



Full wwPDB EM Validation Report ⓘ

Nov 23, 2022 – 03:28 PM EST

PDB ID : 7UPT
EMDB ID : EMD-26675
Title : Human mitochondrial AAA protein ATAD1 (with a catalytic dead mutation)
in complex with a peptide substrate (open conformation)
Authors : Wang, L.; Toutkoushian, H.; Belyy, V.; Kokontis, C.; Walter, P.
Deposited on : 2022-04-16
Resolution : 3.50 Å(reported)

This is a Full wwPDB EM Validation 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.dev43
Mogul : 1.8.5 (274361), CSD as541be (2020)
MolProbity : 4.02b-467
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ : 1.9.9
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.31.2

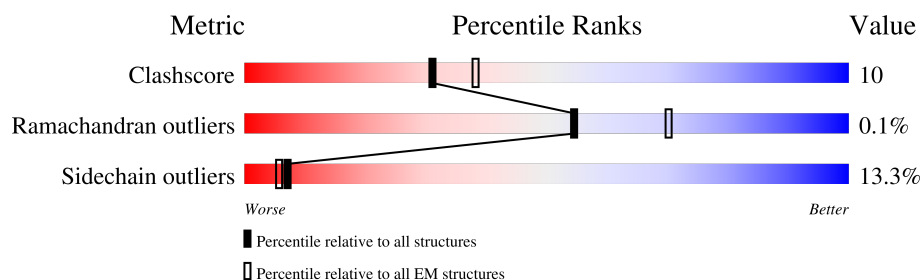
1 Overall quality at a glance

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)
Clashscore	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

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	341	<div> <div>19%</div> <div>55%</div> <div>22%</div> <div>•</div> <div>20%</div> </div>
1	B	341	<div> <div>64%</div> <div>19%</div> <div>•</div> <div>13%</div> </div>
1	C	341	<div> <div>64%</div> <div>20%</div> <div>• •</div> <div>12%</div> </div>
1	D	341	<div> <div>61%</div> <div>21%</div> <div>•</div> <div>14%</div> </div>
1	E	341	<div> <div>60%</div> <div>22%</div> <div>•</div> <div>14%</div> </div>
1	F	341	<div> <div>48%</div> <div>20%</div> <div>•</div> <div>31%</div> </div>
2	G	10	<div> <div>100%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	ADP	A	501	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13567 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 Outer mitochondrial transmembrane helix translocase.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	273	Total	C	N	O	S	0	0
			2148	1355	377	401	15		
1	B	297	Total	C	N	O	S	0	0
			2343	1479	415	433	16		
1	C	299	Total	C	N	O	S	0	0
			2357	1486	418	437	16		
1	D	294	Total	C	N	O	S	0	0
			2318	1464	409	429	16		
1	E	293	Total	C	N	O	S	0	0
			2311	1459	408	428	16		
1	F	236	Total	C	N	O	S	0	0
			1853	1179	319	341	14		

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	21	MET	-	initiating methionine	UNP Q8NBU5
A	22	GLY	-	expression tag	UNP Q8NBU5
A	23	SER	-	expression tag	UNP Q8NBU5
A	24	SER	-	expression tag	UNP Q8NBU5
A	25	HIS	-	expression tag	UNP Q8NBU5
A	26	HIS	-	expression tag	UNP Q8NBU5
A	27	HIS	-	expression tag	UNP Q8NBU5
A	28	HIS	-	expression tag	UNP Q8NBU5
A	29	HIS	-	expression tag	UNP Q8NBU5
A	30	HIS	-	expression tag	UNP Q8NBU5
A	31	SER	-	expression tag	UNP Q8NBU5
A	32	SER	-	expression tag	UNP Q8NBU5
A	33	GLY	-	expression tag	UNP Q8NBU5
A	34	LEU	-	expression tag	UNP Q8NBU5
A	35	VAL	-	expression tag	UNP Q8NBU5
A	36	PRO	-	expression tag	UNP Q8NBU5
A	37	ARG	-	expression tag	UNP Q8NBU5
A	38	GLY	-	expression tag	UNP Q8NBU5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	39	SER	-	expression tag	UNP Q8NBU5
A	40	GLY	-	expression tag	UNP Q8NBU5
A	41	SER	-	expression tag	UNP Q8NBU5
A	193	GLN	GLU	engineered mutation	UNP Q8NBU5
B	21	MET	-	initiating methionine	UNP Q8NBU5
B	22	GLY	-	expression tag	UNP Q8NBU5
B	23	SER	-	expression tag	UNP Q8NBU5
B	24	SER	-	expression tag	UNP Q8NBU5
B	25	HIS	-	expression tag	UNP Q8NBU5
B	26	HIS	-	expression tag	UNP Q8NBU5
B	27	HIS	-	expression tag	UNP Q8NBU5
B	28	HIS	-	expression tag	UNP Q8NBU5
B	29	HIS	-	expression tag	UNP Q8NBU5
B	30	HIS	-	expression tag	UNP Q8NBU5
B	31	SER	-	expression tag	UNP Q8NBU5
B	32	SER	-	expression tag	UNP Q8NBU5
B	33	GLY	-	expression tag	UNP Q8NBU5
B	34	LEU	-	expression tag	UNP Q8NBU5
B	35	VAL	-	expression tag	UNP Q8NBU5
B	36	PRO	-	expression tag	UNP Q8NBU5
B	37	ARG	-	expression tag	UNP Q8NBU5
B	38	GLY	-	expression tag	UNP Q8NBU5
B	39	SER	-	expression tag	UNP Q8NBU5
B	40	GLY	-	expression tag	UNP Q8NBU5
B	41	SER	-	expression tag	UNP Q8NBU5
B	193	GLN	GLU	engineered mutation	UNP Q8NBU5
C	21	MET	-	initiating methionine	UNP Q8NBU5
C	22	GLY	-	expression tag	UNP Q8NBU5
C	23	SER	-	expression tag	UNP Q8NBU5
C	24	SER	-	expression tag	UNP Q8NBU5
C	25	HIS	-	expression tag	UNP Q8NBU5
C	26	HIS	-	expression tag	UNP Q8NBU5
C	27	HIS	-	expression tag	UNP Q8NBU5
C	28	HIS	-	expression tag	UNP Q8NBU5
C	29	HIS	-	expression tag	UNP Q8NBU5
C	30	HIS	-	expression tag	UNP Q8NBU5
C	31	SER	-	expression tag	UNP Q8NBU5
C	32	SER	-	expression tag	UNP Q8NBU5
C	33	GLY	-	expression tag	UNP Q8NBU5
C	34	LEU	-	expression tag	UNP Q8NBU5
C	35	VAL	-	expression tag	UNP Q8NBU5
C	36	PRO	-	expression tag	UNP Q8NBU5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	37	ARG	-	expression tag	UNP Q8NBU5
C	38	GLY	-	expression tag	UNP Q8NBU5
C	39	SER	-	expression tag	UNP Q8NBU5
C	40	GLY	-	expression tag	UNP Q8NBU5
C	41	SER	-	expression tag	UNP Q8NBU5
C	193	GLN	GLU	engineered mutation	UNP Q8NBU5
D	21	MET	-	initiating methionine	UNP Q8NBU5
D	22	GLY	-	expression tag	UNP Q8NBU5
D	23	SER	-	expression tag	UNP Q8NBU5
D	24	SER	-	expression tag	UNP Q8NBU5
D	25	HIS	-	expression tag	UNP Q8NBU5
D	26	HIS	-	expression tag	UNP Q8NBU5
D	27	HIS	-	expression tag	UNP Q8NBU5
D	28	HIS	-	expression tag	UNP Q8NBU5
D	29	HIS	-	expression tag	UNP Q8NBU5
D	30	HIS	-	expression tag	UNP Q8NBU5
D	31	SER	-	expression tag	UNP Q8NBU5
D	32	SER	-	expression tag	UNP Q8NBU5
D	33	GLY	-	expression tag	UNP Q8NBU5
D	34	LEU	-	expression tag	UNP Q8NBU5
D	35	VAL	-	expression tag	UNP Q8NBU5
D	36	PRO	-	expression tag	UNP Q8NBU5
D	37	ARG	-	expression tag	UNP Q8NBU5
D	38	GLY	-	expression tag	UNP Q8NBU5
D	39	SER	-	expression tag	UNP Q8NBU5
D	40	GLY	-	expression tag	UNP Q8NBU5
D	41	SER	-	expression tag	UNP Q8NBU5
D	193	GLN	GLU	engineered mutation	UNP Q8NBU5
E	21	MET	-	initiating methionine	UNP Q8NBU5
E	22	GLY	-	expression tag	UNP Q8NBU5
E	23	SER	-	expression tag	UNP Q8NBU5
E	24	SER	-	expression tag	UNP Q8NBU5
E	25	HIS	-	expression tag	UNP Q8NBU5
E	26	HIS	-	expression tag	UNP Q8NBU5
E	27	HIS	-	expression tag	UNP Q8NBU5
E	28	HIS	-	expression tag	UNP Q8NBU5
E	29	HIS	-	expression tag	UNP Q8NBU5
E	30	HIS	-	expression tag	UNP Q8NBU5
E	31	SER	-	expression tag	UNP Q8NBU5
E	32	SER	-	expression tag	UNP Q8NBU5
E	33	GLY	-	expression tag	UNP Q8NBU5
E	34	LEU	-	expression tag	UNP Q8NBU5

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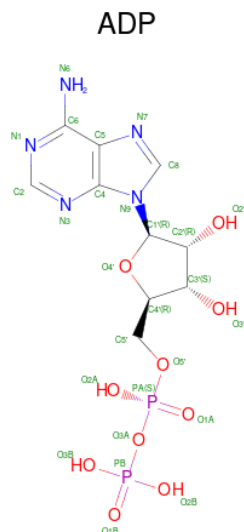
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Chain	Residue	Modelled	Actual	Comment	Reference
E	35	VAL	-	expression tag	UNP Q8NBU5
E	36	PRO	-	expression tag	UNP Q8NBU5
E	37	ARG	-	expression tag	UNP Q8NBU5
E	38	GLY	-	expression tag	UNP Q8NBU5
E	39	SER	-	expression tag	UNP Q8NBU5
E	40	GLY	-	expression tag	UNP Q8NBU5
E	41	SER	-	expression tag	UNP Q8NBU5
E	193	GLN	GLU	engineered mutation	UNP Q8NBU5
F	21	MET	-	initiating methionine	UNP Q8NBU5
F	22	GLY	-	expression tag	UNP Q8NBU5
F	23	SER	-	expression tag	UNP Q8NBU5
F	24	SER	-	expression tag	UNP Q8NBU5
F	25	HIS	-	expression tag	UNP Q8NBU5
F	26	HIS	-	expression tag	UNP Q8NBU5
F	27	HIS	-	expression tag	UNP Q8NBU5
F	28	HIS	-	expression tag	UNP Q8NBU5
F	29	HIS	-	expression tag	UNP Q8NBU5
F	30	HIS	-	expression tag	UNP Q8NBU5
F	31	SER	-	expression tag	UNP Q8NBU5
F	32	SER	-	expression tag	UNP Q8NBU5
F	33	GLY	-	expression tag	UNP Q8NBU5
F	34	LEU	-	expression tag	UNP Q8NBU5
F	35	VAL	-	expression tag	UNP Q8NBU5
F	36	PRO	-	expression tag	UNP Q8NBU5
F	37	ARG	-	expression tag	UNP Q8NBU5
F	38	GLY	-	expression tag	UNP Q8NBU5
F	39	SER	-	expression tag	UNP Q8NBU5
F	40	GLY	-	expression tag	UNP Q8NBU5
F	41	SER	-	expression tag	UNP Q8NBU5
F	193	GLN	GLU	engineered mutation	UNP Q8NBU5

- Molecule 2 is a protein called Unknown peptide substrate.

Mol	Chain	Residues	Atoms				AltConf	Trace
2	G	10	Total	C	N	O	0	0
			50	30	10	10		

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$) (labeled as "Ligand of Interest" by depositor).

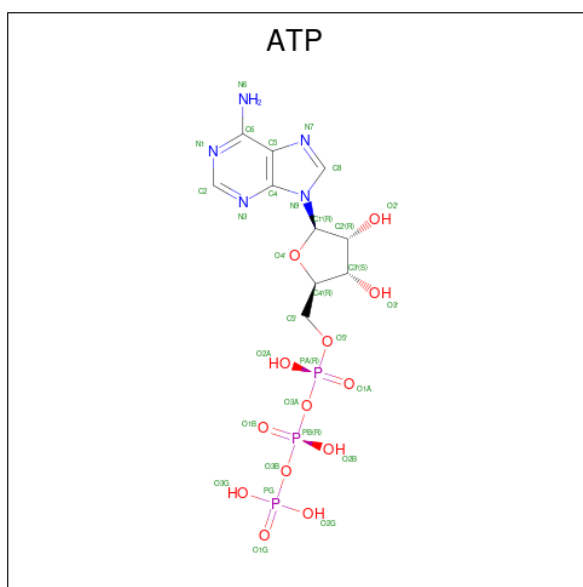


Mol	Chain	Residues	Atoms					AltConf
3	A	1	Total	C	N	O	P	0
			27	10	5	10	2	

- Molecule 4 is MAGNESIUM ION (three-letter code: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	AltConf
4	B	1	Total Mg 1 1	0
4	C	1	Total Mg 1 1	0
4	D	1	Total Mg 1 1	0
4	E	1	Total Mg 1 1	0
4	F	1	Total Mg 1 1	0

- Molecule 5 is ADENOSINE-5'-TRIPHOSPHATE (three-letter code: ATP) (formula: $\text{C}_{10}\text{H}_{16}\text{N}_5\text{O}_{13}\text{P}_3$) (labeled as "Ligand of Interest" by depositor).

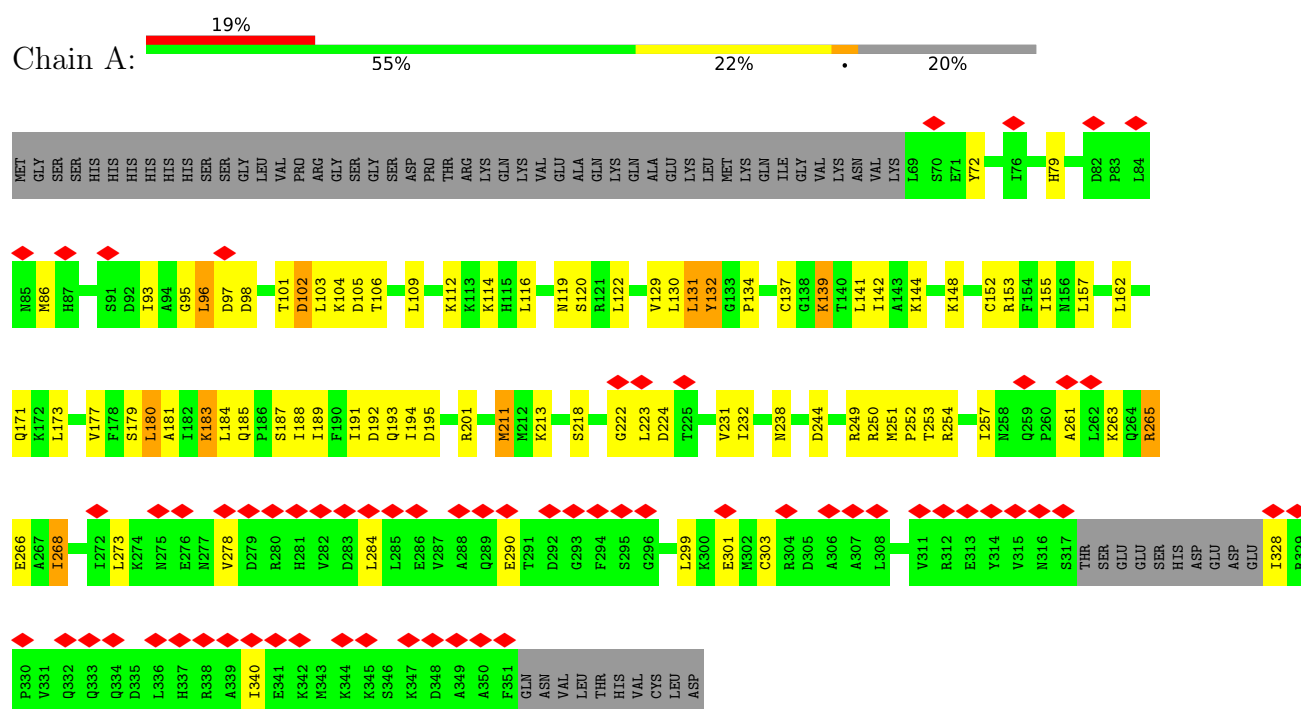


Mol	Chain	Residues	Atoms					AltConf
5	B	1	Total 31	C 10	N 5	O 13	P 3	0
5	C	1	Total 31	C 10	N 5	O 13	P 3	0
5	D	1	Total 31	C 10	N 5	O 13	P 3	0
5	E	1	Total 31	C 10	N 5	O 13	P 3	0
5	F	1	Total 31	C 10	N 5	O 13	P 3	0

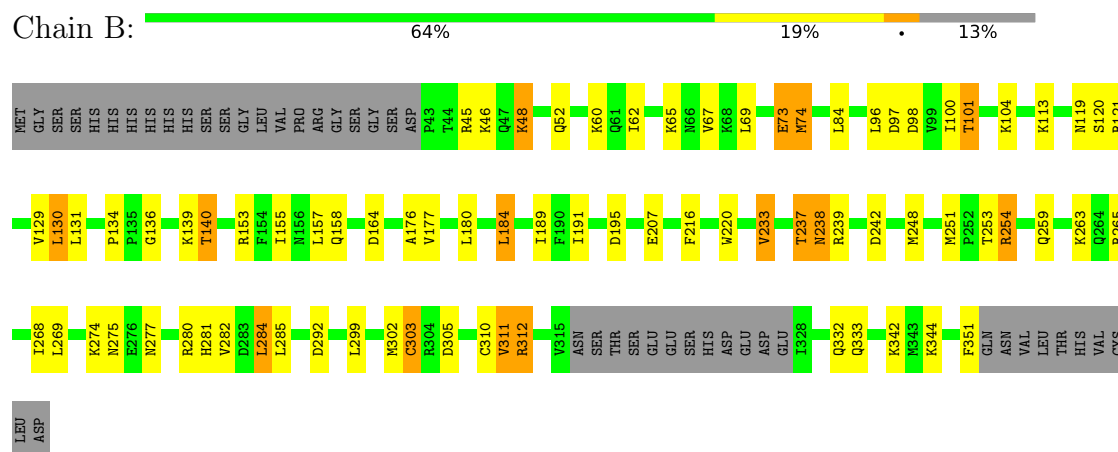
3 Residue-property plots [i](#)

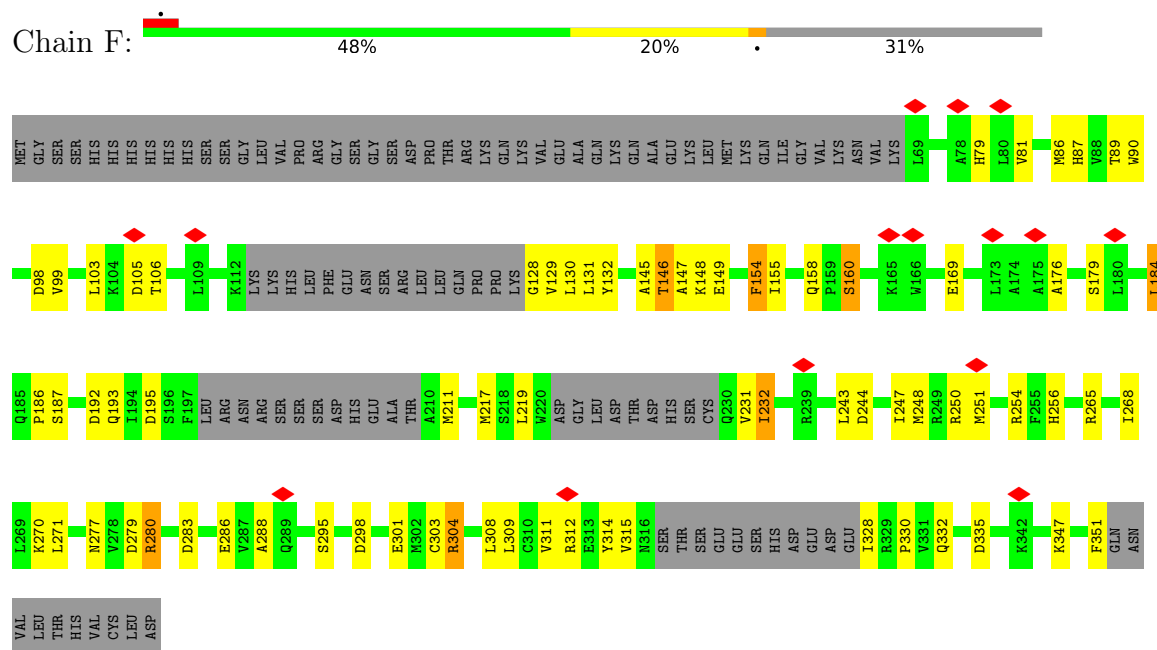
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Outer mitochondrial transmembrane helix translocase



- Molecule 1: Outer mitochondrial transmembrane helix translocase





- Molecule 2: Unknown peptide substrate

Chain G:

There are no outlier residues recorded for this chain.

4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45003	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 ($e^-/\text{\AA}^2$)	67	Depositor
Minimum defocus (nm)	600	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	1.775	Depositor
Minimum map value	-0.751	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.052	Depositor
Recommended contour level	0.25	Depositor
Map size (Å)	266.24, 266.24, 266.24	wwPDB
Map dimensions	320, 320, 320	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.83199996, 0.83199996, 0.83199996	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ATP, ADP, 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	0.24	0/2185	0.47	3/2949 (0.1%)
1	B	0.25	0/2381	0.49	2/3206 (0.1%)
1	C	0.24	0/2395	0.47	4/3225 (0.1%)
1	D	0.25	0/2355	0.48	3/3171 (0.1%)
1	E	0.24	0/2348	0.44	1/3161 (0.0%)
1	F	0.24	0/1881	0.51	8/2535 (0.3%)
All	All	0.24	0/13545	0.48	21/18247 (0.1%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	C	0	1

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	311	VAL	CG1-CB-CG2	7.12	122.30	110.90
1	D	64	VAL	CG1-CB-CG2	7.02	122.14	110.90
1	B	233	VAL	CG1-CB-CG2	6.89	121.92	110.90
1	A	231	VAL	CG1-CB-CG2	6.79	121.76	110.90
1	E	64	VAL	CG1-CB-CG2	6.78	121.75	110.90
1	C	141	LEU	CB-CG-CD1	6.08	121.34	111.00
1	D	103	LEU	CB-CG-CD2	6.04	121.27	111.00
1	F	308	LEU	CB-CG-CD1	5.88	121.00	111.00
1	A	157	LEU	CB-CG-CD2	5.76	120.80	111.00
1	C	284	LEU	CB-CG-CD1	5.76	120.79	111.00

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	271	LEU	CB-CG-CD1	5.70	120.69	111.00
1	F	271	LEU	CB-CG-CD2	5.68	120.65	111.00
1	F	184	LEU	CB-CG-CD1	5.67	120.64	111.00
1	F	243	LEU	CB-CG-CD2	5.65	120.61	111.00
1	F	243	LEU	CB-CG-CD1	5.63	120.58	111.00
1	A	157	LEU	CB-CG-CD1	5.63	120.56	111.00
1	F	184	LEU	CB-CG-CD2	5.57	120.47	111.00
1	C	284	LEU	CB-CG-CD2	5.57	120.46	111.00
1	D	103	LEU	CB-CG-CD1	5.40	120.18	111.00
1	F	308	LEU	CB-CG-CD2	5.33	120.05	111.00
1	C	141	LEU	CB-CG-CD2	5.25	119.93	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	227	HIS	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	A	2148	0	2182	61	0
1	B	2343	0	2410	40	0
1	C	2357	0	2421	43	0
1	D	2318	0	2382	46	0
1	E	2311	0	2373	49	0
1	F	1853	0	1896	39	0
2	G	50	0	13	0	0
3	A	27	0	12	10	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
5	B	31	0	12	2	0
5	C	31	0	12	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	D	31	0	12	2	0
5	E	31	0	12	3	0
5	F	31	0	12	0	0
All	All	13567	0	13749	265	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 10.

All (265) 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:134:PRO:O	1:A:139:LYS:NZ	2.01	0.92
1:C:93:ILE:HD11	1:C:141:LEU:HG	1.51	0.90
1:B:48:LYS:O	1:B:52:GLN:HB2	1.72	0.87
1:B:52:GLN:NE2	1:B:74:MET:SD	2.47	0.87
1:B:134:PRO:O	1:B:139:LYS:NZ	2.09	0.86
1:E:184:LEU:O	1:E:187:SER:OG	1.94	0.85
1:C:254:ARG:NH2	1:E:346:SER:O	2.12	0.83
1:C:195:ASP:OD2	1:C:237:THR:OG1	1.97	0.82
1:C:221:ASP:OD1	1:C:250:ARG:NH1	2.15	0.80
1:D:270:LYS:O	1:D:274:LYS:NZ	2.17	0.77
1:A:96:LEU:HG	3:A:501:ADP:HN62	1.51	0.75
1:E:329:ARG:NH1	1:E:335:ASP:OD2	2.20	0.75
1:A:93:ILE:HG23	3:A:501:ADP:H2	1.51	0.74
1:F:330:PRO:O	1:F:332:GLN:NE2	2.20	0.74
1:A:201:ARG:NH2	1:D:238:ASN:OD1	2.21	0.73
1:A:180:LEU:HD13	1:A:183:LYS:HZ1	1.53	0.73
1:E:173:LEU:O	1:E:177:VAL:HG23	1.87	0.73
1:D:52:GLN:NE2	1:D:56:GLU:OE1	2.22	0.72
1:B:96:LEU:HD12	1:B:96:LEU:O	1.89	0.72
1:E:121:ARG:O	1:E:121:ARG:NE	2.22	0.72
1:F:192:ASP:OD1	1:F:193:GLN:HG2	1.90	0.71
3:A:501:ADP:N3	3:A:501:ADP:H2'	2.05	0.71
1:A:171:GLN:NE2	1:A:211:MET:SD	2.64	0.71
1:E:46:LYS:O	1:E:49:VAL:HG22	1.90	0.71
1:D:59:MET:SD	1:D:64:VAL:HG21	2.31	0.71
1:B:140:THR:OG1	5:B:602:ATP:O1A	2.10	0.70
1:A:102:ASP:O	1:A:106:THR:OG1	2.09	0.70
1:B:238:ASN:N	1:B:238:ASN:OD1	2.23	0.70
1:E:61:GLN:NE2	1:E:82:ASP:OD2	2.26	0.69
1:A:249:ARG:NH1	5:D:501:ATP:O3A	2.27	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:295:SER:OG	1:F:298:ASP:OD1	2.08	0.68
1:D:291:THR:HG22	1:D:294:PHE:HB2	1.75	0.67
1:B:248:MET:SD	1:B:254:ARG:NH2	2.68	0.67
1:C:342:LYS:O	1:C:346:SER:OG	2.12	0.67
1:B:269:LEU:HD12	1:B:299:LEU:HD22	1.77	0.66
1:D:221:ASP:OD2	1:D:249:ARG:NH1	2.28	0.66
1:F:265:ARG:NH1	1:F:288:ALA:O	2.29	0.66
1:F:248:MET:O	1:F:254:ARG:NH1	2.29	0.65
1:D:185:GLN:OE1	1:D:185:GLN:N	2.29	0.64
1:D:158:GLN:O	1:D:161:THR:HG22	1.98	0.64
1:C:158:GLN:O	1:C:161:THR:HG22	1.97	0.64
1:C:265:ARG:NH1	1:C:288:ALA:O	2.31	0.64
1:D:189:ILE:HB	1:D:233:VAL:HG22	1.79	0.64
1:A:141:LEU:CD2	3:A:501:ADP:H3'	2.28	0.64
1:B:269:LEU:HD22	1:B:284:LEU:HD11	1.79	0.64
1:C:96:LEU:HD12	1:C:96:LEU:O	1.98	0.63
1:A:86:MET:O	1:A:148:LYS:NZ	2.27	0.63
1:C:313:GLU:N	1:C:313:GLU:OE1	2.32	0.63
1:E:184:LEU:O	1:E:184:LEU:HD12	2.00	0.62
1:C:93:ILE:CD1	1:C:141:LEU:HG	2.27	0.61
1:F:147:ALA:HB1	1:F:154:PHE:CE1	2.35	0.61
1:E:97:ASP:O	1:E:101:THR:HG23	2.01	0.61
1:A:105:ASP:OD2	1:D:312:ARG:NE	2.31	0.60
1:A:180:LEU:HD13	1:A:183:LYS:NZ	2.15	0.60
1:E:268:ILE:HD13	1:E:268:ILE:O	2.00	0.60
1:F:81:VAL:HG13	1:F:148:LYS:CE	2.31	0.60
1:B:248:MET:O	1:B:254:ARG:NH2	2.34	0.60
1:B:303:CYS:SG	1:D:122:LEU:HD21	2.41	0.60
1:C:254:ARG:NH2	1:E:346:SER:OG	2.35	0.60
1:D:134:PRO:O	1:D:139:LYS:NZ	2.33	0.59
1:B:157:LEU:HD23	1:B:191:ILE:HG12	1.84	0.59
1:B:119:ASN:OD1	1:B:120:SER:N	2.35	0.59
1:B:45:ARG:NH1	1:B:164:ASP:OD1	2.35	0.59
1:E:134:PRO:HG2	1:E:259:GLN:HG3	1.85	0.58
1:D:221:ASP:OD1	1:D:250:ARG:NH1	2.36	0.58
1:E:157:LEU:HD23	1:E:191:ILE:HG12	1.85	0.58
1:E:204:SER:O	1:E:204:SER:OG	2.20	0.58
1:A:119:ASN:OD1	1:A:120:SER:N	2.37	0.58
1:F:158:GLN:O	1:F:160:SER:N	2.37	0.57
1:B:195:ASP:OD2	1:B:237:THR:OG1	2.18	0.57
1:E:62:ILE:HG23	1:E:64:VAL:HG12	1.85	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:238:ASN:OD1	1:C:238:ASN:N	2.38	0.57
1:E:221:ASP:OD1	1:E:250:ARG:NH1	2.37	0.56
1:A:183:LYS:HZ3	1:A:184:LEU:N	2.03	0.56
1:F:217:MET:HG2	1:F:247:ILE:HD11	1.87	0.56
1:A:290:GLU:HB3	1:A:340:ILE:HG21	1.88	0.56
1:A:104:LYS:O	1:A:109:LEU:N	2.37	0.56
1:D:129:VAL:HG23	1:D:253:THR:OG1	2.06	0.56
1:E:117:PHE:CE2	1:F:311:VAL:HG11	2.41	0.56
1:D:205:ASP:OD1	1:D:205:ASP:N	2.37	0.56
1:B:189:ILE:HB	1:B:233:VAL:HG12	1.87	0.55
1:B:73:GLU:N	1:B:73:GLU:OE1	2.39	0.55
1:D:265:ARG:NH1	1:D:288:ALA:O	2.39	0.55
1:F:128:GLY:N	1:F:250:ARG:O	2.39	0.55
1:F:145:ALA:O	1:F:146:THR:HG22	2.06	0.55
1:A:181:ALA:O	1:A:187:SER:OG	2.21	0.54
1:B:129:VAL:HG22	1:B:253:THR:OG1	2.06	0.54
1:F:176:ALA:O	1:F:179:SER:OG	2.09	0.54
1:F:328:ILE:HG23	1:F:328:ILE:O	2.08	0.54
1:B:97:ASP:O	1:B:101:THR:OG1	2.24	0.54
1:A:251:MET:O	1:A:254:ARG:NH2	2.41	0.54
1:D:181:ALA:HB2	1:D:189:ILE:HD11	1.89	0.54
1:E:268:ILE:HD11	5:E:501:ATP:C2	2.43	0.54
1:E:331:VAL:HG11	1:E:336:LEU:HD23	1.90	0.54
1:F:81:VAL:HG13	1:F:148:LYS:HE2	1.89	0.53
1:A:185:GLN:N	1:A:185:GLN:OE1	2.40	0.53
1:C:328:ILE:O	1:C:328:ILE:HG23	2.09	0.53
1:C:136:GLY:N	5:C:602:ATP:O1B	2.41	0.53
1:F:219:LEU:O	1:F:219:LEU:HD23	2.09	0.53
1:A:328:ILE:HG23	1:A:328:ILE:O	2.09	0.53
1:C:131:LEU:HD12	1:C:235:GLY:O	2.09	0.53
1:D:298:ASP:OD1	1:D:298:ASP:N	2.42	0.53
1:A:180:LEU:HA	1:A:183:LYS:HZ2	1.73	0.53
1:A:266:GLU:CG	1:A:284:LEU:HD23	2.39	0.52
1:B:73:GLU:N	1:B:176:ALA:HB1	2.23	0.52
1:E:139:LYS:NZ	1:E:237:THR:O	2.32	0.52
1:A:263:LYS:O	1:A:263:LYS:NZ	2.37	0.52
1:B:180:LEU:O	1:B:184:LEU:HD12	2.09	0.52
1:C:52:GLN:HG2	1:C:74:MET:CE	2.40	0.52
1:E:120:SER:O	1:E:124:GLN:NE2	2.42	0.52
1:E:131:LEU:HD12	1:E:235:GLY:O	2.10	0.51
1:C:195:ASP:OD1	1:C:196:SER:N	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:291:THR:HG23	1:D:340:ILE:HD11	1.92	0.51
1:D:269:LEU:HG	1:D:299:LEU:HD21	1.92	0.51
1:F:129:VAL:HG23	1:F:232:ILE:HG21	1.93	0.51
1:F:130:LEU:HD21	1:F:132:TYR:HB3	1.93	0.51
1:D:100:ILE:HD13	1:D:100:ILE:O	2.11	0.50
1:F:187:SER:C	1:F:231:VAL:HG11	2.32	0.50
1:E:90:TRP:CE3	1:E:100:ILE:HD11	2.46	0.50
1:F:103:LEU:O	1:F:106:THR:N	2.44	0.50
1:E:343:MET:O	1:E:347:LYS:N	2.45	0.50
1:B:184:LEU:HD13	1:B:184:LEU:C	2.33	0.50
1:D:59:MET:O	1:D:62:ILE:HG22	2.12	0.50
1:E:214:ALA:HB1	1:F:193:GLN:HB2	1.93	0.50
1:B:280:ARG:O	1:B:281:HIS:ND1	2.45	0.49
1:B:136:GLY:N	5:B:602:ATP:O1B	2.40	0.49
1:D:279:ASP:OD1	1:D:280:ARG:N	2.43	0.49
1:A:93:ILE:HG23	3:A:501:ADP:C2	2.43	0.49
1:A:95:GLY:HA3	3:A:501:ADP:N6	2.28	0.49
1:D:153:ARG:HG3	1:D:184:LEU:HD13	1.94	0.49
1:E:253:THR:HG23	1:F:301:GLU:OE1	2.12	0.49
1:C:268:ILE:HD13	1:C:268:ILE:O	2.13	0.49
1:A:97:ASP:O	1:A:101:THR:HG23	2.13	0.49
1:A:263:LYS:NZ	1:A:266:GLU:OE1	2.46	0.49
1:C:189:ILE:HB	1:C:233:VAL:HG22	1.94	0.49
1:A:142:ILE:HD12	1:A:257:ILE:HD12	1.95	0.48
1:E:62:ILE:HG23	1:E:64:VAL:CG1	2.44	0.48
1:E:70:SER:OG	1:E:71:GLU:N	2.46	0.48
1:C:119:ASN:OD1	1:C:120:SER:N	2.46	0.48
1:A:95:GLY:HA3	3:A:501:ADP:HN61	1.78	0.48
1:A:141:LEU:HD21	3:A:501:ADP:H3'	1.93	0.48
1:C:137:CYS:O	1:C:257:ILE:HG21	2.13	0.48
1:A:261:ALA:O	1:A:265:ARG:NH1	2.45	0.48
1:A:152:CYS:HB3	1:A:188:ILE:HD11	1.94	0.48
1:E:69:LEU:HD12	1:E:180:LEU:HD12	1.95	0.48
1:E:237:THR:HG21	1:E:243:LEU:HD21	1.96	0.48
1:B:98:ASP:OD1	1:B:98:ASP:N	2.46	0.48
1:B:285:LEU:HD12	1:B:285:LEU:O	2.14	0.48
1:C:194:ILE:HG22	1:C:243:LEU:HD13	1.95	0.48
1:D:118:GLU:OE2	1:D:118:GLU:N	2.44	0.48
1:E:122:LEU:HD21	1:F:304:ARG:HA	1.96	0.48
1:F:146:THR:N	1:F:149:GLU:OE1	2.47	0.47
1:C:252:PRO:HB2	1:E:301:GLU:HG3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:89:THR:OG1	1:F:90:TRP:N	2.47	0.47
1:C:52:GLN:HG2	1:C:74:MET:HE2	1.96	0.47
1:C:92:ASP:O	1:C:271:LEU:HD21	2.15	0.47
1:D:131:LEU:HD12	1:D:131:LEU:H	1.80	0.47
1:F:81:VAL:O	1:F:148:LYS:NZ	2.35	0.47
1:A:193:GLN:HE22	1:A:238:ASN:HD22	1.61	0.47
1:A:218:SER:O	1:A:222:GLY:N	2.48	0.47
1:E:136:GLY:N	5:E:501:ATP:O1B	2.42	0.47
1:A:195:ASP:OD1	1:A:195:ASP:N	2.48	0.46
1:A:268:ILE:HA	3:A:501:ADP:H8	1.80	0.46
1:C:131:LEU:HD12	1:C:131:LEU:H	1.79	0.46
1:A:96:LEU:HD12	1:A:96:LEU:O	2.15	0.46
1:C:84:LEU:HD12	1:C:84:LEU:C	2.36	0.46
1:D:86:MET:SD	1:D:86:MET:N	2.88	0.46
1:C:124:GLN:N	1:C:124:GLN:OE1	2.48	0.46
1:E:269:LEU:HD13	1:E:299:LEU:HD22	1.97	0.46
1:F:187:SER:O	1:F:231:VAL:HG11	2.15	0.46
1:C:335:ASP:N	1:C:335:ASP:OD1	2.49	0.46
1:A:183:LYS:NZ	1:A:184:LEU:HB2	2.31	0.46
1:C:202:SER:OG	1:C:203:SER:N	2.49	0.45
1:A:98:ASP:OD1	1:A:98:ASP:N	2.48	0.45
1:A:72:TYR:HD2	1:A:173:LEU:HD23	1.80	0.45
1:F:311:VAL:O	1:F:315:VAL:HG23	2.16	0.45
1:A:252:PRO:HB2	1:D:301:GLU:HG2	1.98	0.45
1:A:266:GLU:HG3	1:A:284:LEU:HD23	1.97	0.45
1:C:134:PRO:O	1:C:139:LYS:NZ	2.38	0.45
1:C:157:LEU:HD23	1:C:191:ILE:HG12	1.98	0.45
1:F:186:PRO:HB2	1:F:231:VAL:HG12	1.97	0.45
1:C:108:ILE:O	1:C:108:ILE:HD12	2.16	0.45
1:A:273:LEU:HD13	1:A:278:VAL:HG11	1.98	0.45
1:C:140:THR:O	1:C:140:THR:HG22	2.17	0.45
1:C:184:LEU:HD12	1:C:184:LEU:O	2.16	0.45
1:F:335:ASP:N	1:F:335:ASP:OD1	2.48	0.45
1:A:257:ILE:O	1:A:257:ILE:CG2	2.64	0.45
1:F:169:GLU:OE1	1:F:169:GLU:N	2.49	0.45
1:D:146:THR:O	1:D:150:ALA:HB3	2.17	0.44
1:D:161:THR:HG23	1:D:162:LEU:HD23	1.97	0.44
1:B:52:GLN:HE22	1:B:74:MET:C	2.18	0.44
1:B:332:GLN:O	1:B:333:GLN:HB3	2.17	0.44
1:E:331:VAL:HG11	1:E:336:LEU:CD2	2.48	0.44
1:F:195:ASP:OD1	1:F:195:ASP:N	2.50	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:183:LYS:HZ3	1:A:183:LYS:C	2.20	0.44
1:C:121:ARG:NH1	1:C:226:ASP:O	2.51	0.44
1:D:171:GLN:O	1:D:215:GLN:NE2	2.50	0.44
1:A:266:GLU:HG2	1:A:284:LEU:HD23	1.98	0.44
1:B:311:VAL:HG11	1:D:123:LEU:CD1	2.47	0.44
1:F:314:TYR:CD1	1:F:328:ILE:HG22	2.52	0.44
1:C:269:LEU:HG	1:C:284:LEU:HD11	1.99	0.44
1:B:69:LEU:CD1	1:B:180:LEU:HD13	2.48	0.44
1:B:157:LEU:HD11	1:B:177:VAL:HG21	2.00	0.44
1:F:279:ASP:OD1	1:F:280:ARG:N	2.51	0.43
1:A:130:LEU:HD21	1:A:132:TYR:HB3	1.99	0.43
1:A:173:LEU:O	1:A:177:VAL:HG23	2.18	0.43
1:F:251:MET:O	1:F:254:ARG:NH1	2.51	0.43
1:D:62:ILE:O	1:D:62:ILE:HG23	2.18	0.43
1:A:72:TYR:CD2	1:A:173:LEU:HD23	2.54	0.43
1:C:314:TYR:CD2	1:C:328:ILE:HG22	2.54	0.43
1:D:49:VAL:HG13	1:D:50:GLU:N	2.34	0.43
1:E:130:LEU:HD21	1:E:132:TYR:HB3	2.00	0.43
1:B:282:VAL:HG13	1:B:282:VAL:O	2.19	0.43
1:A:129:VAL:HG12	1:A:253:THR:OG1	2.19	0.43
1:A:192:ASP:OD2	1:A:193:GLN:N	2.51	0.43
1:E:94:ALA:HB2	1:E:271:LEU:HD22	2.01	0.43
1:F:98:ASP:OD1	1:F:99:VAL:HG23	2.19	0.43
1:A:257:ILE:O	1:A:257:ILE:HG23	2.19	0.42
1:C:118:GLU:OE2	1:C:118:GLU:N	2.46	0.42
1:A:152:CYS:CB	1:A:188:ILE:HD11	2.48	0.42
1:B:157:LEU:HD23	1:B:191:ILE:CG1	2.48	0.42
1:D:220:TRP:CZ3	1:D:247:ILE:HD11	2.54	0.42
1:E:157:LEU:HD23	1:E:191:ILE:CG1	2.48	0.42
1:A:268:ILE:CB	3:A:501:ADP:H8	2.33	0.42
1:B:312:ARG:NH2	1:D:105:ASP:OD2	2.52	0.42
1:D:96:LEU:HD12	1:D:96:LEU:O	2.19	0.42
1:D:129:VAL:HG13	1:D:129:VAL:O	2.19	0.42
1:E:152:CYS:O	1:E:153:ARG:C	2.58	0.42
1:A:193:GLN:HE22	1:A:238:ASN:ND2	2.18	0.42
1:A:273:LEU:C	1:A:273:LEU:HD12	2.40	0.42
1:D:136:GLY:N	5:D:501:ATP:O1B	2.51	0.42
1:C:271:LEU:O	1:C:271:LEU:HD12	2.20	0.42
1:E:337:HIS:HA	1:E:340:ILE:HG22	2.02	0.42
1:A:131:LEU:HD12	1:A:131:LEU:H	1.85	0.42
1:A:181:ALA:HB2	1:A:189:ILE:HD11	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:193:GLN:HE22	5:E:501:ATP:PG	2.43	0.41
1:F:86:MET:SD	1:F:86:MET:N	2.93	0.41
1:D:96:LEU:O	1:D:96:LEU:CD1	2.69	0.41
1:D:156:ASN:OD1	1:D:157:LEU:N	2.53	0.41
1:E:119:ASN:OD1	1:E:120:SER:N	2.54	0.41
1:B:134:PRO:HG2	1:B:259:GLN:HG3	2.02	0.41
1:D:129:VAL:HG23	1:D:253:THR:CB	2.51	0.41
1:B:184:LEU:HD13	1:B:184:LEU:O	2.20	0.41
1:C:58:LEU:HD23	1:C:58:LEU:O	2.20	0.41
1:D:60:LYS:CD	1:D:60:LYS:H	2.34	0.41
1:E:69:LEU:N	1:E:69:LEU:CD2	2.84	0.41
1:A:179:SER:O	1:A:183:LYS:HG3	2.21	0.41
1:A:268:ILE:HG21	1:A:299:LEU:HD13	2.03	0.41
1:B:265:ARG:NH2	1:B:292:ASP:O	2.51	0.41
1:E:96:LEU:HD13	1:E:257:ILE:CG2	2.50	0.41
1:B:130:LEU:HD11	1:B:237:THR:HG21	2.03	0.41
1:B:220:TRP:HH2	1:B:251:MET:HE3	1.86	0.41
1:D:56:GLU:O	1:D:60:LYS:HD3	2.21	0.41
1:D:57:LYS:HD2	1:D:57:LYS:N	2.36	0.41
1:E:49:VAL:O	1:E:53:LYS:HG2	2.21	0.41
1:E:191:ILE:HG21	1:E:194:ILE:HD12	2.02	0.41
1:F:283:ASP:OD2	1:F:286:GLU:N	2.47	0.41
1:D:311:VAL:O	1:D:315:VAL:HG23	2.21	0.40
1:E:105:ASP:OD1	1:F:312:ARG:NH2	2.54	0.40
1:A:191:ILE:HG21	1:A:194:ILE:HG13	2.03	0.40
1:B:84:LEU:HD12	1:B:84:LEU:C	2.42	0.40
1:C:49:VAL:HG13	1:C:50:GLU:N	2.37	0.40
1:E:156:ASN:OD1	1:E:157:LEU:N	2.55	0.40
1:C:90:TRP:CE3	1:C:100:ILE:HD11	2.57	0.40
1:E:49:VAL:HG23	1:E:50:GLU:N	2.37	0.40

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	269/341 (79%)	247 (92%)	22 (8%)	0	100	100
1	B	293/341 (86%)	275 (94%)	18 (6%)	0	100	100
1	C	295/341 (86%)	271 (92%)	23 (8%)	1 (0%)	41	75
1	D	290/341 (85%)	267 (92%)	23 (8%)	0	100	100
1	E	289/341 (85%)	267 (92%)	22 (8%)	0	100	100
1	F	226/341 (66%)	212 (94%)	14 (6%)	0	100	100
All	All	1662/2046 (81%)	1539 (93%)	122 (7%)	1 (0%)	54	84

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	229	CYS

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	238/299 (80%)	209 (88%)	29 (12%)	5	23
1	B	259/299 (87%)	218 (84%)	41 (16%)	2	15
1	C	261/299 (87%)	225 (86%)	36 (14%)	3	20
1	D	256/299 (86%)	220 (86%)	36 (14%)	3	19
1	E	255/299 (85%)	223 (88%)	32 (12%)	4	23
1	F	203/299 (68%)	181 (89%)	22 (11%)	6	30
All	All	1472/1794 (82%)	1276 (87%)	196 (13%)	7	21

All (196) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	79	HIS

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Mol	Chain	Res	Type
1	A	96	LEU
1	A	102	ASP
1	A	103	LEU
1	A	112	LYS
1	A	114	LYS
1	A	116	LEU
1	A	122	LEU
1	A	131	LEU
1	A	132	TYR
1	A	137	CYS
1	A	139	LYS
1	A	144	LYS
1	A	153	ARG
1	A	155	ILE
1	A	162	LEU
1	A	180	LEU
1	A	183	LYS
1	A	211	MET
1	A	213	LYS
1	A	223	LEU
1	A	224	ASP
1	A	232	ILE
1	A	244	ASP
1	A	250	ARG
1	A	265	ARG
1	A	268	ILE
1	A	301	GLU
1	A	303	CYS
1	B	46	LYS
1	B	48	LYS
1	B	60	LYS
1	B	62	ILE
1	B	65	LYS
1	B	67	VAL
1	B	73	GLU
1	B	74	MET
1	B	100	ILE
1	B	101	THR
1	B	104	LYS
1	B	113	LYS
1	B	121	ARG
1	B	130	LEU

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Mol	Chain	Res	Type
1	B	131	LEU
1	B	140	THR
1	B	153	ARG
1	B	155	ILE
1	B	158	GLN
1	B	184	LEU
1	B	207	GLU
1	B	216	PHE
1	B	237	THR
1	B	238	ASN
1	B	239	ARG
1	B	242	ASP
1	B	254	ARG
1	B	263	LYS
1	B	268	ILE
1	B	274	LYS
1	B	275	ASN
1	B	277	ASN
1	B	284	LEU
1	B	302	MET
1	B	303	CYS
1	B	305	ASP
1	B	310	CYS
1	B	312	ARG
1	B	342	LYS
1	B	344	LYS
1	B	351	PHE
1	C	48	LYS
1	C	53	LYS
1	C	65	LYS
1	C	73	GLU
1	C	79	HIS
1	C	96	LEU
1	C	100	ILE
1	C	108	ILE
1	C	112	LYS
1	C	113	LYS
1	C	116	LEU
1	C	130	LEU
1	C	131	LEU
1	C	141	LEU
1	C	155	ILE

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Mol	Chain	Res	Type
1	C	165	LYS
1	C	183	LYS
1	C	194	ILE
1	C	221	ASP
1	C	232	ILE
1	C	242	ASP
1	C	247	ILE
1	C	250	ARG
1	C	254	ARG
1	C	268	ILE
1	C	276	GLU
1	C	280	ARG
1	C	284	LEU
1	C	304	ARG
1	C	309	LEU
1	C	311	VAL
1	C	335	ASP
1	C	338	ARG
1	C	342	LYS
1	C	346	SER
1	C	351	PHE
1	D	47	GLN
1	D	53	LYS
1	D	59	MET
1	D	60	LYS
1	D	62	ILE
1	D	64	VAL
1	D	65	LYS
1	D	79	HIS
1	D	88	VAL
1	D	92	ASP
1	D	96	LEU
1	D	100	ILE
1	D	102	ASP
1	D	111	ILE
1	D	130	LEU
1	D	131	LEU
1	D	132	TYR
1	D	153	ARG
1	D	155	ILE
1	D	202	SER
1	D	216	PHE

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Mol	Chain	Res	Type
1	D	227	HIS
1	D	229	CYS
1	D	238	ASN
1	D	247	ILE
1	D	250	ARG
1	D	263	LYS
1	D	273	LEU
1	D	274	LYS
1	D	282	VAL
1	D	287	VAL
1	D	308	LEU
1	D	329	ARG
1	D	335	ASP
1	D	338	ARG
1	D	342	LYS
1	E	48	LYS
1	E	57	LYS
1	E	61	GLN
1	E	67	VAL
1	E	68	LYS
1	E	69	LEU
1	E	73	GLU
1	E	86	MET
1	E	96	LEU
1	E	100	ILE
1	E	105	ASP
1	E	112	LYS
1	E	114	LYS
1	E	123	LEU
1	E	131	LEU
1	E	169	GLU
1	E	204	SER
1	E	207	GLU
1	E	216	PHE
1	E	227	HIS
1	E	232	ILE
1	E	250	ARG
1	E	257	ILE
1	E	266	GLU
1	E	268	ILE
1	E	304	ARG
1	E	311	VAL

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Mol	Chain	Res	Type
1	E	314	TYR
1	E	333	GLN
1	E	337	HIS
1	E	341	GLU
1	E	351	PHE
1	F	79	HIS
1	F	87	HIS
1	F	105	ASP
1	F	131	LEU
1	F	146	THR
1	F	154	PHE
1	F	155	ILE
1	F	160	SER
1	F	184	LEU
1	F	211	MET
1	F	232	ILE
1	F	244	ASP
1	F	256	HIS
1	F	268	ILE
1	F	270	LYS
1	F	277	ASN
1	F	280	ARG
1	F	303	CYS
1	F	304	ARG
1	F	309	LEU
1	F	347	LYS
1	F	351	PHE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	193	GLN
1	A	289	GLN
1	A	333	GLN
1	A	337	HIS
1	B	66	ASN
1	D	193	GLN
1	D	227	HIS
1	E	264	GLN
1	F	193	GLN
1	F	241	GLN
1	F	332	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 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
5	ATP	B	602	4	26,33,33	0.93	1 (3%)	31,52,52	1.66	5 (16%)
5	ATP	E	501	4	26,33,33	0.92	1 (3%)	31,52,52	1.63	5 (16%)
5	ATP	D	501	4	26,33,33	0.94	1 (3%)	31,52,52	1.65	6 (19%)
5	ATP	F	602	4	26,33,33	0.92	1 (3%)	31,52,52	1.64	5 (16%)
3	ADP	A	501	-	24,29,29	0.94	1 (4%)	29,45,45	1.46	4 (13%)
5	ATP	C	602	4	26,33,33	0.93	1 (3%)	31,52,52	1.69	5 (16%)

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
5	ATP	B	602	4	-	3/18/38/38	0/3/3/3
5	ATP	E	501	4	-	2/18/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	ATP	D	501	4	-	3/18/38/38	0/3/3/3
5	ATP	F	602	4	-	2/18/38/38	0/3/3/3
3	ADP	A	501	-	-	2/12/32/32	0/3/3/3
5	ATP	C	602	4	-	3/18/38/38	0/3/3/3

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	501	ADP	C5-C4	2.44	1.47	1.40
5	E	501	ATP	C5-C4	2.41	1.47	1.40
5	B	602	ATP	C5-C4	2.40	1.47	1.40
5	D	501	ATP	C5-C4	2.40	1.47	1.40
5	C	602	ATP	C5-C4	2.39	1.47	1.40
5	F	602	ATP	C5-C4	2.39	1.47	1.40

All (30) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	602	ATP	PA-O3A-PB	-4.07	118.86	132.83
3	A	501	ADP	PA-O3A-PB	-3.87	119.55	132.83
5	C	602	ATP	PB-O3B-PG	-3.84	119.66	132.83
5	D	501	ATP	PB-O3B-PG	-3.81	119.75	132.83
5	B	602	ATP	PB-O3B-PG	-3.81	119.77	132.83
5	E	501	ATP	PB-O3B-PG	-3.74	119.98	132.83
5	F	602	ATP	PB-O3B-PG	-3.74	120.00	132.83
5	C	602	ATP	N3-C2-N1	-3.69	122.91	128.68
5	D	501	ATP	N3-C2-N1	-3.68	122.93	128.68
5	E	501	ATP	N3-C2-N1	-3.67	122.94	128.68
5	B	602	ATP	N3-C2-N1	-3.67	122.95	128.68
5	B	602	ATP	PA-O3A-PB	-3.62	120.39	132.83
5	F	602	ATP	N3-C2-N1	-3.62	123.03	128.68
5	D	501	ATP	PA-O3A-PB	-3.54	120.69	132.83
5	B	602	ATP	C3'-C2'-C1'	3.46	106.18	100.98
5	F	602	ATP	C3'-C2'-C1'	3.43	106.14	100.98
5	F	602	ATP	PA-O3A-PB	-3.39	121.19	132.83
5	C	602	ATP	C3'-C2'-C1'	3.39	106.08	100.98
3	A	501	ADP	C3'-C2'-C1'	3.38	106.07	100.98
5	E	501	ATP	PA-O3A-PB	-3.35	121.32	132.83
5	E	501	ATP	C3'-C2'-C1'	3.34	106.00	100.98
5	D	501	ATP	C3'-C2'-C1'	3.33	105.99	100.98
3	A	501	ADP	N3-C2-N1	-3.03	123.94	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	F	602	ATP	C4-C5-N7	-2.71	106.57	109.40
5	C	602	ATP	C4-C5-N7	-2.60	106.69	109.40
5	E	501	ATP	C4-C5-N7	-2.60	106.69	109.40
5	D	501	ATP	C4-C5-N7	-2.60	106.69	109.40
5	B	602	ATP	C4-C5-N7	-2.59	106.70	109.40
3	A	501	ADP	C4-C5-N7	-2.35	106.95	109.40
5	D	501	ATP	C2-N1-C6	2.00	122.18	118.75

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	501	ADP	C5'-O5'-PA-O3A
5	B	602	ATP	C5'-O5'-PA-O2A
5	B	602	ATP	C5'-O5'-PA-O3A
5	C	602	ATP	C5'-O5'-PA-O2A
5	C	602	ATP	C5'-O5'-PA-O3A
5	D	501	ATP	C5'-O5'-PA-O2A
5	D	501	ATP	C5'-O5'-PA-O3A
5	E	501	ATP	C5'-O5'-PA-O2A
5	E	501	ATP	C5'-O5'-PA-O3A
5	F	602	ATP	C5'-O5'-PA-O2A
5	F	602	ATP	C5'-O5'-PA-O3A
3	A	501	ADP	C5'-O5'-PA-O1A
5	D	501	ATP	PA-O3A-PB-O2B
5	B	602	ATP	PA-O3A-PB-O2B
5	C	602	ATP	PA-O3A-PB-O1B

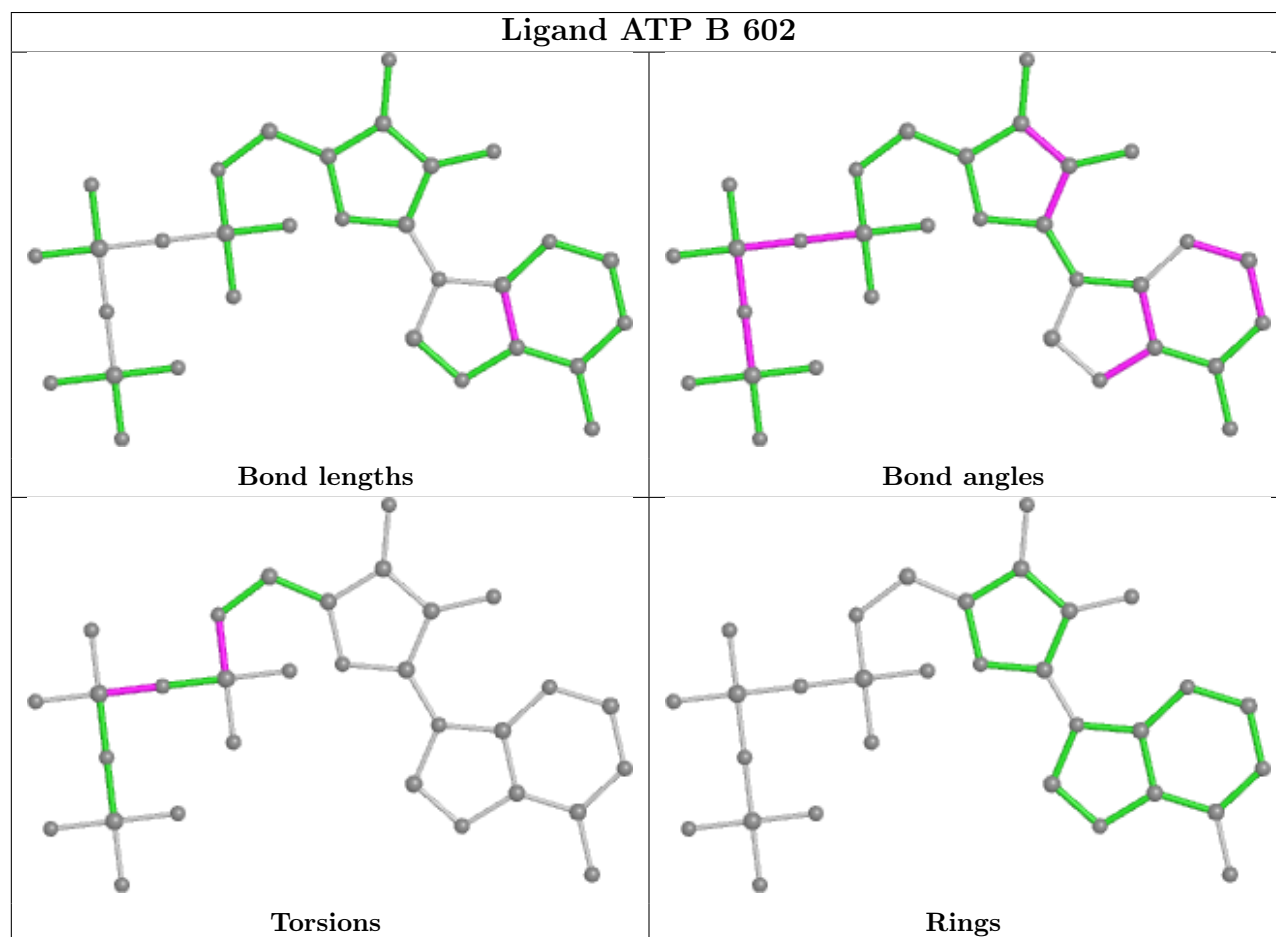
There are no ring outliers.

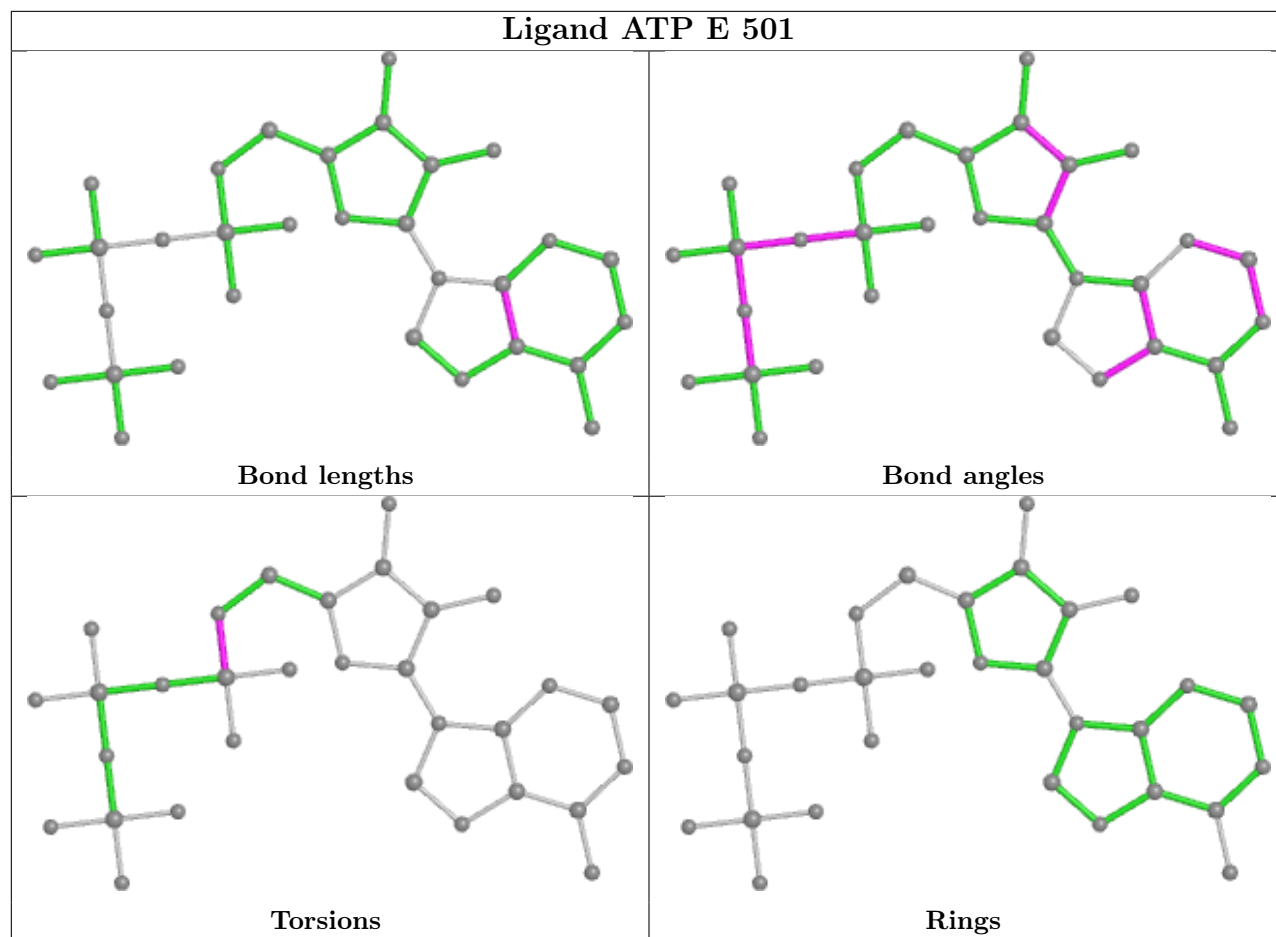
5 monomers are involved in 18 short contacts:

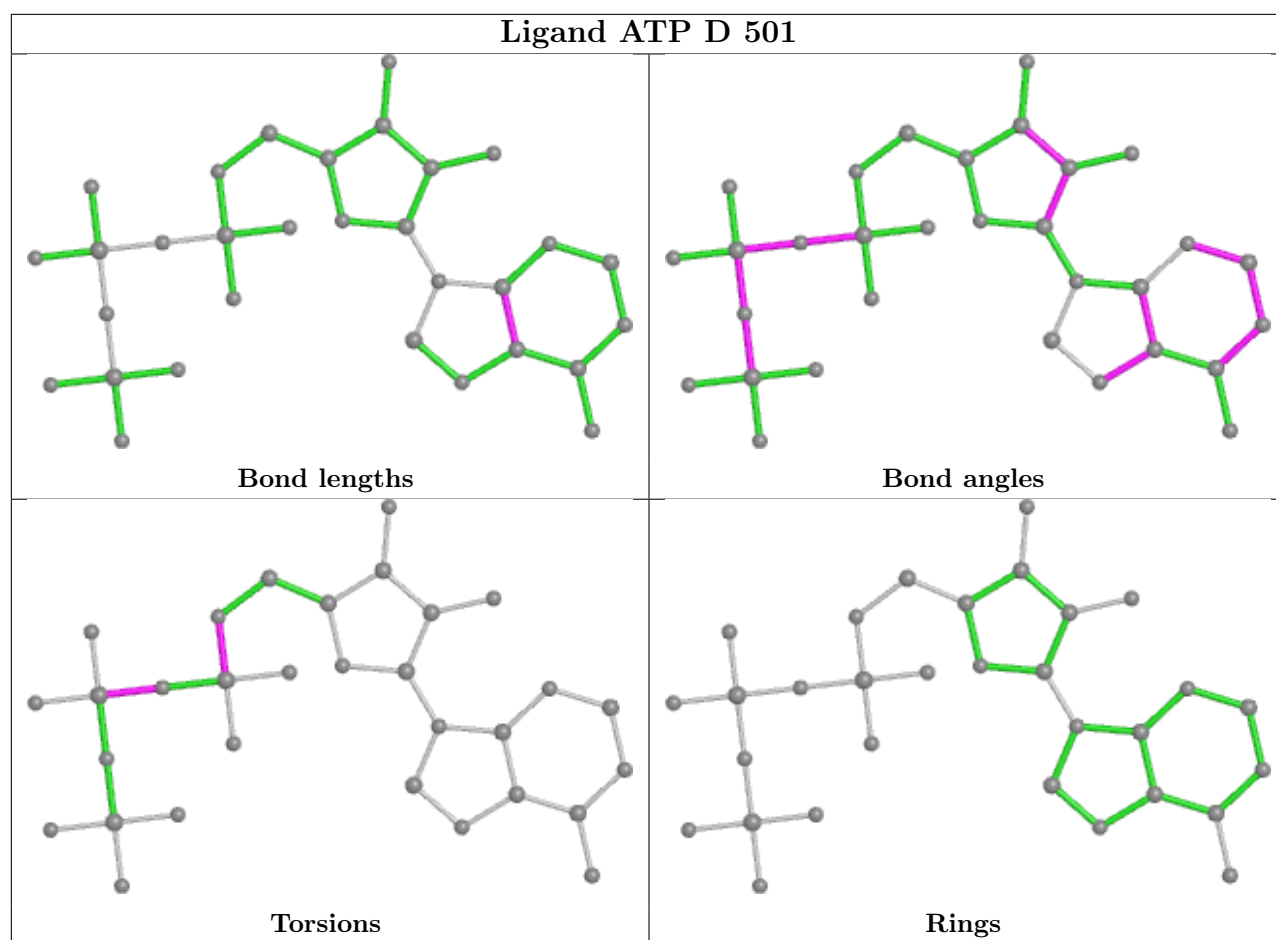
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	602	ATP	2	0
5	E	501	ATP	3	0
5	D	501	ATP	2	0
3	A	501	ADP	10	0
5	C	602	ATP	1	0

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

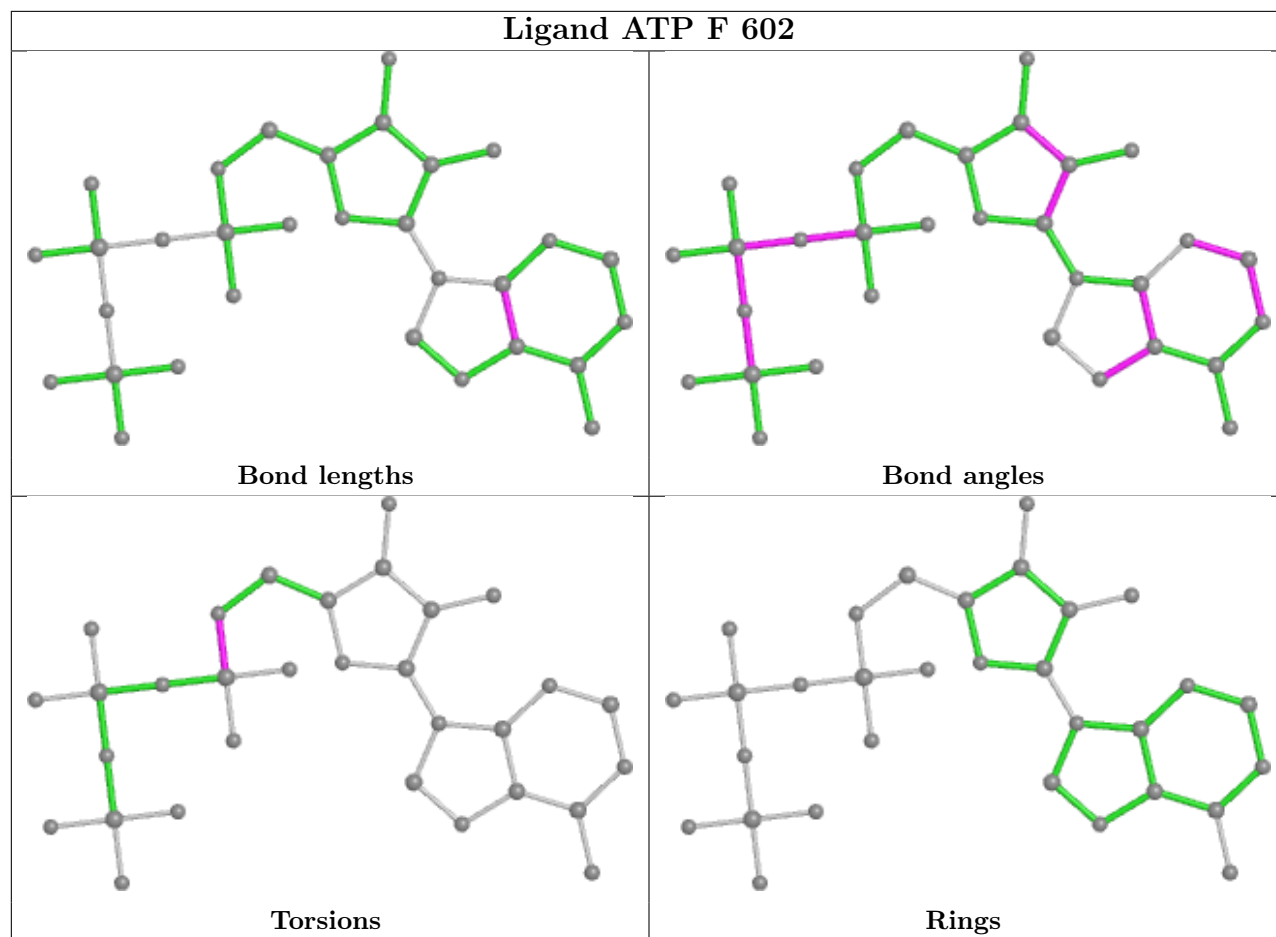
also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted 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.



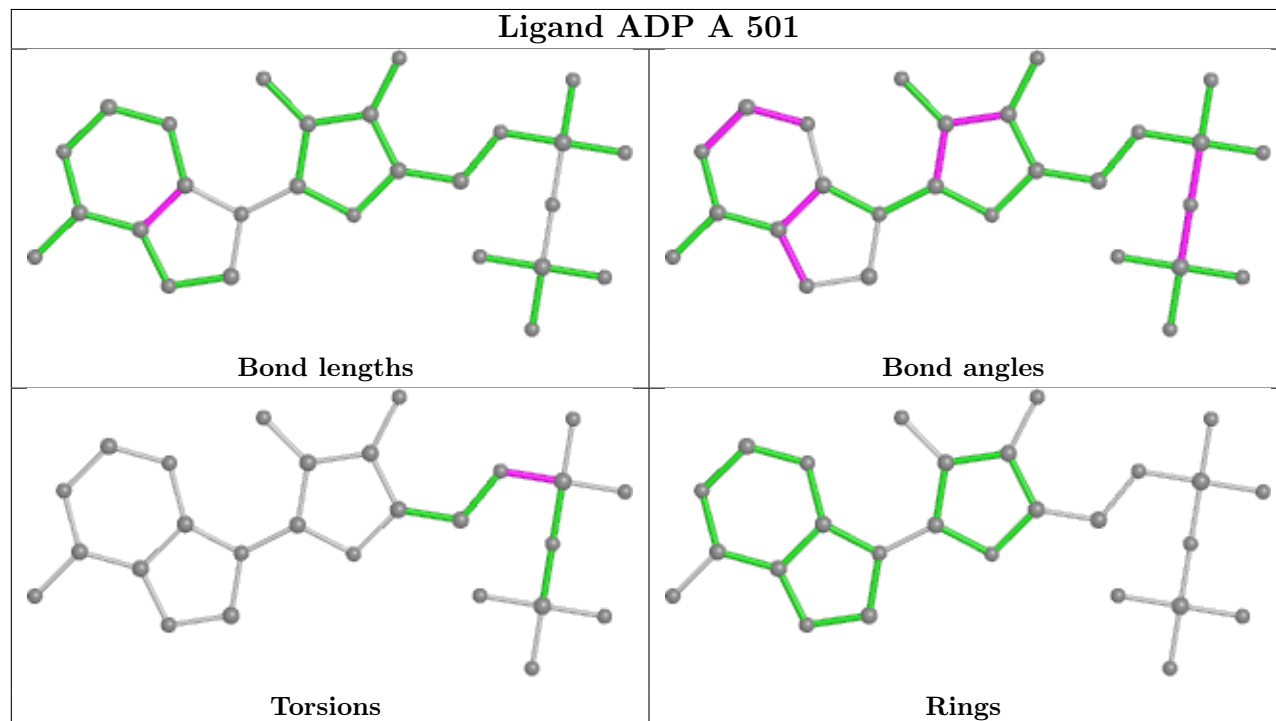


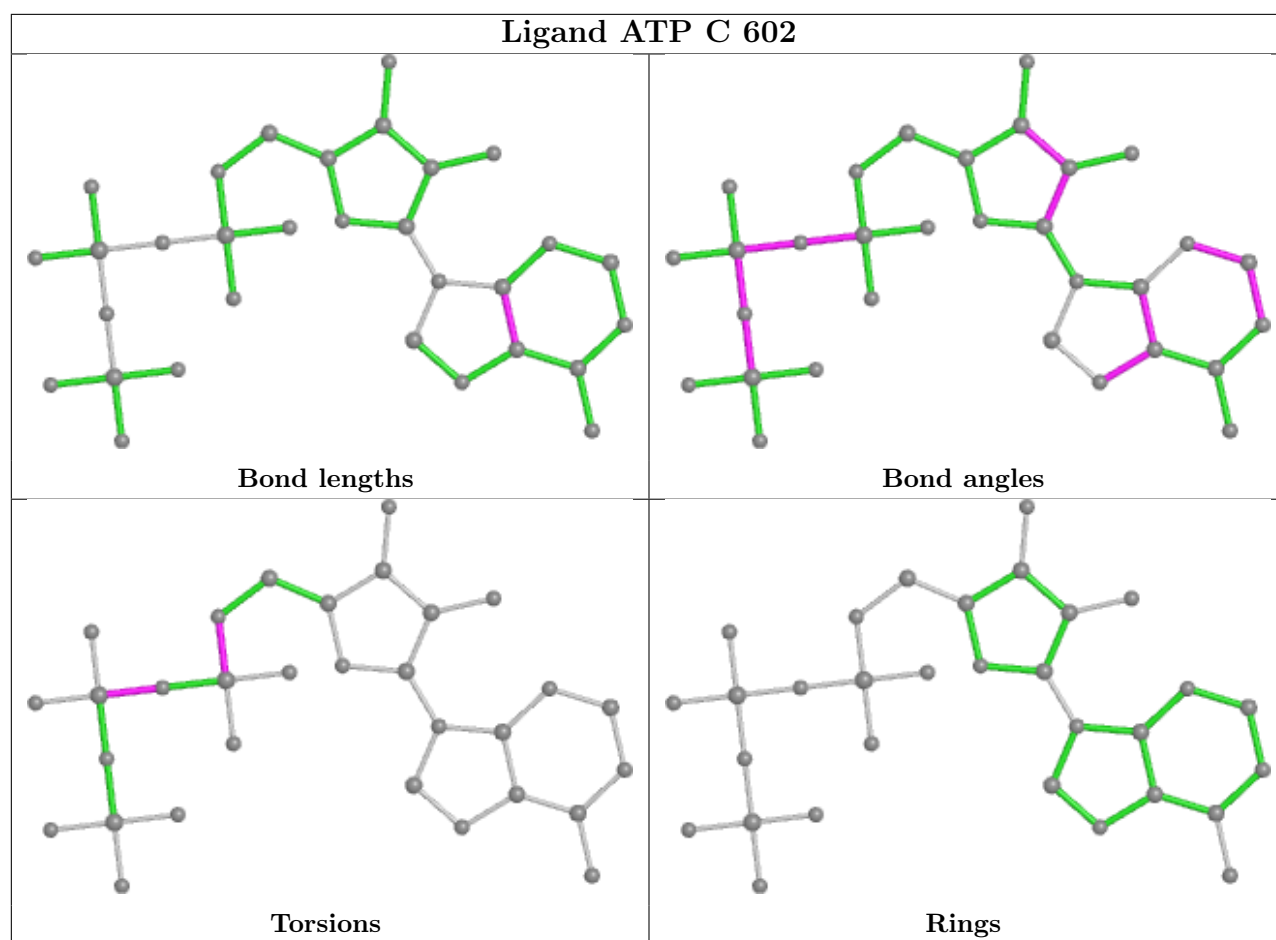


Ligand ATP F 602



Ligand ADP A 501





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.

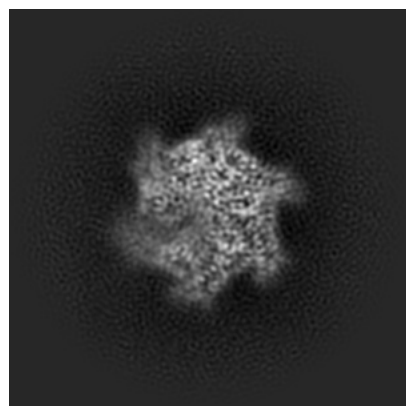
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-26675. These allow visual inspection of the internal detail of the map and identification of artifacts.

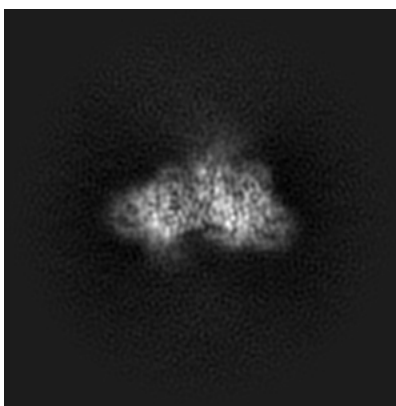
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

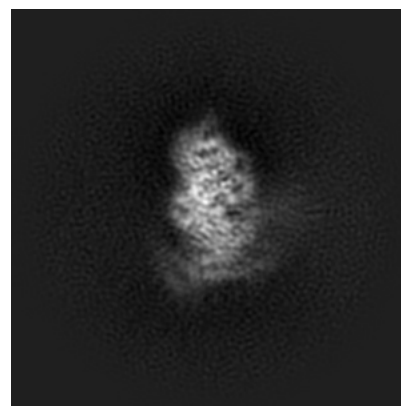
6.1.1 Primary map



X

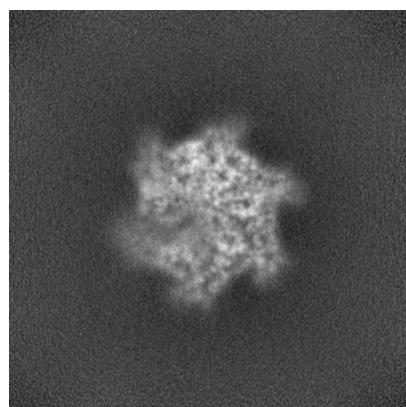


Y

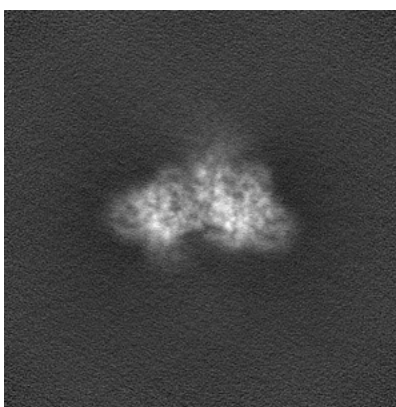


Z

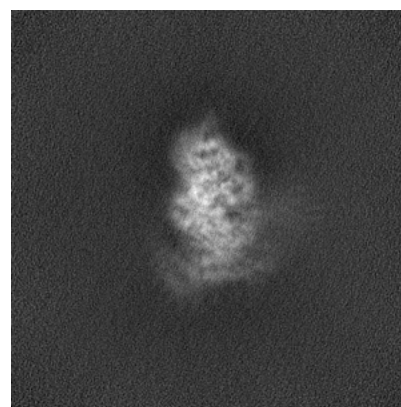
6.1.2 Raw map



X



Y

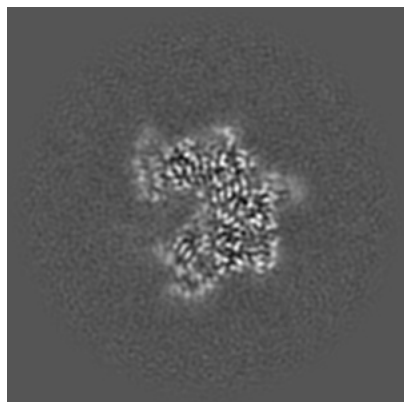


Z

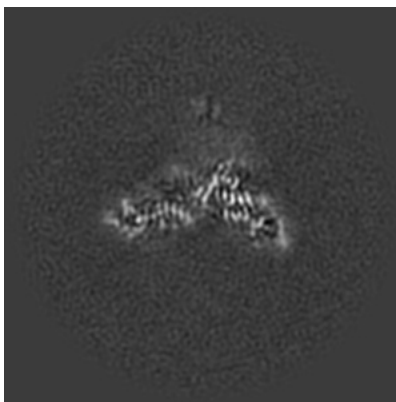
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

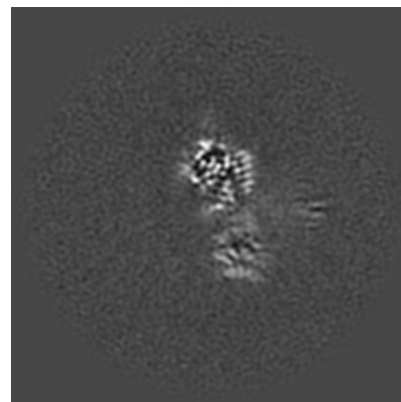
6.2.1 Primary map



X Index: 160

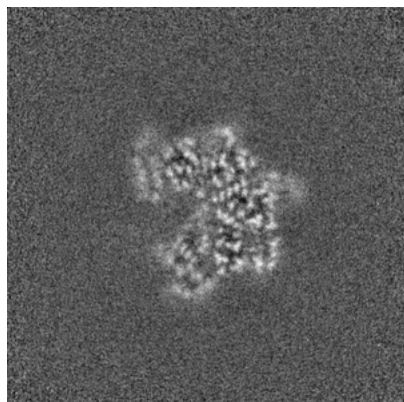


Y Index: 160

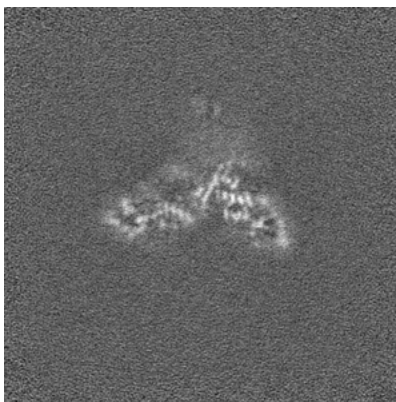


Z Index: 160

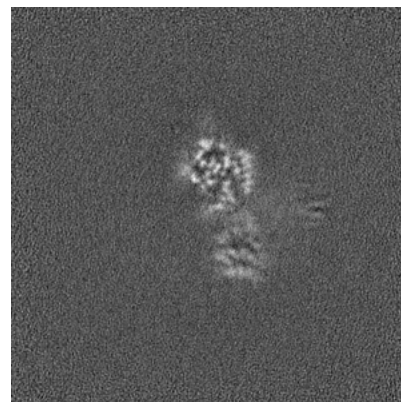
6.2.2 Raw map



X Index: 160



Y Index: 160

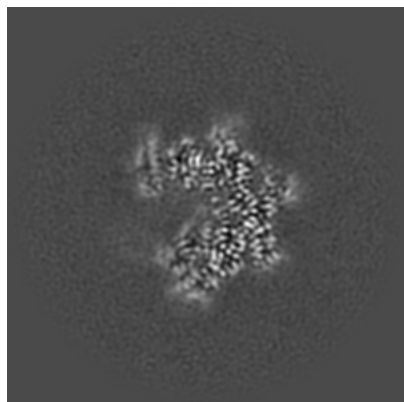


Z Index: 160

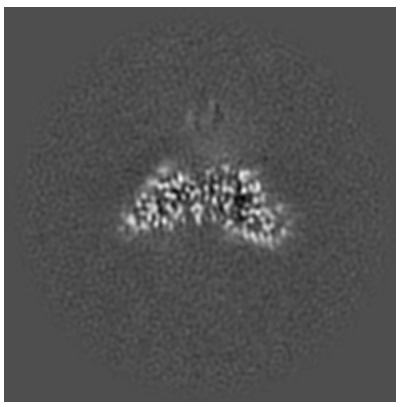
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

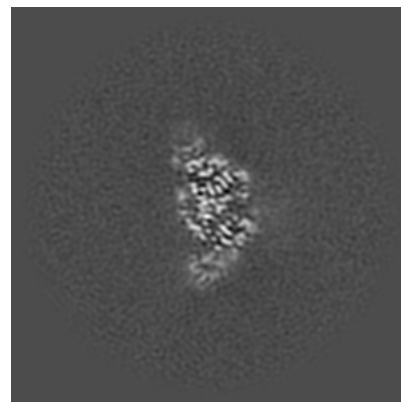
6.3.1 Primary map



X Index: 155

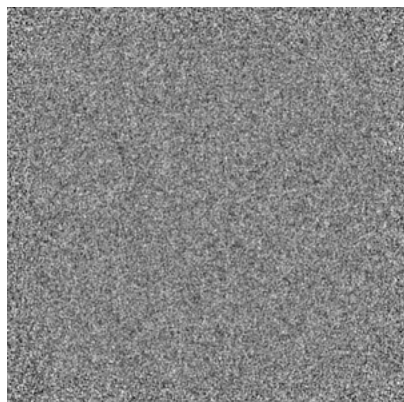


Y Index: 169

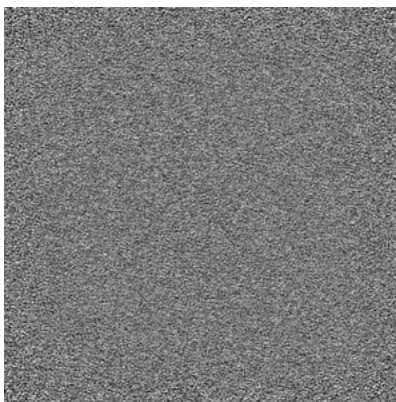


Z Index: 194

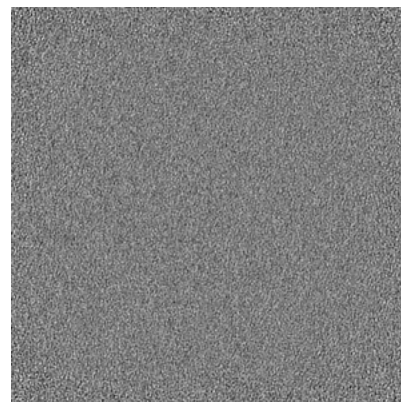
6.3.2 Raw map



X Index: 0



Y Index: 0



Z Index: 0

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

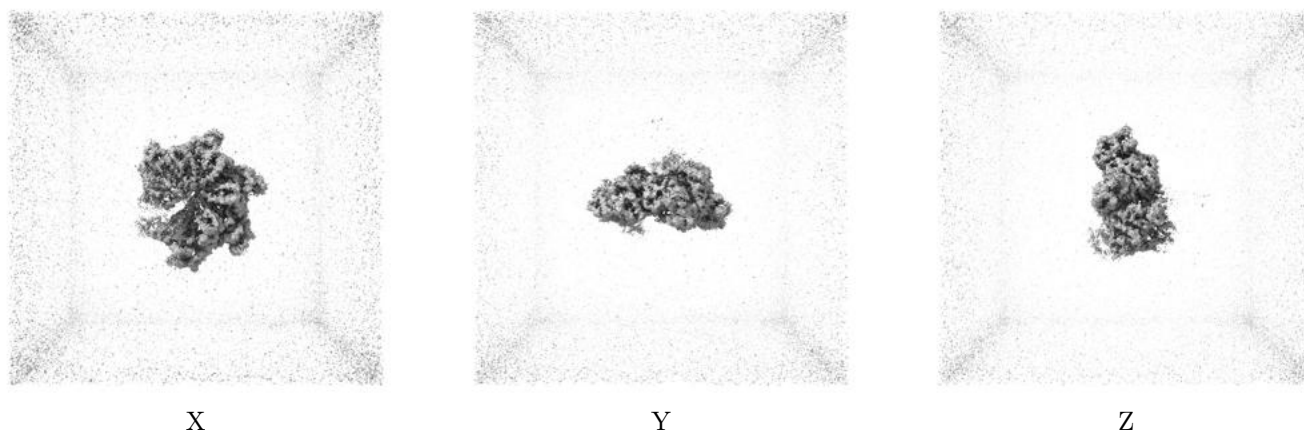
6.4 Orthogonal surface views [i](#)

6.4.1 Primary map



The images above show the 3D surface view of the map at the recommended contour level 0.25. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

6.4.2 Raw map



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.

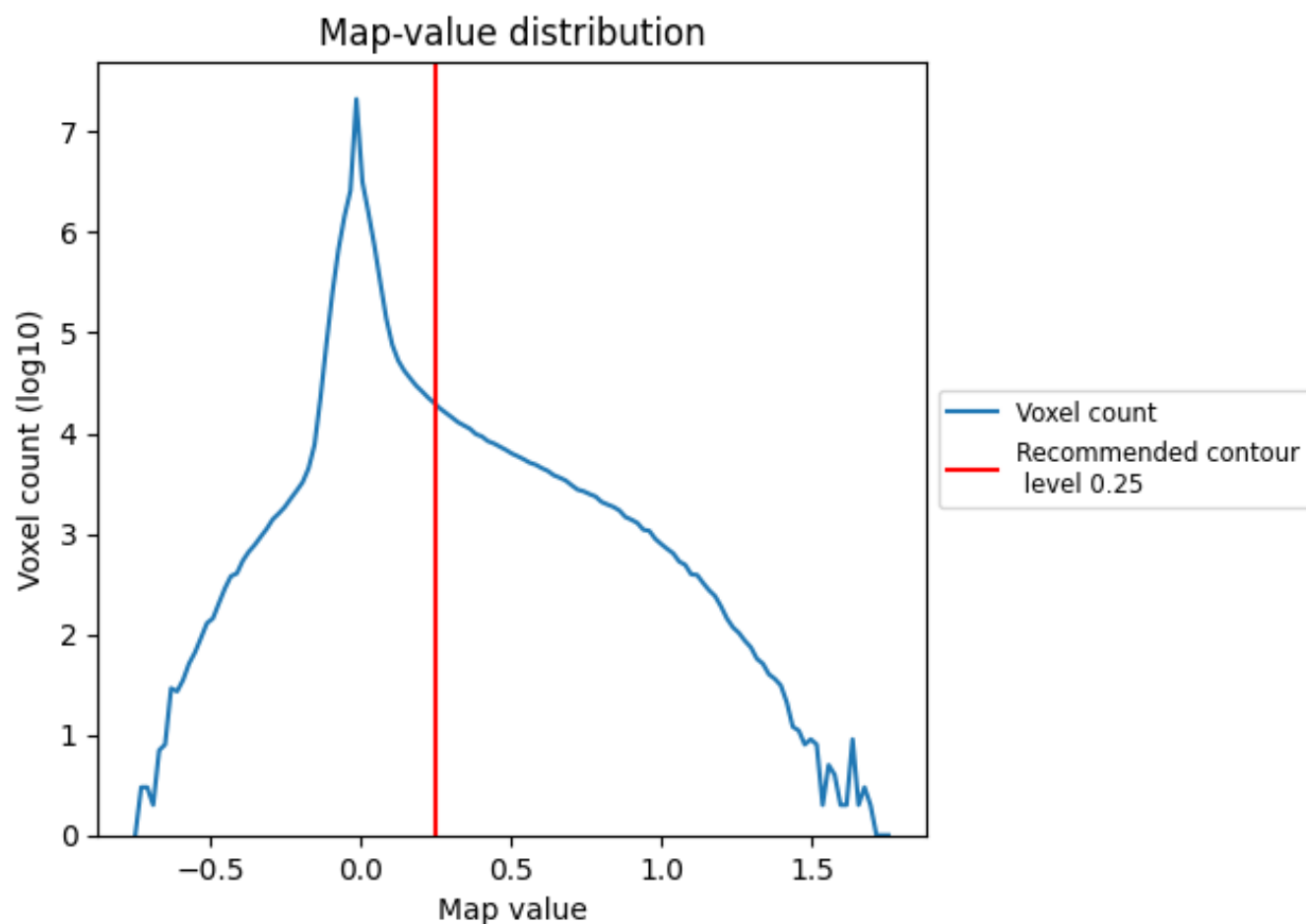
6.5 Mask visualisation [i](#)

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

7 Map analysis [i](#)

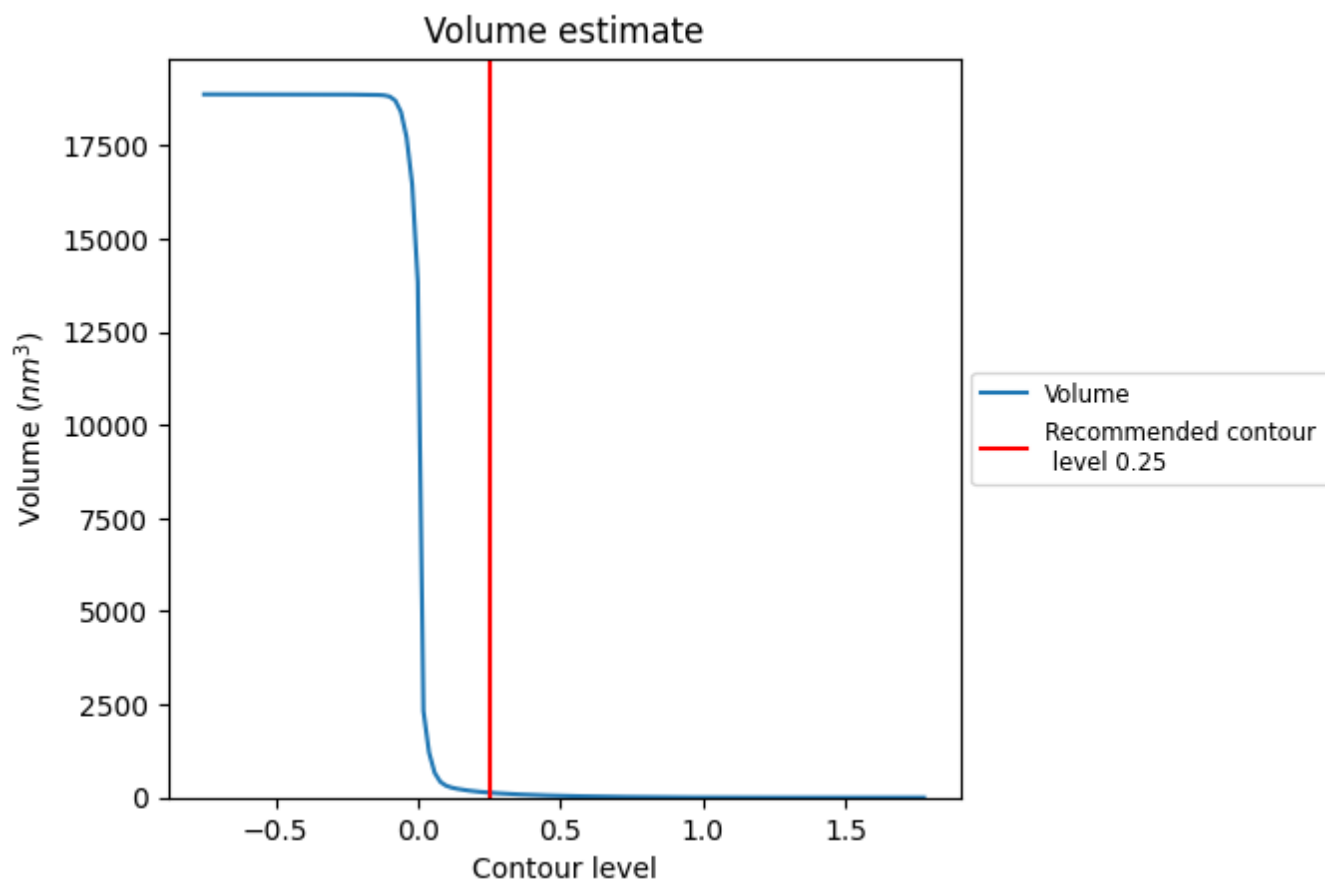
This section contains the results of statistical analysis of the map.

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.

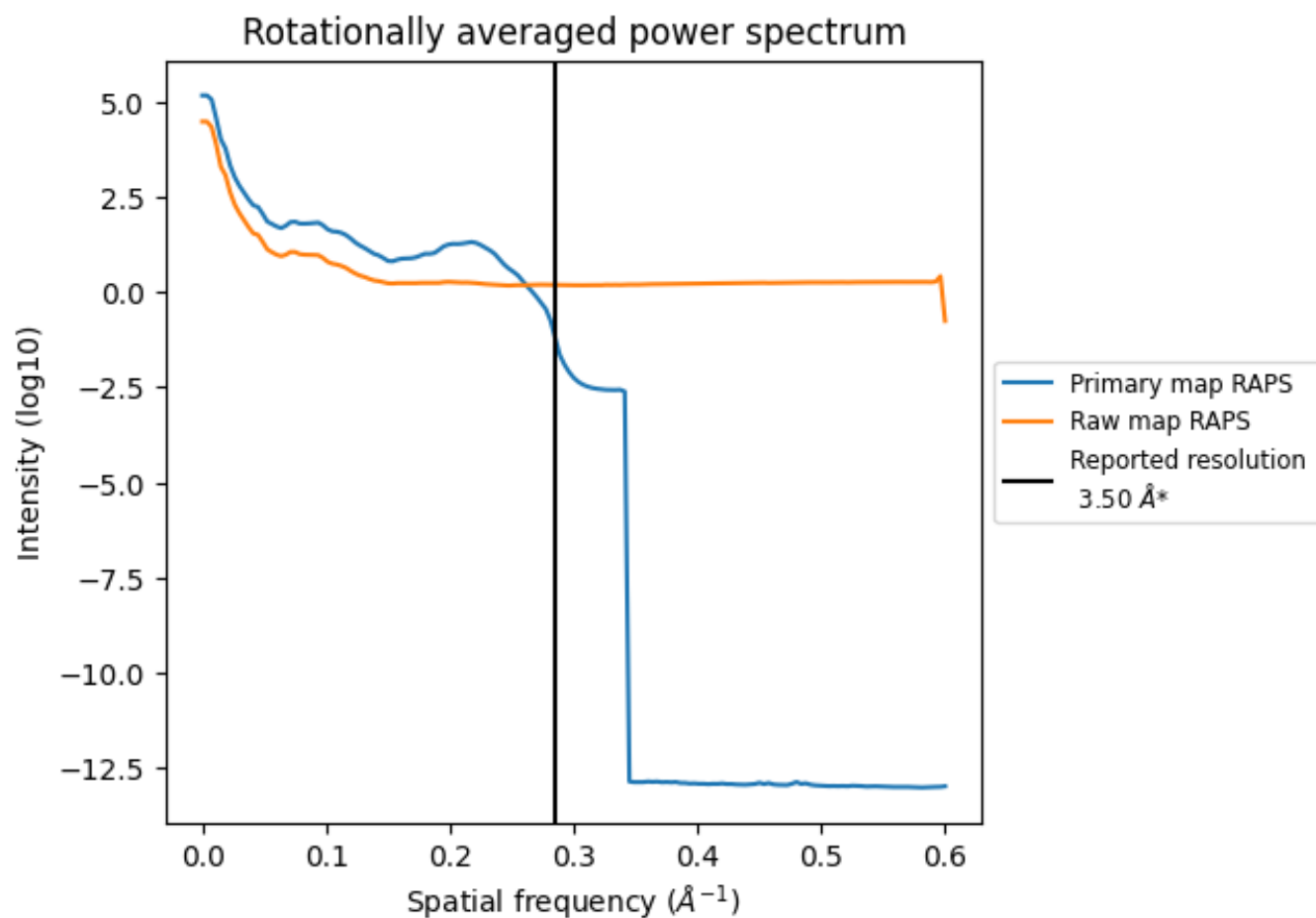
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 132 nm³; this corresponds to an approximate mass of 119 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 ⓘ

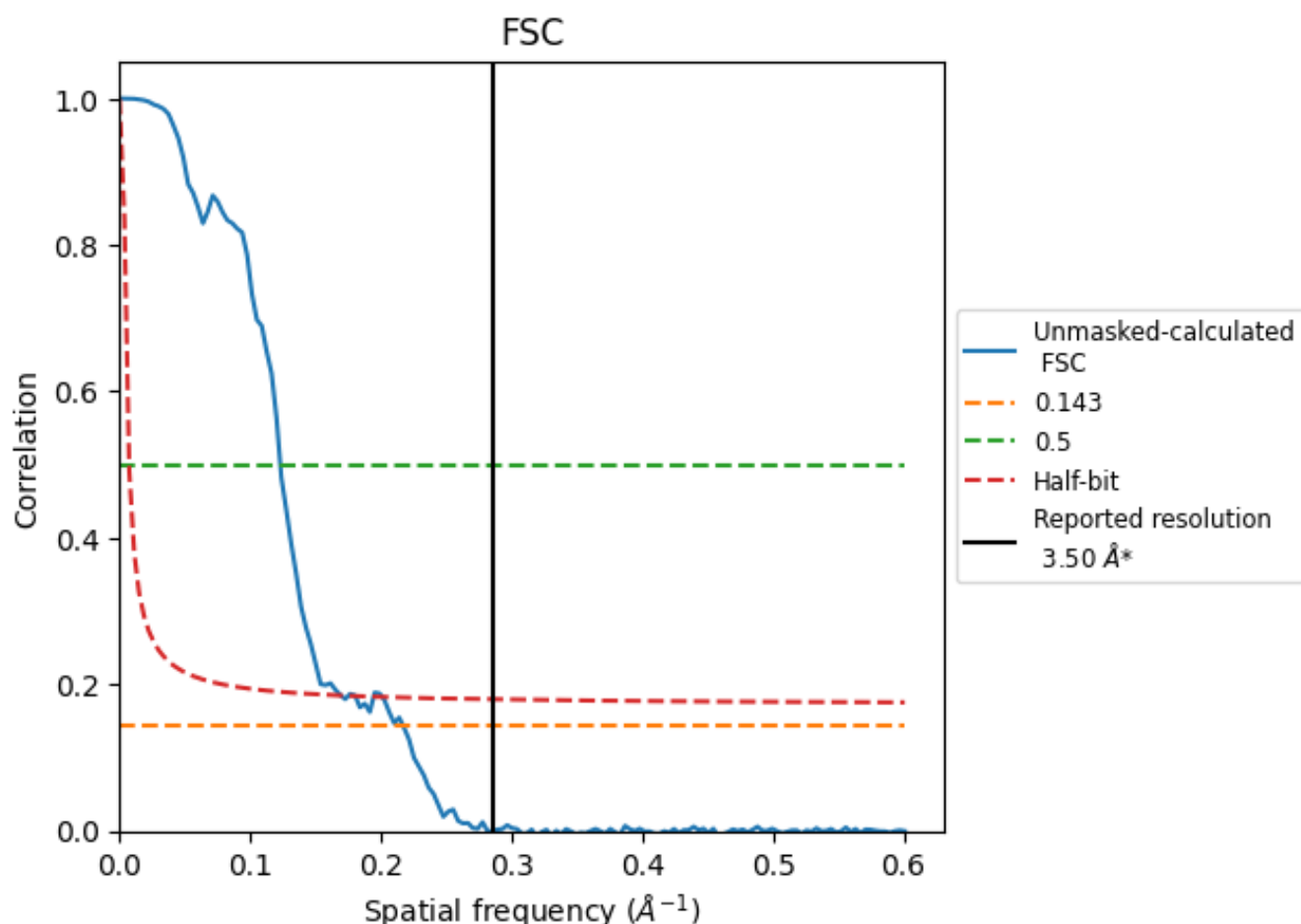


*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8 Fourier-Shell correlation [i](#)

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

8.1 FSC [i](#)



*Reported resolution corresponds to spatial frequency of 0.286 Å⁻¹

8.2 Resolution estimates [i](#)

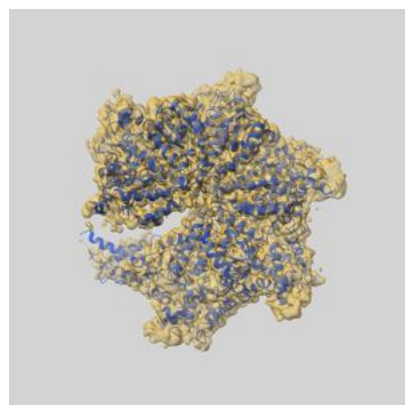
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.50	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	4.60	8.12	5.90

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

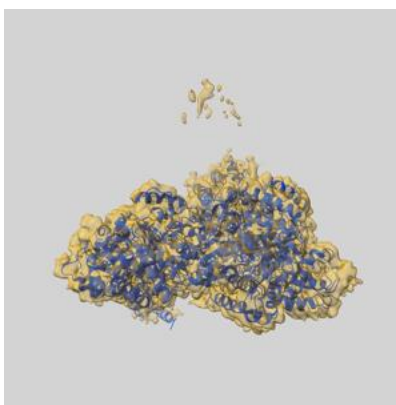
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-26675 and PDB model 7UPT. Per-residue inclusion information can be found in section 3 on page 10.

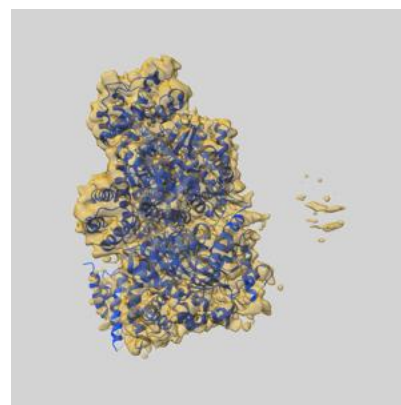
9.1 Map-model overlay [i](#)



X



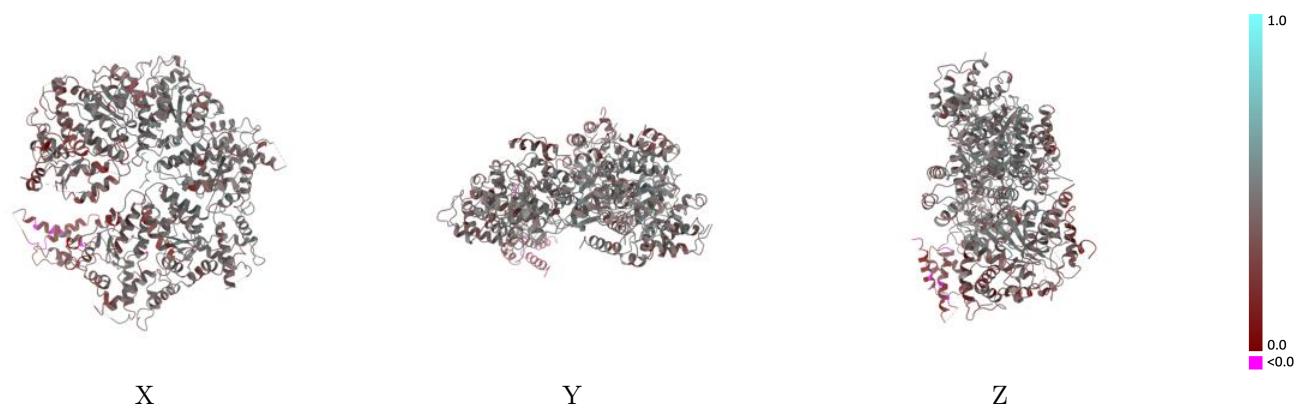
Y



Z

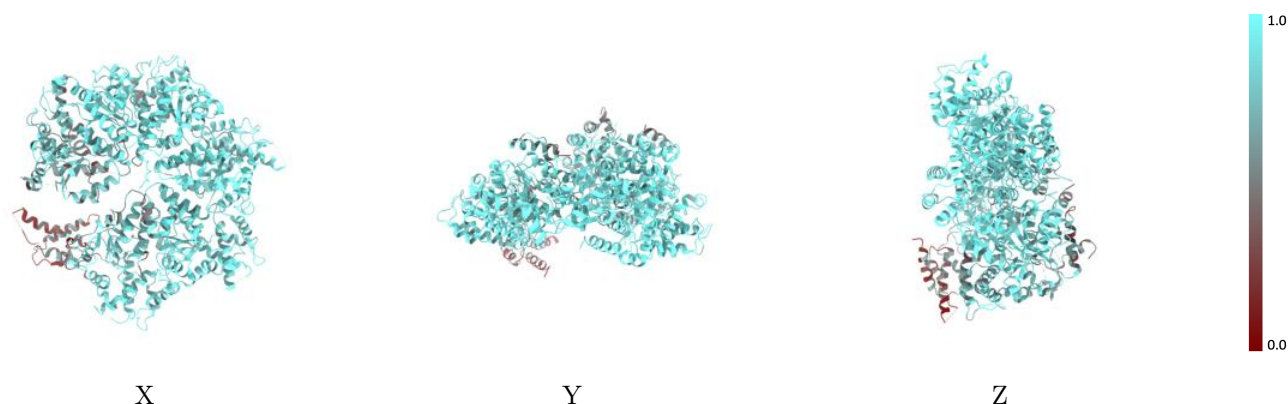
The images above show the 3D surface view of the map at the recommended contour level 0.25 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



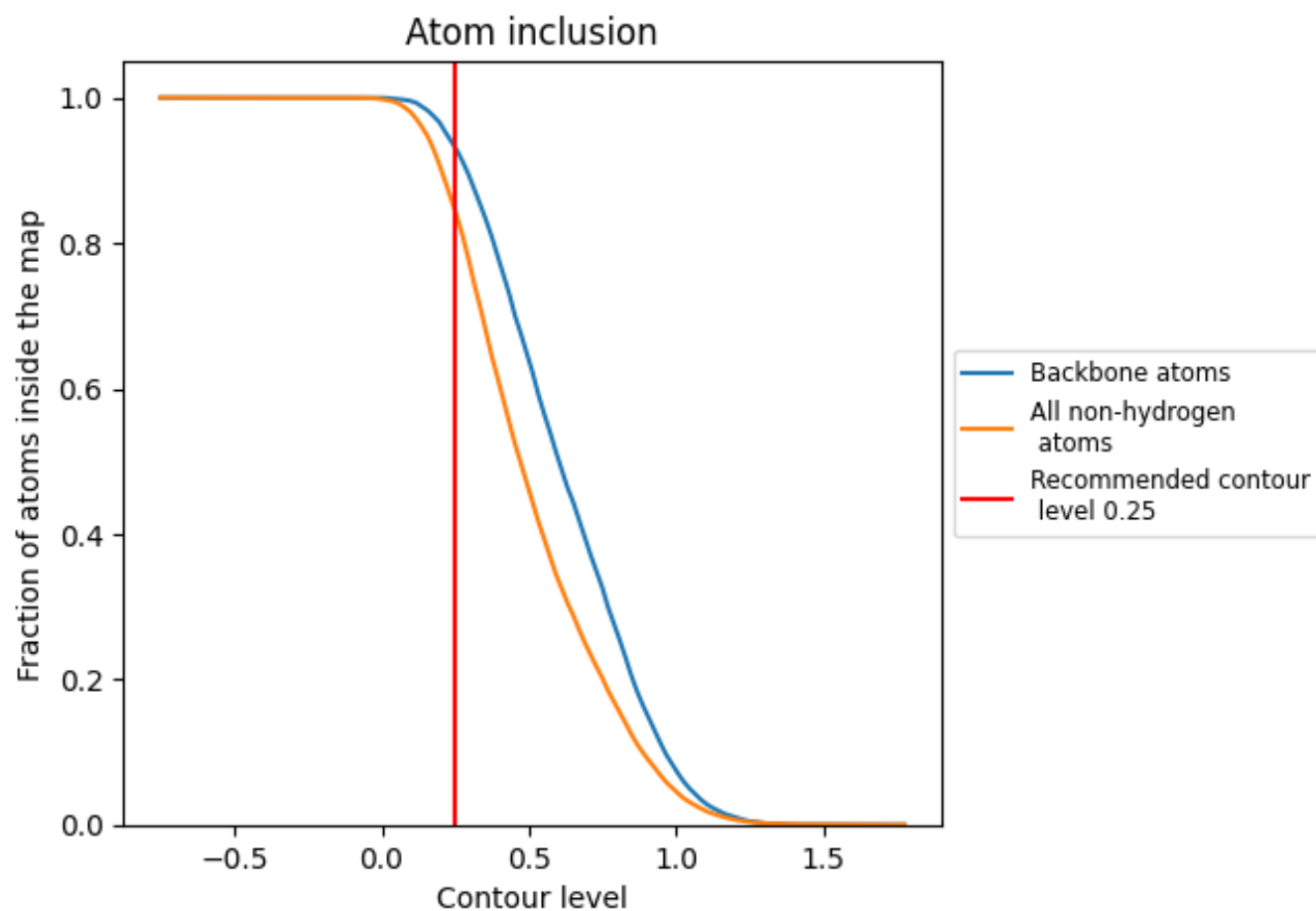
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.25).

9.4 Atom inclusion [i](#)



At the recommended contour level, 93% of all backbone atoms, 84% 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 (0.25) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.8433	<div></div> 0.4040
A	<div></div> 0.6430	<div></div> 0.3130
B	<div></div> 0.9222	<div></div> 0.4460
C	<div></div> 0.9345	<div></div> 0.4500
D	<div></div> 0.8946	<div></div> 0.4260
E	<div></div> 0.9021	<div></div> 0.4230
F	<div></div> 0.7177	<div></div> 0.3400
G	<div></div> 1.0000	<div></div> 0.5560

1.0

0.0

<0.0