



wwPDB EM Validation Summary Report ⓘ

Mar 9, 2026 – 03:02 PM UTC

PDB ID : 5GMK / pdb_00005gmk
EMDB ID : EMD-9525
Title : Cryo-EM structure of the Catalytic Step I spliceosome (C complex) at 3.4 angstrom resolution
Authors : Wan, R.; Yan, C.; Bai, R.; Huang, G.; Shi, Y.
Deposited on : 2016-07-14
Resolution : 3.40 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.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

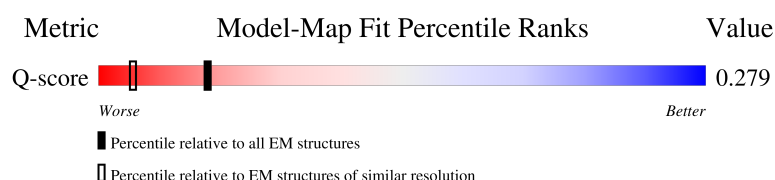
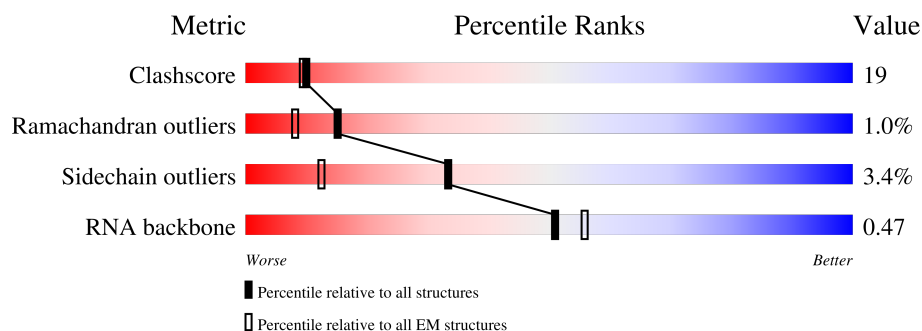
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.40 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	14717 (2.90 - 3.90)

2 Entry composition

There are 38 unique types of molecules in this entry. The entry contains 75273 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 Pre-mRNA-splicing factor 8.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1910	Total	C	N	O	S	0	0
			15775	10142	2709	2867	57		

- Molecule 2 is a protein called Pre-mRNA-splicing factor SNU114.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	C	878	Total	C	N	O	S	0	0
			7019	4529	1166	1295	29		

- Molecule 3 is a RNA chain called U5 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	117	Total	C	N	O	P	0	0
			2465	1104	414	830	117		

- Molecule 4 is a RNA chain called U6 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	E	103	Total	C	N	O	P	0	0
			2192	982	391	716	103		

- Molecule 5 is a RNA chain called U2 snRNA.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	L	127	Total	C	N	O	P	0	0
			2673	1197	445	904	127		

- Molecule 6 is a RNA chain called Intron_BPS.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	M	29	Total	C	N	O	P	0	0
			608	274	101	204	29		

- Molecule 7 is a RNA chain called 5'-Exon.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	B	13	Total	C	N	O	P	0	0
			275	124	47	91	13		

- Molecule 8 is a RNA chain called 5'-Splicing Site.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	N	15	Total	C	N	O	P	0	0
			312	140	45	112	15		

- Molecule 9 is a protein called Pre-mRNA-splicing factor CWC21.

Mol	Chain	Residues	Atoms				AltConf	Trace
9	J	27	Total	C	N	O	0	0
			190	112	38	40		

- Molecule 10 is a protein called Pre-mRNA-splicing factor PRP46.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	O	337	Total	C	N	O	S	0	0
			2646	1669	466	501	10		

- Molecule 11 is a protein called Pre-mRNA-processing protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	P	201	Total	C	N	O	S	0	0
			1583	988	290	298	7		

- Molecule 12 is a protein called Pre-mRNA-splicing factor SLT11.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	Q	185	Total	C	N	O	S	0	0
			1472	930	256	271	15		

- Molecule 13 is a protein called Pre-mRNA-splicing factor CWC2.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	R	261	Total	C	N	O	S	0	0
			2089	1320	369	388	12		

- Molecule 14 is a protein called Pre-mRNA-splicing factor CWC15.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	S	69	Total	C	N	O	S	0	0
			560	351	112	96	1		

- Molecule 15 is a protein called Pre-mRNA-splicing factor BUD31.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	T	157	Total	C	N	O	S	0	0
			1291	808	240	232	11		

- Molecule 16 is a protein called Pre-mRNA-splicing factor CWC22.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	Z	447	Total	C	N	O	S	0	0
			3651	2343	602	688	18		

- Molecule 17 is a protein called Pre-mRNA-splicing factor CEF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
17	c	436	Total	C	N	O	S	0	0
			2971	1841	549	573	8		

- Molecule 18 is a protein called Pre-mRNA-splicing factor CLF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
18	d	549	Total	C	N	O	S	0	0
			3590	2232	675	675	8		

- Molecule 19 is a protein called Protein CWC16.

Mol	Chain	Residues	Atoms					AltConf	Trace
19	F	115	Total	C	N	O	S	0	0
			937	592	167	169	9		

- Molecule 20 is a protein called Pre-mRNA-splicing factor CWC25.

Mol	Chain	Residues	Atoms					AltConf	Trace
20	G	41	Total	C	N	O	S	0	0
			342	215	63	63	1		

- Molecule 21 is a protein called Pre-mRNA-splicing factor ISY1.

Mol	Chain	Residues	Atoms					AltConf	Trace
21	H	95	Total	C	N	O	S	0	0
			810	506	152	151	1		

- Molecule 22 is a protein called Pre-mRNA-splicing factor SYF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
22	I	102	Total	C	N	O	S	0	0
			822	504	152	165	1		

- Molecule 23 is a protein called Pre-mRNA-splicing factor SYF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
23	v	673	Total	C	N	O	S	0	0
			3580	2190	683	706	1		

- Molecule 24 is a protein called Pre-mRNA-processing factor 17.

Mol	Chain	Residues	Atoms					AltConf	Trace
24	n	299	Total	C	N	O	S	0	0
			1890	1175	340	369	6		

- Molecule 25 is a protein called Pre-mRNA-processing factor 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
25	o	126	Total	C	N	O	S	0	0
			830	525	134	169	2		
25	p	128	Total	C	N	O	S	0	0
			843	532	136	173	2		
25	q	387	Total	C	N	O	S	0	0
			2345	1471	402	464	8		
25	r	125	Total	C	N	O	S	0	0
			823	521	133	167	2		

- Molecule 26 is a protein called Pre-mRNA-splicing factor SNT309.

Mol	Chain	Residues	Atoms					AltConf	Trace
26	t	156	Total	C	N	O	S	0	0
			926	585	160	180	1		

- Molecule 27 is a protein called Small nuclear ribonucleoprotein-associated protein B.

Mol	Chain	Residues	Atoms					AltConf	Trace
27	k	80	Total	C	N	O	S	0	0
			631	403	114	111	3		
27	s	78	Total	C	N	O	S	0	0
			610	389	110	108	3		

- Molecule 28 is a protein called Small nuclear ribonucleoprotein E.

Mol	Chain	Residues	Atoms					AltConf	Trace
28	i	75	Total	C	N	O	S	0	0
			575	379	92	101	3		
28	u	75	Total	C	N	O	S	0	0
			575	379	92	101	3		

- Molecule 29 is a protein called Small nuclear ribonucleoprotein F.

Mol	Chain	Residues	Atoms					AltConf	Trace
29	h	70	Total	C	N	O	S	0	0
			554	355	98	100	1		
29	w	70	Total	C	N	O	S	0	0
			554	355	98	100	1		

- Molecule 30 is a protein called Small nuclear ribonucleoprotein G.

Mol	Chain	Residues	Atoms					AltConf	Trace
30	j	69	Total	C	N	O	S	0	0
			529	337	93	97	2		
30	x	69	Total	C	N	O	S	0	0
			529	337	93	97	2		

- Molecule 31 is a protein called Small nuclear ribonucleoprotein Sm D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
31	l	82	Total	C	N	O	S	0	0
			625	399	109	115	2		
31	y	82	Total	C	N	O	S	0	0
			625	399	109	115	2		

- Molecule 32 is a protein called Small nuclear ribonucleoprotein Sm D1.

Mol	Chain	Residues	Atoms					AltConf	Trace
32	m	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

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Mol	Chain	Residues	Atoms					AltConf	Trace
32	z	82	Total	C	N	O	S	0	0
			644	409	110	123	2		

- Molecule 33 is a protein called Small nuclear ribonucleoprotein Sm D2.

Mol	Chain	Residues	Atoms					AltConf	Trace
33	g	94	Total	C	N	O	S	0	0
			741	477	141	119	4		
33	e	65	Total	C	N	O	S	0	0
			528	340	102	84	2		

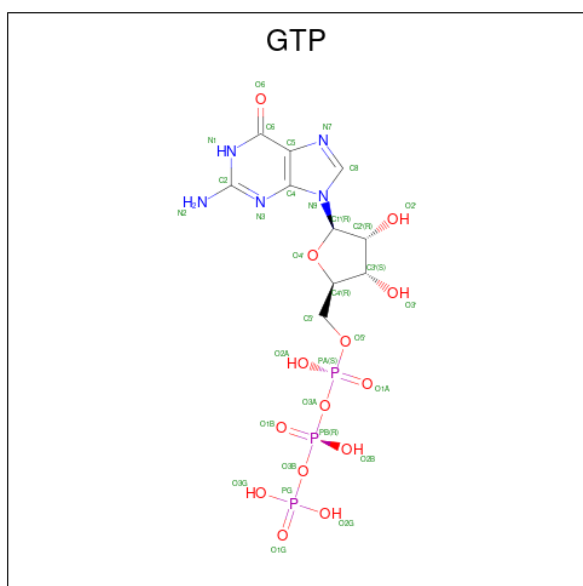
- Molecule 34 is a protein called U2 small nuclear ribonucleoprotein B''.

Mol	Chain	Residues	Atoms				AltConf	Trace
34	a	81	Total	C	N	O	0	0
			513	332	89	92		

- Molecule 35 is a protein called U2 small nuclear ribonucleoprotein A'.

Mol	Chain	Residues	Atoms				AltConf	Trace
35	b	135	Total	C	N	O	0	0
			841	538	142	161		

- Molecule 36 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					AltConf
36	C	1	Total	C	N	O	P	0
			32	10	5	14	3	

- Molecule 37 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
37	C	1	Total	Mg	0
			1	1	
37	E	5	Total	Mg	0
			5	5	

- Molecule 38 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		AltConf
38	Q	2	Total	Zn	0
			2	2	
38	R	1	Total	Zn	0
			1	1	
38	T	3	Total	Zn	0
			3	3	
38	F	1	Total	Zn	0
			1	1	

SEQUENCE-PLOTS INFOmissingINFO

3 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	161066	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	4.7	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.240	Depositor
Minimum map value	-0.120	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.0413	Depositor
Map size (Å)	522.4, 522.4, 522.4	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.3060001, 1.3060001, 1.3060001	Depositor

4 Model quality ⓘ

4.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, GTP, MG

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	A	0.43	5/16178 (0.0%)	0.63	9/21929 (0.0%)
2	C	0.41	3/7168 (0.0%)	0.57	6/9707 (0.1%)
3	D	0.36	0/2747	0.38	0/4267
4	E	0.38	1/2452 (0.0%)	0.37	0/3817
5	L	0.87	32/2974 (1.1%)	1.30	47/4610 (1.0%)
6	M	0.40	1/678 (0.1%)	0.68	3/1051 (0.3%)
7	B	0.65	1/307 (0.3%)	0.34	0/475
8	N	0.66	1/346 (0.3%)	0.51	0/535
9	J	0.37	0/191	0.56	0/254
10	O	0.52	0/2704	0.67	3/3676 (0.1%)
11	P	0.37	1/1604 (0.1%)	0.62	2/2160 (0.1%)
12	Q	0.45	1/1496 (0.1%)	0.75	2/2014 (0.1%)
13	R	0.37	0/2135	0.58	0/2871
14	S	0.42	1/574 (0.2%)	0.57	0/766
15	T	0.41	0/1315	0.66	0/1759
16	Z	0.55	0/3712	1.10	15/5004 (0.3%)
17	c	0.40	1/2405 (0.0%)	0.72	1/3218 (0.0%)
18	d	0.42	0/2107	0.58	1/2852 (0.0%)
19	F	0.28	0/955	0.57	0/1277
20	G	0.21	0/346	0.58	0/462
21	H	0.26	0/826	0.69	0/1108
22	I	0.27	0/826	0.44	0/1097
23	v	0.87	9/905 (1.0%)	1.11	9/1214 (0.7%)
24	n	1.12	16/1900 (0.8%)	1.13	24/2537 (0.9%)
25	o	0.54	0/835	0.85	0/1126
25	p	0.53	0/848	0.91	0/1143
25	q	0.64	0/2342	0.93	2/3139 (0.1%)
25	r	0.53	0/828	0.86	0/1117
26	t	0.58	0/924	1.06	2/1244 (0.2%)
27	k	0.55	0/636	0.76	0/856
27	s	0.54	0/615	0.76	0/829
28	i	0.63	0/585	0.86	0/795

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
28	u	0.63	0/585	0.86	0/795
29	h	0.61	0/564	0.87	0/761
29	w	0.60	0/564	0.87	0/761
30	j	0.53	0/532	0.82	1/715 (0.1%)
30	x	0.53	0/532	0.82	1/715 (0.1%)
31	l	0.55	0/634	0.96	2/859 (0.2%)
31	y	0.55	0/634	0.96	2/859 (0.2%)
32	m	0.58	0/649	0.81	0/880
32	z	0.58	0/649	0.81	0/880
33	e	0.64	0/535	0.86	2/717 (0.3%)
33	g	0.65	0/753	0.96	2/1013 (0.2%)
34	a	1.00	2/514 (0.4%)	1.86	7/686 (1.0%)
35	b	1.24	6/839 (0.7%)	2.35	45/1127 (4.0%)
All	All	0.54	81/72448 (0.1%)	0.81	188/99677 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	8
2	C	0	2
10	O	0	6
11	P	0	1
12	Q	0	3
16	Z	0	5
17	c	0	1
20	G	0	1
24	n	0	4
30	j	0	1
30	x	0	1
31	l	0	2
31	y	0	2
33	e	0	2
33	g	0	2
All	All	0	41

The worst 5 of 81 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	399	CYS	CB-SG	-12.11	1.41	1.81

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
24	n	444	CYS	CB-SG	-11.45	1.43	1.81
35	b	69	ASP	CA-CB	-10.58	1.38	1.53
24	n	454	CYS	CB-SG	-9.99	1.48	1.81
24	n	218	CYS	CB-SG	-9.77	1.49	1.81

The worst 5 of 188 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	483	PRO	O-C-N	-33.46	77.47	122.64
6	M	502	C	O3'-P-O5'	-16.03	79.95	104.00
35	b	44	PRO	N-CA-CB	15.91	113.89	103.23
35	b	81	LEU	CA-C-N	12.08	131.57	120.10
35	b	81	LEU	C-N-CA	12.08	131.57	120.10

There are no chirality outliers.

5 of 41 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	1014	LYS	Peptide
1	A	257	ASN	Peptide
1	A	483	PRO	Mainchain
1	A	539	PRO	Peptide
1	A	773	SER	Peptide

4.2 Too-close contacts [i](#)

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	A	15775	0	15756	748	0
2	C	7019	0	7201	319	0
3	D	2465	0	1251	79	0
4	E	2192	0	1106	134	0
5	L	2673	0	1360	331	0
6	M	608	0	307	45	0
7	B	275	0	137	20	0
8	N	312	0	156	19	0
9	J	190	0	186	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
10	O	2646	0	2639	131	0
11	P	1583	0	1608	91	0
12	Q	1472	0	1485	183	0
13	R	2089	0	2053	121	0
14	S	560	0	545	68	0
15	T	1291	0	1312	56	0
16	Z	3651	0	3707	187	0
17	c	2971	0	2336	81	0
18	d	3590	0	2359	96	0
19	F	937	0	962	59	0
20	G	342	0	360	16	0
21	H	810	0	799	36	0
22	I	822	0	845	72	0
23	v	3580	0	1298	68	0
24	n	1890	0	1407	89	0
25	o	830	0	663	6	0
25	p	843	0	675	8	0
25	q	2345	0	1636	43	0
25	r	823	0	654	7	0
26	t	926	0	606	15	0
27	k	631	0	670	3	0
27	s	610	0	640	17	0
28	i	575	0	597	21	0
28	u	575	0	597	21	0
29	h	554	0	556	17	0
29	w	554	0	556	18	0
30	j	529	0	557	2	0
30	x	529	0	557	3	0
31	l	625	0	647	7	0
31	y	625	0	647	8	0
32	m	644	0	686	14	0
32	z	644	0	686	14	0
33	e	528	0	573	37	0
33	g	741	0	778	18	0
34	a	513	0	402	13	0
35	b	841	0	614	17	0
36	C	32	0	12	1	0
37	C	1	0	0	0	0
37	E	5	0	0	0	0
38	F	1	0	0	0	0
38	Q	2	0	0	0	0
38	R	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
38	T	3	0	0	0	0
All	All	75273	0	65184	2725	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 19.

The worst 5 of 2725 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)
1:A:426:PRO:HB3	16:Z:201:ARG:CG	1.38	1.50
1:A:1327:THR:CG2	5:L:35:U:H5'	1.41	1.48
1:A:1327:THR:HG22	5:L:35:U:C5'	1.47	1.44
5:L:15:C:H1'	5:L:16:U:C5	1.50	1.42
23:v:729:TYR:CZ	23:v:748:UNK:CB	2.03	1.42

There are no symmetry-related clashes.

4.3 Torsion angles [i](#)

4.3.1 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	A	1902/2413 (79%)	1744 (92%)	149 (8%)	9 (0%)	24	54
2	C	872/1008 (86%)	796 (91%)	72 (8%)	4 (0%)	24	54
9	J	25/135 (18%)	20 (80%)	5 (20%)	0	100	100
10	O	335/451 (74%)	299 (89%)	31 (9%)	5 (2%)	8	30
11	P	193/379 (51%)	174 (90%)	17 (9%)	2 (1%)	12	40
12	Q	177/364 (49%)	154 (87%)	21 (12%)	2 (1%)	11	38
13	R	259/339 (76%)	241 (93%)	18 (7%)	0	100	100
14	S	63/175 (36%)	55 (87%)	5 (8%)	3 (5%)	2	11

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
15	T	155/157 (99%)	137 (88%)	16 (10%)	2 (1%)	9	33
16	Z	443/577 (77%)	390 (88%)	44 (10%)	9 (2%)	6	25
17	c	312/587 (53%)	291 (93%)	17 (5%)	4 (1%)	9	33
18	d	238/332 (72%)	221 (93%)	17 (7%)	0	100	100
19	F	-	104 (92%)	8 (7%)	1 (1%)	14	42
20	G	-	37 (95%)	1 (3%)	1 (3%)	4	21
21	H	-	78 (84%)	14 (15%)	1 (1%)	11	38
22	I	98/170 (58%)	95 (97%)	3 (3%)	0	100	100
23	v	121/859 (14%)	110 (91%)	7 (6%)	4 (3%)	3	17
24	n	279/455 (61%)	242 (87%)	29 (10%)	8 (3%)	3	19
25	o	120/503 (24%)	115 (96%)	4 (3%)	1 (1%)	16	44
25	p	122/503 (24%)	116 (95%)	6 (5%)	0	100	100
25	q	355/503 (71%)	327 (92%)	16 (4%)	12 (3%)	3	17
25	r	119/503 (24%)	111 (93%)	5 (4%)	3 (2%)	4	21
26	t	150/175 (86%)	134 (89%)	13 (9%)	3 (2%)	6	25
27	k	76/196 (39%)	69 (91%)	7 (9%)	0	100	100
27	s	74/196 (38%)	67 (90%)	7 (10%)	0	100	100
28	i	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
28	u	71/94 (76%)	65 (92%)	6 (8%)	0	100	100
29	h	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	30
29	w	66/86 (77%)	61 (92%)	4 (6%)	1 (2%)	8	30
30	j	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
30	x	65/77 (84%)	64 (98%)	1 (2%)	0	100	100
31	l	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	33
31	y	80/101 (79%)	70 (88%)	9 (11%)	1 (1%)	9	33
32	m	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
32	z	78/146 (53%)	74 (95%)	4 (5%)	0	100	100
33	e	63/110 (57%)	58 (92%)	4 (6%)	1 (2%)	7	29
33	g	92/110 (84%)	85 (92%)	6 (6%)	1 (1%)	11	38
34	a	77/111 (69%)	75 (97%)	2 (3%)	0	100	100
35	b	125/238 (52%)	111 (89%)	12 (10%)	2 (2%)	7	29

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	7810/12557 (62%)	7124 (91%)	604 (8%)	82 (1%)	15	40

5 of 82 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	483	PRO
2	C	364	PHE
2	C	463	THR
16	Z	206	LYS
20	G	17	MET

4.3.2 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	A	1736/2182 (80%)	1722 (99%)	14 (1%)	73	77
2	C	794/910 (87%)	788 (99%)	6 (1%)	73	77
9	J	21/121 (17%)	21 (100%)	0	100	100
10	O	295/397 (74%)	292 (99%)	3 (1%)	68	75
11	P	173/328 (53%)	173 (100%)	0	100	100
12	Q	171/332 (52%)	156 (91%)	15 (9%)	9	31
13	R	224/296 (76%)	223 (100%)	1 (0%)	84	83
14	S	56/151 (37%)	53 (95%)	3 (5%)	20	47
15	T	141/141 (100%)	138 (98%)	3 (2%)	47	64
16	Z	417/538 (78%)	382 (92%)	35 (8%)	10	34
17	c	212/316 (67%)	204 (96%)	8 (4%)	29	54
18	d	219/249 (88%)	216 (99%)	3 (1%)	59	70
19	F	-	104 (99%)	1 (1%)	68	75
20	G	-	39 (100%)	0	100	100
21	H	-	87 (99%)	1 (1%)	65	74
22	I	92/150 (61%)	92 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
23	v	58/152 (38%)	47 (81%)	11 (19%)	1	6
24	n	124/413 (30%)	103 (83%)	21 (17%)	2	9
25	o	60/451 (13%)	54 (90%)	6 (10%)	7	26
25	p	62/451 (14%)	54 (87%)	8 (13%)	4	16
25	q	124/451 (28%)	106 (86%)	18 (14%)	3	13
25	r	60/451 (13%)	55 (92%)	5 (8%)	10	35
26	t	40/165 (24%)	27 (68%)	13 (32%)	0	0
27	k	70/176 (40%)	69 (99%)	1 (1%)	59	70
27	s	67/176 (38%)	66 (98%)	1 (2%)	57	69
28	i	65/83 (78%)	60 (92%)	5 (8%)	12	37
28	u	65/83 (78%)	60 (92%)	5 (8%)	12	37
29	h	61/77 (79%)	60 (98%)	1 (2%)	55	68
29	w	61/77 (79%)	60 (98%)	1 (2%)	55	68
30	j	58/66 (88%)	56 (97%)	2 (3%)	32	57
30	x	58/66 (88%)	56 (97%)	2 (3%)	32	57
31	l	69/89 (78%)	68 (99%)	1 (1%)	59	70
31	y	69/89 (78%)	68 (99%)	1 (1%)	59	70
32	m	77/129 (60%)	74 (96%)	3 (4%)	28	53
32	z	77/129 (60%)	74 (96%)	3 (4%)	28	53
33	e	59/103 (57%)	54 (92%)	5 (8%)	10	33
33	g	79/103 (77%)	73 (92%)	6 (8%)	12	38
34	a	26/100 (26%)	26 (100%)	0	100	100
35	b	47/219 (22%)	44 (94%)	3 (6%)	16	42
All	All	6319/10410 (61%)	6104 (97%)	215 (3%)	33	57

5 of 215 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
24	n	258	THR
25	q	56	SER
28	u	81	LEU
24	n	327	PRO
25	o	134	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 133 such sidechains are listed below:

Mol	Chain	Res	Type
29	h	52	GLN
32	m	30	GLN
32	z	86	ASN
2	C	764	ASN
2	C	683	ASN

4.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	D	114/214 (53%)	30 (26%)	3 (2%)
4	E	102/112 (91%)	34 (33%)	7 (6%)
5	L	120/1175 (10%)	25 (20%)	5 (4%)
6	M	28/29 (96%)	7 (25%)	0
7	B	12/13 (92%)	5 (41%)	0
8	N	14/15 (93%)	7 (50%)	1 (7%)
All	All	390/1558 (25%)	108 (27%)	16 (4%)

5 of 108 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
3	D	29	G
3	D	31	G
3	D	32	G
3	D	33	U
3	D	42	A

5 of 16 RNA pucker outliers are listed below:

Mol	Chain	Res	Type
5	L	1111	U
5	L	1107	C
4	E	66	C
5	L	117	U
4	E	64	U

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

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

4.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

4.6 Ligand geometry [i](#)

Of 14 ligands modelled in this entry, 13 are monoatomic - leaving 1 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	$\# Z > 2$
36	GTP	C	1500	37	33,34,34	0.94	1 (3%)	50,54,54	1.63	10 (20%)

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
36	GTP	C	1500	37	-	5/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
36	C	1500	GTP	C5-N7	-2.31	1.34	1.39

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
36	C	1500	GTP	C5-C4-N3	-4.94	120.52	128.39
36	C	1500	GTP	C2-N3-C4	4.47	120.00	112.30
36	C	1500	GTP	N9-C4-N3	3.24	132.43	125.95
36	C	1500	GTP	C2-N1-C6	-3.13	119.44	125.11
36	C	1500	GTP	N9-C8-N7	-2.93	107.98	113.40

There are no chirality outliers.

All (5) torsion outliers are listed below:

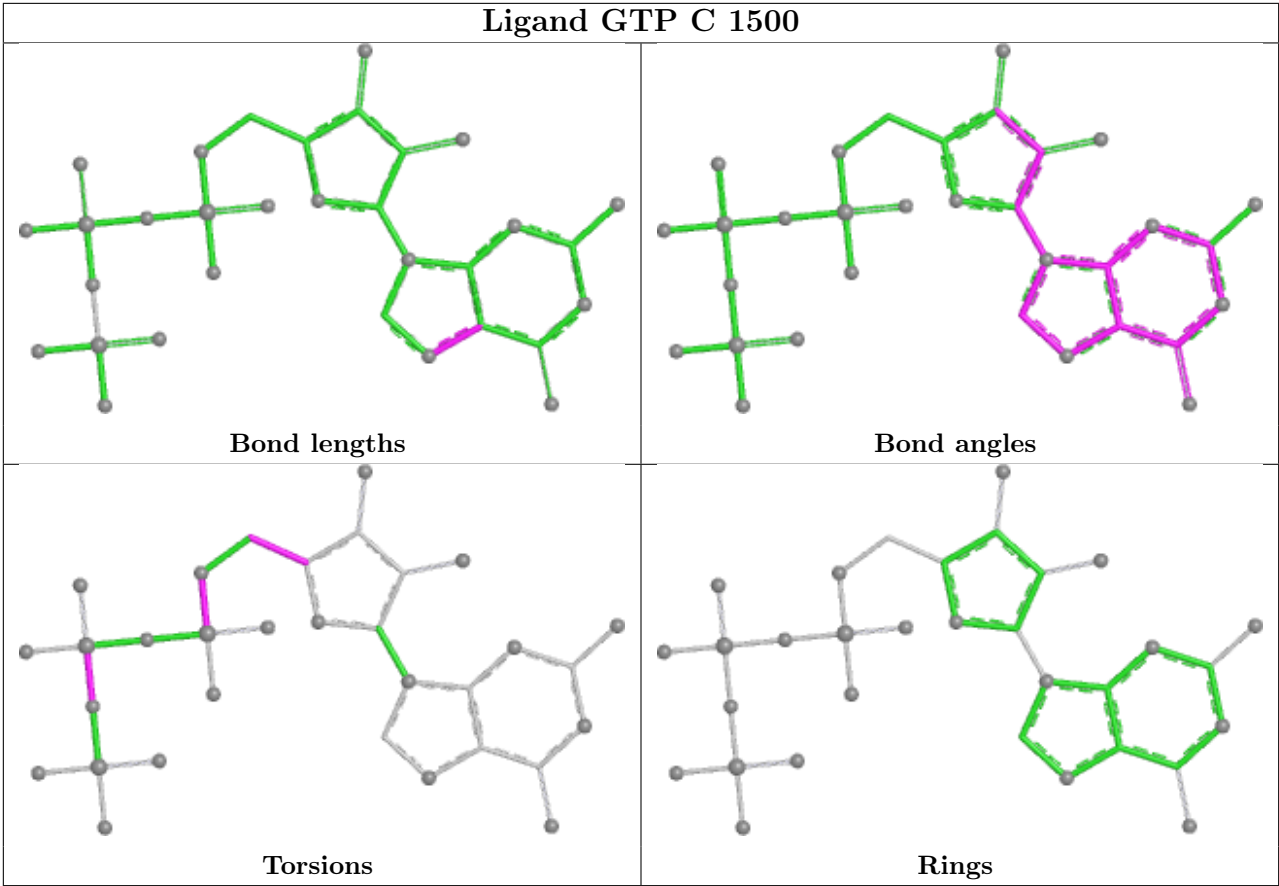
Mol	Chain	Res	Type	Atoms
36	C	1500	GTP	C5'-O5'-PA-O3A
36	C	1500	GTP	C5'-O5'-PA-O1A
36	C	1500	GTP	C5'-O5'-PA-O2A
36	C	1500	GTP	C3'-C4'-C5'-O5'
36	C	1500	GTP	PG-O3B-PB-O2B

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
36	C	1500	GTP	1	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.



4.7 Other polymers ⓘ

There are no such residues in this entry.

4.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
23	v	33
18	d	21
17	c	6

The worst 5 of 60 chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	d	275:PRO	C	295:UNK	N	28.30
1	v	103:UNK	C	106:UNK	N	18.26
1	d	377:UNK	C	379:UNK	N	14.04
1	c	382:UNK	C	384:UNK	N	13.70

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Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	c	469:UNK	C	482:GLU	N	13.69

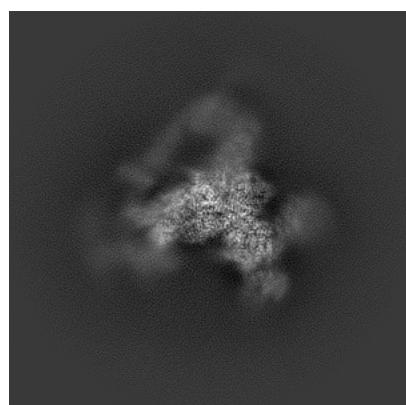
5 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-9525. These allow visual inspection of the internal detail of the map and identification of artifacts.

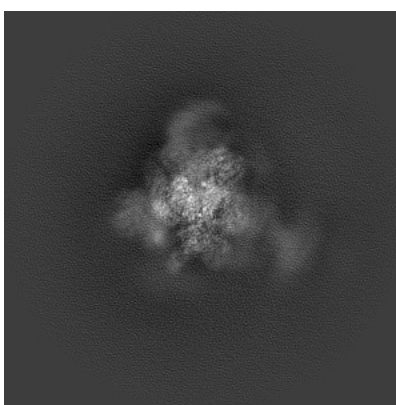
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

5.1 Orthogonal projections [i](#)

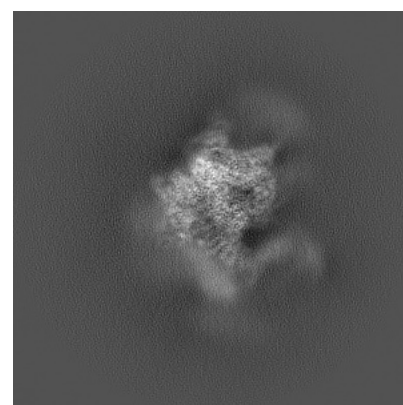
5.1.1 Primary map



X



Y

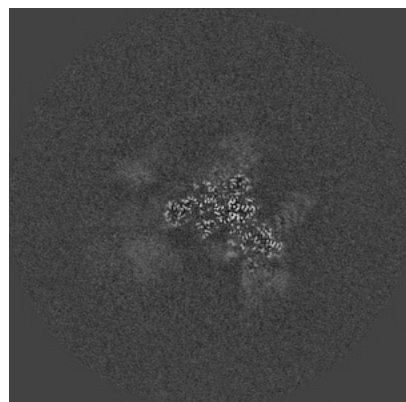


Z

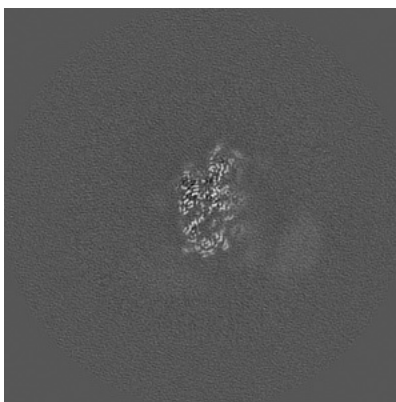
The images above show the map projected in three orthogonal directions.

5.2 Central slices [i](#)

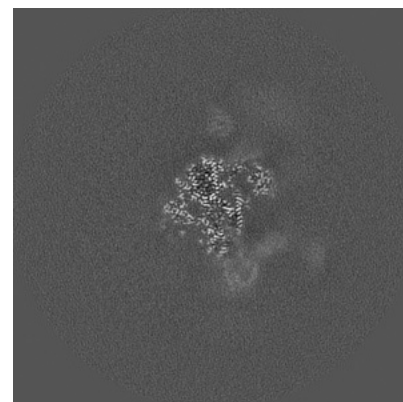
5.2.1 Primary map



X Index: 200



Y Index: 200

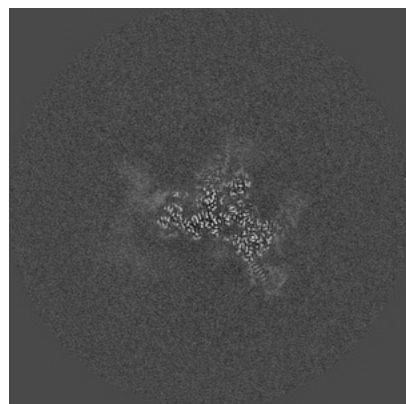


Z Index: 200

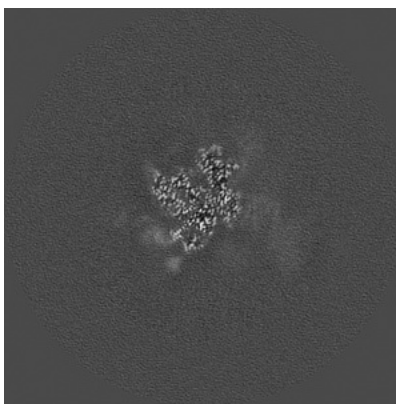
The images above show central slices of the map in three orthogonal directions.

5.3 Largest variance slices [i](#)

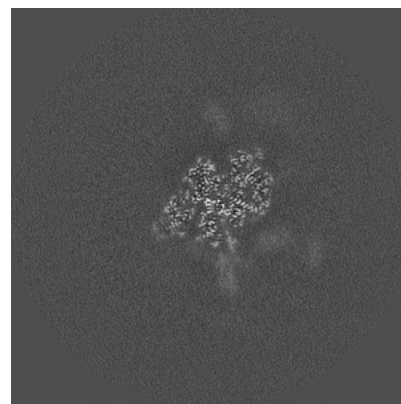
5.3.1 Primary map



X Index: 211



Y Index: 230

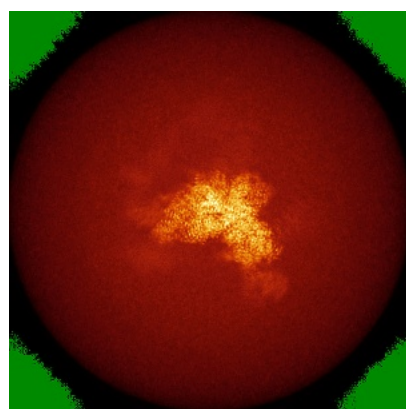


Z Index: 207

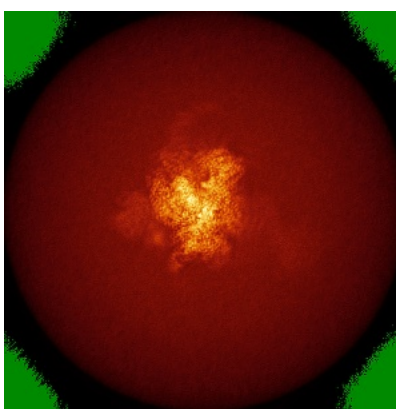
The images above show the largest variance slices of the map in three orthogonal directions.

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

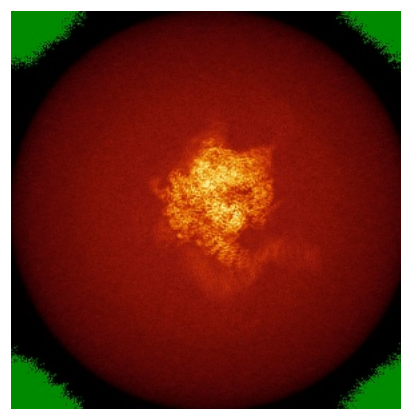
5.4.1 Primary map



X



Y



Z

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

5.5 Orthogonal surface views [i](#)

5.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.0413. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

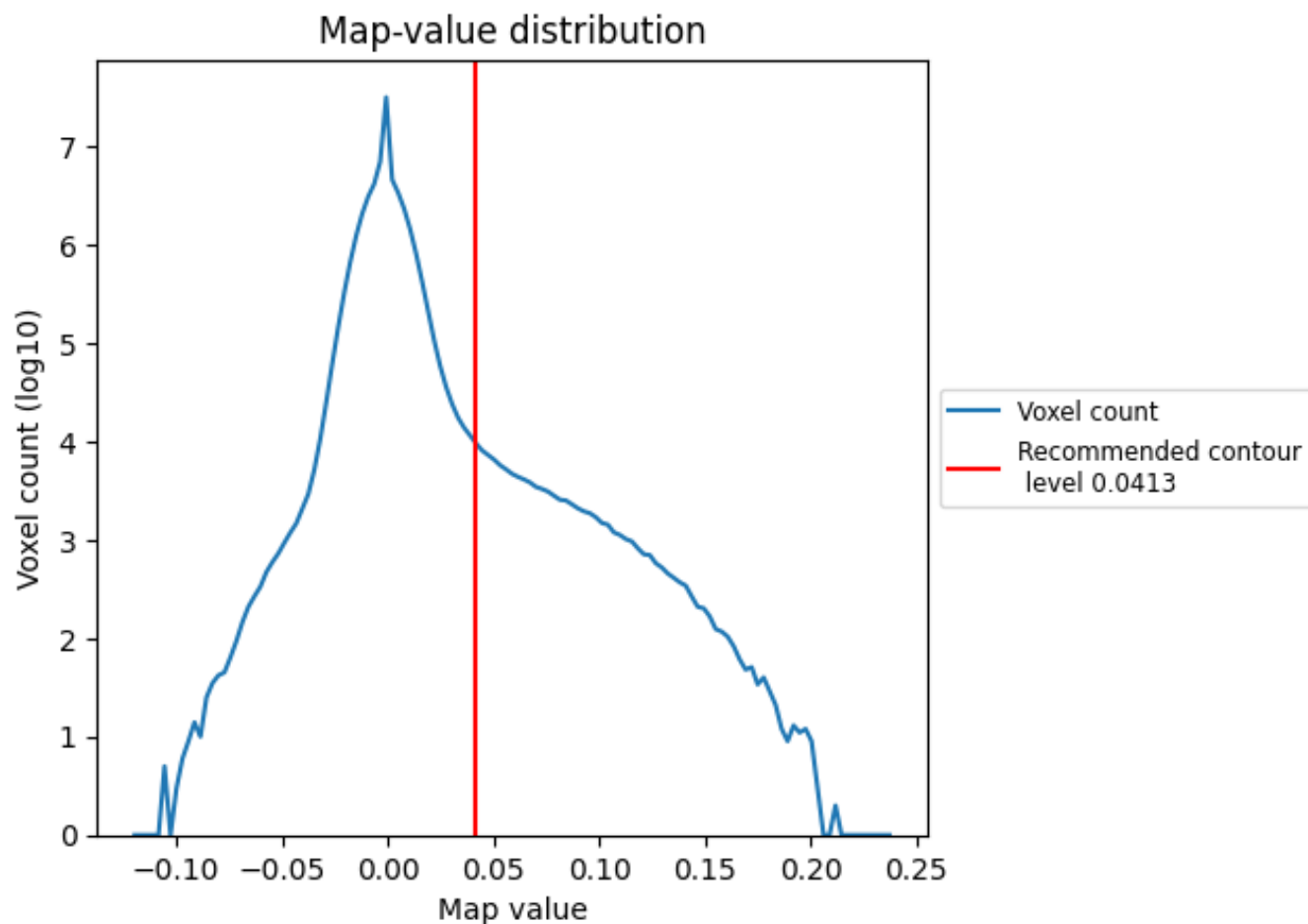
5.6 Mask visualisation [i](#)

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

6 Map analysis [i](#)

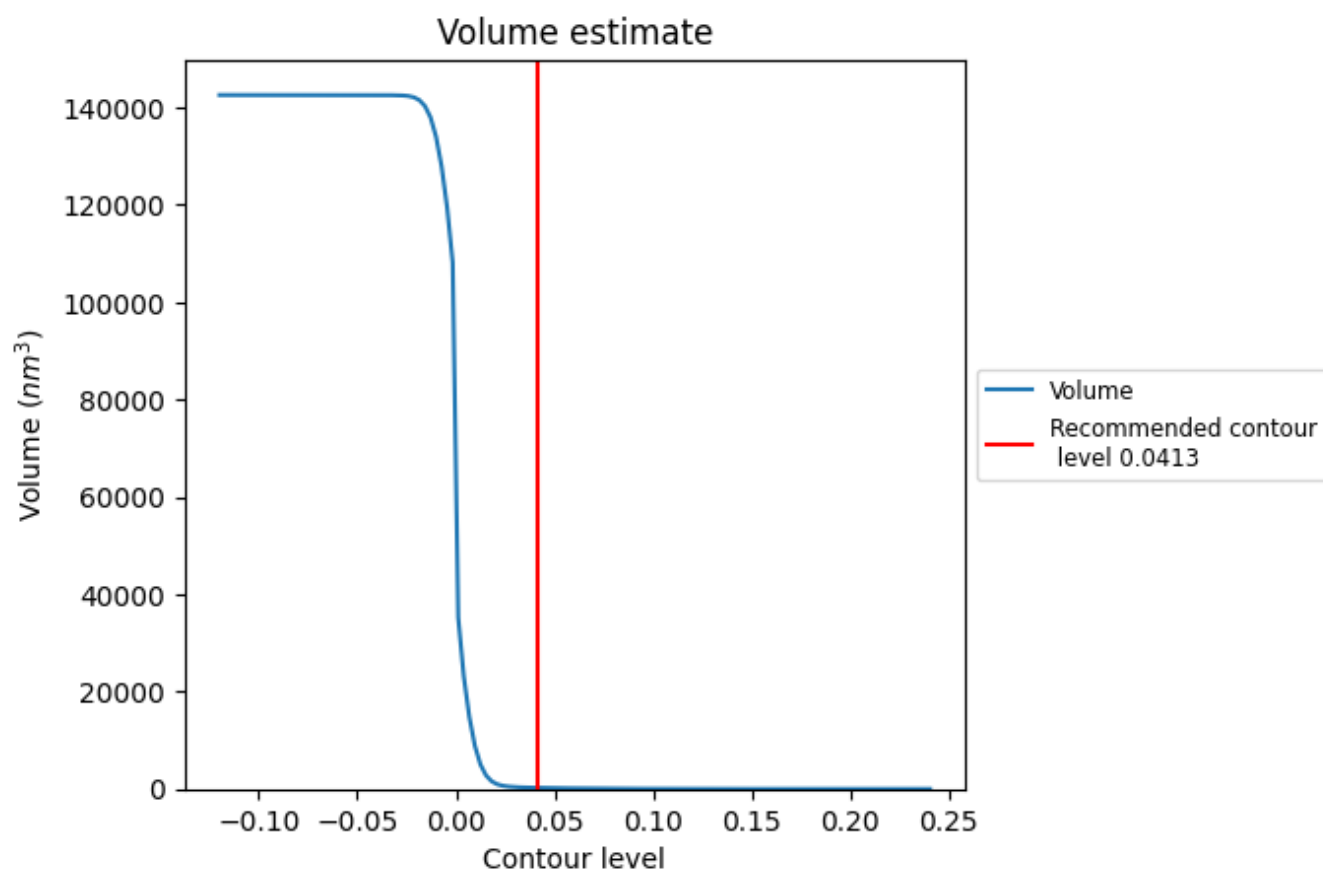
This section contains the results of statistical analysis of the map.

6.1 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.

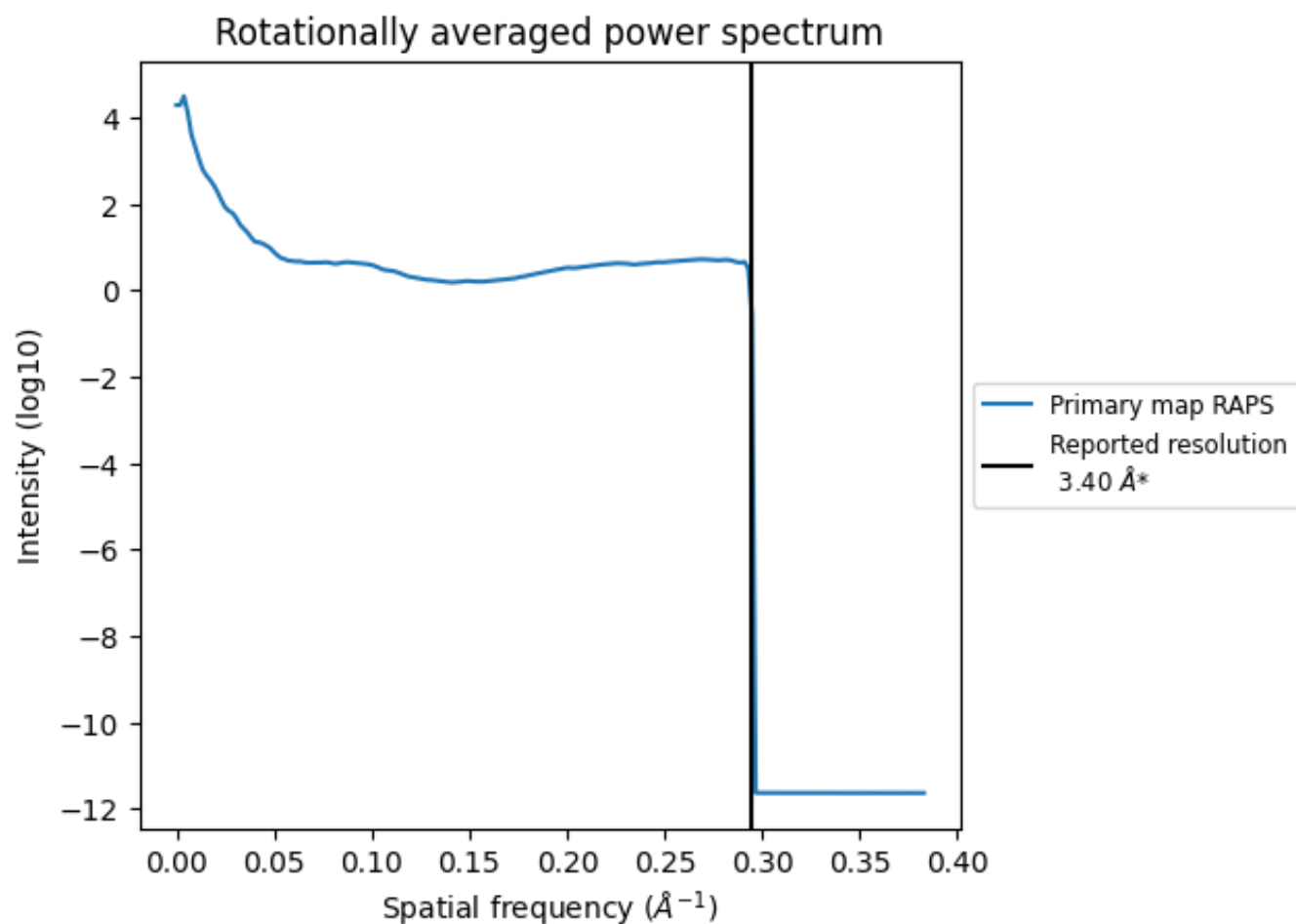
6.2 Volume estimate [i](#)



The volume at the recommended contour level is 230 nm^3 ; this corresponds to an approximate mass of 208 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.

6.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of $0.294 \text{ \AA}^{-1}$

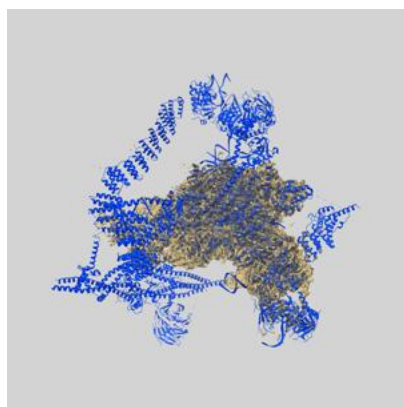
7 Fourier-Shell correlation ⓘ

This section was not generated. No FSC curve or half-maps provided.

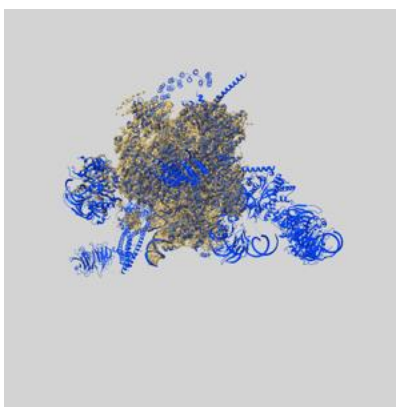
8 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-9525 and PDB model 5GMK. Per-residue inclusion information can be found in section ?? on page ??.

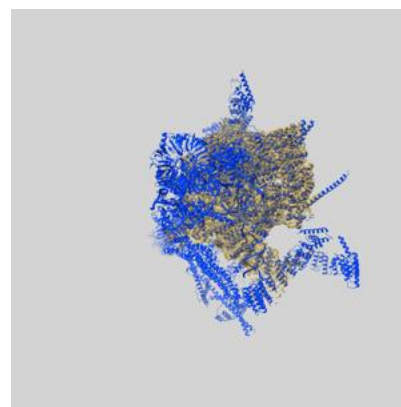
8.1 Map-model overlay [i](#)



X



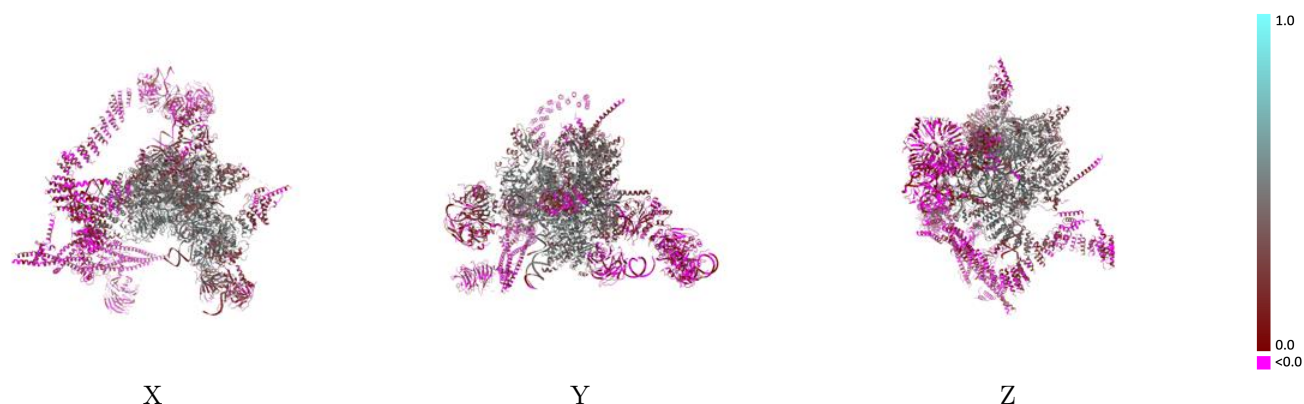
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0413 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.

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

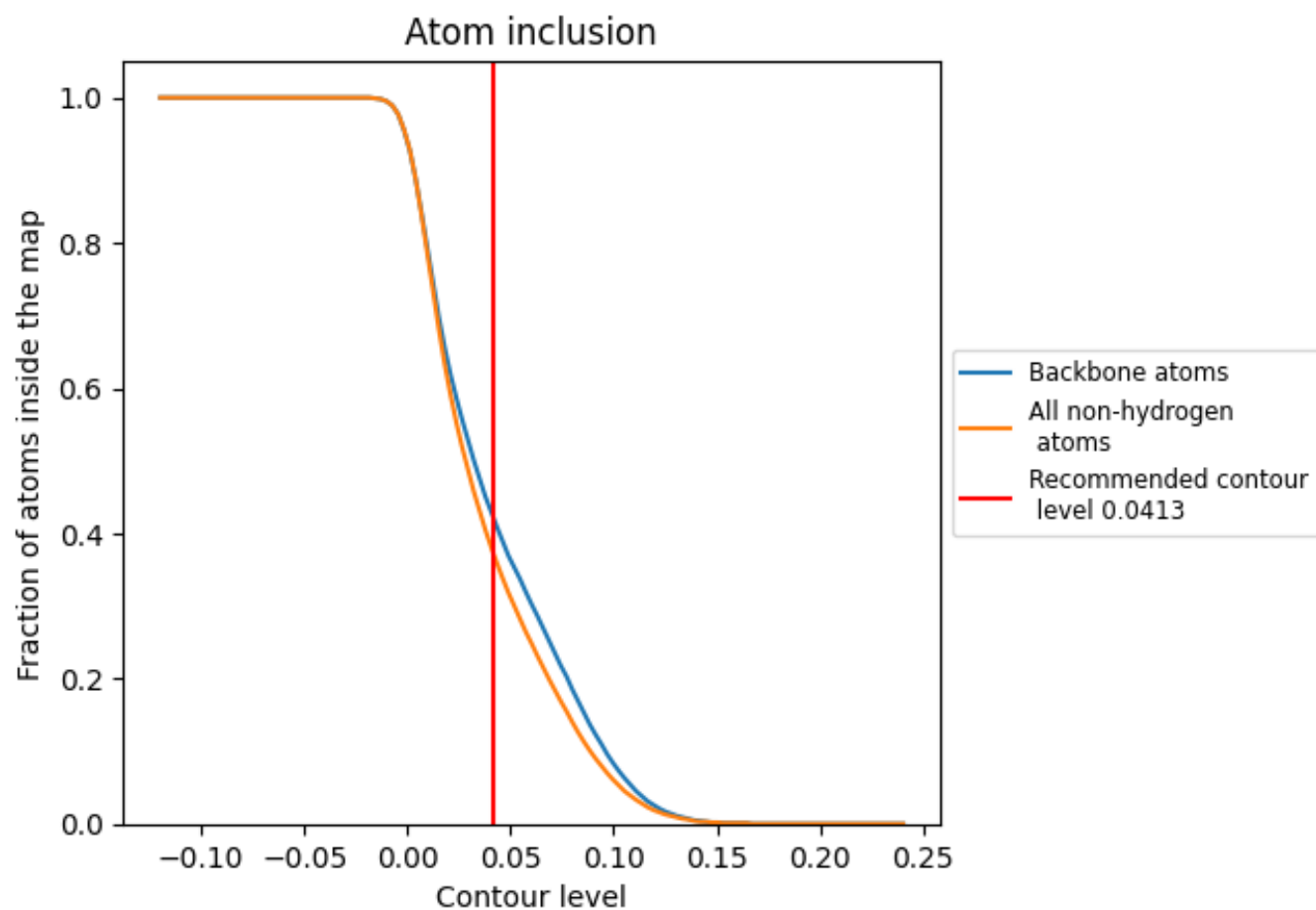


The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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

This section was not generated.

8.4 Atom inclusion [i](#)



At the recommended contour level, 42% of all backbone atoms, 38% of all non-hydrogen atoms, are inside the map.

8.5 Map-model fit summary ⓘ

The table lists the average atom inclusion at the recommended contour level (0.0413) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.3750	 0.2790
A	 0.5810	 0.4060
B	 0.5600	 0.4420
C	 0.6550	 0.4330
D	 0.6350	 0.3920
E	 0.7210	 0.4230
F	 0.1440	 0.3760
G	 0.1400	 0.3200
H	 0.0990	 0.3320
I	 0.4220	 0.3730
J	 0.5450	 0.4740
L	 0.1590	 0.1240
M	 0.1170	 0.1810
N	 0.6030	 0.4150
O	 0.7510	 0.4890
P	 0.5040	 0.3740
Q	 0.5390	 0.4270
R	 0.6400	 0.4260
S	 0.4460	 0.4390
T	 0.6920	 0.4540
Z	 0.2320	 0.2360
a	 0.0000	 0.0020
b	 0.0000	 0.0090
c	 0.3240	 0.2250
d	 0.3840	 0.2600
e	 0.0000	 -0.0120
g	 0.0110	 0.1290
h	 0.0070	 0.0820
i	 0.0140	 0.1390
j	 0.0690	 0.2270
k	 0.0810	 0.2660
l	 0.2740	 0.3460
m	 0.0250	 0.1360
n	 0.0570	 0.0280
o	 0.0000	 -0.0230



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Chain	Atom inclusion	Q-score
p	 0.0000	 0.0070
q	 0.0000	 -0.0060
r	 0.0000	 0.0490
s	 0.0000	 0.0380
t	 0.0000	 -0.0000
u	 0.0000	 -0.0020
v	 0.0400	 0.0590
w	 0.0000	 0.0260
x	 0.0000	 0.0060
y	 0.0000	 0.0170
z	 0.0000	 0.0090