Full wwPDB EM Validation Report (i)

Aug 10, 2026 – 01:19 pm BST

PDB ID	:	9RC1 / pdb_00009rc1
EMDB ID	:	EMD-53911
Title	:	Cryo-ET structure of N-terminally truncated membrane-bound EHD2 complex
Authors	:	Vazquez-Sarandeses, E.; Mikirtumov, V.; Noel, J.; Kudryashev, M.; Daumke, O.
Deposited on	:	2025-05-27
Resolution	:	10.10 Å(reported)
Based on initial model	:	4cid

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

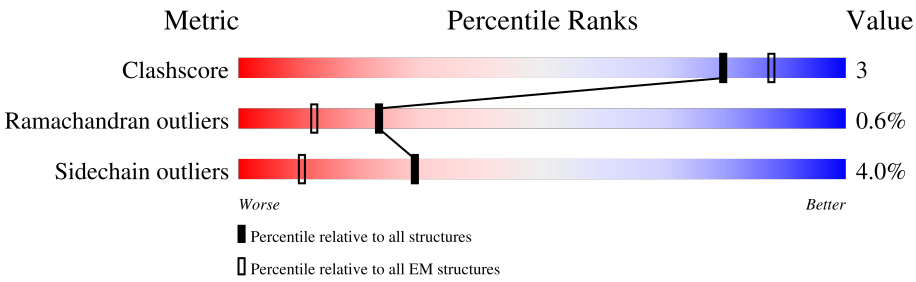
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data 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

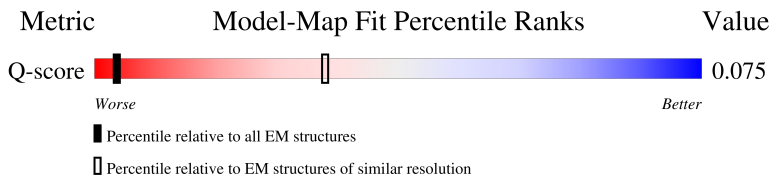
1 Overall quality at a glance (i)

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

The reported resolution of this entry is 10.10 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	127 (9.60 - 10.60)

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	525	46% 83% 9% 7%
1	B	525	44% 83% 9% • 7%
1	C	525	44% 85% 7% • 7%
1	D	525	46% 82% 10% • 7%

2 Entry composition (i)

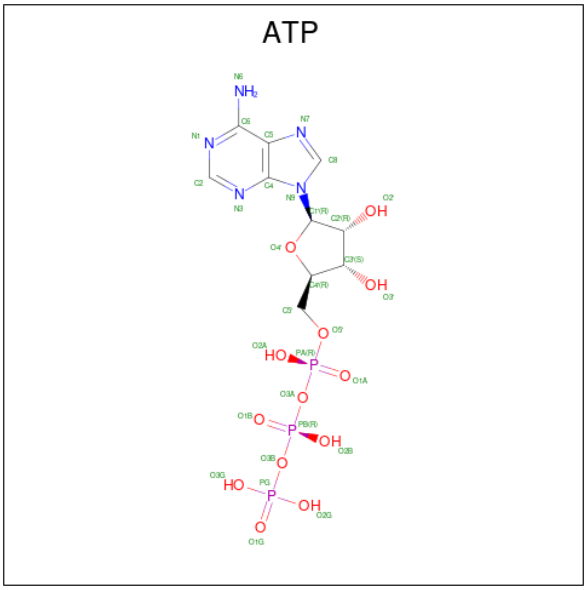
There are 3 unique types of molecules in this entry. The entry contains 15664 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 EH domain-containing protein 2.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	488	3884	2498	667	703	16	0	0
1	B	488	3884	2498	667	703	16	0	0
1	C	488	3884	2498	667	703	16	0	0
1	D	488	3884	2498	667	703	16	0	0

- Molecule 2 is ADENOSINE-5'-TRIPHOSPHATE (CCD ID: ATP) (formula: $C_{10}H_{16}N_5O_{13}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					AltConf
			Total	C	N	O	P	
2	A	1	31	10	5	13	3	0
2	B	1	31	10	5	13	3	0

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

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

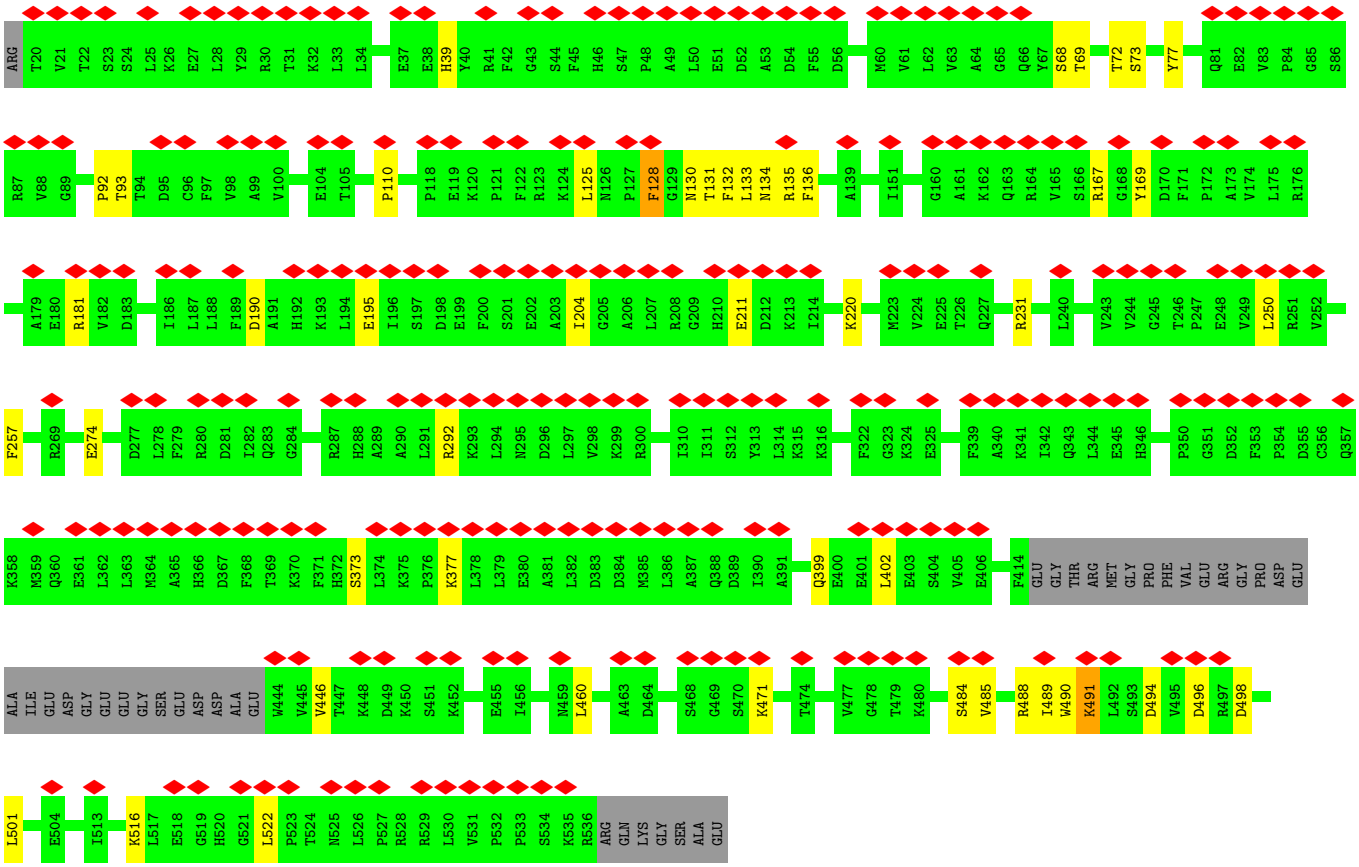
Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
3	A	1	1	1	0
3	B	1	1	1	0
3	C	1	1	1	0
3	D	1	1	1	0

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.

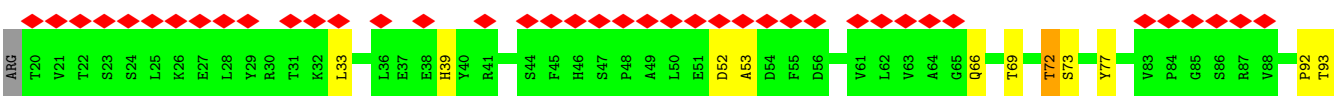
- Molecule 1: EH domain-containing protein 2

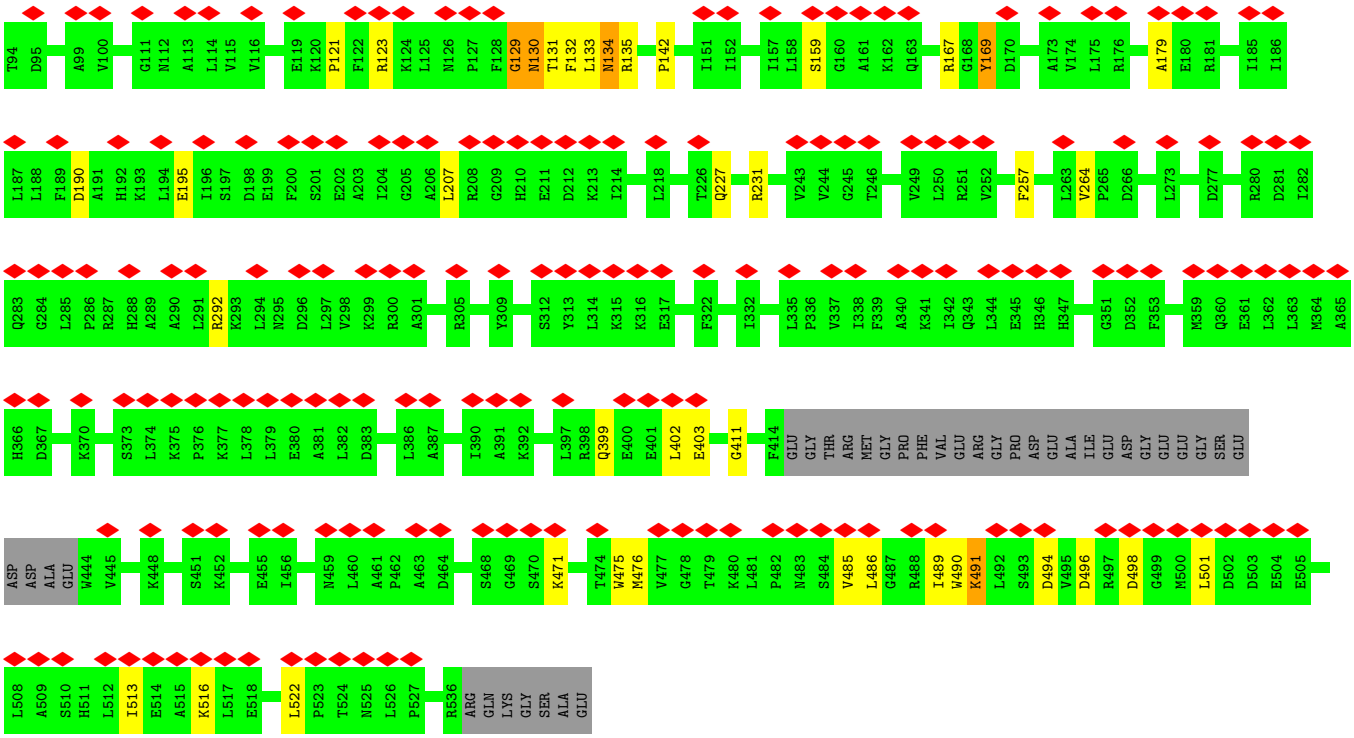
Chain A:



- Molecule 1: EH domain-containing protein 2

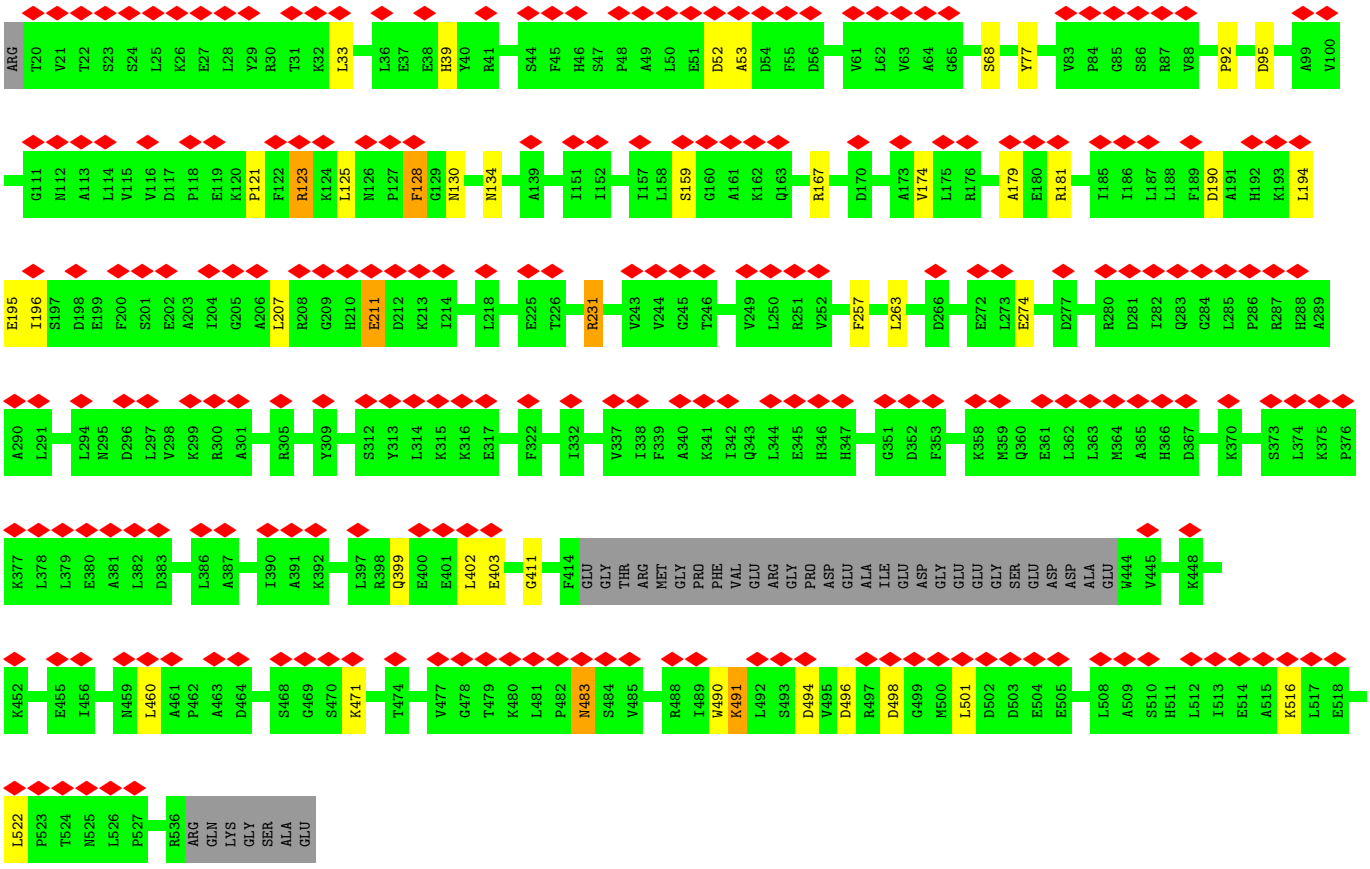
Chain B:





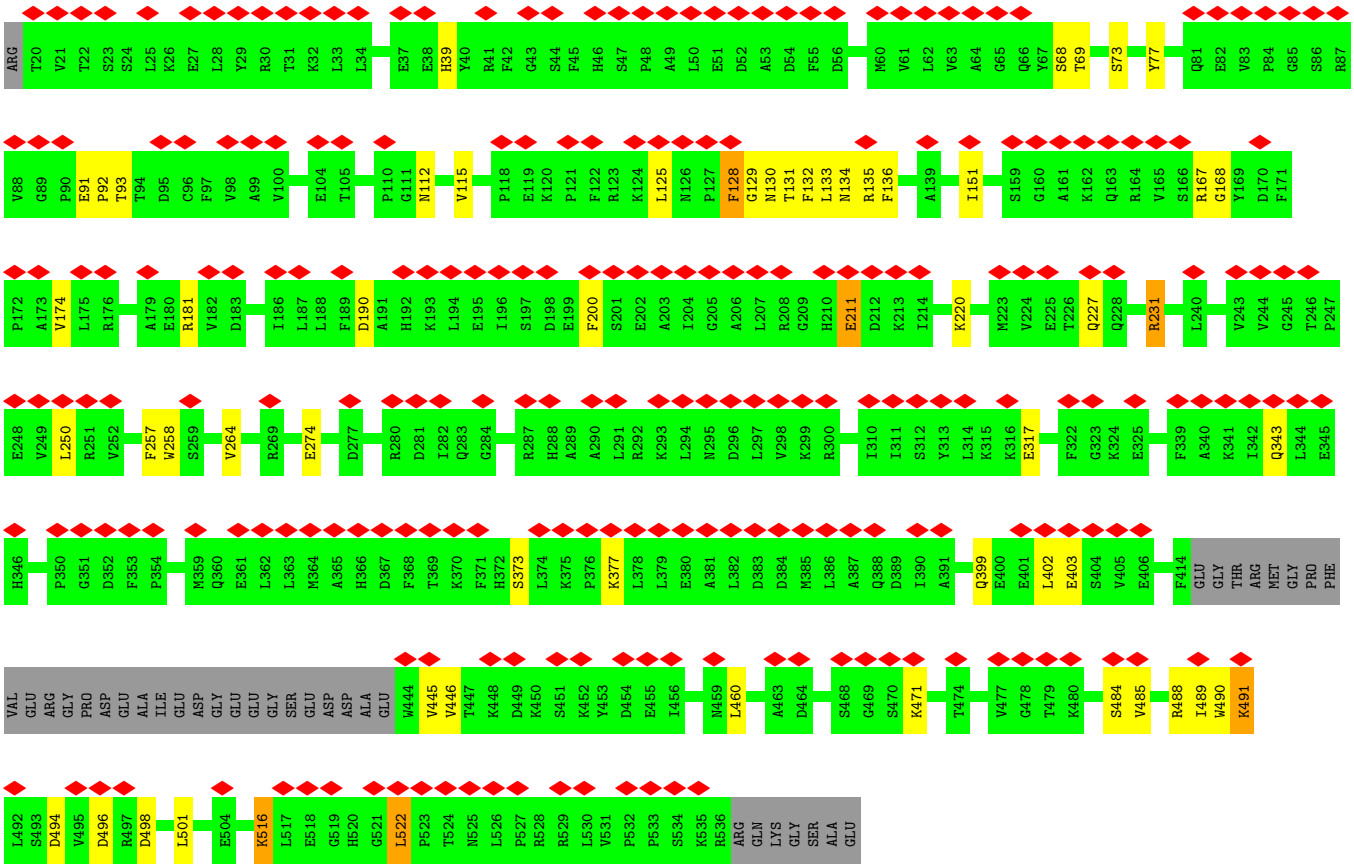
- Molecule 1: EH domain-containing protein 2

Chain C:



- Molecule 1: EH domain-containing protein 2

Chain D:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SUBTOMOGRAM AVERAGING	Depositor
Imposed symmetry	POINT, C2	Depositor
Number of subtomograms used	17204	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 ($e^-/Å^2$)	158	Depositor
Minimum defocus (nm)	2000	Depositor
Maximum defocus (nm)	7000	Depositor
Magnification	42000	Depositor
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.700	Depositor
Minimum map value	-0.376	Depositor
Average map value	0.003	Depositor
Map value standard deviation	0.030	Depositor
Recommended contour level	0.254	Depositor
Map size (Å)	410.496, 410.496, 410.496	wwPDB
Map dimensions	192, 192, 192	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	2.138, 2.138, 2.138	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: ATP, 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	0.89	0/3971	1.41	10/5368 (0.2%)
1	B	0.88	0/3971	1.43	9/5368 (0.2%)
1	C	0.88	0/3971	1.43	9/5368 (0.2%)
1	D	0.89	0/3971	1.42	11/5368 (0.2%)
All	All	0.88	0/15884	1.42	39/21472 (0.2%)

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

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	6
1	C	0	5
1	D	0	4
All	All	0	19

There are no bond length outliers.

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	129	GLY	N-CA-C	10.29	124.78	112.33
1	B	494	ASP	CA-CB-CG	8.30	120.91	112.60
1	C	494	ASP	CA-CB-CG	8.19	120.79	112.60
1	A	494	ASP	CA-CB-CG	8.08	120.68	112.60
1	D	494	ASP	CA-CB-CG	8.00	120.60	112.60
1	B	190	ASP	CA-CB-CG	7.78	120.38	112.60
1	D	190	ASP	CA-CB-CG	7.55	120.15	112.60
1	A	190	ASP	CA-CB-CG	7.30	119.90	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	190	ASP	CA-CB-CG	7.16	119.75	112.60
1	B	498	ASP	CA-CB-CG	6.22	118.83	112.60
1	C	399	GLN	OE1-CD-NE2	-6.07	116.53	122.60
1	A	211	GLU	CA-C-N	6.05	128.99	120.28
1	A	211	GLU	C-N-CA	6.05	128.99	120.28
1	B	39	HIS	CB-CG-CD2	-5.89	123.54	131.20
1	A	39	HIS	CB-CG-CD2	-5.85	123.60	131.20
1	C	496	ASP	CA-CB-CG	5.71	118.31	112.60
1	C	498	ASP	CA-CB-CG	5.70	118.30	112.60
1	D	39	HIS	CB-CG-CD2	-5.66	123.85	131.20
1	A	399	GLN	OE1-CD-NE2	-5.65	116.95	122.60
1	C	39	HIS	CB-CG-CD2	-5.64	123.87	131.20
1	B	399	GLN	OE1-CD-NE2	-5.50	117.10	122.60
1	D	317	GLU	CB-CG-CD	5.44	121.85	112.60
1	D	343	GLN	OE1-CD-NE2	-5.34	117.25	122.60
1	B	496	ASP	CA-CB-CG	5.32	117.92	112.60
1	B	142	PRO	N-CA-CB	5.30	105.89	102.92
1	D	498	ASP	CA-CB-CG	5.29	117.89	112.60
1	D	496	ASP	CA-CB-CG	5.25	117.85	112.60
1	A	496	ASP	CA-CB-CG	5.19	117.79	112.60
1	D	211	GLU	CA-C-N	5.18	127.73	120.28
1	D	211	GLU	C-N-CA	5.18	127.73	120.28
1	B	227	GLN	OE1-CD-NE2	-5.16	117.44	122.60
1	A	110	PRO	CA-C-N	5.16	125.70	119.98
1	A	110	PRO	C-N-CA	5.16	125.70	119.98
1	C	211	GLU	CA-C-N	5.09	128.04	120.31
1	C	211	GLU	C-N-CA	5.09	128.04	120.31
1	A	498	ASP	CA-CB-CG	5.08	117.68	112.60
1	D	227	GLN	OE1-CD-NE2	-5.07	117.53	122.60
1	C	483	ASN	OD1-CG-ND2	-5.06	117.54	122.60
1	D	399	GLN	OE1-CD-NE2	-5.04	117.56	122.60

There are no chirality outliers.

All (19) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	181	ARG	Sidechain
1	A	231	ARG	Sidechain
1	A	257	PHE	Peptide
1	A	77	TYR	Sidechain
1	B	167	ARG	Sidechain
1	B	169	TYR	Sidechain

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Mol	Chain	Res	Type	Group
1	B	257	PHE	Peptide
1	B	292	ARG	Sidechain
1	B	411	GLY	Peptide
1	B	77	TYR	Sidechain
1	C	181	ARG	Sidechain
1	C	231	ARG	Sidechain
1	C	257	PHE	Peptide
1	C	411	GLY	Peptide
1	C	77	TYR	Sidechain
1	D	181	ARG	Sidechain
1	D	231	ARG	Sidechain
1	D	257	PHE	Peptide
1	D	77	TYR	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	3884	0	3948	19	0
1	B	3884	0	3948	23	0
1	C	3884	0	3948	14	0
1	D	3884	0	3948	33	0
2	A	31	0	12	3	0
2	B	31	0	12	2	0
2	C	31	0	12	1	0
2	D	31	0	12	4	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
All	All	15664	0	15840	86	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 3.

All (86) 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:130:ASN:HA	1:B:133:LEU:HB2	1.38	0.99
1:A:130:ASN:HA	1:A:133:LEU:HB2	1.63	0.81
1:D:129:GLY:HA3	1:D:133:LEU:HG	1.66	0.76
1:D:125:LEU:HD23	1:D:128:PHE:HE2	1.53	0.74
1:B:133:LEU:C	1:B:135:ARG:H	1.98	0.72
1:C:130:ASN:HB3	1:C:134:ASN:ND2	2.06	0.71
1:D:131:THR:HG21	1:D:168:GLY:HA3	1.76	0.67
1:D:129:GLY:C	1:D:133:LEU:H	2.05	0.65
1:B:130:ASN:O	1:B:134:ASN:N	2.26	0.64
1:D:130:ASN:N	1:D:133:LEU:HB2	2.13	0.64
1:B:485:VAL:O	1:B:489:ILE:HG13	2.00	0.62
1:C:128:PHE:CE1	1:C:174:VAL:HB	2.37	0.60
1:D:125:LEU:HD23	1:D:128:PHE:CE2	2.36	0.60
1:A:134:ASN:C	1:A:136:PHE:H	2.10	0.59
1:D:112:ASN:HA	1:D:133:LEU:HD22	1.85	0.58
1:B:53:ALA:HB1	1:B:121:PRO:HA	1.86	0.58
1:D:125:LEU:HA	1:D:128:PHE:CE2	2.40	0.57
1:B:133:LEU:C	1:B:135:ARG:N	2.63	0.57
1:A:220:LYS:HG2	2:A:601:ATP:C6	2.40	0.56
1:D:134:ASN:C	1:D:136:PHE:H	2.13	0.56
1:D:73:SER:OG	2:D:601:ATP:O2A	2.21	0.55
1:D:484:SER:O	1:D:488:ARG:HD3	2.07	0.55
1:A:490:TRP:CZ3	1:A:501:LEU:HG	2.42	0.54
1:C:491:LYS:HA	1:C:491:LYS:HE3	1.88	0.54
1:A:73:SER:OG	2:A:601:ATP:O2A	2.22	0.54
1:D:485:VAL:HG22	1:D:488:ARG:NH2	2.23	0.53
1:D:220:LYS:HG2	2:D:601:ATP:C6	2.42	0.53
1:A:130:ASN:O	1:A:131:THR:C	2.51	0.53
1:B:73:SER:OG	2:B:601:ATP:O2A	2.21	0.53
1:D:115:VAL:HG21	1:D:133:LEU:HD21	1.91	0.53
1:D:129:GLY:CA	1:D:133:LEU:HG	2.35	0.52
1:B:490:TRP:CH2	1:B:501:LEU:HG	2.44	0.52
1:D:485:VAL:O	1:D:489:ILE:HG13	2.09	0.52
1:D:491:LYS:HA	1:D:491:LYS:HE3	1.91	0.52
1:A:134:ASN:O	1:A:136:PHE:N	2.41	0.52
1:C:130:ASN:HB3	1:C:134:ASN:HD22	1.74	0.51
1:B:130:ASN:HA	1:B:133:LEU:CB	2.27	0.51
1:D:68:SER:O	2:D:601:ATP:H5'1	2.11	0.50
1:A:68:SER:O	2:A:601:ATP:H5'1	2.12	0.50
1:D:115:VAL:HG11	1:D:133:LEU:HD21	1.93	0.50
1:C:53:ALA:HB1	1:C:121:PRO:HA	1.94	0.49
1:A:130:ASN:HB2	1:A:134:ASN:OD1	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:491:LYS:HA	1:A:491:LYS:HE3	1.95	0.48
1:B:130:ASN:O	1:B:131:THR:C	2.56	0.48
1:C:52:ASP:HB2	1:C:123:ARG:HH12	1.79	0.48
1:D:490:TRP:CZ3	1:D:501:LEU:HG	2.49	0.46
1:C:179:ALA:HB2	1:C:207:LEU:HD13	1.97	0.46
1:A:131:THR:OG1	1:A:169:TYR:HB3	2.15	0.46
1:B:491:LYS:HE3	1:B:491:LYS:HA	1.98	0.46
1:A:134:ASN:C	1:A:136:PHE:N	2.75	0.45
1:C:68:SER:O	2:C:601:ATP:H5'1	2.16	0.45
1:B:129:GLY:O	1:B:133:LEU:HG	2.17	0.45
1:C:274:GLU:CD	1:D:231:ARG:HH22	2.26	0.44
1:A:484:SER:OG	1:A:488:ARG:NH1	2.50	0.44
1:B:66:GLN:HE22	1:B:195:GLU:HB2	1.82	0.44
1:D:115:VAL:CG2	1:D:133:LEU:HD21	2.47	0.44
1:B:489:ILE:HD13	1:B:513:ILE:HG12	1.99	0.44
1:B:72:THR:OG1	2:B:601:ATP:O2B	2.31	0.43
1:C:490:TRP:CZ3	1:C:501:LEU:HG	2.54	0.43
1:D:130:ASN:CG	1:D:131:THR:H	2.26	0.43
1:B:52:ASP:HB2	1:B:123:ARG:HH12	1.83	0.43
1:B:486:LEU:HA	1:B:489:ILE:HD12	2.00	0.43
1:B:491:LYS:HA	1:B:491:LYS:CE	2.48	0.43
1:D:133:LEU:HA	1:D:133:LEU:HD23	1.60	0.43
1:A:485:VAL:O	1:A:489:ILE:HG13	2.19	0.42
1:B:179:ALA:HB2	1:B:207:LEU:HD13	2.01	0.42
1:D:112:ASN:CG	1:D:133:LEU:HB3	2.45	0.42
1:A:125:LEU:HD23	1:A:128:PHE:CE2	2.55	0.42
1:D:134:ASN:C	1:D:136:PHE:N	2.78	0.42
1:A:125:LEU:HD22	1:A:132:PHE:CE2	2.55	0.42
1:C:490:TRP:CD1	1:C:490:TRP:C	2.97	0.42
1:D:258:TRP:HB2	2:D:601:ATP:N6	2.34	0.41
1:A:128:PHE:H	1:A:128:PHE:HD2	1.68	0.41
1:C:130:ASN:HB3	1:C:134:ASN:HD21	1.83	0.41
1:C:231:ARG:HH22	1:D:274:GLU:CD	2.28	0.41
1:B:475:TRP:CE3	1:B:476:MET:HG3	2.56	0.41
1:D:134:ASN:O	1:D:136:PHE:N	2.48	0.41
1:B:132:PHE:HB2	1:B:169:TYR:CD2	2.55	0.41
1:D:115:VAL:CG1	1:D:133:LEU:HD21	2.50	0.41
1:D:130:ASN:CG	1:D:131:THR:N	2.78	0.41
1:D:516:LYS:HG2	1:D:522:LEU:HD13	2.02	0.41
1:A:274:GLU:CD	1:B:231:ARG:HH22	2.29	0.40
1:B:130:ASN:CA	1:B:133:LEU:HB2	2.28	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:125:LEU:HD23	1:C:128:PHE:CE2	2.56	0.40
1:A:130:ASN:O	1:A:134:ASN:N	2.40	0.40
1:D:132:PHE:CE1	1:D:174:VAL:HG21	2.56	0.40

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	484/525 (92%)	455 (94%)	25 (5%)	4 (1%)	16	54
1	B	484/525 (92%)	461 (95%)	21 (4%)	2 (0%)	30	67
1	C	484/525 (92%)	454 (94%)	28 (6%)	2 (0%)	30	67
1	D	484/525 (92%)	455 (94%)	26 (5%)	3 (1%)	21	59
All	All	1936/2100 (92%)	1825 (94%)	100 (5%)	11 (1%)	23	59

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	128	PHE
1	C	128	PHE
1	A	135	ARG
1	D	135	ARG
1	B	134	ASN
1	D	92	PRO
1	D	377	LYS
1	A	92	PRO
1	A	377	LYS
1	B	92	PRO
1	C	92	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	423/452 (94%)	407 (96%)	16 (4%)	29	50
1	B	423/452 (94%)	410 (97%)	13 (3%)	35	56
1	C	423/452 (94%)	405 (96%)	18 (4%)	26	47
1	D	423/452 (94%)	403 (95%)	20 (5%)	23	45
All	All	1692/1808 (94%)	1625 (96%)	67 (4%)	29	49

All (67) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	THR
1	A	72	THR
1	A	93	THR
1	A	167	ARG
1	A	195	GLU
1	A	204	ILE
1	A	250	LEU
1	A	292	ARG
1	A	373	SER
1	A	402	LEU
1	A	446	VAL
1	A	460	LEU
1	A	471	LYS
1	A	491	LYS
1	A	516	LYS
1	A	522	LEU
1	B	33	LEU
1	B	69	THR
1	B	72	THR
1	B	93	THR
1	B	130	ASN
1	B	159	SER
1	B	264	VAL
1	B	402	LEU

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Mol	Chain	Res	Type
1	B	403	GLU
1	B	471	LYS
1	B	491	LYS
1	B	516	LYS
1	B	522	LEU
1	C	33	LEU
1	C	95	ASP
1	C	123	ARG
1	C	159	SER
1	C	167	ARG
1	C	194	LEU
1	C	195	GLU
1	C	196	ILE
1	C	211	GLU
1	C	263	LEU
1	C	402	LEU
1	C	403	GLU
1	C	460	LEU
1	C	471	LYS
1	C	483	ASN
1	C	491	LYS
1	C	516	LYS
1	C	522	LEU
1	D	69	THR
1	D	91	GLU
1	D	93	THR
1	D	128	PHE
1	D	151	ILE
1	D	167	ARG
1	D	200	PHE
1	D	211	GLU
1	D	250	LEU
1	D	264	VAL
1	D	373	SER
1	D	402	LEU
1	D	403	GLU
1	D	445	VAL
1	D	446	VAL
1	D	460	LEU
1	D	471	LYS
1	D	491	LYS
1	D	516	LYS

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Mol	Chain	Res	Type
1	D	522	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	39	HIS
1	A	210	HIS
1	A	366	HIS
1	A	399	GLN
1	B	66	GLN
1	B	81	GLN
1	B	130	ASN
1	B	143	ASN
1	B	192	HIS
1	B	288	HIS
1	B	399	GLN
1	C	39	HIS
1	C	126	ASN
1	C	134	ASN
1	C	143	ASN
1	C	295	ASN
1	C	399	GLN
1	C	410	GLN
1	D	39	HIS
1	D	112	ASN
1	D	144	GLN
1	D	192	HIS
1	D	260	GLN
1	D	399	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	$\#\|Z\| > 2$
2	ATP	D	601	3	29,33,33	1.72	7 (24%)	44,52,52	1.99	11 (25%)
2	ATP	C	601	3	29,33,33	1.66	7 (24%)	44,52,52	1.94	9 (20%)
2	ATP	A	601	3	29,33,33	1.45	6 (20%)	44,52,52	2.05	11 (25%)
2	ATP	B	601	3	29,33,33	1.51	5 (17%)	44,52,52	2.10	13 (29%)

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
2	ATP	D	601	3	-	0/22/38/38	0/3/3/3
2	ATP	C	601	3	-	2/22/38/38	0/3/3/3
2	ATP	A	601	3	-	1/22/38/38	0/3/3/3
2	ATP	B	601	3	-	0/22/38/38	0/3/3/3

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	ATP	C5-C4	5.00	1.48	1.39
2	B	601	ATP	C5-C4	3.98	1.46	1.39
2	A	601	ATP	C5-C4	3.83	1.46	1.39
2	C	601	ATP	C5-C4	3.69	1.45	1.39
2	B	601	ATP	C8-N7	3.44	1.38	1.31
2	C	601	ATP	C5-N7	-3.40	1.32	1.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	601	ATP	C4-N3	3.14	1.40	1.34
2	D	601	ATP	C8-N7	3.11	1.37	1.31
2	C	601	ATP	C8-N9	-3.10	1.32	1.37
2	D	601	ATP	C5-N7	-2.94	1.33	1.39
2	D	601	ATP	C5-C6	2.77	1.48	1.41
2	C	601	ATP	O3'-C3'	2.62	1.49	1.43
2	B	601	ATP	C5-N7	-2.59	1.34	1.39
2	A	601	ATP	C8-N7	2.58	1.36	1.31
2	B	601	ATP	C5-C6	2.56	1.48	1.41
2	A	601	ATP	C4-N9	-2.56	1.32	1.37
2	C	601	ATP	C4-N9	-2.43	1.32	1.37
2	A	601	ATP	C5-N7	-2.41	1.34	1.39
2	A	601	ATP	C2-N3	2.40	1.38	1.33
2	B	601	ATP	PG-O2G	-2.32	1.45	1.54
2	D	601	ATP	C1'-N9	2.24	1.52	1.46
2	C	601	ATP	C5-C6	2.21	1.47	1.41
2	D	601	ATP	C8-N9	-2.20	1.33	1.37
2	A	601	ATP	C5-C6	2.15	1.47	1.41
2	C	601	ATP	C8-N7	2.13	1.35	1.31

All (44) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	D	601	ATP	C5-C4-N3	-6.65	118.07	126.75
2	A	601	ATP	C5-C4-N3	-6.59	118.16	126.75
2	C	601	ATP	C5-C4-N3	-5.86	119.10	126.75
2	B	601	ATP	C5-C4-N3	-5.72	119.29	126.75
2	B	601	ATP	N3-C4-N9	5.26	135.74	127.08
2	D	601	ATP	N3-C4-N9	5.20	135.65	127.08
2	C	601	ATP	N3-C4-N9	4.99	135.31	127.08
2	A	601	ATP	C2-N3-C4	4.42	122.19	111.75
2	C	601	ATP	PB-O3B-PG	-4.39	117.77	132.83
2	A	601	ATP	N3-C4-N9	4.36	134.26	127.08
2	B	601	ATP	C2-N3-C4	4.22	121.72	111.75
2	B	601	ATP	PB-O3B-PG	-4.12	118.69	132.83
2	A	601	ATP	PB-O3B-PG	-4.06	118.89	132.83
2	B	601	ATP	N3-C2-N1	-4.02	122.32	128.60
2	D	601	ATP	C2-N3-C4	3.86	120.87	111.75
2	B	601	ATP	C4-N9-C8	3.85	109.90	105.73
2	C	601	ATP	C2-N3-C4	3.71	120.52	111.75
2	D	601	ATP	PB-O3B-PG	-3.59	120.50	132.83
2	D	601	ATP	PA-O3A-PB	-3.45	121.00	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	601	ATP	PA-O3A-PB	-3.45	121.00	132.83
2	A	601	ATP	C5-C6-N6	-3.41	116.01	123.43
2	A	601	ATP	PA-O3A-PB	-3.39	121.18	132.83
2	A	601	ATP	N3-C2-N1	-3.37	123.32	128.60
2	B	601	ATP	N9-C8-N7	-3.14	109.62	113.91
2	C	601	ATP	C5-C6-N6	-3.08	116.72	123.43
2	D	601	ATP	C4-C5-N7	-3.03	106.92	110.62
2	B	601	ATP	PA-O3A-PB	-3.01	122.49	132.83
2	C	601	ATP	N6-C6-N1	2.96	124.83	118.35
2	C	601	ATP	N3-C2-N1	-2.85	124.14	128.60
2	B	601	ATP	C5-C6-N6	-2.80	117.34	123.43
2	B	601	ATP	N6-C6-N1	2.70	124.27	118.35
2	D	601	ATP	N3-C2-N1	-2.67	124.42	128.60
2	D	601	ATP	O3G-PG-O2G	2.60	117.57	107.64
2	A	601	ATP	N6-C6-N1	2.48	123.79	118.35
2	A	601	ATP	N9-C8-N7	-2.43	110.59	113.91
2	D	601	ATP	C6-C5-N7	2.40	136.48	132.02
2	A	601	ATP	C4-C5-N7	-2.38	107.72	110.62
2	D	601	ATP	C4-N9-C8	2.35	108.28	105.73
2	A	601	ATP	C5-N7-C8	2.32	106.81	103.51
2	B	601	ATP	C5-N7-C8	2.30	106.78	103.51
2	C	601	ATP	C4-N9-C8	2.25	108.16	105.73
2	D	601	ATP	C5-N7-C8	2.22	106.66	103.51
2	B	601	ATP	O3G-PG-O2G	2.21	116.08	107.64
2	B	601	ATP	O2B-PB-O1B	2.20	123.12	112.24

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	601	ATP	C5'-O5'-PA-O3A
2	A	601	ATP	C5'-O5'-PA-O1A
2	C	601	ATP	C5'-O5'-PA-O1A

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	601	ATP	4	0
2	C	601	ATP	1	0
2	A	601	ATP	3	0

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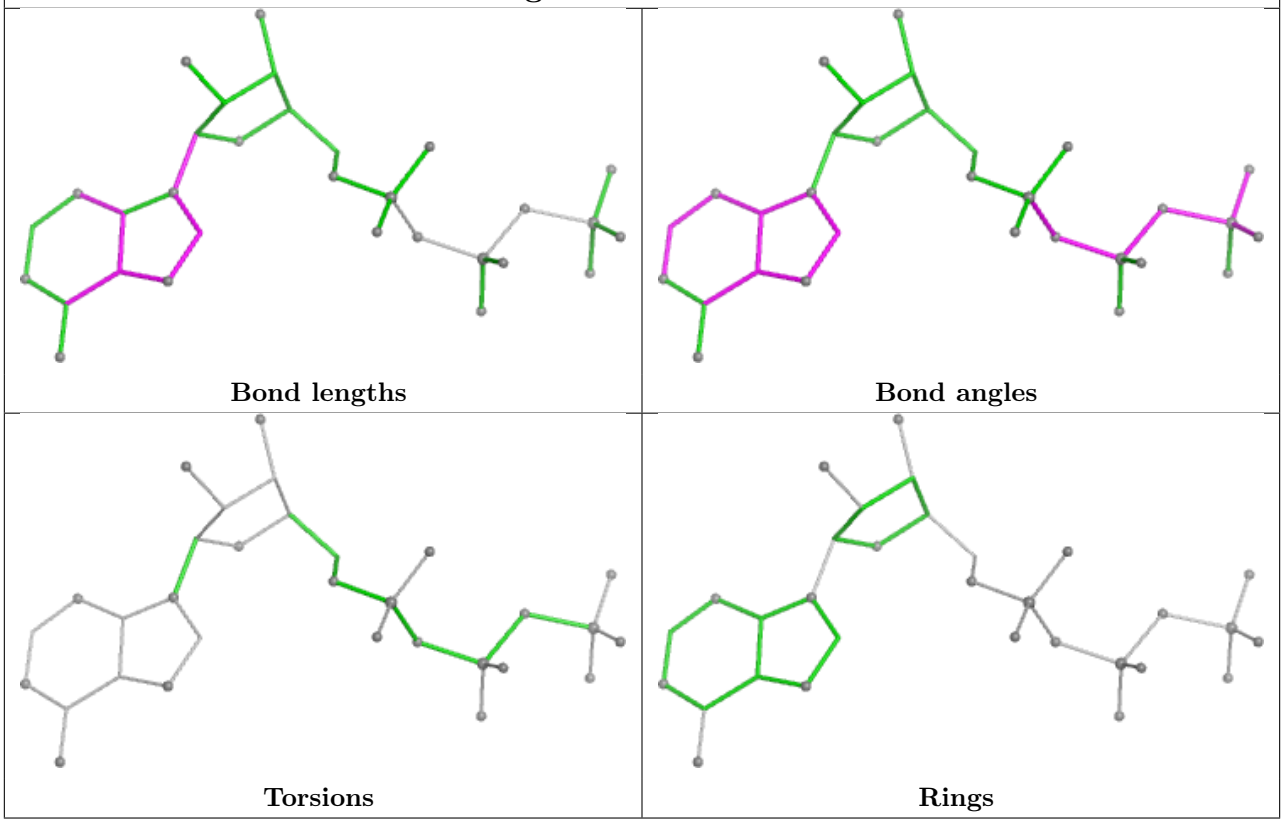
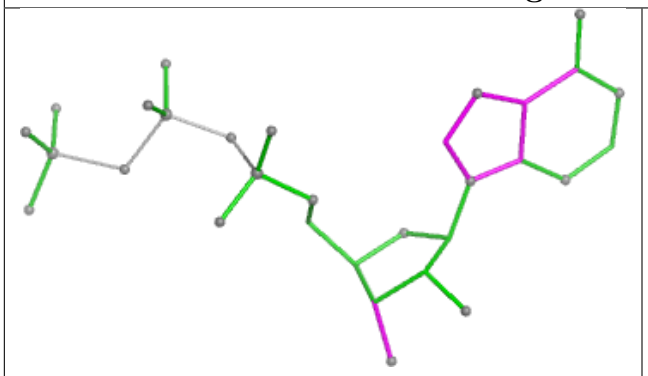
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	601	ATP	2	0

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 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.

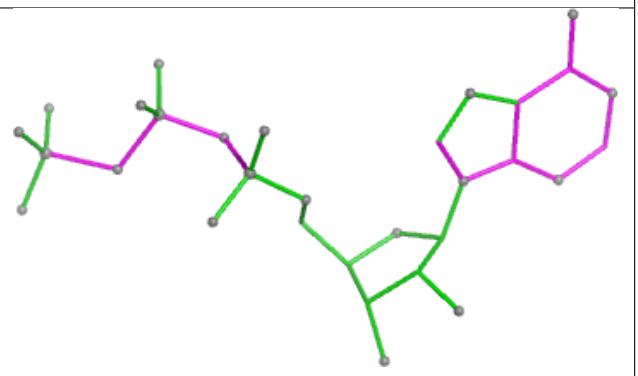
Ligand ATP D 601



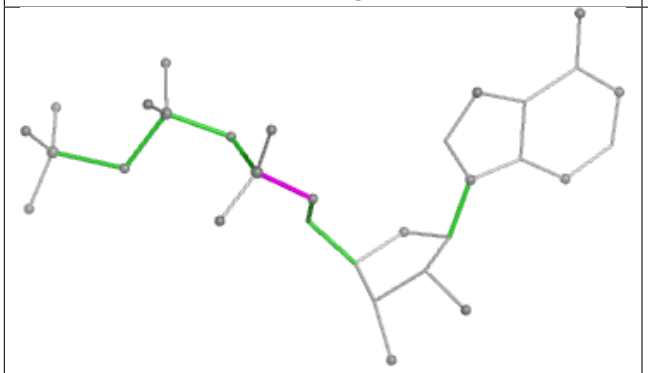
Ligand ATP C 601



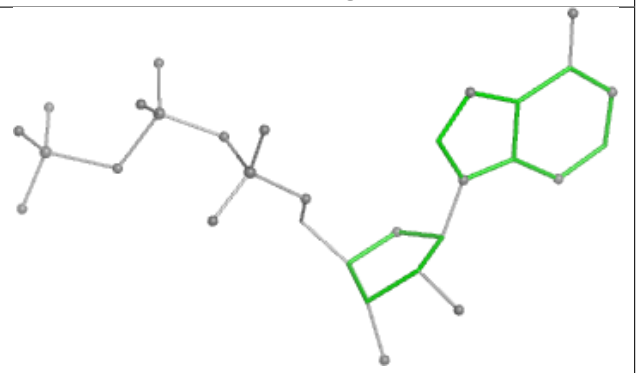
Bond lengths



Bond angles

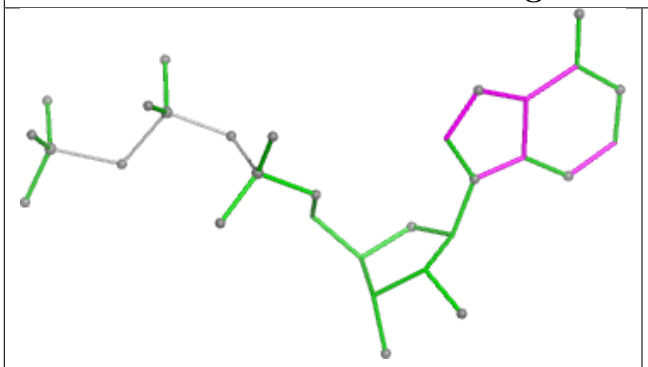


Torsions

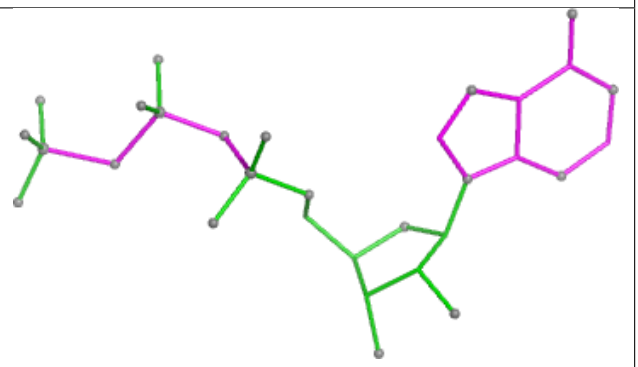


Rings

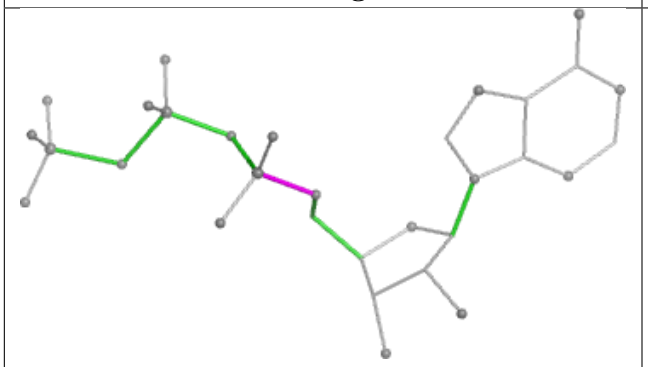
Ligand ATP A 601



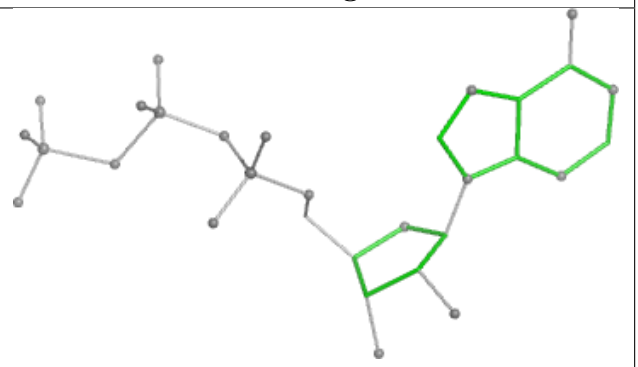
Bond lengths



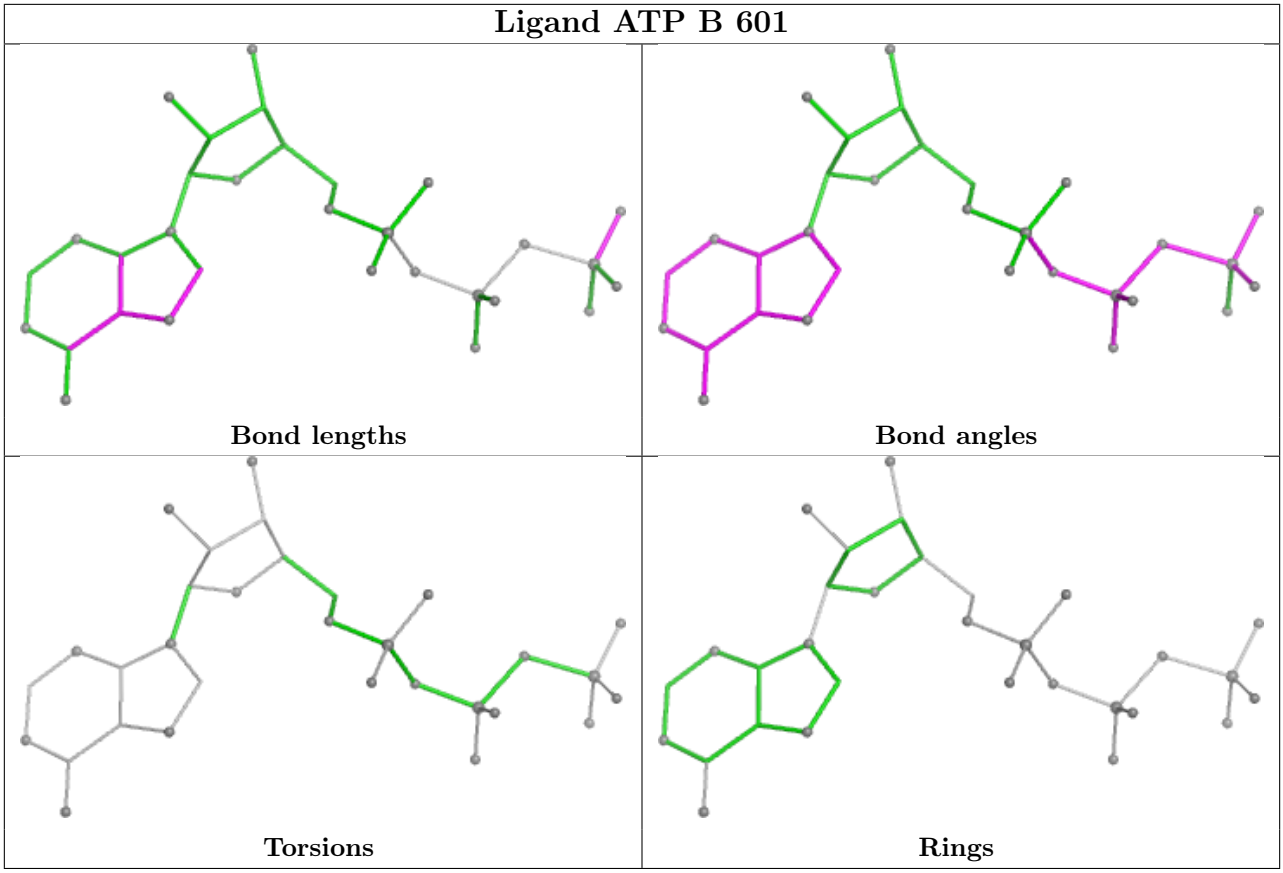
Bond angles



Torsions



Rings



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-53911. 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)

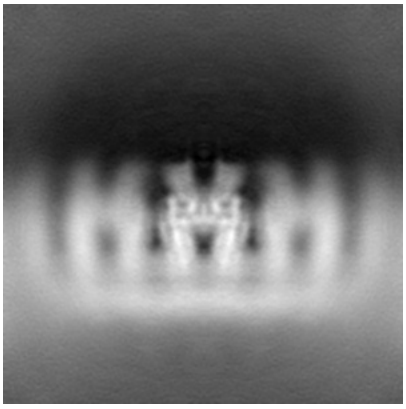
6.1.1 Primary map

X

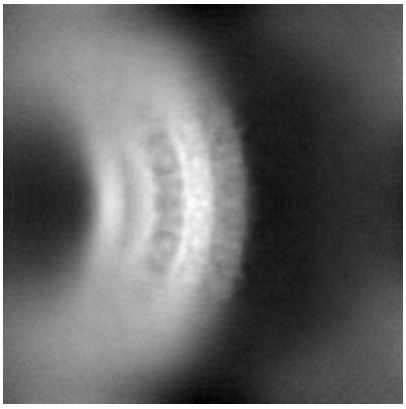
Y

Z

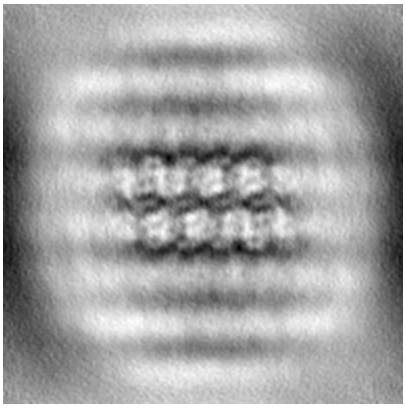
6.1.2 Raw map



X



Y



Z

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

6.2 Central slices (i)

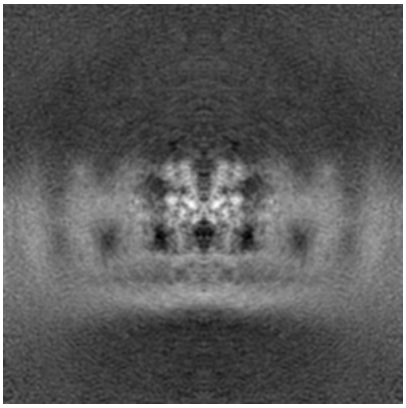
6.2.1 Primary map

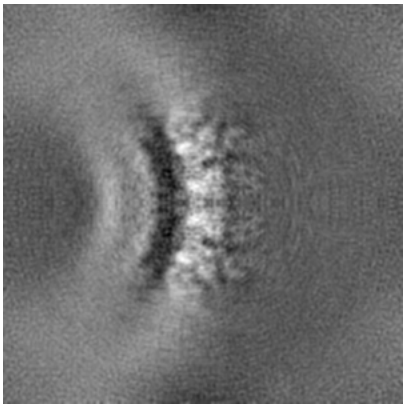
X Index: 96

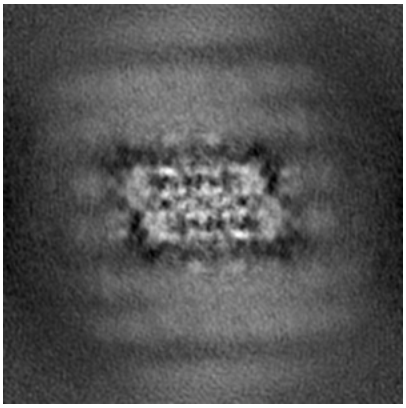
Y Index: 96

Z Index: 96

6.2.2 Raw map


X Index: 96


Y Index: 96

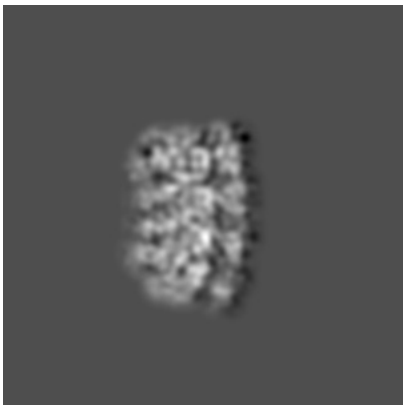

Z Index: 96

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

6.3 Largest variance slices (i)

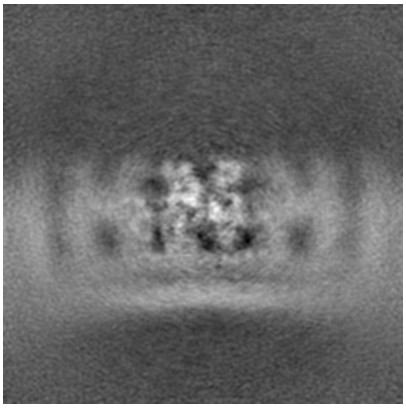
6.3.1 Primary map

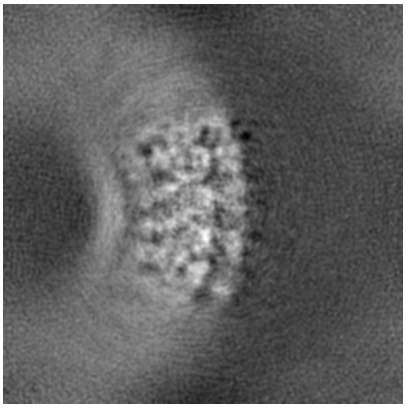
X Index: 76

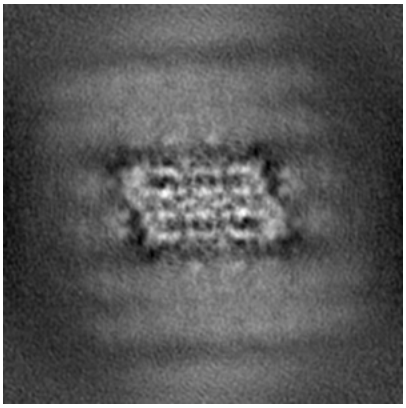

Y Index: 110

Z Index: 96

6.3.2 Raw map


X Index: 94

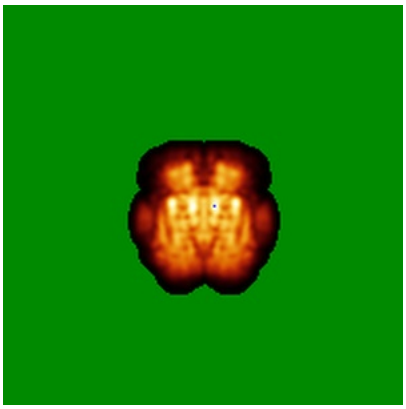

Y Index: 110


Z Index: 95

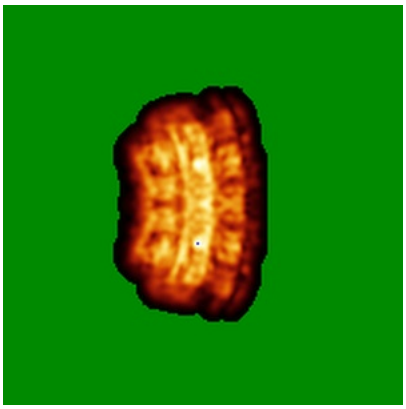
The images above show the largest variance slices of the map in three orthogonal directions.

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

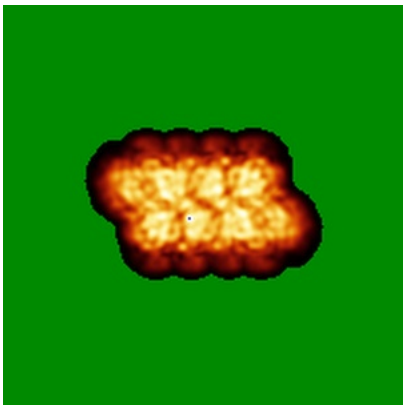
6.4.1 Primary map



X

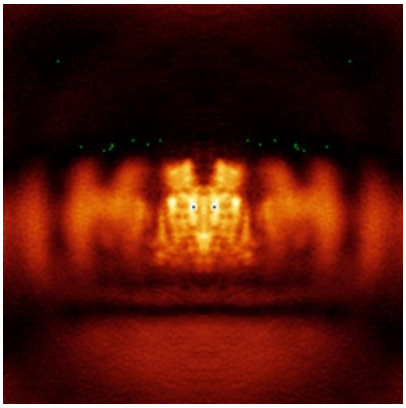


Y

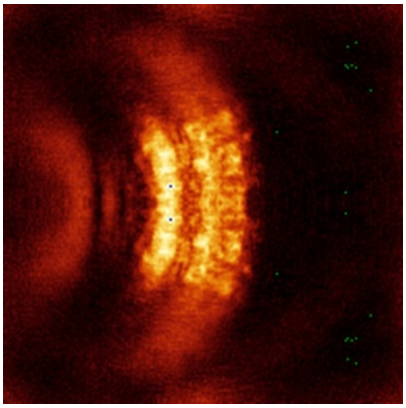


Z

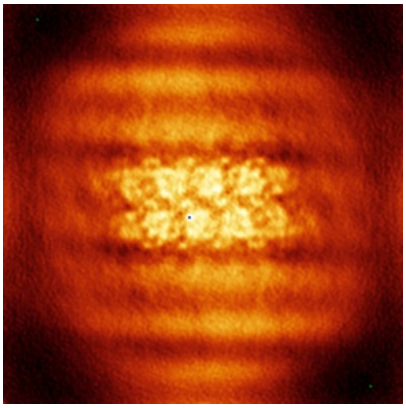
6.4.2 Raw map



X



Y

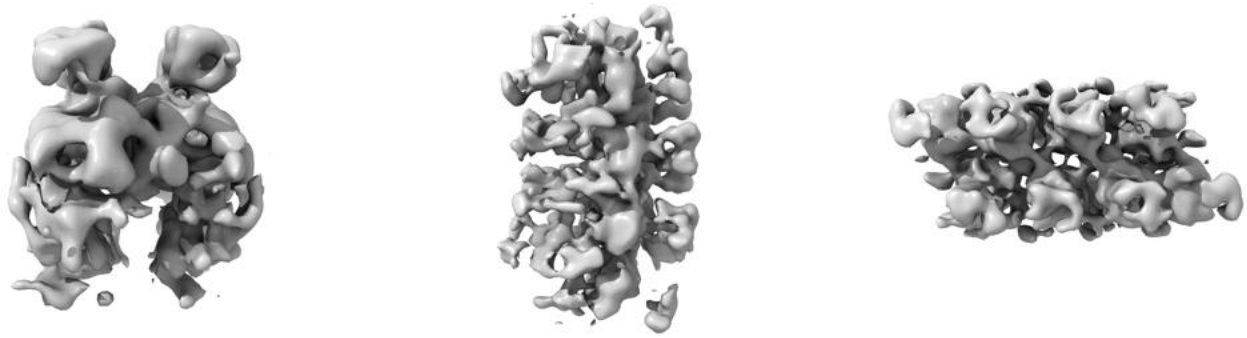


Z

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)

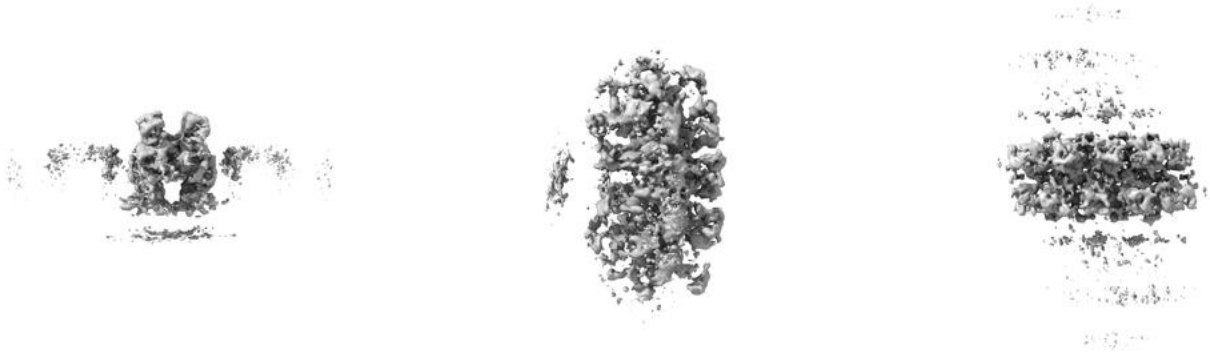
6.5.1 Primary map



X Y Z

The images above show the 3D surface view of the map at the recommended contour level 0.254. 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.

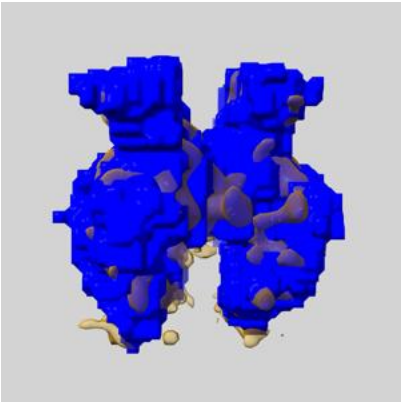
6.6 Mask visualisation (i)

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

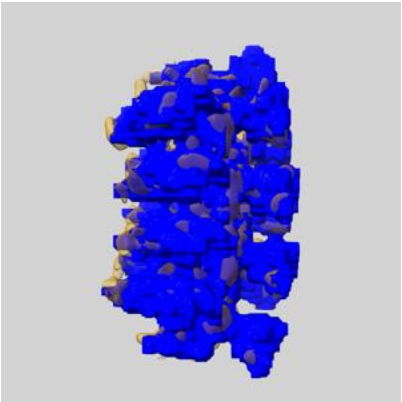
A mask typically either:

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

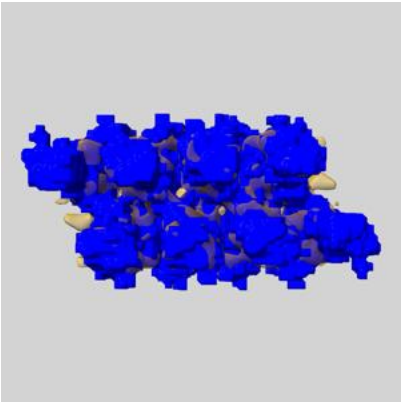
6.6.1 emd_53911_msk_1.map (i)



X



Y

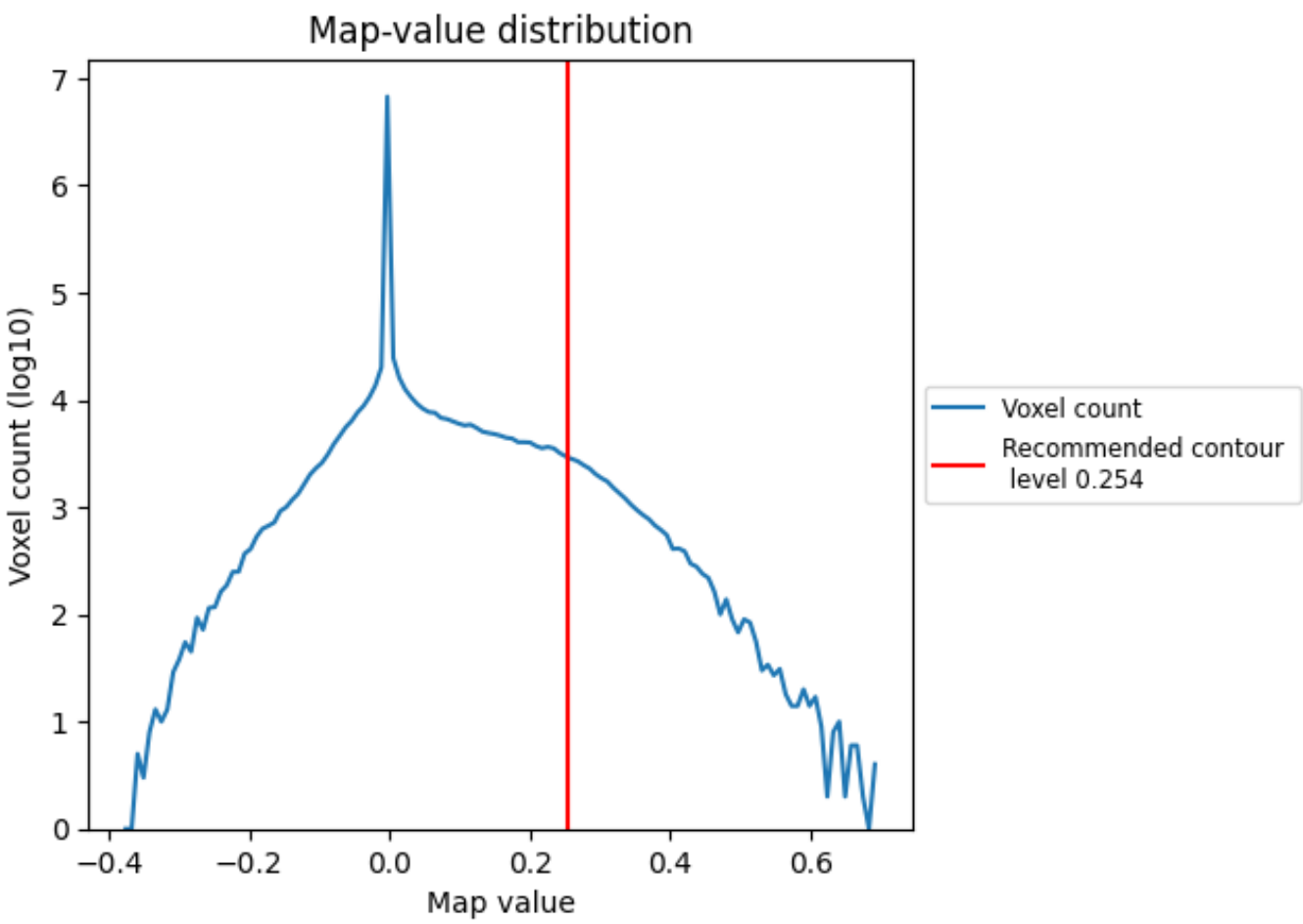


Z

7 Map analysis (i)

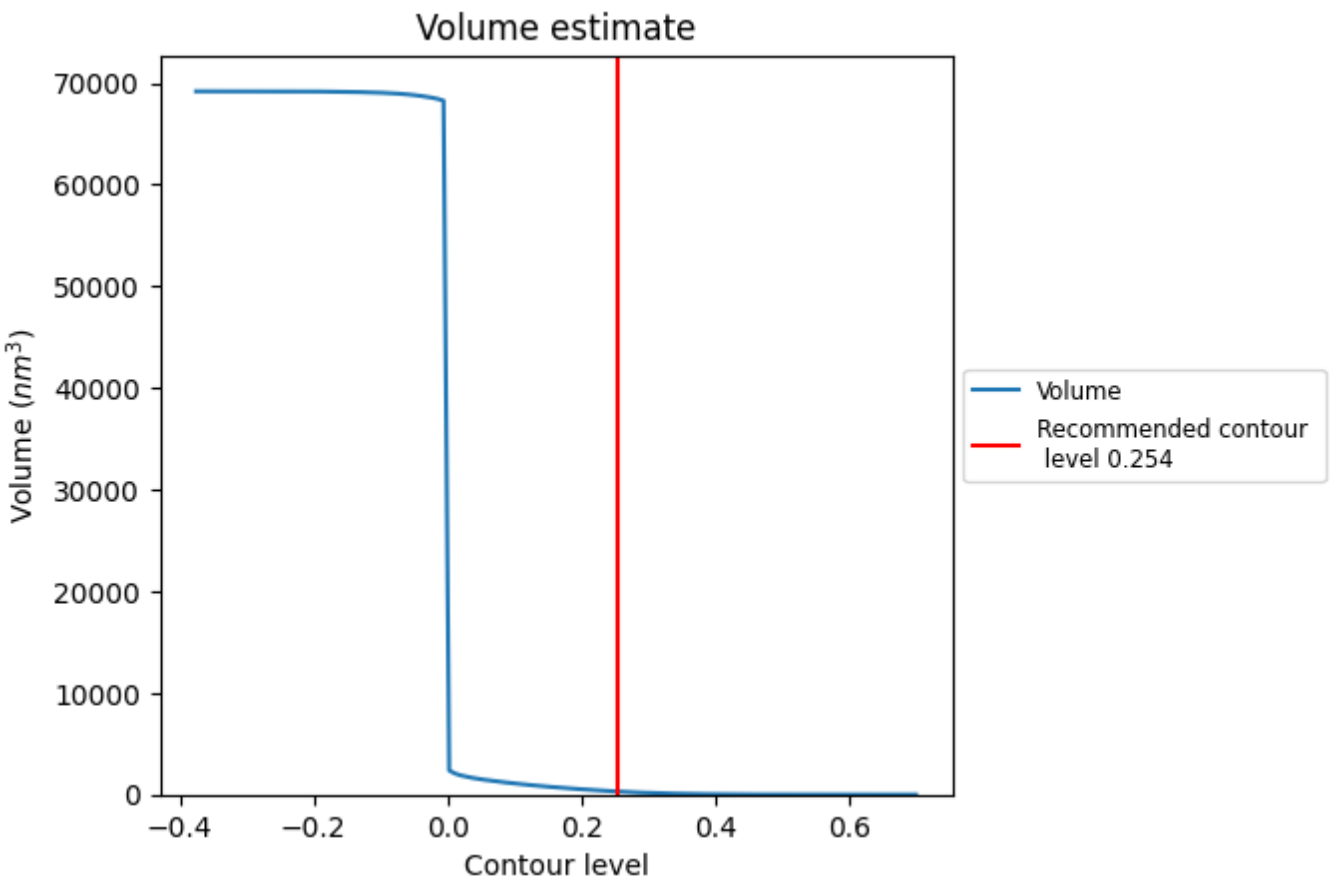
This section contains the results of statistical analysis of the map.

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.

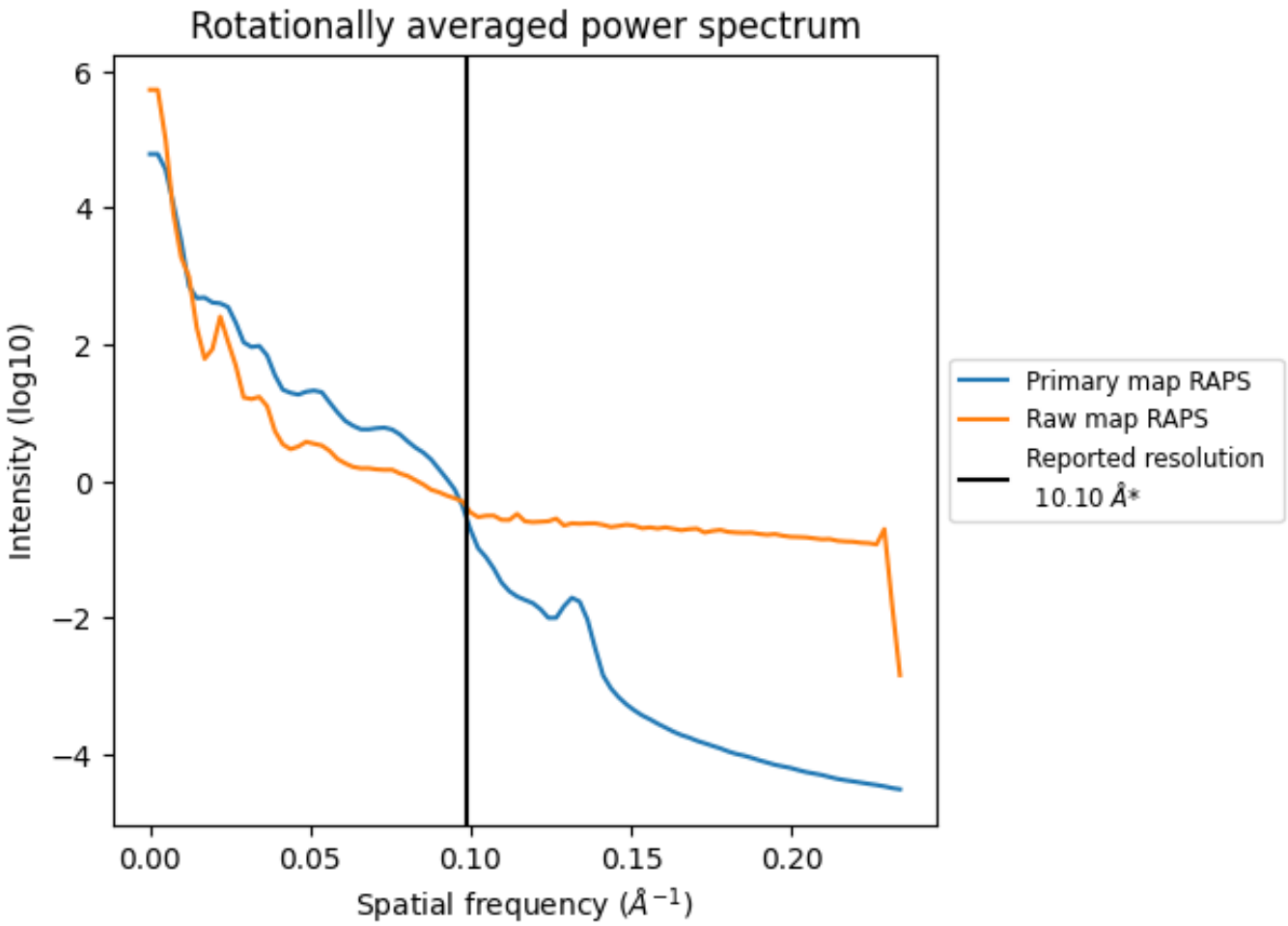
7.2 Volume estimate (i)



The volume at the recommended contour level is 300 nm^3; this corresponds to an approximate mass of 271 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)

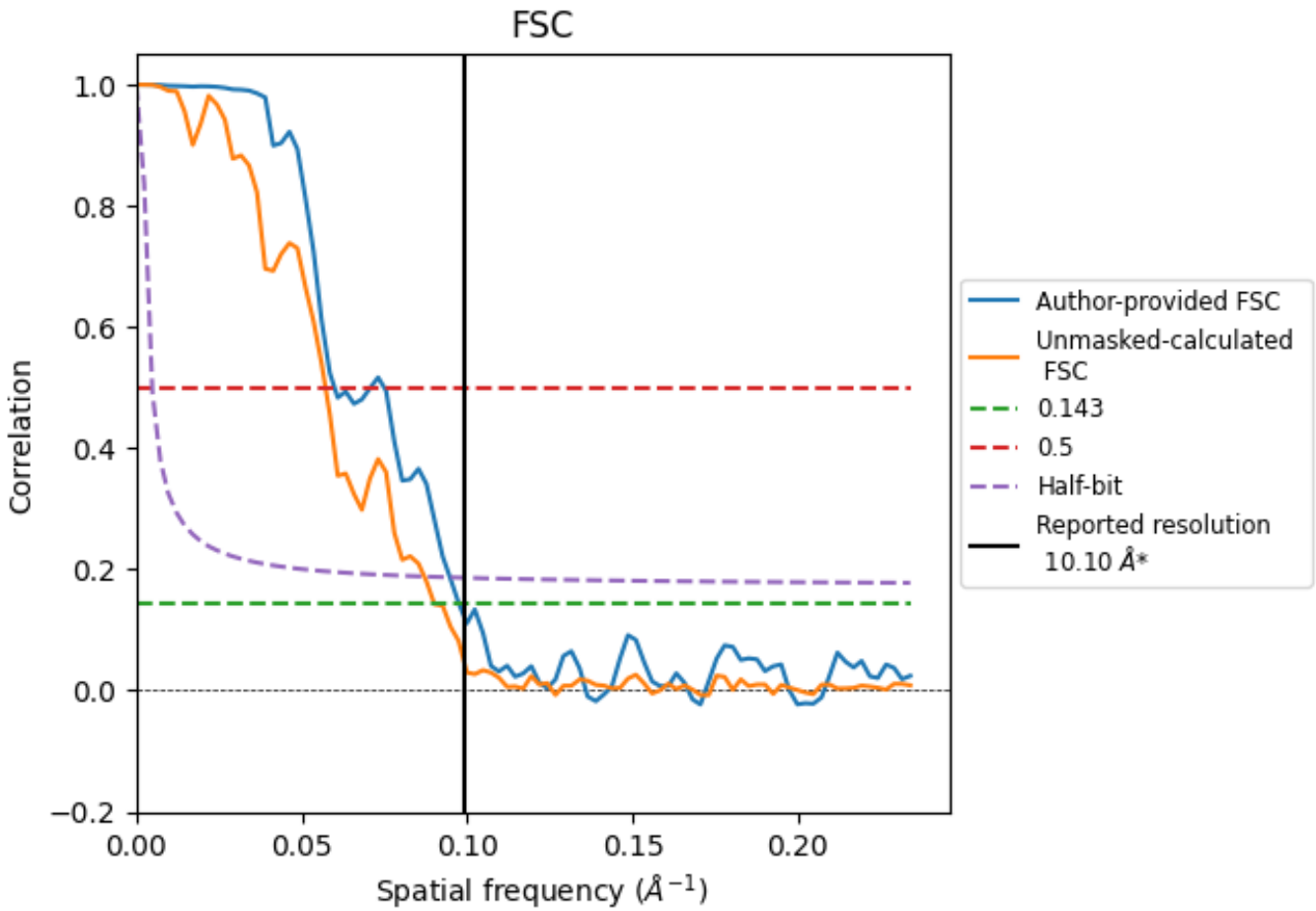


*Reported resolution corresponds to spatial frequency of 0.099 Å^{-1}

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 0.099 Å^{-1}

8.2 Resolution estimates (i)

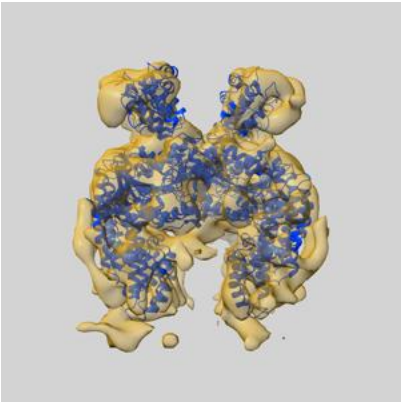
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	10.10	-	-
Author-provided FSC curve	10.25	16.69	10.54
Unmasked-calculated*	11.10	17.48	11.49

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps.

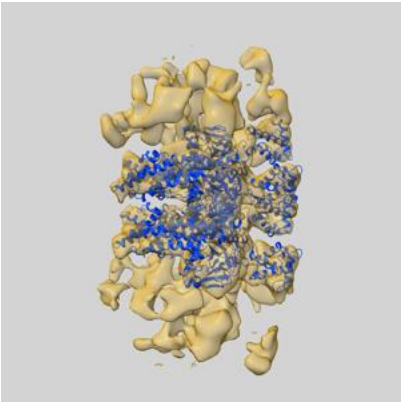
9 Map-model fit (i)

This section contains information regarding the fit between EMDB map EMD-53911 and PDB model 9RC1. Per-residue inclusion information can be found in section 3 on page 5.

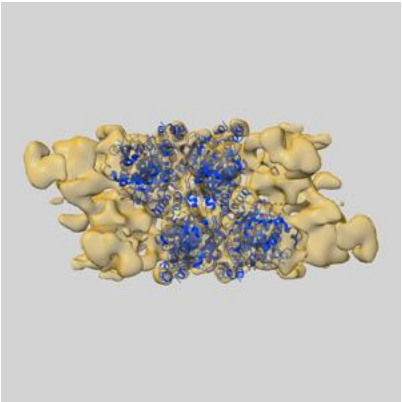
9.1 Map-model overlay (i)



X



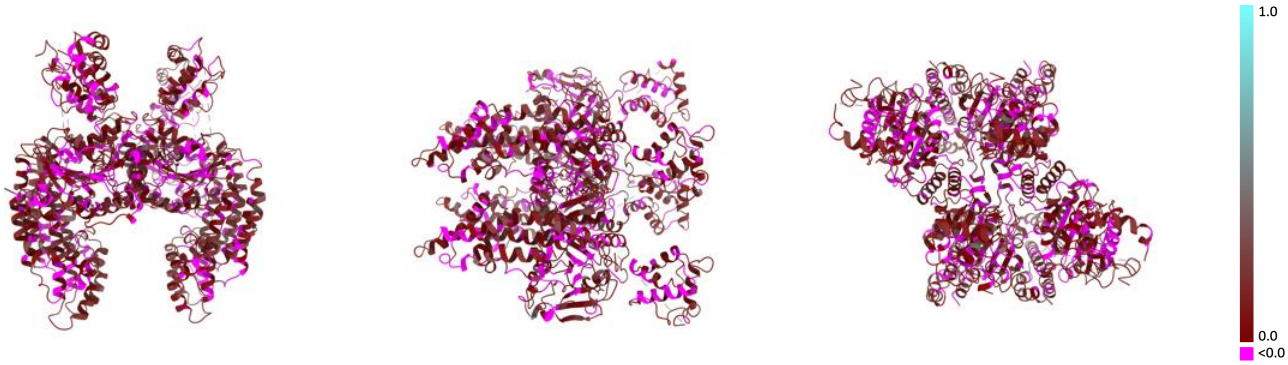
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.254 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.

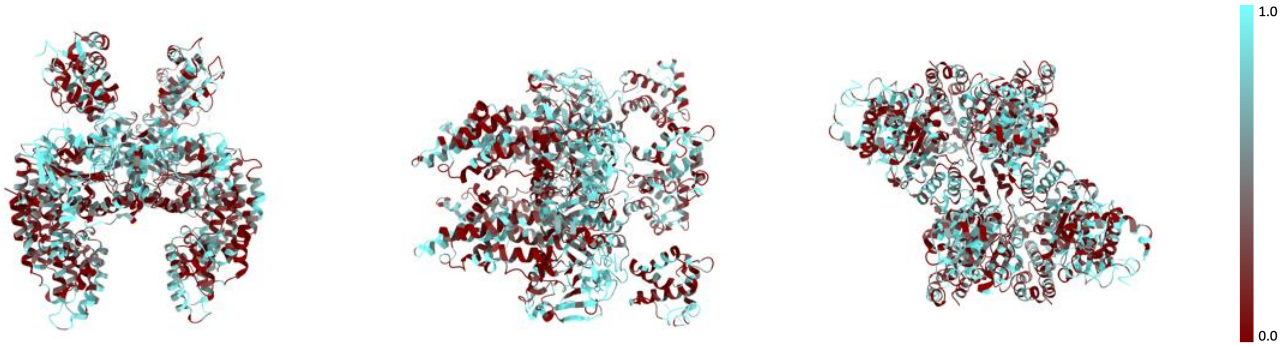
9.2 Q-score mapped to coordinate model (i)



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.

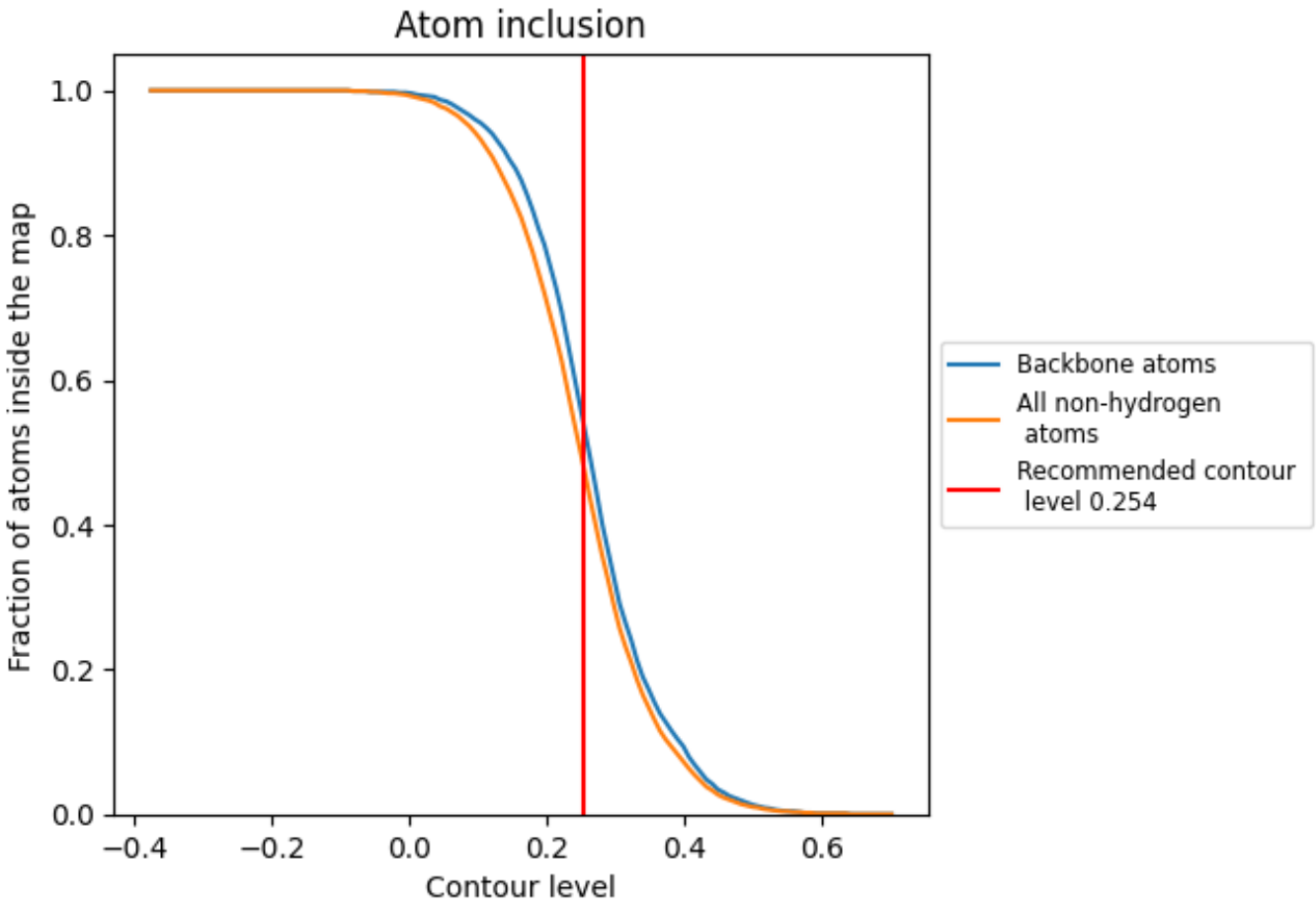
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.254).

9.4 Atom inclusion (i)



At the recommended contour level, 53% of all backbone atoms, 48% 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 (0.254) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.4750	0.0750
A	0.4710	0.0760
B	0.4800	0.0730
C	0.4820	0.0710
D	0.4670	0.0780