



wwPDB EM Validation Summary Report ⓘ

Sep 12, 2026 – 01:11 PM EDT

PDB ID : 12DL / pdb_000012dl
EMDB ID : EMD-76334
Title : Native structure of the cytoplasmic lattice (CPL) asymmetric unit from mouse MII eggs
Authors : Li, Y.; Zheng, W.; Leem, J.; Wu, C.; Tang, S.; Mogessie, B.; Xiong, Y.
Deposited on : 2026-03-29
Resolution : 3.50 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:

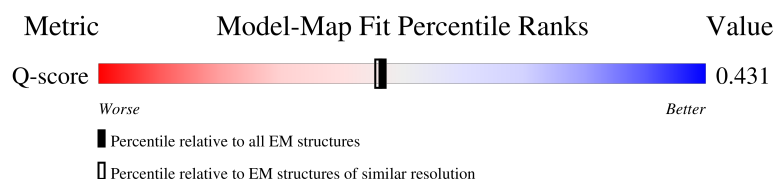
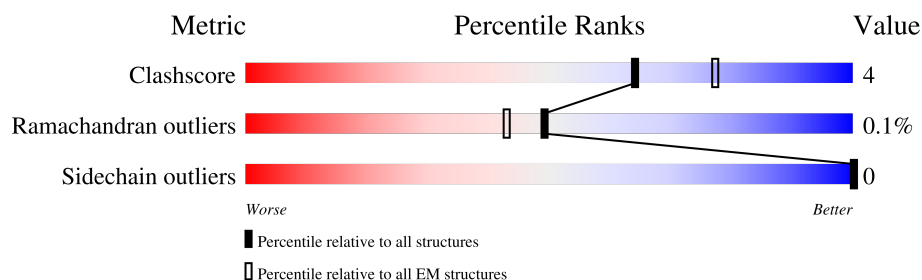
EMDB validation analysis : 0.0.1.dev133
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics : 202505.v01 (Using data 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) : 2.50

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 3.50 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.



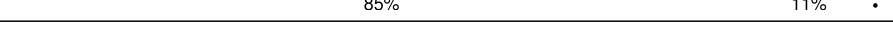
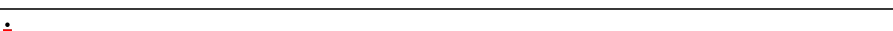
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	13950 (3.00 - 4.00)

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	FA	445	
2	GA	1163	
2	GB	1163	
3	IA	164	

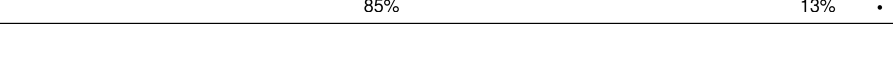
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Mol	Chain	Length	Quality of chain
3	JA	164	
4	HA	581	
4	HB	581	
5	KA	227	
6	LA	440	
7	MA	937	
8	AA	682	
8	AB	682	
8	AC	682	
8	AD	682	
8	AE	682	
8	AF	682	
8	AG	682	
8	AH	682	
8	AI	682	
8	AJ	682	
9	EA	449	
10	DA	993	
10	DB	993	
11	BA	782	
11	BB	782	
12	CA	147	
12	CB	147	
13	OA	466	
14	QA	163	

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Mol	Chain	Length	Quality of chain
14	QB	163	
14	QC	163	
15	NA	469	
16	PA	468	

2 Entry composition [i](#)

There are 20 unique types of molecules in this entry. The entry contains 133296 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 Tubulin beta-4B chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	FA	429	Total	C	N	O	S	0	0
			3365	2114	577	649	25		

- Molecule 2 is a protein called NACHT, LRR and PYD domains-containing protein 5.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	GB	949	Total	C	N	O	S	0	0
			7479	4758	1266	1390	65		
2	GA	946	Total	C	N	O	S	0	0
			7453	4744	1260	1384	65		

- Molecule 3 is a protein called Oocyte-expressed protein homolog.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	IA	128	Total	C	N	O	S	0	0
			1026	660	177	184	5		
3	JA	118	Total	C	N	O	S	0	0
			953	609	165	174	5		

- Molecule 4 is a protein called Transducin-like enhancer protein 6.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	HB	363	Total	C	N	O	S	0	0
			2868	1820	502	526	20		
4	HA	363	Total	C	N	O	S	0	0
			2868	1820	502	526	20		

- Molecule 5 is a protein called Zinc finger BED domain-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
5	KA	57	Total	C	N	O	S	0	0
			460	293	85	76	6		

- Molecule 6 is a protein called KH domain-containing protein 3.

Mol	Chain	Residues	Atoms					AltConf	Trace
6	LA	133	Total	C	N	O	S	0	0
			1100	709	199	184	8		

- Molecule 7 is a protein called NLR family, pyrin domain containing 4F.

Mol	Chain	Residues	Atoms					AltConf	Trace
7	MA	935	Total	C	N	O	S	0	0
			7536	4813	1256	1397	70		

- Molecule 8 is a protein called Inactive protein-arginine deiminase type-6.

Mol	Chain	Residues	Atoms					AltConf	Trace
8	AC	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AD	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AE	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AF	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AG	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AH	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AA	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AB	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AI	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		
8	AJ	656	Total	C	N	O	S	0	0
			5185	3316	856	975	38		

- Molecule 9 is a protein called Tubulin alpha-1C chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
9	EA	444	Total	C	N	O	S	0	0
			3464	2188	588	666	22		

- Molecule 10 is a protein called NACHT, LRR and PYD domains-containing protein 14.

Mol	Chain	Residues	Atoms					AltConf	Trace
10	DA	958	Total	C	N	O	S	0	0
			7662	4875	1313	1412	62		
10	DB	958	Total	C	N	O	S	0	0
			7663	4875	1313	1413	62		

- Molecule 11 is a protein called E3 ubiquitin-protein ligase UHRF1.

Mol	Chain	Residues	Atoms					AltConf	Trace
11	BA	629	Total	C	N	O	S	0	0
			5082	3184	925	939	34		
11	BB	629	Total	C	N	O	S	0	0
			5082	3184	925	939	34		

- Molecule 12 is a protein called Ubiquitin-conjugating enzyme E2 D3.

Mol	Chain	Residues	Atoms					AltConf	Trace
12	CA	146	Total	C	N	O	S	0	0
			1166	746	199	214	7		
12	CB	146	Total	C	N	O	S	0	0
			1166	746	199	214	7		

- Molecule 13 is a protein called F-box and WD-40 domain protein 19.

Mol	Chain	Residues	Atoms					AltConf	Trace
13	OA	456	Total	C	N	O	S	0	0
			3683	2371	628	655	29		

- Molecule 14 is a protein called S-phase kinase-associated protein 1.

Mol	Chain	Residues	Atoms					AltConf	Trace
14	QB	154	Total	C	N	O	S	0	0
			1236	778	200	252	6		
14	QA	157	Total	C	N	O	S	0	0
			1260	793	205	256	6		
14	QC	157	Total	C	N	O	S	0	0
			1260	794	204	255	7		

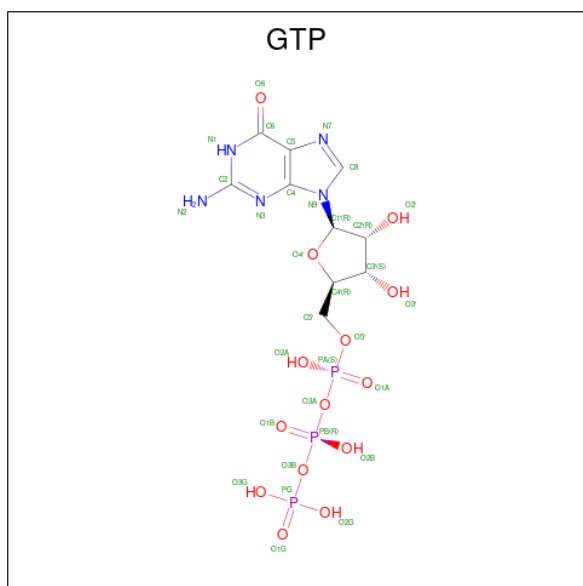
- Molecule 15 is a protein called Expressed sequence C85627.

Mol	Chain	Residues	Atoms					AltConf	Trace
15	NA	463	Total	C	N	O	S	0	0
			3755	2421	625	680	29		

- Molecule 16 is a protein called F-box and WD-40 domain protein 21.

Mol	Chain	Residues	Atoms					AltConf	Trace
16	PA	461	Total	C	N	O	S	0	0
			3781	2451	632	674	24		

- Molecule 17 is GUANOSINE-5'-TRIPHOSPHATE (CCD ID: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 18 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
18	FA	1	Total	Mg	0
			1	1	
18	EA	1	Total	Mg	0
			1	1	

- Molecule 19 is ZINC ION (CCD ID: ZN) (formula: Zn) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
19	KA	1	Total 1	Zn 1	0
19	BA	5	Total 5	Zn 5	0
19	BB	5	Total 5	Zn 5	0

- Molecule 20 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

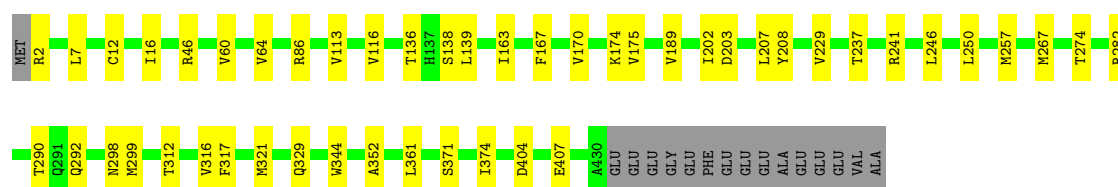
Mol	Chain	Residues	Atoms		AltConf
20	EA	1	Total 1	Ca 1	0

3 Residue-property plots

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

- Molecule 1: Tubulin beta-4B chain

Chain FA: 



- Molecule 2: NACHT, LRR and PYD domains-containing protein 5

Chain GB: 



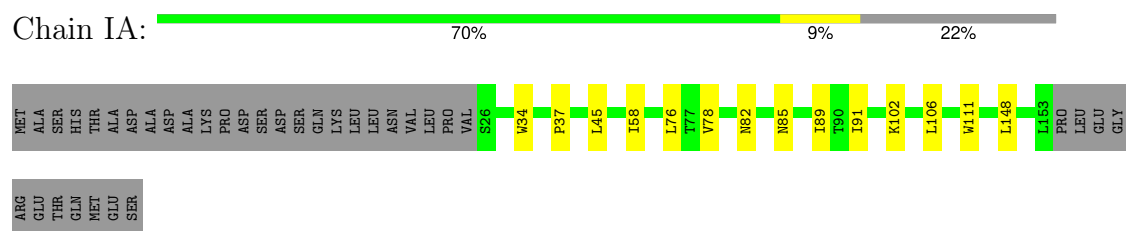
- Molecule 2: NACHT, LRR and PYD domains-containing protein 5

Chain GA:



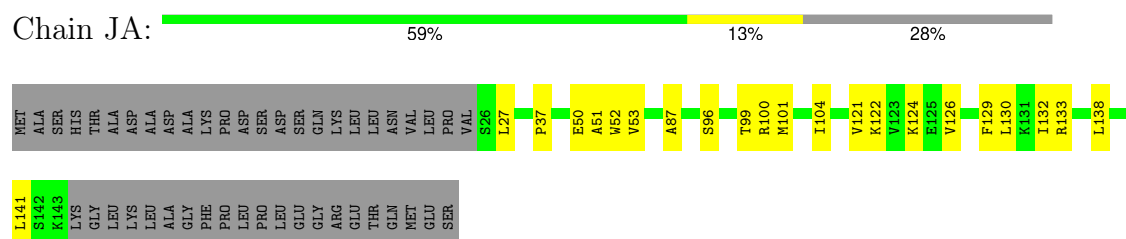
- Molecule 3: Oocyte-expressed protein homolog

Chain IA:

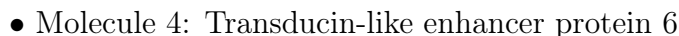


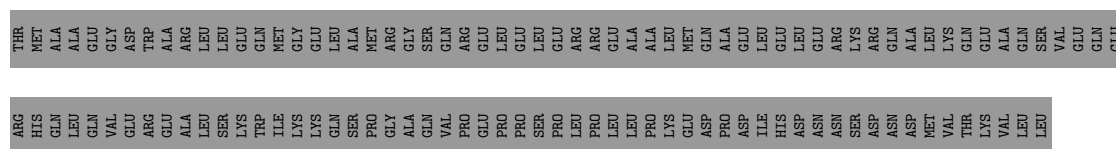
- Molecule 3: Oocyte-expressed protein homolog

Chain JA:

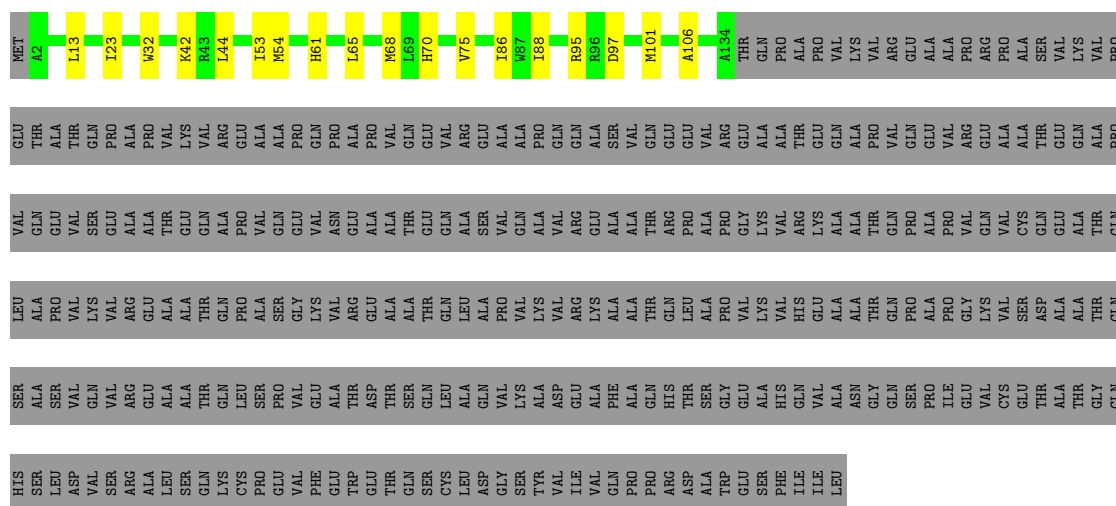


- Molecule 4: Transducin-like enhancer protein 6

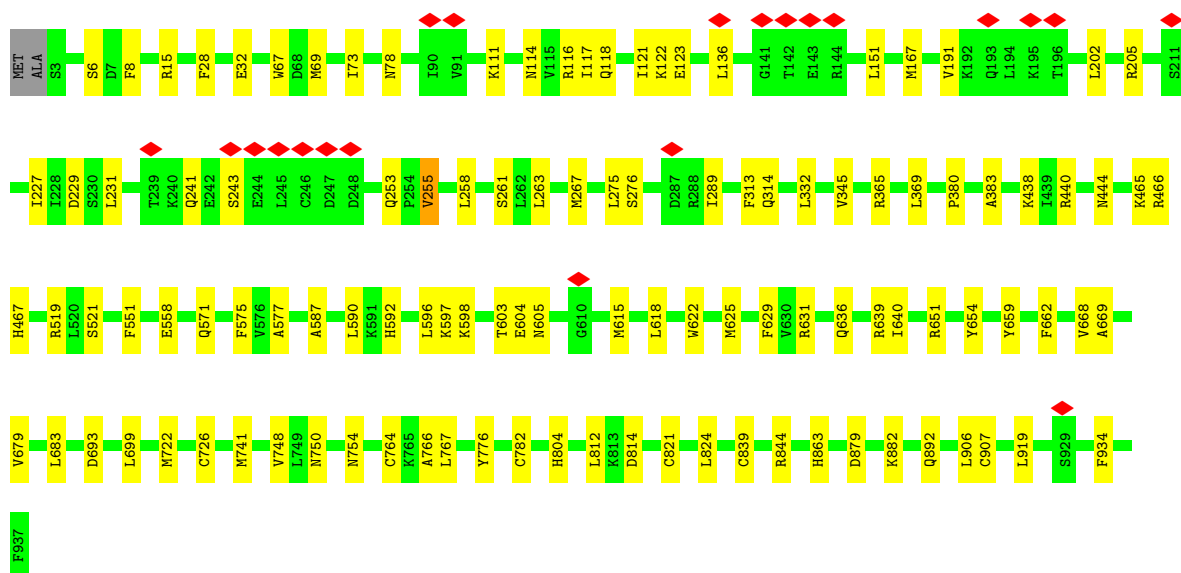




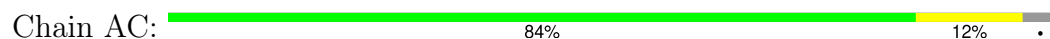
- Molecule 6: KH domain-containing protein 3

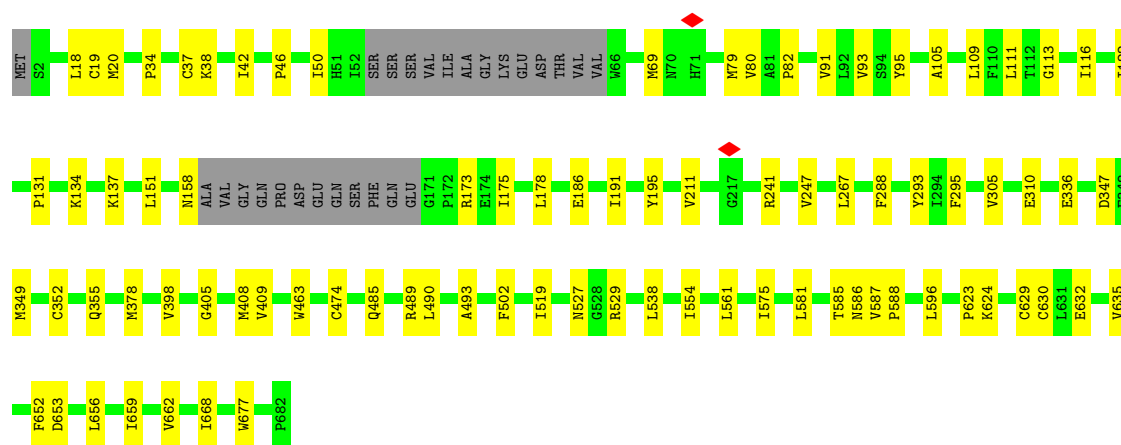


- Molecule 7: NLR family, pyrin domain containing 4F



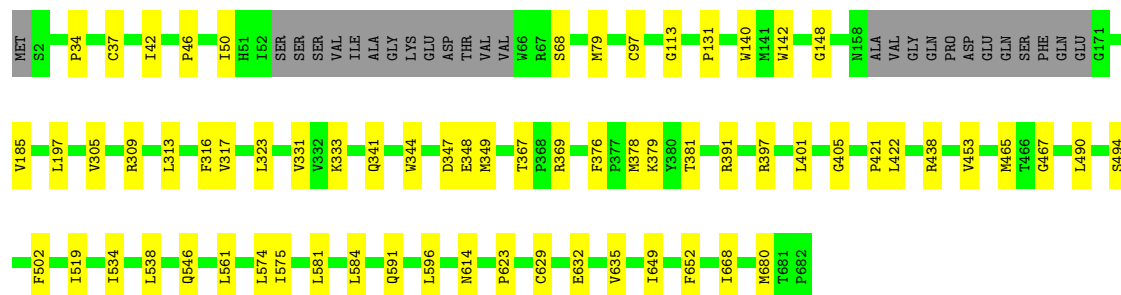
- Molecule 8: Inactive protein-arginine deiminase type-6





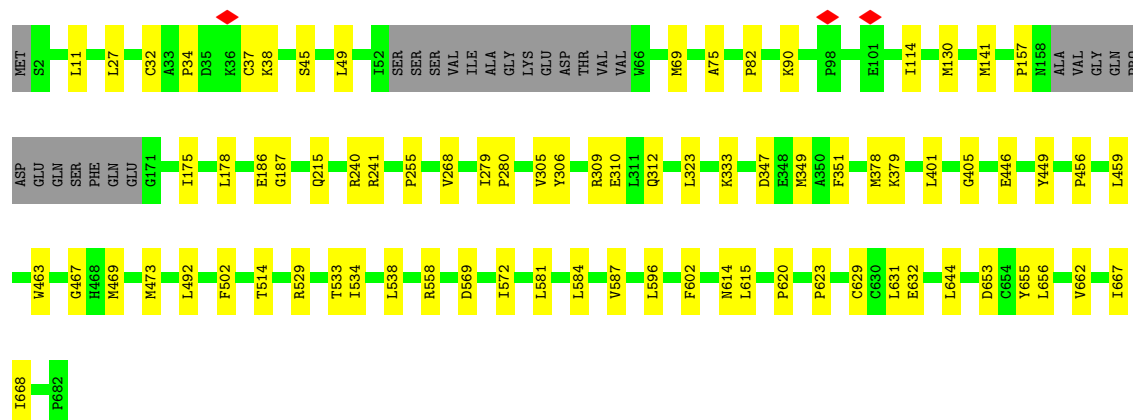
- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AD: 86% 10% •



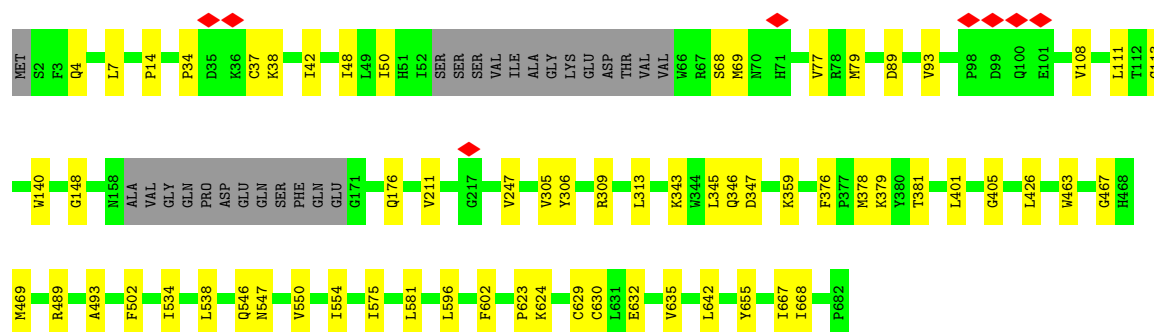
- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AE: 85% 11% •



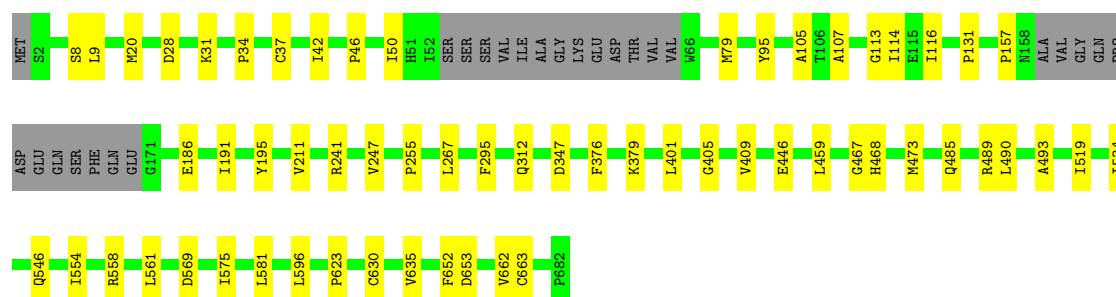
- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AF: 87% 10% •



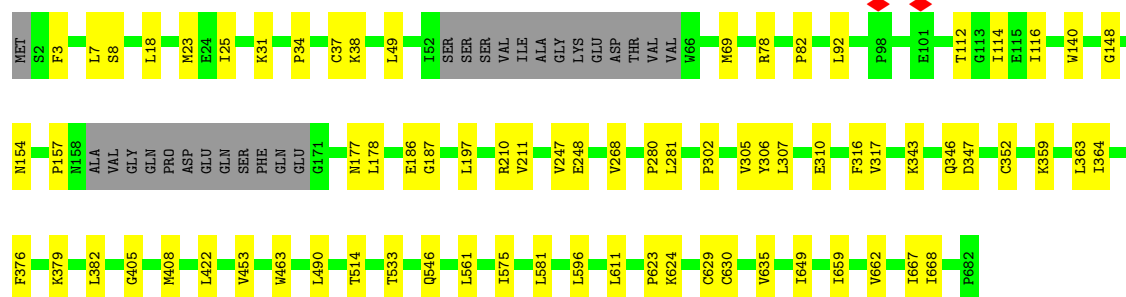
- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AG: 87% 9% .



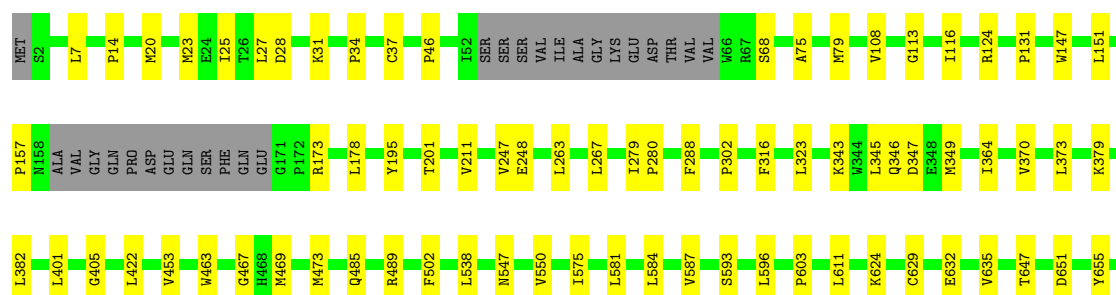
- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AH: 85% 11% .



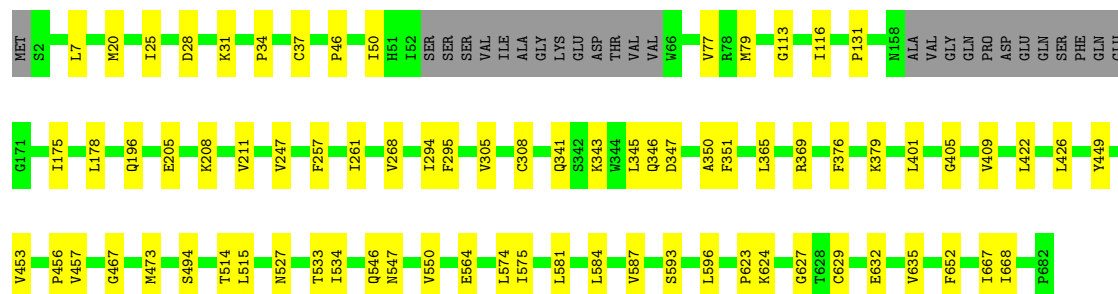
- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AA: 85% 11% .

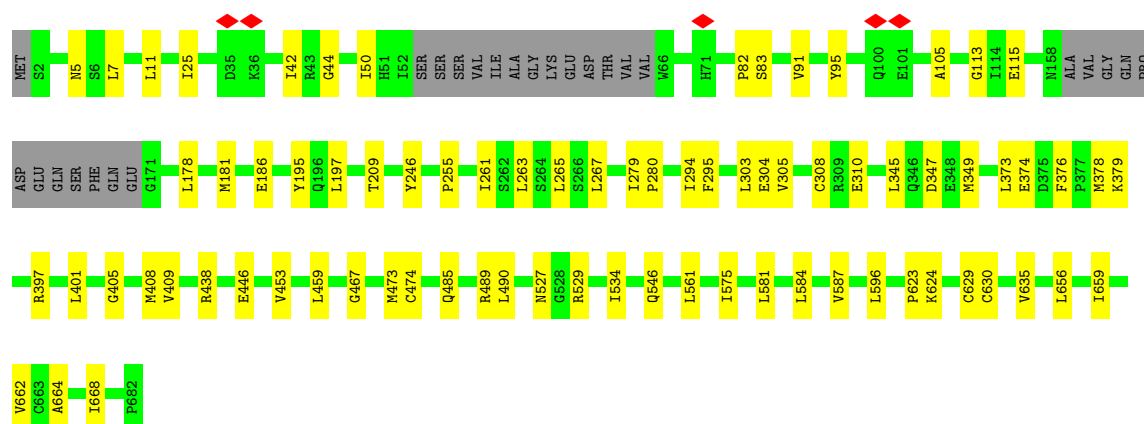


P682

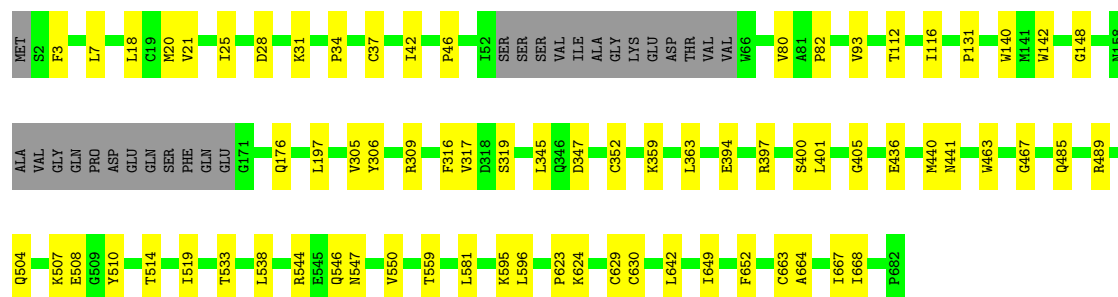
- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AB:  85% 11%

- Molecule 8: Inactive protein-arginine deiminase type-6

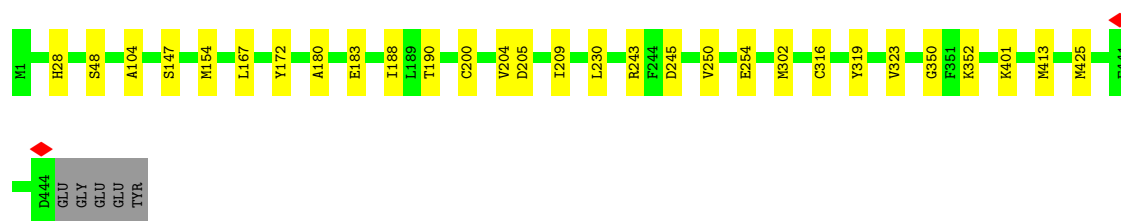
Chain AI:  85% 11%

- Molecule 8: Inactive protein-arginine deiminase type-6

Chain AJ:  85% 11%

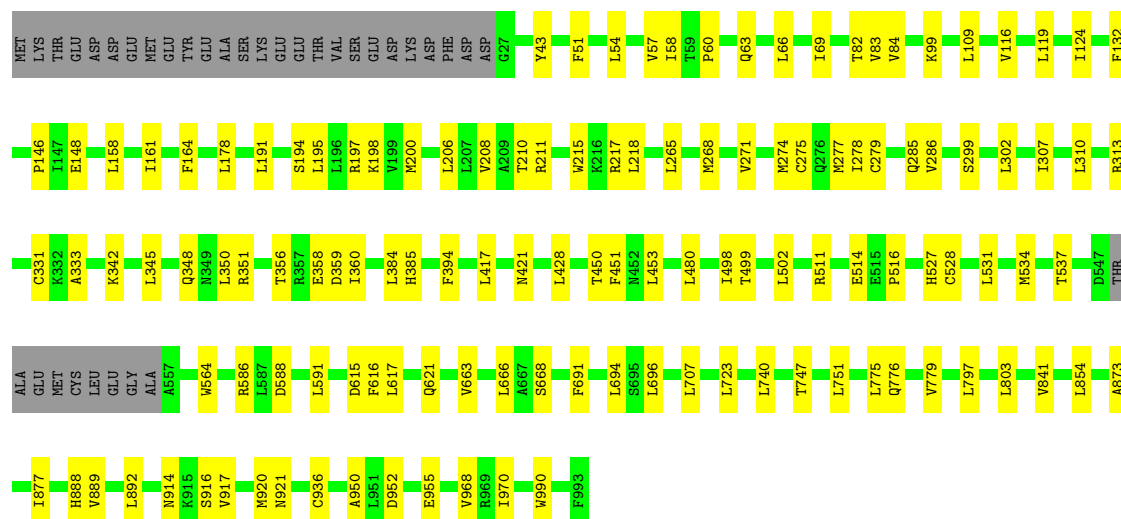
- Molecule 9: Tubulin alpha-1C chain

Chain EA:  92% 6%



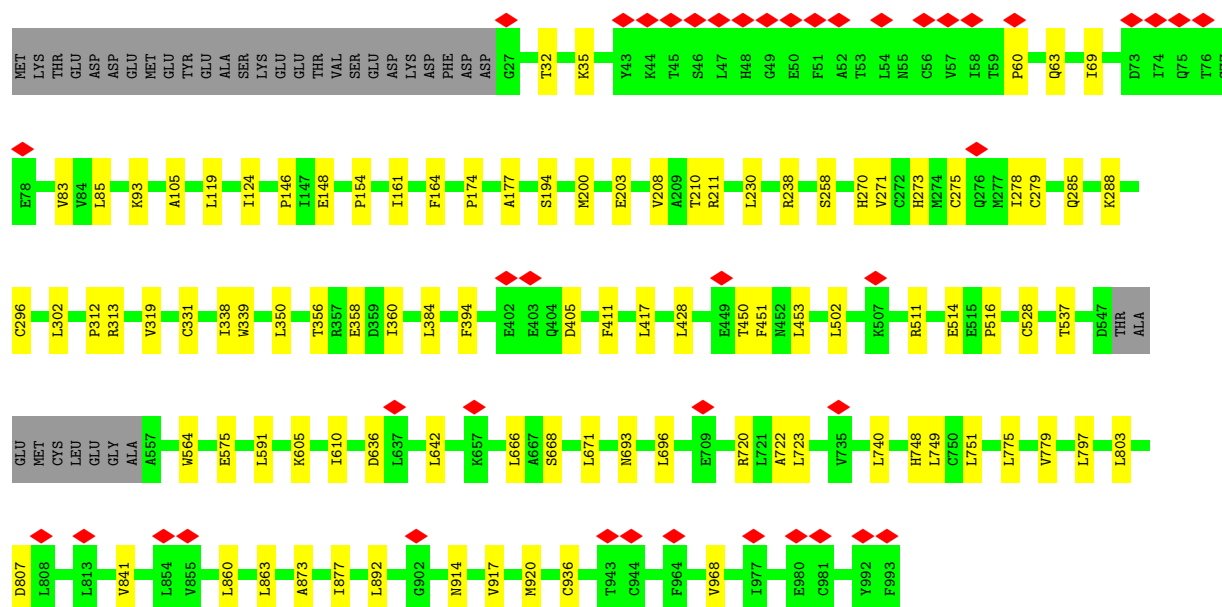
- Molecule 10: NACHT, LRR and PYD domains-containing protein 14

Chain DA: 84% 13% .



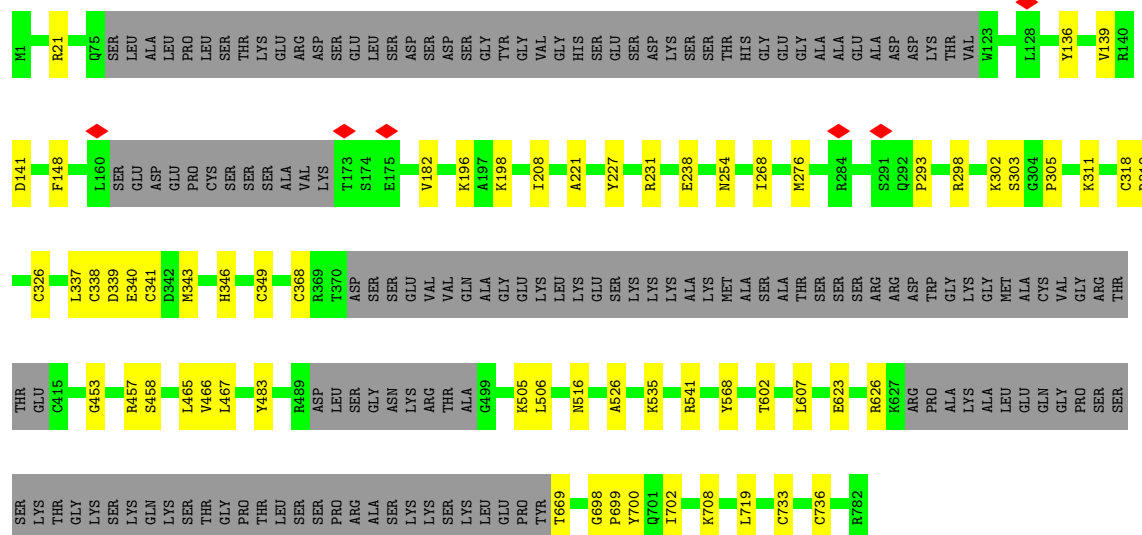
- Molecule 10: NACHT, LRR and PYD domains-containing protein 14

Chain DB: 87% 10% .



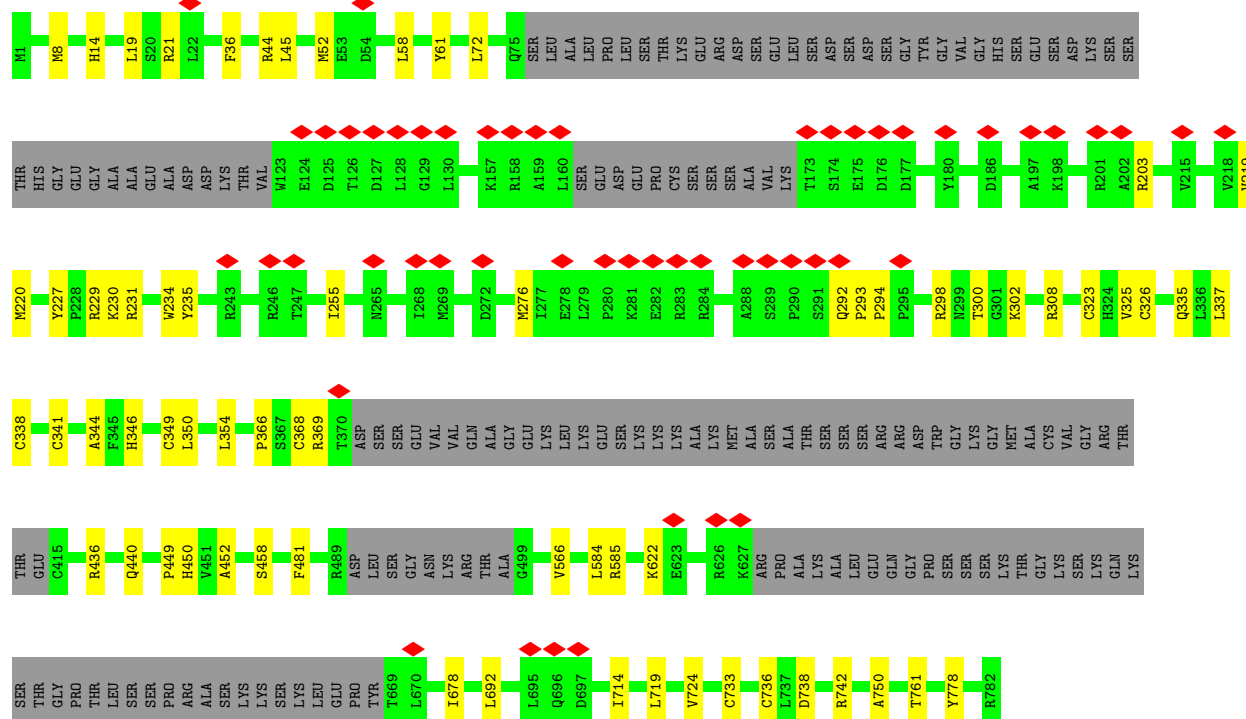
- Molecule 11: E3 ubiquitin-protein ligase UHRF1

Chain BA:  73% 8% 20%



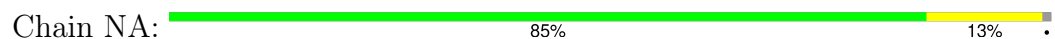
• Molecule 11: E3 ubiquitin-protein ligase UHRF1

Chain BB:  7% 72% 9% 20%



• Molecule 12: Ubiquitin-conjugating enzyme E2 D3

Chain CA:  89% 10%



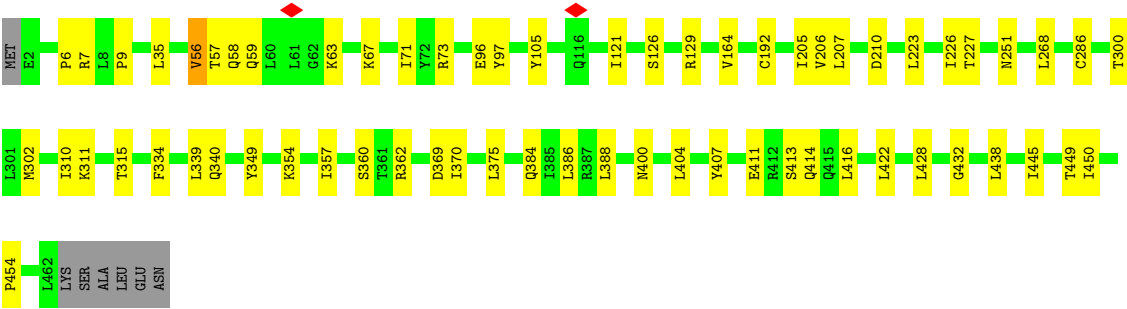


- Molecule 16: F-box and WD-40 domain protein 21

Chain PA:

85%

13%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	249541	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 ($e^-/\text{\AA}^2$)	50	Depositor
Minimum defocus (nm)	1800	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.702	Depositor
Minimum map value	0.000	Depositor
Average map value	0.004	Depositor
Map value standard deviation	0.031	Depositor
Recommended contour level	0.1	Depositor
Map size (Å)	546.816, 546.816, 546.816	wwPDB
Map dimensions	512, 512, 512	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.068, 1.068, 1.068	Depositor

5 Model quality

5.1 Standard geometry

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

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	FA	0.21	0/3440	0.36	0/4663
2	GA	0.19	0/7585	0.36	1/10258 (0.0%)
2	GB	0.18	0/7611	0.34	0/10293
3	IA	0.18	0/1046	0.30	0/1415
3	JA	0.20	0/971	0.36	0/1315
4	HA	0.20	0/2934	0.36	0/3982
4	HB	0.21	0/2934	0.36	0/3982
5	KA	0.17	0/477	0.28	0/649
6	LA	0.17	0/1131	0.32	0/1527
7	MA	0.12	0/7678	0.34	0/10339
8	AA	0.13	0/5302	0.32	0/7189
8	AB	0.13	0/5302	0.31	0/7189
8	AC	0.16	0/5302	0.32	0/7189
8	AD	0.14	0/5302	0.32	0/7189
8	AE	0.15	0/5302	0.32	0/7189
8	AF	0.14	0/5302	0.31	0/7189
8	AG	0.15	0/5302	0.33	0/7189
8	AH	0.15	0/5302	0.32	0/7189
8	AI	0.16	0/5302	0.31	0/7189
8	AJ	0.16	0/5302	0.33	0/7189
9	EA	0.21	0/3542	0.30	0/4809
10	DA	0.19	0/7806	0.36	0/10553
10	DB	0.10	0/7807	0.29	0/10553
11	BA	0.18	0/5198	0.30	0/7027
11	BB	0.10	0/5198	0.27	0/7027
12	CA	0.21	0/1201	0.33	0/1637
12	CB	0.14	0/1201	0.36	0/1637
13	OA	0.18	0/3774	0.33	0/5124
14	QA	0.13	0/1281	0.33	0/1731
14	QB	0.13	0/1256	0.30	0/1697
14	QC	0.10	0/1281	0.29	0/1731
15	NA	0.20	0/3848	0.33	0/5228

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
16	PA	0.18	0/3883	0.32	0/5270
All	All	0.16	0/136103	0.33	1/184337 (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
15	NA	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	GA	441	CYS	CA-CB-SG	5.70	127.51	114.40

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
15	NA	8	LEU	Peptide

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	FA	3365	0	3244	29	0
2	GA	7453	0	7533	67	0
2	GB	7479	0	7557	82	0
3	IA	1026	0	1060	10	0
3	JA	953	0	974	22	0
4	HA	2868	0	2848	33	0
4	HB	2868	0	2848	25	0
5	KA	460	0	431	1	0
6	LA	1100	0	1112	14	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	MA	7536	0	7597	67	0
8	AA	5185	0	5185	43	0
8	AB	5185	0	5185	43	0
8	AC	5185	0	5185	52	0
8	AD	5185	0	5185	37	0
8	AE	5185	0	5185	44	0
8	AF	5185	0	5185	35	0
8	AG	5185	0	5185	36	0
8	AH	5185	0	5185	44	0
8	AI	5185	0	5185	45	0
8	AJ	5185	0	5185	43	0
9	EA	3464	0	3361	19	0
10	DA	7662	0	7769	73	0
10	DB	7663	0	7769	52	0
11	BA	5082	0	4956	37	0
11	BB	5082	0	4956	41	0
12	CA	1166	0	1147	8	0
12	CB	1166	0	1147	19	0
13	OA	3683	0	3733	29	0
14	QA	1260	0	1244	11	0
14	QB	1236	0	1218	11	0
14	QC	1260	0	1249	10	0
15	NA	3755	0	3766	34	0
16	PA	3781	0	3787	37	0
17	EA	32	0	12	0	0
17	FA	32	0	12	0	0
18	EA	1	0	0	0	0
18	FA	1	0	0	0	0
19	BA	5	0	0	0	0
19	BB	5	0	0	0	0
19	KA	1	0	0	0	0
20	EA	1	0	0	0	0
All	All	133296	0	133180	1098	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 1098 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)
2:GA:437:CYS:HA	2:GA:441:CYS:HB3	1.54	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:GA:462:THR:HG21	2:GA:601:GLY:HA3	1.61	0.82
11:BA:338:CYS:SG	11:BA:341:CYS:HB2	2.25	0.75
3:IA:37:PRO:HB3	4:HB:322:VAL:HG21	1.69	0.73
14:QA:4:ILE:HD13	14:QA:21:ALA:HB2	1.72	0.71

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	FA	427/445 (96%)	407 (95%)	20 (5%)	0	100	100
2	GA	942/1163 (81%)	874 (93%)	68 (7%)	0	100	100
2	GB	945/1163 (81%)	881 (93%)	64 (7%)	0	100	100
3	IA	126/164 (77%)	122 (97%)	4 (3%)	0	100	100
3	JA	116/164 (71%)	114 (98%)	2 (2%)	0	100	100
4	HA	359/581 (62%)	330 (92%)	29 (8%)	0	100	100
4	HB	359/581 (62%)	328 (91%)	29 (8%)	2 (1%)	21	54
5	KA	55/227 (24%)	50 (91%)	4 (7%)	1 (2%)	6	34
6	LA	131/440 (30%)	129 (98%)	2 (2%)	0	100	100
7	MA	933/937 (100%)	867 (93%)	64 (7%)	2 (0%)	43	74
8	AA	650/682 (95%)	623 (96%)	26 (4%)	1 (0%)	43	74
8	AB	650/682 (95%)	624 (96%)	26 (4%)	0	100	100
8	AC	650/682 (95%)	613 (94%)	37 (6%)	0	100	100
8	AD	650/682 (95%)	623 (96%)	26 (4%)	1 (0%)	43	74
8	AE	650/682 (95%)	623 (96%)	27 (4%)	0	100	100
8	AF	650/682 (95%)	615 (95%)	34 (5%)	1 (0%)	43	74

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
8	AG	650/682 (95%)	622 (96%)	28 (4%)	0	100	100
8	AH	650/682 (95%)	622 (96%)	28 (4%)	0	100	100
8	AI	650/682 (95%)	619 (95%)	31 (5%)	0	100	100
8	AJ	650/682 (95%)	622 (96%)	28 (4%)	0	100	100
9	EA	442/449 (98%)	431 (98%)	11 (2%)	0	100	100
10	DA	954/993 (96%)	914 (96%)	39 (4%)	1 (0%)	48	79
10	DB	954/993 (96%)	915 (96%)	38 (4%)	1 (0%)	48	79
11	BA	617/782 (79%)	592 (96%)	24 (4%)	1 (0%)	43	74
11	BB	617/782 (79%)	590 (96%)	27 (4%)	0	100	100
12	CA	144/147 (98%)	144 (100%)	0	0	100	100
12	CB	144/147 (98%)	140 (97%)	4 (3%)	0	100	100
13	OA	452/466 (97%)	430 (95%)	21 (5%)	1 (0%)	43	74
14	QA	153/163 (94%)	148 (97%)	5 (3%)	0	100	100
14	QB	150/163 (92%)	146 (97%)	4 (3%)	0	100	100
14	QC	153/163 (94%)	149 (97%)	4 (3%)	0	100	100
15	NA	461/469 (98%)	433 (94%)	27 (6%)	1 (0%)	43	74
16	PA	459/468 (98%)	429 (94%)	28 (6%)	2 (0%)	30	62
All	All	16593/18870 (88%)	15769 (95%)	809 (5%)	15 (0%)	49	79

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
13	OA	451	SER
7	MA	255	VAL
5	KA	35	TYR
7	MA	467	HIS
11	BA	700	TYR

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	FA	367/380 (97%)	367 (100%)	0	100	100
2	GA	845/1054 (80%)	845 (100%)	0	100	100
2	GB	848/1054 (80%)	848 (100%)	0	100	100
3	IA	112/143 (78%)	112 (100%)	0	100	100
3	JA	105/143 (73%)	105 (100%)	0	100	100
4	HA	320/516 (62%)	320 (100%)	0	100	100
4	HB	320/516 (62%)	320 (100%)	0	100	100
5	KA	48/196 (24%)	48 (100%)	0	100	100
6	LA	117/357 (33%)	117 (100%)	0	100	100
7	MA	861/862 (100%)	861 (100%)	0	100	100
8	AA	589/613 (96%)	589 (100%)	0	100	100
8	AB	589/613 (96%)	589 (100%)	0	100	100
8	AC	589/613 (96%)	589 (100%)	0	100	100
8	AD	589/613 (96%)	589 (100%)	0	100	100
8	AE	589/613 (96%)	589 (100%)	0	100	100
8	AF	589/613 (96%)	589 (100%)	0	100	100
8	AG	589/613 (96%)	589 (100%)	0	100	100
8	AH	589/613 (96%)	589 (100%)	0	100	100
8	AI	589/613 (96%)	589 (100%)	0	100	100
8	AJ	589/613 (96%)	589 (100%)	0	100	100
9	EA	372/376 (99%)	372 (100%)	0	100	100
10	DA	878/909 (97%)	878 (100%)	0	100	100
10	DB	878/909 (97%)	878 (100%)	0	100	100
11	BA	556/682 (82%)	556 (100%)	0	100	100
11	BB	556/682 (82%)	556 (100%)	0	100	100
12	CA	131/132 (99%)	131 (100%)	0	100	100
12	CB	131/132 (99%)	131 (100%)	0	100	100
13	OA	421/430 (98%)	421 (100%)	0	100	100
14	QA	144/150 (96%)	144 (100%)	0	100	100
14	QB	141/150 (94%)	141 (100%)	0	100	100
14	QC	144/150 (96%)	144 (100%)	0	100	100
15	NA	429/435 (99%)	429 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
16	PA	425/431 (99%)	425 (100%)	0	100	100
All	All	15039/16919 (89%)	15039 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 113 such sidechains are listed below:

Mol	Chain	Res	Type
8	AG	358	HIS
14	QA	158	GLN
8	AI	592	GLN
12	CB	46	GLN
11	BA	217	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 16 ligands modelled in this entry, 14 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
17	GTP	FA	501	18	33,34,34	0.93	1 (3%)	50,54,54	1.60	8 (16%)
17	GTP	EA	502	18	33,34,34	0.90	0	50,54,54	1.55	9 (18%)

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
17	GTP	FA	501	18	-	6/22/38/38	0/3/3/3
17	GTP	EA	502	18	-	3/22/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
17	FA	501	GTP	C2-N3	2.02	1.38	1.33

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
17	FA	501	GTP	C5-C4-N3	-5.14	120.21	128.39
17	EA	502	GTP	C5-C4-N3	-5.03	120.38	128.39
17	FA	501	GTP	C2-N3-C4	4.69	120.37	112.30
17	EA	502	GTP	C2-N3-C4	4.46	119.98	112.30
17	EA	502	GTP	N9-C4-N3	3.29	132.54	125.95

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

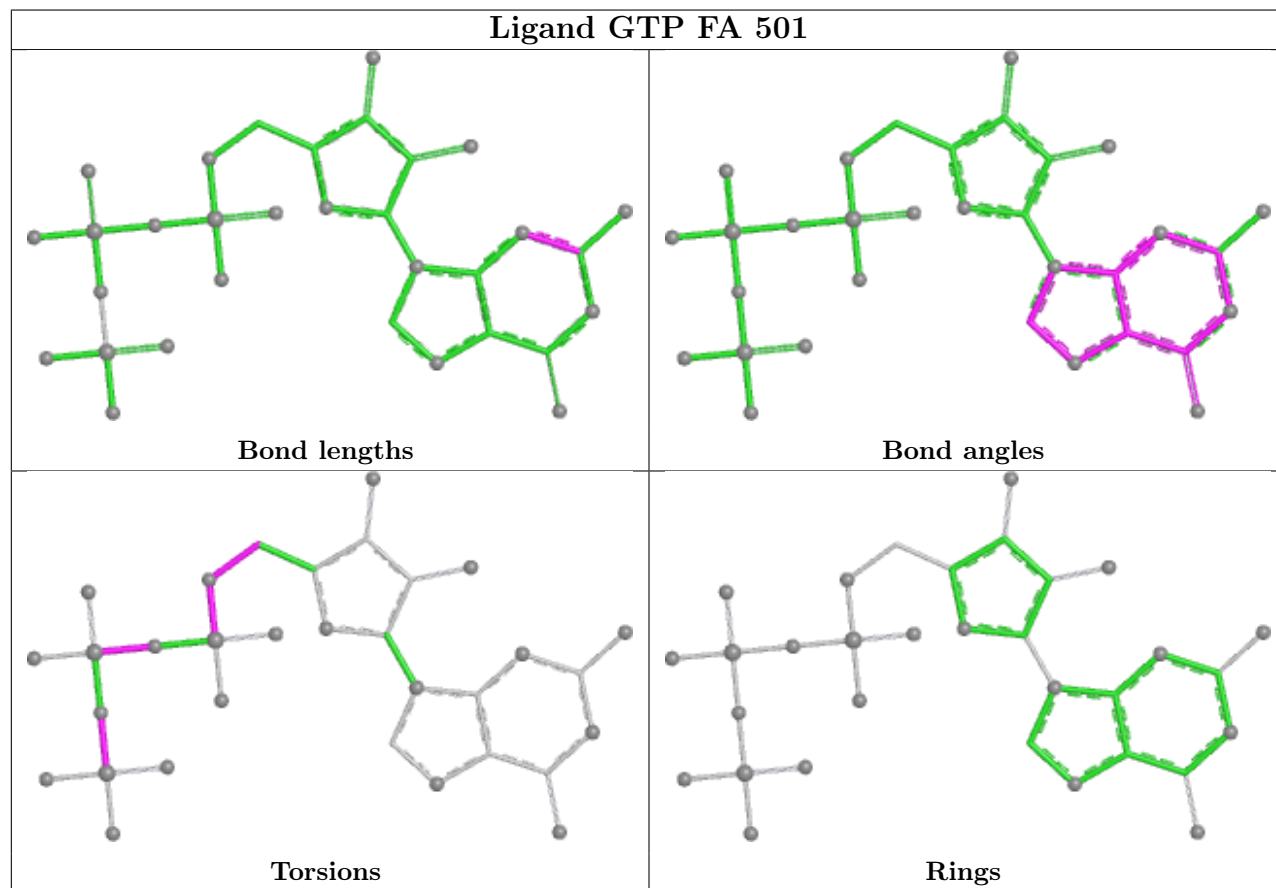
Mol	Chain	Res	Type	Atoms
17	FA	501	GTP	C5'-O5'-PA-O3A
17	FA	501	GTP	C5'-O5'-PA-O1A
17	FA	501	GTP	C5'-O5'-PA-O2A
17	EA	502	GTP	C5'-O5'-PA-O3A
17	EA	502	GTP	C5'-O5'-PA-O2A

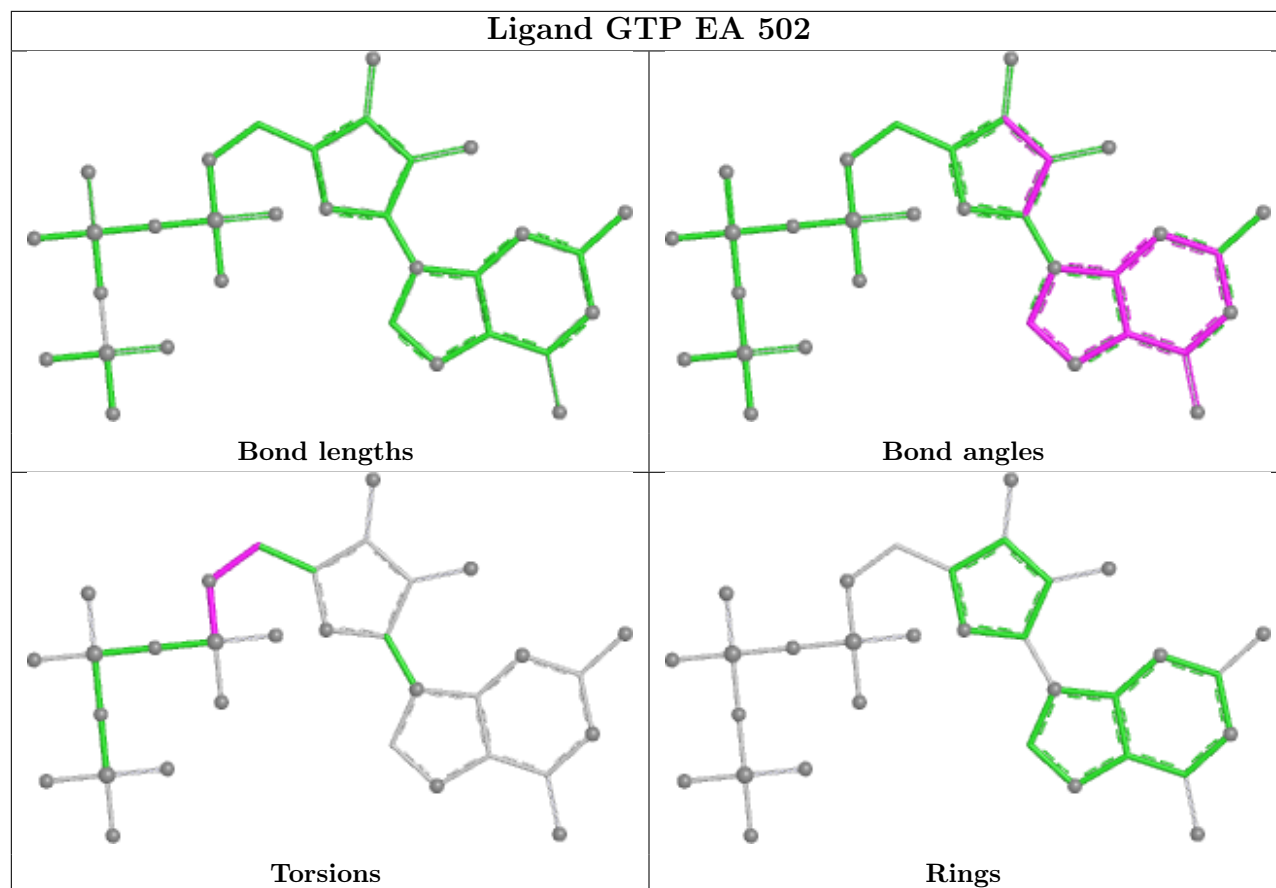
There are no ring outliers.

No monomer is involved in short contacts.

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.

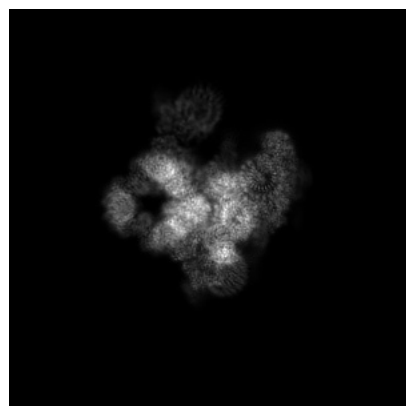
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-76334. These allow visual inspection of the internal detail of the map and identification of artifacts.

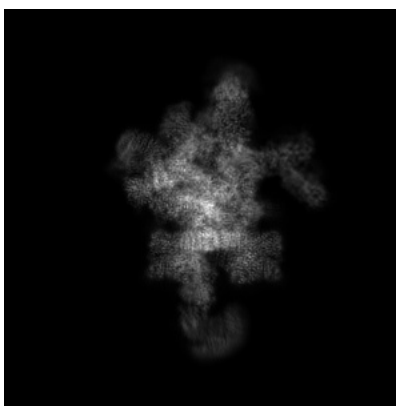
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

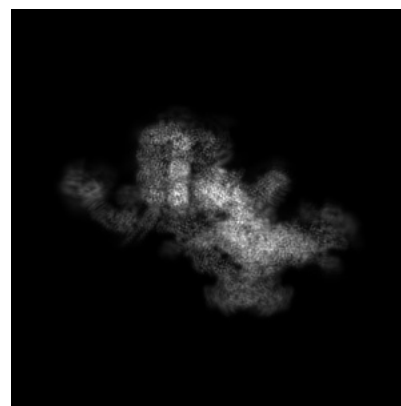
6.1.1 Primary map



X

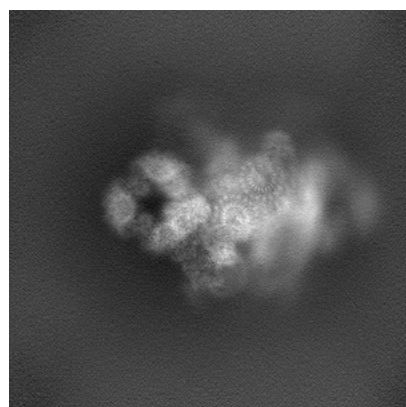


Y

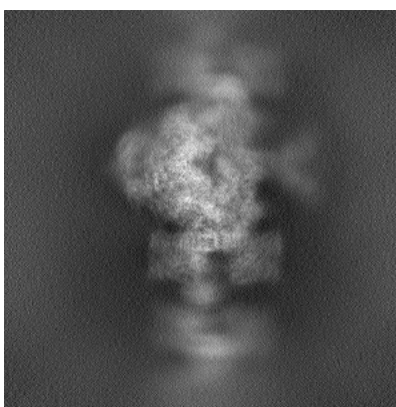


Z

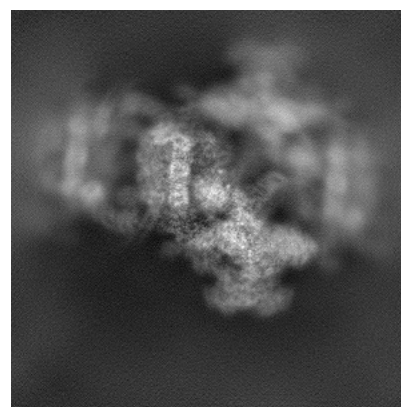
6.1.2 Raw map



X



Y

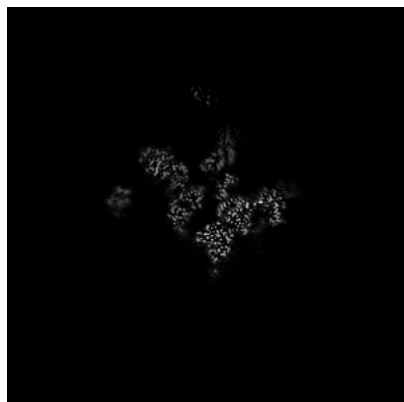


Z

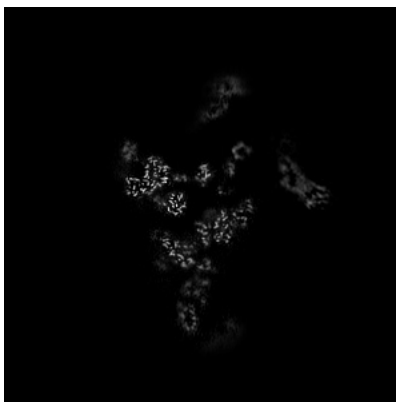
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

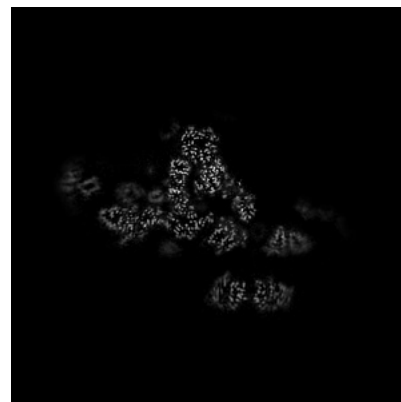
6.2.1 Primary map



X Index: 256

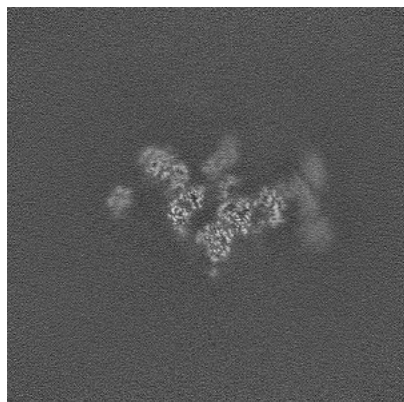


Y Index: 256

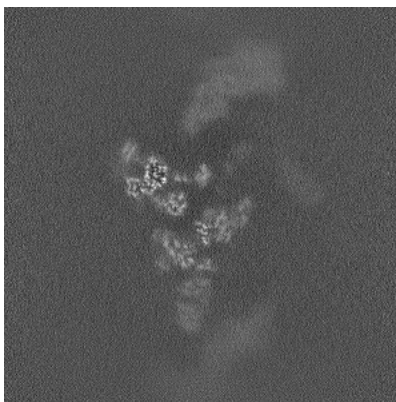


Z Index: 256

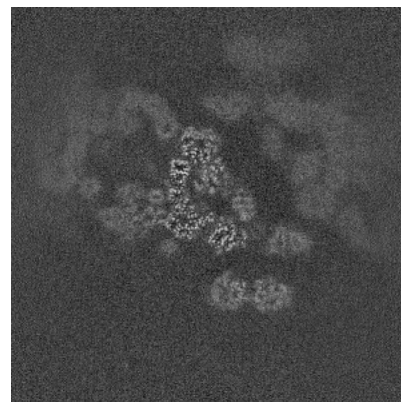
6.2.2 Raw map



X Index: 256



Y Index: 256

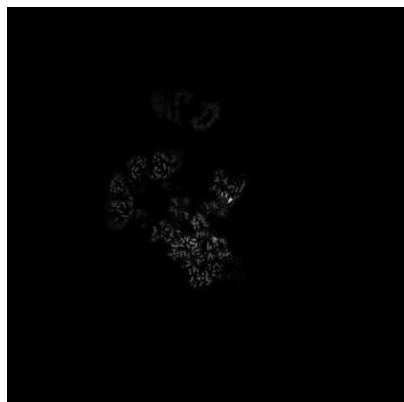


Z Index: 256

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: 291

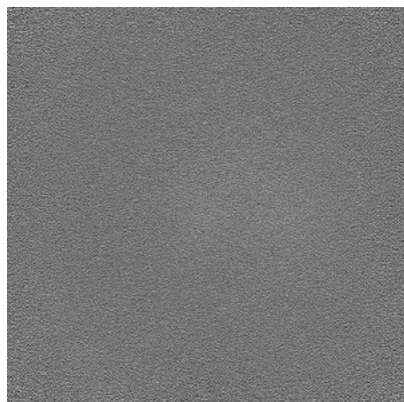


Y Index: 275

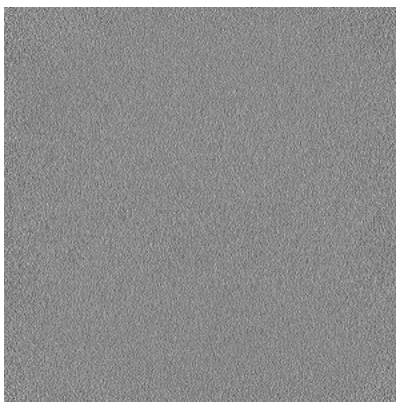


Z Index: 258

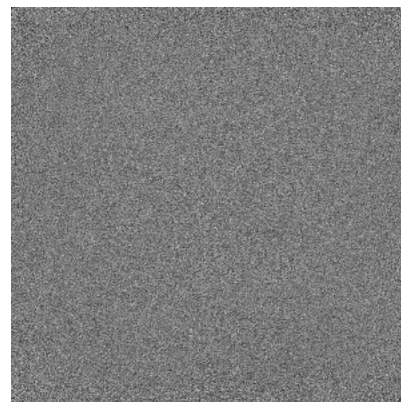
6.3.2 Raw map



X Index: 0



Y Index: 0

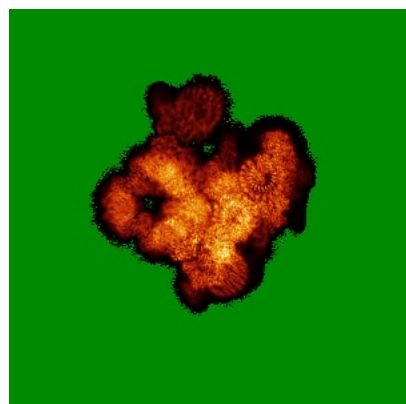


Z Index: 0

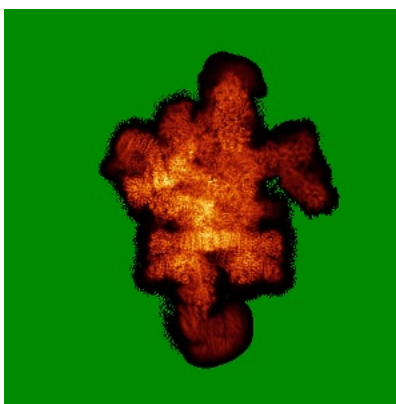
The images above show the largest variance slices of the map in three orthogonal directions.

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

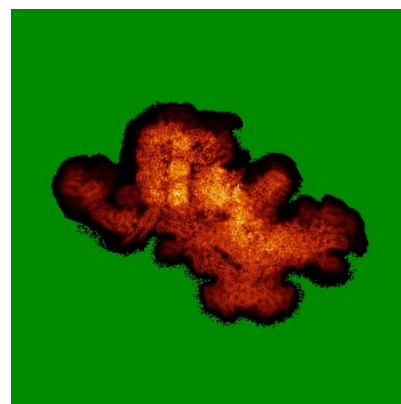
6.4.1 Primary map



X

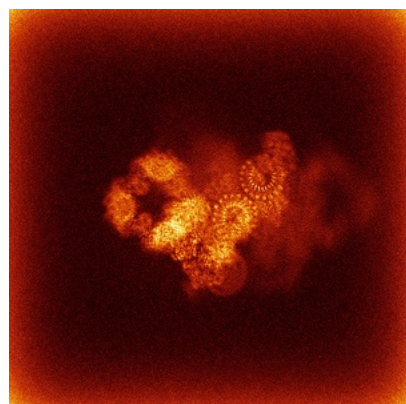


Y

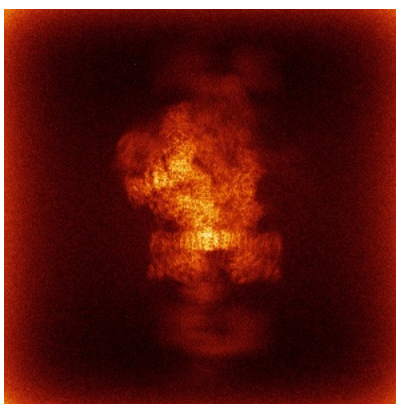


Z

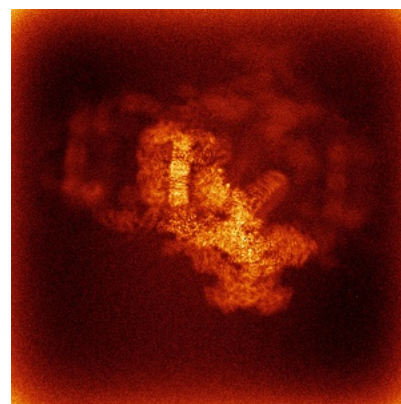
6.4.2 Raw map



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



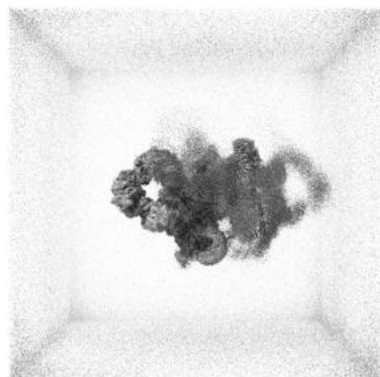
Y



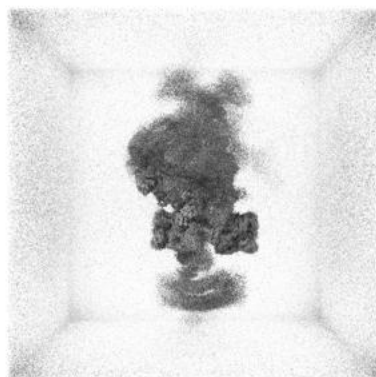
Z

The images above show the 3D surface view of the map at the recommended contour level 0.1. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

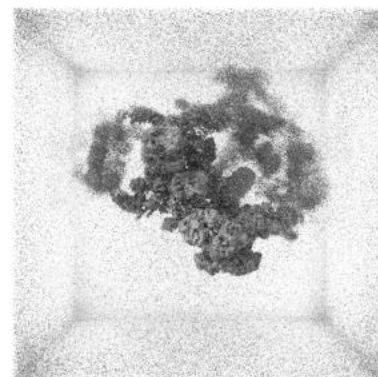
6.5.2 Raw map



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.

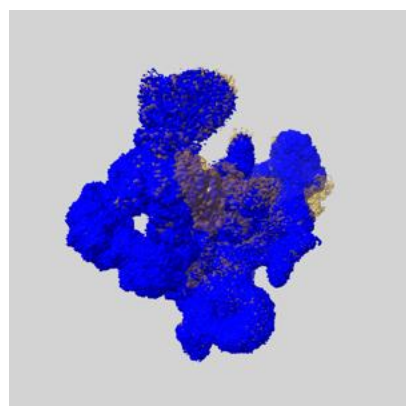
6.6 Mask visualisation [i](#)

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

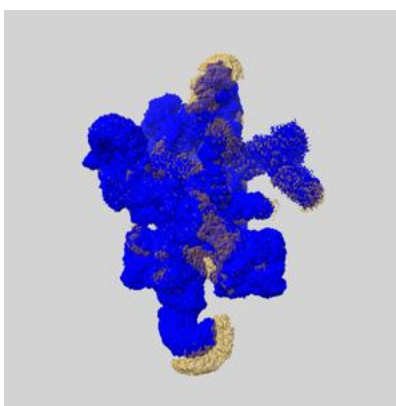
A mask typically either:

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

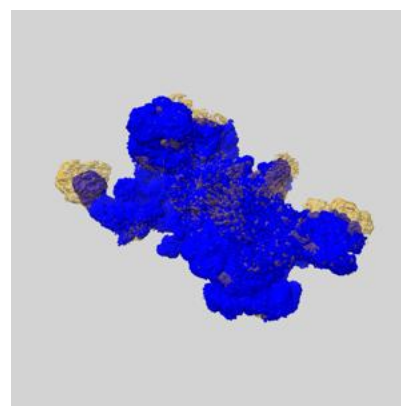
6.6.1 emd_76334_msk_1.map [i](#)



X



Y

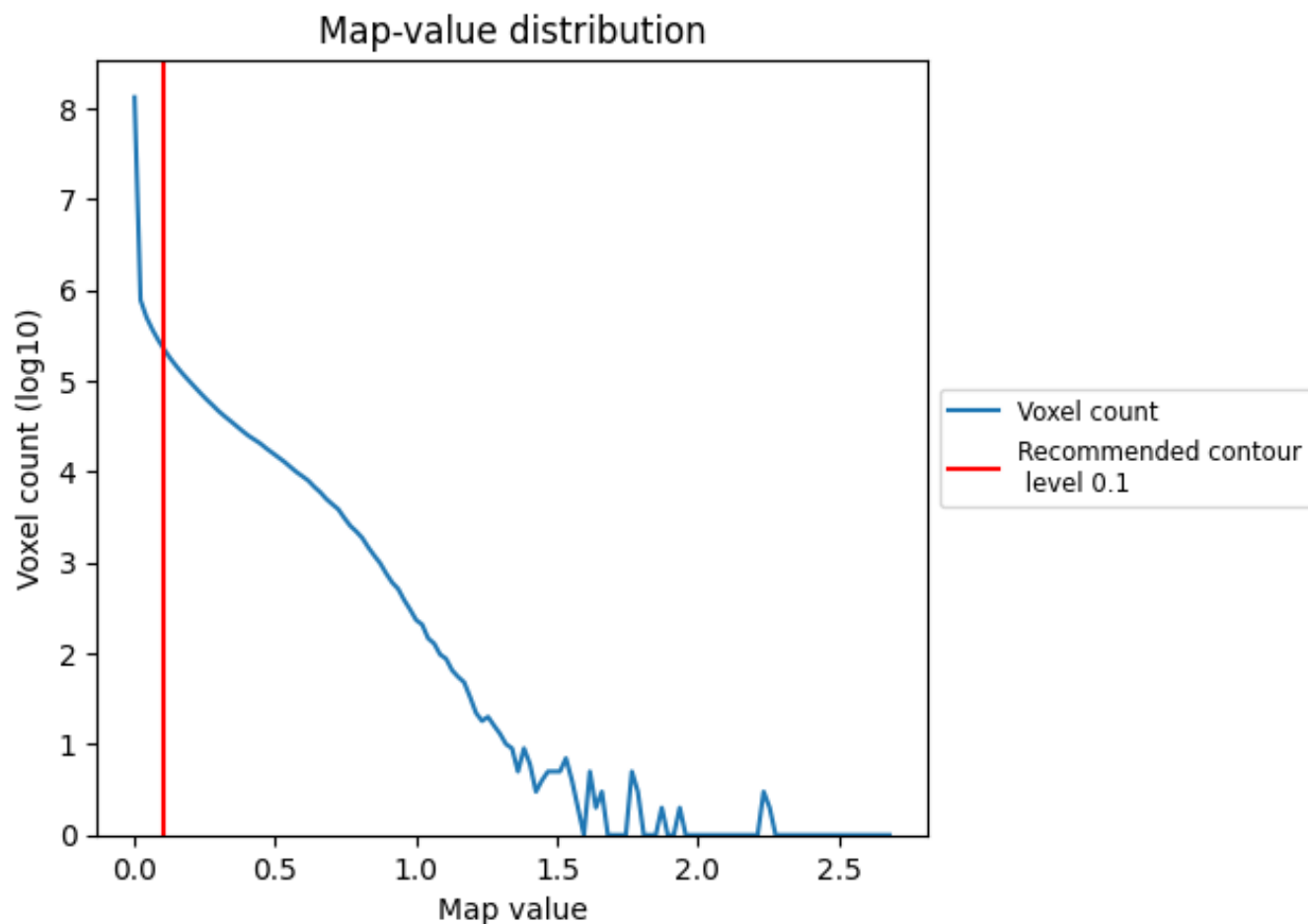


Z

7 Map analysis [i](#)

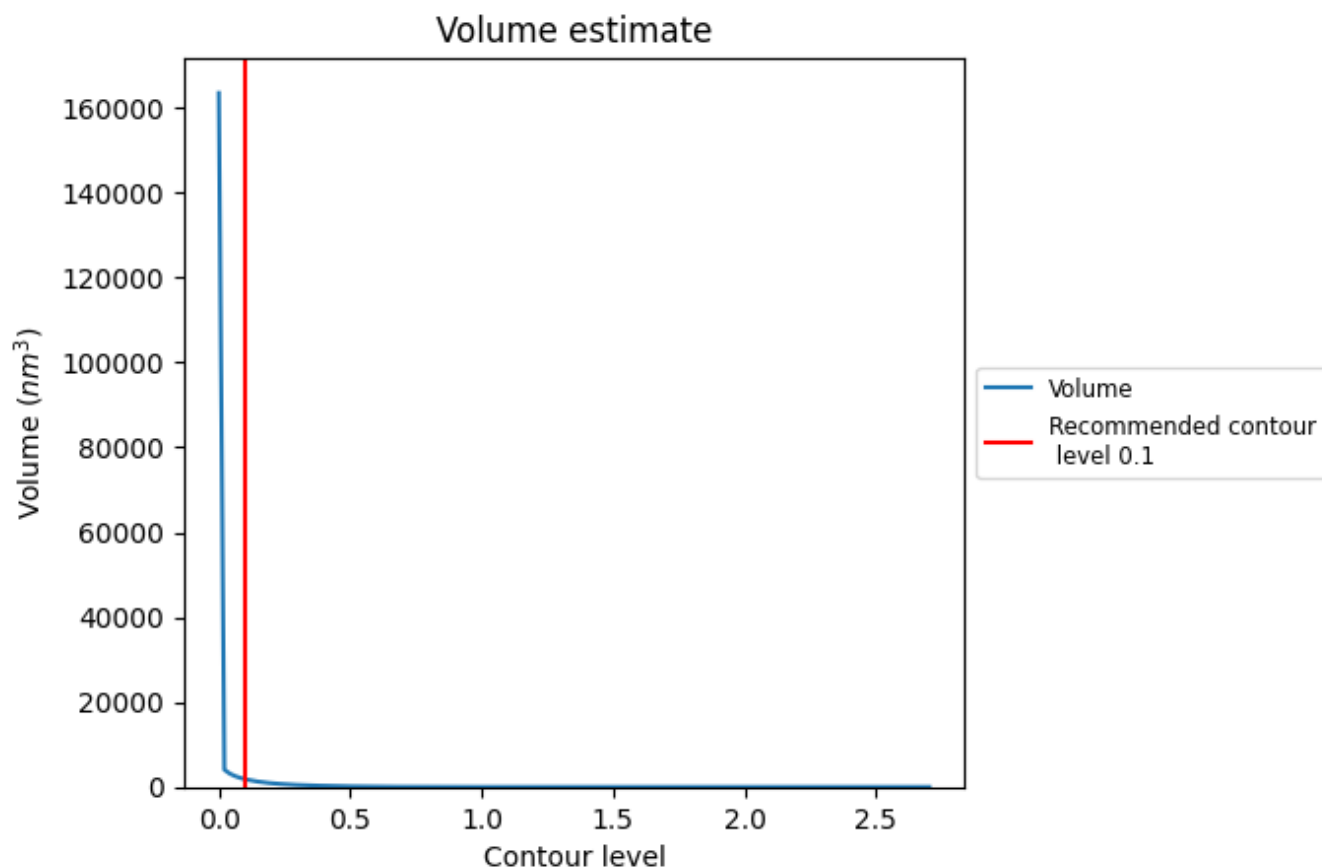
This section contains the results of statistical analysis of the map.

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.

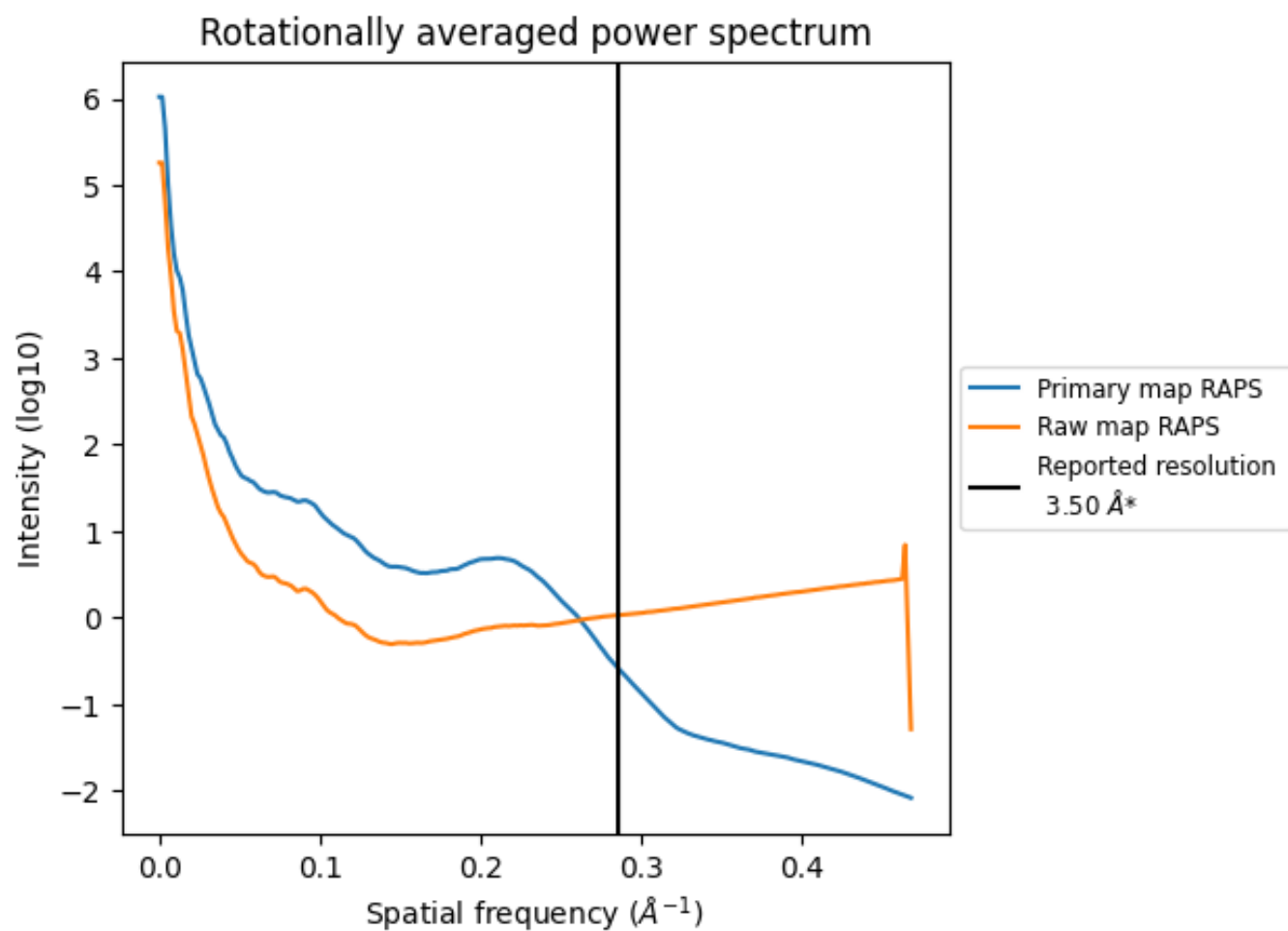
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 1833 nm^3 ; this corresponds to an approximate mass of 1656 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 ⓘ

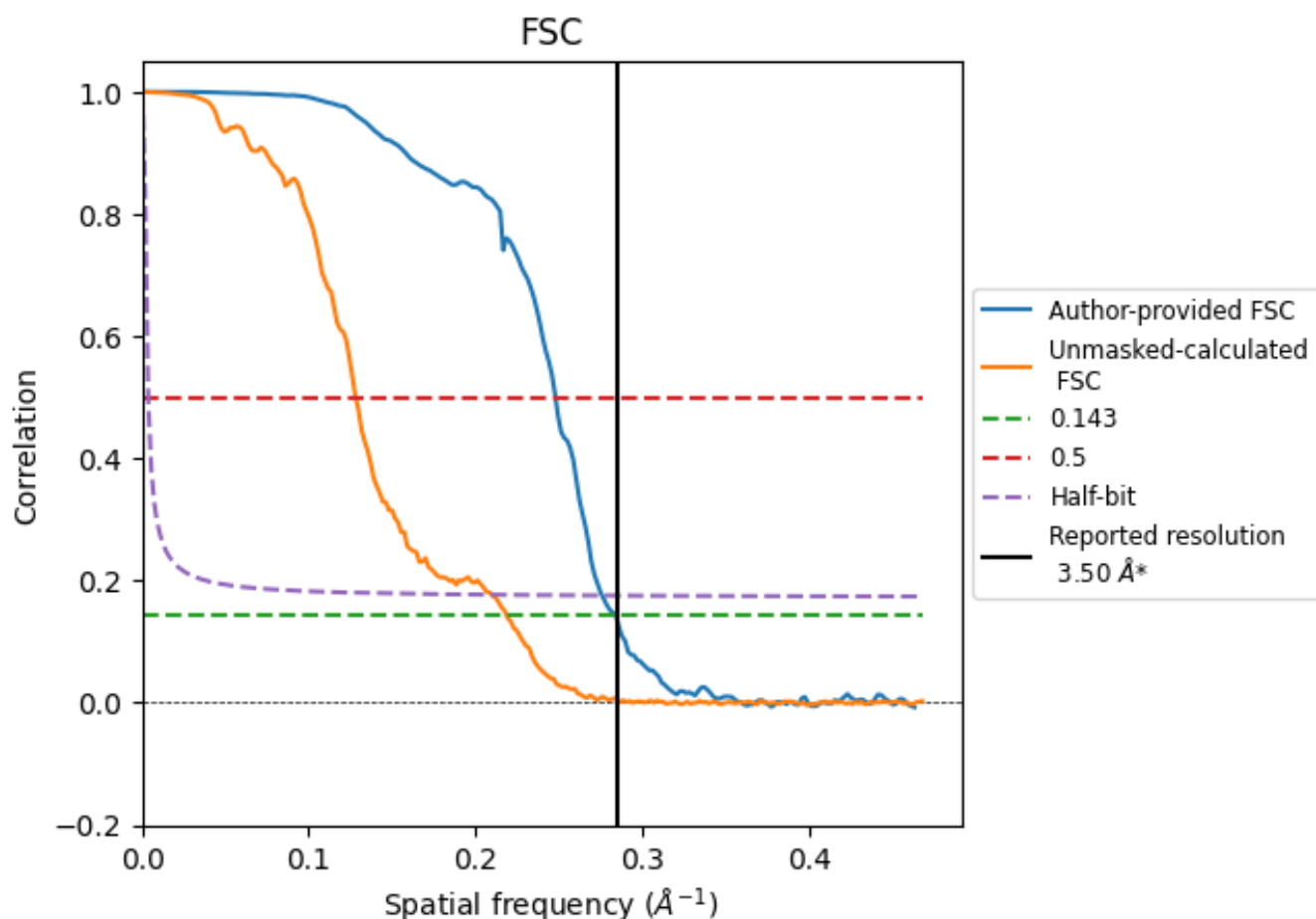


*Reported resolution corresponds to spatial frequency of 0.286 $\text{\AA}^{-1}$

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 0.286 $\text{\AA}^{-1}$

8.2 Resolution estimates [i](#)

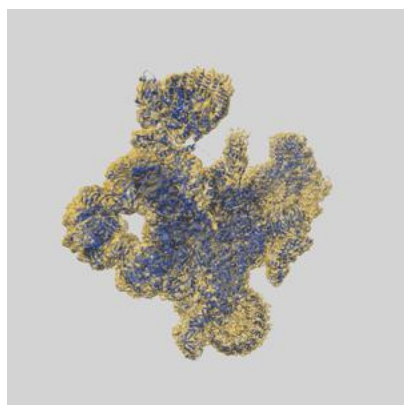
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	3.52	4.03	3.62
Unmasked-calculated*	4.57	7.81	4.77

*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 4.57 differs from the reported value 3.5 by more than 10 %

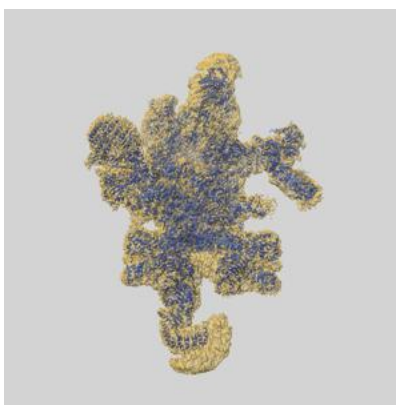
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-76334 and PDB model 12DL. Per-residue inclusion information can be found in section [3](#) on page [10](#).

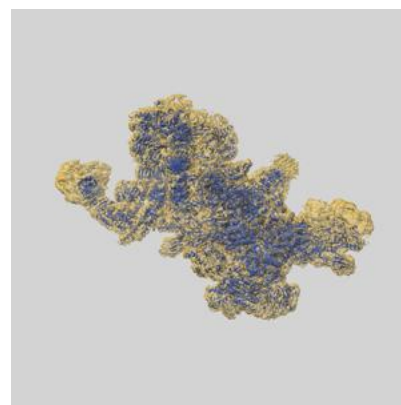
9.1 Map-model overlay [i](#)



X



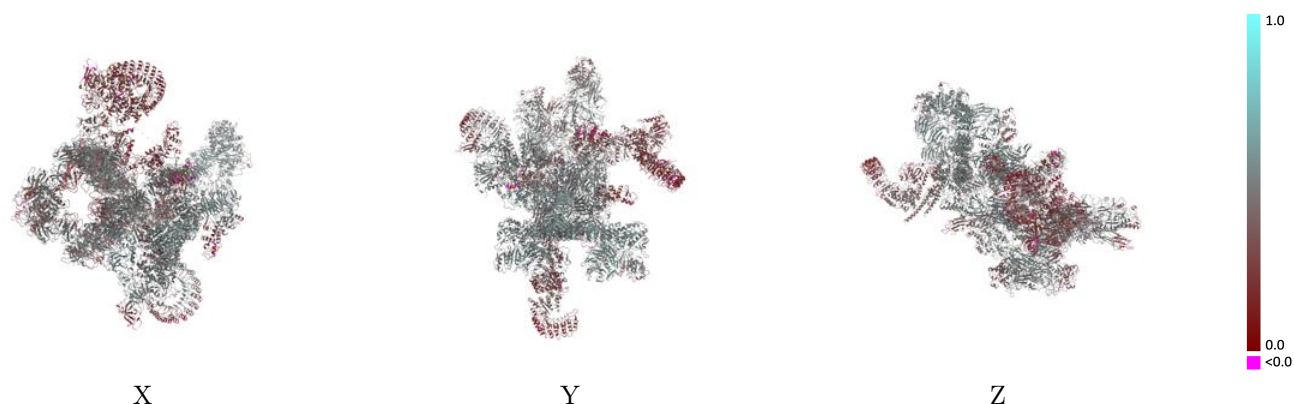
Y



Z

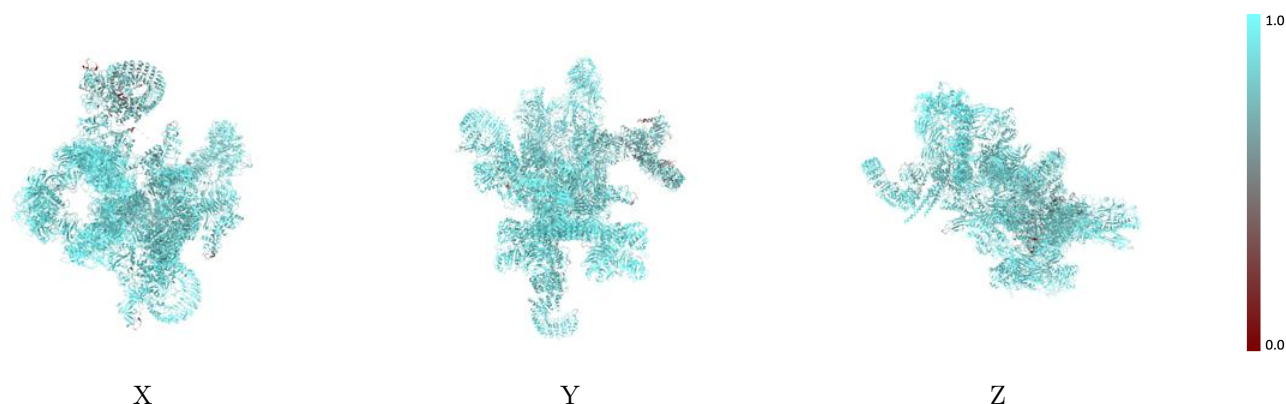
The images above show the 3D surface view of the map at the recommended contour level 0.1 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



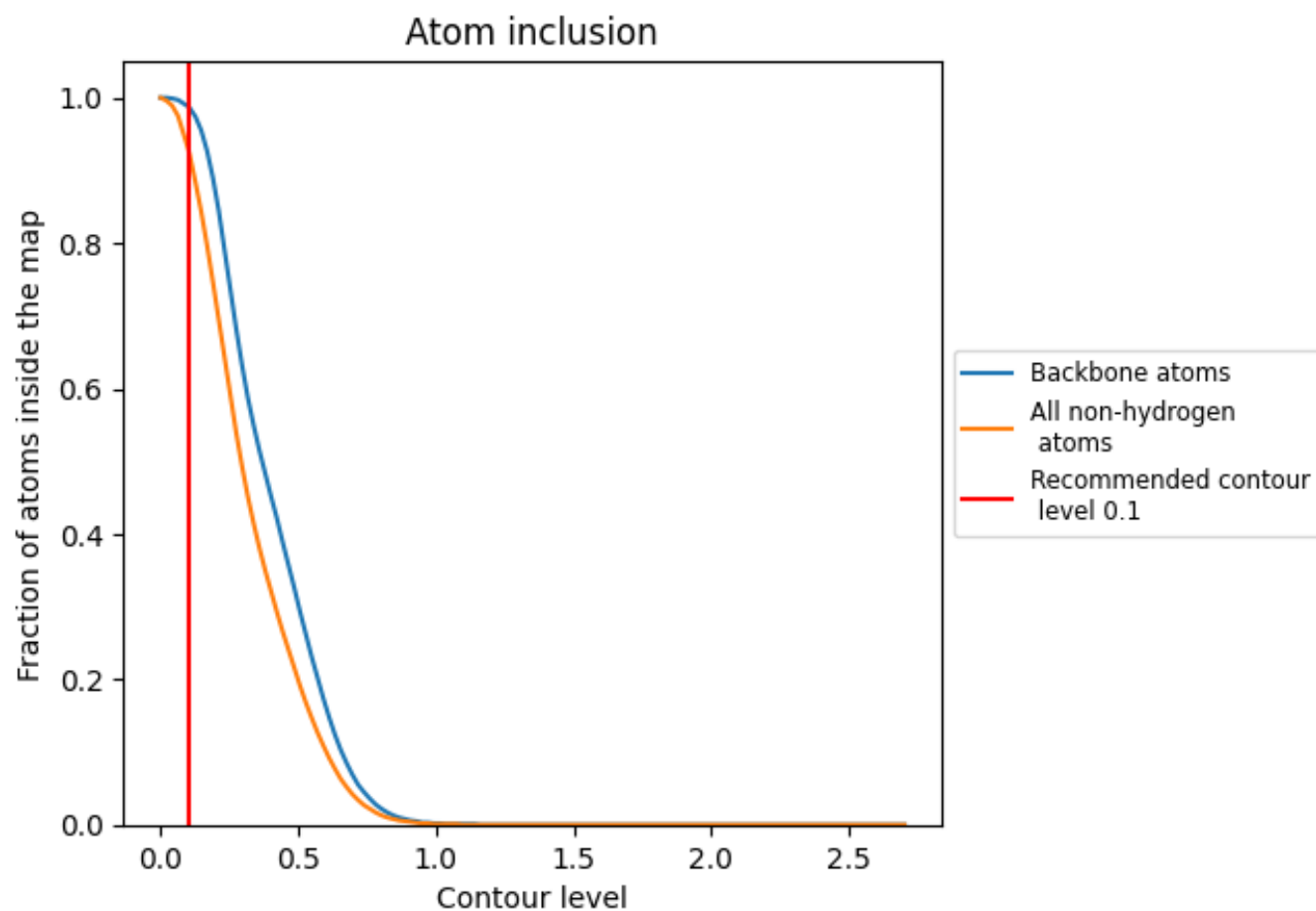
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.1).

9.4 Atom inclusion ⓘ



At the recommended contour level, 99% of all backbone atoms, 93% 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 (0.1) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.9300	 0.4310
AA	 0.9590	 0.4380
AB	 0.9600	 0.4330
AC	 0.9710	 0.4570
AD	 0.9650	 0.4560
AE	 0.9540	 0.4690
AF	 0.9460	 0.4380
AG	 0.9590	 0.4580
AH	 0.9590	 0.4430
AI	 0.9570	 0.4350
AJ	 0.9520	 0.4360
BA	 0.9470	 0.4550
BB	 0.7530	 0.2770
CA	 0.9800	 0.4890
CB	 0.8570	 0.2900
DA	 0.9440	 0.4420
DB	 0.7330	 0.2550
EA	 0.9770	 0.5300
FA	 0.9780	 0.4950
GA	 0.9770	 0.4960
GB	 0.9620	 0.5030
HA	 0.9710	 0.4960
HB	 0.9570	 0.5160
IA	 0.9440	 0.4930
JA	 0.9630	 0.4660
KA	 0.9930	 0.5360
LA	 0.9380	 0.4140
MA	 0.8760	 0.3050
NA	 0.9710	 0.5090
OA	 0.9650	 0.4760
PA	 0.9610	 0.4730
QA	 0.8290	 0.2650
QB	 0.8270	 0.2650
QC	 0.8290	 0.2470

