



Full wwPDB EM Validation Report ⓘ

Mar 9, 2026 – 07:41 AM UTC

PDB ID : 7VGH / pdb_00007vgh
EMDB ID : EMD-31969
Title : Cryo-EM structure of the human P4-type flippase ATP8B1-CDC50B in the auto-inhibited E2P state
Authors : Chen, M.T.; Chen, Y.
Deposited on : 2021-09-16
Resolution : 3.39 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/EMValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

EMDB validation analysis : 0.0.1.dev132
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4-5-2 with Phenix2.0
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) : 2.49

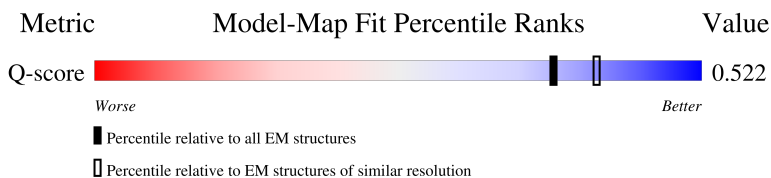
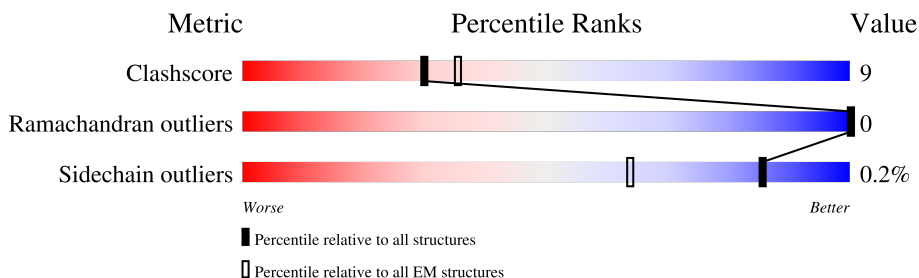
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.39 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	14220 (2.89 - 3.89)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion $< 40\%$). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	363	
2	B	1294	
3	C	4	
4	D	6	

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Mol	Chain	Length	Quality of chain
5	E	2	 100%

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 12404 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 Cell cycle control protein 50B.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	338	Total	C	N	O	S	0	0
			2654	1719	459	465	11		

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	initiating methionine	UNP Q3MIR4
A	-10	SER	-	expression tag	UNP Q3MIR4
A	-9	HIS	-	expression tag	UNP Q3MIR4
A	-8	HIS	-	expression tag	UNP Q3MIR4
A	-7	HIS	-	expression tag	UNP Q3MIR4
A	-6	HIS	-	expression tag	UNP Q3MIR4
A	-5	HIS	-	expression tag	UNP Q3MIR4
A	-4	HIS	-	expression tag	UNP Q3MIR4
A	-3	GLY	-	expression tag	UNP Q3MIR4
A	-2	SER	-	expression tag	UNP Q3MIR4
A	-1	GLY	-	expression tag	UNP Q3MIR4
A	0	SER	-	expression tag	UNP Q3MIR4

- Molecule 2 is a protein called Phospholipid-transporting ATPase IC.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	B	1183	Total	C	N	O	P S	0	0
			9584	6165	1618	1754	1 46		

There are 43 discrepancies between the modelled and reference sequences:

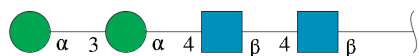
Chain	Residue	Modelled	Actual	Comment	Reference
B	-42	MET	-	initiating methionine	UNP O43520
B	-41	ALA	-	expression tag	UNP O43520
B	-40	SER	-	expression tag	UNP O43520
B	-39	TRP	-	expression tag	UNP O43520
B	-38	SER	-	expression tag	UNP O43520

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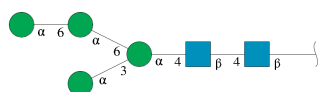
Chain	Residue	Modelled	Actual	Comment	Reference
B	-37	HIS	-	expression tag	UNP O43520
B	-36	PRO	-	expression tag	UNP O43520
B	-35	GLN	-	expression tag	UNP O43520
B	-34	PHE	-	expression tag	UNP O43520
B	-33	GLU	-	expression tag	UNP O43520
B	-32	LYS	-	expression tag	UNP O43520
B	-31	GLY	-	expression tag	UNP O43520
B	-30	GLY	-	expression tag	UNP O43520
B	-29	GLY	-	expression tag	UNP O43520
B	-28	ALA	-	expression tag	UNP O43520
B	-27	ARG	-	expression tag	UNP O43520
B	-26	GLY	-	expression tag	UNP O43520
B	-25	GLY	-	expression tag	UNP O43520
B	-24	SER	-	expression tag	UNP O43520
B	-23	GLY	-	expression tag	UNP O43520
B	-22	GLY	-	expression tag	UNP O43520
B	-21	GLY	-	expression tag	UNP O43520
B	-20	SER	-	expression tag	UNP O43520
B	-19	TRP	-	expression tag	UNP O43520
B	-18	SER	-	expression tag	UNP O43520
B	-17	HIS	-	expression tag	UNP O43520
B	-16	PRO	-	expression tag	UNP O43520
B	-15	GLN	-	expression tag	UNP O43520
B	-14	PHE	-	expression tag	UNP O43520
B	-13	GLU	-	expression tag	UNP O43520
B	-12	LYS	-	expression tag	UNP O43520
B	-11	GLY	-	expression tag	UNP O43520
B	-10	PHE	-	expression tag	UNP O43520
B	-9	ASP	-	expression tag	UNP O43520
B	-8	TYR	-	expression tag	UNP O43520
B	-7	LYS	-	expression tag	UNP O43520
B	-6	ASP	-	expression tag	UNP O43520
B	-5	ASP	-	expression tag	UNP O43520
B	-4	ASP	-	expression tag	UNP O43520
B	-3	ASP	-	expression tag	UNP O43520
B	-2	LYS	-	expression tag	UNP O43520
B	-1	GLY	-	expression tag	UNP O43520
B	0	THR	-	expression tag	UNP O43520

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
3	C	4	Total	C	N	O	0	0
			51	28	2	21		

- Molecule 4 is an oligosaccharide called alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



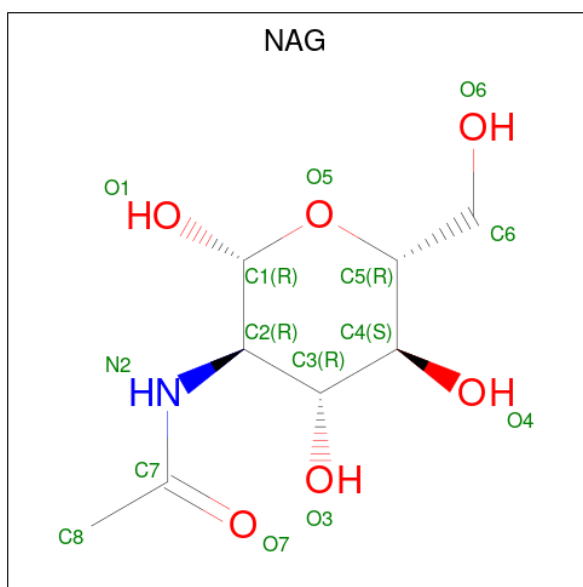
Mol	Chain	Residues	Atoms				AltConf	Trace
4	D	6	Total	C	N	O	0	0
			72	40	2	30		

- Molecule 5 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				AltConf	Trace
5	E	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
6	A	1	14	8	1	5	0

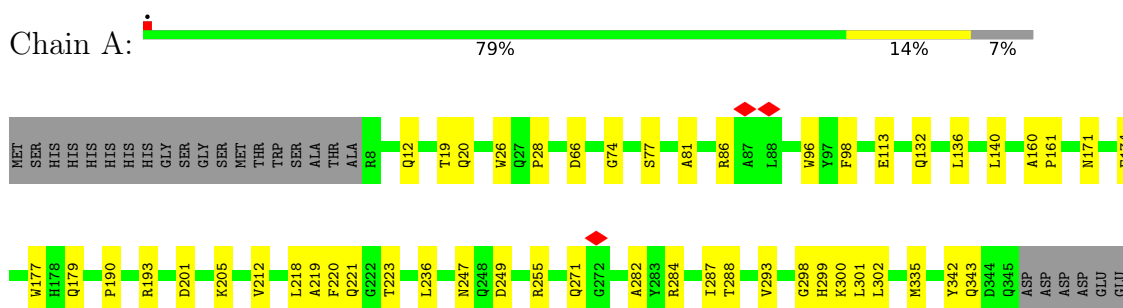
- Molecule 7 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		AltConf
			Total	Mg	
7	B	1	1	1	0

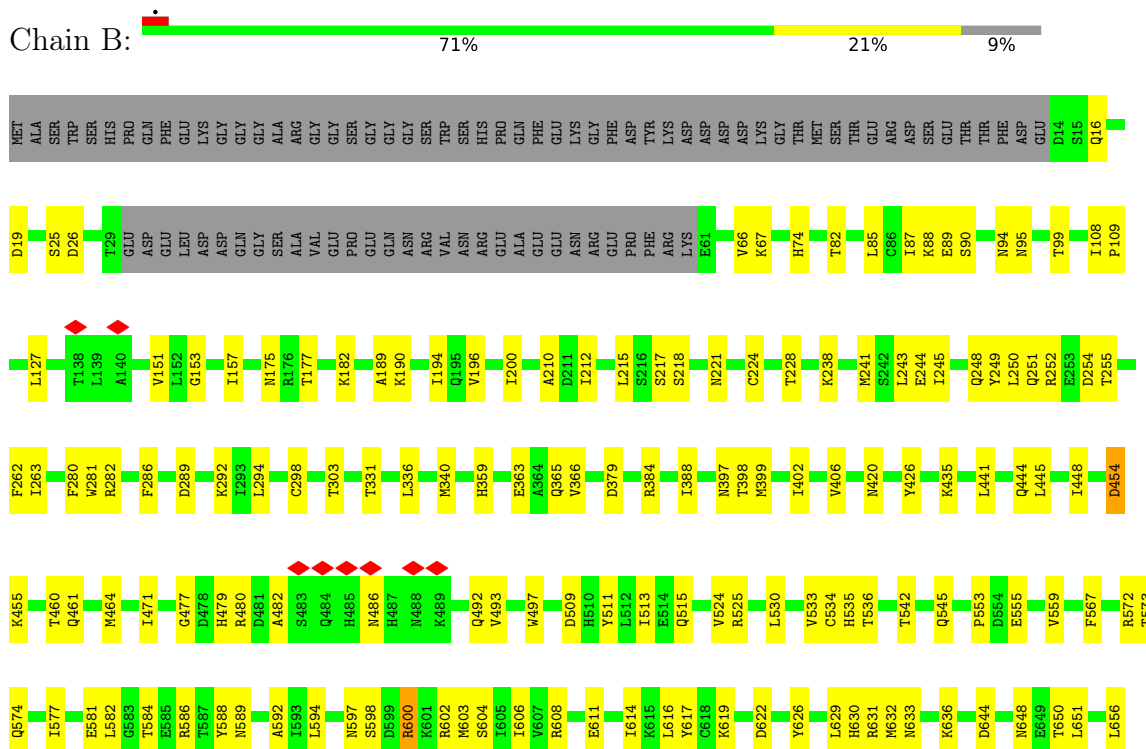
3 Residue-property plots

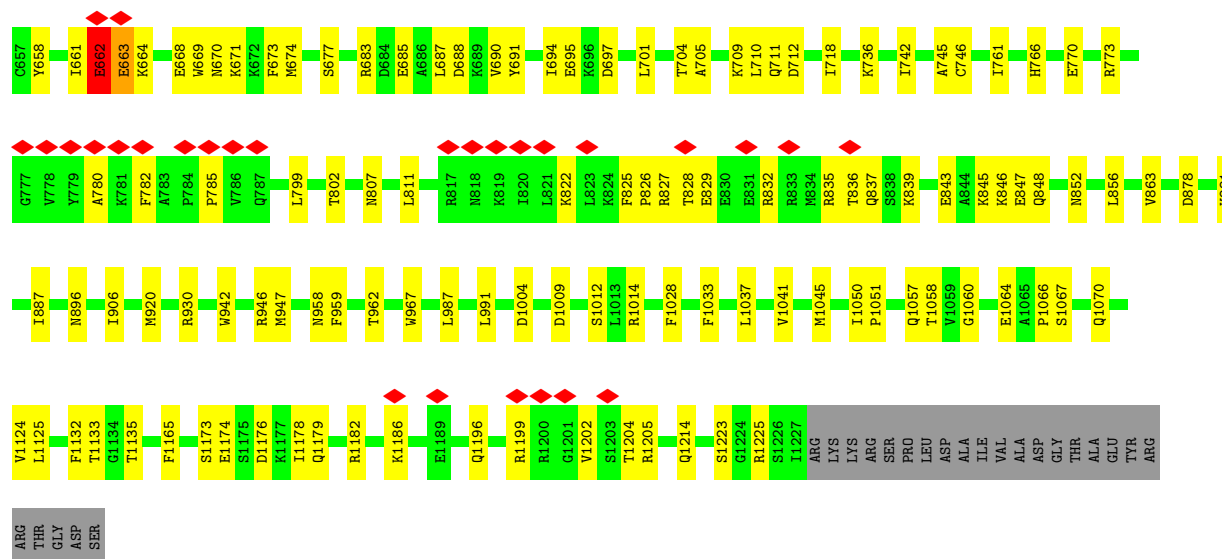
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion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

- Molecule 1: Cell cycle control protein 50B



- Molecule 2: Phospholipid-transporting ATPase IC





- Molecule 3: alpha-D-mannopyranose-(1-3)-alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C: 75% 25%



- Molecule 4: alpha-D-mannopyranose-(1-6)-alpha-D-mannopyranose-(1-6)-[alpha-D-mannopyranose-(1-3)]alpha-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 83% 17%



- Molecule 5: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain E: 100%



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	160435	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	60	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.105	Depositor
Minimum map value	-0.053	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.004	Depositor
Recommended contour level	0.0125	Depositor
Map size ($\text{\AA}$)	257.76, 257.76, 257.76	wwPDB
Map dimensions	240, 240, 240	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	1.074, 1.074, 1.074	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: PHD, MAN, MG, NAG

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	0.19	0/2744	0.40	0/3752
2	B	0.20	0/9787	0.42	1/13241 (0.0%)
All	All	0.20	0/12531	0.42	1/16993 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	662	GLU	CB-CA-C	-6.24	108.75	117.23

There are no chirality outliers.

There are no planarity outliers.

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	2654	0	2565	32	0
2	B	9584	0	9543	193	0
3	C	51	0	44	2	0
4	D	72	0	61	2	0
5	E	28	0	25	1	0
6	A	14	0	13	1	0
7	B	1	0	0	0	0
All	All	12404	0	12251	225	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 9.

All (225) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:614:ILE:HG22	2:B:661:ILE:HG22	1.52	0.91
2:B:614:ILE:CG2	2:B:661:ILE:CG2	2.55	0.84
2:B:614:ILE:HG22	2:B:661:ILE:CG2	2.07	0.83
2:B:262:PHE:HB2	2:B:280:PHE:HB2	1.65	0.77
2:B:811:LEU:HD21	2:B:845:LYS:HG3	1.67	0.76
2:B:399:MET:HG2	2:B:962:THR:HG21	1.69	0.73
2:B:127:LEU:HD13	2:B:397:ASN:HD22	1.54	0.73
2:B:946:ARG:NH2	2:B:1004:ASP:O	2.22	0.73
2:B:629:LEU:HD12	2:B:633:ASN:HD22	1.54	0.70
2:B:614:ILE:CG2	2:B:661:ILE:HG22	2.20	0.69
2:B:614:ILE:CG2	2:B:661:ILE:HG21	2.21	0.68
2:B:66:VAL:O	2:B:74:HIS:NE2	2.27	0.68
1:A:132:GLN:NE2	1:A:160:ALA:O	2.28	0.67
1:A:179:GLN:HG2	1:A:282:ALA:HB3	1.77	0.67
1:A:236:LEU:HD13	1:A:247:ASN:HD22	1.60	0.67
2:B:420:ASN:HB3	2:B:435:LYS:HA	1.77	0.66
2:B:340:MET:HE1	2:B:1028:PHE:HE2	1.60	0.66
2:B:492:GLN:NE2	2:B:493:VAL:O	2.29	0.66
2:B:614:ILE:HG21	2:B:661:ILE:HG21	1.77	0.66
1:A:218:LEU:HA	1:A:221:GLN:HE22	1.62	0.65
1:A:298:GLY:O	1:A:299:HIS:ND1	2.30	0.65
2:B:1179:GLN:OE1	2:B:1182:ARG:NH2	2.28	0.65
2:B:959:PHE:CE2	2:B:1037:LEU:HD22	2.31	0.65
2:B:835:ARG:NH1	2:B:836:THR:OG1	2.30	0.64
2:B:533:VAL:HG23	2:B:577:ILE:HD11	1.79	0.62
2:B:215:LEU:HD13	2:B:250:LEU:HD12	1.82	0.62
2:B:629:LEU:HD11	2:B:636:LYS:HE2	1.82	0.62
2:B:26:ASP:OD1	2:B:807:ASN:ND2	2.33	0.61
2:B:497:TRP:HE1	2:B:513:ILE:HD11	1.65	0.61
2:B:535:HIS:CE1	2:B:572:ARG:HH22	2.19	0.61
1:A:132:GLN:HE21	1:A:140:LEU:HD12	1.64	0.61
2:B:482:ALA:O	2:B:486:ASN:ND2	2.33	0.61
2:B:651:LEU:HD13	2:B:705:ALA:HB1	1.83	0.61
2:B:471:ILE:HG21	2:B:524:VAL:HG12	1.82	0.60
4:D:2:NAG:H3	4:D:2:NAG:H83	1.82	0.60
2:B:331:THR:HG22	2:B:441:LEU:HD13	1.84	0.60
2:B:597:ASN:OD1	2:B:598:SER:N	2.34	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1057:GLN:HG3	2:B:1058:THR:H	1.66	0.59
2:B:482:ALA:HB2	2:B:511:TYR:HB2	1.85	0.58
2:B:535:HIS:O	2:B:572:ARG:NH1	2.36	0.58
1:A:171:ASN:HD22	4:D:1:NAG:H83	1.69	0.58
2:B:289:ASP:OD1	2:B:292:LYS:NZ	2.36	0.58
2:B:536:THR:HG23	2:B:603:MET:HE1	1.85	0.58
2:B:766:HIS:NE2	2:B:770:GLU:OE1	2.35	0.58
2:B:835:ARG:HG2	2:B:836:THR:HG23	1.86	0.58
1:A:19:THR:HG23	1:A:20:GLN:HG2	1.86	0.57
2:B:542:THR:OG1	2:B:545:GLN:NE2	2.36	0.57
2:B:848:GLN:O	2:B:852:ASN:ND2	2.35	0.57
1:A:190:PRO:HB2	1:A:271:GLN:HG3	1.86	0.57
1:A:160:ALA:HB3	1:A:161:PRO:HD3	1.86	0.57
2:B:664:LYS:HD3	2:B:664:LYS:C	2.30	0.56
2:B:710:LEU:O	2:B:711:GLN:HG3	2.04	0.56
2:B:525:ARG:HG2	2:B:567:PHE:HZ	1.71	0.56
2:B:66:VAL:HG12	2:B:263:ILE:HB	1.87	0.56
2:B:600:ARG:HH11	2:B:600:ARG:HB2	1.70	0.56
3:C:1:NAG:H83	3:C:1:NAG:H3	1.87	0.56
2:B:829:GLU:OE2	2:B:837:GLN:N	2.39	0.56
1:A:220:PHE:O	1:A:223:THR:OG1	2.24	0.56
2:B:597:ASN:HB3	2:B:600:ARG:HB3	1.87	0.55
2:B:614:ILE:HG21	2:B:661:ILE:CG2	2.33	0.55
1:A:96:TRP:CZ3	1:A:98:PHE:HB3	2.41	0.55
3:C:1:NAG:H61	3:C:2:NAG:HN2	1.72	0.55
1:A:12:GLN:HG2	2:B:426:TYR:CZ	2.42	0.54
2:B:600:ARG:HG3	2:B:602:ARG:HG2	1.89	0.54
2:B:228:THR:HG22	2:B:298:CYS:SG	2.47	0.54
1:A:255:ARG:HH21	2:B:1070:GLN:HG3	1.72	0.54
1:A:177:TRP:CG	1:A:284:ARG:HH21	2.26	0.54
2:B:822:LYS:HG3	2:B:827:ARG:HH22	1.73	0.53
2:B:942:TRP:O	2:B:946:ARG:HG3	2.09	0.53
2:B:846:LYS:C	2:B:848:GLN:H	2.17	0.53
2:B:644:ASP:O	2:B:648:ASN:N	2.41	0.53
2:B:217:SER:OG	2:B:218:SER:N	2.42	0.53
2:B:589:ASN:OD1	2:B:608:ARG:HB3	2.09	0.53
2:B:477:GLY:HA2	2:B:509:ASP:HB2	1.90	0.53
2:B:573:THR:OG1	2:B:574:GLN:N	2.42	0.53
2:B:626:TYR:HA	2:B:629:LEU:HD22	1.89	0.52
2:B:94:ASN:OD1	2:B:95:ASN:N	2.39	0.52
2:B:1058:THR:HG23	2:B:1066:PRO:HB3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1173:SER:OG	2:B:1176:ASP:OD2	2.28	0.52
1:A:212:VAL:HG12	1:A:219:ALA:HB2	1.92	0.52
2:B:799:LEU:HB3	2:B:863:VAL:HG22	1.91	0.52
2:B:832:ARG:HG3	2:B:835:ARG:HD2	1.92	0.52
2:B:825:PHE:CE1	2:B:827:ARG:HB3	2.45	0.52
2:B:359:HIS:CD2	2:B:388:ILE:HG13	2.45	0.51
2:B:602:ARG:HH11	2:B:695:GLU:HG2	1.75	0.51
2:B:16:GLN:CD	2:B:16:GLN:H	2.18	0.51
2:B:454:PHD:OD1	2:B:455:LYS:N	2.43	0.51
1:A:81:ALA:HA	1:A:86:ARG:CZ	2.41	0.50
2:B:718:ILE:HD12	2:B:746:CYS:HB2	1.94	0.50
2:B:454:PHD:OP1	2:B:896:ASN:ND2	2.35	0.50
2:B:448:ILE:HD11	2:B:906:ILE:HD12	1.93	0.50
2:B:1223:SER:HB3	2:B:1225:ARG:NH2	2.26	0.50
2:B:1033:PHE:CZ	2:B:1037:LEU:HD11	2.47	0.49
2:B:363:GLU:OE2	2:B:384:ARG:NH2	2.46	0.49
2:B:89:GLU:HG2	2:B:90:SER:H	1.78	0.49
1:A:205:LYS:HD3	2:B:1133:THR:HB	1.93	0.49
1:A:342:TYR:O	1:A:343:GLN:NE2	2.38	0.49
2:B:251:GLN:O	2:B:252:ARG:HG3	2.13	0.49
2:B:674:MET:HE2	2:B:674:MET:HA	1.95	0.49
2:B:200:ILE:HD11	2:B:212:ILE:HG21	1.93	0.49
2:B:644:ASP:OD2	2:B:1205:ARG:NH2	2.46	0.49
2:B:664:LYS:C	2:B:664:LYS:CD	2.85	0.49
2:B:252:ARG:NH2	2:B:254:ASP:OD2	2.46	0.48
2:B:151:VAL:HG21	2:B:402:ILE:HG13	1.95	0.48
2:B:685:GLU:OE1	2:B:685:GLU:N	2.46	0.48
2:B:221:ASN:HB3	2:B:241:MET:HE1	1.95	0.48
2:B:677:SER:HA	2:B:687:LEU:HD13	1.95	0.48
2:B:687:LEU:HA	2:B:690:VAL:HG12	1.95	0.48
2:B:987:LEU:HD22	2:B:991:LEU:HD12	1.96	0.48
1:A:74:GLY:O	1:A:77:SER:OG	2.24	0.48
2:B:630:HIS:O	2:B:633:ASN:ND2	2.46	0.48
2:B:832:ARG:CG	2:B:835:ARG:HD2	2.43	0.48
2:B:379:ASP:HB2	2:B:384:ARG:HE	1.79	0.48
2:B:761:ILE:HD12	2:B:856:LEU:HD21	1.95	0.47
2:B:99:THR:HG21	2:B:920:MET:HE3	1.96	0.47
2:B:477:GLY:N	2:B:509:ASP:OD2	2.44	0.47
2:B:1037:LEU:O	2:B:1041:VAL:HG13	2.13	0.47
1:A:201:ASP:OD1	1:A:255:ARG:NH1	2.48	0.47
2:B:773:ARG:NH2	2:B:785:PRO:HB3	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:967:TRP:CZ2	2:B:1045:MET:HE2	2.49	0.47
2:B:1050:ILE:HB	2:B:1051:PRO:HD3	1.96	0.47
2:B:153:GLY:O	2:B:157:ILE:HG12	2.15	0.46
2:B:461:GLN:HG2	2:B:709:LYS:O	2.14	0.46
2:B:398:THR:HG23	2:B:962:THR:HB	1.97	0.46
2:B:445:LEU:HD12	2:B:906:ILE:HD13	1.96	0.46
2:B:1060:GLY:HA3	2:B:1064:GLU:HA	1.97	0.46
2:B:1199:ARG:HH21	2:B:1204:THR:H	1.64	0.46
2:B:464:MET:HE2	2:B:553:PRO:HB2	1.98	0.46
1:A:113:GLU:HB3	1:A:301:LEU:HB2	1.98	0.46
2:B:82:THR:HG23	2:B:88:LYS:HE2	1.98	0.46
2:B:238:LYS:HD2	2:B:1214:GLN:NE2	2.31	0.46
2:B:1174:GLU:O	2:B:1178:ILE:HG12	2.16	0.46
2:B:243:LEU:HD12	2:B:244:GLU:H	1.80	0.46
2:B:250:LEU:O	2:B:252:ARG:N	2.49	0.46
2:B:594:LEU:HD12	2:B:604:SER:OG	2.16	0.46
2:B:281:TRP:CD1	2:B:282:ARG:HG2	2.51	0.45
2:B:224:CYS:HA	2:B:303:THR:HG21	1.99	0.45
2:B:243:LEU:HG	2:B:245:ILE:HG22	1.98	0.45
2:B:245:ILE:HG21	2:B:286:PHE:CE2	2.52	0.45
2:B:600:ARG:HD2	2:B:602:ARG:CZ	2.47	0.45
1:A:26:TRP:CZ2	1:A:28:PRO:HB3	2.51	0.44
2:B:108:ILE:HB	2:B:109:PRO:HD3	1.98	0.44
2:B:95:ASN:HB2	2:B:194:ILE:O	2.17	0.44
2:B:822:LYS:HB2	2:B:828:THR:HG21	1.98	0.44
2:B:835:ARG:HD3	2:B:835:ARG:H	1.82	0.44
2:B:622:ASP:OD1	2:B:622:ASP:N	2.47	0.44
2:B:85:LEU:HB3	2:B:87:ILE:HD12	1.99	0.44
2:B:177:THR:HA	2:B:189:ALA:O	2.17	0.44
2:B:712:ASP:O	2:B:930:ARG:NH2	2.42	0.44
2:B:843:GLU:N	2:B:843:GLU:OE1	2.51	0.44
1:A:66:ASP:HA	1:A:301:LEU:HG	1.99	0.44
2:B:25:SER:OG	2:B:26:ASP:N	2.51	0.44
2:B:611:GLU:N	2:B:611:GLU:OE1	2.50	0.44
1:A:96:TRP:HZ3	1:A:98:PHE:HB3	1.80	0.44
2:B:336:LEU:O	2:B:340:MET:HG3	2.18	0.44
2:B:594:LEU:HD22	2:B:691:TYR:CD1	2.53	0.44
2:B:669:TRP:CG	2:B:694:ILE:HD11	2.53	0.44
2:B:736:LYS:HB3	2:B:736:LYS:HE3	1.72	0.44
2:B:19:ASP:HA	2:B:802:THR:HG21	1.99	0.43
2:B:668:GLU:HA	2:B:671:LYS:NZ	2.32	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:293:VAL:HG21	1:A:300:LYS:HG3	2.01	0.43
2:B:127:LEU:HD11	2:B:397:ASN:HB2	2.00	0.43
2:B:515:GLN:OE1	2:B:524:VAL:HG21	2.18	0.43
2:B:662:GLU:HB3	2:B:663:GLU:H	1.50	0.43
1:A:174:PHE:CE1	1:A:302:LEU:HD21	2.54	0.43
2:B:365:GLN:HG2	2:B:366:VAL:HG23	2.01	0.43
2:B:210:ALA:O	2:B:212:ILE:HG23	2.18	0.43
2:B:455:LYS:HD2	2:B:742:ILE:HG13	2.00	0.43
2:B:780:ALA:C	2:B:782:PHE:H	2.26	0.43
2:B:947:MET:HE2	2:B:947:MET:HB2	1.81	0.43
2:B:958:ASN:O	2:B:962:THR:HG22	2.19	0.43
2:B:479:HIS:O	2:B:480:ARG:HD3	2.18	0.43
2:B:534:CYS:O	2:B:619:LYS:NZ	2.52	0.43
2:B:878:ASP:HA	2:B:881:LYS:HG2	2.01	0.43
2:B:1124:VAL:O	2:B:1125:LEU:HG	2.19	0.43
2:B:212:ILE:HD11	2:B:294:LEU:HD12	2.00	0.43
2:B:670:ASN:HA	2:B:673:PHE:CE1	2.54	0.43
2:B:688:ASP:HA	2:B:691:TYR:HD2	1.84	0.43
2:B:704:THR:OG1	2:B:705:ALA:N	2.52	0.43
1:A:287:ILE:HG22	1:A:288:THR:N	2.34	0.42
1:A:284:ARG:NH1	6:A:401:NAG:H5	2.34	0.42
2:B:839:LYS:HD2	2:B:839:LYS:HA	1.62	0.42
2:B:1199:ARG:NE	2:B:1202:VAL:HA	2.34	0.42
2:B:592:ALA:HB3	2:B:606:ILE:HD12	2.02	0.42
2:B:66:VAL:HG23	2:B:196:VAL:HG12	2.01	0.42
2:B:127:LEU:HD23	2:B:127:LEU:HA	1.84	0.42
2:B:586:ARG:NH2	2:B:588:TYR:OH	2.52	0.42
2:B:606:ILE:HG12	2:B:616:LEU:HD12	2.01	0.42
2:B:773:ARG:HA	2:B:773:ARG:NE	2.35	0.42
2:B:555:GLU:O	2:B:559:VAL:HG23	2.20	0.42
1:A:193:ARG:NH1	1:A:249:ASP:OD2	2.53	0.41
2:B:811:LEU:CD2	2:B:845:LYS:HG3	2.46	0.41
2:B:1009:ASP:HA	2:B:1012:SER:HB3	2.02	0.41
2:B:248:GLN:HG3	2:B:249:TYR:CD1	2.56	0.41
2:B:248:GLN:HG3	2:B:249:TYR:HD1	1.85	0.41
2:B:530:LEU:HD12	2:B:617:TYR:HD2	1.85	0.41
2:B:648:ASN:CG	2:B:1196:GLN:HE22	2.29	0.41
1:A:136:LEU:HD23	1:A:136:LEU:HA	1.84	0.41
2:B:826:PRO:HA	2:B:829:GLU:O	2.20	0.41
2:B:444:GLN:HE21	2:B:887:ILE:HG21	1.85	0.41
2:B:650:THR:HG21	2:B:745:ALA:HA	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:677:SER:OG	2:B:683:ARG:NH1	2.53	0.41
2:B:1014:ARG:NH2	2:B:1186:LYS:O	2.50	0.41
2:B:1045:MET:HE3	2:B:1045:MET:HB2	1.87	0.41
2:B:460:THR:HA	2:B:710:LEU:HA	2.03	0.41
2:B:1132:PHE:HB3	2:B:1135:THR:CG2	2.51	0.41
1:A:335:MET:HE3	2:B:1165:PHE:CD2	2.55	0.41
2:B:151:VAL:HG22	2:B:406:VAL:HG21	2.01	0.41
2:B:480:ARG:HB3	2:B:486:ASN:HA	2.02	0.41
2:B:631:ARG:HH22	2:B:632:MET:HE1	1.86	0.41
2:B:658:TYR:CE2	2:B:701:LEU:HD21	2.56	0.41
2:B:668:GLU:OE1	2:B:668:GLU:N	2.51	0.41
2:B:822:LYS:HG3	2:B:827:ARG:NH2	2.35	0.41
2:B:1066:PRO:O	2:B:1067:SER:C	2.63	0.41
5:E:1:NAG:O3	5:E:2:NAG:O5	2.37	0.41
2:B:254:ASP:OD1	2:B:255:THR:N	2.54	0.40
2:B:581:GLU:O	2:B:584:THR:OG1	2.38	0.40
2:B:630:HIS:ND1	2:B:697:ASP:OD1	2.54	0.40
2:B:525:ARG:HH11	2:B:582:LEU:HG	1.86	0.40
2:B:843:GLU:O	2:B:847:GLU:HB3	2.20	0.40
2:B:66:VAL:HG13	2:B:67:LYS:N	2.37	0.40
2:B:175:ASN:HA	2:B:190:LYS:HD2	2.03	0.40
2:B:182:LYS:HD3	2:B:182:LYS:HA	1.85	0.40
2:B:530:LEU:HD22	2:B:656:LEU:HD23	2.03	0.40
2:B:825:PHE:CD1	2:B:827:ARG:HB3	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	336/363 (93%)	310 (92%)	26 (8%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	B	1178/1294 (91%)	1016 (86%)	162 (14%)	0	100	100
All	All	1514/1657 (91%)	1326 (88%)	188 (12%)	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	275/296 (93%)	275 (100%)	0	100	100
2	B	1035/1126 (92%)	1032 (100%)	3 (0%)	86	84
All	All	1310/1422 (92%)	1307 (100%)	3 (0%)	85	85

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	600	ARG
2	B	662	GLU
2	B	663	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	21	GLN
1	A	132	GLN
1	A	178	HIS
1	A	271	GLN
2	B	131	GLN
2	B	221	ASN
2	B	397	ASN
2	B	449	HIS
2	B	462	ASN
2	B	472	ASN

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Mol	Chain	Res	Type
2	B	535	HIS
2	B	545	GLN
2	B	549	GLN
2	B	633	ASN
2	B	913	GLN
2	B	1039	HIS
2	B	1196	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	PHD	B	454	2,7	9,11,12	3.51	1 (11%)	9,15,17	1.95	4 (44%)

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	PHD	B	454	2,7	-	2/8/11/13	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	454	PHD	P-OD1	10.14	1.78	1.59

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	454	PHD	CA-CB-CG	3.08	119.38	112.78
2	B	454	PHD	OP2-P-OD1	-2.86	96.98	105.32
2	B	454	PHD	OD1-CG-CB	2.57	116.99	110.95
2	B	454	PHD	OP3-P-OP1	2.18	119.34	110.83

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	454	PHD	CA-CB-CG-OD1
2	B	454	PHD	C-CA-CB-CG

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	454	PHD	2	0

5.5 Carbohydrates [i](#)

12 monosaccharides are modelled in this entry.

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	NAG	C	1	2,3	14,14,15	0.42	0	17,19,21	1.38	2 (11%)
3	NAG	C	2	3	14,14,15	0.21	0	17,19,21	0.40	0
3	MAN	C	3	3	11,11,12	0.63	0	15,15,17	1.08	2 (13%)
3	MAN	C	4	3	12,12,12	0.46	0	17,17,17	0.95	2 (11%)
4	NAG	D	1	1,4	14,14,15	0.41	0	17,19,21	0.50	0
4	NAG	D	2	4	14,14,15	0.38	0	17,19,21	1.45	2 (11%)
4	MAN	D	3	4	11,11,12	1.06	1 (9%)	15,15,17	0.88	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	MAN	D	4	4	11,11,12	0.55	0	15,15,17	0.97	1 (6%)
4	MAN	D	5	4	11,11,12	0.81	1 (9%)	15,15,17	1.26	2 (13%)
4	MAN	D	6	4	11,11,12	0.95	1 (9%)	15,15,17	1.32	2 (13%)
5	NAG	E	1	5,1	14,14,15	0.43	0	17,19,21	0.43	0
5	NAG	E	2	5	14,14,15	0.33	0	17,19,21	0.54	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	NAG	C	1	2,3	-	6/6/23/26	0/1/1/1
3	NAG	C	2	3	-	2/6/23/26	0/1/1/1
3	MAN	C	3	3	-	1/2/19/22	1/1/1/1
3	MAN	C	4	3	-	2/2/22/22	0/1/1/1
4	NAG	D	1	1,4	-	4/6/23/26	0/1/1/1
4	NAG	D	2	4	-	5/6/23/26	0/1/1/1
4	MAN	D	3	4	-	2/2/19/22	0/1/1/1
4	MAN	D	4	4	-	0/2/19/22	0/1/1/1
4	MAN	D	5	4	-	2/2/19/22	0/1/1/1
4	MAN	D	6	4	-	1/2/19/22	1/1/1/1
5	NAG	E	1	5,1	-	4/6/23/26	0/1/1/1
5	NAG	E	2	5	-	4/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	6	MAN	C1-C2	2.62	1.58	1.52
4	D	3	MAN	C2-C3	2.20	1.55	1.52
4	D	5	MAN	C1-C2	2.08	1.57	1.52

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	2	NAG	C2-N2-C7	4.73	129.24	122.90
3	C	1	NAG	C2-N2-C7	4.60	129.06	122.90
4	D	6	MAN	C1-O5-C5	3.55	116.94	112.19
4	D	5	MAN	C1-O5-C5	3.43	116.78	112.19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	6	MAN	O2-C2-C3	-2.98	103.98	110.15
3	C	3	MAN	C1-O5-C5	2.94	116.13	112.19
4	D	4	MAN	C1-O5-C5	2.63	115.71	112.19
4	D	2	NAG	C1-C2-N2	2.40	114.22	110.43
3	C	3	MAN	O2-C2-C3	-2.31	105.37	110.15
3	C	1	NAG	C1-C2-N2	2.28	114.03	110.43
4	D	5	MAN	O2-C2-C3	-2.24	105.51	110.15
3	C	4	MAN	O5-C1-C2	2.17	114.12	110.30
3	C	4	MAN	O2-C2-C3	-2.05	105.55	110.38

There are no chirality outliers.

All (33) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	C	2	NAG	C4-C5-C6-O6
5	E	2	NAG	O5-C5-C6-O6
3	C	2	NAG	O5-C5-C6-O6
4	D	3	MAN	O5-C5-C6-O6
3	C	1	NAG	O5-C5-C6-O6
5	E	2	NAG	C4-C5-C6-O6
5	E	1	NAG	O5-C5-C6-O6
4	D	3	MAN	C4-C5-C6-O6
4	D	1	NAG	O5-C5-C6-O6
3	C	4	MAN	O5-C5-C6-O6
4	D	1	NAG	C4-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
3	C	1	NAG	C8-C7-N2-C2
3	C	1	NAG	O7-C7-N2-C2
4	D	1	NAG	C8-C7-N2-C2
4	D	1	NAG	O7-C7-N2-C2
4	D	2	NAG	C8-C7-N2-C2
4	D	2	NAG	O7-C7-N2-C2
5	E	1	NAG	C8-C7-N2-C2
5	E	1	NAG	O7-C7-N2-C2
5	E	2	NAG	C8-C7-N2-C2
5	E	2	NAG	O7-C7-N2-C2
5	E	1	NAG	C4-C5-C6-O6
4	D	5	MAN	O5-C5-C6-O6
3	C	3	MAN	O5-C5-C6-O6
4	D	5	MAN	C4-C5-C6-O6
4	D	6	MAN	O5-C5-C6-O6
4	D	2	NAG	C4-C5-C6-O6

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Mol	Chain	Res	Type	Atoms
4	D	2	NAG	C3-C2-N2-C7
3	C	4	MAN	C4-C5-C6-O6
3	C	1	NAG	C1-C2-N2-C7
4	D	2	NAG	C1-C2-N2-C7
3	C	1	NAG	C3-C2-N2-C7

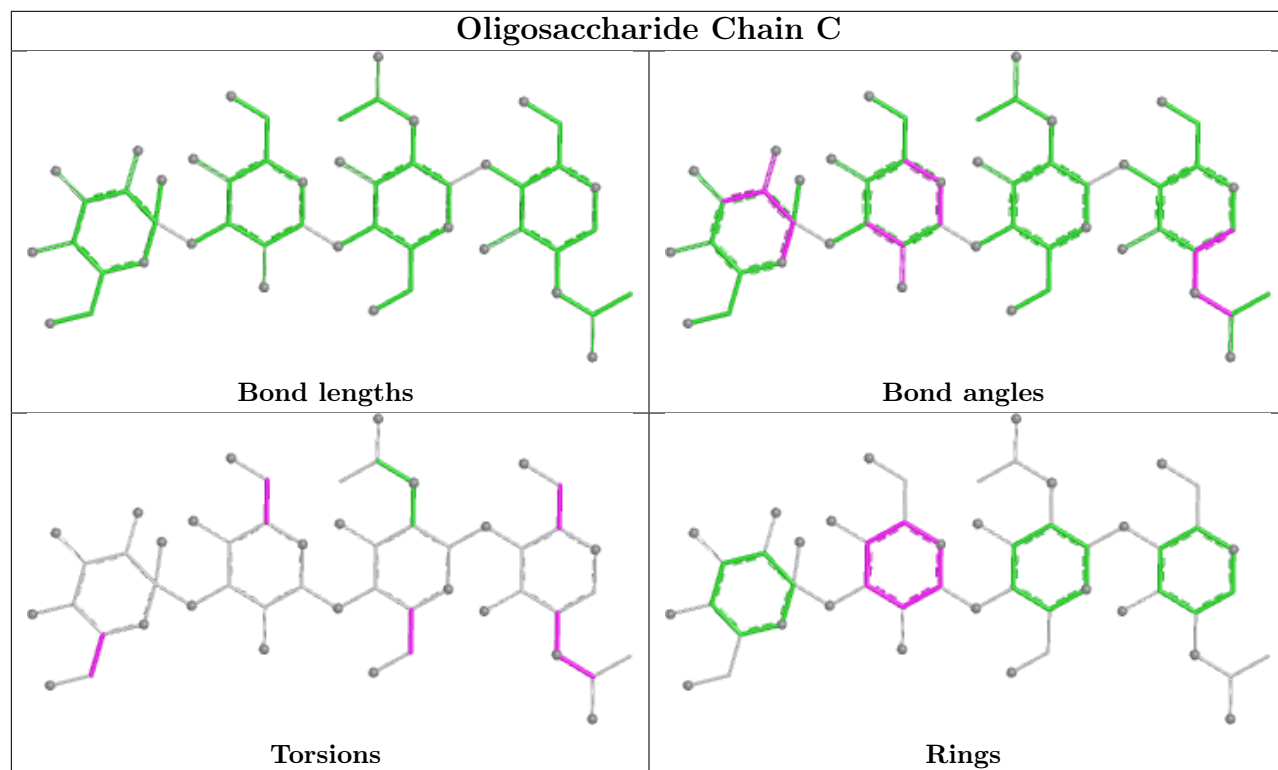
All (2) ring outliers are listed below:

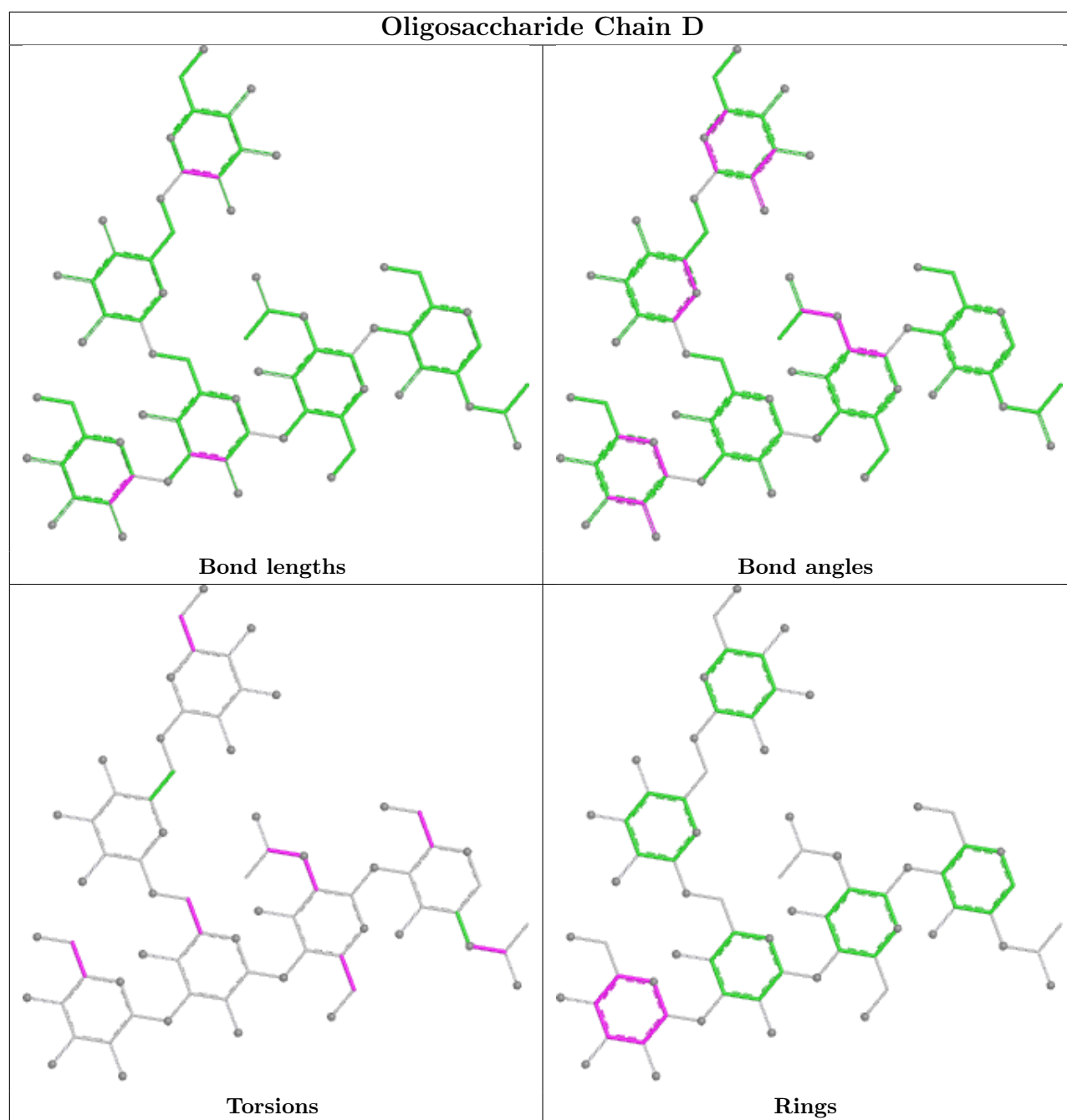
Mol	Chain	Res	Type	Atoms
3	C	3	MAN	C1-C2-C3-C4-C5-O5
4	D	6	MAN	C1-C2-C3-C4-C5-O5

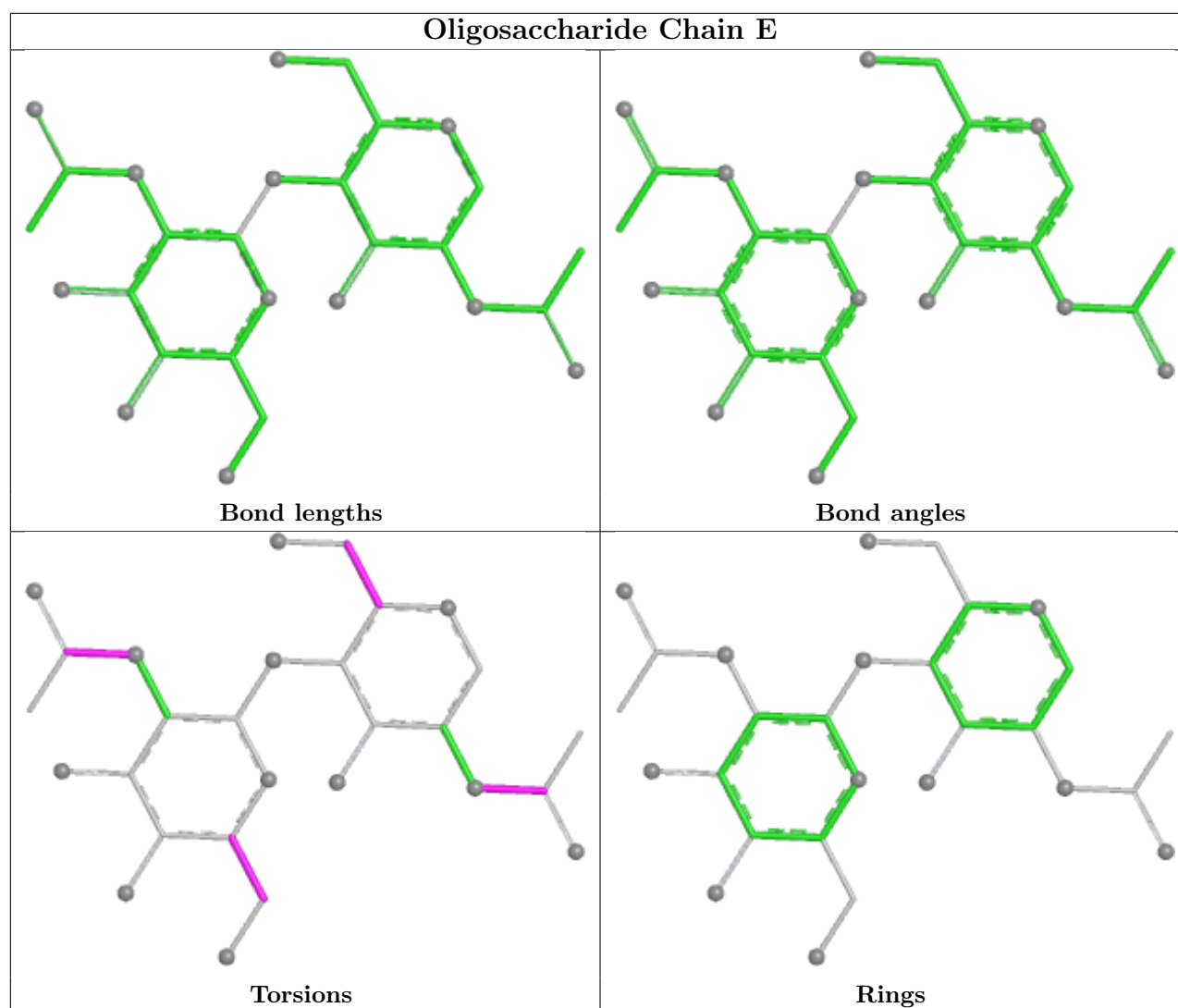
6 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	2	NAG	1	0
4	D	2	NAG	1	0
4	D	1	NAG	1	0
3	C	1	NAG	2	0
5	E	2	NAG	1	0
5	E	1	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.







5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 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	$\# Z > 2$
6	NAG	A	401	1	14,14,15	0.36	0	17,19,21	0.43	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
6	NAG	A	401	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	401	NAG	C4-C5-C6-O6
6	A	401	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	401	NAG	1	0

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.

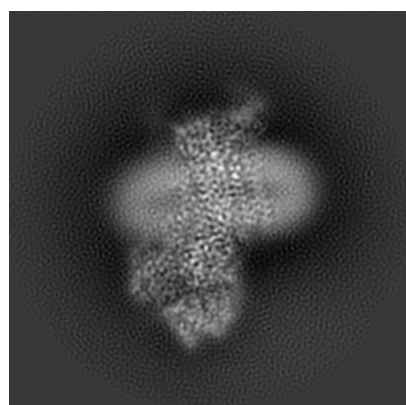
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-31969. These allow visual inspection of the internal detail of the map and identification of artifacts.

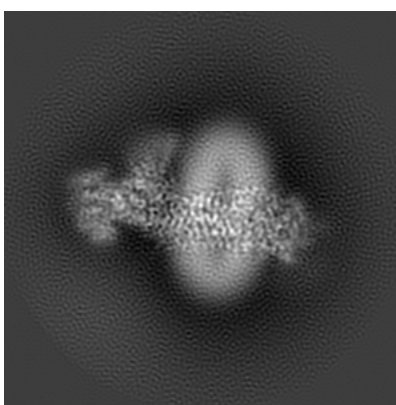
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

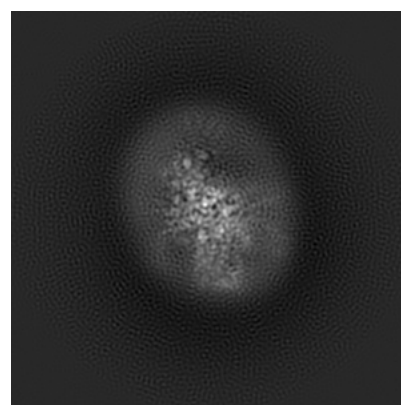
6.1.1 Primary map



X



Y

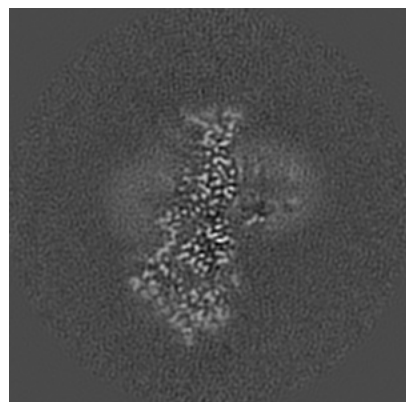


Z

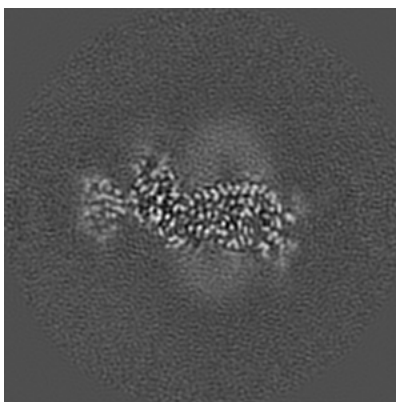
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

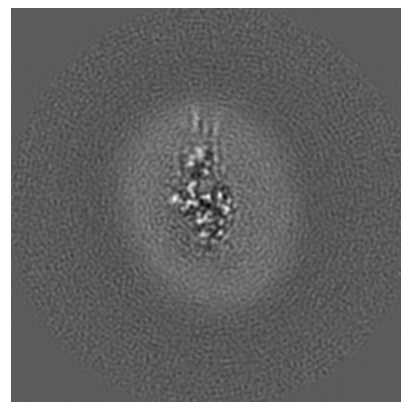
6.2.1 Primary map



X Index: 120



Y Index: 120

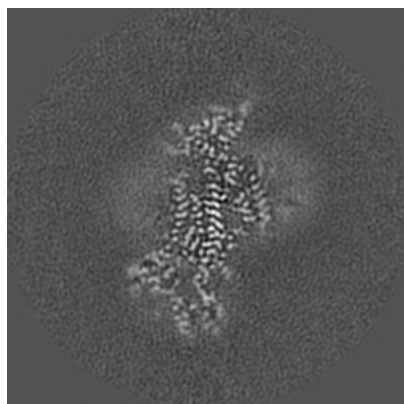


Z Index: 120

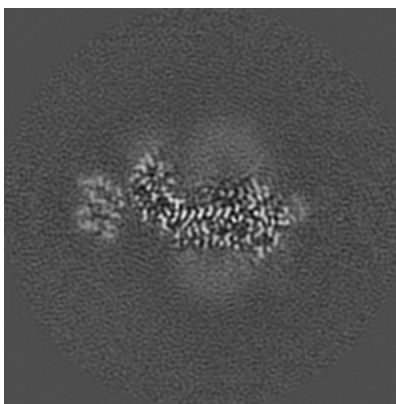
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

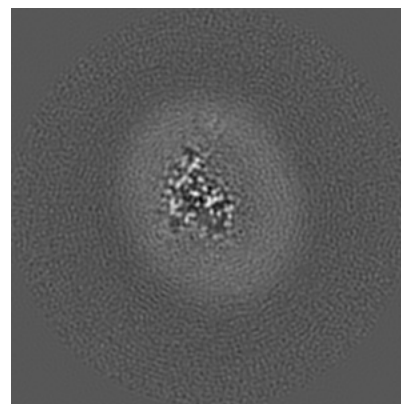
6.3.1 Primary map



X Index: 115



Y Index: 123

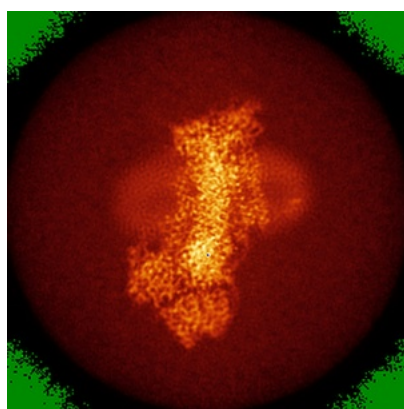


Z Index: 139

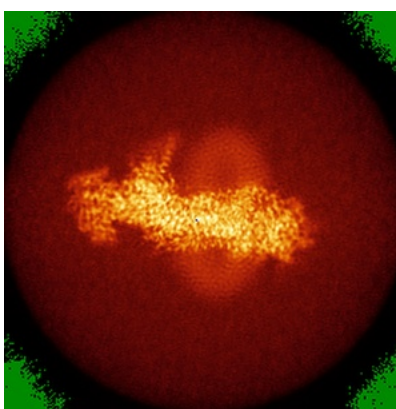
The images above show the largest variance slices of the map in three orthogonal directions.

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

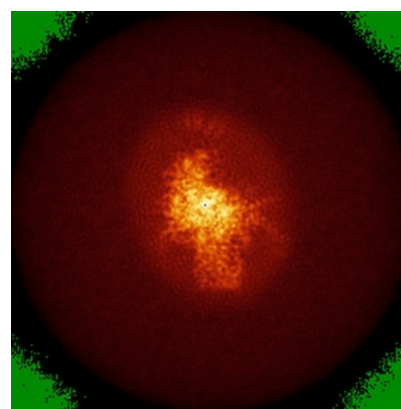
6.4.1 Primary map



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

This section was not generated.

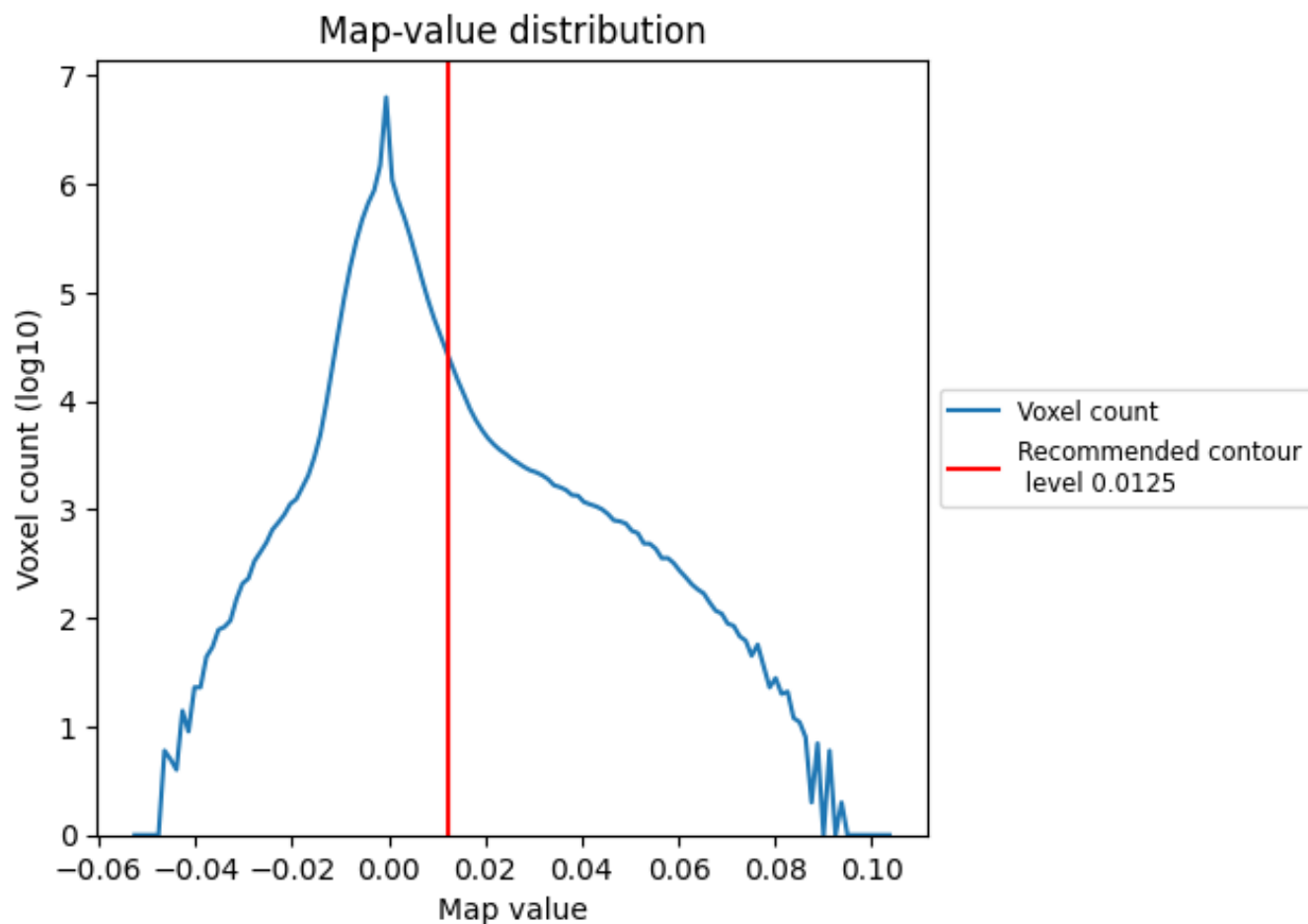
6.6 Mask visualisation

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

7 Map analysis [i](#)

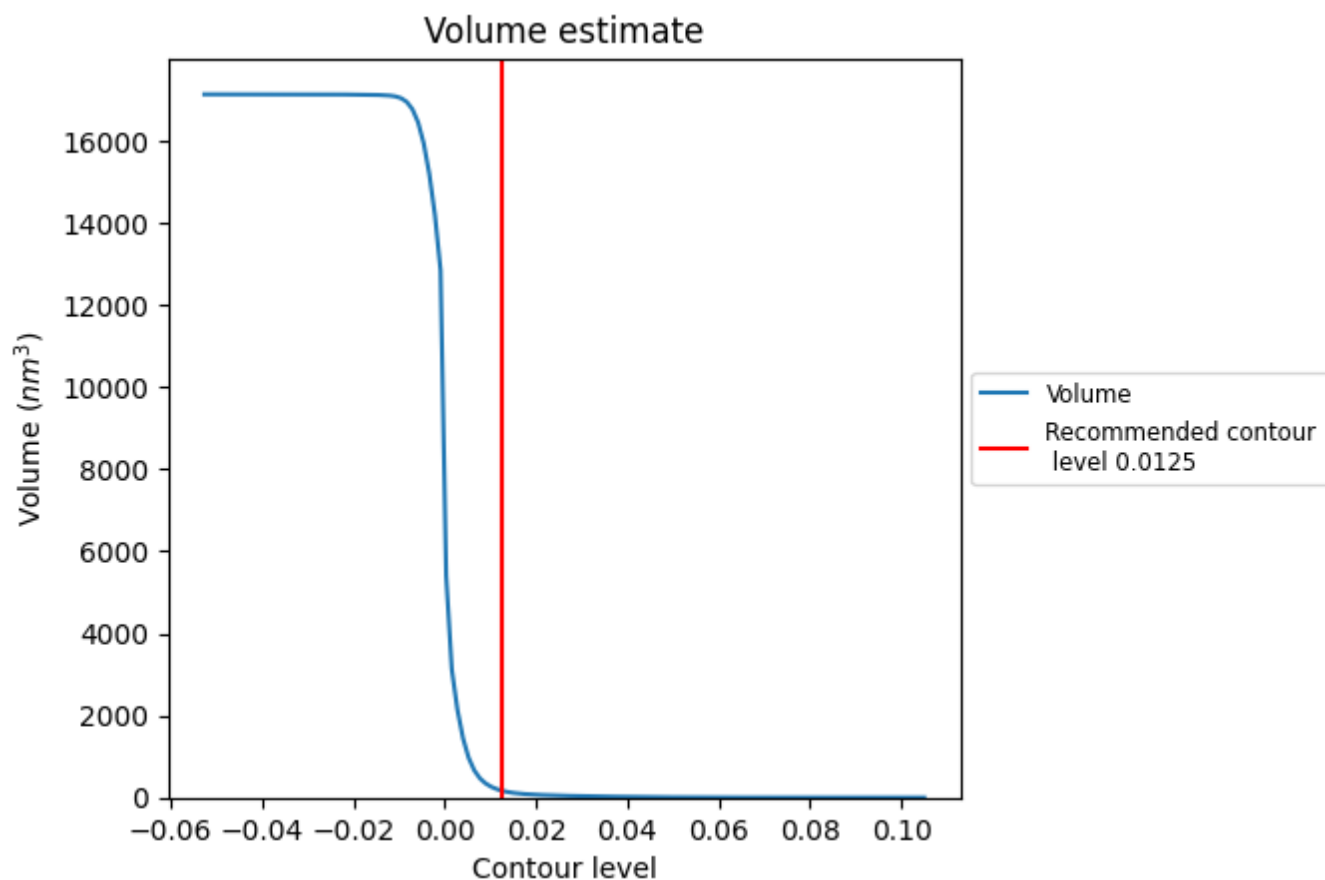
This section contains the results of statistical analysis of the map.

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.

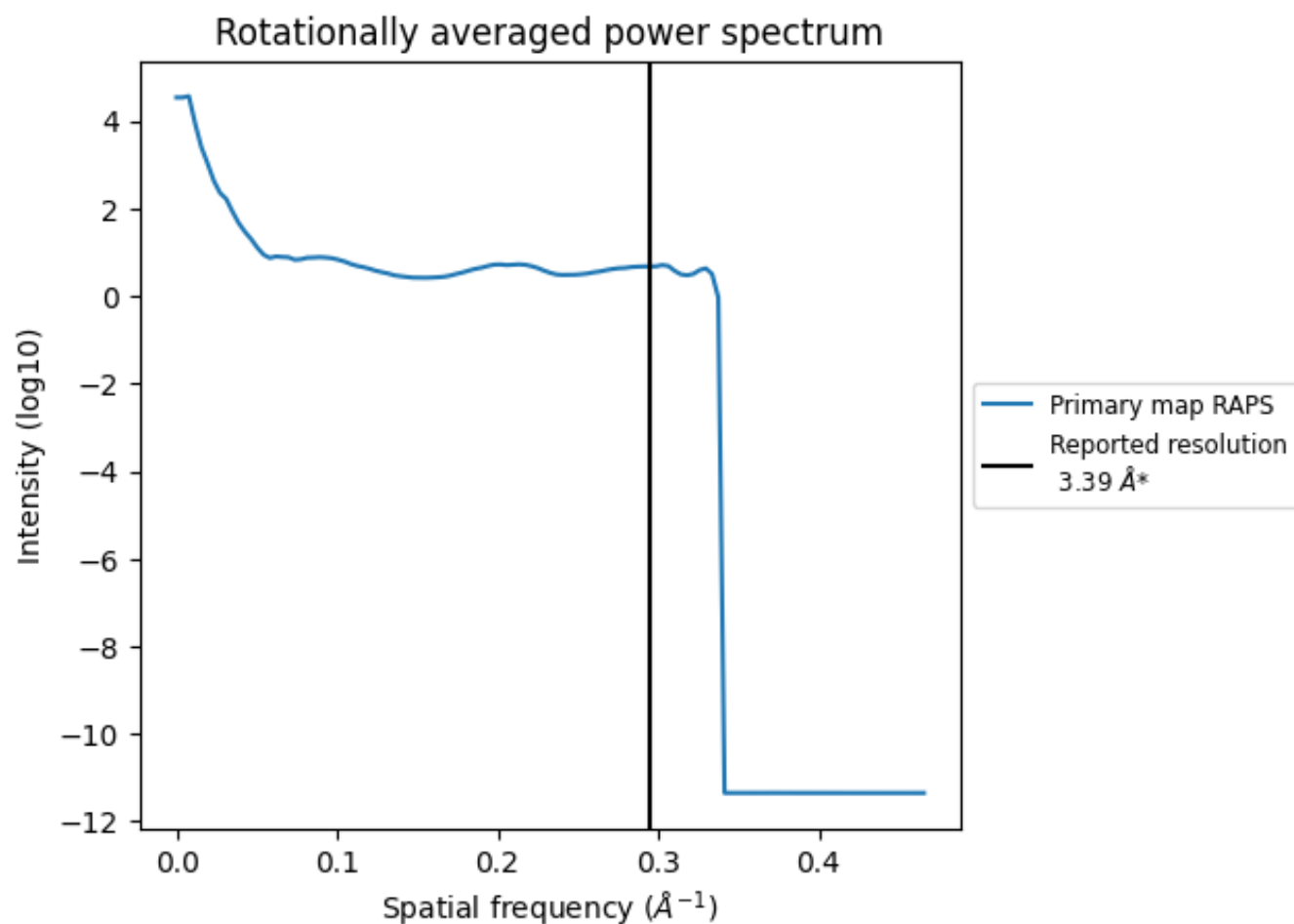
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 169 nm³; this corresponds to an approximate mass of 153 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum ⓘ



*Reported resolution corresponds to spatial frequency of 0.295 Å⁻¹

8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

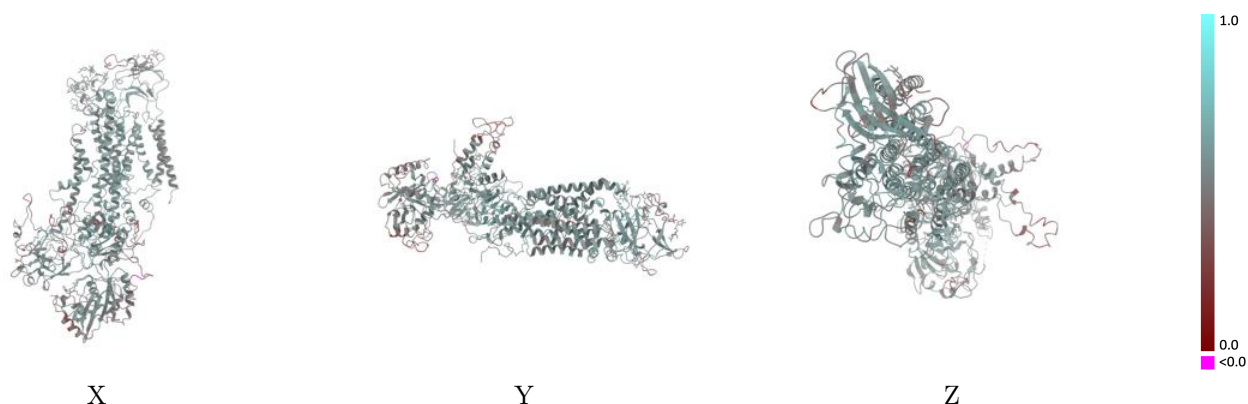
This section contains information regarding the fit between EMDB map EMD-31969 and PDB model 7VGH. Per-residue inclusion information can be found in [section 3](#) on [page 8](#).

9.1 Map-model overlay [i](#)



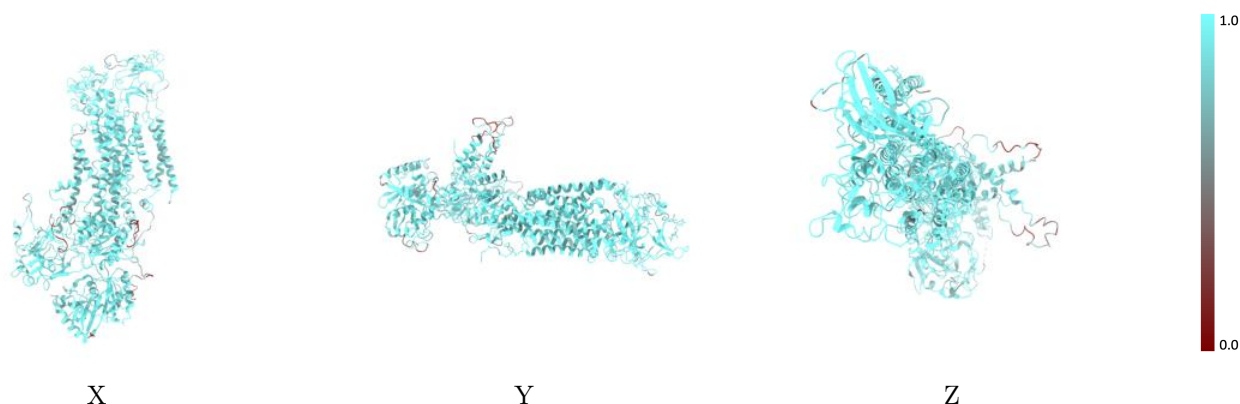
The images above show the 3D surface view of the map at the recommended contour level 0.0125 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



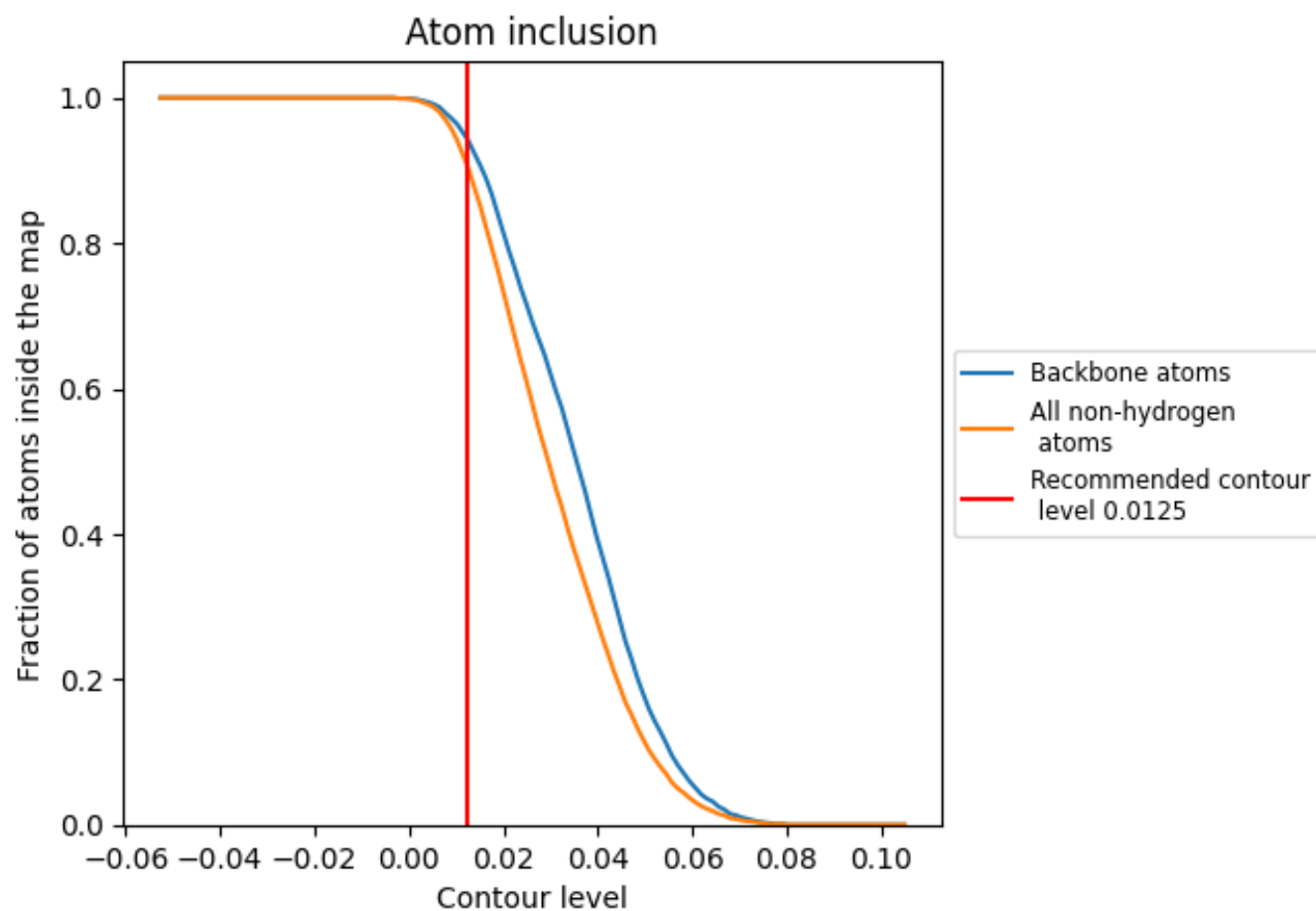
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

9.3 Atom inclusion mapped to coordinate model [i](#)



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.0125).

9.4 Atom inclusion [i](#)



At the recommended contour level, 94% of all backbone atoms, 90% 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 (0.0125) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9050	0.5220
A	0.9360	0.5300
B	0.8970	0.5200
C	0.9410	0.5270
D	0.9030	0.5000
E	0.7860	0.4190

