Full wwPDB EM Validation Report

Aug 23, 2026 – 03:12 pm BST

PDB ID	:	7OU0 / pdb_00007ou0
EMDB ID	:	EMD-13071
Title	:	The structure of MutS bound to two molecules of ADP-Vanadate
Authors	:	Lamers, M.H.; Borsellini, A.; Friedhoff, P.; Kunetsky, V.
Deposited on	:	2021-06-10
Resolution	:	3.80 Å(reported)
Based on initial model	:	1E3M

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:

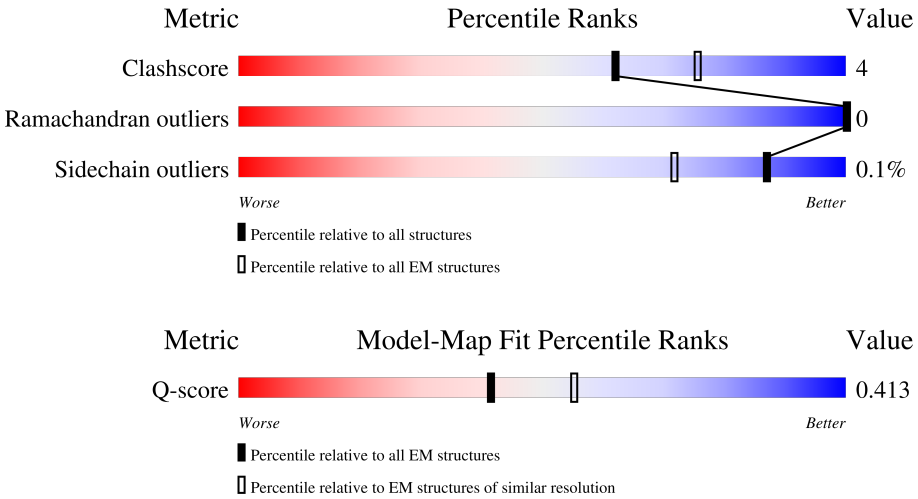
EMDB validation analysis	:	0.0.1.dev133
Mogul	:	1.8.4, CSD as541be (2020)
MolProbity	:	4-5-2 with Phenix2.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
EM percentile statistics	:	202505.v01 (Using data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

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

The reported resolution of this entry is 3.80 Å.

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



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

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=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	806	6% 81% 8% 12%
1	B	806	9% 67% 7% 25%

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
4	VO4	A	901	-	-	X	-
4	VO4	A	904	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 10335 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called DNA mismatch repair protein MutS.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	B	602	Total 4697	C 2947	N 839	O 888	S 23	0	0
1	A	711	Total 5572	C 3505	N 990	O 1049	S 28	0	0

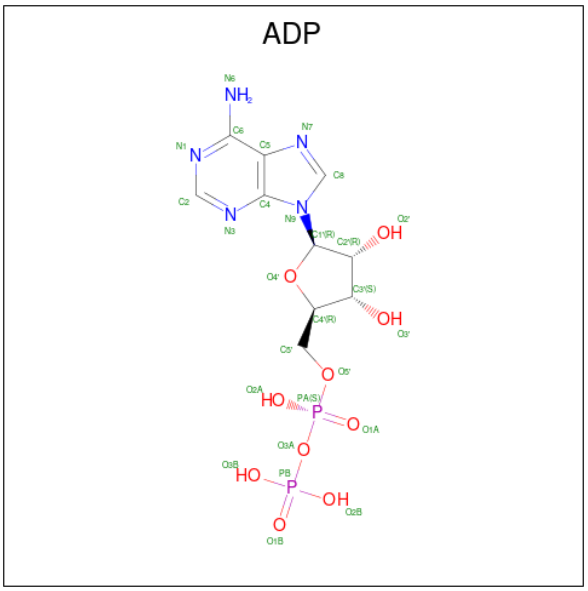
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-5	HIS	-	expression tag	UNP P23909
B	-4	HIS	-	expression tag	UNP P23909
B	-3	HIS	-	expression tag	UNP P23909
B	-2	HIS	-	expression tag	UNP P23909
B	-1	HIS	-	expression tag	UNP P23909
B	0	HIS	-	expression tag	UNP P23909
B	800	SER	-	expression tag	UNP P23909
A	-5	HIS	-	expression tag	UNP P23909
A	-4	HIS	-	expression tag	UNP P23909
A	-3	HIS	-	expression tag	UNP P23909
A	-2	HIS	-	expression tag	UNP P23909
A	-1	HIS	-	expression tag	UNP P23909
A	0	HIS	-	expression tag	UNP P23909
A	800	SER	-	expression tag	UNP P23909

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

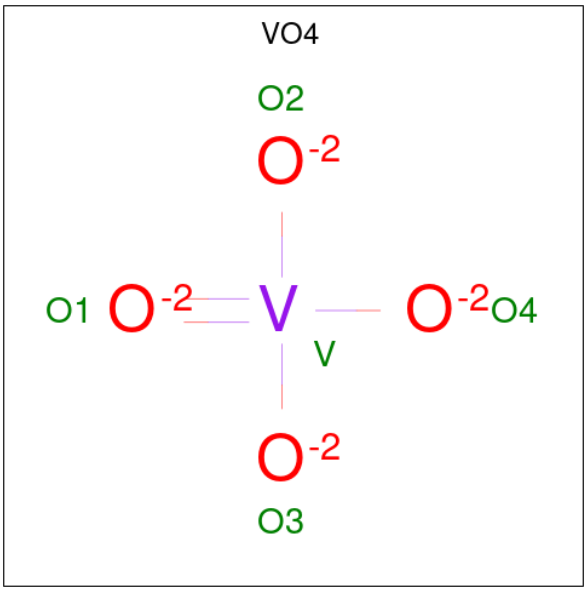
Mol	Chain	Residues	Atoms		AltConf
2	B	1	Total 1	Mg 1	0
2	A	1	Total 1	Mg 1	0

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



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

- Molecule 4 is VANADATE ION (CCD ID: VO4) (formula: O_4V) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			AltConf
4	A	1	Total	O	V	0
			5	4	1	

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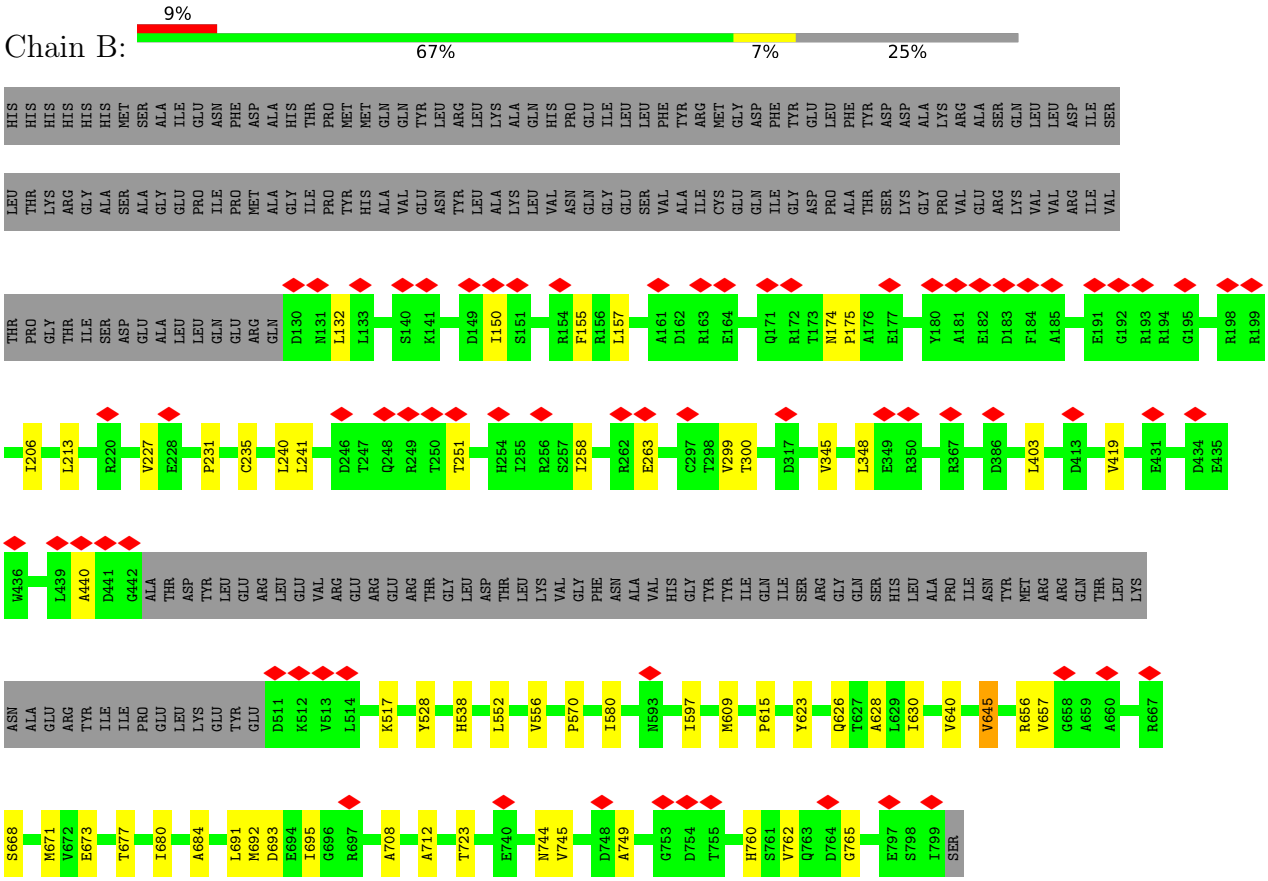
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Mol	Chain	Residues	Atoms			AltConf
			Total	O	V	
4	A	1	5	4	1	0

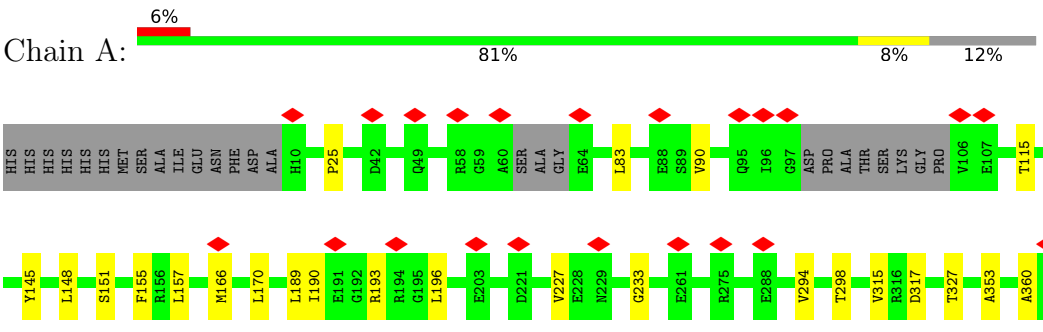
3 Residue-property plots (i)

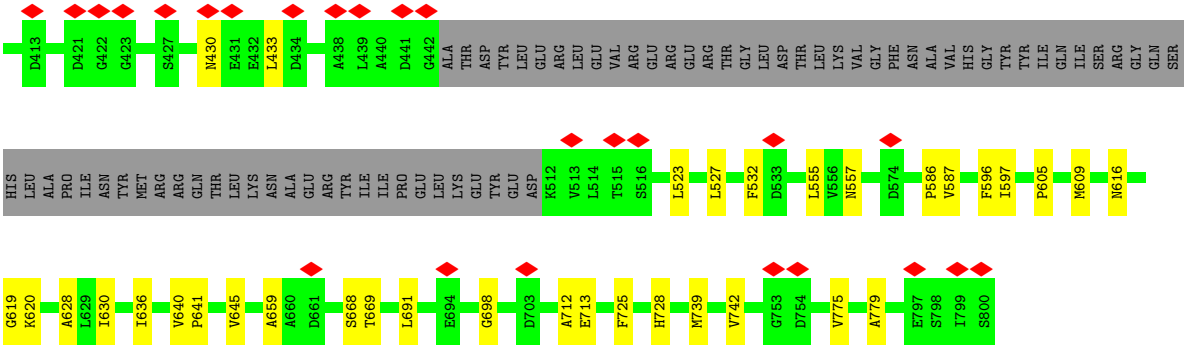
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: DNA mismatch repair protein MutS



• Molecule 1: DNA mismatch repair protein MutS




D413 D421 G422 G423 S427 M430 E431 E432 L433 D434 A438 L439 A440 D441 G442 ALA THR ASP TYR LEU GLU ARG LEU GLU VAL ARG GLU ARG GLU ARG THR GLY LEU ASP THR LEU LYS VAL GLY PHE ASN ALA VAL HIS GLY TYR TYR ILE GLN ILE SER ARG GLY GLN SER
HIS LEU ALA PRO ILE ASN TYR MET ARG ARG GLN THR LEU LYS ASN ALA GLU ARG TYR ILE ILE PRO GLU LEU LYS GLU TYR GLU ASP K512 V513 L514 T515 S516 L523 L527 F532 D533 L555 V556 N557 D574 P586 V587 F596 I597 P605 M609 N616
G619 K620 A628 L629 I630 I636 V640 P641 V645 A659 A660 D661 S668 T669 L691 E694 G698 D703 A712 E713 F725 H728 M739 V742 G753 D754 V775 A779 E797 S798 I799 S800

4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	81316	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 ($e^-/Å^2$)	57	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	105000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	0.122	Depositor
Minimum map value	-0.058	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.009	Depositor
Recommended contour level	0.029	Depositor
Map size (Å)	128.04001, 147.84001, 113.520004	wwPDB
Map dimensions	97, 112, 86	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.32, 1.32, 1.32	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: VO4, MG, ADP

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	0.97	0/5662	1.32	6/7661 (0.1%)
1	B	0.97	0/4771	1.36	3/6460 (0.0%)
All	All	0.97	0/10433	1.34	9/14121 (0.1%)

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	725	PHE	CA-CB-CG	6.42	120.22	113.80
1	A	25	PRO	N-CA-C	6.09	121.56	113.40
1	B	231	PRO	CB-CA-C	-5.93	103.64	113.06
1	B	263	GLU	N-CA-C	-5.67	103.88	111.87
1	A	605	PRO	N-CA-C	-5.44	106.31	113.65
1	A	636	ILE	N-CA-C	-5.28	107.60	112.83
1	A	728	HIS	N-CA-C	-5.25	106.56	113.17
1	B	174	ASN	CB-CA-C	5.14	115.54	110.71
1	A	139	ASP	N-CA-C	-5.04	103.00	110.46

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	5572	0	5627	43	0
1	B	4697	0	4743	47	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	27	0	12	7	0
3	B	27	0	12	3	0
4	A	10	0	0	6	0
All	All	10335	0	10394	89	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (89) 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:206:ILE:HD13	1:B:235:CYS:SG	2.15	0.87
1:A:586:PRO:HG3	1:A:641:PRO:HG3	1.62	0.79
1:B:760:HIS:HB3	3:B:1002:ADP:C6	2.20	0.76
1:A:597:ILE:O	3:A:903:ADP:N6	2.23	0.70
1:B:206:ILE:HB	1:B:235:CYS:SG	2.32	0.70
1:A:315:VAL:HG12	1:A:317:ASP:H	1.60	0.67
1:B:623:TYR:O	1:B:626:GLN:HG2	1.95	0.67
1:B:745:VAL:HG13	1:B:762:VAL:HG13	1.75	0.67
1:B:656:ARG:HE	1:B:673:GLU:HG3	1.60	0.66
1:A:616:ASN:ND2	4:A:904:VO4:O4	2.29	0.64
1:B:745:VAL:CG1	1:B:762:VAL:HG13	2.29	0.62
1:A:157:LEU:HD21	1:A:233:GLY:HA3	1.81	0.62
1:B:206:ILE:HD13	1:B:235:CYS:HG	1.63	0.61
1:B:299:VAL:HG23	1:B:300:THR:HG23	1.84	0.60
1:A:630:ILE:HG23	1:A:640:VAL:CG1	2.33	0.59
1:B:628:ALA:HB2	1:B:691:LEU:HD11	1.85	0.58
1:A:83:LEU:HD13	1:A:90:VAL:HG11	1.85	0.58
1:B:615:PRO:HG3	1:B:749:ALA:HB2	1.85	0.58
1:A:148:LEU:HD13	1:A:155:PHE:HD2	1.68	0.57
1:A:628:ALA:HB2	1:A:691:LEU:HD11	1.87	0.56
1:A:640:VAL:HG11	1:A:645:VAL:HG21	1.87	0.56
1:A:189:LEU:HD12	1:A:190:ILE:N	2.22	0.55
1:B:760:HIS:HB3	3:B:1002:ADP:N6	2.21	0.55
1:A:619:GLY:HA2	3:A:903:ADP:O1A	2.08	0.54
1:B:630:ILE:HG23	1:B:640:VAL:HG11	1.89	0.54
1:B:345:VAL:HG12	1:B:348:LEU:HD13	1.90	0.54
1:B:671:MET:SD	1:A:779:ALA:HB2	2.49	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:PHE:HA	3:A:903:ADP:C2	2.44	0.53
1:A:327:THR:HG21	1:A:555:LEU:HD13	1.92	0.52
1:B:640:VAL:HG11	1:B:645:VAL:HG21	1.91	0.52
1:B:656:ARG:C	1:B:656:ARG:HH21	2.17	0.52
1:B:630:ILE:HG23	1:B:640:VAL:CG1	2.39	0.52
1:A:151:SER:O	1:A:353:ALA:HB2	2.10	0.51
1:B:440:ALA:HB1	1:B:517:LYS:HG2	1.92	0.51
1:B:628:ALA:HB2	1:B:691:LEU:CD1	2.40	0.51
1:A:157:LEU:HD13	1:A:227:VAL:HG21	1.93	0.51
1:B:570:PRO:HG3	1:B:640:VAL:HG23	1.92	0.51
1:A:115:THR:O	1:A:119:ILE:HG23	2.11	0.51
1:A:630:ILE:HG23	1:A:640:VAL:HG11	1.92	0.50
1:B:668:SER:HB2	3:A:903:ADP:O2B	2.12	0.50
1:B:609:MET:HE1	1:B:712:ALA:O	2.13	0.49
1:B:227:VAL:HG21	1:B:258:ILE:HG12	1.95	0.48
1:A:597:ILE:N	3:A:903:ADP:N1	2.43	0.48
1:B:657:VAL:HG22	1:B:693:ASP:HB2	1.95	0.48
1:A:170:LEU:HD21	1:A:190:ILE:HD13	1.96	0.48
1:B:206:ILE:CD1	1:B:235:CYS:SG	2.97	0.48
1:A:433:LEU:HD22	1:A:527:LEU:HD22	1.95	0.47
1:A:713:GLU:HA	1:A:739:MET:HE1	1.96	0.47
1:A:360:ALA:HB3	1:A:532:PHE:CE1	2.50	0.47
1:A:630:ILE:HG23	1:A:640:VAL:HG13	1.97	0.47
1:A:193:ARG:HB2	1:A:196:LEU:HD21	1.98	0.46
1:A:609:MET:HE1	1:A:712:ALA:HB1	1.98	0.46
1:B:419:VAL:HG21	1:B:528:TYR:CD2	2.51	0.45
3:A:903:ADP:O2B	4:A:904:VO4:O3	2.33	0.45
1:B:157:LEU:HD21	1:B:227:VAL:HB	1.98	0.45
1:B:597:ILE:HG12	3:B:1002:ADP:N1	2.32	0.45
1:A:294:VAL:HG21	1:A:587:VAL:HA	1.99	0.45
1:A:659:ALA:HB1	1:A:669:THR:CG2	2.47	0.45
1:A:668:SER:HB2	4:A:901:VO4:O1	2.17	0.44
1:B:403:LEU:HD11	1:B:538:HIS:CD2	2.52	0.44
1:B:656:ARG:NE	1:B:673:GLU:HG3	2.29	0.44
1:B:695:ILE:HG23	1:B:708:ALA:HB2	2.00	0.44
1:A:298:THR:HG23	1:A:557:ASN:HD22	1.83	0.44
1:A:136:ILE:CD1	1:A:190:ILE:HD11	2.48	0.44
1:B:132:LEU:HD22	1:B:175:PRO:HB3	2.00	0.44
1:B:609:MET:HG3	1:B:723:THR:OG1	2.18	0.43
1:B:692:MET:HE1	1:B:695:ILE:HD12	2.00	0.43
1:B:668:SER:OG	4:A:904:VO4:O3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:744:ASN:HB3	1:B:765:GLY:O	2.19	0.43
1:B:150:ILE:HG23	1:B:251:THR:HG21	2.00	0.43
1:A:136:ILE:HD13	1:A:190:ILE:HD11	2.01	0.42
1:A:620:LYS:NZ	4:A:904:VO4:O1	2.48	0.42
1:A:433:LEU:HA	1:A:523:LEU:HD23	2.02	0.42
1:A:430:ASN:CB	1:A:527:LEU:HD21	2.50	0.42
1:A:430:ASN:HB2	1:A:527:LEU:HD21	2.01	0.42
1:B:692:MET:HE2	1:B:692:MET:HB3	1.94	0.42
1:A:145:TYR:CG	1:A:166:MET:HE1	2.55	0.42
1:A:145:TYR:HB2	1:A:166:MET:HE1	2.02	0.41
1:B:132:LEU:CD2	1:B:175:PRO:HB3	2.50	0.41
1:B:580:ILE:HG12	1:B:645:VAL:HG22	2.01	0.41
1:B:677:THR:HG21	1:B:695:ILE:CD1	2.50	0.41
1:B:552:LEU:O	1:B:556:VAL:HG23	2.21	0.41
1:B:671:MET:HE2	1:A:775:VAL:HG13	2.02	0.40
1:A:619:GLY:CA	3:A:903:ADP:O1A	2.68	0.40
1:B:680:ILE:O	1:B:684:ALA:HB2	2.21	0.40
1:A:698:GLY:O	4:A:901:VO4:O4	2.39	0.40
1:B:155:PHE:HE1	1:B:240:LEU:HD23	1.86	0.40
1:B:213:LEU:HD23	1:B:241:LEU:HD22	2.04	0.40
1:A:739:MET:HE3	1:A:742:VAL:HG21	2.03	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	703/806 (87%)	695 (99%)	8 (1%)	0	100	100
1	B	598/806 (74%)	586 (98%)	12 (2%)	0	100	100
All	All	1301/1612 (81%)	1281 (98%)	20 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	589/670 (88%)	589 (100%)	0	100 100
1	B	495/670 (74%)	494 (100%)	1 (0%)	87 87
All	All	1084/1340 (81%)	1083 (100%)	1 (0%)	87 89

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	645	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	138	GLN
1	B	214	ASN
1	B	339	GLN
1	B	391	GLN
1	B	538	HIS
1	B	557	ASN
1	B	746	HIS
1	A	23	GLN
1	A	24	HIS
1	A	95	GLN
1	A	126	GLN
1	A	214	ASN
1	A	254	HIS
1	A	543	GLN
1	A	616	ASN
1	A	643	GLN
1	A	683	ASN
1	A	714	ASN

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Mol	Chain	Res	Type
1	A	728	HIS
1	A	791	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 6 ligands modelled in this entry, 2 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	$\#\|Z\| > 2$
3	ADP	A	903	2,4	27,29,29	0.77	1 (3%)	42,45,45	0.52	0
4	VO4	A	904	2,3	0,4,4	-	-	-		
4	VO4	A	901	2	0,4,4	-	-	-		
3	ADP	B	1002	2	27,29,29	0.55	0	42,45,45	0.52	0

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
3	ADP	A	903	2,4	-	4/16/32/32	0/3/3/3
3	ADP	B	1002	2	-	2/16/32/32	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	903	ADP	PB-O2B	-3.00	1.43	1.54

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1002	ADP	PA-O3A-PB-O3B
3	A	903	ADP	PA-O3A-PB-O3B
3	A	903	ADP	C5'-O5'-PA-O3A
3	A	903	ADP	C5'-O5'-PA-O1A
3	A	903	ADP	PA-O3A-PB-O1B
3	B	1002	ADP	PA-O3A-PB-O2B

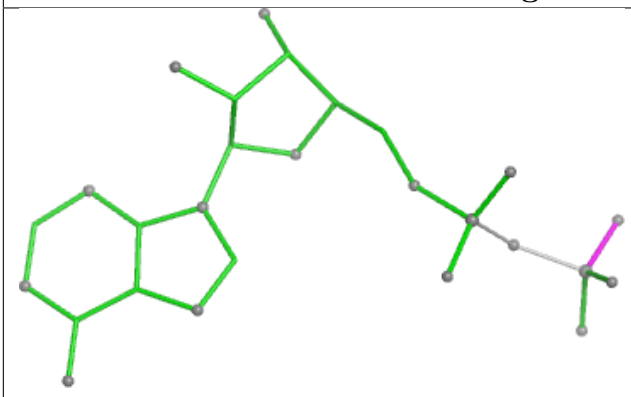
There are no ring outliers.

4 monomers are involved in 15 short contacts:

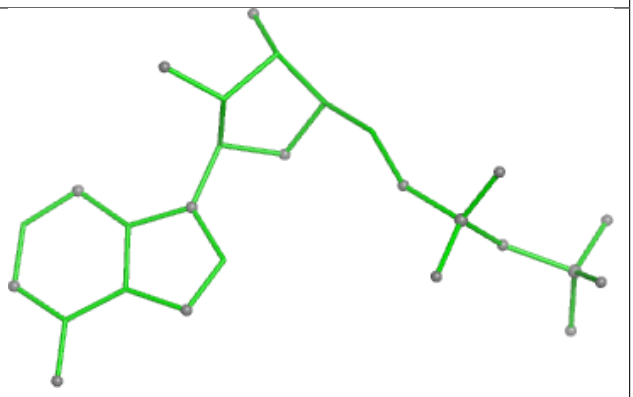
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	903	ADP	7	0
4	A	904	VO4	4	0
4	A	901	VO4	2	0
3	B	1002	ADP	3	0

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.

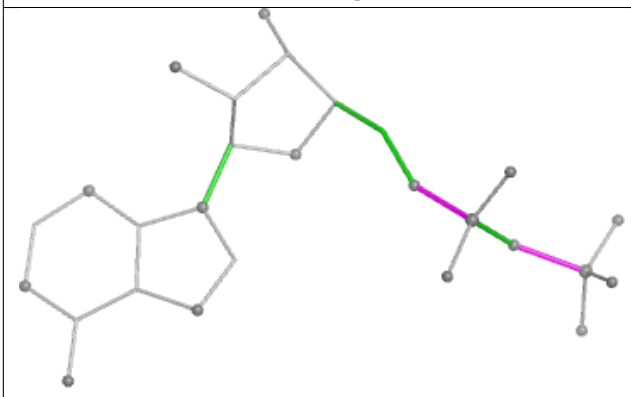
Ligand ADP A 903



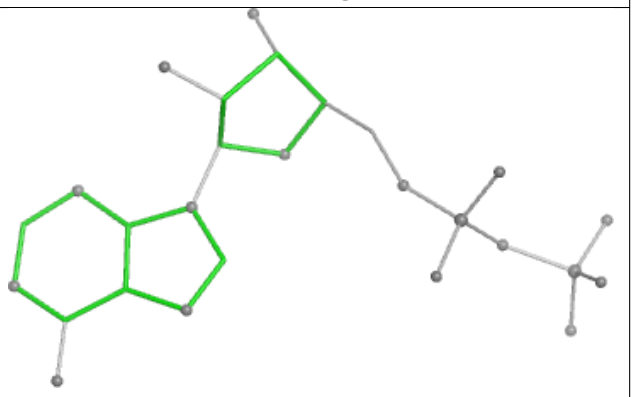
Bond lengths



Bond angles

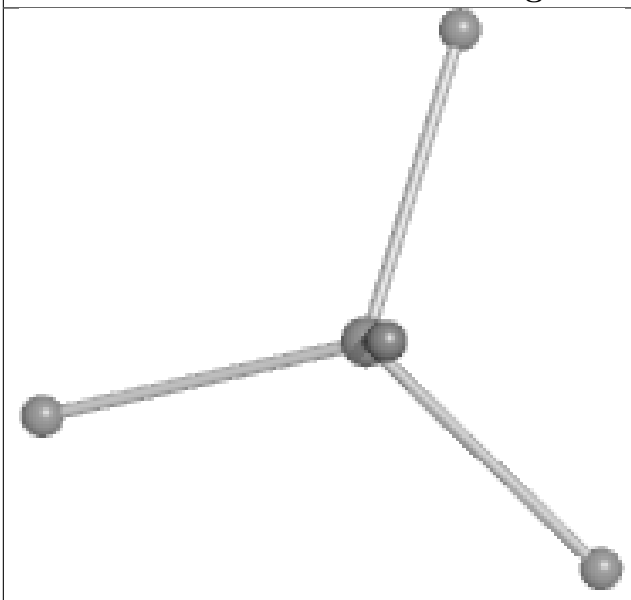


Torsions

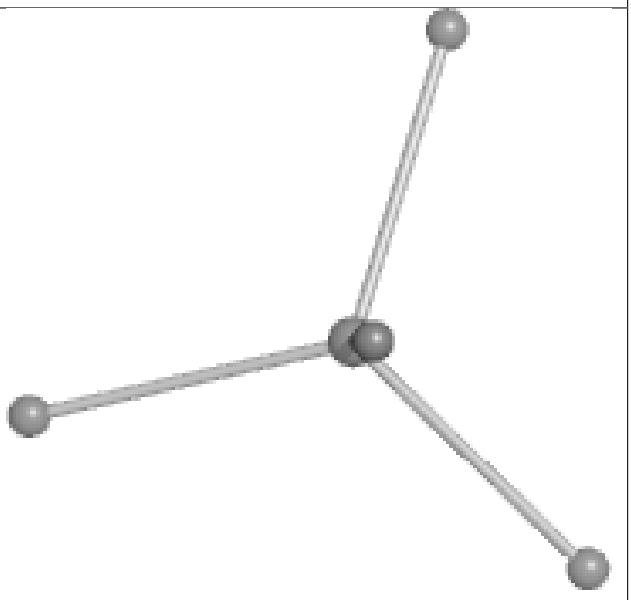


Rings

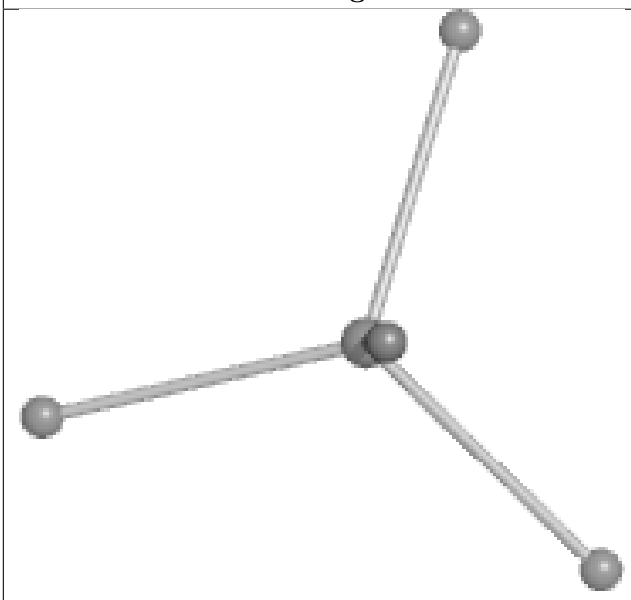
Ligand VO4 A 904



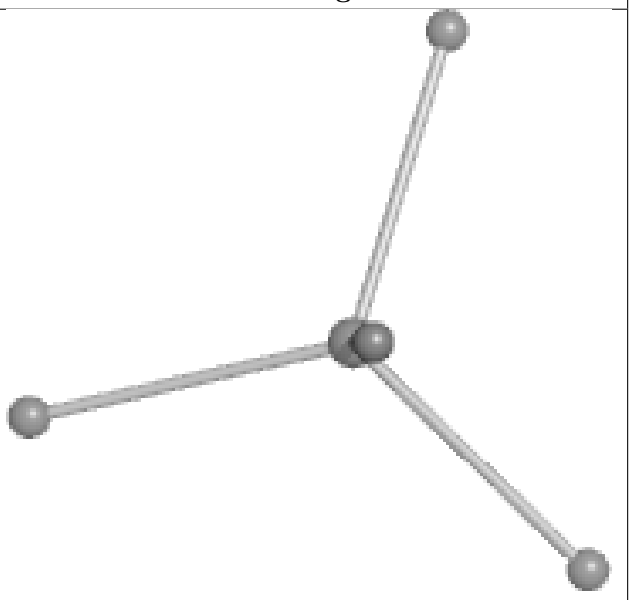
Bond lengths



Bond angles

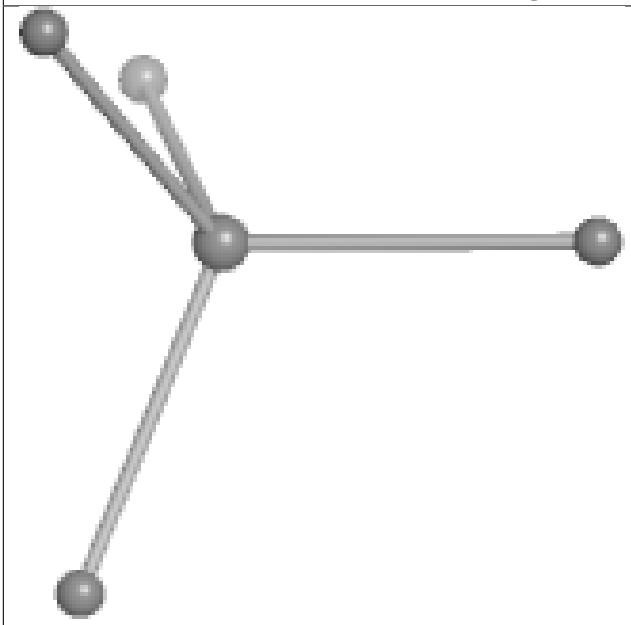


Torsions

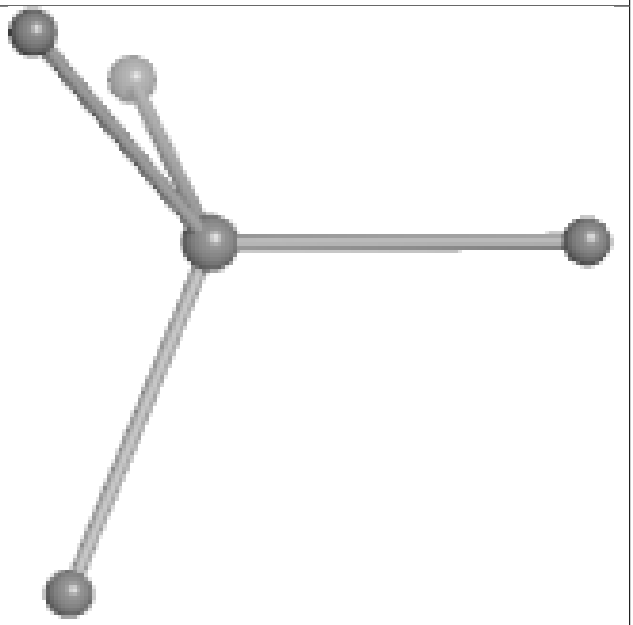


Rings

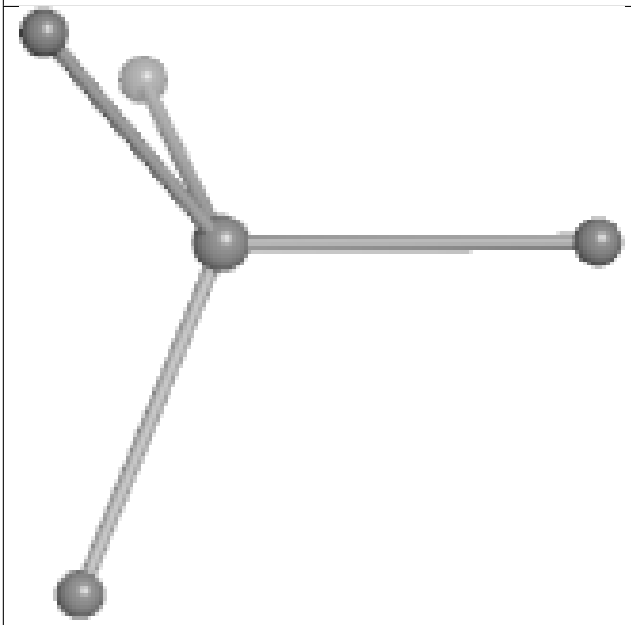
Ligand VO4 A 901



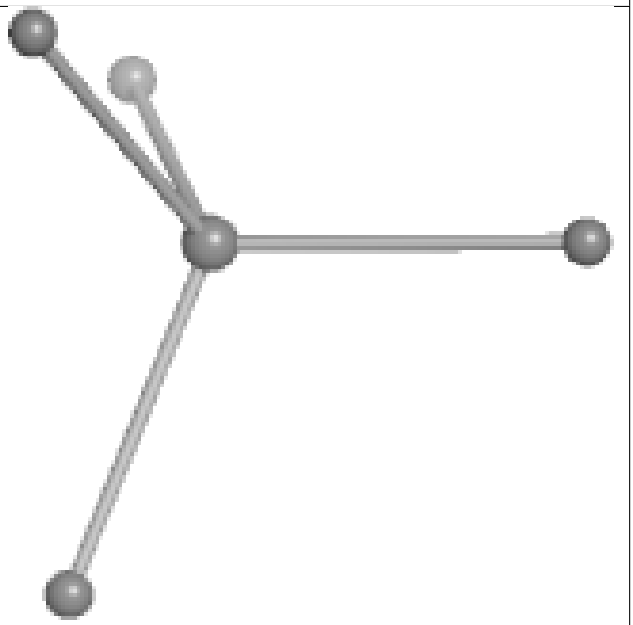
Bond lengths



Bond angles

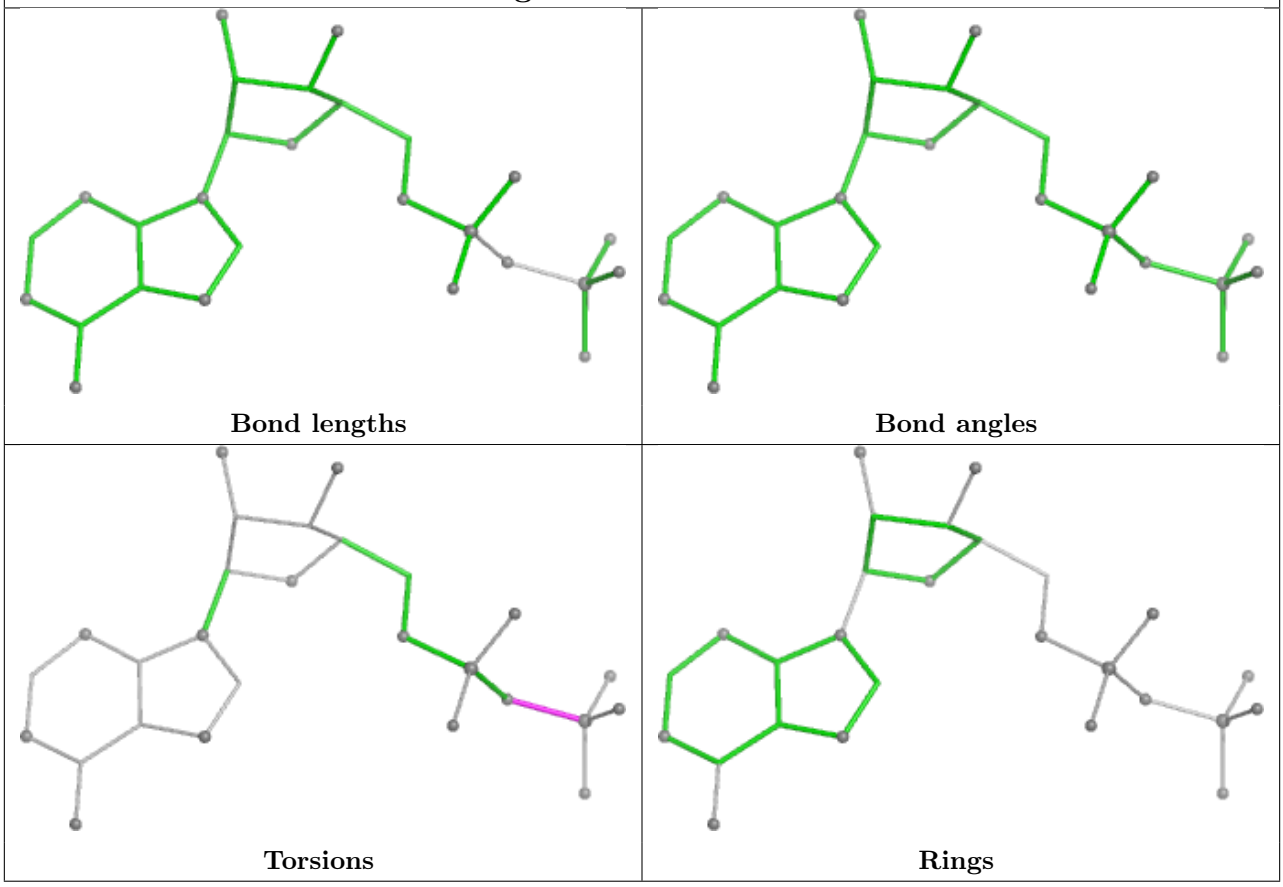


Torsions



Rings

Ligand ADP B 1002



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.

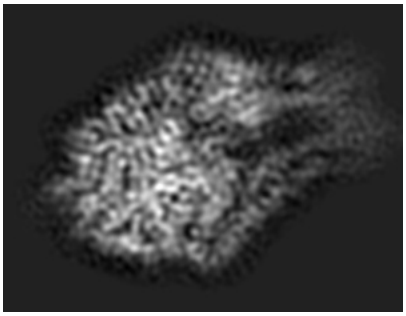
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-13071. These allow visual inspection of the internal detail of the map and identification of artifacts.

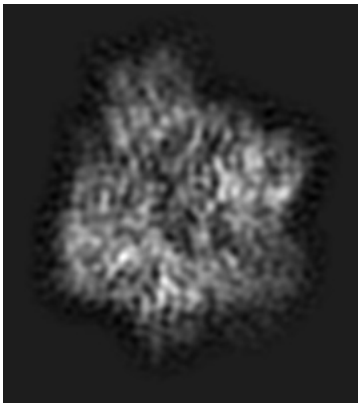
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections

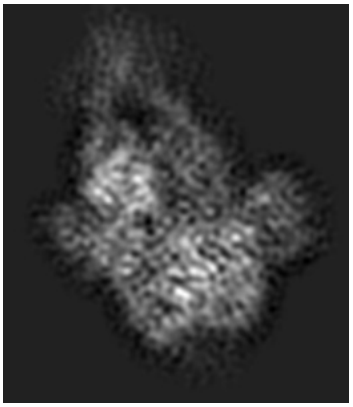
6.1.1 Primary map



X



Y

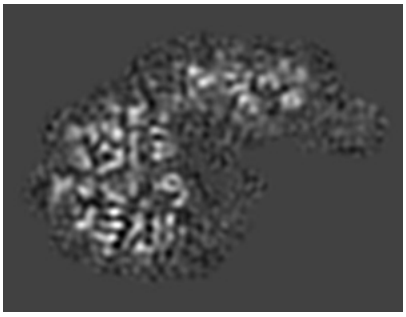


Z

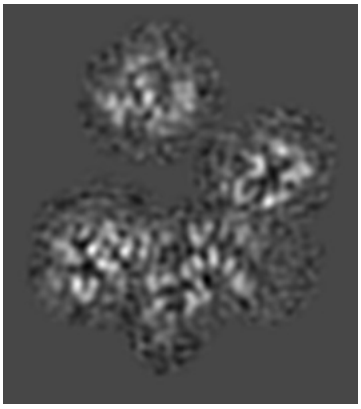
The images above show the map projected in three orthogonal directions.

6.2 Central slices

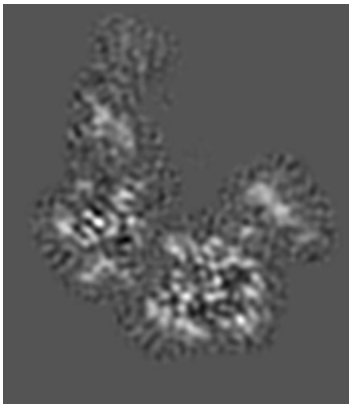
6.2.1 Primary map



X Index: 48



Y Index: 56

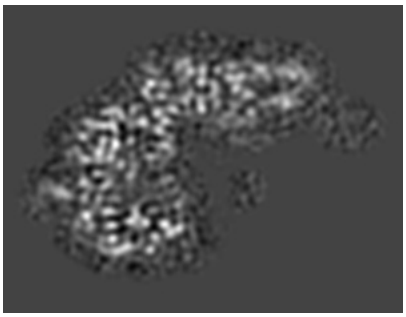


Z Index: 43

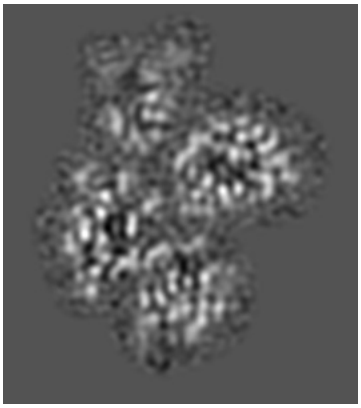
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices (i)

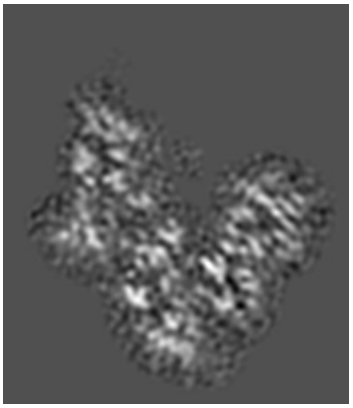
6.3.1 Primary map



X Index: 50



Y Index: 45

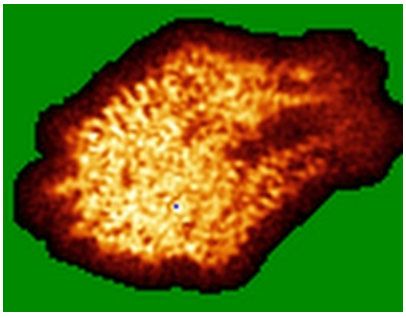


Z Index: 34

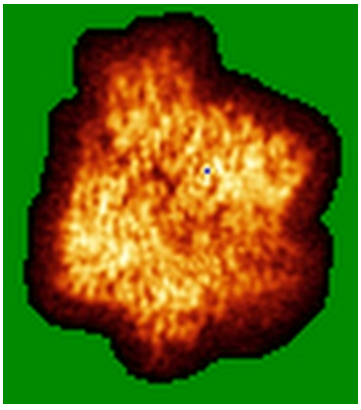
The images above show the largest variance slices of the map in three orthogonal directions.

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

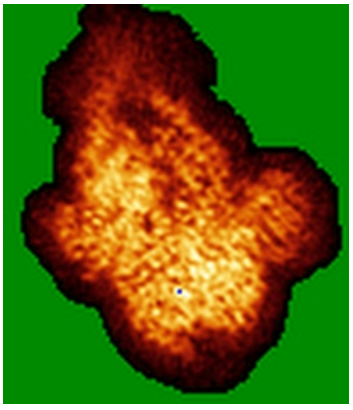
6.4.1 Primary map



X



Y

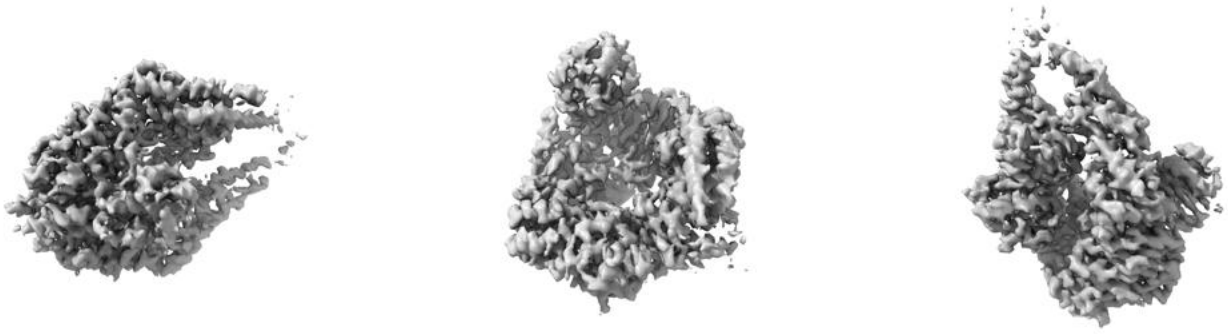


Z

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 0.029. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

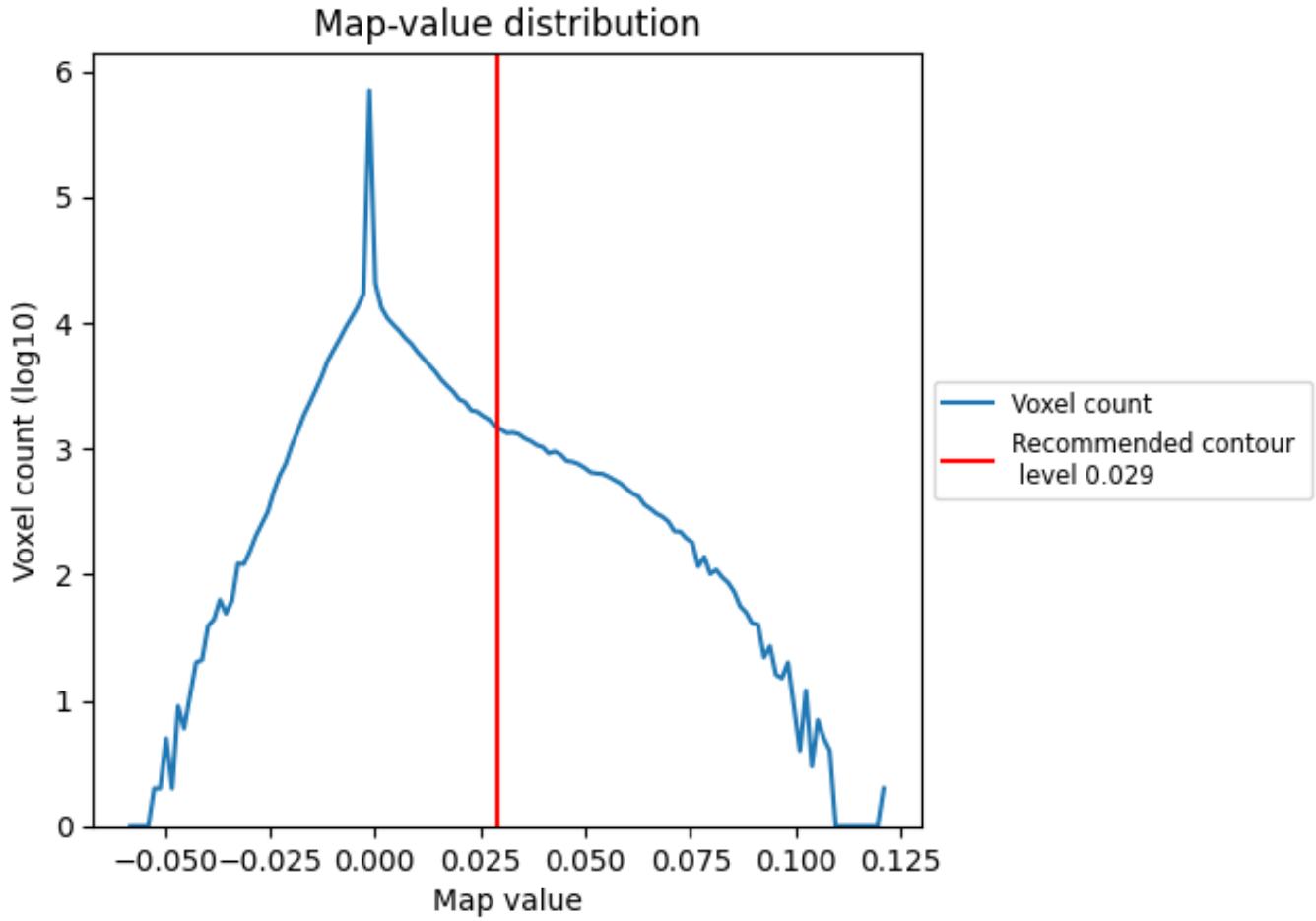
6.6 Mask visualisation (i)

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

7 Map analysis

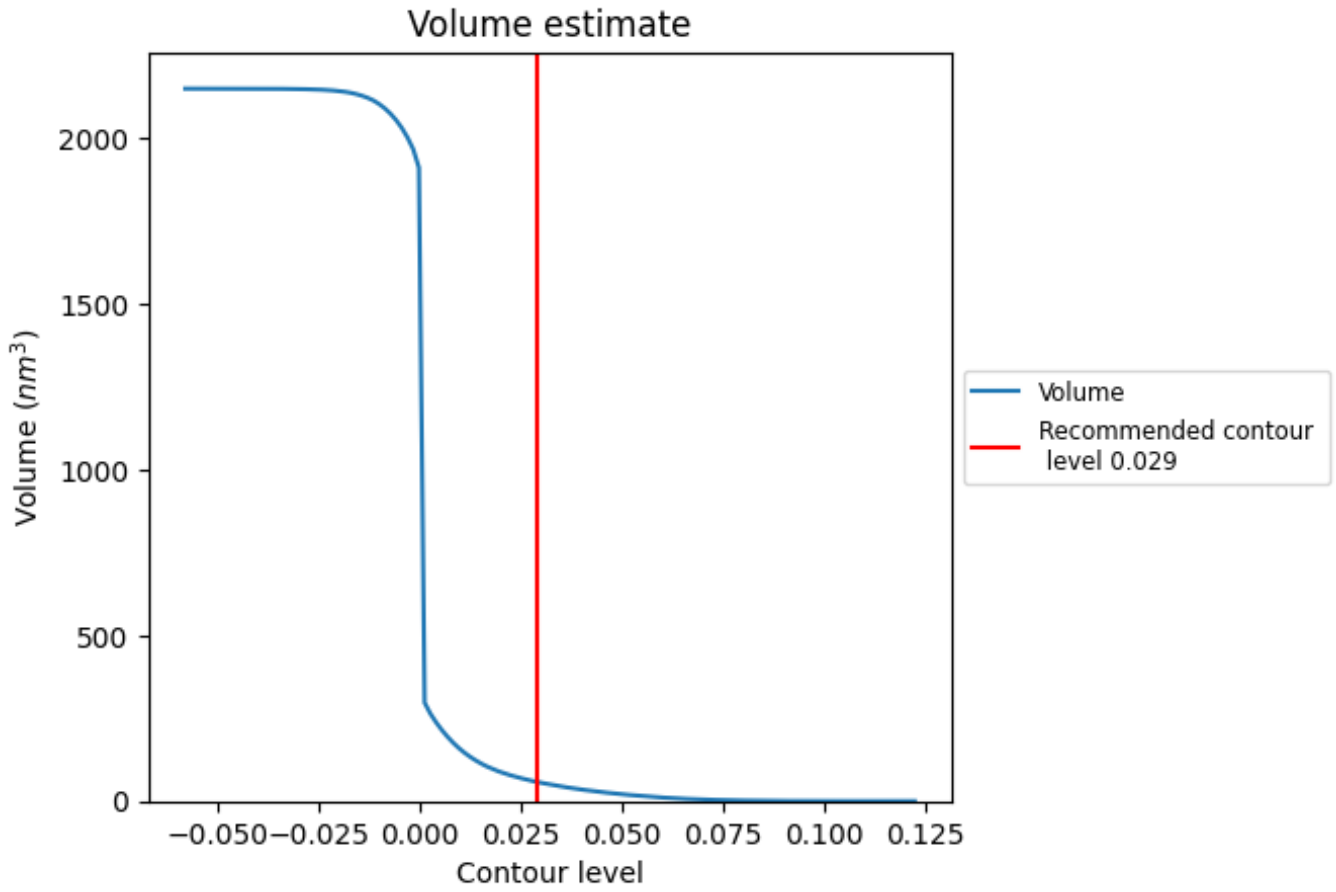
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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 58 nm^3; this corresponds to an approximate mass of 52 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.

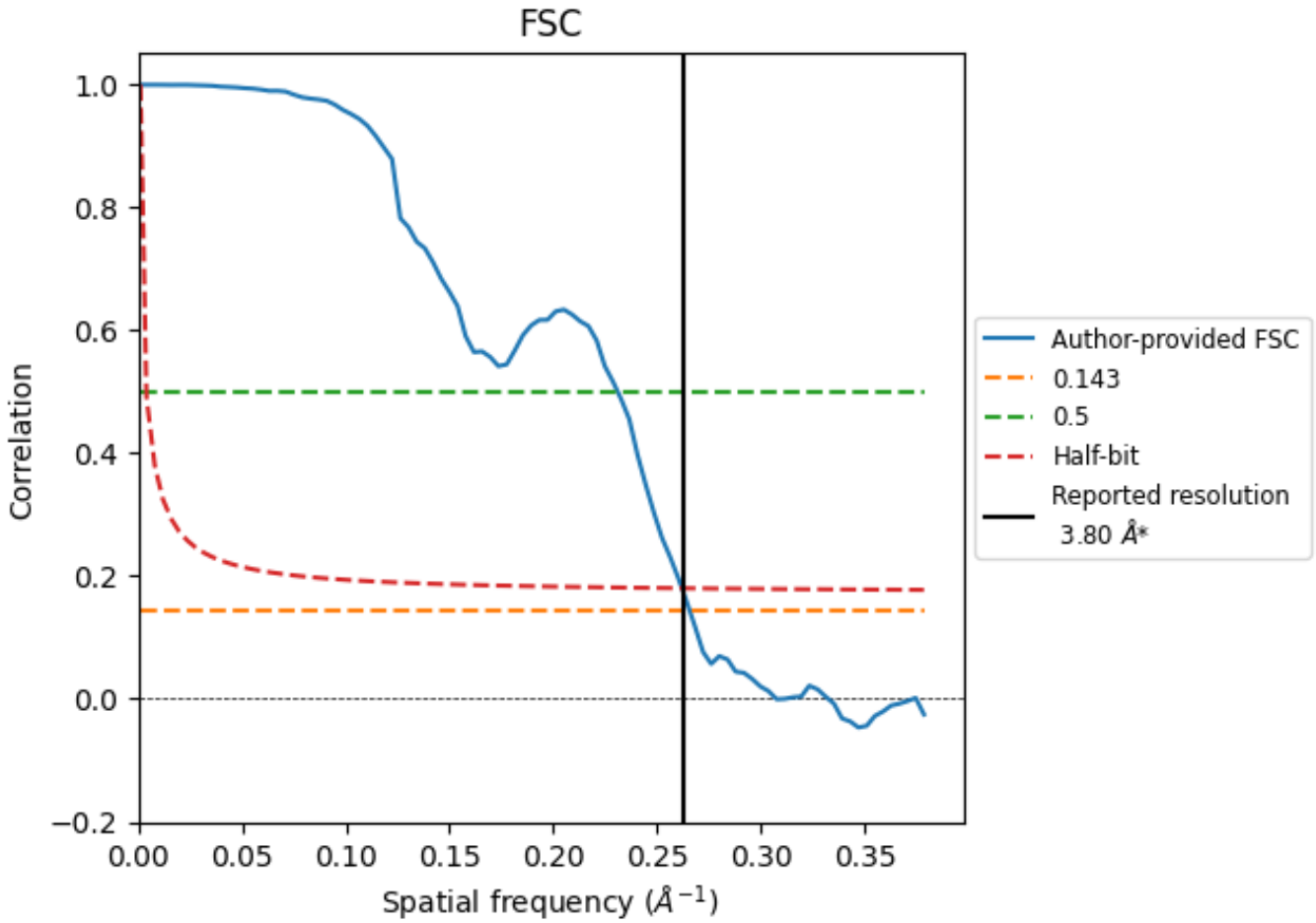
7.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

8 Fourier-Shell correlation

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



*Reported resolution corresponds to spatial frequency of 0.263 Å^{-1}

8.2 Resolution estimates (i)

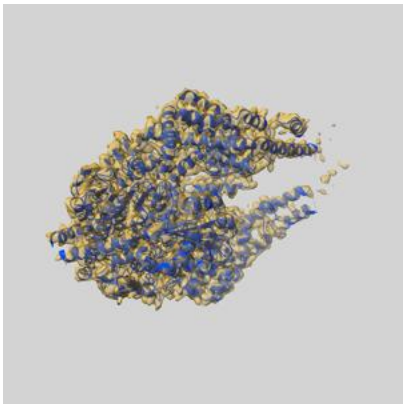
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.80	-	-
Author-provided FSC curve	3.76	4.33	3.82
Unmasked-calculated*	-	-	-

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

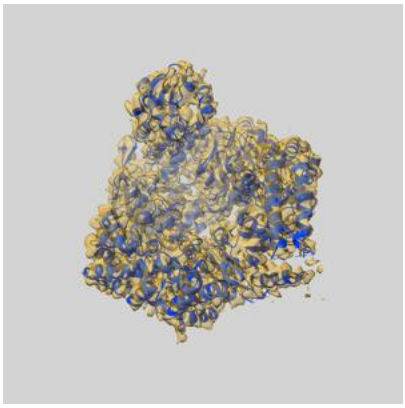
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-13071 and PDB model 7OU0. Per-residue inclusion information can be found in section 3 on page 7.

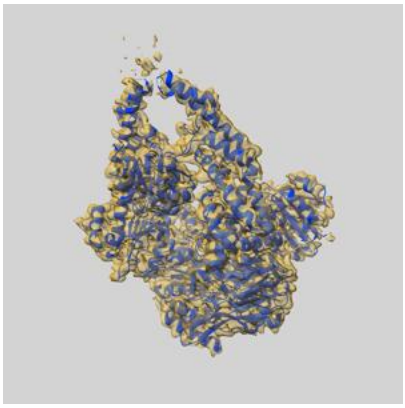
9.1 Map-model overlay



X



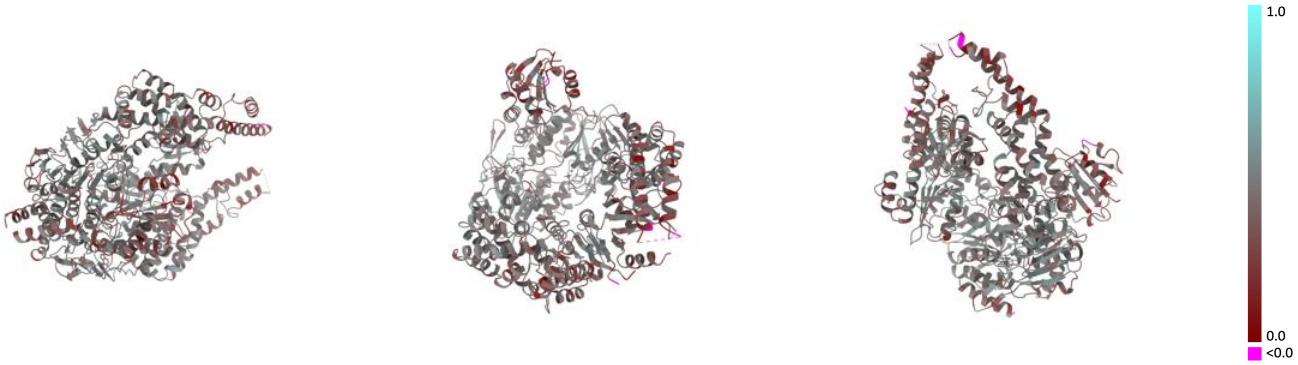
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.029 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.

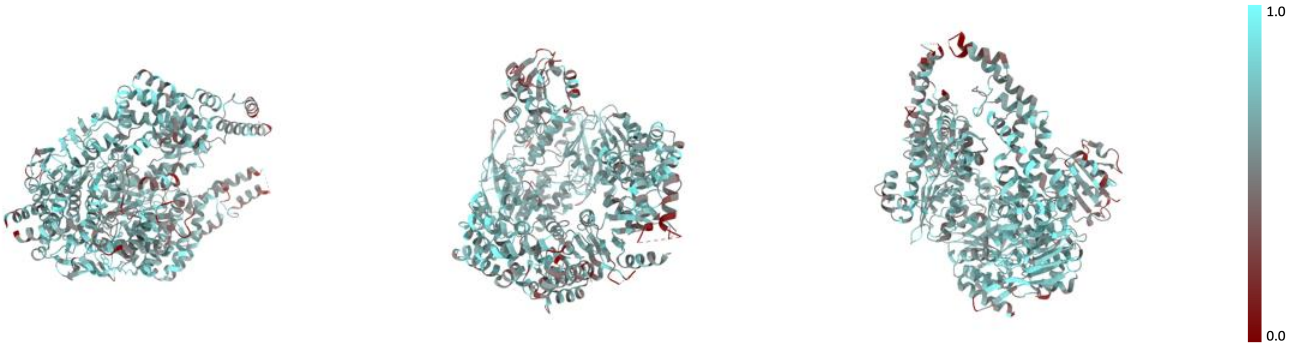
9.2 Q-score mapped to coordinate model (i)



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.

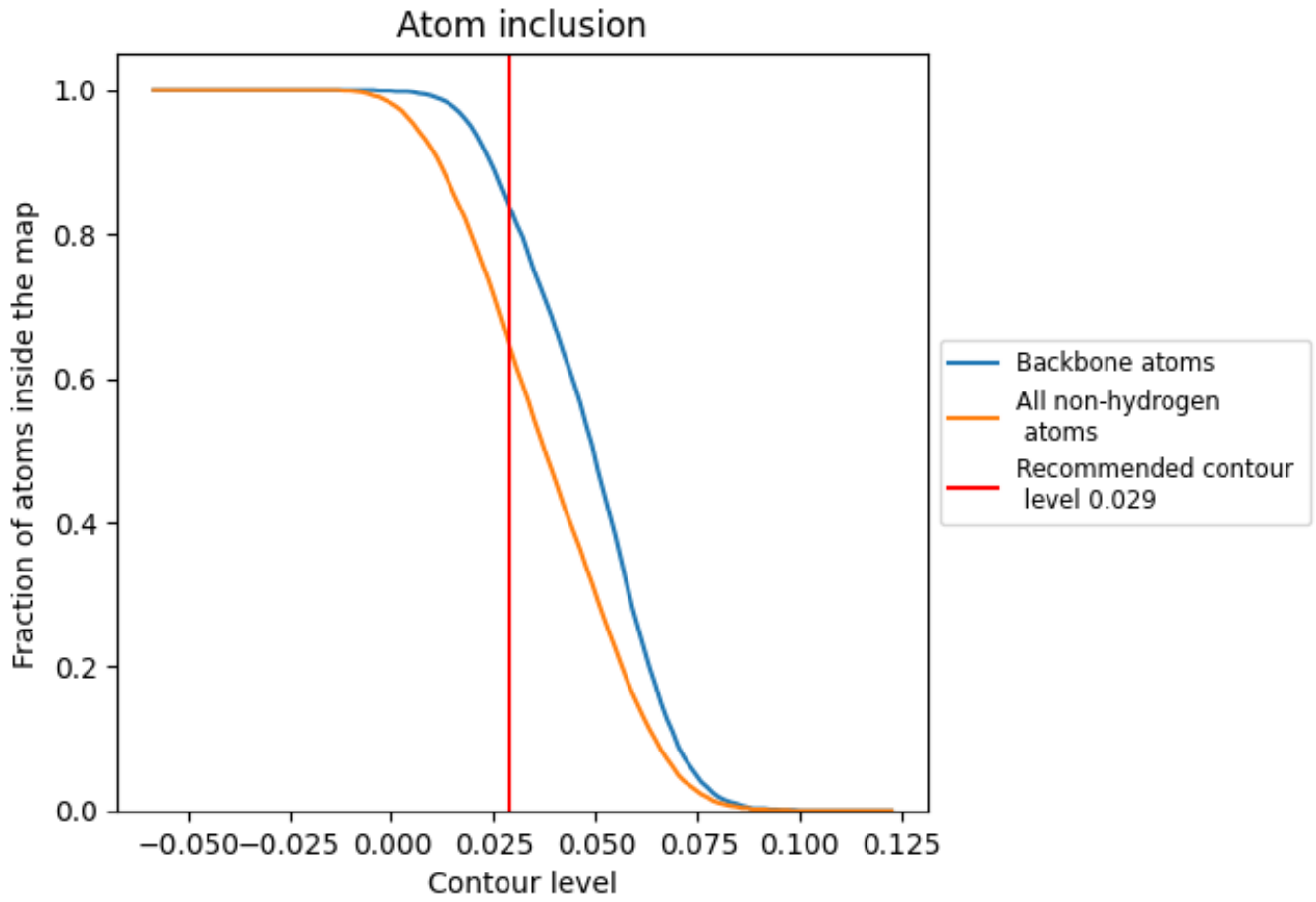
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.029).

9.4 Atom inclusion (i)



At the recommended contour level, 84% of all backbone atoms, 64% 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 (0.029) and Q-score for the entire model and for each chain.



Chain	Atom inclusion	Q-score
All	0.6420	0.4130
A	0.6500	0.4240
B	0.6330	0.4000