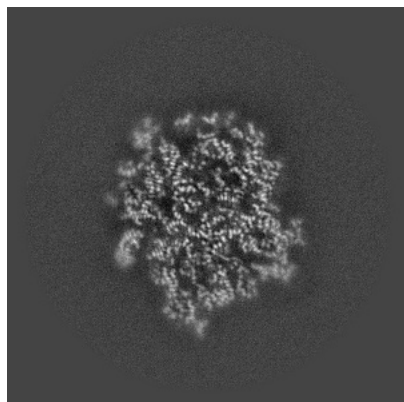


Y Index: 215

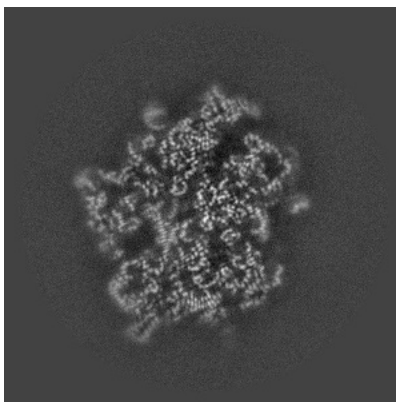


Z Index: 240

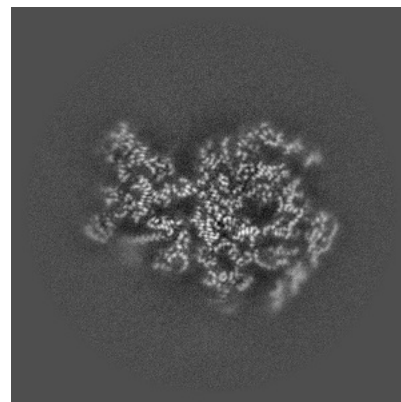
6.3.2 Raw map



X Index: 253



Y Index: 215

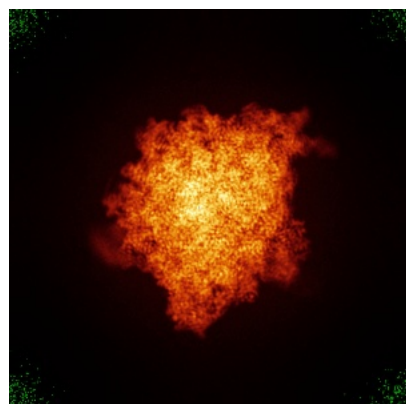


Z Index: 240

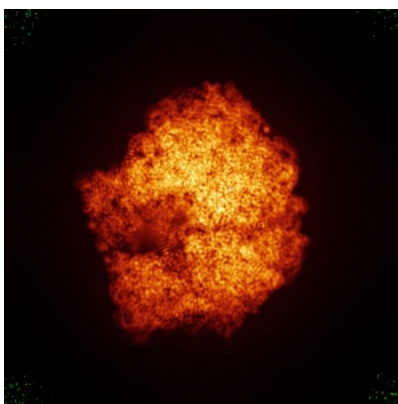
The images above show the largest variance slices of the map in three orthogonal directions.

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

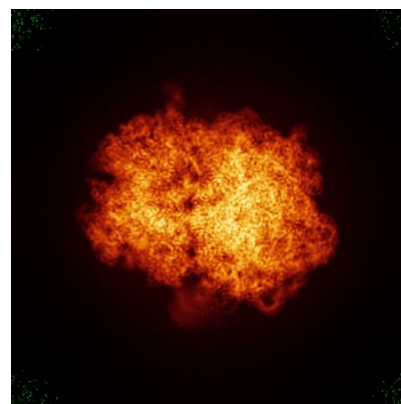
6.4.1 Primary map



X

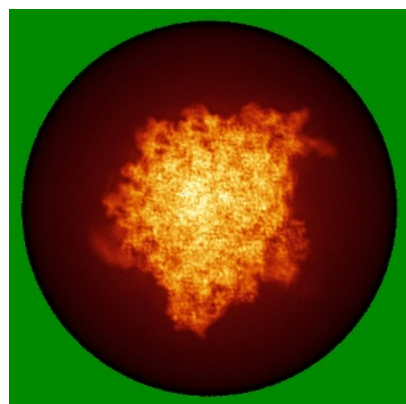


Y

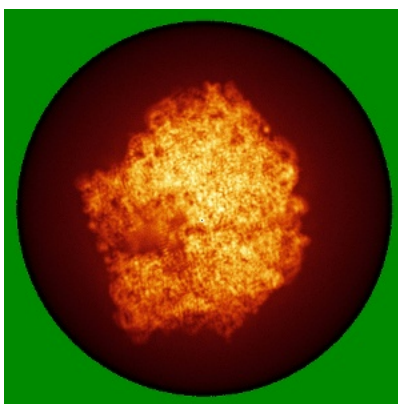


Z

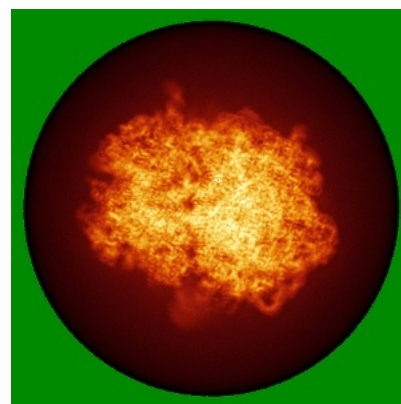
6.4.2 Raw map



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



X



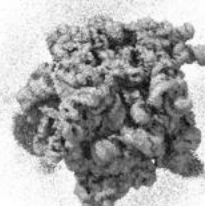
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 1.35. 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



X



Y



Z

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.

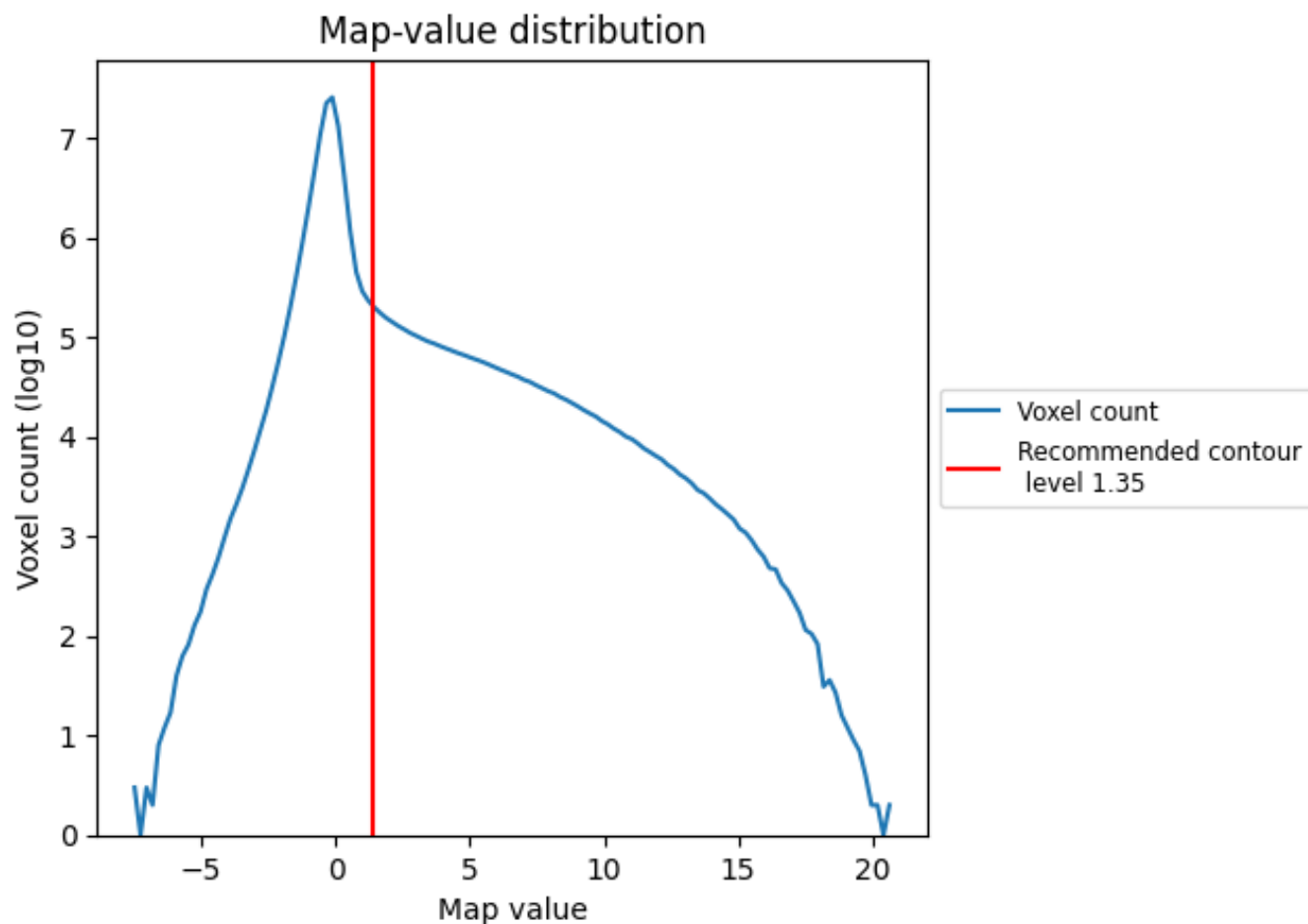
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

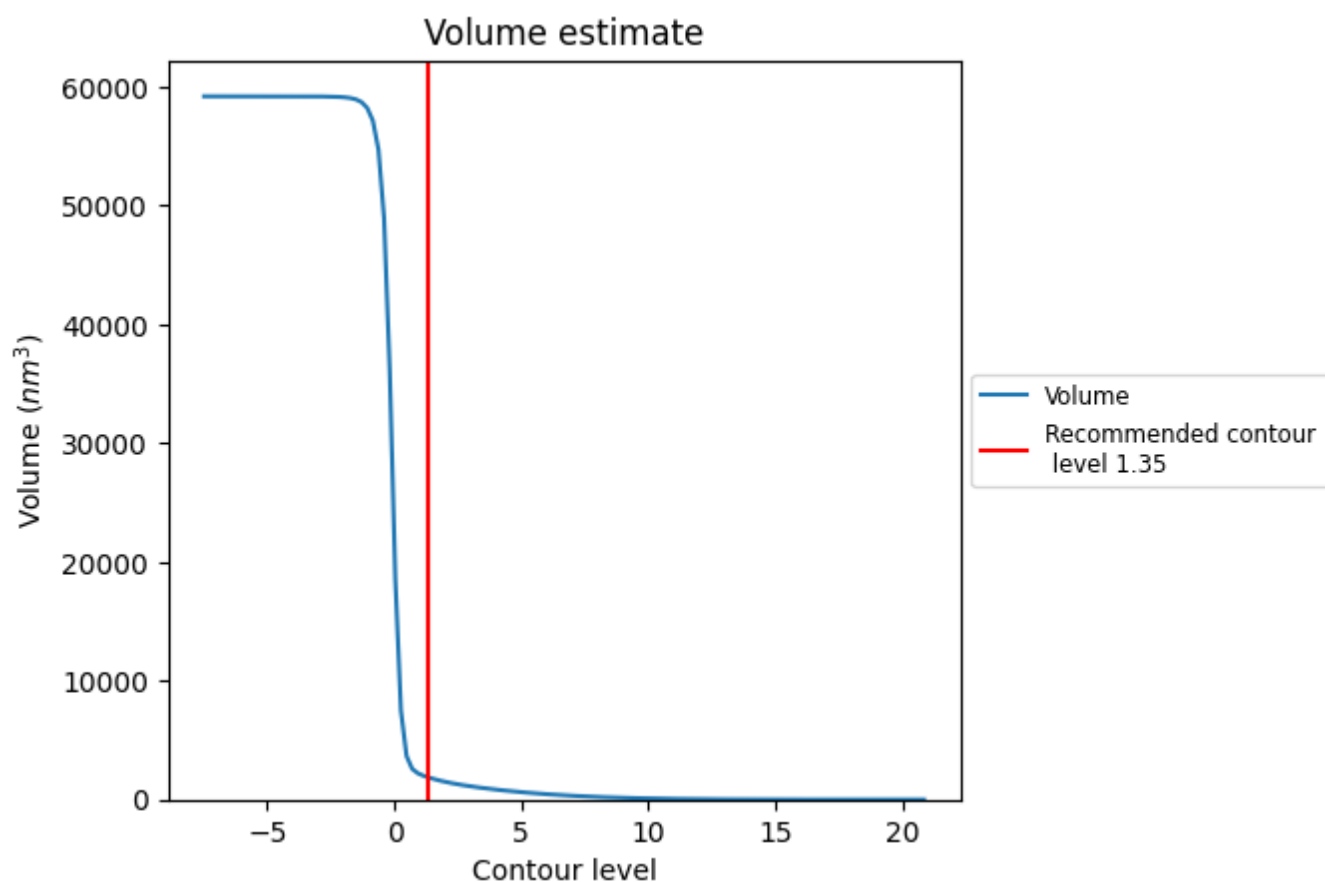
This section contains the results of statistical analysis of the map.

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.

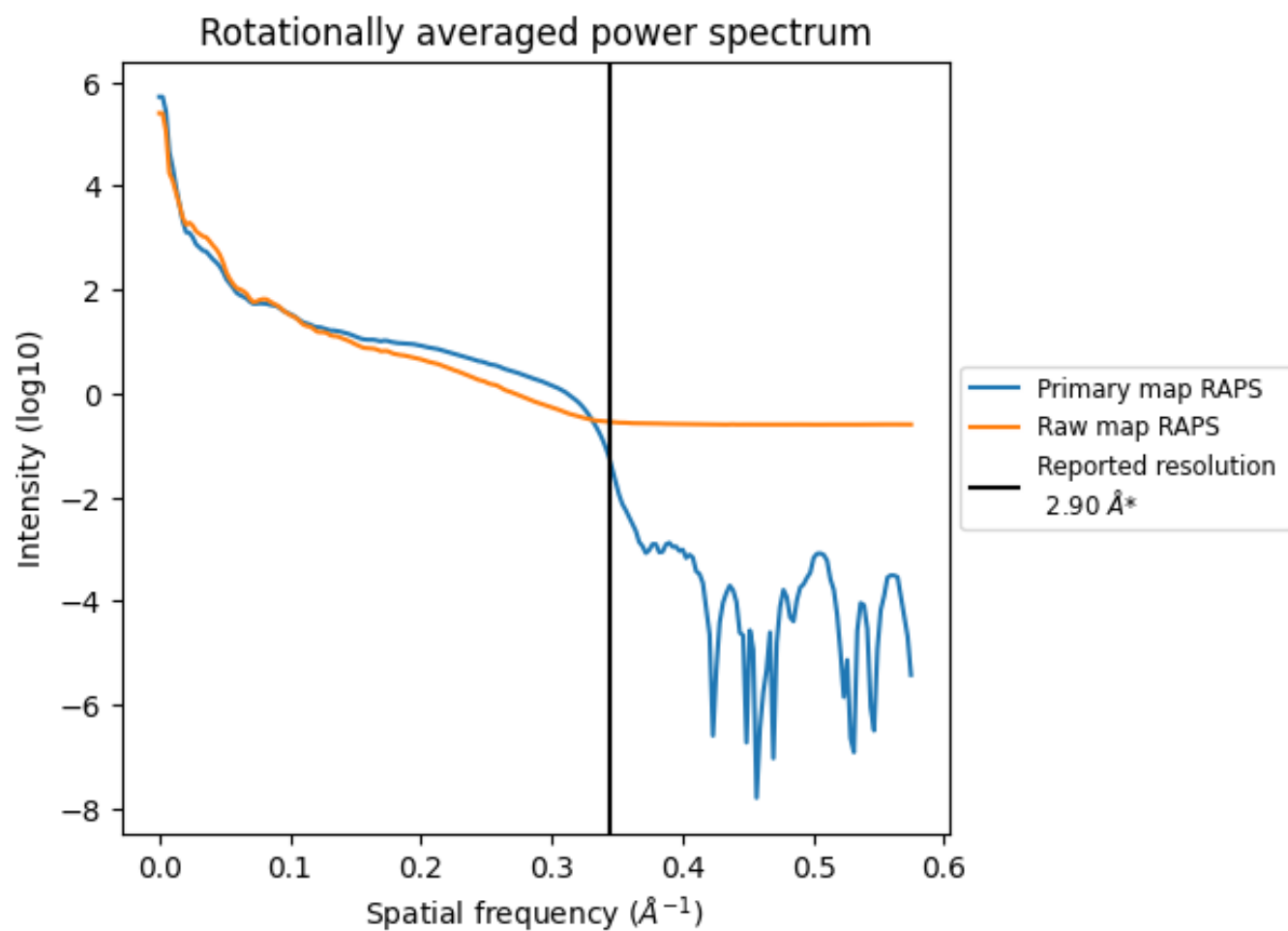
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1857 nm³; this corresponds to an approximate mass of 1677 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 ⓘ

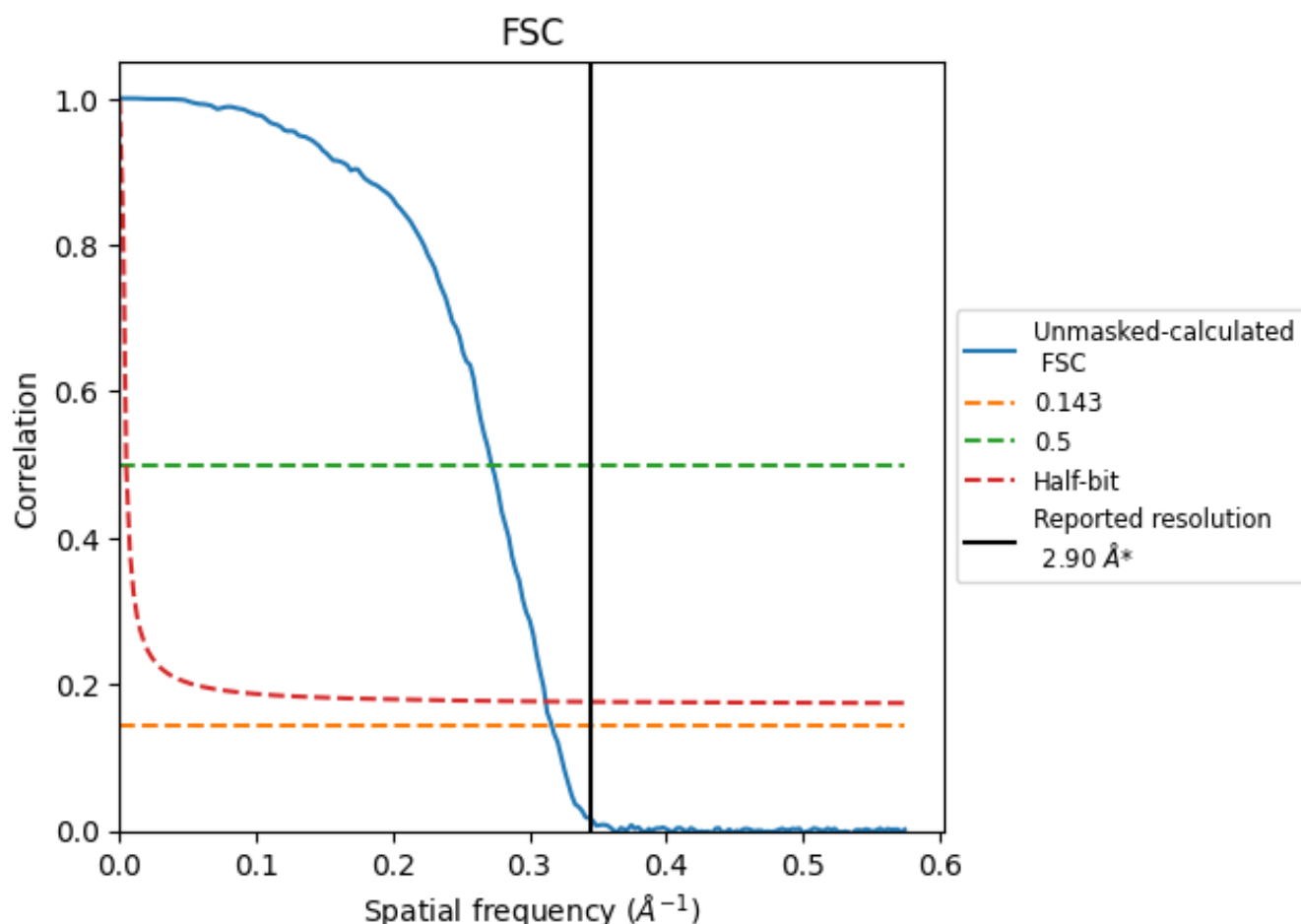


*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.345 Å⁻¹

8.2 Resolution estimates [i](#)

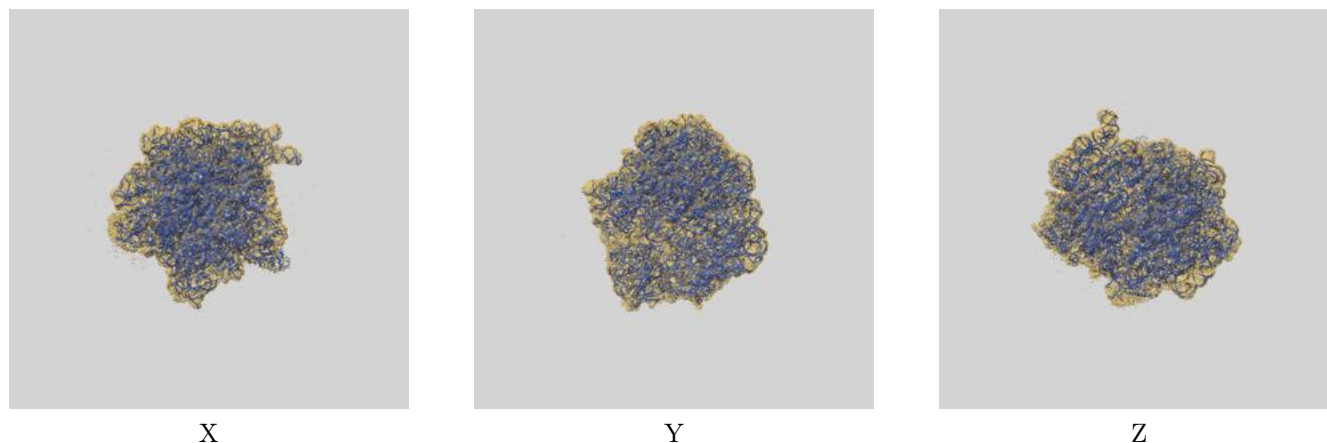
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.90	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.16	3.67	3.21

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

9 Map-model fit [i](#)

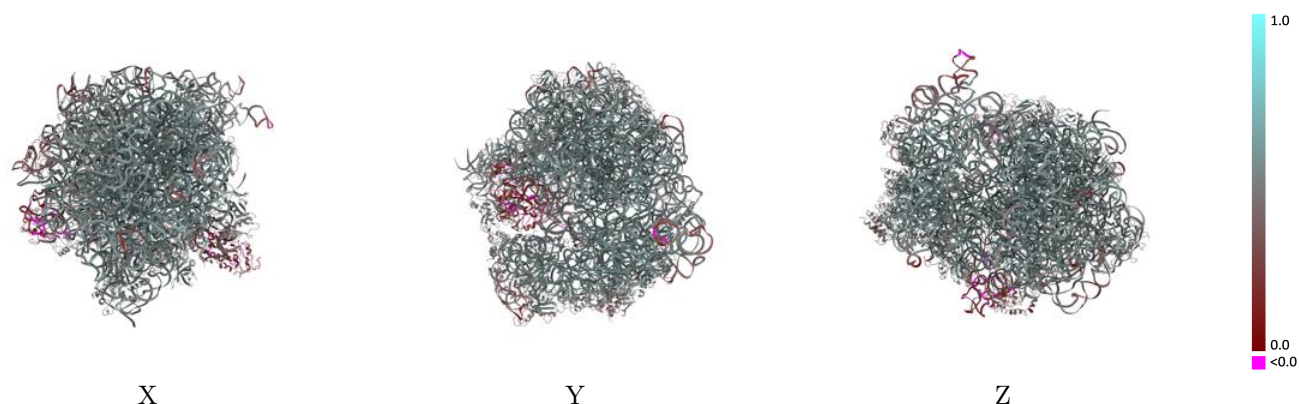
This section contains information regarding the fit between EMDB map EMD-25418 and PDB model 7ST2. Per-residue inclusion information can be found in section [3](#) on page [14](#).

9.1 Map-model overlay [i](#)



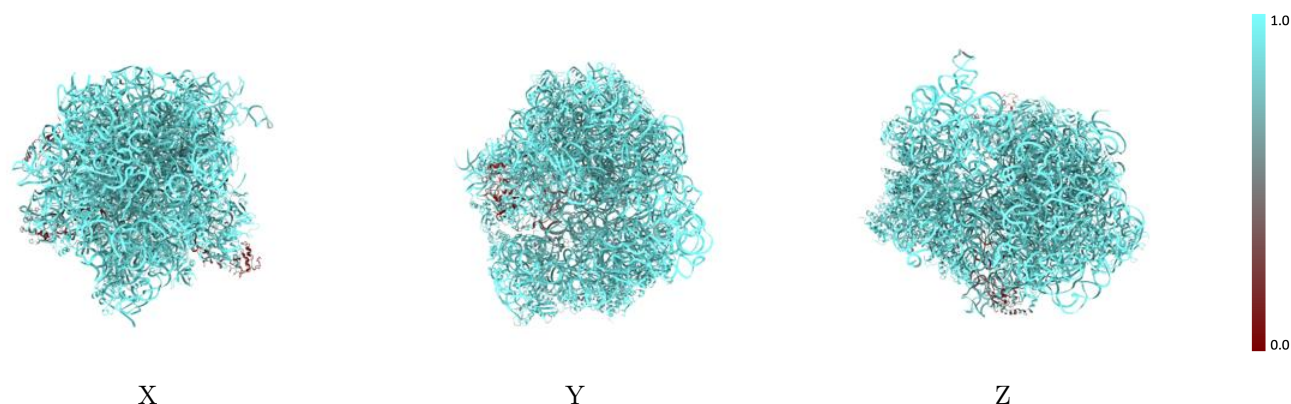
The images above show the 3D surface view of the map at the recommended contour level 1.35 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



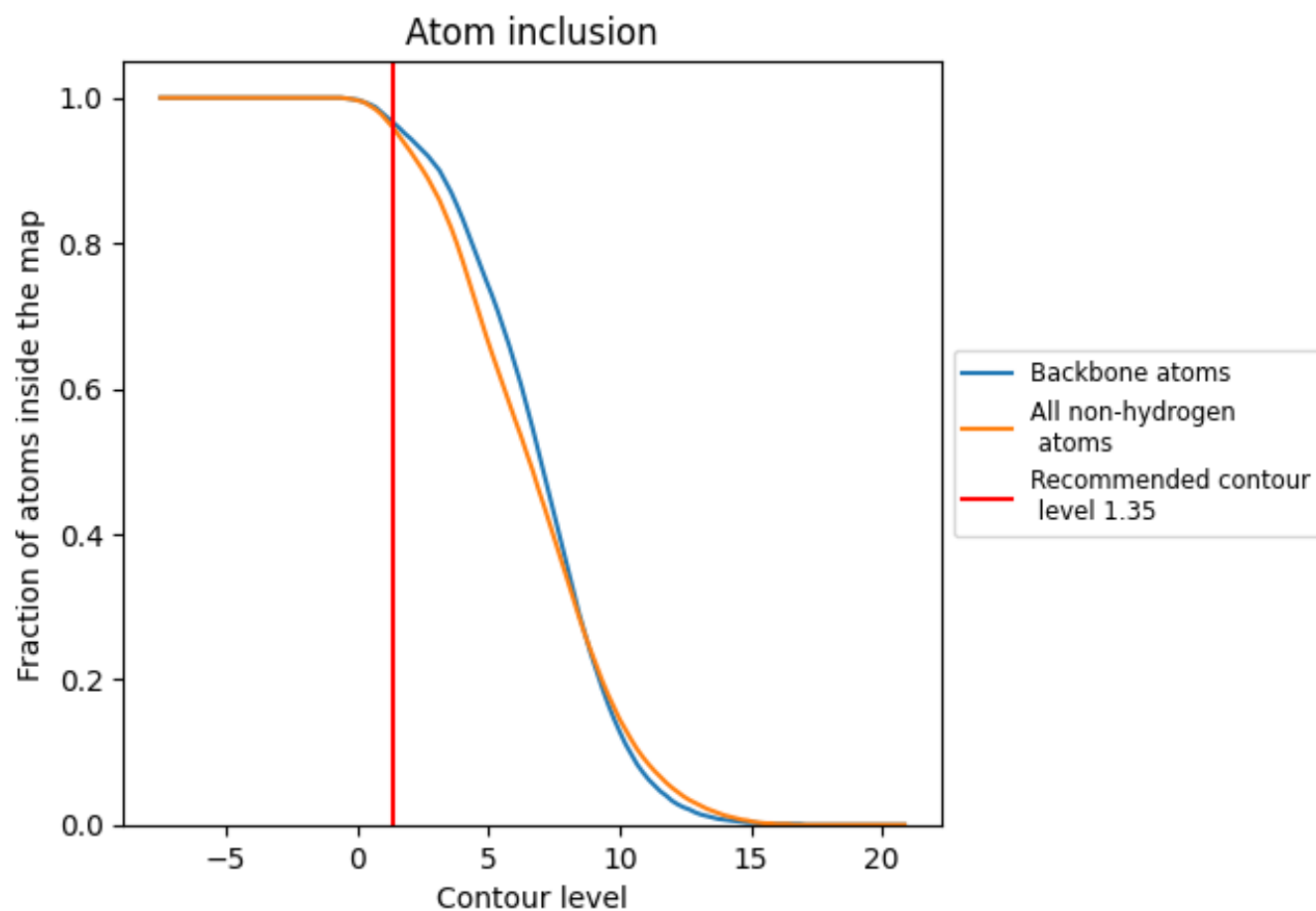
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (1.35).







































































9.4 Atom inclusion [i](#)



At the recommended contour level, 97% of all backbone atoms, 96% 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 (1.35) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9600	 0.5090
1	 0.9890	 0.5190
2	 0.9980	 0.5200
3	 0.9960	 0.5350
4	 0.9180	 0.3070
5	 0.9950	 0.5100
6	 0.2760	 0.3070
A	 0.9350	 0.4240
B	 0.9720	 0.5370
C	 0.8460	 0.5230
D	 0.9660	 0.5560
E	 0.9780	 0.5670
F	 0.9760	 0.5480
G	 0.9060	 0.4560
H	 0.9510	 0.5190
I	 0.9400	 0.4730
J	 0.9630	 0.5320
K	 0.9670	 0.4820
L	 0.9350	 0.4770
M	 0.9570	 0.5330
N	 0.9510	 0.4870
O	 0.8960	 0.4650
P	 0.9700	 0.5140
Q	 0.9610	 0.5400
R	 0.9450	 0.4810
S	 0.9610	 0.5030
T	 0.9780	 0.5110
U	 0.9590	 0.5080
V	 0.9510	 0.5190
W	 0.9710	 0.4950
X	 0.9610	 0.4840
Y	 0.9460	 0.4990
Z	 0.8570	 0.3510
a	 0.4660	 0.1910
b	 0.9780	 0.5630



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Chain	Atom inclusion	Q-score
c	 0.9810	 0.5460
d	 0.9460	 0.5040
e	 0.9630	 0.4860
f	 0.9750	 0.4860
g	 0.5350	 0.3510
h	 0.3520	 0.1820
i	 0.6260	 0.1690
j	 0.9660	 0.5350
k	 0.9640	 0.5480
l	 0.9660	 0.5270
m	 0.9760	 0.5510
n	 0.9740	 0.5410
o	 0.9770	 0.5040
p	 0.9640	 0.5470
q	 0.9790	 0.5390
r	 0.9650	 0.5250
s	 0.9590	 0.5240
t	 0.9520	 0.5040
u	 0.9670	 0.4890
v	 0.9590	 0.5190
w	 0.9710	 0.5540
x	 0.9670	 0.5340
y	 0.9480	 0.4370
z	 0.9540	 0.5270