Full wwPDB EM Validation Report (i)

Feb 13, 2024 – 04:52 AM EST

PDB ID	:	3JBI
EMDB ID	:	EMD-6446
Title	:	MDFF model of the vinculin tail domain bound to F-actin
Authors	:	Kim, L.Y.; Thompson, P.M.; Lee, H.T.; Pershad, M.; Campbell, S.L.; Alushin, G.M.
Deposited on	:	2015-09-02
Resolution	:	8.50 Å(reported)
Based on initial models	:	3J8A, 1QKR

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 (i) 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 (1)) were used in the production of this report:

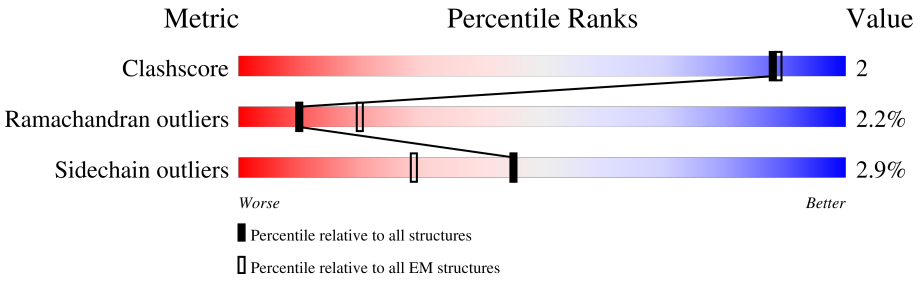
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.9
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 8.50 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 <=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	375	87% 9% • • •
1	B	375	• 83% 13% • • •
2	V	254	10% 48% • 48%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 6777 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 Actin, alpha skeletal muscle.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	367	2861	1812	481	548	20	0	0
1	B	367	2861	1812	481	548	20	0	0

- Molecule 2 is a protein called Vinculin.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	V	131	999	608	187	195	9	0	0

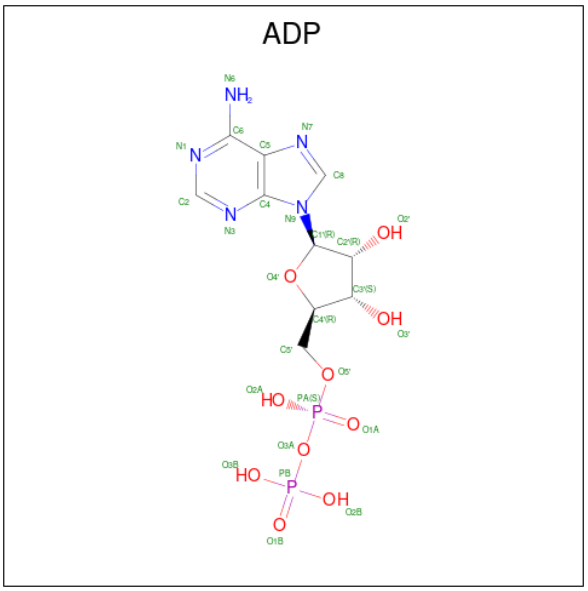
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
V	808	GLY	-	expression tag	UNP P12003
V	809	SER	-	expression tag	UNP P12003

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
3	A	1	1	1	0
3	B	1	1	1	0

- Molecule 4 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



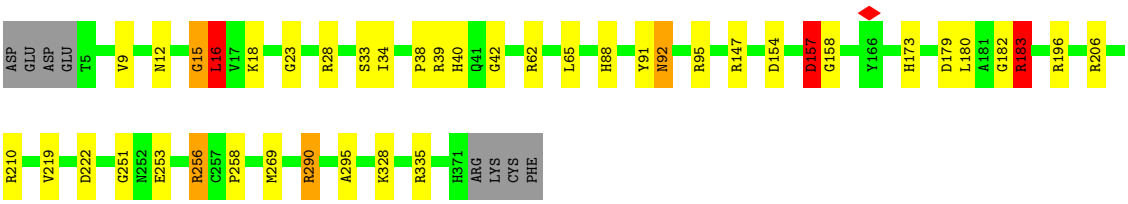
Mol	Chain	Residues	Atoms					AltConf
4	A	1	Total	C	N	O	P	0
			27	10	5	10	2	
4	B	1	Total	C	N	O	P	0
			27	10	5	10	2	

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.

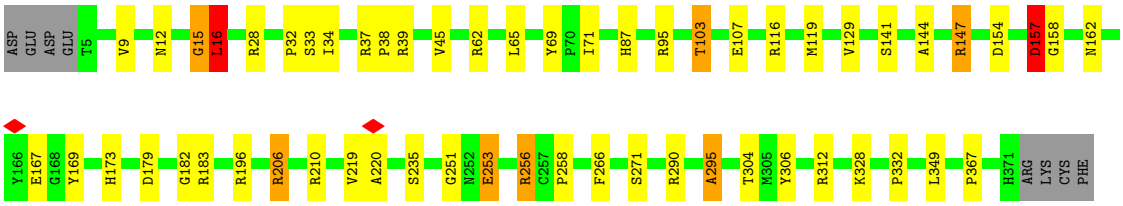
- Molecule 1: Actin, alpha skeletal muscle

Chain A:



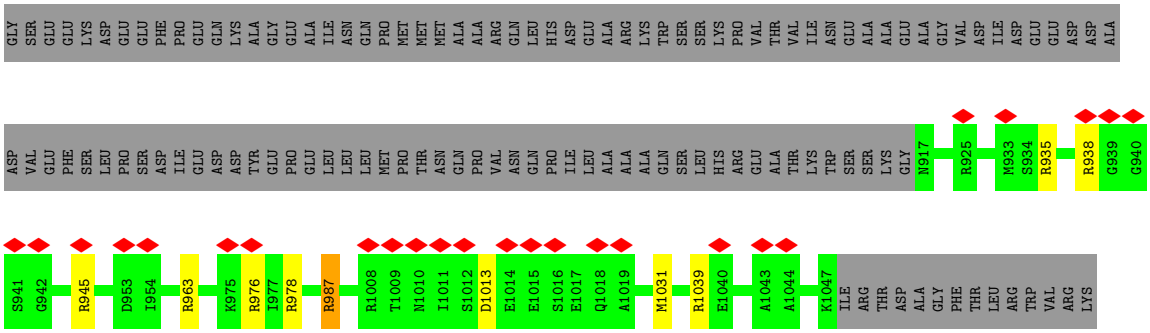
- Molecule 1: Actin, alpha skeletal muscle

Chain B:



- Molecule 2: Vinculin

Chain V:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	HELICAL	Depositor
Imposed symmetry	HELICAL, twist=166.82°, rise=27.80 Å, axial sym=C1	Depositor
Number of segments used	Not provided	
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	FREALIGN (per segment)	Depositor
Microscope	FEI TECNAI F20	Depositor
Voltage (kV)	120	Depositor
Electron dose ($e^-/Å^2$)	25	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	3000	Depositor
Magnification	137615	Depositor
Image detector	GATAN ULTRASCAN 4000 (4k x 4k)	Depositor
Maximum map value	20.806	Depositor
Minimum map value	-7.766	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	5.5	Depositor
Map size (Å)	436.0, 436.0, 436.0	wwPDB
Map dimensions	200, 200, 200	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.18, 2.18, 2.18	Depositor

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.83	0/2923	1.23	16/3963 (0.4%)
1	B	0.83	0/2923	1.22	20/3963 (0.5%)
2	V	0.71	0/1000	1.09	9/1339 (0.7%)
All	All	0.82	0/6846	1.21	45/9265 (0.5%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	9
2	V	0	1
All	All	0	15

There are no bond length outliers.

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	147	ARG	NE-CZ-NH1	9.27	124.94	120.30
1	A	39	ARG	NE-CZ-NH1	8.04	124.32	120.30
1	B	196	ARG	NE-CZ-NH1	7.69	124.14	120.30
1	A	256	ARG	NE-CZ-NH1	7.68	124.14	120.30
1	B	196	ARG	NE-CZ-NH2	-7.52	116.54	120.30
2	V	935	ARG	NE-CZ-NH1	7.31	123.95	120.30
1	A	147	ARG	NE-CZ-NH2	-7.27	116.67	120.30
1	A	39	ARG	NE-CZ-NH2	-7.16	116.72	120.30
1	A	28	ARG	NE-CZ-NH1	7.05	123.83	120.30
1	A	196	ARG	NE-CZ-NH2	-7.04	116.78	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	V	1039	ARG	NE-CZ-NH1	7.03	123.81	120.30
1	B	37	ARG	NE-CZ-NH1	6.86	123.73	120.30
1	B	147	ARG	NE-CZ-NH2	-6.85	116.88	120.30
1	B	37	ARG	NE-CZ-NH2	-6.84	116.88	120.30
1	A	290	ARG	NE-CZ-NH1	6.80	123.70	120.30
1	A	290	ARG	NE-CZ-NH2	-6.78	116.91	120.30
1	B	62	ARG	NE-CZ-NH1	6.72	123.66	120.30
2	V	963	ARG	NE-CZ-NH2	-6.69	116.96	120.30
2	V	978	ARG	NE-CZ-NH1	6.69	123.64	120.30
1	B	256	ARG	NE-CZ-NH1	6.68	123.64	120.30
1	A	183	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	B	116	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	B	119	MET	CG-SD-CE	-6.30	90.12	100.20
1	B	39	ARG	NE-CZ-NH1	6.06	123.33	120.30
1	B	154	ASP	CB-CG-OD2	5.99	123.69	118.30
2	V	976	ARG	NE-CZ-NH1	5.97	123.29	120.30
1	A	154	ASP	CB-CG-OD2	5.94	123.64	118.30
1	B	206	ARG	NE-CZ-NH2	-5.91	117.34	120.30
2	V	987	ARG	NE-CZ-NH1	5.91	123.25	120.30
1	B	116	ARG	NE-CZ-NH2	-5.79	117.41	120.30
2	V	963	ARG	NE-CZ-NH1	5.79	123.19	120.30
1	A	16	LEU	N-CA-CB	5.72	121.84	110.40
1	A	196	ARG	NE-CZ-NH1	5.62	123.11	120.30
1	A	15	GLY	C-N-CA	5.56	135.61	121.70
2	V	938	ARG	NE-CZ-NH2	-5.54	117.53	120.30
2	V	945	ARG	NE-CZ-NH1	5.32	122.96	120.30
1	B	15	GLY	O-C-N	-5.30	114.21	122.70
1	A	210	ARG	NE-CZ-NH1	5.24	122.92	120.30
1	A	157	ASP	C-N-CA	5.22	133.26	122.30
1	B	206	ARG	NE-CZ-NH1	5.18	122.89	120.30
1	B	157	ASP	C-N-CA	5.16	133.14	122.30
1	B	154	ASP	OD1-CG-OD2	-5.15	113.51	123.30
1	B	16	LEU	N-CA-CB	5.15	120.70	110.40
1	B	15	GLY	C-N-CA	5.14	134.55	121.70
1	B	266	PHE	CB-CG-CD2	-5.12	117.22	120.80

There are no chirality outliers.

All (15) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	183	ARG	Sidechain
1	A	206	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	290	ARG	Sidechain
1	A	335	ARG	Sidechain
1	A	62	ARG	Sidechain
1	B	206	ARG	Sidechain
1	B	210	ARG	Sidechain
1	B	28	ARG	Sidechain
1	B	290	ARG	Sidechain
1	B	312	ARG	Sidechain
1	B	332	PRO	Peptide
1	B	349	LEU	Peptide
1	B	69	TYR	Sidechain
1	B	95	ARG	Sidechain
2	V	987	ARG	Sidechain

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2861	0	2831	14	0
1	B	2861	0	2831	14	0
2	V	999	0	1059	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	27	0	12	0	0
4	B	27	0	12	0	0
All	All	6777	0	6745	26	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 2.

All (26) 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:B:141:SER:HA	1:B:144:ALA:HB3	1.78	0.65
1:B:295:ALA:HA	1:B:328:LYS:H	1.63	0.64
1:B:219:VAL:HG22	1:B:258:PRO:HB2	1.85	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:38:PRO:HA	1:A:65:LEU:HA	1.90	0.53
1:B:157:ASP:HA	1:B:182:GLY:H	1.74	0.51
1:A:295:ALA:HA	1:A:328:LYS:H	1.75	0.50
1:A:157:ASP:HA	1:A:182:GLY:H	1.76	0.50
1:B:15:GLY:HA3	1:B:16:LEU:HB2	1.92	0.50
1:A:15:GLY:HA3	1:A:16:LEU:HB2	1.96	0.48
1:A:40:HIS:CE1	1:B:173:HIS:CE1	3.02	0.47
1:A:158:GLY:HA2	1:A:183:ARG:H	1.78	0.47
1:B:295:ALA:HA	1:B:328:LYS:N	2.29	0.47
1:A:88:HIS:CE1	1:A:92:ASN:HD21	2.32	0.47
1:B:38:PRO:HA	1:B:65:LEU:HA	1.97	0.47
1:B:158:GLY:HA2	1:B:183:ARG:H	1.81	0.46
1:A:295:ALA:HA	1:A:328:LYS:N	2.33	0.44
1:A:42:GLY:HA2	1:B:169:TYR:HA	2.00	0.43
1:A:158:GLY:HA2	1:A:182:GLY:H	1.84	0.43
1:B:16:LEU:H	1:B:32:PRO:HA	1.82	0.43
1:A:91:TYR:O	1:A:95:ARG:HA	2.20	0.42
1:B:103:THR:HG22	1:B:129:VAL:HG11	2.02	0.42
1:B:219:VAL:HG23	1:B:306:TYR:HB3	2.02	0.42
1:B:253:GLU:HA	1:B:256:ARG:HB3	2.03	0.41
1:A:253:GLU:H	1:A:253:GLU:CD	2.24	0.41
1:A:253:GLU:HA	1:A:256:ARG:HB3	2.03	0.41
1:A:219:VAL:HG22	1:A:258:PRO:HB2	2.03	0.41

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	A	365/375 (97%)	330 (90%)	28 (8%)	7 (2%)	8 38
1	B	365/375 (97%)	317 (87%)	36 (10%)	12 (3%)	4 26

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	V	129/254 (51%)	128 (99%)	1 (1%)	0	100	100
All	All	859/1004 (86%)	775 (90%)	65 (8%)	19 (2%)	10	35

All (19) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	34	ILE
1	B	34	ILE
1	A	16	LEU
1	A	23	GLY
1	B	16	LEU
1	B	295	ALA
1	A	33	SER
1	A	180	LEU
1	A	251	GLY
1	B	167	GLU
1	B	235	SER
1	B	251	GLY
1	B	304	THR
1	B	45	VAL
1	A	269	MET
1	B	33	SER
1	B	220	ALA
1	B	271	SER
1	B	367	PRO

5.3.2 Protein sidechains (i)

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	310/318 (98%)	302 (97%)	8 (3%)	46	66
1	B	310/318 (98%)	299 (96%)	11 (4%)	36	59
2	V	110/214 (51%)	108 (98%)	2 (2%)	59	77
All	All	730/850 (86%)	709 (97%)	21 (3%)	45	64

All (21) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	VAL
1	A	12	ASN
1	A	18	LYS
1	A	92	ASN
1	A	157	ASP
1	A	173	HIS
1	A	179	ASP
1	A	222	ASP
1	B	9	VAL
1	B	12	ASN
1	B	71	ILE
1	B	87	HIS
1	B	103	THR
1	B	107	GLU
1	B	147	ARG
1	B	157	ASP
1	B	162	ASN
1	B	179	ASP
1	B	253	GLU
2	V	1013	ASP
2	V	1031	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	HIS
1	A	92	ASN
1	A	275	HIS
1	B	173	HIS
2	V	949	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 4 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
4	ADP	B	402	3	24,29,29	0.81	0	29,45,45	1.55	3 (10%)
4	ADP	A	402	3	24,29,29	0.79	0	29,45,45	1.58	3 (10%)

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
4	ADP	B	402	3	-	3/12/32/32	0/3/3/3
4	ADP	A	402	3	-	3/12/32/32	0/3/3/3

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	402	ADP	PA-O3A-PB	-6.14	111.74	132.83
4	B	402	ADP	PA-O3A-PB	-5.71	113.22	132.83
4	B	402	ADP	O3B-PB-O3A	3.24	115.50	104.64
4	A	402	ADP	O3B-PB-O3A	3.17	115.27	104.64
4	B	402	ADP	C5-C6-N6	2.38	123.97	120.35
4	A	402	ADP	C2'-C3'-C4'	2.13	106.78	102.64

There are no chirality outliers.

All (6) torsion outliers are listed below:

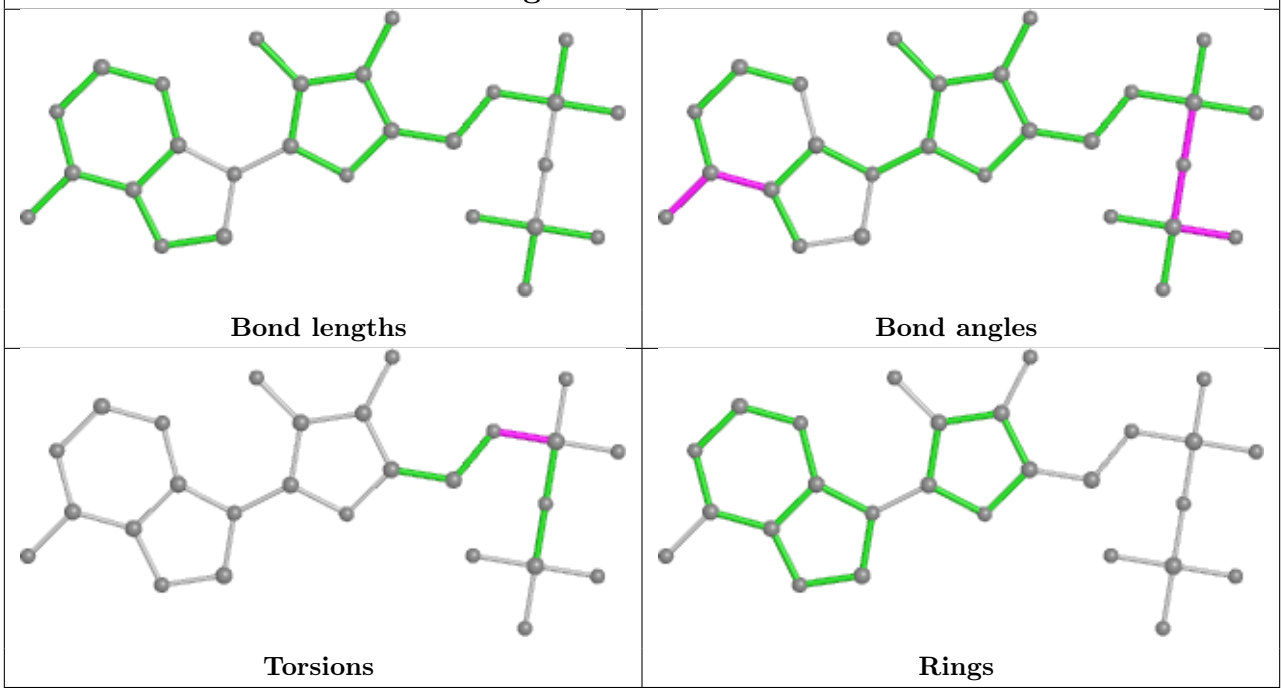
Mol	Chain	Res	Type	Atoms
4	A	402	ADP	C5'-O5'-PA-O1A
4	A	402	ADP	C5'-O5'-PA-O2A
4	B	402	ADP	C5'-O5'-PA-O1A
4	B	402	ADP	C5'-O5'-PA-O2A
4	A	402	ADP	C5'-O5'-PA-O3A
4	B	402	ADP	C5'-O5'-PA-O3A

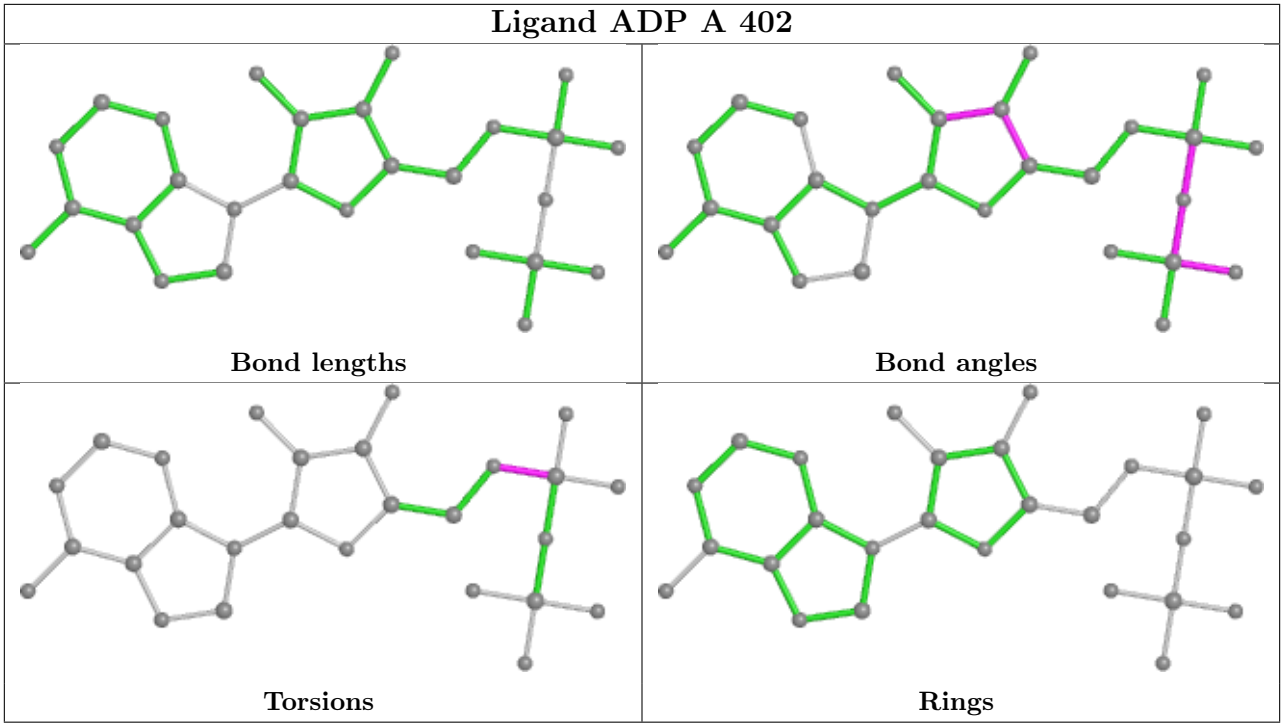
There are no ring outliers.

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 then 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 ADP B 402





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.

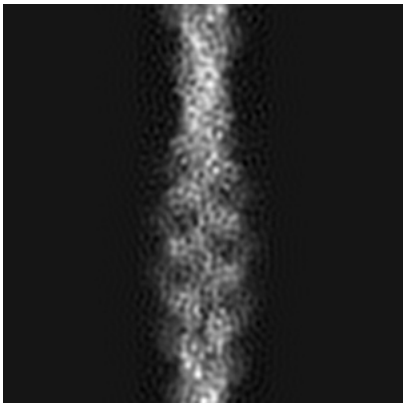
6 Map visualisation (i)

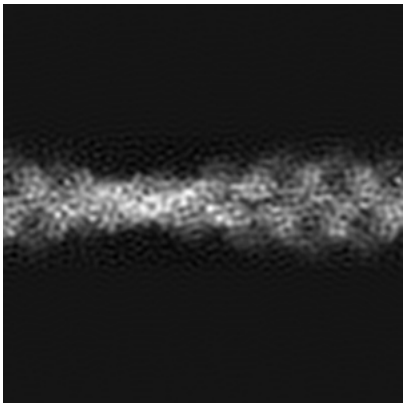
This section contains visualisations of the EMDB entry EMD-6446. These allow visual inspection of the internal detail of the map and identification of artifacts.

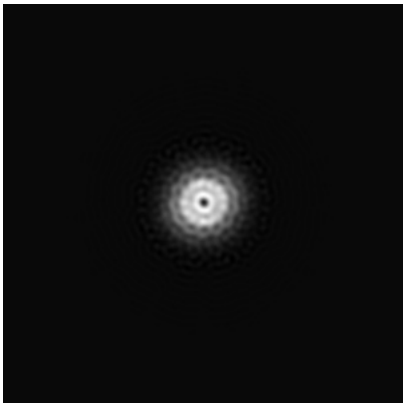
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

6.1.1 Primary map


X

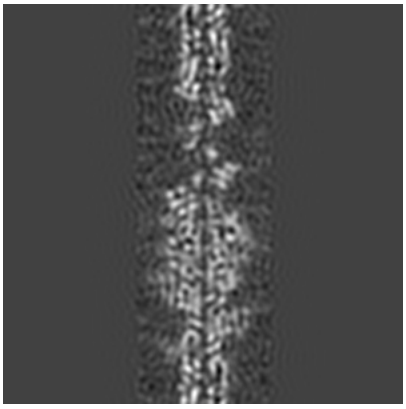

Y

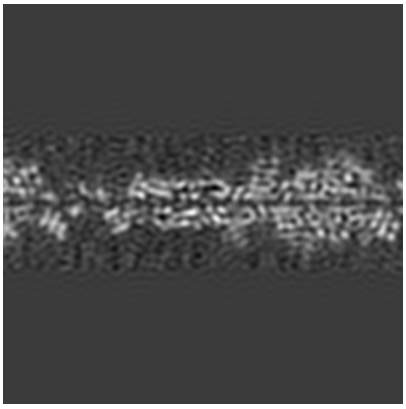

Z

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

6.2 Central slices (i)

6.2.1 Primary map


X Index: 100

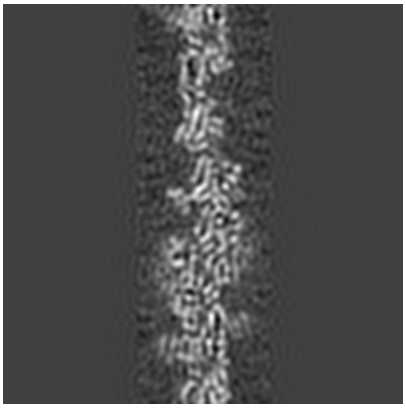

Y Index: 100

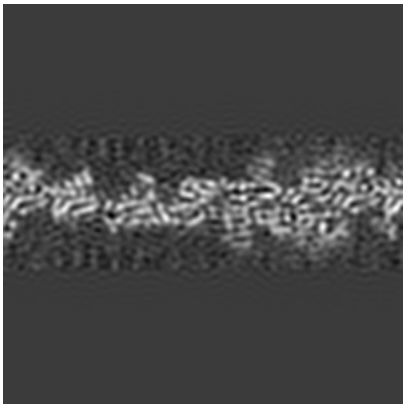
Z Index: 100

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: 97

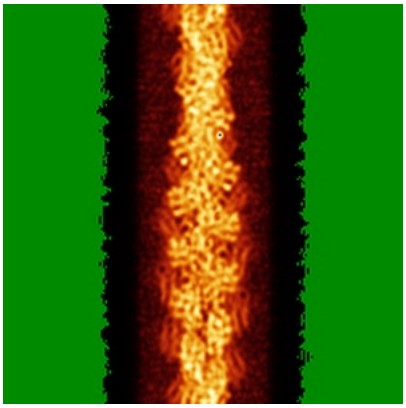

Y Index: 103

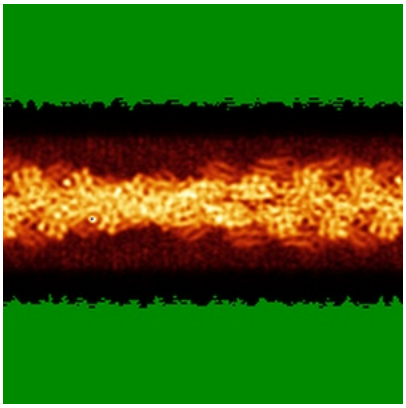
Z Index: 103

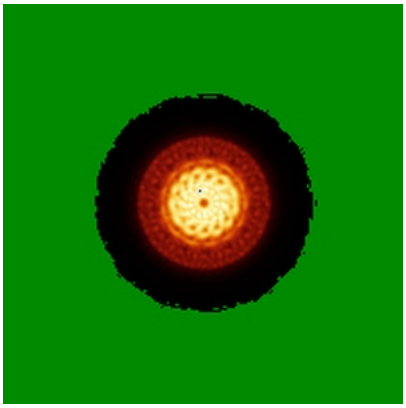
The images above show the largest variance slices of the map in three orthogonal directions.

6.4 Orthogonal standard-deviation projections (False-color) (i)

6.4.1 Primary map


X

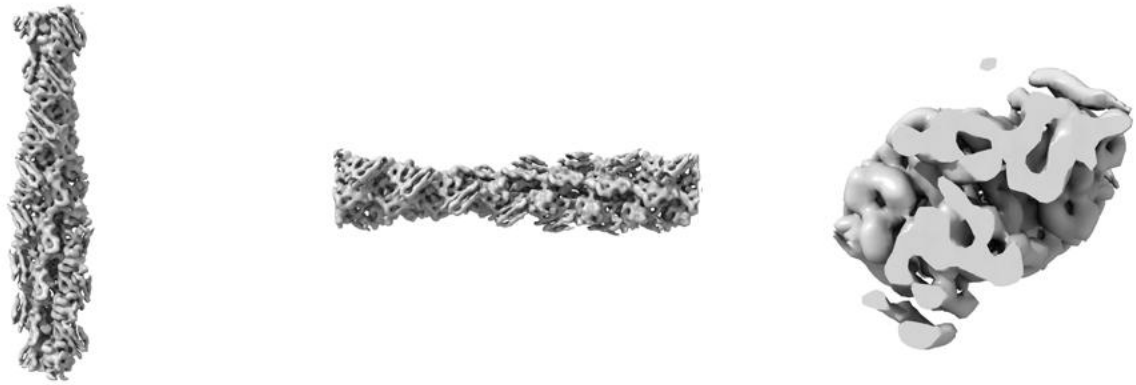

Y


Z

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

6.5 Orthogonal surface views (i)

6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 5.5. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

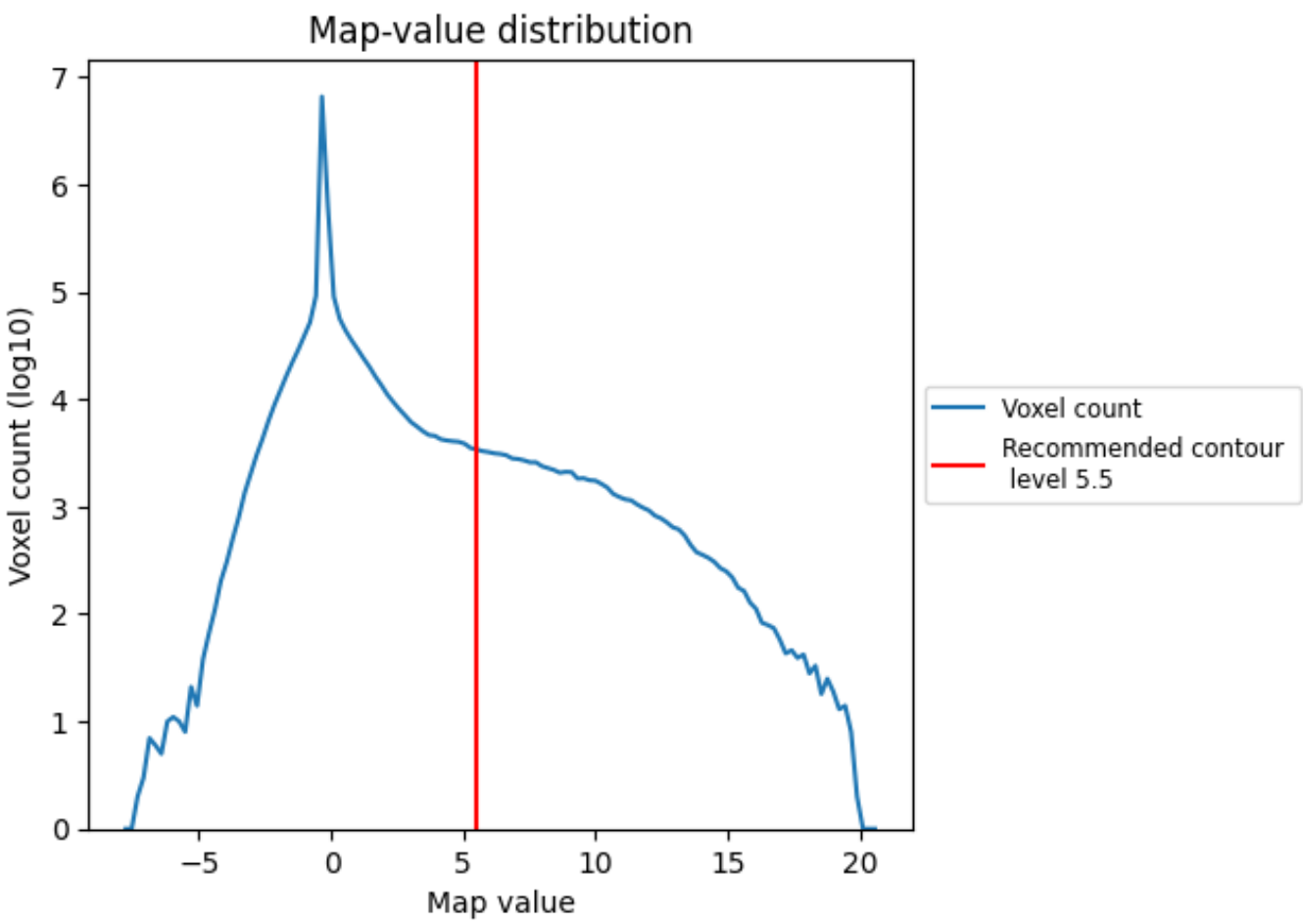
6.6 Mask visualisation (i)

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

7 Map analysis (i)

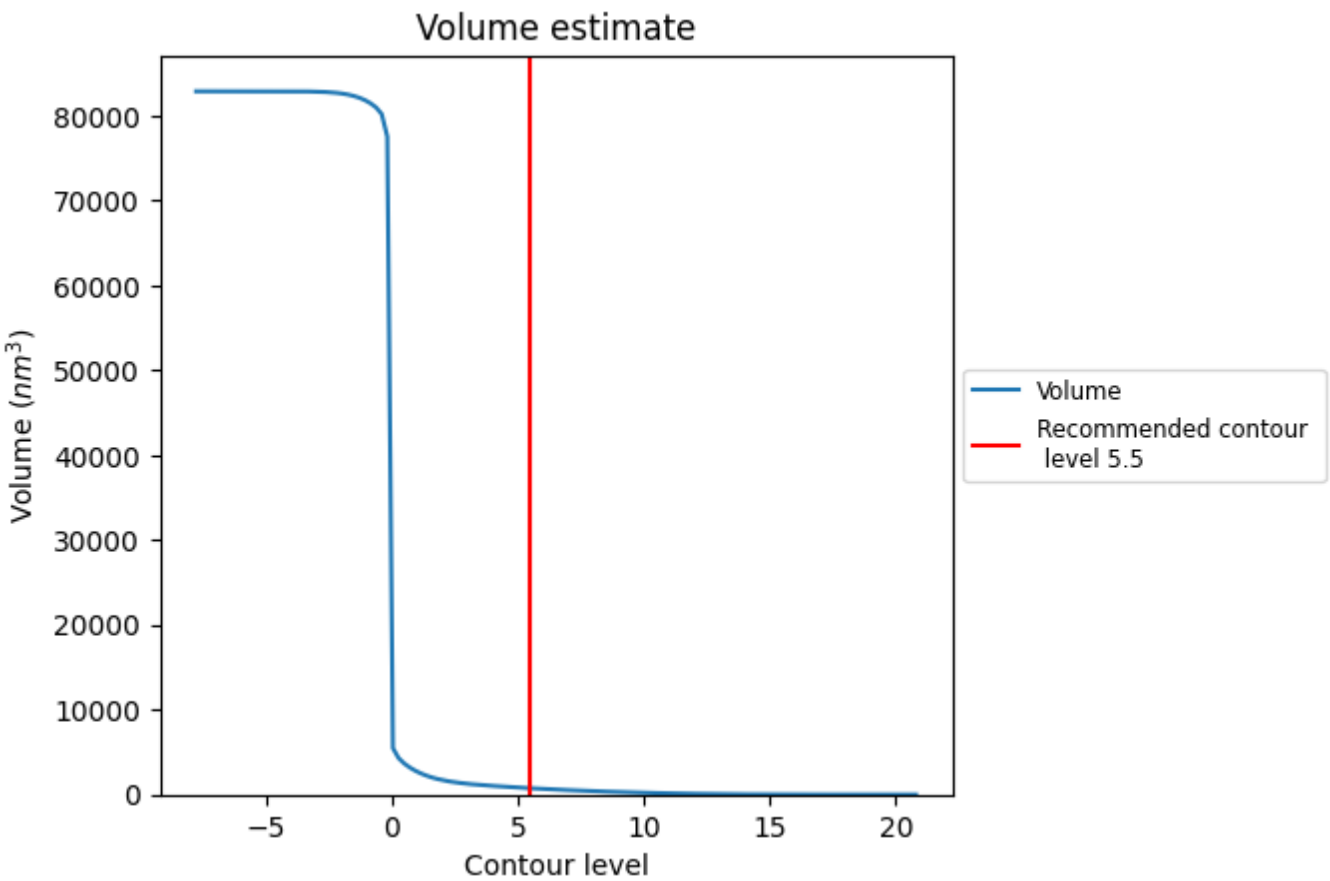
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)



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

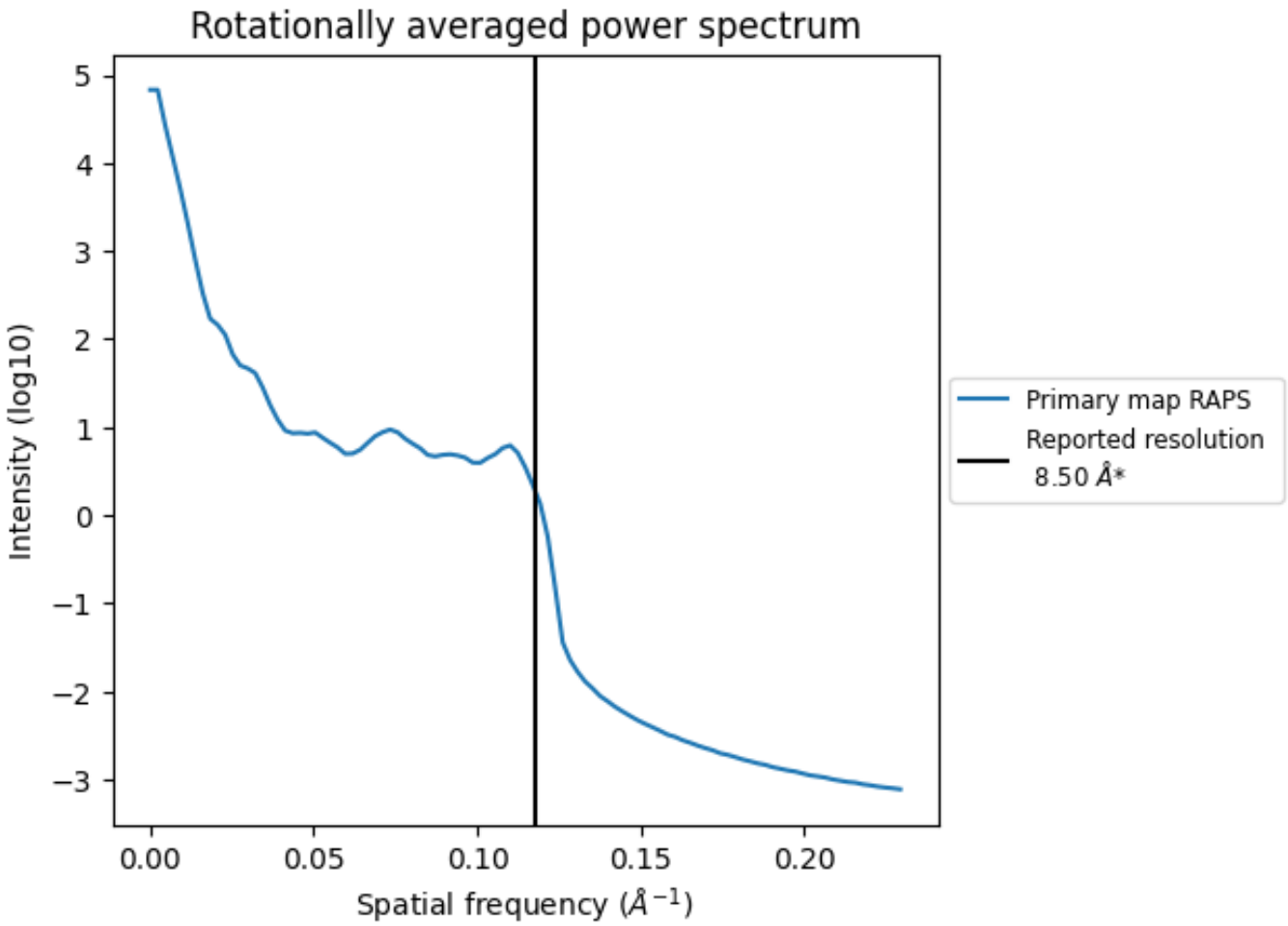
7.2 Volume estimate (i)



The volume at the recommended contour level is 745 nm^3; this corresponds to an approximate mass of 673 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 (i)



*Reported resolution corresponds to spatial frequency of 0.118 Å^{-1}

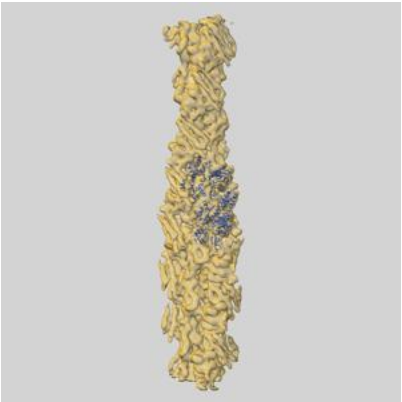
8 Fourier-Shell correlation (i)

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

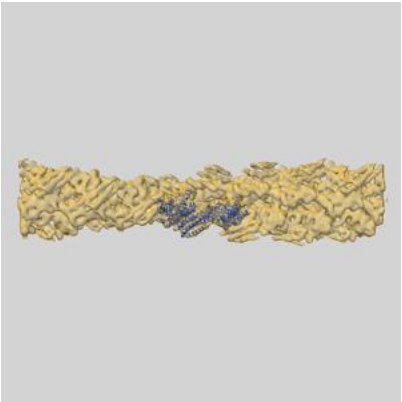
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-6446 and PDB model 3JBI. Per-residue inclusion information can be found in section 3 on page 5.

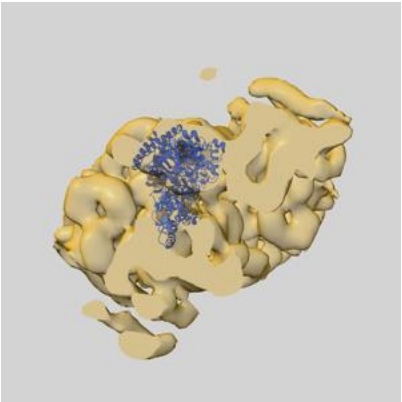
9.1 Map-model overlay (i)



X



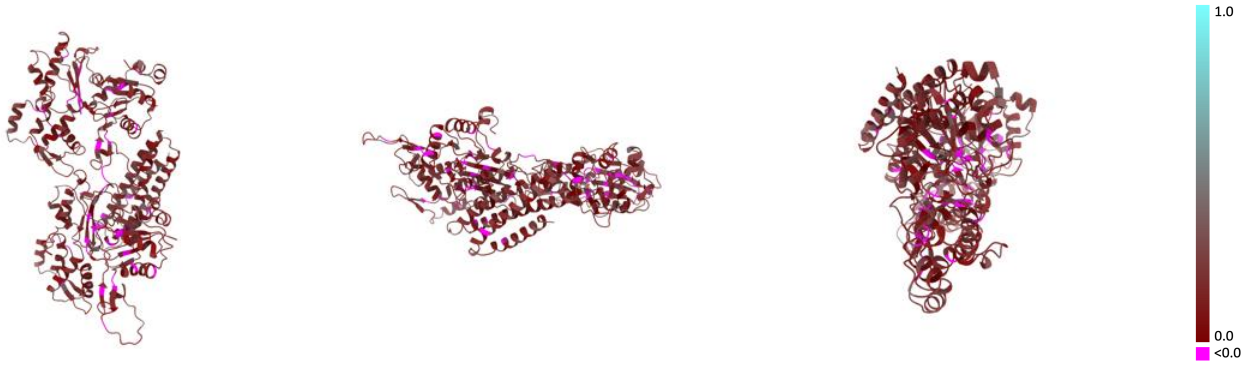
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 5.5 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.

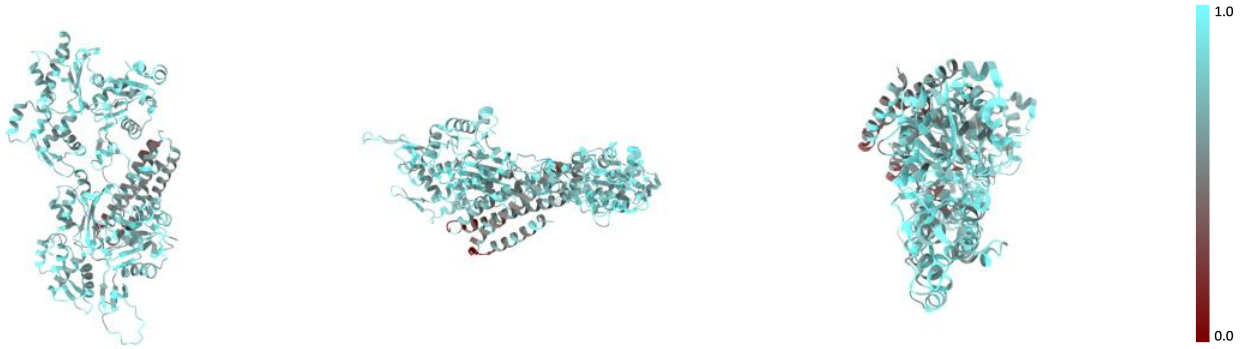
9.2 Q-score mapped to coordinate model (i)



X Y Z

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

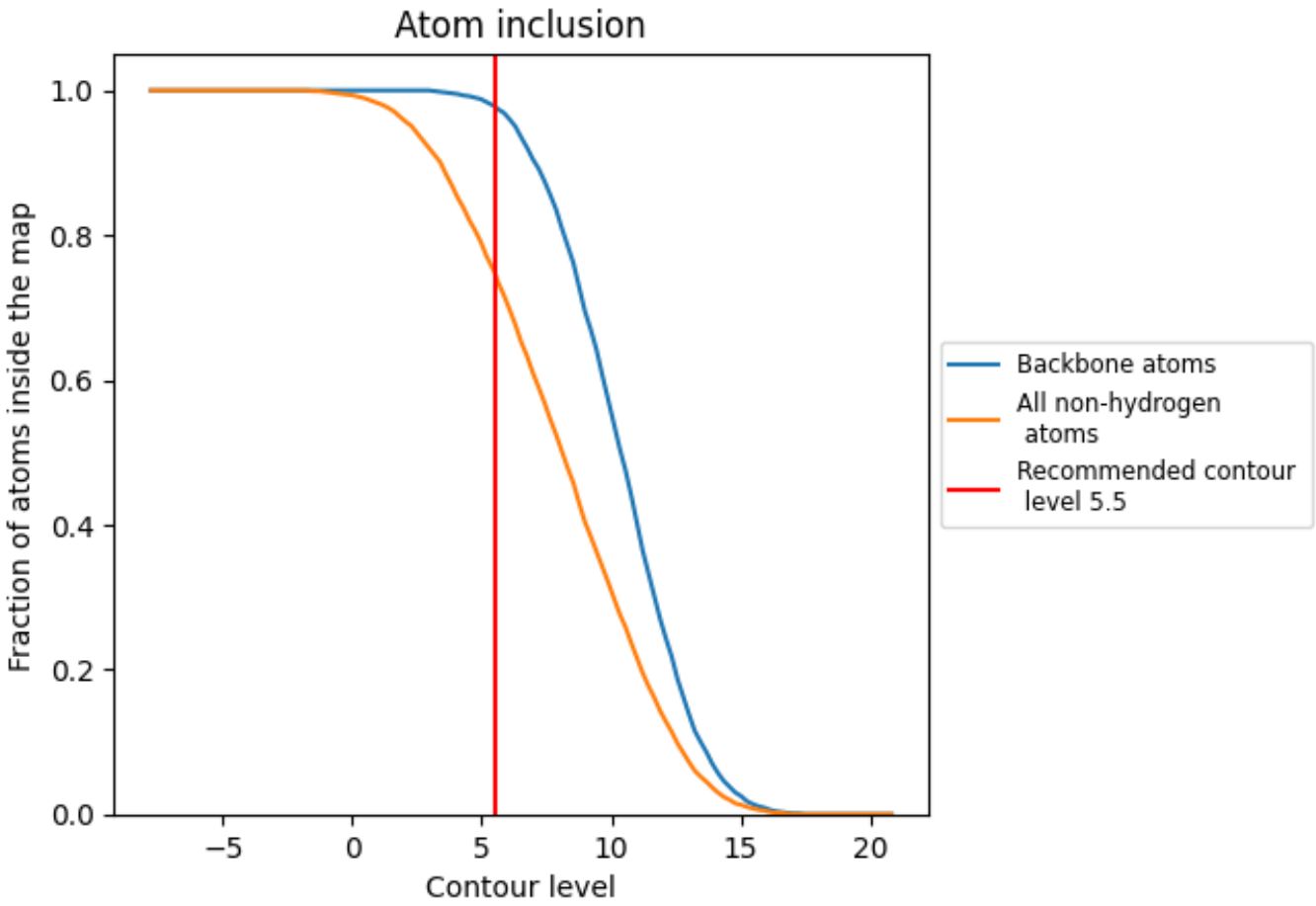
9.3 Atom inclusion mapped to coordinate model (i)



X Y Z

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 (5.5).

9.4 Atom inclusion (i)



At the recommended contour level, 98% of all backbone atoms, 75% of all non-hydrogen atoms, are inside the map.

9.5 Map-model fit summary (i)

The table lists the average atom inclusion at the recommended contour level (5.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.7480	0.1530
A	0.7790	0.1530
B	0.7830	0.1520
V	0.5560	0.1570