



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 05:36 PM UTC

PDB ID : 6PTJ / pdb_00006ptj
EMDB ID : EMD-20471
Title : Structure of Ctf4 trimer in complex with one CMG helicase
Authors : Yuan, Z.; Georgescu, R.; Bai, L.; Santos, R.; Donnell, M.; Li, H.
Deposited on : 2019-07-15
Resolution : 3.80 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:

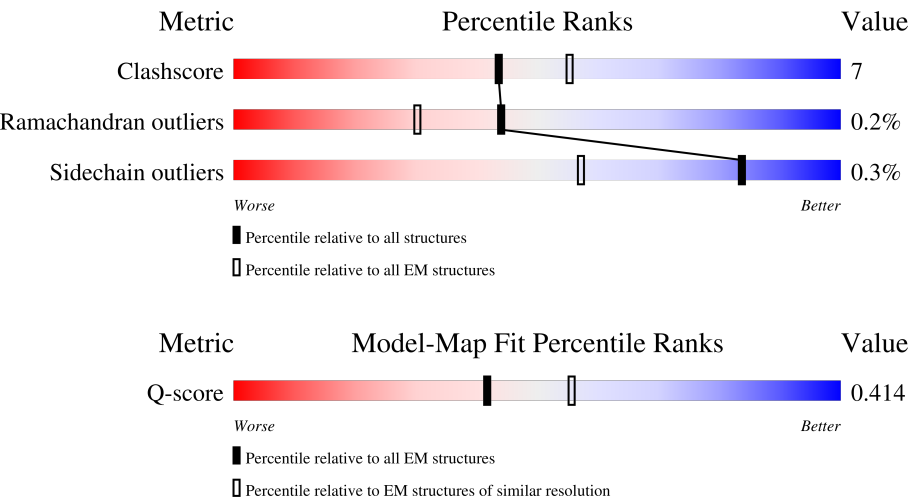
EMDB validation analysis : 0.0.1.dev132
MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)
MapQ : 1.9.13
Ideal geometry (proteins) : Engh &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

1 Overall quality at a glance i

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

The reported resolution of this entry is 3.80 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	10198 (3.30 - 4.30)

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	A	208	
2	B	213	
3	C	194	
4	D	294	

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Mol	Chain	Length	Quality of chain
5	c	650	76%9%15%
6	2	868	27%70%
7	3	971	23%5%72%
8	4	933	24%6%69%
9	5	775	25%7%67%
10	6	1017	23%73%
11	7	845	6%33%5%61%
12	E	927	41%54%
12	F	927	6%37%9%54%
12	G	927	11%40%6%54%

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 34361 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 DNA replication complex GINS protein PSF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	208	Total	C	N	O	S	0	0
			1696	1065	290	331	10		

- Molecule 2 is a protein called DNA replication complex GINS protein PSF2.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	186	Total	C	N	O	S	0	0
			1557	1005	271	277	4		

- Molecule 3 is a protein called DNA replication complex GINS protein PSF3.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	C	159	Total	C	N	O	S	0	0
			1288	843	207	232	6		

- Molecule 4 is a protein called DNA replication complex GINS protein SLD5.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	230	Total	C	N	O	S	0	0
			1891	1206	309	364	12		

- Molecule 5 is a protein called Cell division control protein 45.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	c	553	Total	C	N	O	S	0	0
			4482	2862	763	844	13		

- Molecule 6 is a protein called DNA replication licensing factor MCM2.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	2	260	Total	C	N	O	S	0	0
			2025	1284	361	374	6		

- Molecule 7 is a protein called DNA replication licensing factor MCM3.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	3	270	Total	C	N	O	S	0	0
			2139	1361	371	403	4		

- Molecule 8 is a protein called DNA replication licensing factor MCM4.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	4	285	Total	C	N	O	S	0	0
			2299	1450	400	432	17		

- Molecule 9 is a protein called Minichromosome maintenance protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	5	252	Total	C	N	O	S	0	0
			2006	1271	344	382	9		

- Molecule 10 is a protein called DNA replication licensing factor MCM6.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	6	273	Total	C	N	O	S	0	0
			2081	1314	371	390	6		

- Molecule 11 is a protein called DNA replication licensing factor MCM7.

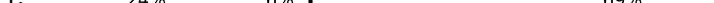
Mol	Chain	Residues	Atoms					AltConf	Trace
11	7	326	Total	C	N	O	S	0	0
			2615	1655	454	493	13		

- Molecule 12 is a protein called DNA polymerase alpha-binding protein.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	E	424	Total	C	N	O	S	0	0
			3408	2189	564	640	15		
12	F	431	Total	C	N	O	S	1	0
			3472	2227	576	653	16		
12	G	423	Total	C	N	O	S	1	0
			3402	2186	563	638	15		

PRO	GLU	GLU	GLU	LYS	PHE	SER	ALA	GLN	GLU	TYR	LEU	ALA	GLY	LEU	LYS	ILE	MET	SER	ASP	ARG	ASN	ASN	LEU	MET	VAL	ALA	ASP	ASP	LYS	VAL	TRP	ARG	VAL
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- Molecule 8: DNA replication licensing factor MCM4

Chain 4:  24% 6% 69%

ASN ILE ARG ALA ALA ILE GLY SER SER PRO LEU PHE ASN PRO SER SER GLN ARG GLN ASN SER ASP VAL PHE GLN SER SER GLY ARG GLN GLY ARG ILE SER SER SER SER SER SER SER GLY ARG ARG ARG TYR HIS SER ASP ARG LEU ARG SER ASP ARG ALA ALA PRO THR SER SER

SER	SER	LEU	GLY	ARG	ASN	GLY	GLN	ASN	ASN	ARG	VAL	HIS	HIS	MET	ARG	ARG	ARG	ASN	ASP	ILE	HIS	THR	SER	SER	ASP	LEU	SER	SER	PRO	ARG	ARG	ILE	VAL	ASP	PHE	ASP	THR	ARG	SER	SER	GLY	VAL	ASN	THR	LEU	ASP	THR	THR	SER	SER	SER	SER	ALA	PRO	PRO	SER	GLU	ALA	SER	GLU	PRO	L177	R178	L179	L180
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Protein A	R428	0.85	High	
	R432	0.75	High	
	K433	0.90	High	
	E434	0.70	High	
	G437	0.65	High	
	I442	0.80	High	
	S448	0.75	High	
	R449	0.85	High	
	V452	0.60	High	
	V463	0.70	High	
Protein B	V185	0.75	High	
	E189	0.80	High	
	F201	0.65	High	
	K202	0.70	High	
	F205	0.85	High	
	R206	0.75	High	
	D210	0.80	High	
	E211	0.70	High	
	R212	0.75	High	
	GLU	0.60	High	
Protein C	GLU	0.60	High	
	PHE	0.65	High	
	ILE	0.70	High	
	ASN	0.65	High	
	ASN	0.60	High	
	THR	0.65	High	
	THR	0.60	High	
	D221	0.85	High	
	L224	0.70	High	
	R234	0.75	High	
Protein D	T238	0.70	High	
	S239	0.75	High	
	N240	0.65	High	
	L241	0.80	High	
	N242	0.75	High	
	Y251	0.70	High	
	D256	0.65	High	
	L262	0.70	High	
	L271	0.75	High	
	M272	0.70	High	
Protein E	V285	0.80	High	
	D286	0.75	High	
	N287	0.80	High	
	N288	0.75	High	
	L289	0.70	High	
	D290	0.75	High	
	Y291	0.70	High	
	D292	0.75	High	
	L293	0.70	High	
	D294	0.75	High	
Protein F	E295	0.70	High	
	L296	0.75	High	
	E297	0.70	High	
	R304	0.65	High	
	S310	0.80	High	
	Protein G	C311	0.65	High
		K312	0.70	High
		G313	0.75	High
		K314	0.80	High
		R315	0.70	High
L322		0.65	High	
L326		0.70	High	
K329		0.75	High	
G330		0.70	High	
F346		0.65	High	
Protein H	D353	0.70	High	
	V358	0.75	High	
	F359	0.70	High	
	L360	0.65	High	
	D361	0.70	High	
	R362	0.75	High	
	S365	0.65	High	
	R370	0.70	High	
	C371	0.65	High	
	E372	0.70	High	
Protein I	R373	0.75	High	
	L374	0.65	High	
	D375	0.70	High	
	C376	0.75	High	
	N377	0.70	High	
	E378	0.65	High	
	P379	0.70	High	
	C389	0.65	High	
	D393	0.70	High	
	E401	0.65	High	
Protein J	T402	0.70	High	
	P403	0.75	High	
	D404	0.70	High	
	F405	0.65	High	
	V406	0.70	High	
	P407	0.75	High	
	D408	0.70	High	
	G409	0.75	High	
	G410	0.70	High	
	I411	0.65	High	
Protein K	T412	0.70	High	
	THR	0.65	High	
	ASP	0.70	High	
	H413	0.65	High	
	S414	0.70	High	
	ASP	0.65	High	
	LEU	0.70	High	
	ALA	0.65	High	
	L423	0.70	High	
	V424	0.65	High	
D425	0.75	High		

[illegible]

VAL	CYS	CYS	ILE	ASP	GLU	PHE	ASP	MET	SER	ASP	SER	THR	ARG	SER	VAL	VAL	HIS	GLU	VAL	MET	GLU	GLN	THR	ILE	ILE	ALA	LYS	ALA	ALA	GLY	ILE	ILE	THR	THR	THR	LEU	ASN	ALA	ARG	SER	SER	ILE	LEU	ALA	ALA	ALA	ASN	GLY	SER	ARG	TYR	ASN	PRO	ASN	LEU	PRO
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VAL	THR	GLU	ASN	ASP	LEU	PRO	PRO	PRO	LEU	LEU	SER	ARG	PHE	ASP	LEU	VAL	TYR	LEU	VAL	GLU	LYS	ASP	ASP	ARG	GLU	LEU	ALA	LYS	HIS	LEU	THR	ASN	LEU	TYR	LEU	LEU	GLU	ASP	LYS	PRO	GLU	HIS	ILE	SER	GLN	ASP	ASP	VAL	LEU	PRO	VAL	VAL	GLU	PHE	LEU
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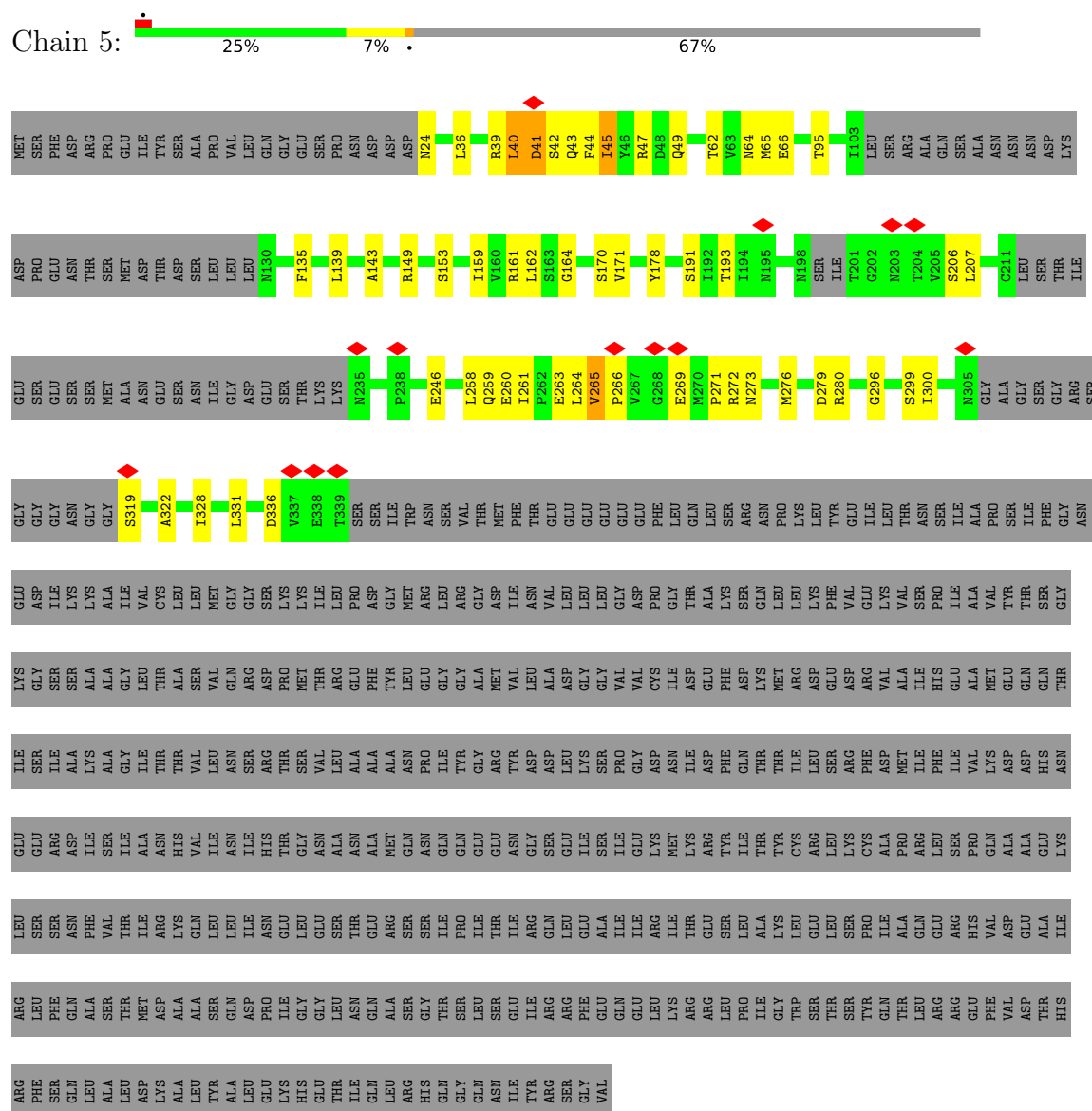
THR	MET	TYR.	ILE	SER	TYR.	ALA	LYS	GLU	HIS	HIS	PRO	ILE	ILE	THR.	GLU	LEU	VAL	ARG	ALA	LYS	THR.	GLU	GLY	VAL	GLY	Gly	MET	ARG	ASP	ASP	SER	ARG	SER	ASP	GLU	Lys	Arg	ILE	THR.	ALA	ALA	THR.	THR.	THR.	ARG	GLN	LEU	GLU	SER	MET	ILE	ARG	LEU	ALA	ALA	GLY
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HIS	ALA	LYS	MET	LEU	LYS	ASN	VAL	VAL	GLU	GLU	ASP	VAL	GLN	GLU	ALA	VAL	ARG	ILE	ILE	ARG	SER	ALA	LYS	ASP	LYS	THR	ALA	THR	PRO	ASP	ILE	ILE	ASP	MET	ASN	LEU	VAL	GLN	THR	GLY	LYS	SER	VAL	ILE	GLN	ARG	LYS	LEU	GLN	ASP	LEU	SER	ARG
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[illegible]

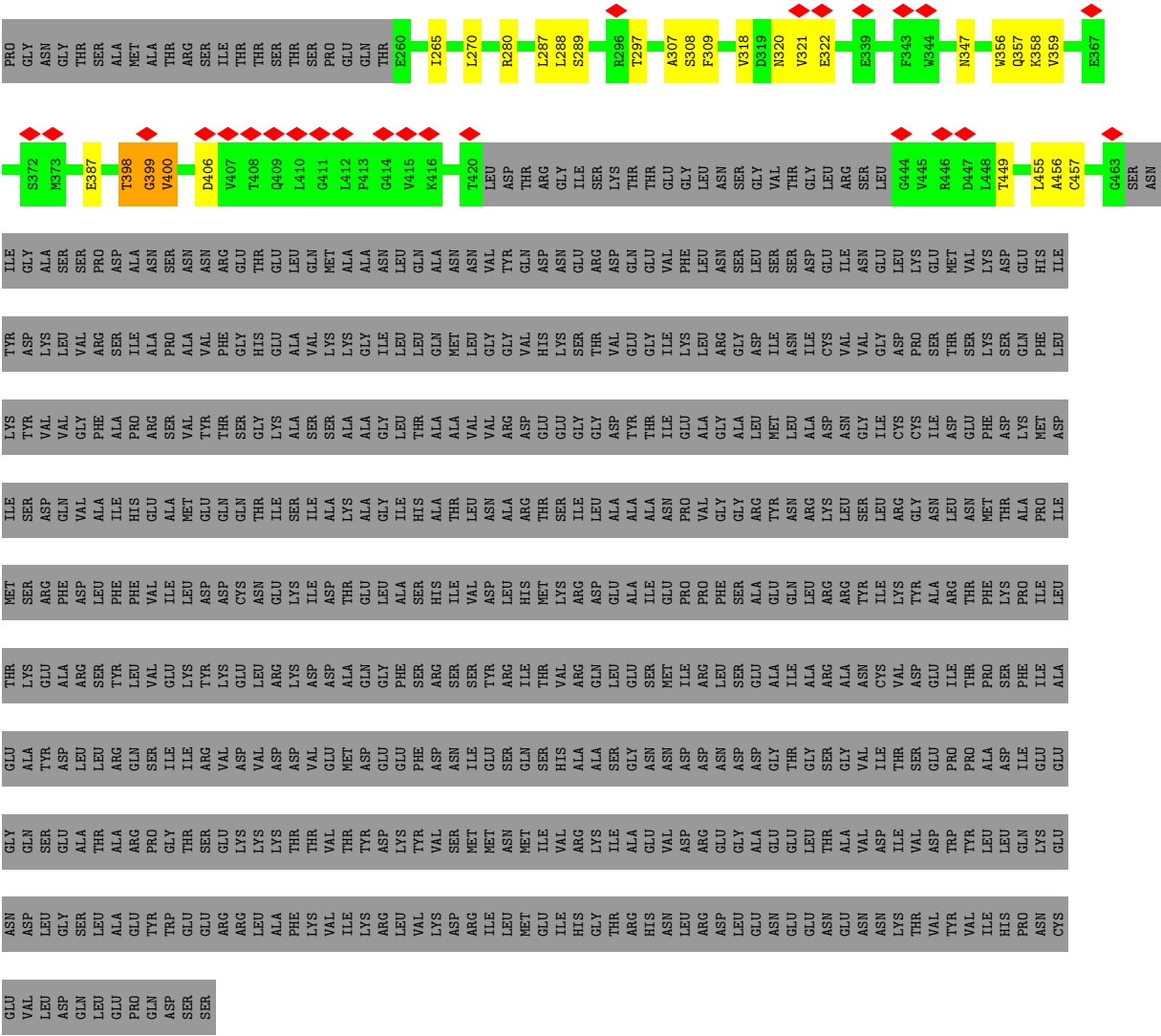
ARG
LEU
ASN
ASN
ARG
VAL

- Molecule 9: Minichromosome maintenance protein 5

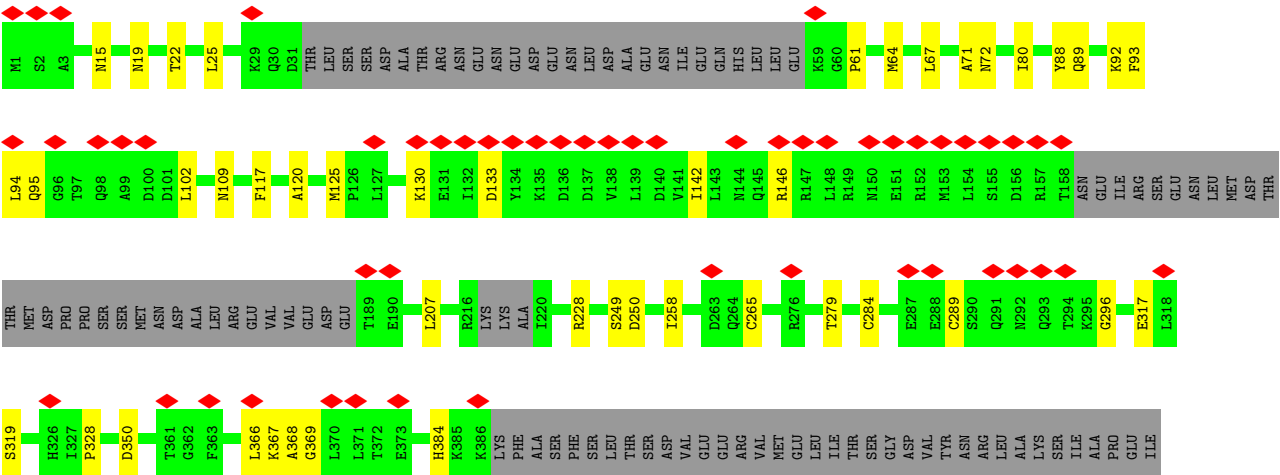


- Molecule 10: DNA replication licensing factor MCM6



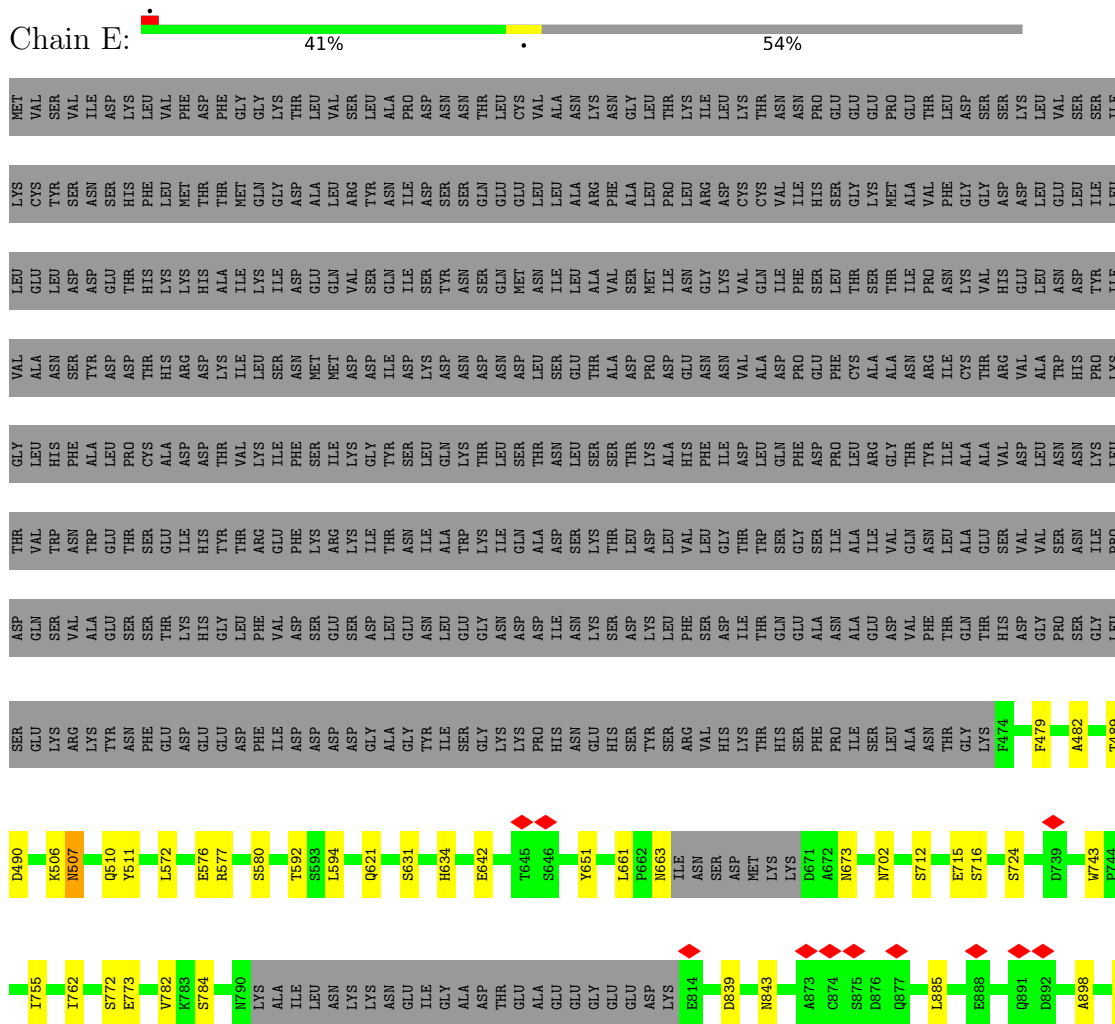


● Molecule 11: DNA replication licensing factor MCM7



[illegible]

- Molecule 12: DNA polymerase alpha-binding protein



L883	S884	L885	A886	H887	E888	L889	K890	Q891	D892	R893	A894	L895	T896	A897	A898	V899	K900	I901	S902	E903	R904	A905	E906	L907	P908	S909	L910	V911	K912	K913	I914	N915	N916	I917	R918	E919	A920	R921	Y922	E923	GLN	GLN	LYS										
THR	GLU	ALA	GLU	GLY	GLU	GLU	ASP	LYS	E814	I817	E825	E826	Y827	L833	L836	E842	N843	D844	G845	E846	N847	Y848	G849	N850	E851	N852	E853	V854	L855	L858	N859	G860	A861	Y862	D863	K864	A865	L866	L867	R868	L869	F870	A871	S872	A873	C874	S875	D876	Q877	N878	V879	E880	
ASN	SER	ASP	MET	LYS	D671	A672	F689	S690	S691	Y692	G693	L722	E727	K730	K735	E736	T737	T738	L745	Y749	N753	C754	P771	S772	E775	I776	R777	M778	P779	K783	E788	E789	N790	K791	A792	I793	LEU	ASN	LYS	ASN	ASN	GLU	ILE	ALA	ALA	ASP							
GLY	T495	M496	M497	E498	V499	S508	E509	T514	D519	V520	R524	D530	Y534	D535	L539	N540	E541	D560	S561	I562	A574	G575	E576	L594	N601	V605	F626	S631	Q632	F633	H634	L643	G644	T645	S646	S647	R653	M659	S660	N663	ILE												
SER	GLU	LYS	ARG	LYS	TYR	ASN	PHE	GLU	GLU	ASP	PHE	ILE	ASP	ASP	ASP	GLY	TYR	GLY	ILE	SER	GLY	LYS	LYS	PRO	HIS	ASN	GLU	ARG	VAL	HIS	ASN	GLU	VAL	HIS	THR	GLY	LYS	F474	M477	P478	G487	F488											
ASP	GLN	SER	VAL	ALA	TRP	GLU	SER	SER	THR	THR	HIS	GLY	TYR	THR	ARG	PHE	VAL	SER	LYS	GLU	ARG	ILE	LYS	ASP	ASP	GLN	THR	ILE	ASN	GLY	THR	ALA	ASP	ASN	ALA	ASN	ALA	THR	GLN	THR	VAL	THR	GLY	PRO	SER	GLY	PRO	LEU					
THR	VAL	TRP	ASN	TRP	GLU	THR	SER	SER	THR	GLU	ILE	HIS	GLY	TYR	THR	ARG	PHE	ASP	SER	LYS	GLU	ARG	ILE	LYS	ASP	ASP	GLU	ILE	ASN	GLY	THR	THR	GLN	THR	THR	ASN	ASN	ALA	ALA	ALA	THR	VAL	THR	GLN	THR	VAL	THR	GLY	PRO	SER	GLY	PRO	LEU
VAL	ALA	SER	ASP	TRP	ASP	THR	HIS	LYS	LYS	ALA	ILE	LYS	VAL	LEU	SER	ILE	ASP	MET	GLN	TYR	ASN	ALA	LYS	ASN	ASP	ASN	GLN	THR	ILE	ASN	GLY	THR	ALA	ASP	PRO	PHE	GLU	THR	CYS	ALA	ASP	ALA	THR	ASN	ILE	ARG	THR	VAL	ALA	TRP	HIS	PRO	LYS
LEU	GLU	LEU	ASP	GLU	THR	HIS	LYS	LYS	ALA	ILE	LYS	VAL	ILE	LYS	ILE	SER	ASP	ASN	GLU	MET	GLN	VAL	ASP	VAL	SER	THR	ALA	ALA	VAL	ASP	PRO	PHE	GLU	THR	CYS	ALA	ASP	ALA	THR	ASN	ILE	ARG	THR	VAL	ALA	TRP	HIS	PRO	LYS				

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	200491	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 ($e^-/\text{\AA}^2$)	50	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	0.230	Depositor
Minimum map value	-0.128	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.034	Depositor
Map size (Å)	300.72, 300.72, 300.72	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.074, 1.074, 1.074	Depositor

5 Model quality

5.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.36	0/1718	0.72	1/2314 (0.0%)
2	B	0.46	0/1589	0.82	2/2150 (0.1%)
3	C	0.39	0/1320	0.72	1/1784 (0.1%)
4	D	0.42	0/1923	0.82	4/2594 (0.2%)
5	c	0.41	0/4563	0.69	2/6173 (0.0%)
6	2	0.34	0/2063	0.72	2/2794 (0.1%)
7	3	0.39	0/2189	0.78	5/2975 (0.2%)
8	4	0.28	0/2336	0.80	4/3155 (0.1%)
9	5	0.46	0/2035	0.87	5/2752 (0.2%)
10	6	0.29	0/2114	0.77	6/2862 (0.2%)
11	7	0.29	0/2660	0.68	1/3595 (0.0%)
12	E	0.41	0/3493	0.62	3/4730 (0.1%)
12	F	0.28	0/3558	0.58	1/4817 (0.0%)
12	G	0.29	0/3487	0.60	0/4724
All	All	0.36	0/35048	0.71	37/47419 (0.1%)

There are no bond length outliers.

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	5	45	ILE	N-CA-C	16.83	127.79	110.62
8	4	373	ARG	N-CA-C	-16.59	90.28	111.02
10	6	399	GLY	N-CA-C	16.19	132.16	112.73
7	3	325	THR	CA-C-O	-12.06	105.72	119.95
9	5	265	VAL	N-CA-C	11.48	120.20	108.95

There are no chirality outliers.

There are no planarity outliers.

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	A	1696	0	1698	19	0
2	B	1557	0	1610	18	0
3	C	1288	0	1298	24	0
4	D	1891	0	1899	28	0
5	c	4482	0	4499	35	0
6	2	2025	0	1993	20	0
7	3	2139	0	2112	38	0
8	4	2299	0	2292	59	0
9	5	2006	0	2038	41	0
10	6	2081	0	1987	35	0
11	7	2615	0	2627	30	0
12	E	3408	0	3351	24	0
12	F	3472	0	3418	63	0
12	G	3402	0	3345	37	0
All	All	34361	0	34167	448	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 7.

The worst 5 of 448 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)
8:4:289:LEU:HD21	8:4:293:LEU:CD2	1.49	1.40
8:4:289:LEU:CD2	8:4:293:LEU:HD23	1.61	1.28
7:3:187:THR:HG21	7:3:259:GLN:NE2	1.46	1.26
8:4:370:ARG:HG2	8:4:378:GLU:CB	1.73	1.17
12:F:493:TYR:CZ	12:F:768:LEU:HD21	1.79	1.16

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	206/208 (99%)	180 (87%)	25 (12%)	1 (0%)	24	57
2	B	182/213 (85%)	149 (82%)	32 (18%)	1 (0%)	24	57
3	C	151/194 (78%)	136 (90%)	14 (9%)	1 (1%)	18	51
4	D	222/294 (76%)	197 (89%)	24 (11%)	1 (0%)	24	57
5	c	543/650 (84%)	482 (89%)	61 (11%)	0	100	100
6	2	258/868 (30%)	218 (84%)	40 (16%)	0	100	100
7	3	262/971 (27%)	221 (84%)	40 (15%)	1 (0%)	30	62
8	4	281/933 (30%)	247 (88%)	31 (11%)	3 (1%)	11	41
9	5	242/775 (31%)	214 (88%)	28 (12%)	0	100	100
10	6	267/1017 (26%)	221 (83%)	45 (17%)	1 (0%)	30	62
11	7	318/845 (38%)	282 (89%)	36 (11%)	0	100	100
12	E	418/927 (45%)	392 (94%)	26 (6%)	0	100	100
12	F	428/927 (46%)	404 (94%)	24 (6%)	0	100	100
12	G	418/927 (45%)	398 (95%)	20 (5%)	0	100	100
All	All	4196/9749 (43%)	3741 (89%)	446 (11%)	9 (0%)	44	73

5 of 9 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	114	GLU
8	4	375	ASP
8	4	378	GLU
7	3	281	ASP
3	C	101	ASN

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	A	193/193 (100%)	193 (100%)	0	100	100
2	B	176/198 (89%)	176 (100%)	0	100	100
3	C	144/173 (83%)	143 (99%)	1 (1%)	76	77
4	D	221/279 (79%)	221 (100%)	0	100	100
5	c	499/586 (85%)	498 (100%)	1 (0%)	87	87
6	2	212/770 (28%)	212 (100%)	0	100	100
7	3	236/835 (28%)	233 (99%)	3 (1%)	61	71
8	4	260/848 (31%)	259 (100%)	1 (0%)	84	83
9	5	237/688 (34%)	233 (98%)	4 (2%)	53	67
10	6	210/886 (24%)	209 (100%)	1 (0%)	81	81
11	7	296/753 (39%)	294 (99%)	2 (1%)	76	77
12	E	376/825 (46%)	376 (100%)	0	100	100
12	F	384/825 (46%)	384 (100%)	0	100	100
12	G	375/825 (46%)	375 (100%)	0	100	100
All	All	3819/8684 (44%)	3806 (100%)	13 (0%)	84	84

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
9	5	45	ILE
9	5	159	ILE
11	7	258	ILE
10	6	129	THR
11	7	207	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 54 such sidechains are listed below:

Mol	Chain	Res	Type
9	5	284	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
11	7	150	ASN
12	F	877	GLN
10	6	149	ASN
10	6	347	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

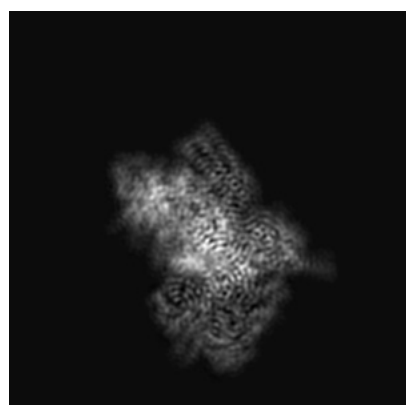
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-20471. These allow visual inspection of the internal detail of the map and identification of artifacts.

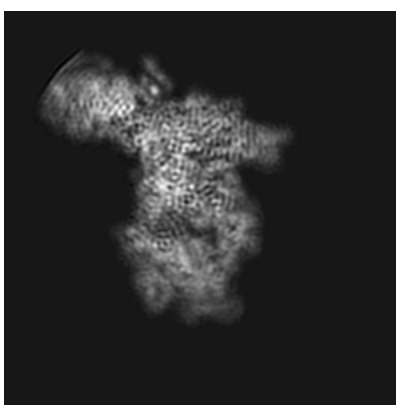
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

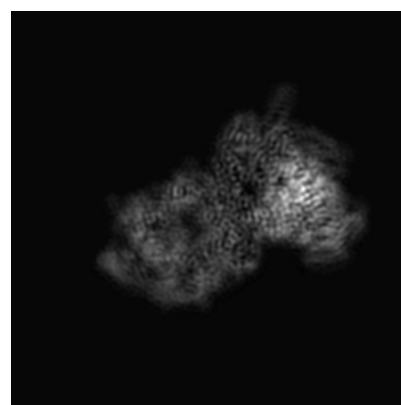
6.1.1 Primary map



X



Y



Z

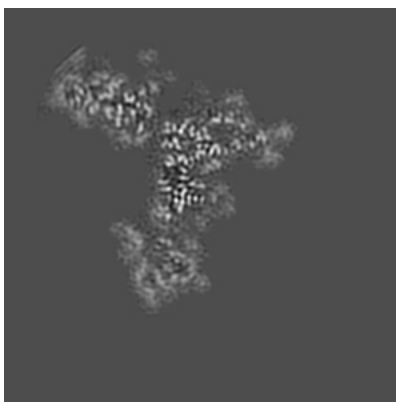
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

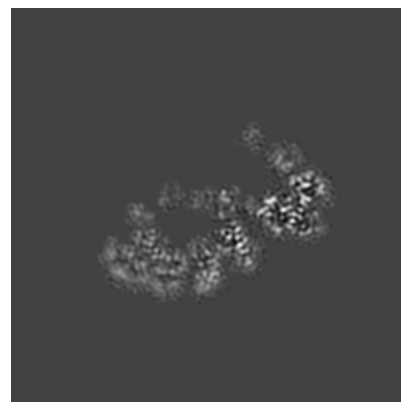
6.2.1 Primary map



X Index: 140



Y Index: 140

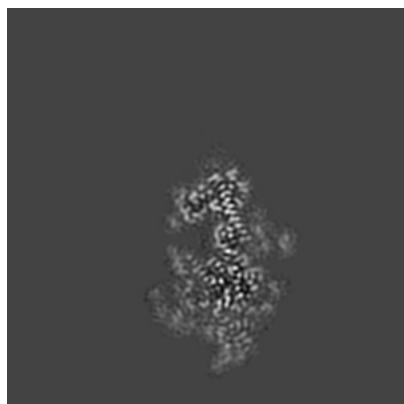


Z Index: 140

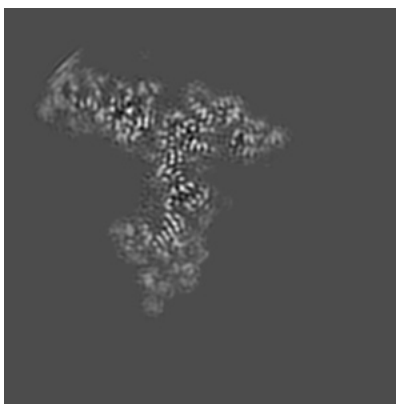
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

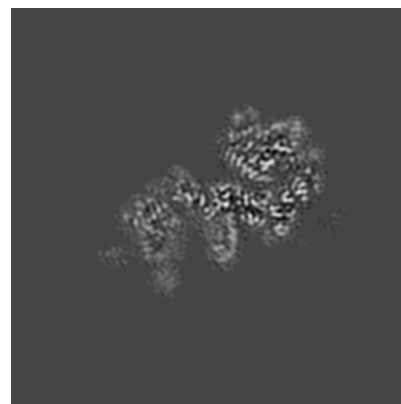
6.3.1 Primary map



X Index: 204



Y Index: 146

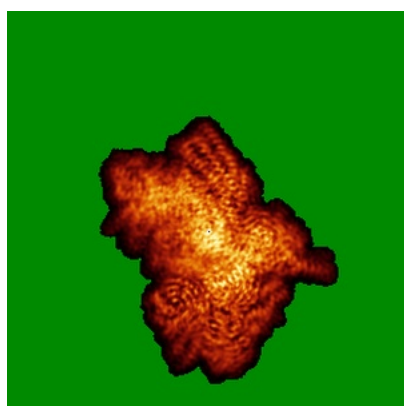


Z Index: 121

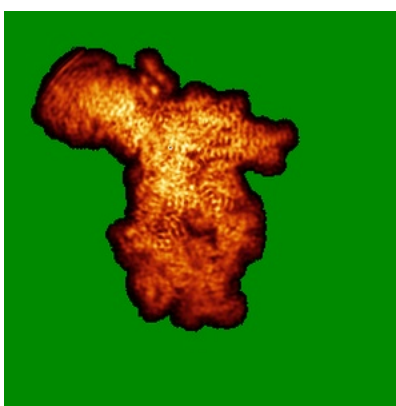
The images above show the largest variance slices of the map in three orthogonal directions.

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

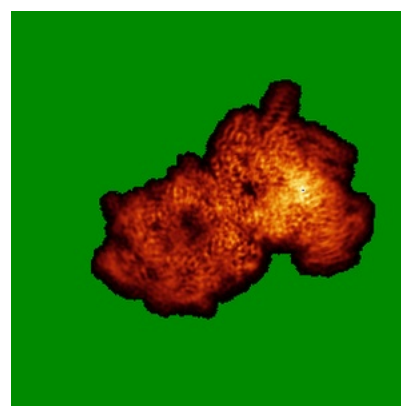
6.4.1 Primary map



X



Y

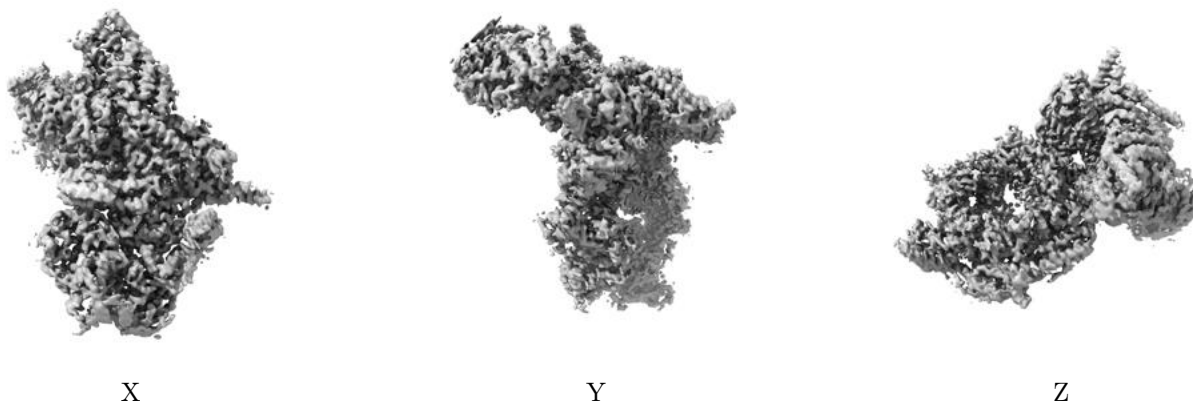


Z

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

6.5 Orthogonal surface views [i](#)

6.5.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.034. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

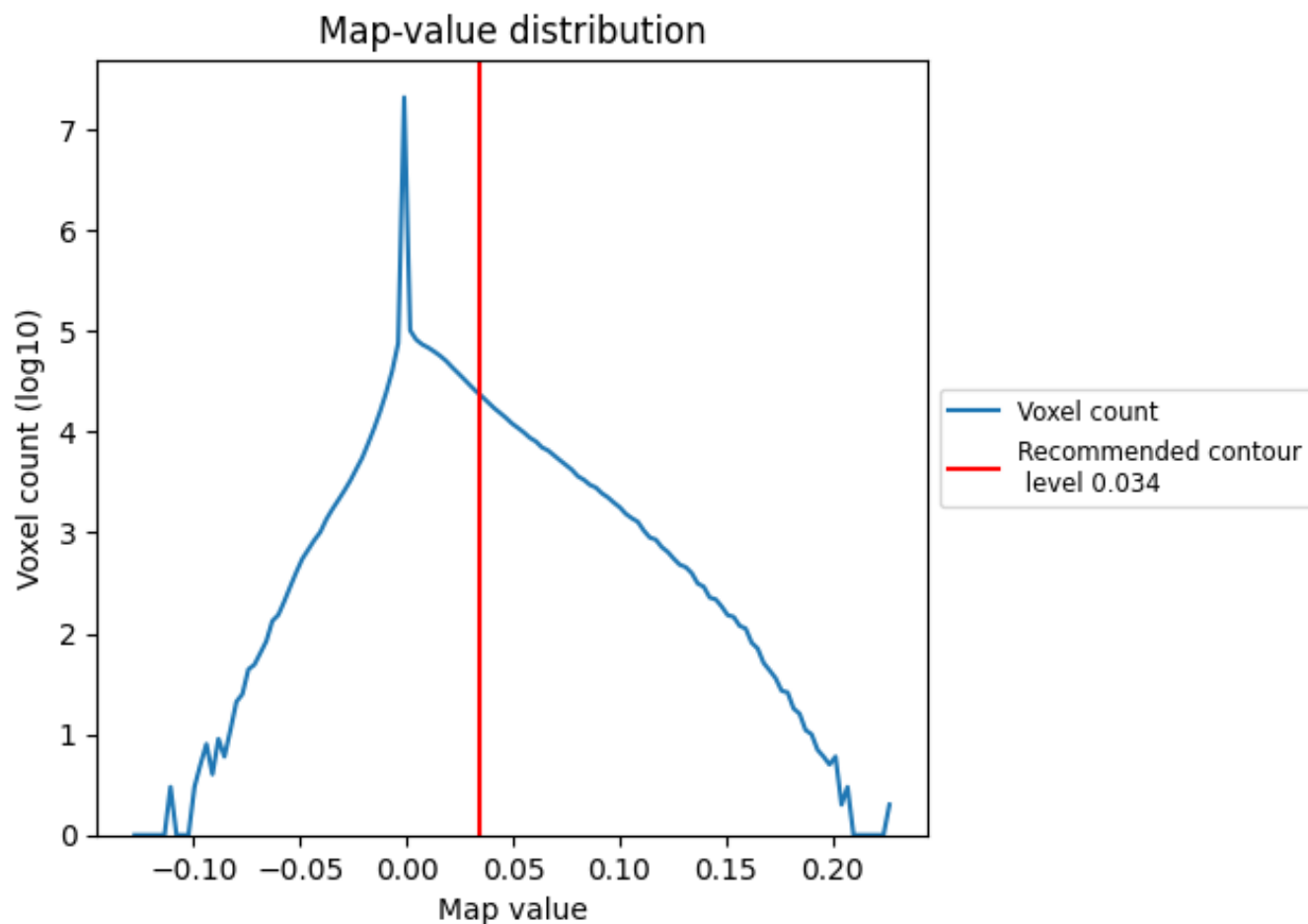
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

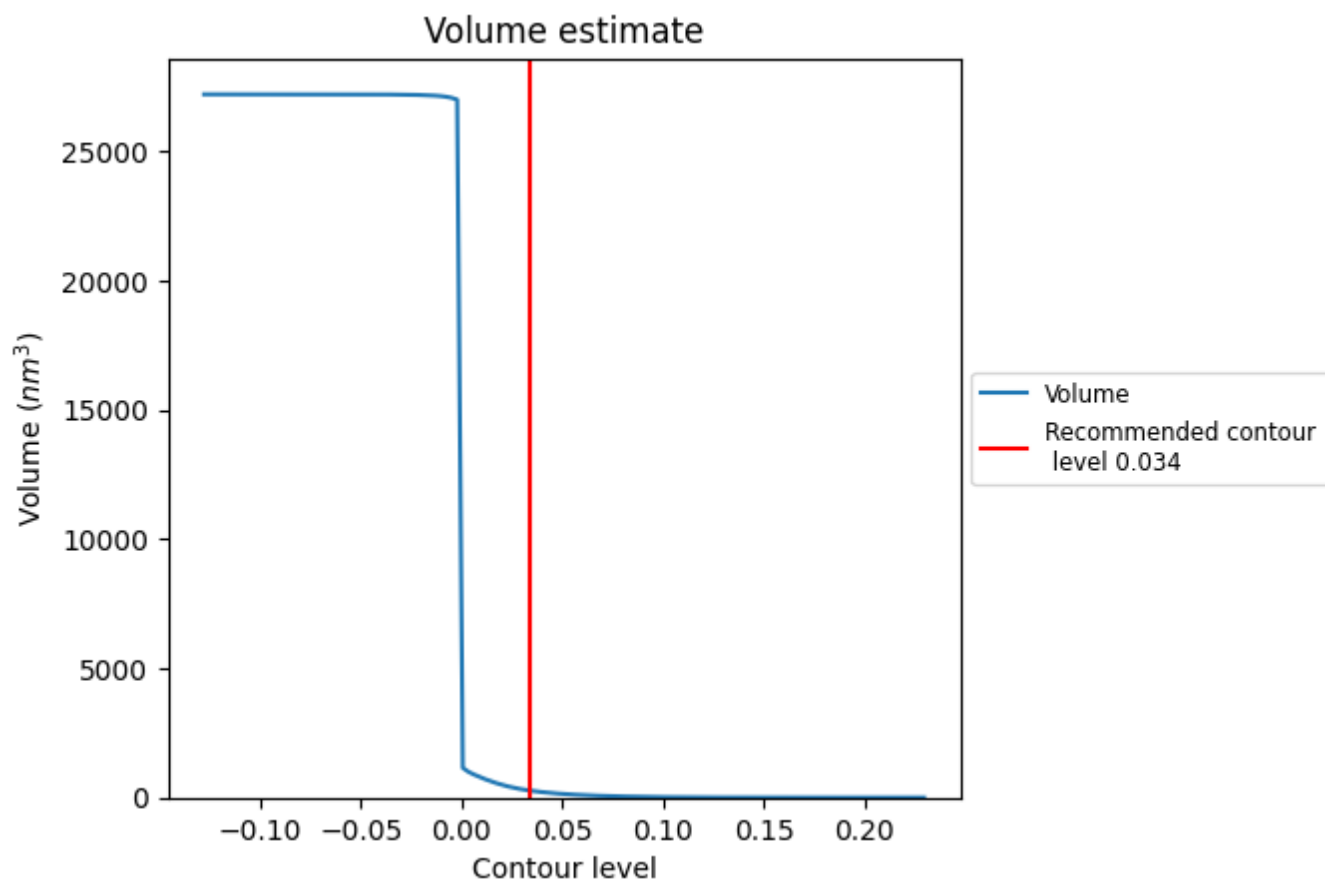
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

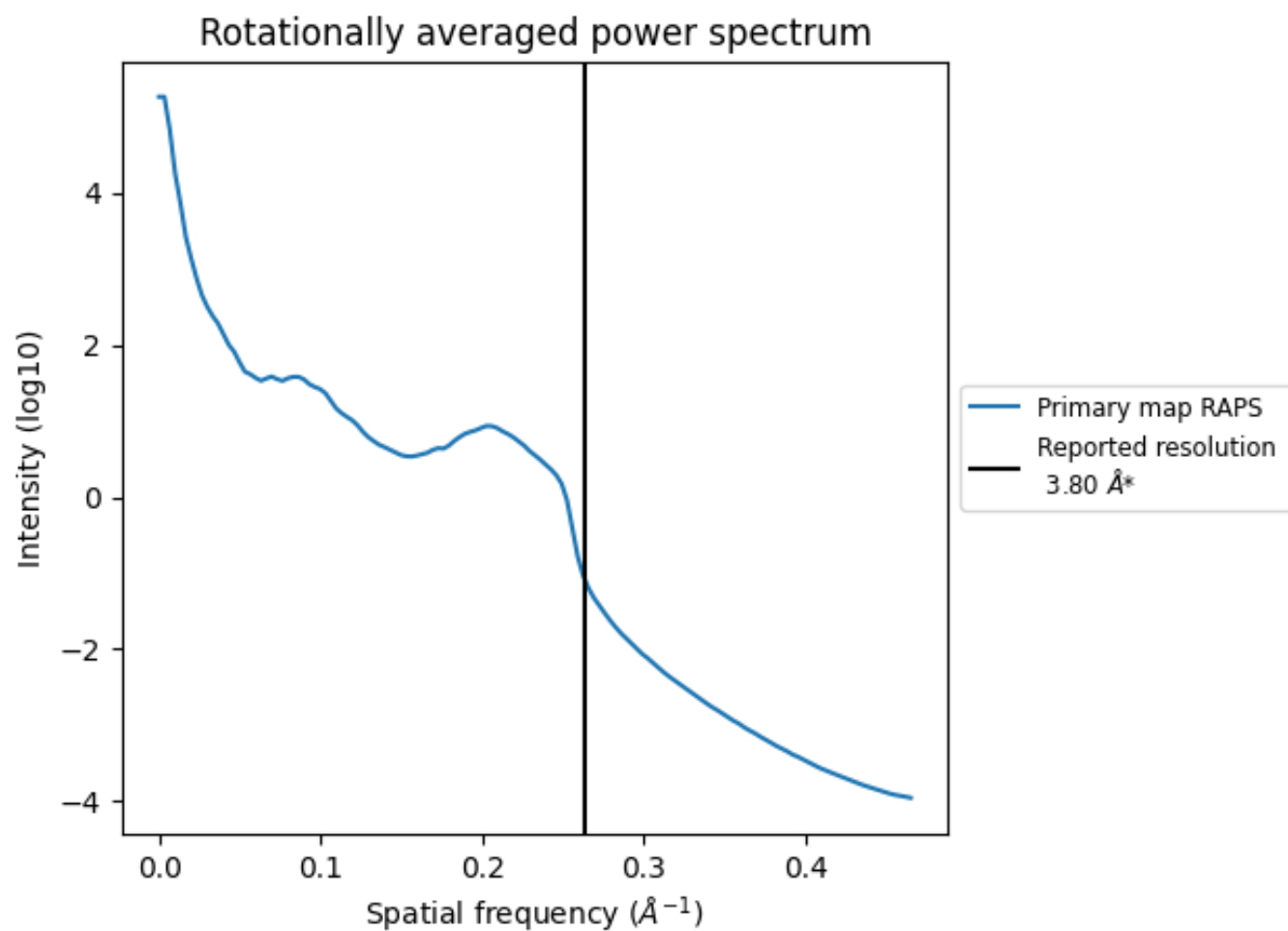
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 270 nm³; this corresponds to an approximate mass of 244 kDa.

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

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.263 Å⁻¹

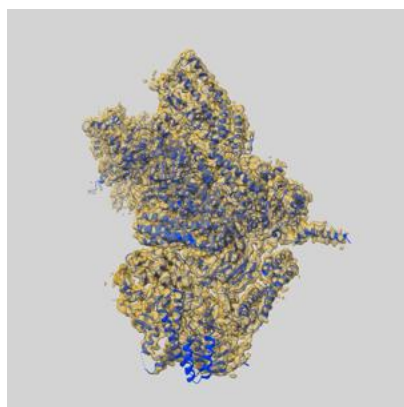
8 Fourier-Shell correlation

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

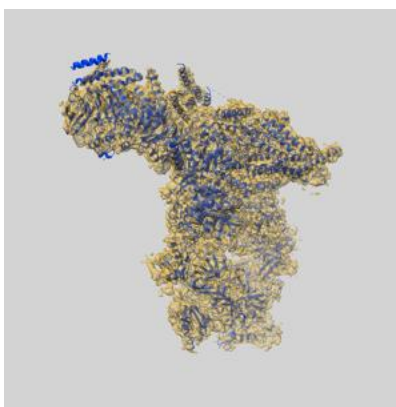
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-20471 and PDB model 6PTJ. Per-residue inclusion information can be found in [section 3](#) on [page 6](#).

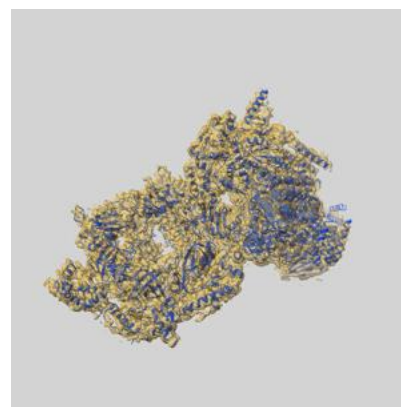
9.1 Map-model overlay [i](#)



X



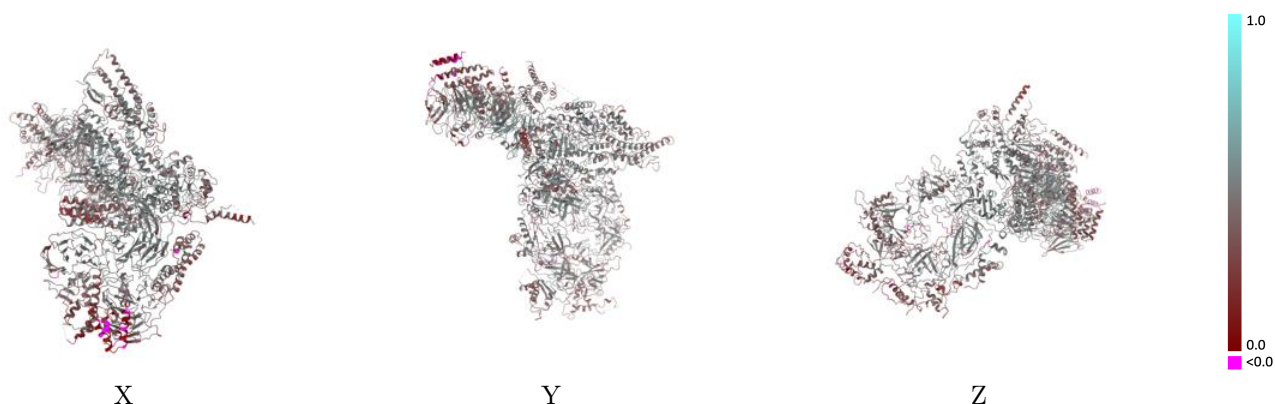
Y



Z

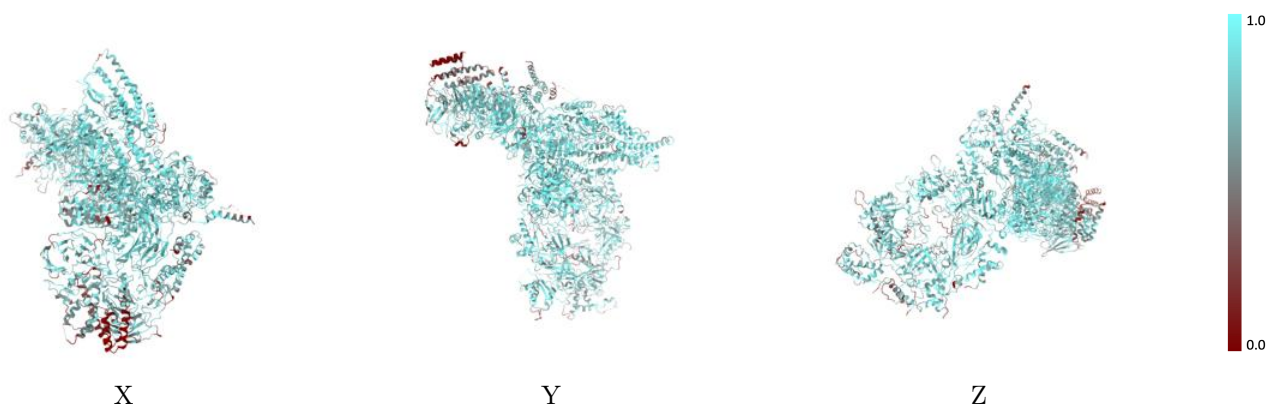
The images above show the 3D surface view of the map at the recommended contour level 0.034 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



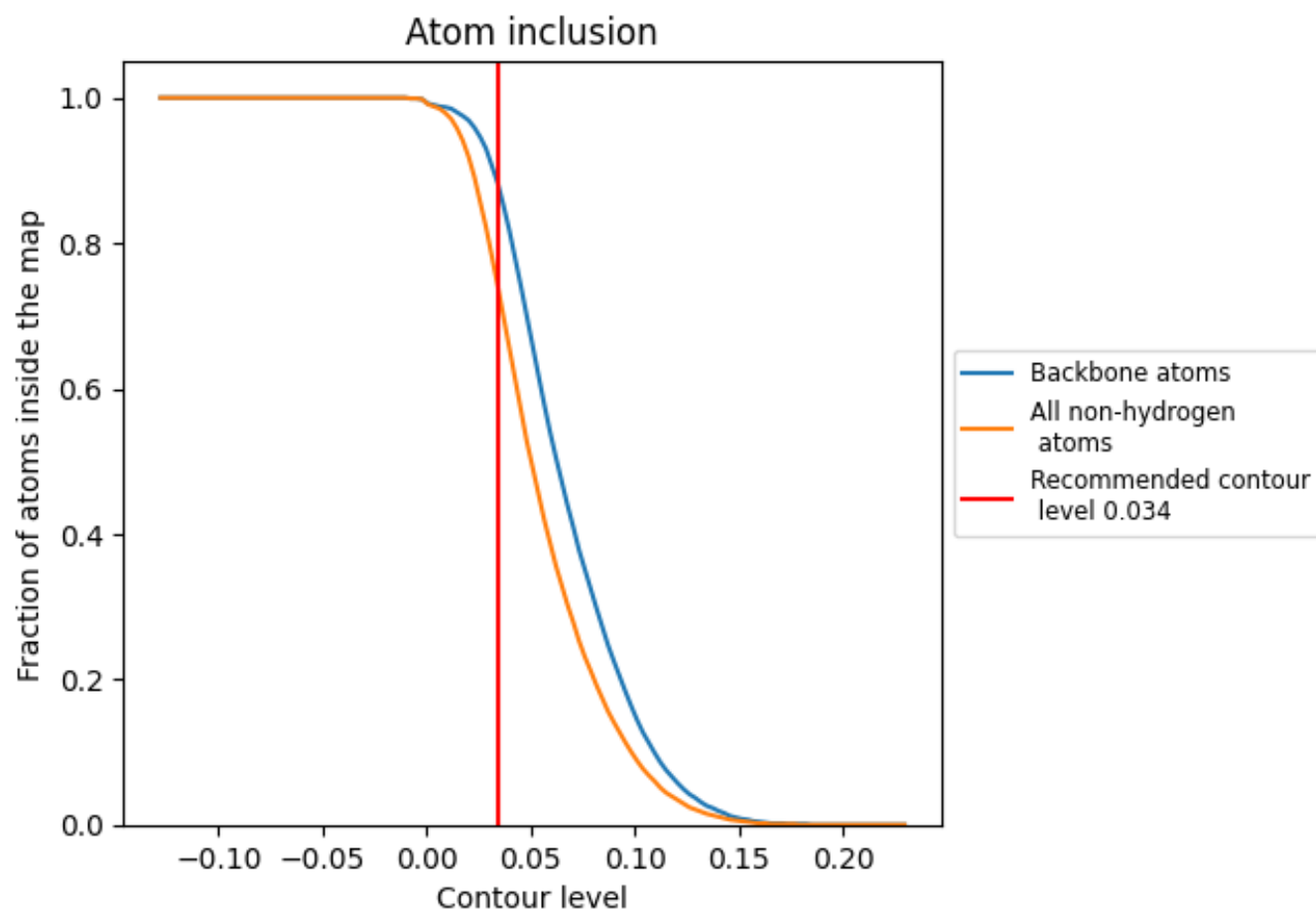
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.034).

9.4 Atom inclusion [i](#)



At the recommended contour level, 88% of all backbone atoms, 74% 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 (0.034) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7440	0.4140
2	0.7350	0.4080
3	0.7820	0.4310
4	0.6830	0.3360
5	0.8300	0.4740
6	0.7020	0.3820
7	0.6650	0.3640
A	0.7460	0.4030
B	0.8420	0.4790
C	0.8430	0.4660
D	0.7880	0.4380
E	0.8070	0.4620
F	0.6930	0.3990
G	0.6120	0.3620
c	0.8000	0.4380

1.0

0.0

<0.0