



wwPDB EM Validation Summary Report ⓘ

Jun 21, 2026 – 02:59 pm BST

PDB ID : 9GHA / pdb_00009gha
EMDB ID : EMD-51350
Title : Fusidic acid-locked Escherichia coli 70S ribosome with Staphylococcus aureus EF-G and a tRNA in pe/E chimeric state (CHI)
Authors : Gonzalez-Lopez, A.; Selmer, M.
Deposited on : 2024-08-15
Resolution : 2.24 Å (reported)
Based on initial models : 7N2C, 9GHE, 8P2H

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:

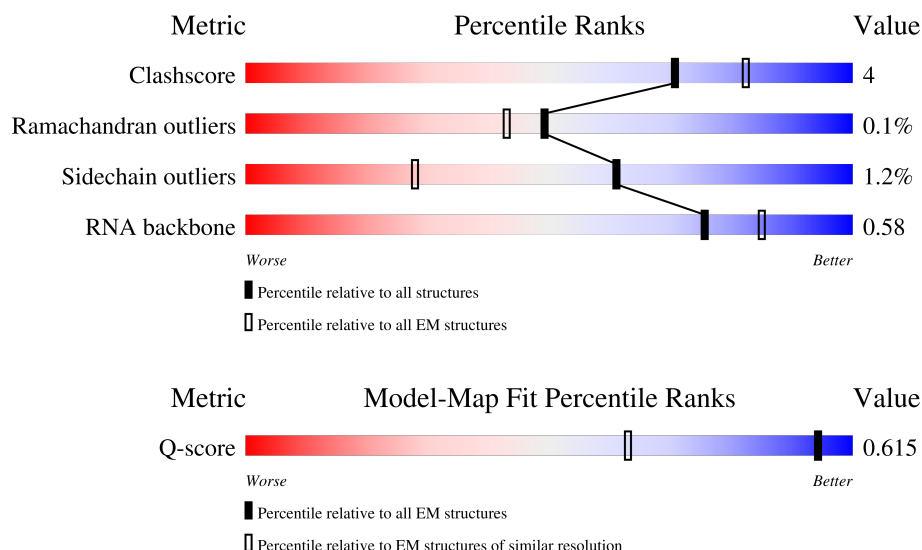
EMDB validation analysis : 0.0.1.dev132
Mogul : 1.8.4, CSD as541be (2020)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

1 Overall quality at a glance

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

The reported resolution of this entry is 2.24 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
RNA backbone	8273	3508	-
Q-score	-	25397	3381 (1.75 - 2.74)

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

Mol	Chain	Length	Quality of chain
1	0	55	
2	1	46	
3	2	65	

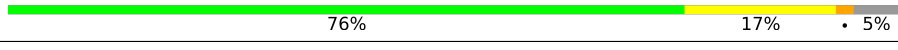
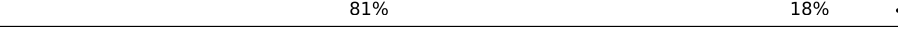
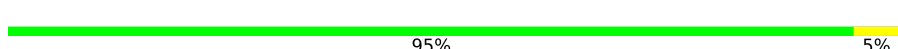
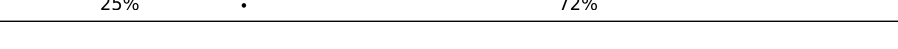
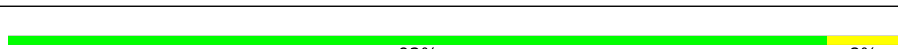
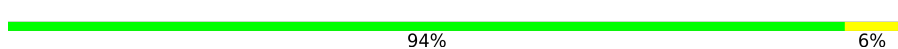
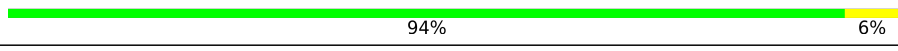
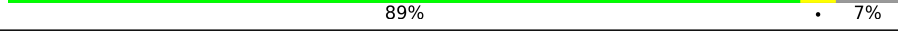
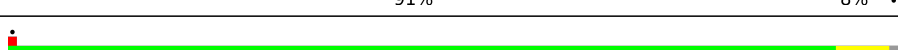
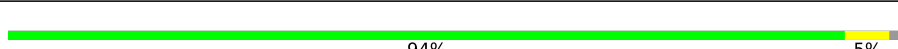
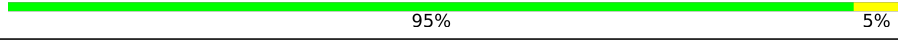
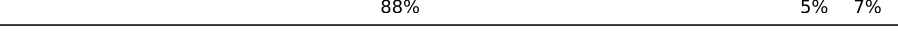
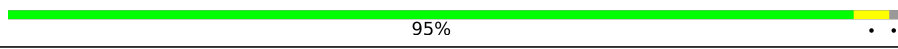
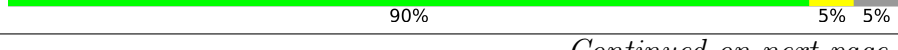
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Mol	Chain	Length	Quality of chain
4	3	38	
5	4	70	
6	8	77	
7	9	24	
8	A	1554	
9	B	241	
10	C	233	
11	D	206	
12	E	167	
13	F	135	
14	G	179	
15	H	130	
16	I	130	
17	J	103	
18	K	129	
19	L	124	
20	M	118	
21	N	101	
22	O	89	
23	P	82	
24	Q	84	
25	R	75	
26	S	92	
27	T	87	
28	U	71	

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Mol	Chain	Length	Quality of chain
29	W	693	
30	a	2930	
31	b	119	
32	c	273	
33	d	209	
34	e	201	
35	f	179	
36	g	177	
37	h	149	
38	i	142	
39	j	123	
40	k	144	
41	l	136	
42	m	127	
43	n	117	
44	o	115	
45	p	118	
46	q	103	
47	r	110	
48	s	100	
49	t	104	
50	u	94	
51	v	85	
52	w	78	
53	x	63	

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Mol	Chain	Length	Quality of chain
54	y	59	95%
55	z	57	93% • 5%

2 Entry composition

There are 60 unique types of molecules in this entry. The entry contains 145564 atoms, of which 0 are hydrogens and 0 are deuteriums.

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

- Molecule 1 is a protein called 50S ribosomal protein L33.

Mol	Chain	Residues	Atoms				AltConf	Trace
1	0	50	Total	C	N	O	0	0
			413	267	75	71		

- Molecule 2 is a protein called 50S ribosomal protein L34.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	1	45	Total	C	N	O	S	0	0
			367	222	88	55	2		

- Molecule 3 is a protein called 50S ribosomal protein L35.

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

- Molecule 4 is a protein called 50S ribosomal protein L36.

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

- Molecule 5 is a protein called 50S ribosomal protein L31.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	4	48	Total	C	N	O	S	0	0
			373	232	66	69	6		

- Molecule 6 is a RNA chain called tRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	8	77	Total	C	N	O	P	0	0
			1640	732	297	535	76		

- Molecule 7 is a RNA chain called mRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	9	5	Total	C	N	O	P	0	0
			110	49	22	34	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
8	A	1526	Total	C	N	O	P	0	0
			32757	14617	6009	10605	1526		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
9	B	222	Total	C	N	O	S	0	0
			1737	1099	312	318	8		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	154	Total	C	N	O	S	0	0
			1135	706	215	208	6		

- Molecule 13 is a protein called 30S ribosomal protein S6.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	F	101	Total	C	N	O	S	0	0
			824	520	149	149	6		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
14	G	150	Total	C	N	O	S	0	0
			1176	732	226	214	4		

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
16	I	125	Total	C	N	O	S	0	0
			1001	622	200	176	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
17	J	96	Total	C	N	O	S	0	0
			775	487	148	139	1		

- Molecule 18 is a protein called Small ribosomal subunit protein uS11.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	K	117	Total	C	N	O	S	0	0
			877	540	173	161	3		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
K	119	IAS	ASN	modified residue	UNP P0A7R9

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

Mol	Chain	Residues	Atoms					AltConf	Trace
19	L	121	Total	C	N	O	S	0	0
			942	582	193	162	5		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
20	M	115	Total	C	N	O	S	0	0
			891	552	179	157	3		

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

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

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

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

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

Mol	Chain	Residues	Atoms					AltConf	Trace
23	P	79	Total	C	N	O	S	0	0
			629	394	124	110	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
24	Q	79	Total	C	N	O	S	0	0
			641	406	120	112	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
25	R	64	Total	C	N	O	S	0	0
			524	330	99	94	1		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
26	S	84	Total	C	N	O	S	0	0
			668	427	127	112	2		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
27	T	86	Total	C	N	O	S	0	0
			670	414	138	115	3		

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

Mol	Chain	Residues	Atoms					AltConf	Trace
28	U	55	Total	C	N	O	S	0	0
			460	287	95	77	1		

- Molecule 29 is a protein called Elongation factor G.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	W	666	Total	C	N	O	S	0	0
			5154	3232	865	1028	29		

- Molecule 30 is a RNA chain called 23S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	a	2782	Total	C	N	O	P	0	0
			59756	26665	11017	19292	2782		

- Molecule 31 is a RNA chain called 5S rRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	b	119	Total	C	N	O	P	0	0
			2549	1135	466	829	119		

- Molecule 32 is a protein called 50S ribosomal protein L2.

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

- Molecule 33 is a protein called 50S ribosomal protein L3.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	d	207	Total	C	N	O	S	0	0
			1552	972	286	291	3		

- Molecule 34 is a protein called 50S ribosomal protein L4.

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

- Molecule 35 is a protein called 50S ribosomal protein L5.

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

- Molecule 36 is a protein called 50S ribosomal protein L6.

Mol	Chain	Residues	Atoms					AltConf	Trace
36	g	170	Total	C	N	O	S	0	0
			1273	803	232	236	2		

- Molecule 37 is a protein called 50S ribosomal protein L9.

Mol	Chain	Residues	Atoms					AltConf	Trace
37	h	41	Total	C	N	O	S	0	0
			303	194	54	54	1		

- Molecule 38 is a protein called 50S ribosomal protein L13.

Mol	Chain	Residues	Atoms					AltConf	Trace
38	i	141	Total	C	N	O	S	0	0
			1121	709	211	198	3		

- Molecule 39 is a protein called 50S ribosomal protein L14.

Mol	Chain	Residues	Atoms					AltConf	Trace
39	j	123	Total	C	N	O	S	0	0
			946	593	181	166	6		

- Molecule 40 is a protein called 50S ribosomal protein L15.

Mol	Chain	Residues	Atoms					AltConf	Trace
40	k	144	Total	C	N	O	S	0	0
			1053	654	207	190	2		

- Molecule 41 is a protein called 50S ribosomal protein L16.

Mol	Chain	Residues	Atoms					AltConf	Trace
41	l	136	Total	C	N	O	S	0	0
			1075	686	205	177	7		

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
l	82	MS6	MET	modified residue	UNP P0ADY7

- Molecule 42 is a protein called 50S ribosomal protein L17.

Mol	Chain	Residues	Atoms					AltConf	Trace
42	m	118	Total	C	N	O	S	0	0
			945	585	194	161	5		

- Molecule 43 is a protein called 50S ribosomal protein L18.

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

- Molecule 44 is a protein called 50S ribosomal protein L19.

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

- Molecule 45 is a protein called 50S ribosomal protein L20.

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

- Molecule 46 is a protein called 50S ribosomal protein L21.

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

- Molecule 47 is a protein called 50S ribosomal protein L22.

Mol	Chain	Residues	Atoms					AltConf	Trace
47	r	109	Total	C	N	O	S	0	0
			845	526	162	154	3		

- Molecule 48 is a protein called 50S ribosomal protein L23.

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

- Molecule 49 is a protein called 50S ribosomal protein L24.

Mol	Chain	Residues	Atoms					AltConf	Trace
49	t	93	Total	C	N	O	S	0	0
			717	452	135	130			

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

Mol	Chain	Residues	Atoms					AltConf	Trace
50	u	93	Total	C	N	O	S	0	0
			745	474	136	133	2		

- Molecule 51 is a protein called 50S ribosomal protein L27.

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

- Molecule 52 is a protein called 50S ribosomal protein L28.

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

- Molecule 53 is a protein called 50S ribosomal protein L29.

Mol	Chain	Residues	Atoms					AltConf	Trace
53	x	60	Total	C	N	O	S	0	0
			491	303	96	91	1		

- Molecule 54 is a protein called 50S ribosomal protein L30.

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

- Molecule 55 is a protein called 50S ribosomal protein L32.

Mol	Chain	Residues	Atoms					AltConf	Trace
55	z	54	Total	C	N	O	S	0	0
			429	260	91	77	1		

- Molecule 56 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
56	3	1	Total	Zn	0
			1	1	
56	4	1	Total	Zn	0
			1	1	

- Molecule 57 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		AltConf
57	A	14	Total	K	0
			14	14	
57	F	1	Total	K	0
			1	1	
57	a	74	Total	K	0
			74	74	
57	c	3	Total	K	0
			3	3	
57	e	1	Total	K	0
			1	1	
57	t	1	Total	K	0
			1	1	

- Molecule 58 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

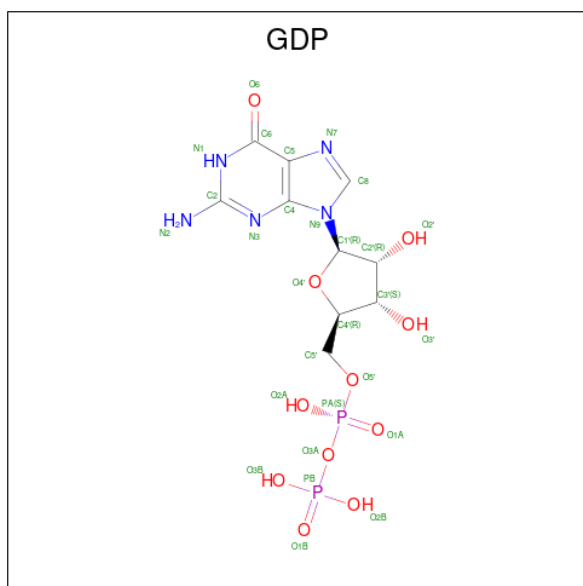
Mol	Chain	Residues	Atoms		AltConf
58	A	27	Total	Mg	0
			27	27	
58	W	1	Total	Mg	0
			1	1	
58	a	233	Total	Mg	0
			233	233	

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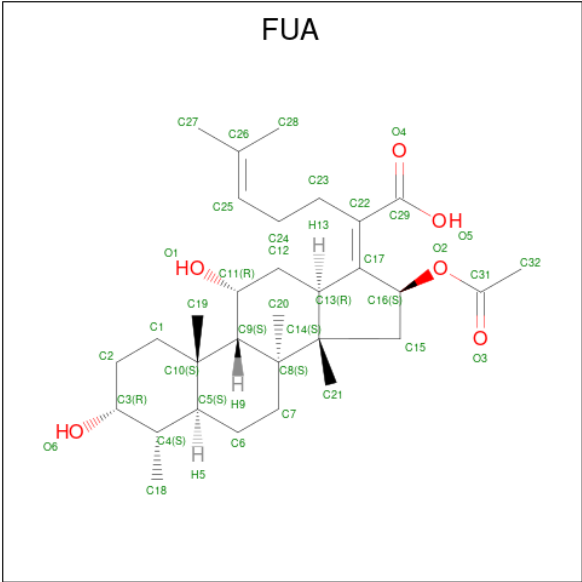
Mol	Chain	Residues	Atoms		AltConf
58	b	3	Total	Mg	0
			3	3	
58	c	3	Total	Mg	0
			3	3	
58	d	2	Total	Mg	0
			2	2	
58	k	1	Total	Mg	0
			1	1	
58	z	1	Total	Mg	0
			1	1	

- Molecule 59 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					AltConf
59	W	1	Total	C	N	O	P	0
			28	10	5	11	2	

- Molecule 60 is FUSIDIC ACID (CCD ID: FUA) (formula: $C_{31}H_{48}O_6$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
60	W	1	Total	C	O	0
			37	31	6	

3 Residue-property plots [i](#)

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

- Molecule 1: 50S ribosomal protein L33

Chain 0:  80% 9% 9%



- Molecule 2: 50S ribosomal protein L34

Chain 1:  93% . .



- Molecule 3: 50S ribosomal protein L35

Chain 2:  86% 12% .



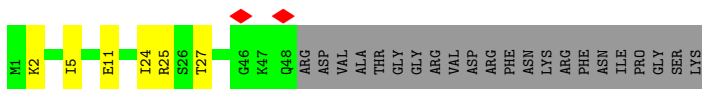
- Molecule 4: 50S ribosomal protein L36

Chain 3:  87% 13%

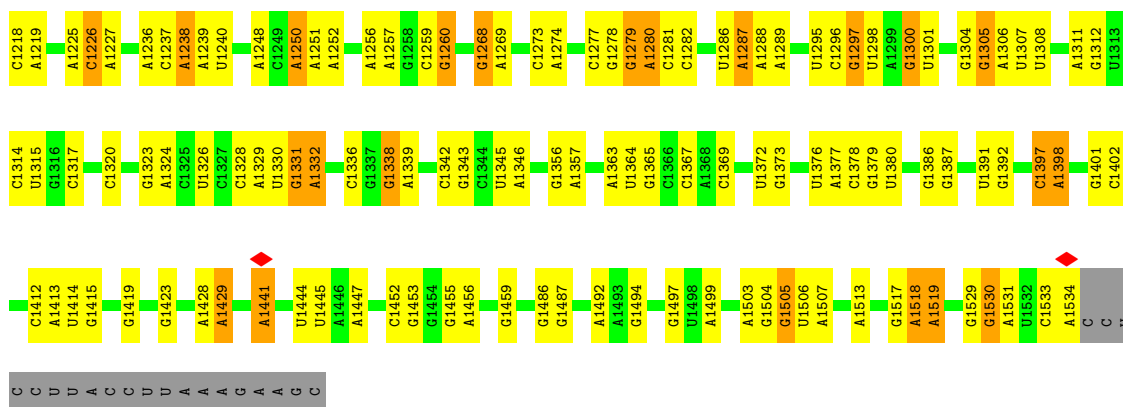


- Molecule 5: 50S ribosomal protein L31

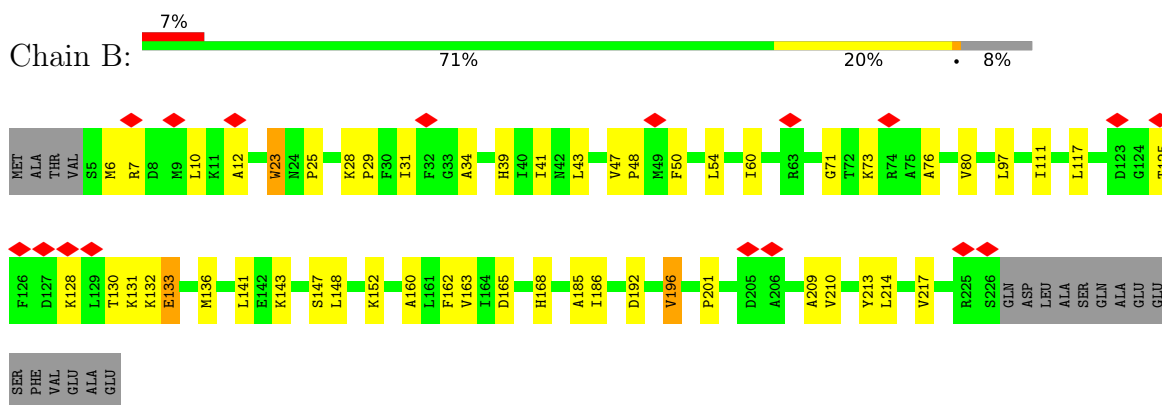
Chain 4:  60% 9% 31%



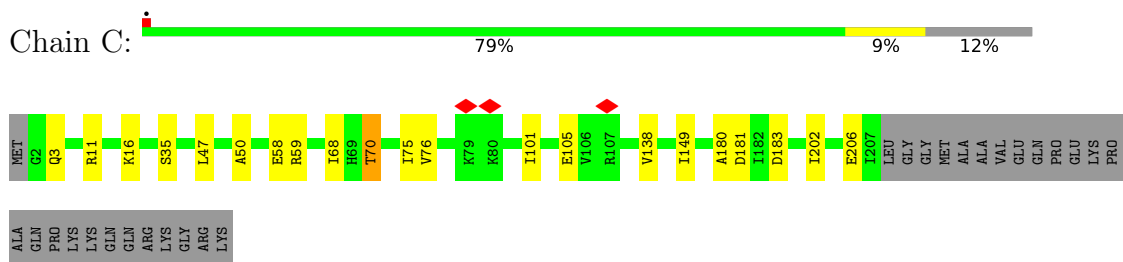
- Molecule 6: tRNA



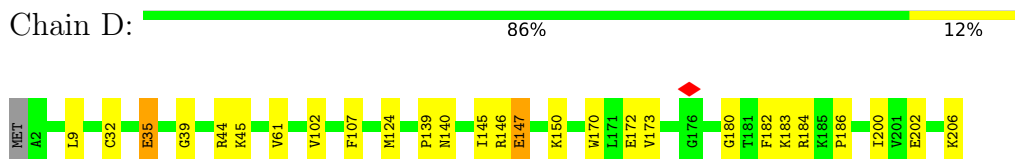
• Molecule 9: 30S ribosomal protein S2



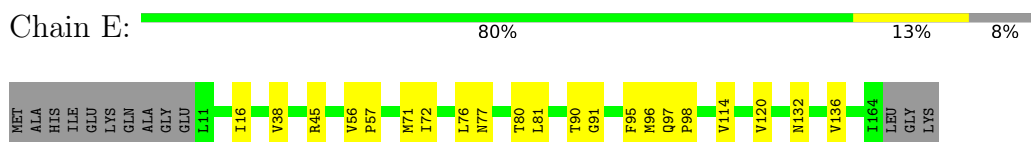
• Molecule 10: 30S ribosomal protein S3



• Molecule 11: 30S ribosomal protein S4

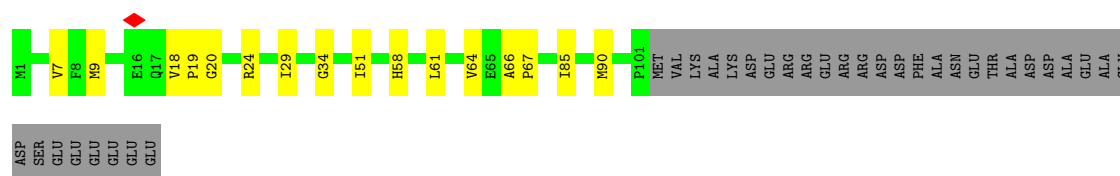


• Molecule 12: 30S ribosomal protein S5



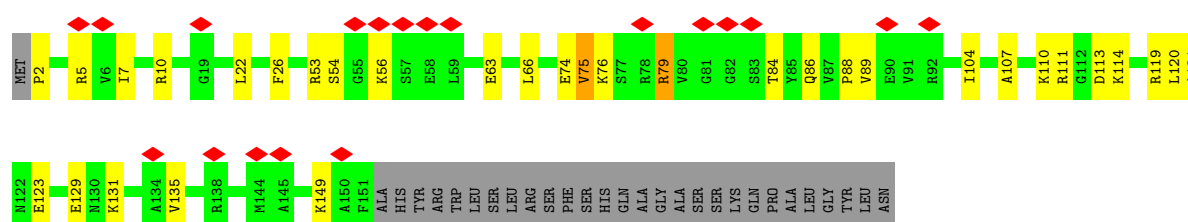
- Molecule 13: 30S ribosomal protein S6

Chain F:  63% 12% 25%



- Molecule 14: 30S ribosomal protein S7

Chain G:  11% 65% 17% 16%



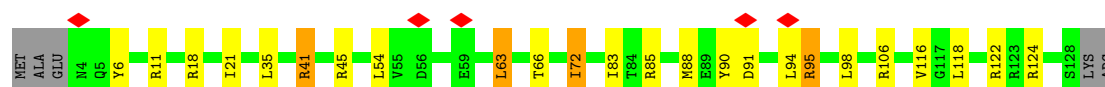
- Molecule 15: 30S ribosomal protein S8

Chain H:  86% 12% ..



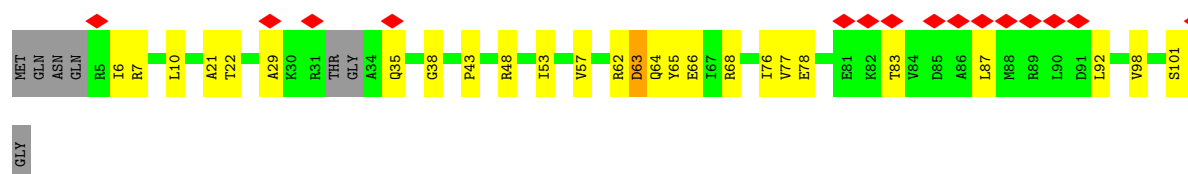
- Molecule 16: 30S ribosomal protein S9

Chain I:  78% 15% ..



- Molecule 17: 30S ribosomal protein S10

Chain J:  15% 67% 25% 7%



- Molecule 18: Small ribosomal subunit protein uS11

Chain K:  84% 7% 9%



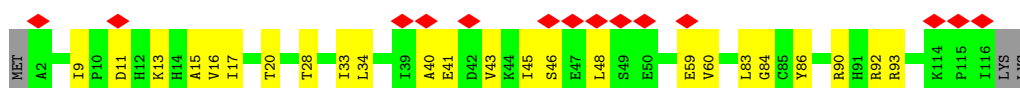
- Molecule 19: 30S ribosomal protein S12

Chain L: 84% 13% ..



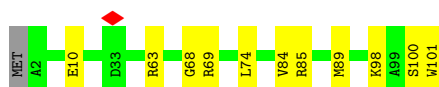
- Molecule 20: 30S ribosomal protein S13

Chain M: 12% 77% 20% .



- Molecule 21: 30S ribosomal protein S14

Chain N: 88% 11% .



- Molecule 22: 30S ribosomal protein S15

Chain O: 94% ..



- Molecule 23: 30S ribosomal protein S16

Chain P: 87% 10% .



- Molecule 24: 30S ribosomal protein S17

Chain Q: 81% 12% 6%

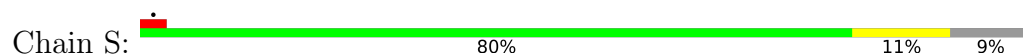


- Molecule 25: 30S ribosomal protein S18

Chain R: 75% 11% 15%



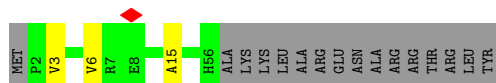
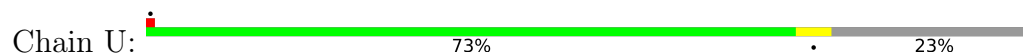
- Molecule 26: 30S ribosomal protein S19



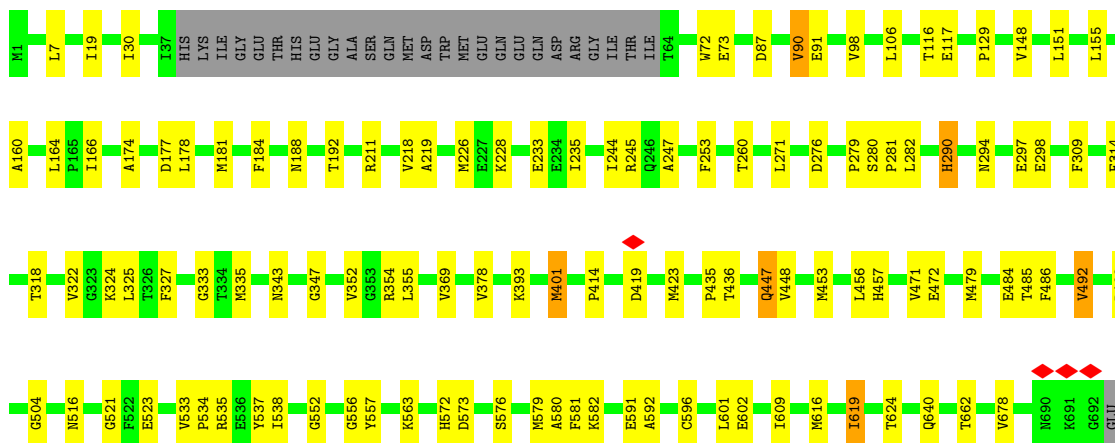
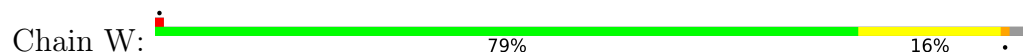
- Molecule 27: 30S ribosomal protein S20



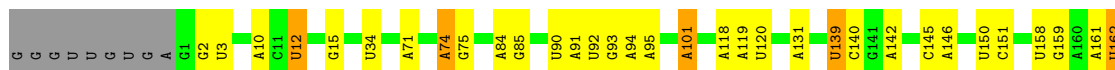
- Molecule 28: 30S ribosomal protein S21



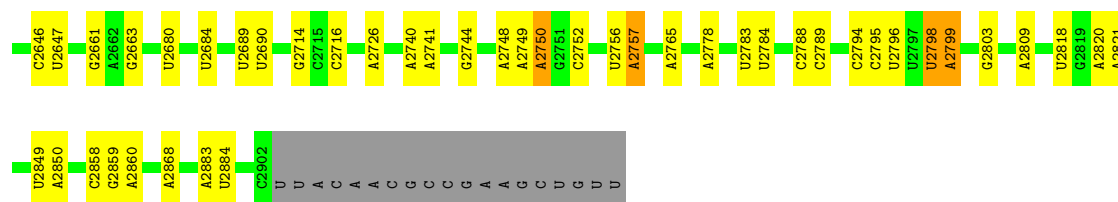
- Molecule 29: Elongation factor G



- Molecule 30: 23S rRNA

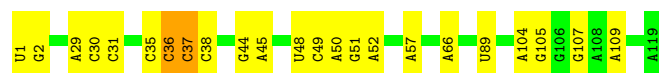


A2468	G2315	A1791	A1580	U1405	C1170	U1060	U746	A547	C351	A181
A2469	A2322	C1800	U1584	U1406	G1171	U1061	U747	G548	C352	A191
U2473	G2323	A1801	G1585	U1409	U	G1062		G549	C353	C192
U2474	U2324	A1908	A1586	U1412	U	U1065	A764	G555	A354	
A2476	G2325	C1816	C1605	A1413	U	A1069	C765	A556	G356	A196
A2477	A2327	A2015	C1606	A1416	G	A1070	G775	A563	C357	A199
U2478	A2328	A2020	C1607	G1419	C1178	A1071	G776	U568	U358	U200
U2491	U2329	A1829	A1608	G1419	G1179	C1072	A781	U573	U359	
G2502	U2330	C1838	A1609	A1419	U1180	U1072	A782	U574	G361	A204
A2503	A2333	A1847	G1619	C1428	G1182	A1077	A783	A575	A362	
U2504	U2334	A1948	A1637	C1428	U1183	U1078	G784			C210
G2505	A2346	A1948	A1637	C1428	G1187	C1079	G785	U586	U366	
A2518	C2347	A1853	U1647	A1434	U1188	A1080	A792	C587	U366	G215
U2522	G2350	A1858	U1648	G1451	U1198	U1082	G805	U588	G366	A216
A2529	A2358	U1859	G1674	G1452	G1225	U1083	U811	U589	A411	A221
G2530	C2359	G1960	G1674	A1453	U1225	A1086	U812	U593	U448	A244
A2546	A2366	G1960	G1674	C1454	A1253	U1087	U813	C595	U451	G246
A2547	A2376	A1871	U1680	U1458	G1256	A1089	U814	A603	A454	G247
U2548	A2377	A1872	G1681	G1459	U1256	A1090	U827	A609	C455	G248
G2552	A2378	A1898	U1682	U1460	G1271	G1093	U828	C610	A476	A255
G2553	U2383	C1905	G1682	A1469	A1272	U1094	A833	A614	A477	A265
U2554	U2384	G1906	U1683	A1470	A1276	A1097	G834	U615	A478	
U2555	C2385	G1907	G1715	G1482	A1287	U1101	A845	A627	A479	A272
G2556	U2402	U1911	G1721	A1490	C1296	C1102	U846	G638	A480	G273
G2557	A2406	A1912	G1721	A1490	U1300	A1103	U846	U639	G481	C274
A2566	U2419	C1914	C1727	C1493	G1300	G1104	A849	C634	A482	C275
G2567	U2425	3TD1915	C1728	U1506	A1301	U1105	U850	C635	A483	
U2573	A2425	U1917	U1729	C1507	A1301	G1106	C851	A637	G491	A278
U2580	G2429	A1918	C1730	U1508	A1321	G1112	U852	G638	A492	A279
G2591	A2430	A1927	G1734	A1509	A1327	G1116	G858	C640	G493	U280
G2592	U2431	A1928	G1737	G1510	A1328	U1116	A861	A644	G494	C281
A2602	A2435	A1928	G1738	A1515	U1352	G1125	G862	U499	U499	G285
G2603	U2441	G1929	A1744	A1528	C1357	G1128	G869	C645	G500	U288
U2604	U2441	G1930	C1760	G1529	G1358	A1129	U870	U646	A501	G289
U2605	G2445	A1932	C1760	U1534	G1361	U1130	U871	G647	A502	G308
U2609	A2448	G1933	C1764	A1535	G1362	G1131	U872	U653	A503	A309
U2613	U2449	A1937	A1773	C1536	A1365	U1132	A378	A654	A504	A310
A2614	G2307	U1939	A1773	G1537	A1378	A1133	G	A655	A505	A311
U2615	G2308	U1955	U1778	G1538	U1379	A1134	G	U696	C509	
U2629	A2311	C1967	U1782	A1569	A1383	C1135	G	C531	G	A322
C2636	U2312	A1970	A1784	A1570	A1386	A1142	G	A716	A532	A330
U2637	A2314	U1971	C1790	A1578	A1387	A1143	G	C717	G533	A340
				A1579		A1144	U	A718	U534	C341
						A1151	C	G728	C544	A345
						A1169	U	A730	U546	A346



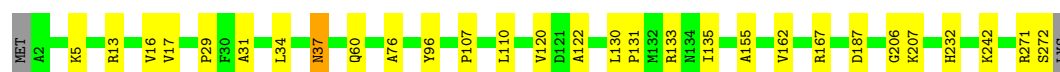
• Molecule 31: 5S rRNA

Chain b: 81% 18% .



• Molecule 32: 50S ribosomal protein L2

Chain c: 89% 10% .



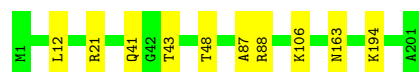
• Molecule 33: 50S ribosomal protein L3

Chain d: 92% 7% .



• Molecule 34: 50S ribosomal protein L4

Chain e: 95% 5%



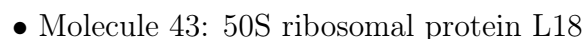
• Molecule 35: 50S ribosomal protein L5

Chain f: 76% 22% ..

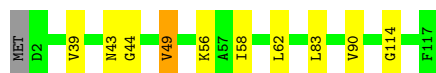


• Molecule 36: 50S ribosomal protein L6

Chain g: 81% 13% . .

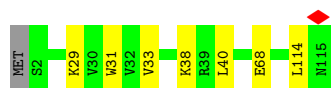


Chain n:  91% 8% ..



- Molecule 44: 50S ribosomal protein L19

Chain o:  93% 6% .



- Molecule 45: 50S ribosomal protein L20

Chain p:  94% 5% .

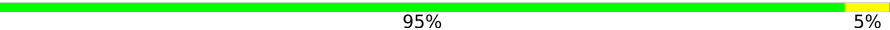


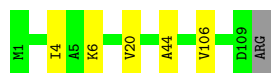
- Molecule 46: 50S ribosomal protein L21

Chain q:  89% 11%



- Molecule 47: 50S ribosomal protein L22

Chain r:  95% 5% .



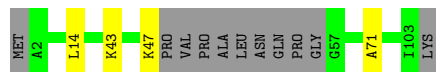
- Molecule 48: 50S ribosomal protein L23

Chain s:  88% 5% 7%

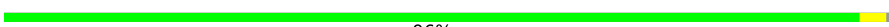


- Molecule 49: 50S ribosomal protein L24

Chain t:  86% 11%



- Molecule 50: 50S ribosomal protein L25

Chain u:  96% ..



- Molecule 51: 50S ribosomal protein L27

Chain v:  82% 6% 12%



- Molecule 52: 50S ribosomal protein L28

Chain w:  95% ..

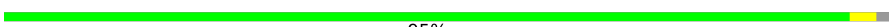


- Molecule 53: 50S ribosomal protein L29

Chain x:  90% 5% 5%



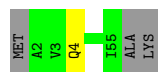
- Molecule 54: 50S ribosomal protein L30

Chain y:  95% ..



- Molecule 55: 50S ribosomal protein L32

Chain z:  93% • 5%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	88568	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	40	Depositor
Minimum defocus (nm)	700	Depositor
Maximum defocus (nm)	1000	Depositor
Magnification	130000	Depositor
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.714	Depositor
Minimum map value	-0.317	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.014	Depositor
Recommended contour level	0.02	Depositor
Map size (Å)	388.8, 388.8, 388.8	wwPDB
Map dimensions	600, 600, 600	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.648, 0.648, 0.648	Depositor

5 Model quality ⓘ

5.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: D2T, K, OMC, IAS, 3TD, 6MZ, OMG, PSU, 4D4, 2MA, H2U, MEQ, MS6, GDP, 1MG, MA6, OMU, 2MG, 5MC, MG, ZN, FUA, 5MU, UR3, G7M, 4OC

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	0	0.47	0/420	0.79	0/560
2	1	0.48	0/370	0.88	0/487
3	2	0.50	0/513	0.85	0/676
4	3	0.48	0/303	0.72	0/397
5	4	0.49	0/380	0.84	0/508
6	8	0.54	0/1832	0.76	0/2855
7	9	0.59	0/123	0.75	0/190
8	A	0.54	0/36398	0.75	0/56774
9	B	0.46	0/1768	0.94	0/2381
10	C	0.47	0/1651	0.82	0/2225
11	D	0.45	0/1665	0.88	0/2227
12	E	0.49	0/1148	0.83	0/1545
13	F	0.45	0/843	0.81	0/1140
14	G	0.47	0/1190	0.91	0/1595
15	H	0.48	0/989	0.83	0/1326
16	I	0.45	0/1013	0.85	0/1350
17	J	0.48	0/784	0.87	0/1059
18	K	0.52	0/884	0.83	0/1191
19	L	0.47	0/945	0.79	0/1268
20	M	0.47	0/900	0.91	0/1204
21	N	0.47	0/817	0.89	0/1088
22	O	0.43	0/722	0.91	0/964
23	P	0.46	0/639	0.81	0/859
24	Q	0.46	0/650	0.74	0/871
25	R	0.45	0/532	0.91	0/715
26	S	0.49	0/685	0.84	0/922
27	T	0.46	0/676	0.93	0/895
28	U	0.47	0/467	0.90	0/620
29	W	0.46	0/5244	0.84	0/7091
30	a	0.52	1/66355 (0.0%)	0.77	8/103511 (0.0%)
31	b	0.53	0/2850	0.76	0/4444

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
32	c	0.49	0/2121	0.79	0/2852
33	d	0.47	0/1562	0.78	0/2102
34	e	0.46	0/1571	0.84	0/2113
35	f	0.45	0/1434	0.87	0/1926
36	g	0.49	0/1291	0.83	1/1747 (0.1%)
37	h	0.48	0/306	0.79	0/413
38	i	0.46	0/1144	0.83	0/1541
39	j	0.47	0/955	0.79	0/1279
40	k	0.48	0/1062	0.83	0/1413
41	l	0.47	0/1073	0.80	0/1433
42	m	0.46	0/958	0.85	0/1281
43	n	0.47	0/902	0.86	0/1209
44	o	0.47	0/929	0.73	0/1242
45	p	0.46	0/960	0.89	0/1278
46	q	0.46	0/829	0.73	0/1107
47	r	0.47	0/852	0.83	0/1142
48	s	0.46	0/744	0.79	0/994
49	t	0.46	0/721	0.75	0/956
50	u	0.46	0/758	0.81	0/1015
51	v	0.48	0/576	0.76	0/762
52	w	0.47	0/635	0.83	0/848
53	x	0.41	0/492	0.89	0/655
54	y	0.46	0/453	0.81	0/605
55	z	0.47	0/435	0.84	0/581
All	All	0.51	1/156519 (0.0%)	0.79	9/233432 (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
3	2	0	1
4	3	0	1
10	C	0	1
11	D	0	1
14	G	0	1
16	I	0	2
17	J	0	2
18	K	0	1
19	L	0	1
36	g	0	1

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Mol	Chain	#Chirality outliers	#Planarity outliers
38	i	0	1
45	p	0	1
52	w	0	1
53	x	0	1
All	All	0	16

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2069	G7M	O3'-P	5.17	1.61	1.56

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2546	U	O3'-P-O5'	-7.53	92.71	104.00
30	a	1905	C	O3'-P-O5'	-6.46	94.32	104.00
30	a	781	A	O3'-P-O5'	-6.03	94.96	104.00
30	a	2324	U	C2'-C3'-O3'	-5.88	104.89	113.70
30	a	1378	A	O3'-P-O5'	-5.77	95.34	104.00

There are no chirality outliers.

5 of 16 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
3	2	13	ARG	Sidechain
4	3	36	ARG	Sidechain
10	C	11	ARG	Sidechain
11	D	184	ARG	Sidechain
14	G	79	ARG	Sidechain

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	0	413	0	448	4	0
2	1	367	0	405	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	2	504	0	572	4	0
4	3	302	0	340	3	0
5	4	373	0	370	4	0
6	8	1640	0	837	13	0
7	9	110	0	55	1	0
8	A	32757	0	16505	265	0
9	B	1737	0	1763	28	0
10	C	1624	0	1696	13	0
11	D	1643	0	1707	15	0
12	E	1135	0	1179	12	0
13	F	824	0	815	10	0
14	G	1176	0	1233	20	0
15	H	979	0	1031	9	0
16	I	1001	0	1044	14	0
17	J	775	0	817	24	0
18	K	877	0	883	4	0
19	L	942	0	999	9	0
20	M	891	0	952	16	0
21	N	805	0	844	12	0
22	O	714	0	734	3	0
23	P	629	0	643	6	0
24	Q	641	0	682	5	0
25	R	524	0	543	5	0
26	S	668	0	693	7	0
27	T	670	0	719	3	0
28	U	460	0	486	2	0
29	W	5154	0	5064	68	0
30	a	59756	0	30054	195	0
31	b	2549	0	1291	11	0
32	c	2082	0	2153	16	0
33	d	1552	0	1601	8	0
34	e	1552	0	1619	7	0
35	f	1410	0	1444	31	0
36	g	1273	0	1322	12	0
37	h	303	0	327	2	0
38	i	1121	0	1150	1	0
39	j	946	0	1023	8	0
40	k	1053	0	1129	4	0
41	l	1075	0	1145	4	0
42	m	945	0	989	3	0
43	n	892	0	923	4	0
44	o	917	0	962	5	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
45	p	947	0	1019	4	0
46	q	816	0	839	6	0
47	r	845	0	909	4	0
48	s	738	0	807	3	0
49	t	717	0	766	3	0
50	u	745	0	768	2	0
51	v	569	0	581	3	0
52	w	625	0	652	1	0
53	x	491	0	523	1	0
54	y	449	0	488	1	0
55	z	429	0	440	1	0
56	3	1	0	0	0	0
56	4	1	0	0	0	0
57	A	14	0	0	0	0
57	F	1	0	0	0	0
57	a	74	0	0	0	0
57	c	3	0	0	0	0
57	e	1	0	0	0	0
57	t	1	0	0	0	0
58	A	27	0	0	0	0
58	W	1	0	0	0	0
58	a	233	0	0	0	0
58	b	3	0	0	0	0
58	c	3	0	0	0	0
58	d	2	0	0	0	0
58	k	1	0	0	0	0
58	z	1	0	0	0	0
59	W	28	0	12	0	0
60	W	37	0	47	5	0
All	All	145564	0	99042	845	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

The worst 5 of 845 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
14:G:79:ARG:HA	14:G:84:THR:HA	1.23	1.10
8:A:1016:A:H1'	8:A:1017:U:H4'	1.45	0.96
17:J:48:ARG:HG2	17:J:66:GLU:HG3	1.50	0.91
8:A:424:G:O2'	8:A:425:G:H5'	1.77	0.84

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
8:A:411:A:N3	8:A:413:G:H5''	1.95	0.81

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	0	48/55 (87%)	48 (100%)	0	0	100	100
2	1	43/46 (94%)	43 (100%)	0	0	100	100
3	2	62/65 (95%)	60 (97%)	2 (3%)	0	100	100
4	3	36/38 (95%)	36 (100%)	0	0	100	100
5	4	46/70 (66%)	45 (98%)	1 (2%)	0	100	100
9	B	220/241 (91%)	214 (97%)	5 (2%)	1 (0%)	24	23
10	C	204/233 (88%)	197 (97%)	7 (3%)	0	100	100
11	D	203/206 (98%)	201 (99%)	2 (1%)	0	100	100
12	E	152/167 (91%)	148 (97%)	4 (3%)	0	100	100
13	F	99/135 (73%)	95 (96%)	4 (4%)	0	100	100
14	G	148/179 (83%)	145 (98%)	3 (2%)	0	100	100
15	H	127/130 (98%)	124 (98%)	2 (2%)	1 (1%)	16	13
16	I	123/130 (95%)	118 (96%)	5 (4%)	0	100	100
17	J	92/103 (89%)	88 (96%)	3 (3%)	1 (1%)	11	7
18	K	113/129 (88%)	107 (95%)	6 (5%)	0	100	100
19	L	118/124 (95%)	111 (94%)	7 (6%)	0	100	100
20	M	113/118 (96%)	110 (97%)	3 (3%)	0	100	100
21	N	98/101 (97%)	95 (97%)	2 (2%)	1 (1%)	12	9
22	O	86/89 (97%)	85 (99%)	1 (1%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
23	P	77/82 (94%)	74 (96%)	3 (4%)	0	100	100
24	Q	77/84 (92%)	74 (96%)	3 (4%)	0	100	100
25	R	62/75 (83%)	62 (100%)	0	0	100	100
26	S	82/92 (89%)	81 (99%)	1 (1%)	0	100	100
27	T	84/87 (97%)	84 (100%)	0	0	100	100
28	U	53/71 (75%)	52 (98%)	1 (2%)	0	100	100
29	W	662/693 (96%)	647 (98%)	15 (2%)	0	100	100
32	c	269/273 (98%)	263 (98%)	6 (2%)	0	100	100
33	d	204/209 (98%)	198 (97%)	6 (3%)	0	100	100
34	e	199/201 (99%)	194 (98%)	5 (2%)	0	100	100
35	f	175/179 (98%)	170 (97%)	4 (2%)	1 (1%)	21	20
36	g	166/177 (94%)	164 (99%)	2 (1%)	0	100	100
37	h	39/149 (26%)	37 (95%)	2 (5%)	0	100	100
38	i	139/142 (98%)	138 (99%)	1 (1%)	0	100	100
39	j	121/123 (98%)	117 (97%)	4 (3%)	0	100	100
40	k	142/144 (99%)	136 (96%)	5 (4%)	1 (1%)	18	16
41	l	132/136 (97%)	129 (98%)	3 (2%)	0	100	100
42	m	116/127 (91%)	112 (97%)	4 (3%)	0	100	100
43	n	114/117 (97%)	110 (96%)	4 (4%)	0	100	100
44	o	112/115 (97%)	110 (98%)	2 (2%)	0	100	100
45	p	115/118 (98%)	114 (99%)	1 (1%)	0	100	100
46	q	101/103 (98%)	100 (99%)	0	1 (1%)	12	9
47	r	107/110 (97%)	105 (98%)	2 (2%)	0	100	100
48	s	91/100 (91%)	88 (97%)	3 (3%)	0	100	100
49	t	89/104 (86%)	88 (99%)	1 (1%)	0	100	100
50	u	91/94 (97%)	88 (97%)	3 (3%)	0	100	100
51	v	73/85 (86%)	71 (97%)	2 (3%)	0	100	100
52	w	75/78 (96%)	75 (100%)	0	0	100	100
53	x	58/63 (92%)	58 (100%)	0	0	100	100
54	y	56/59 (95%)	55 (98%)	1 (2%)	0	100	100
55	z	52/57 (91%)	51 (98%)	1 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	6064/6606 (92%)	5915 (98%)	142 (2%)	7 (0%)	49 54

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
17	J	57	VAL
35	f	42	GLU
9	B	165	ASP
40	k	29	LYS
15	H	75	ILE

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	0	46/49 (94%)	45 (98%)	1 (2%)	45 54
2	1	37/38 (97%)	37 (100%)	0	100 100
3	2	51/52 (98%)	51 (100%)	0	100 100
4	3	34/34 (100%)	34 (100%)	0	100 100
5	4	44/62 (71%)	44 (100%)	0	100 100
9	B	184/199 (92%)	178 (97%)	6 (3%)	33 39
10	C	170/190 (90%)	168 (99%)	2 (1%)	63 72
11	D	172/173 (99%)	167 (97%)	5 (3%)	37 44
12	E	117/126 (93%)	116 (99%)	1 (1%)	70 78
13	F	88/116 (76%)	88 (100%)	0	100 100
14	G	124/147 (84%)	120 (97%)	4 (3%)	34 40
15	H	104/105 (99%)	103 (99%)	1 (1%)	68 76
16	I	103/107 (96%)	100 (97%)	3 (3%)	37 44
17	J	85/90 (94%)	84 (99%)	1 (1%)	63 72
18	K	89/98 (91%)	87 (98%)	2 (2%)	45 54
19	L	101/103 (98%)	98 (97%)	3 (3%)	36 43

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
20	M	93/96 (97%)	92 (99%)	1 (1%)	65	74
21	N	83/84 (99%)	83 (100%)	0	100	100
22	O	76/77 (99%)	76 (100%)	0	100	100
23	P	64/65 (98%)	64 (100%)	0	100	100
24	Q	73/78 (94%)	69 (94%)	4 (6%)	19	18
25	R	55/65 (85%)	55 (100%)	0	100	100
26	S	72/79 (91%)	72 (100%)	0	100	100
27	T	65/66 (98%)	64 (98%)	1 (2%)	57	66
28	U	48/61 (79%)	48 (100%)	0	100	100
29	W	556/579 (96%)	545 (98%)	11 (2%)	48	58
32	c	216/218 (99%)	215 (100%)	1 (0%)	81	86
33	d	162/163 (99%)	162 (100%)	0	100	100
34	e	165/165 (100%)	165 (100%)	0	100	100
35	f	148/150 (99%)	145 (98%)	3 (2%)	48	58
36	g	132/138 (96%)	128 (97%)	4 (3%)	36	43
37	h	32/114 (28%)	32 (100%)	0	100	100
38	i	115/116 (99%)	113 (98%)	2 (2%)	53	63
39	j	104/104 (100%)	104 (100%)	0	100	100
40	k	103/103 (100%)	102 (99%)	1 (1%)	68	76
41	l	107/107 (100%)	105 (98%)	2 (2%)	50	59
42	m	98/103 (95%)	98 (100%)	0	100	100
43	n	86/87 (99%)	83 (96%)	3 (4%)	32	37
44	o	99/100 (99%)	99 (100%)	0	100	100
45	p	89/90 (99%)	89 (100%)	0	100	100
46	q	84/84 (100%)	83 (99%)	1 (1%)	63	72
47	r	92/93 (99%)	92 (100%)	0	100	100
48	s	80/84 (95%)	80 (100%)	0	100	100
49	t	76/85 (89%)	76 (100%)	0	100	100
50	u	77/78 (99%)	77 (100%)	0	100	100
51	v	56/63 (89%)	56 (100%)	0	100	100
52	w	67/68 (98%)	67 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
53	x	54/55 (98%)	54 (100%)	0	100	100
54	y	48/49 (98%)	48 (100%)	0	100	100
55	z	46/48 (96%)	46 (100%)	0	100	100
All	All	5070/5404 (94%)	5007 (99%)	63 (1%)	61	72

5 of 63 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
19	L	120	LYS
38	i	95	ARG
29	W	90	VAL
38	i	9	GLU
43	n	49	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 60 such sidechains are listed below:

Mol	Chain	Res	Type
23	P	26	ASN
50	u	12	GLN
29	W	158	ASN
50	u	5	ASN
54	y	20	HIS

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
30	a	2778/2930 (94%)	309 (11%)	0
31	b	118/119 (99%)	7 (5%)	0
6	8	76/77 (98%)	15 (19%)	3 (3%)
7	9	4/24 (16%)	0	0
8	A	1524/1554 (98%)	240 (15%)	47 (3%)
All	All	4500/4704 (95%)	571 (12%)	50 (1%)

5 of 571 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
6	8	7	G
6	8	8	U
6	8	9	G

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Mol	Chain	Res	Type
6	8	16	C
6	8	17(A)	U

5 of 50 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
8	A	1031	C
8	A	1157	A
8	A	1505	G
8	A	1092	A
8	A	1124	G

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

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

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
30	6MZ	a	2030	30	22,25,26	0.30	0	30,36,39	0.59	0
30	5MU	a	1939	30,57	19,22,23	0.30	0	28,32,35	0.37	0
30	PSU	a	2457	30	18,21,22	0.88	1 (5%)	22,30,33	0.62	0
30	3TD	a	1915	30	18,22,23	0.98	1 (5%)	22,32,35	0.62	0
8	5MC	A	1407	8	18,22,23	0.32	0	26,32,35	0.54	0
30	PSU	a	1911	30	18,21,22	0.92	1 (5%)	22,30,33	0.66	0
30	PSU	a	2605	30	18,21,22	0.90	1 (5%)	22,30,33	0.75	0
8	PSU	A	516	8	18,21,22	0.91	1 (5%)	22,30,33	0.59	0
41	4D4	l	81	41	9,11,12	0.55	0	8,13,15	0.70	0
30	PSU	a	2580	30,57	18,21,22	0.90	1 (5%)	22,30,33	0.85	1 (4%)
30	2MA	a	2503	30,58,57	22,25,26	0.91	1 (4%)	33,37,40	1.07	4 (12%)
30	5MU	a	747	30	19,22,23	0.26	0	28,32,35	0.42	0
8	MA6	A	1519	8	23,26,27	0.25	0	34,38,41	0.72	1 (2%)
8	4OC	A	1402	8	20,23,24	0.39	0	26,32,35	0.42	0
30	1MG	a	745	30	22,26,27	0.52	0	33,39,42	0.46	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	G7M	A	527	8	23,26,27	0.71	1 (4%)	35,39,42	0.55	0
30	PSU	a	1917	30	18,21,22	0.89	1 (5%)	22,30,33	0.52	0
8	MA6	A	1518	8	23,26,27	0.26	0	34,38,41	0.65	1 (2%)
33	MEQ	d	150	33	8,9,10	0.43	0	5,10,12	0.54	0
18	IAS	K	119	18	6,7,8	0.91	0	6,8,10	0.99	0
30	6MZ	a	1618	30	22,25,26	0.39	0	30,36,39	0.57	0
8	5MC	A	967	8	18,22,23	0.33	0	26,32,35	0.49	0
30	H2U	a	2449	30	18,21,22	0.60	0	21,30,33	0.88	2 (9%)
30	PSU	a	746	30,58	18,21,22	0.95	1 (5%)	22,30,33	0.60	0
30	5MC	a	1962	30	18,22,23	0.34	0	26,32,35	0.50	0
30	OMG	a	2251	30,57	23,26,27	0.32	0	33,38,41	0.39	0
30	PSU	a	2504	30,57	18,21,22	0.85	1 (5%)	22,30,33	0.76	0
30	PSU	a	955	30	18,21,22	0.88	1 (5%)	22,30,33	0.65	0
30	2MG	a	1835	30	23,26,27	0.39	0	32,38,41	0.36	0
30	G7M	a	2069	30	23,26,27	0.69	1 (4%)	35,39,42	0.64	0
30	2MG	a	2445	30	23,26,27	0.39	0	32,38,41	0.42	0
19	D2T	L	89	19	7,9,10	0.94	0	6,11,13	1.85	4 (66%)
41	MS6	l	82	41	5,7,8	0.22	0	2,7,9	0.01	0
8	2MG	A	966	8	23,26,27	0.41	0	32,38,41	0.35	0
30	OMU	a	2552	30	19,22,23	0.21	0	26,31,34	0.40	0
8	UR3	A	1498	8	19,22,23	0.28	0	26,32,35	0.64	0
8	2MG	A	1516	8	23,26,27	0.39	0	32,38,41	0.49	0
30	OMC	a	2498	30,58	19,22,23	0.28	0	26,31,34	0.53	0
8	2MG	A	1207	8	23,26,27	0.40	0	32,38,41	0.38	0
30	PSU	a	2604	30	18,21,22	0.91	1 (5%)	22,30,33	0.75	1 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
30	6MZ	a	2030	30	-	2/9/27/28	0/3/3/3
30	5MU	a	1939	30,57	-	0/7/25/26	0/2/2/2
30	PSU	a	2457	30	-	0/7/25/26	0/2/2/2
30	3TD	a	1915	30	-	0/7/25/26	0/2/2/2
8	5MC	A	1407	8	-	0/7/25/26	0/2/2/2
30	PSU	a	1911	30	-	2/7/25/26	0/2/2/2
30	PSU	a	2605	30	-	0/7/25/26	0/2/2/2
8	PSU	A	516	8	-	0/7/25/26	0/2/2/2

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
41	4D4	l	81	41	-	1/11/12/14	-
30	PSU	a	2580	30,57	-	0/7/25/26	0/2/2/2
30	2MA	a	2503	30,58,57	-	1/7/25/26	0/3/3/3
30	5MU	a	747	30	-	1/7/25/26	0/2/2/2
8	MA6	A	1519	8	-	0/11/29/30	0/3/3/3
8	4OC	A	1402	8	-	0/9/29/30	0/2/2/2
30	1MG	a	745	30	-	0/7/25/26	0/3/3/3
8	G7M	A	527	8	-	2/7/25/26	0/3/3/3
30	PSU	a	1917	30	-	0/7/25/26	0/2/2/2
8	MA6	A	1518	8	-	0/11/29/30	0/3/3/3
33	MEQ	d	150	33	-	2/8/9/11	-
18	IAS	K	119	18	-	2/7/7/8	-
30	6MZ	a	1618	30	-	0/9/27/28	0/3/3/3
8	5MC	A	967	8	-	0/7/25/26	0/2/2/2
30	H2U	a	2449	30	-	0/7/38/39	0/2/2/2
30	PSU	a	746	30,58	-	2/7/25/26	0/2/2/2
30	5MC	a	1962	30	-	2/7/25/26	0/2/2/2
30	OMG	a	2251	30,57	-	1/9/27/28	0/3/3/3
30	PSU	a	2504	30,57	-	2/7/25/26	0/2/2/2
30	PSU	a	955	30	-	0/7/25/26	0/2/2/2
30	2MG	a	1835	30	-	0/9/27/28	0/3/3/3
30	G7M	a	2069	30	-	2/7/25/26	0/3/3/3
30	2MG	a	2445	30	-	1/9/27/28	0/3/3/3
19	D2T	L	89	19	-	4/7/12/14	-
41	MS6	l	82	41	-	1/4/6/8	-
8	2MG	A	966	8	-	2/9/27/28	0/3/3/3
30	OMU	a	2552	30	-	0/9/27/28	0/2/2/2
8	UR3	A	1498	8	-	0/7/25/26	0/2/2/2
8	2MG	A	1516	8	-	0/9/27/28	0/3/3/3
30	OMC	a	2498	30,58	-	0/9/27/28	0/2/2/2
8	2MG	A	1207	8	-	0/9/27/28	0/3/3/3
30	PSU	a	2604	30	-	0/7/25/26	0/2/2/2

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	746	PSU	C6-C5	3.77	1.39	1.35
30	a	1915	3TD	C6-C5	3.71	1.39	1.35
30	a	1911	PSU	C6-C5	3.65	1.39	1.35
8	A	516	PSU	C6-C5	3.58	1.39	1.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
30	a	2580	PSU	C6-C5	3.58	1.39	1.35

The worst 5 of 14 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
30	a	2503	2MA	C5-C4-N3	-2.99	123.83	127.19
8	A	1518	MA6	C2-N1-C6	2.92	118.65	111.75
8	A	1519	MA6	C2-N1-C6	2.91	118.64	111.75
30	a	2580	PSU	C3'-C2'-C1'	2.75	104.84	101.64
19	L	89	D2T	OD1-CG-CB	-2.58	117.03	122.44

There are no chirality outliers.

5 of 30 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
19	L	89	D2T	CA-CB-CG-OD1
19	L	89	D2T	CA-CB-CG-OD2
30	a	746	PSU	C2'-C1'-C5-C4
30	a	1911	PSU	O4'-C1'-C5-C4
30	a	1911	PSU	O4'-C1'-C5-C6

There are no ring outliers.

12 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
30	a	2030	6MZ	1	0
30	a	1939	5MU	1	0
30	a	1915	3TD	1	0
30	a	1911	PSU	1	0
30	a	747	5MU	1	0
8	A	1519	MA6	1	0
8	A	1402	4OC	2	0
8	A	1518	MA6	1	0
30	a	2449	H2U	1	0
30	a	2445	2MG	1	0
30	a	2552	OMU	1	0
30	a	2604	PSU	1	0

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 369 ligands modelled in this entry, 367 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
59	GDP	W	701	58	28,30,30	0.46	0	44,47,47	0.41	0
60	FUA	W	703	-	39,40,40	1.48	2 (5%)	49,64,64	0.91	2 (4%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
59	GDP	W	701	58	-	1/16/32/32	0/3/3/3
60	FUA	W	703	-	-	7/15/92/92	0/4/4/4

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
60	W	703	FUA	C29-C22	-8.49	1.35	1.47
60	W	703	FUA	O5-C29	-2.32	1.23	1.30

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
60	W	703	FUA	C14-C8-C9	-2.20	105.10	109.40
60	W	703	FUA	C16-O2-C31	2.16	120.34	117.06

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
60	W	703	FUA	C13-C17-C22-C29
60	W	703	FUA	C32-C31-O2-C16

Continued on next page...

Continued from previous page...

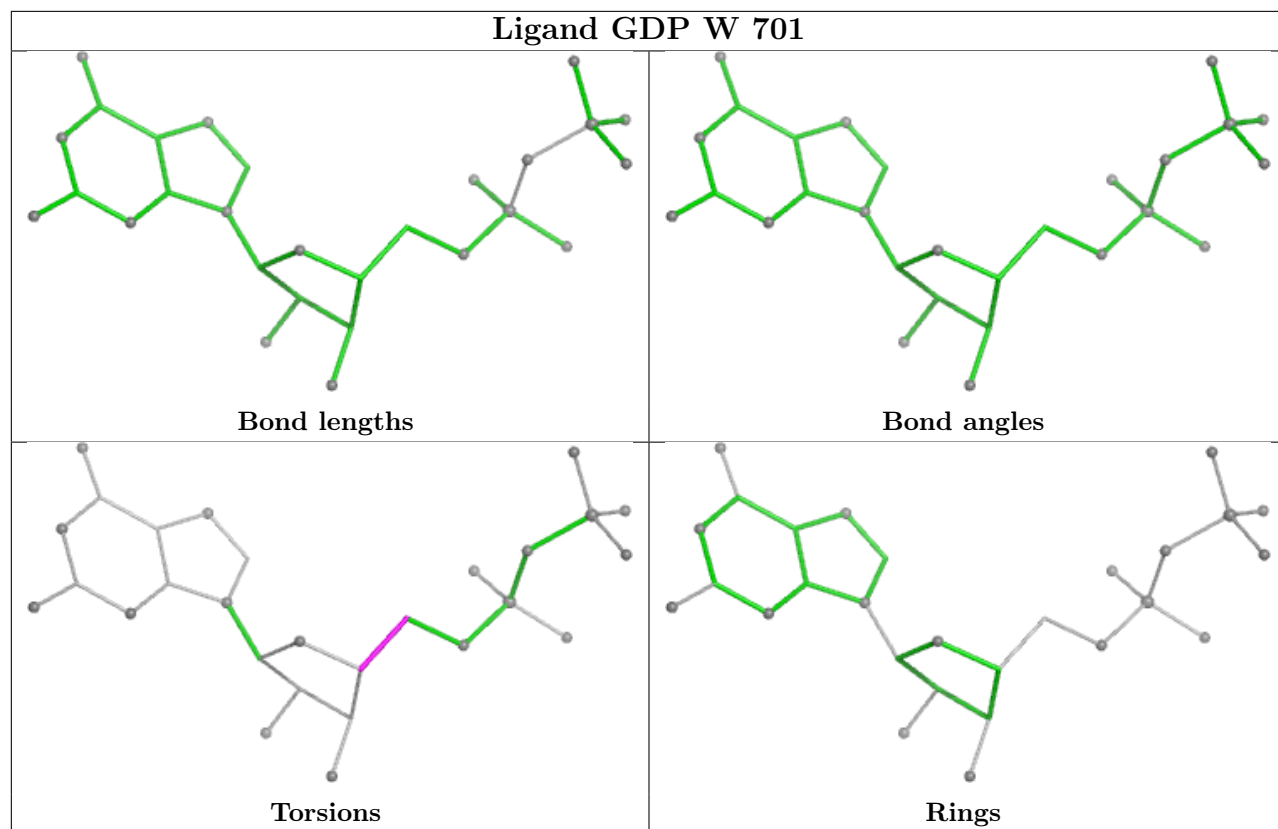
Mol	Chain	Res	Type	Atoms
60	W	703	FUA	O3-C31-O2-C16
60	W	703	FUA	C29-C22-C23-C24
60	W	703	FUA	C17-C22-C29-O4

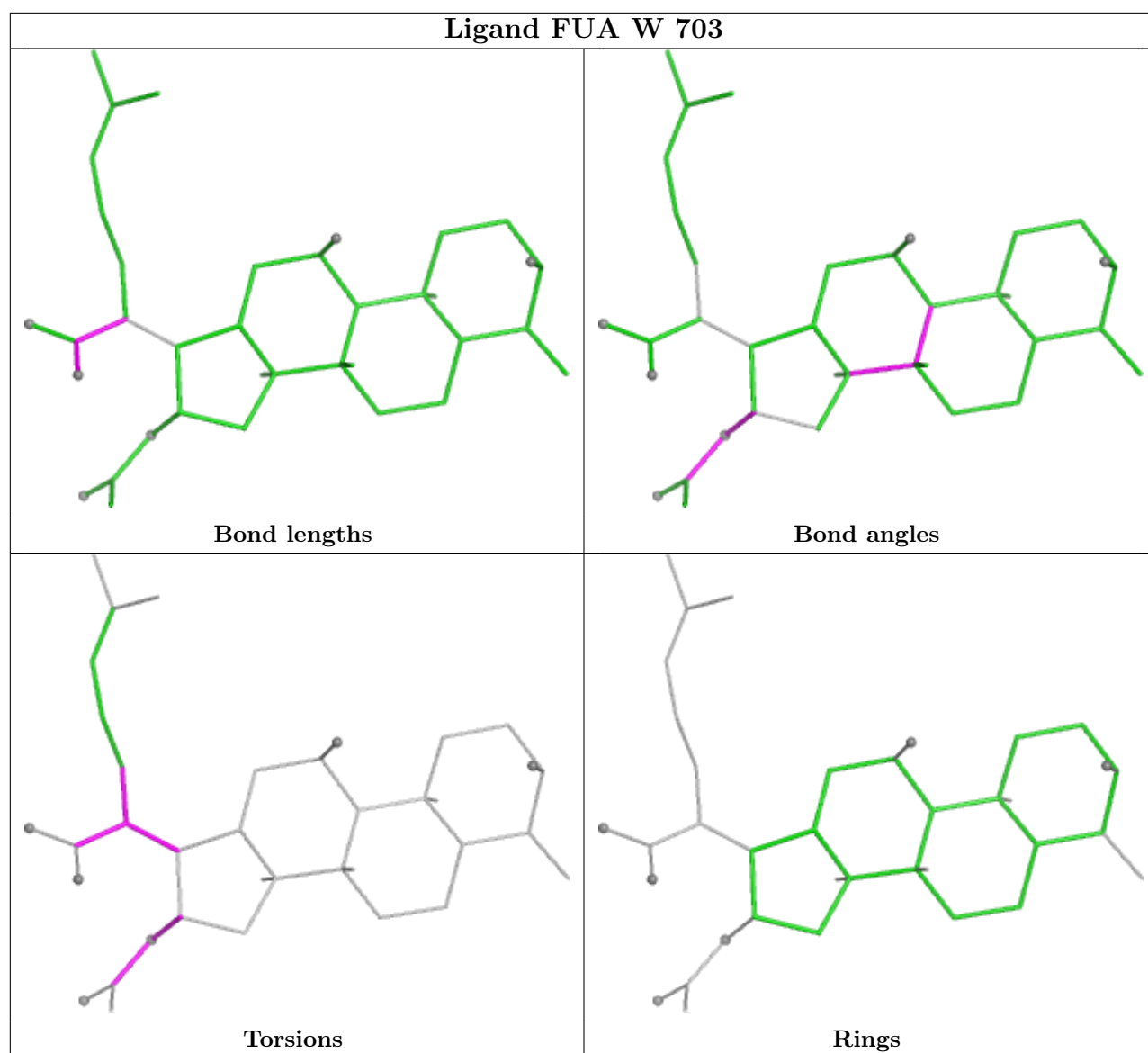
There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
60	W	703	FUA	5	0

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





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

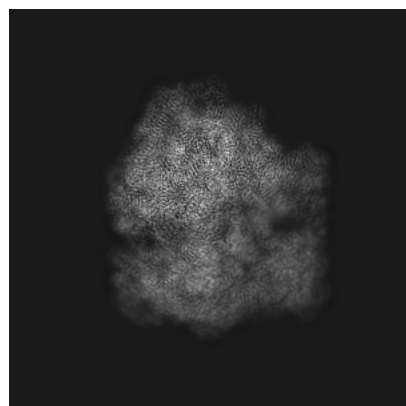
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-51350. These allow visual inspection of the internal detail of the map and identification of artifacts.

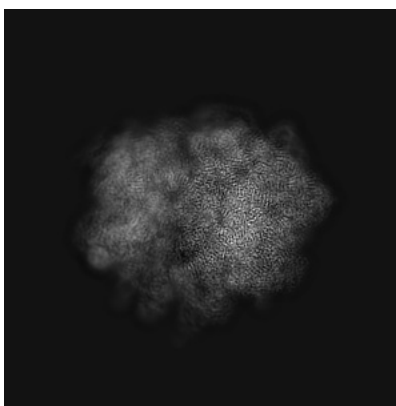
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

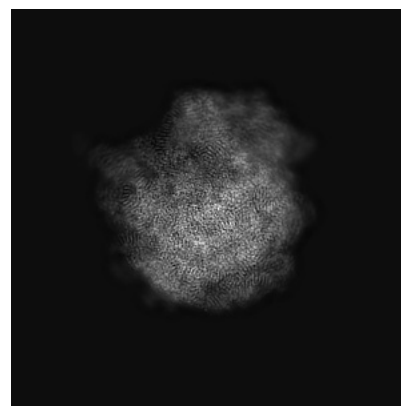
6.1.1 Primary map



X

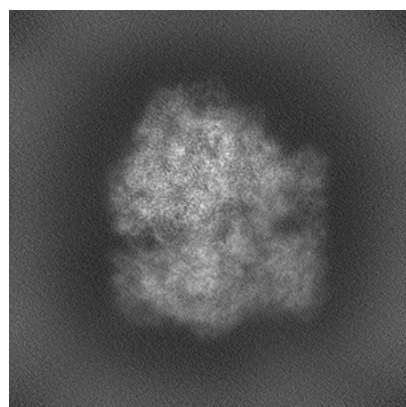


Y

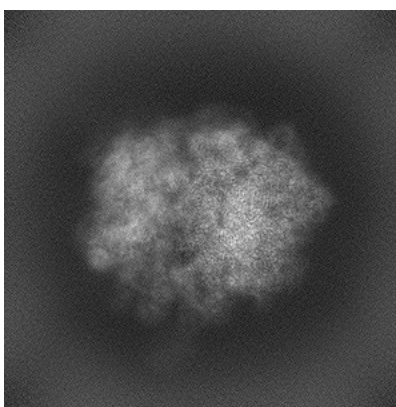


Z

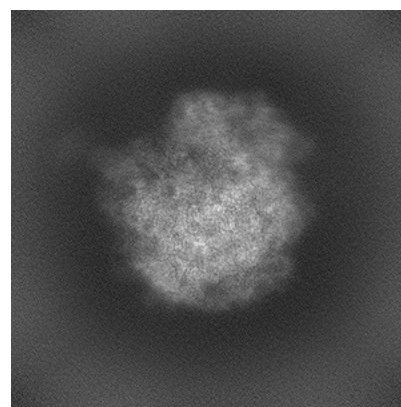
6.1.2 Raw map



X



Y

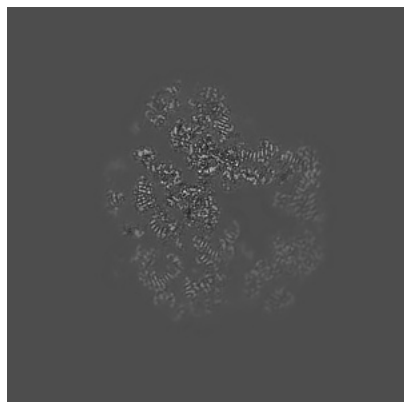


Z

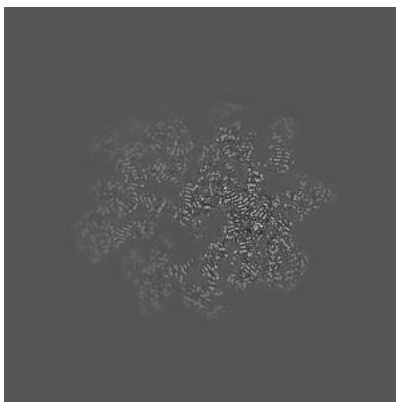
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

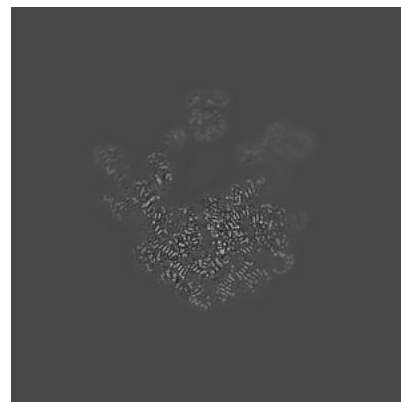
6.2.1 Primary map



X Index: 300

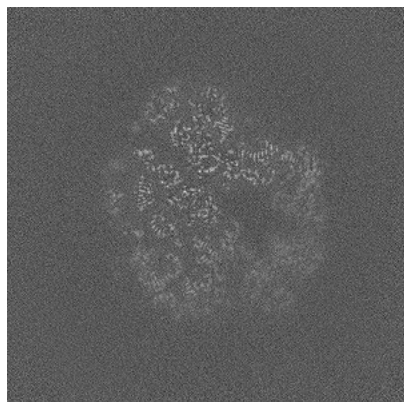


Y Index: 300

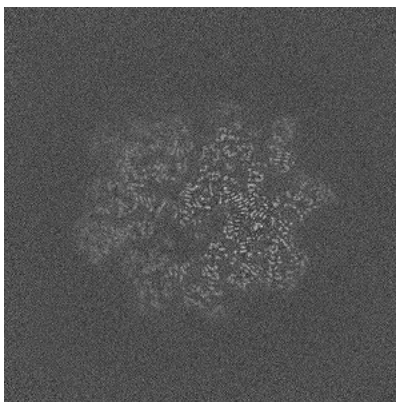


Z Index: 300

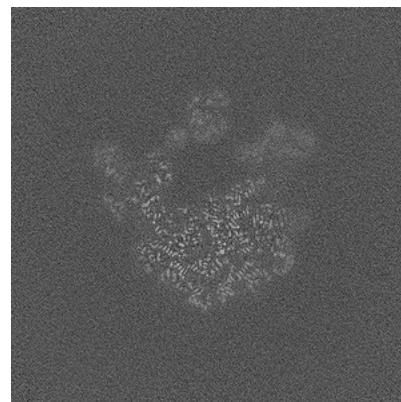
6.2.2 Raw map



X Index: 300



Y Index: 300

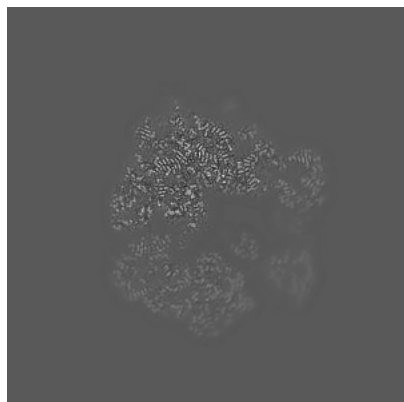


Z Index: 300

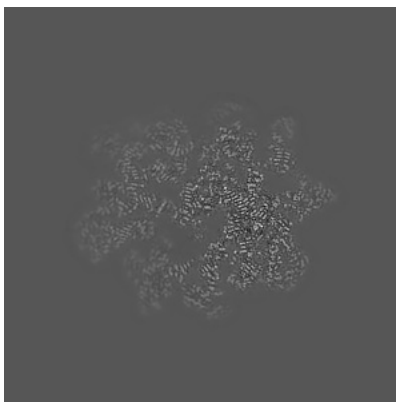
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

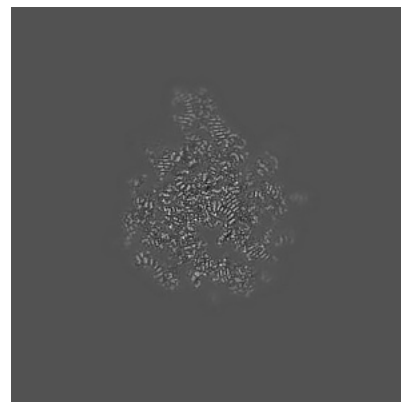
6.3.1 Primary map



X Index: 268

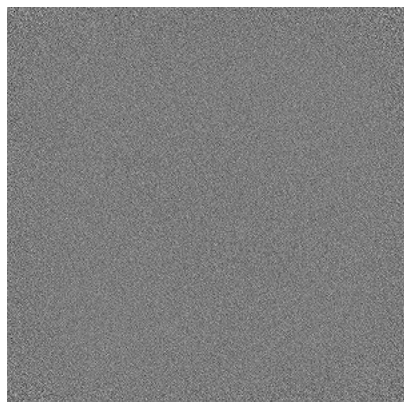


Y Index: 300

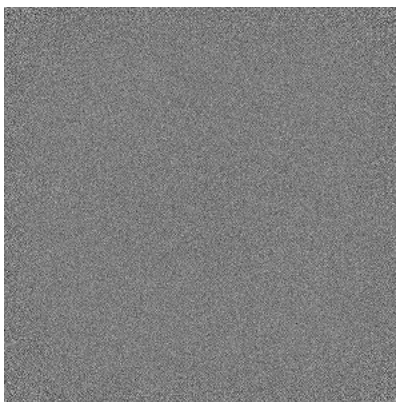


Z Index: 372

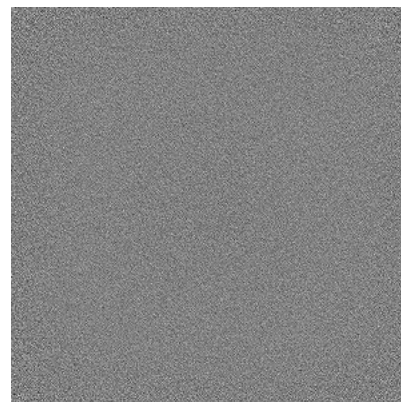
6.3.2 Raw map



X Index: 0



Y Index: 0

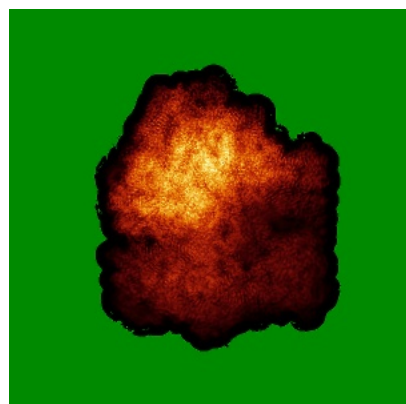


Z Index: 0

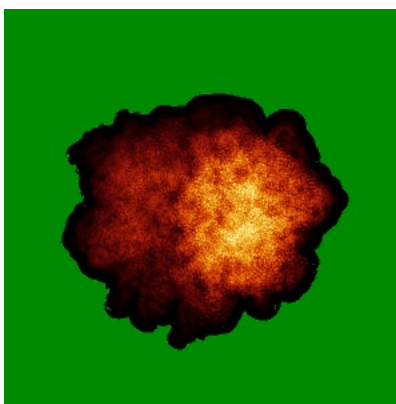
The images above show the largest variance slices of the map in three orthogonal directions.

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

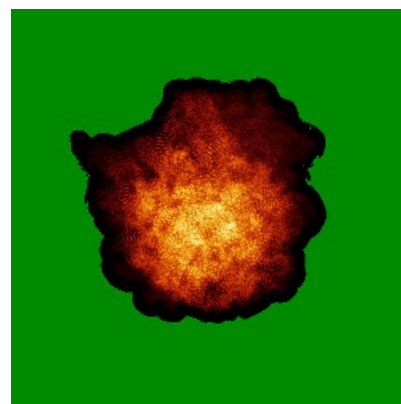
6.4.1 Primary map



X

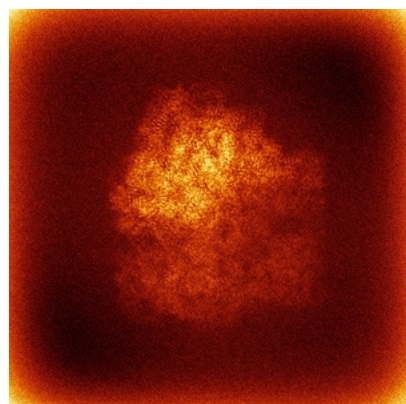


Y

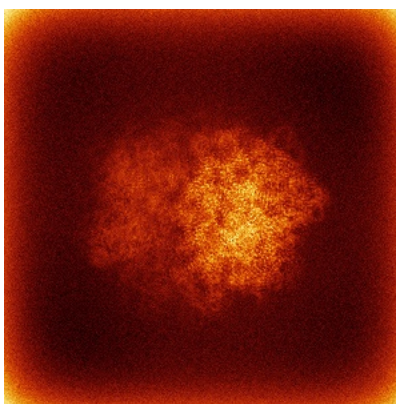


Z

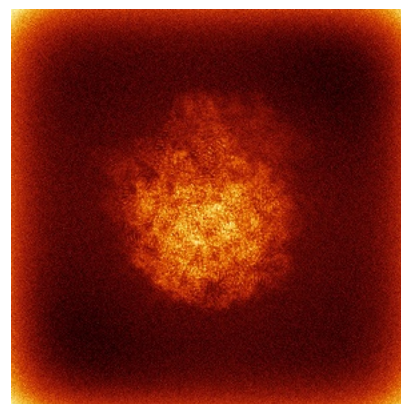
6.4.2 Raw map



X



Y



Z

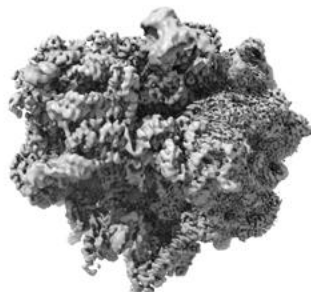
The images above show the map standard deviation projections with false color in three orthogonal directions. Minimum values are shown in green, max in blue, and dark to light orange shades represent small to large values respectively.

6.5 Orthogonal surface views [i](#)

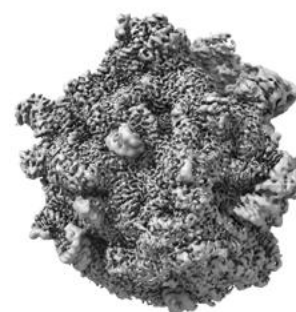
6.5.1 Primary map



X



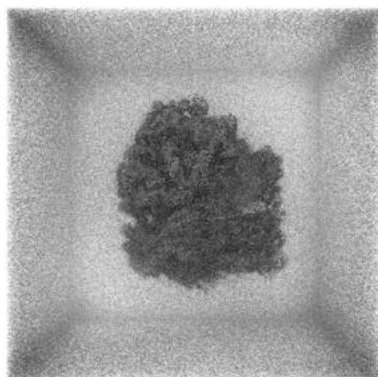
Y



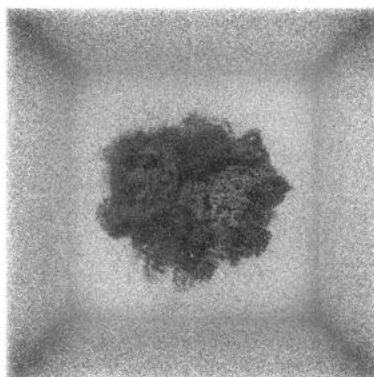
Z

The images above show the 3D surface view of the map at the recommended contour level 0.02. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

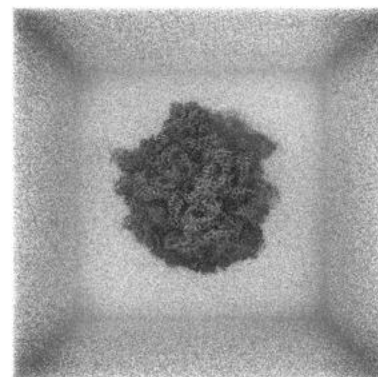
6.5.2 Raw map



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.

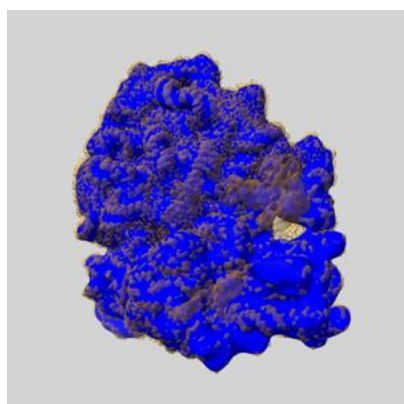
6.6 Mask visualisation [i](#)

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

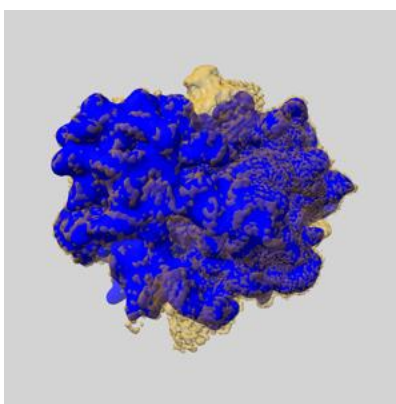
A mask typically either:

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

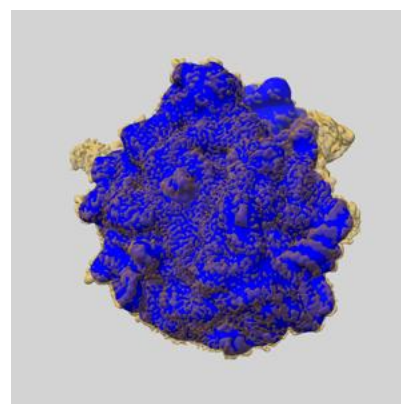
6.6.1 emd_51350_msk_1.map [i](#)



X



Y

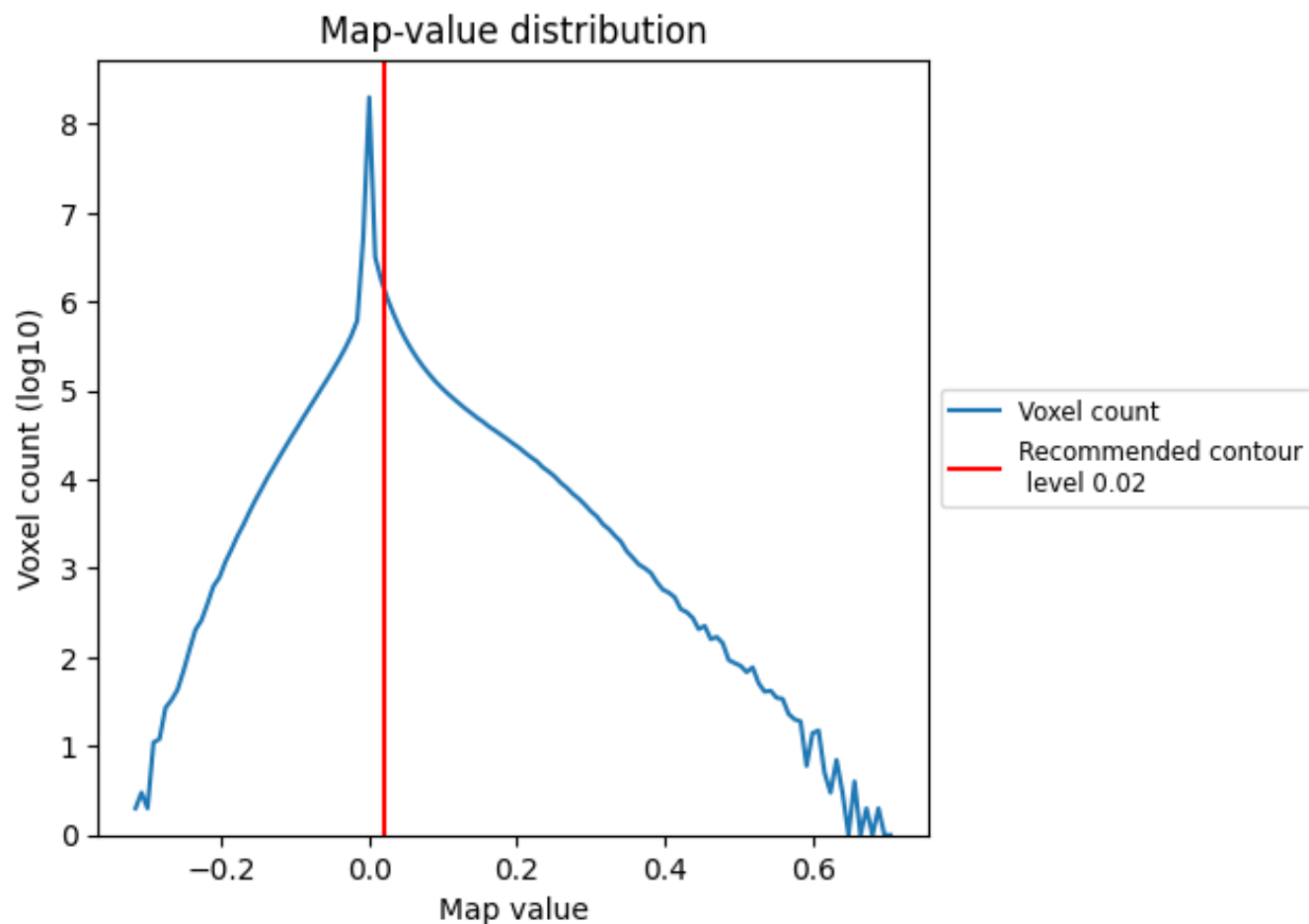


Z

7 Map analysis [i](#)

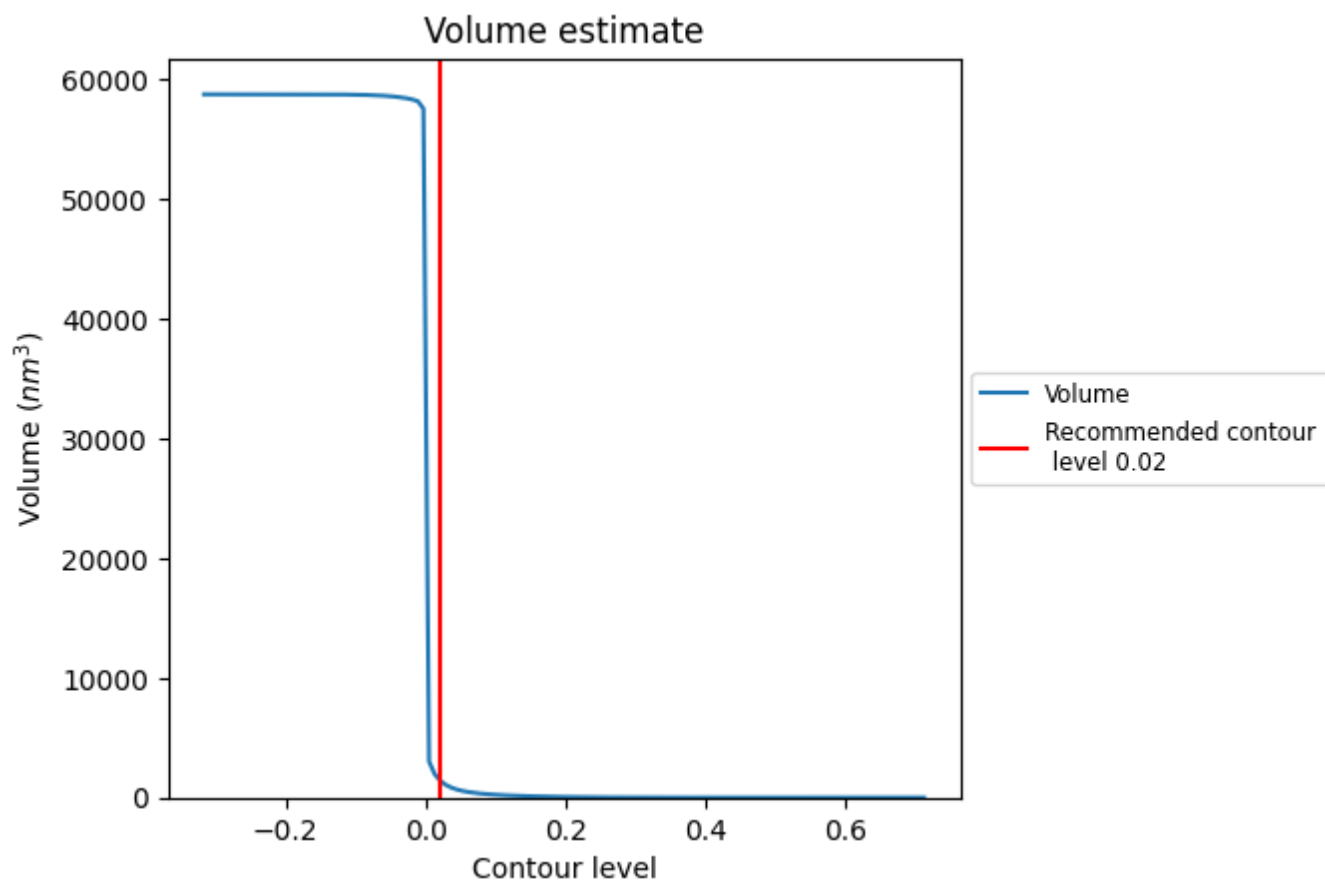
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

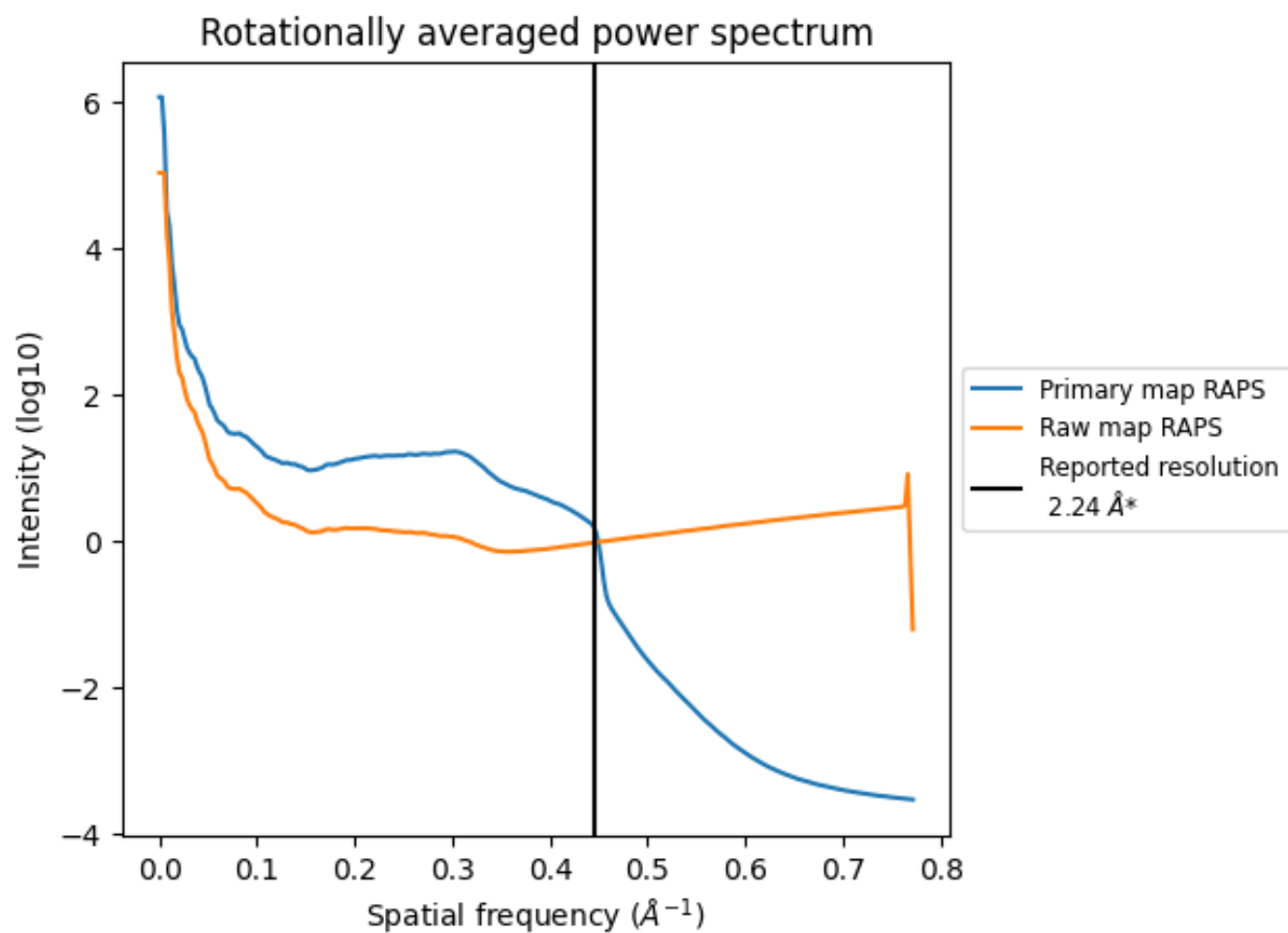
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1500 nm³; this corresponds to an approximate mass of 1355 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 ⓘ

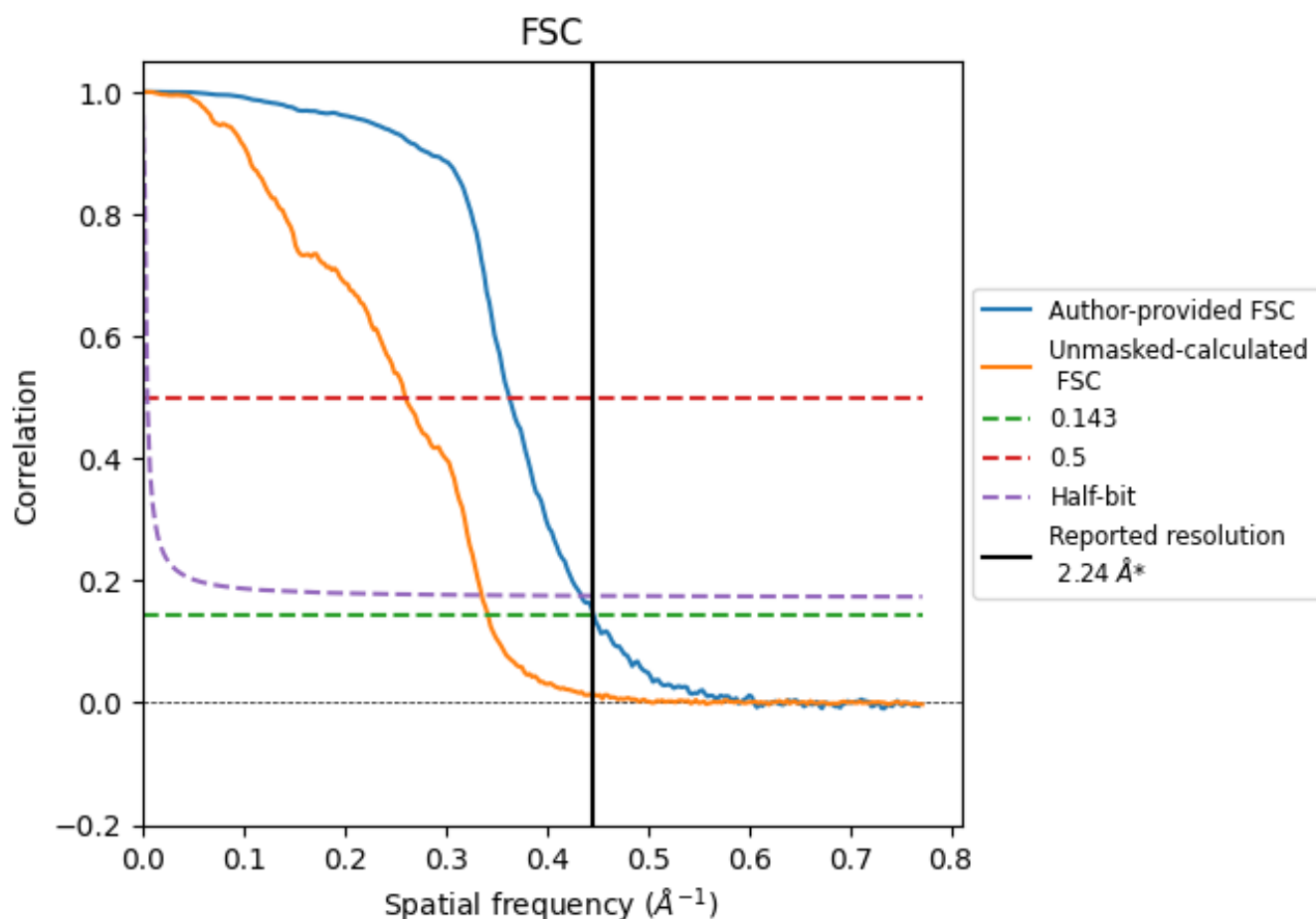


*Reported resolution corresponds to spatial frequency of 0.446 Å⁻¹

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 $0.446 \text{ \AA}^{-1}$

8.2 Resolution estimates [i](#)

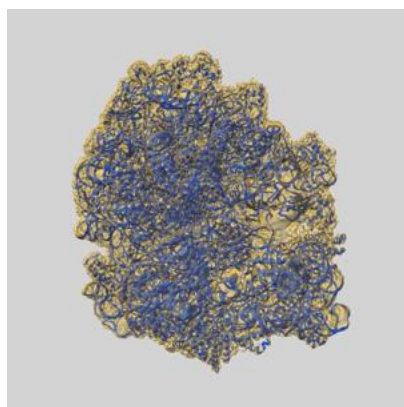
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.24	-	-
Author-provided FSC curve	2.24	2.75	2.30
Unmasked-calculated*	2.92	3.84	2.98

*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 2.92 differs from the reported value 2.24 by more than 10 %

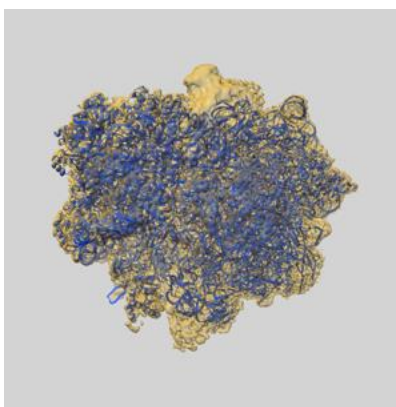
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-51350 and PDB model 9GHA. Per-residue inclusion information can be found in [section 3](#) on [page 17](#).

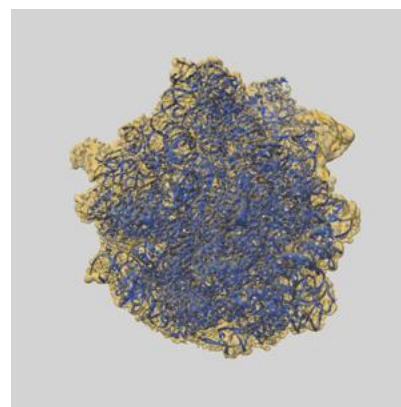
9.1 Map-model overlay [i](#)



X



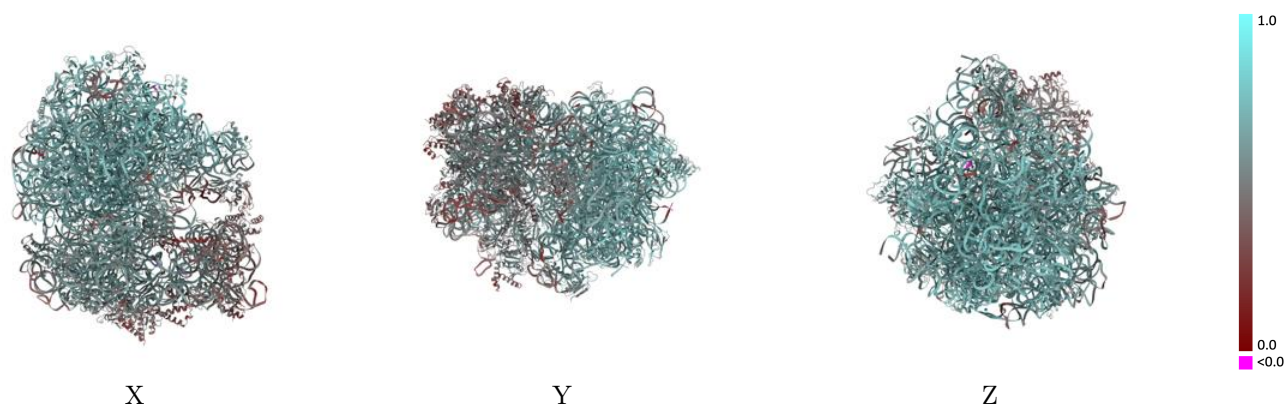
Y



Z

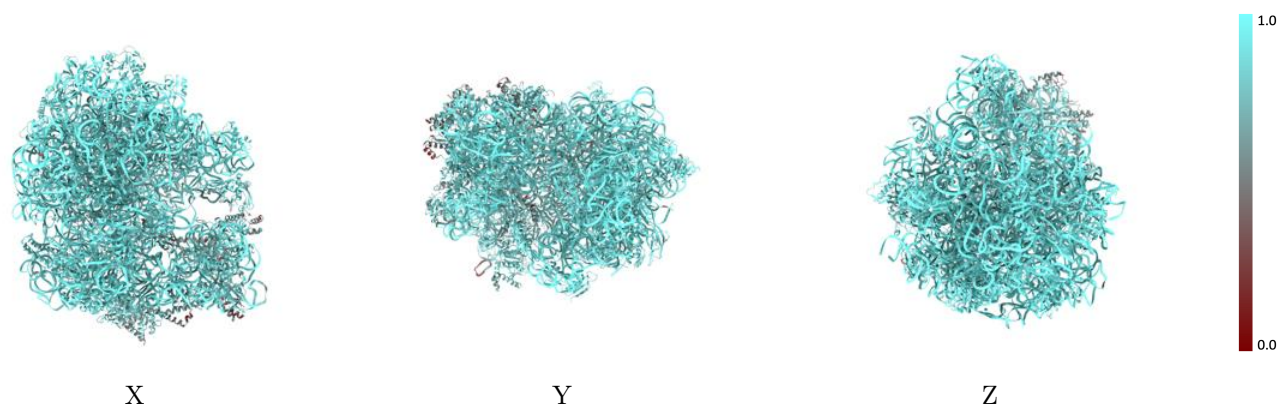
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



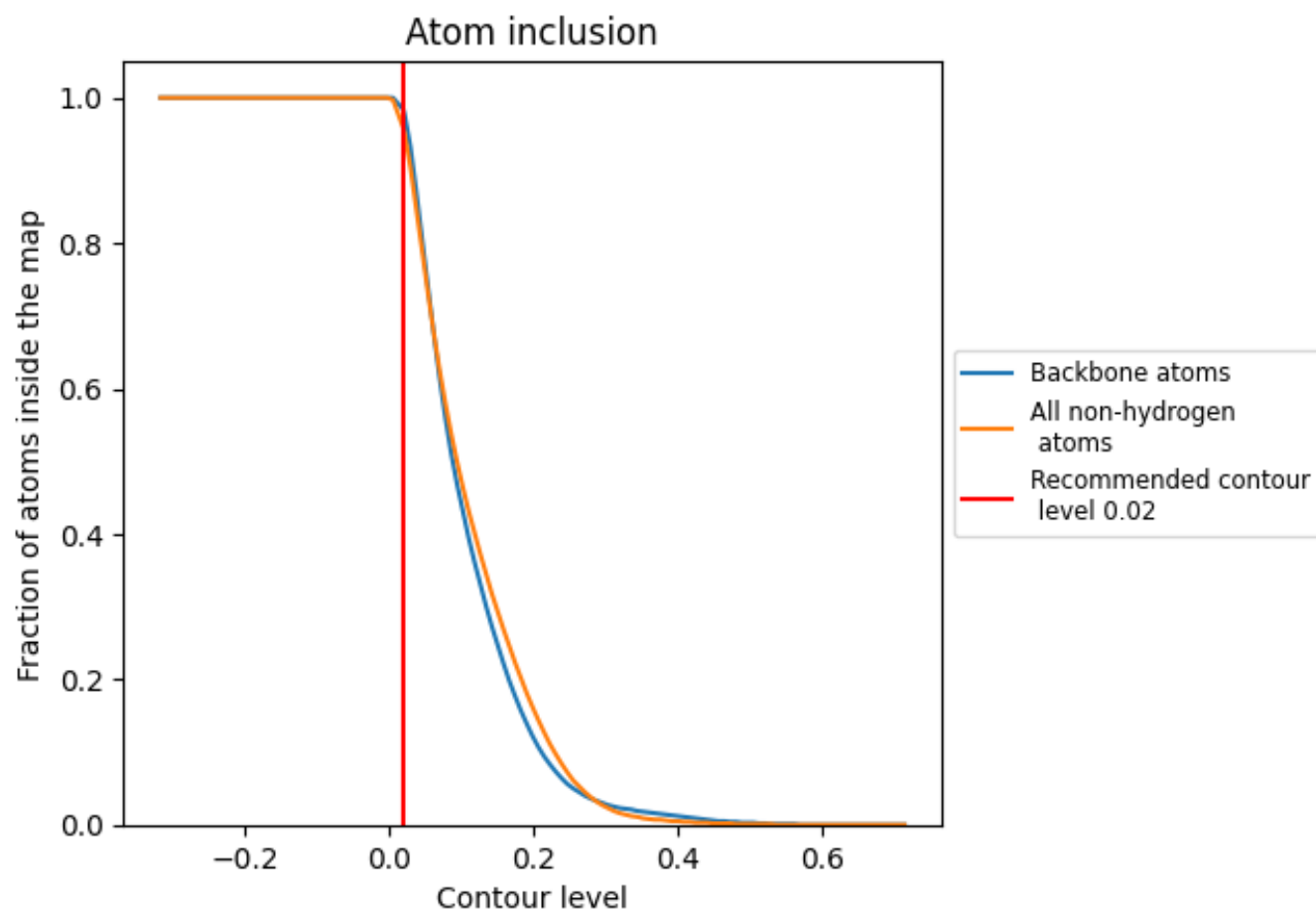
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

9.4 Atom inclusion [i](#)



At the recommended contour level, 98% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9570	 0.6150
0	 0.9460	 0.6380
1	 0.9970	 0.7540
2	 0.9940	 0.7340
3	 0.9930	 0.6730
4	 0.7980	 0.3930
8	 0.9290	 0.4840
9	 0.8730	 0.5040
A	 0.9740	 0.5540
B	 0.6740	 0.3880
C	 0.8280	 0.4780
D	 0.8720	 0.4780
E	 0.9200	 0.5390
F	 0.8780	 0.4970
G	 0.6590	 0.3370
H	 0.9170	 0.5450
I	 0.8110	 0.4350
J	 0.7150	 0.4190
K	 0.9040	 0.5440
L	 0.9340	 0.5650
M	 0.7040	 0.4140
N	 0.8820	 0.4880
O	 0.9250	 0.5580
P	 0.9490	 0.5510
Q	 0.9330	 0.5690
R	 0.9180	 0.5330
S	 0.8220	 0.4580
T	 0.9360	 0.5530
U	 0.8500	 0.5020
W	 0.8390	 0.4790
a	 0.9930	 0.6860
b	 0.9950	 0.6280
c	 0.9890	 0.7120
d	 0.9730	 0.7060
e	 0.9590	 0.6740



Continued on next page...

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Chain	Atom inclusion	Q-score
f	 0.8550	 0.4730
g	 0.9410	 0.5910
h	 0.9430	 0.5840
i	 0.9790	 0.7090
j	 0.9780	 0.6920
k	 0.9800	 0.7030
l	 0.9760	 0.6830
m	 0.9970	 0.7360
n	 0.9570	 0.6110
o	 0.9550	 0.6700
p	 0.9920	 0.7360
q	 0.9510	 0.6680
r	 0.9810	 0.7100
s	 0.9520	 0.6460
t	 0.9660	 0.6480
u	 0.9340	 0.6210
v	 0.9730	 0.6990
w	 0.9770	 0.6920
x	 0.9400	 0.6260
y	 0.9660	 0.6950
z	 0.9830	 0.7150