Full wwPDB EM Validation Report

May 14, 2025 – 01:13 AM EDT

PDB ID	:	9DIY / pdb_00009diy
EMDB ID	:	EMD-46921
Title	:	Local Cryo-EM structure of HCMV gH/UL116 interaction
Authors	:	Norris, M.J.; Benedict, C.A.; Kamil, J.P.; Saphire, E.O.
Deposited on	:	2024-09-06
Resolution	:	5.36 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:

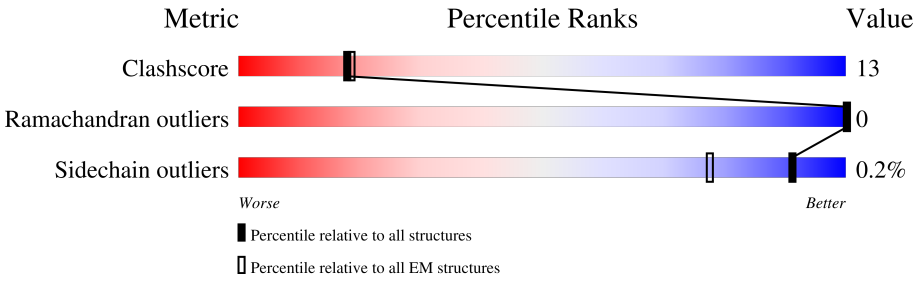
EMDB validation analysis	:	0.0.1.dev118
Mogul	:	2022.3.0, CSD as543be (2022)
MolProbity	:	4-5-2 with Phenix2.0rc1
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

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 5.36 Å.

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



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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	680	23% 9% 68%
2	C	332	20% 12% 68%
3	B	273	64% 16% 19%
4	D	2	100%
5	E	3	67% 33%

2 Entry composition (i)

There are 6 unique types of molecules in this entry. The entry contains 9026 atoms, of which 4401 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 Envelope glycoprotein H.

Mol	Chain	Residues	Atoms						AltConf	Trace
1	A	219	Total	C	H	N	O	S	0	0
			3522	1162	1727	296	330	7		

- Molecule 2 is a protein called UL116.

Mol	Chain	Residues	Atoms						AltConf	Trace
2	C	106	Total	C	H	N	O	S	0	0
			1646	548	794	145	156	3		

There are 43 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	314	GLY	-	expression tag	UNP A8T7J8
C	315	GLY	-	expression tag	UNP A8T7J8
C	316	SER	-	expression tag	UNP A8T7J8
C	317	GLY	-	expression tag	UNP A8T7J8
C	318	GLY	-	expression tag	UNP A8T7J8
C	319	SER	-	expression tag	UNP A8T7J8
C	320	GLY	-	expression tag	UNP A8T7J8
C	321	SER	-	expression tag	UNP A8T7J8
C	322	ASP	-	expression tag	UNP A8T7J8
C	323	ASP	-	expression tag	UNP A8T7J8
C	324	ASP	-	expression tag	UNP A8T7J8
C	325	ASP	-	expression tag	UNP A8T7J8
C	326	LYS	-	expression tag	UNP A8T7J8
C	327	ALA	-	expression tag	UNP A8T7J8
C	328	GLY	-	expression tag	UNP A8T7J8
C	329	TRP	-	expression tag	UNP A8T7J8
C	330	SER	-	expression tag	UNP A8T7J8
C	331	HIS	-	expression tag	UNP A8T7J8
C	332	PRO	-	expression tag	UNP A8T7J8
C	333	GLN	-	expression tag	UNP A8T7J8
C	334	PHE	-	expression tag	UNP A8T7J8

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Chain	Residue	Modelled	Actual	Comment	Reference
C	335	GLU	-	expression tag	UNP A8T7J8
C	336	LYS	-	expression tag	UNP A8T7J8
C	337	GLY	-	expression tag	UNP A8T7J8
C	338	GLY	-	expression tag	UNP A8T7J8
C	339	GLY	-	expression tag	UNP A8T7J8
C	340	SER	-	expression tag	UNP A8T7J8
C	341	GLY	-	expression tag	UNP A8T7J8
C	342	GLY	-	expression tag	UNP A8T7J8
C	343	GLY	-	expression tag	UNP A8T7J8
C	344	SER	-	expression tag	UNP A8T7J8
C	345	GLY	-	expression tag	UNP A8T7J8
C	346	GLY	-	expression tag	UNP A8T7J8
C	347	GLY	-	expression tag	UNP A8T7J8
C	348	SER	-	expression tag	UNP A8T7J8
C	349	TRP	-	expression tag	UNP A8T7J8
C	350	SER	-	expression tag	UNP A8T7J8
C	351	HIS	-	expression tag	UNP A8T7J8
C	352	PRO	-	expression tag	UNP A8T7J8
C	353	GLN	-	expression tag	UNP A8T7J8
C	354	PHE	-	expression tag	UNP A8T7J8
C	355	GLU	-	expression tag	UNP A8T7J8
C	356	LYS	-	expression tag	UNP A8T7J8

- Molecule 3 is a protein called Protein UL141.

Mol	Chain	Residues	Atoms						AltConf	Trace
3	B	221	Total	C	H	N	O	S	0	0
			3475	1125	1690	316	327	17		

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	280	GLY	-	expression tag	UNP Q6RJQ3
B	281	SER	-	expression tag	UNP Q6RJQ3
B	282	GLY	-	expression tag	UNP Q6RJQ3
B	283	GLY	-	expression tag	UNP Q6RJQ3
B	284	GLY	-	expression tag	UNP Q6RJQ3
B	285	SER	-	expression tag	UNP Q6RJQ3
B	286	LEU	-	expression tag	UNP Q6RJQ3
B	287	GLU	-	expression tag	UNP Q6RJQ3
B	288	VAL	-	expression tag	UNP Q6RJQ3
B	289	LEU	-	expression tag	UNP Q6RJQ3

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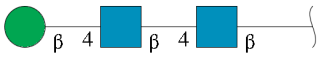
Chain	Residue	Modelled	Actual	Comment	Reference
B	290	PHE	-	expression tag	UNP Q6RJQ3
B	291	GLN	-	expression tag	UNP Q6RJQ3
B	292	GLY	-	expression tag	UNP Q6RJQ3
B	293	PRO	-	expression tag	UNP Q6RJQ3
B	294	GLY	-	expression tag	UNP Q6RJQ3
B	295	HIS	-	expression tag	UNP Q6RJQ3
B	296	HIS	-	expression tag	UNP Q6RJQ3
B	297	HIS	-	expression tag	UNP Q6RJQ3
B	298	HIS	-	expression tag	UNP Q6RJQ3
B	299	HIS	-	expression tag	UNP Q6RJQ3
B	300	HIS	-	expression tag	UNP Q6RJQ3
B	301	HIS	-	expression tag	UNP Q6RJQ3
B	302	HIS	-	expression tag	UNP Q6RJQ3

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

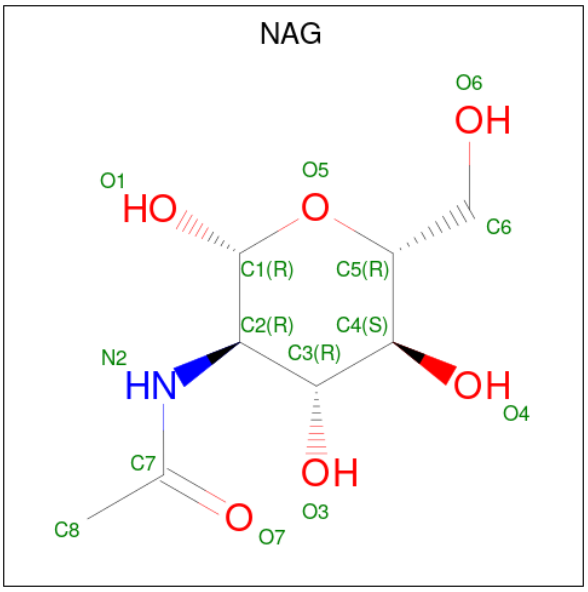
Mol	Chain	Residues	Atoms					AltConf	Trace
4	D	2	Total	C	H	N	O	0	0
			55	16	27	2	10		

- Molecule 5 is an oligosaccharide called beta-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
5	E	3	Total	C	H	N	O	0	0
			76	22	37	2	15		

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



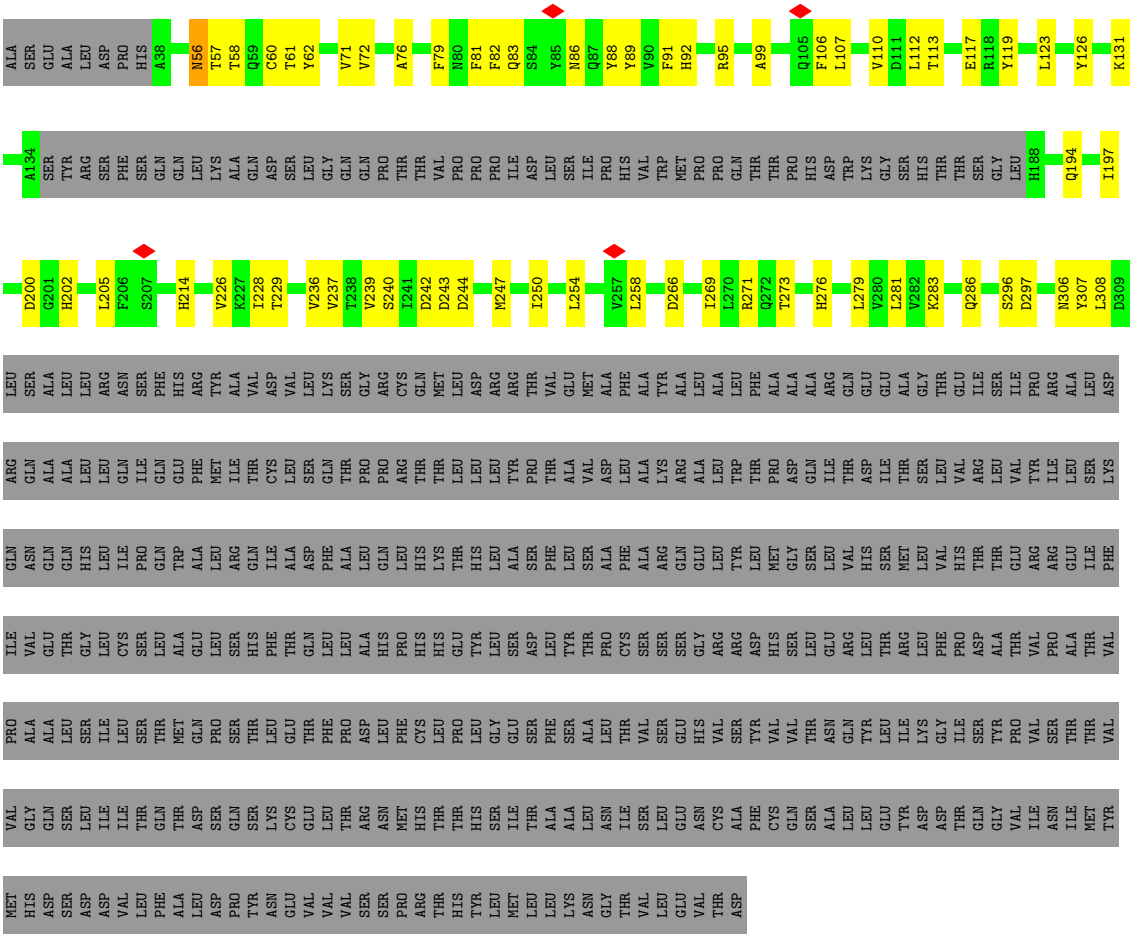
Mol	Chain	Residues	Atoms					AltConf
6	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	A	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	C	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	B	1	Total	C	H	N	O	0
			28	8	14	1	5	
6	B	1	Total	C	H	N	O	0
			28	8	14	1	5	

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.

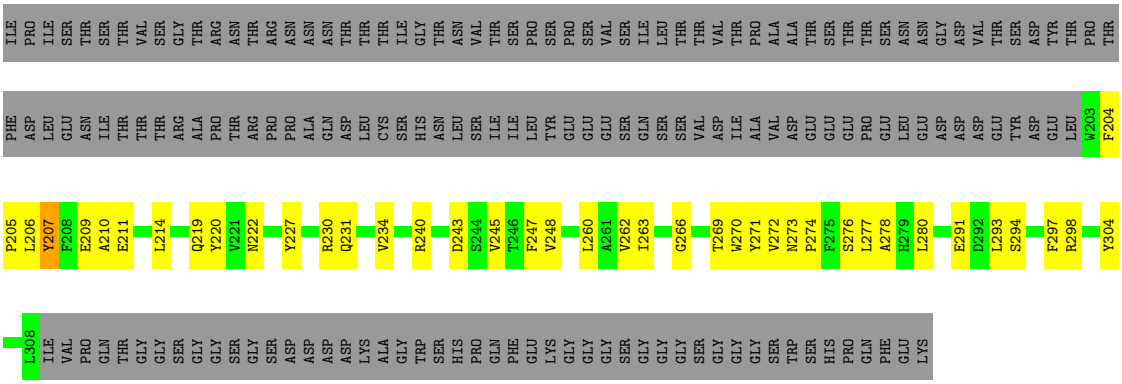
- Molecule 1: Envelope glycoprotein H

Chain A:



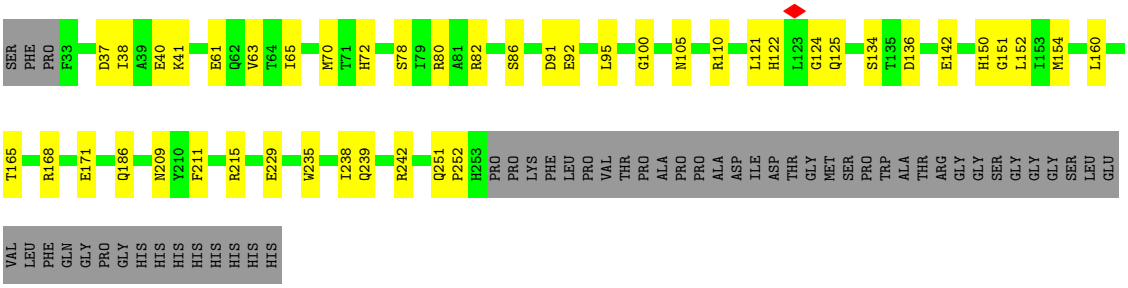
- Molecule 2: UL116

Chain C:



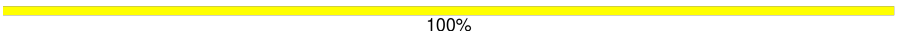
• Molecule 3: Protein UL141

Chain B:



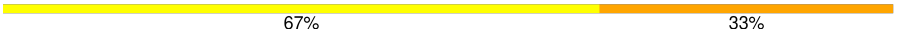
• Molecule 4: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D:



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

Chain E:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	112666	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 ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2500	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.791	Depositor
Minimum map value	-0.404	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.016	Depositor
Recommended contour level	0.0625	Depositor
Map size (Å)	211.20001, 211.20001, 211.20001	wwPDB
Map dimensions	160, 160, 160	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: BMA, 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	0.20	0/1840	0.50	0/2502
2	C	0.19	0/879	0.48	0/1207
3	B	0.14	0/1838	0.36	0/2504
All	All	0.17	0/4557	0.44	0/6213

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	1
2	C	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	58	THR	Peptide
2	C	207	TYR	Peptide

5.2 Too-close contacts

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

the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1795	1727	1723	61	0
2	C	852	794	792	48	0
3	B	1785	1690	1689	36	0
4	D	28	27	25	0	0
5	E	39	37	34	1	0
6	A	28	28	26	0	0
6	B	28	28	26	0	0
6	C	70	70	65	5	0
All	All	4625	4401	4380	118	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 13.

All (118) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:200:ASP:OD2	3:B:110:ARG:NE	2.09	0.84
1:A:112:LEU:HD23	2:C:272:VAL:HG12	1.61	0.81
1:A:243:ASP:O	3:B:80:ARG:NH2	2.12	0.81
2:C:231:GLN:N	2:C:231:GLN:OE1	2.18	0.77
1:A:247:MET:SD	1:A:286:GLN:NE2	2.60	0.74
1:A:194:GLN:NE2	3:B:229:GLU:OE2	2.22	0.73
1:A:99:ALA:O	2:C:240:ARG:NH2	2.22	0.72
1:A:86:ASN:OD1	2:C:214:LEU:N	2.23	0.71
1:A:240:SER:OG	1:A:242:ASP:OD1	2.09	0.71
1:A:214:HIS:ND1	1:A:229:THR:OG1	2.24	0.71
6:C:404:NAG:O7	6:C:404:NAG:O3	2.09	0.70
1:A:117:GLU:N	1:A:117:GLU:OE1	2.26	0.68
1:A:88:TYR:O	2:C:211:GLU:N	2.27	0.67
1:A:89:TYR:CD1	2:C:210:ALA:HB2	2.31	0.66
2:C:214:LEU:O	6:C:403:NAG:H83	1.98	0.64
1:A:214:HIS:ND1	1:A:228:ILE:O	2.30	0.64
1:A:283:LYS:NZ	3:B:37:ASP:OD2	2.32	0.63
3:B:215:ARG:O	3:B:215:ARG:NE	2.31	0.61
3:B:121:LEU:O	3:B:124:GLY:N	2.34	0.61
2:C:211:GLU:N	2:C:211:GLU:OE1	2.34	0.60
1:A:306:ASN:OD1	1:A:307:TYR:N	2.35	0.59
1:A:269:ILE:HG22	1:A:271:ARG:N	2.18	0.58
1:A:269:ILE:HG22	1:A:271:ARG:H	1.68	0.58
1:A:131:LYS:NZ	1:A:266:ASP:O	2.27	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:106:PHE:CE1	2:C:280:LEU:HD21	2.40	0.57
3:B:160:LEU:HD11	3:B:238:ILE:HD13	1.85	0.57
3:B:125:GLN:N	3:B:125:GLN:OE1	2.38	0.56
3:B:165:THR:OG1	3:B:209:ASN:O	2.20	0.56
1:A:82:PHE:CE1	2:C:248:VAL:HG23	2.40	0.56
1:A:243:ASP:OD2	3:B:82:ARG:NH1	2.39	0.56
3:B:95:LEU:HD11	3:B:100:GLY:O	2.06	0.55
1:A:82:PHE:HA	1:A:88:TYR:HA	1.87	0.55
1:A:205:LEU:HD11	1:A:258:LEU:HG	1.88	0.54
1:A:126:TYR:CE1	1:A:281:LEU:HD12	2.43	0.53
1:A:250:ILE:N	1:A:279:LEU:O	2.39	0.53
2:C:204:PHE:CG	2:C:293:LEU:HD21	2.44	0.53
1:A:89:TYR:HA	2:C:210:ALA:HA	1.90	0.53
2:C:243:ASP:OD2	2:C:266:GLY:N	2.42	0.52
1:A:273:THR:OG1	1:A:276:HIS:O	2.27	0.52
1:A:88:TYR:CZ	2:C:214:LEU:HD23	2.45	0.51
3:B:134:SER:OG	3:B:136:ASP:OD1	2.28	0.51
1:A:83:GLN:O	1:A:83:GLN:NE2	2.42	0.51
1:A:243:ASP:OD2	3:B:80:ARG:NH1	2.43	0.51
1:A:228:ILE:HG13	1:A:237:VAL:HG12	1.92	0.51
1:A:242:ASP:O	1:A:244:ASP:N	2.41	0.51
3:B:105:ASN:O	3:B:105:ASN:OD1	2.28	0.50
1:A:112:LEU:HG	2:C:276:SER:OG	2.12	0.50
1:A:112:LEU:HD23	2:C:272:VAL:CG1	2.38	0.49
1:A:61:THR:HG22	1:A:62:TYR:N	2.26	0.49
1:A:296:SER:OG	1:A:297:ASP:N	2.45	0.49
1:A:88:TYR:CE1	2:C:214:LEU:HD23	2.48	0.48
2:C:206:LEU:HD12	2:C:206:LEU:N	2.29	0.47
2:C:219:GLN:OE1	2:C:219:GLN:N	2.45	0.47
1:A:72:VAL:HG22	1:A:76:ALA:HB3	1.94	0.47
3:B:168:ARG:HB2	3:B:171:GLU:OE1	2.14	0.47
3:B:251:GLN:OE1	3:B:251:GLN:N	2.47	0.47
3:B:61:GLU:OE2	3:B:63:VAL:N	2.47	0.47
3:B:186:GLN:NE2	3:B:242:ARG:HE	2.13	0.47
3:B:91:ASP:OD2	3:B:91:ASP:N	2.48	0.47
2:C:291:GLU:O	2:C:298:ARG:NH2	2.44	0.47
3:B:70:MET:O	3:B:72:HIS:ND1	2.48	0.46
2:C:277:LEU:HD12	2:C:278:ALA:N	2.30	0.46
1:A:61:THR:HG22	1:A:62:TYR:H	1.81	0.46
2:C:266:GLY:O	6:C:402:NAG:N2	2.48	0.46
1:A:56:ASN:HA	2:C:206:LEU:HD22	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:150:HIS:ND1	5:E:1:NAG:H5	2.31	0.46
1:A:106:PHE:O	1:A:107:LEU:C	2.58	0.46
2:C:230:ARG:O	2:C:230:ARG:NH1	2.44	0.45
1:A:60:CYS:HA	2:C:209:GLU:OE1	2.17	0.45
2:C:266:GLY:O	6:C:402:NAG:H82	2.17	0.45
3:B:78:SER:OG	3:B:92:GLU:OE1	2.32	0.45
2:C:263:ILE:O	2:C:269:THR:HG23	2.17	0.45
1:A:226:VAL:HG22	1:A:239:VAL:HG23	1.98	0.44
1:A:106:PHE:HE1	1:A:110:VAL:HG13	1.82	0.44
3:B:38:ILE:HG23	3:B:41:LYS:HE3	2.00	0.44
3:B:65:ILE:O	3:B:65:ILE:HG13	2.16	0.44
1:A:119:TYR:O	1:A:123:LEU:HG	2.17	0.44
1:A:307:TYR:O	1:A:308:LEU:HG	2.18	0.44
2:C:220:TYR:O	2:C:222:ASN:ND2	2.49	0.44
3:B:92:GLU:OE2	3:B:92:GLU:HA	2.17	0.44
1:A:81:PHE:HZ	2:C:304:TYR:HH	1.63	0.43
1:A:95:ARG:O	1:A:99:ALA:N	2.51	0.43
2:C:204:PHE:CD1	2:C:293:LEU:HD21	2.53	0.43
3:B:38:ILE:HD11	3:B:151:GLY:N	2.34	0.43
1:A:113:THR:HG22	2:C:272:VAL:HG22	1.99	0.43
2:C:260:LEU:HA	2:C:274:PRO:HD3	2.00	0.43
6:C:404:NAG:HO3	6:C:404:NAG:C7	2.23	0.43
3:B:121:LEU:O	3:B:122:HIS:C	2.62	0.43
2:C:231:GLN:O	2:C:234:VAL:HG12	2.19	0.43
3:B:235:TRP:O	3:B:239:GLN:OE1	2.36	0.43
2:C:263:ILE:HD11	2:C:270:TRP:CH2	2.54	0.42
3:B:160:LEU:HD11	3:B:238:ILE:CD1	2.48	0.42
1:A:197:ILE:CG2	3:B:86:SER:OG	2.66	0.42
1:A:250:ILE:HG22	1:A:254:LEU:HD22	2.01	0.42
2:C:209:GLU:OE1	2:C:210:ALA:C	2.62	0.42
2:C:273:ASN:OD1	2:C:273:ASN:C	2.62	0.42
2:C:274:PRO:O	2:C:277:LEU:HG	2.19	0.42
3:B:239:GLN:HB3	3:B:252:PRO:HD3	2.01	0.42
3:B:121:LEU:HB3	3:B:124:GLY:O	2.19	0.42
1:A:71:VAL:HG11	1:A:92:HIS:CE1	2.55	0.42
3:B:40:GLU:OE2	3:B:150:HIS:CG	2.72	0.42
2:C:227:TYR:O	2:C:227:TYR:CG	2.73	0.42
2:C:294:SER:HA	2:C:297:PHE:CE1	2.54	0.42
2:C:247:PHE:CG	2:C:248:VAL:N	2.88	0.41
1:A:113:THR:HG22	2:C:272:VAL:HG13	2.02	0.41
2:C:262:VAL:HG22	2:C:271:TYR:CD2	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:152:LEU:HG	3:B:154:MET:CE	2.50	0.41
1:A:56:ASN:HB3	2:C:206:LEU:HD22	2.02	0.41
1:A:89:TYR:HD1	2:C:210:ALA:HB2	1.81	0.41
1:A:126:TYR:CD1	1:A:281:LEU:HD12	2.55	0.41
3:B:82:ARG:NH2	3:B:142:GLU:OE2	2.54	0.41
1:A:91:PHE:HZ	2:C:297:PHE:CB	2.33	0.41
1:A:236:VAL:HG12	1:A:250:ILE:HG23	2.03	0.41
1:A:79:PHE:HD1	2:C:245:VAL:HG13	1.86	0.41
1:A:202:HIS:ND1	1:A:205:LEU:HB3	2.37	0.41
1:A:57:THR:HG23	2:C:207:TYR:O	2.21	0.40
2:C:204:PHE:HB3	2:C:205:PRO:HD2	2.03	0.40
3:B:165:THR:HG21	3:B:211:PHE:CE2	2.57	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	215/680 (32%)	192 (89%)	23 (11%)	0	100	100
2	C	104/332 (31%)	97 (93%)	7 (7%)	0	100	100
3	B	219/273 (80%)	210 (96%)	9 (4%)	0	100	100
All	All	538/1285 (42%)	499 (93%)	39 (7%)	0	100	100

There are no Ramachandran outliers to report.

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	199/616 (32%)	198 (100%)	1 (0%)	86 89
2	C	93/289 (32%)	93 (100%)	0	100 100
3	B	193/235 (82%)	193 (100%)	0	100 100
All	All	485/1140 (42%)	484 (100%)	1 (0%)	91 94

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

Mol	Chain	Res	Type
1	A	56	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	191	HIS
1	A	267	ASN
1	A	272	GLN
2	C	279	HIS
3	B	198	HIS
3	B	253	HIS

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)

5 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	$\#\|Z\| > 2$
4	NAG	D	1	1,4	14,14,15	0.70	0	17,19,21	1.10	2 (11%)
4	NAG	D	2	4	14,14,15	0.77	0	17,19,21	1.01	1 (5%)
5	NAG	E	1	3,5	14,14,15	0.68	0	17,19,21	1.03	2 (11%)
5	NAG	E	2	5	14,14,15	0.73	0	17,19,21	0.87	1 (5%)
5	BMA	E	3	5	11,11,12	0.85	0	15,15,17	2.90	6 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	D	1	1,4	-	1/6/23/26	0/1/1/1
4	NAG	D	2	4	-	2/6/23/26	0/1/1/1
5	NAG	E	1	3,5	-	1/6/23/26	0/1/1/1
5	NAG	E	2	5	-	1/6/23/26	0/1/1/1
5	BMA	E	3	5	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
5	E	3	BMA	C1-O5-C5	8.46	123.52	112.19
5	E	3	BMA	C3-C4-C5	4.22	117.89	110.23
5	E	3	BMA	C2-C3-C4	3.12	116.34	110.86
5	E	3	BMA	O4-C4-C3	-2.68	104.06	110.38
5	E	3	BMA	O5-C5-C4	2.65	117.27	110.83
4	D	1	NAG	O4-C4-C3	-2.64	104.15	110.38
4	D	1	NAG	O5-C1-C2	-2.62	107.23	111.29
4	D	2	NAG	O5-C1-C2	-2.50	107.42	111.29
5	E	2	NAG	O5-C1-C2	-2.46	107.48	111.29
5	E	1	NAG	C1-O5-C5	2.43	115.44	112.19
5	E	3	BMA	O3-C3-C2	-2.29	105.38	110.05
5	E	1	NAG	O5-C1-C2	-2.09	108.06	111.29

There are no chirality outliers.

All (5) torsion outliers are listed below:

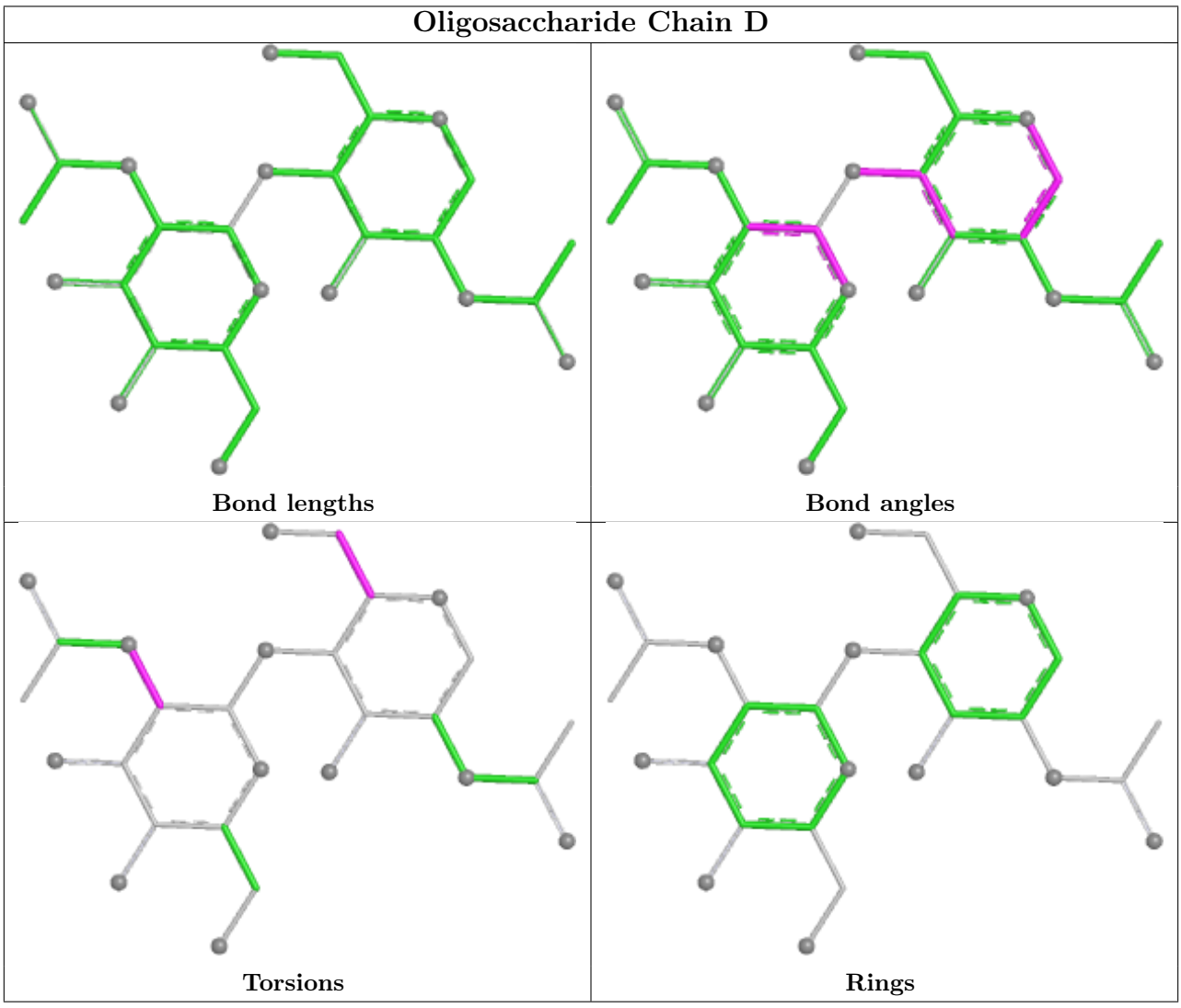
Mol	Chain	Res	Type	Atoms
4	D	2	NAG	C1-C2-N2-C7
4	D	1	NAG	O5-C5-C6-O6
5	E	2	NAG	O5-C5-C6-O6
5	E	1	NAG	O5-C5-C6-O6
4	D	2	NAG	C3-C2-N2-C7

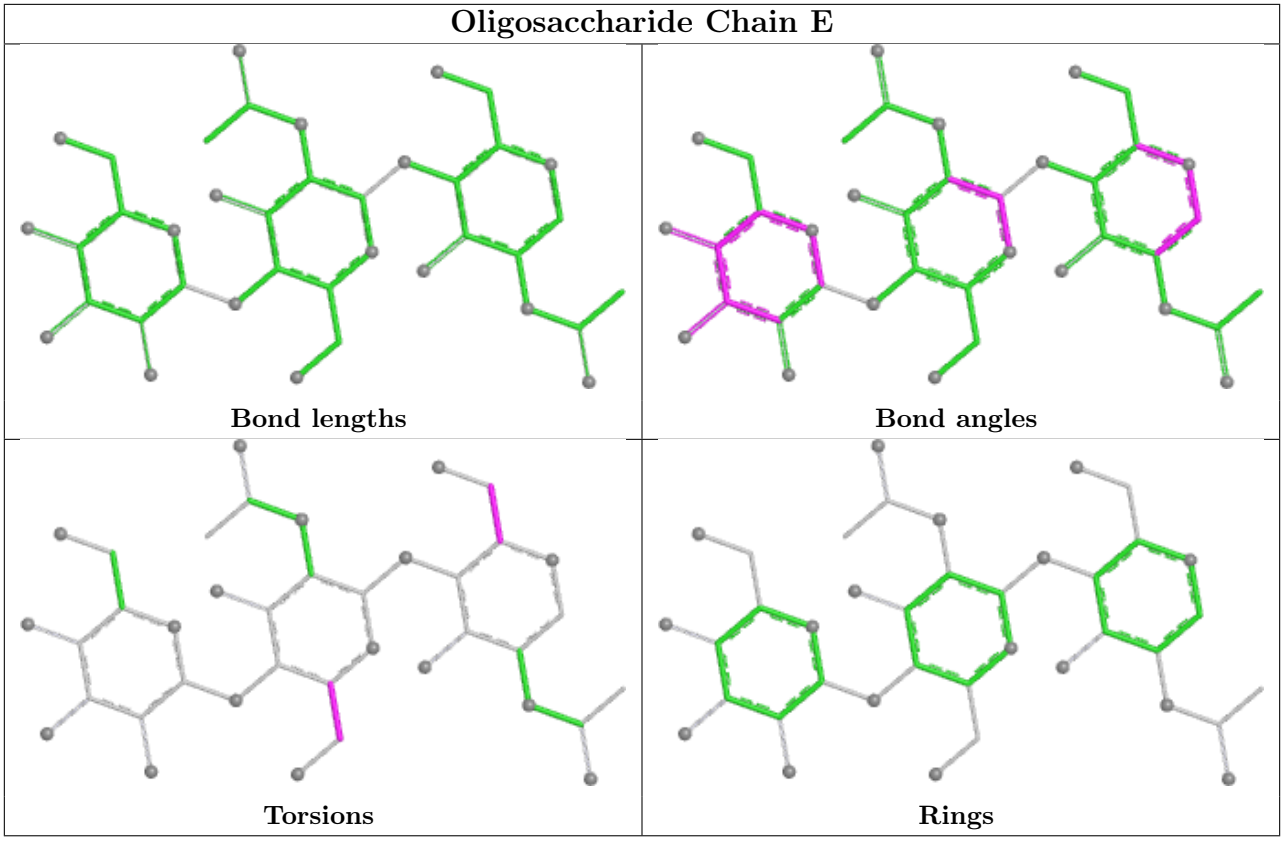
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
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)

9 ligands 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	$\#\|Z\| > 2$
6	NAG	C	402	2	14,14,15	0.74	0	17,19,21	0.96	0
6	NAG	B	402	3	14,14,15	0.72	0	17,19,21	1.14	2 (11%)
6	NAG	C	403	2	14,14,15	0.71	0	17,19,21	1.25	2 (11%)
6	NAG	C	404	2	14,14,15	0.79	0	17,19,21	0.97	1 (5%)
6	NAG	A	802	1	14,14,15	0.78	0	17,19,21	1.08	2 (11%)
6	NAG	A	801	1	14,14,15	0.73	0	17,19,21	0.84	0
6	NAG	B	401	3	14,14,15	0.73	0	17,19,21	0.92	0
6	NAG	C	401	2	14,14,15	0.67	0	17,19,21	1.10	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
6	NAG	C	405	2	14,14,15	0.71	0	17,19,21	0.82	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	C	402	2	-	0/6/23/26	0/1/1/1
6	NAG	B	402	3	-	1/6/23/26	0/1/1/1
6	NAG	C	403	2	-	1/6/23/26	0/1/1/1
6	NAG	C	404	2	-	1/6/23/26	0/1/1/1
6	NAG	A	802	1	-	1/6/23/26	0/1/1/1
6	NAG	A	801	1	-	0/6/23/26	0/1/1/1
6	NAG	B	401	3	-	0/6/23/26	0/1/1/1
6	NAG	C	401	2	-	0/6/23/26	0/1/1/1
6	NAG	C	405	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
6	C	403	NAG	C2-N2-C7	2.80	126.65	122.90
6	A	802	NAG	C1-O5-C5	2.69	115.80	112.19
6	C	401	NAG	O5-C1-C2	-2.55	107.34	111.29
6	B	402	NAG	C2-N2-C7	2.46	126.20	122.90
6	C	403	NAG	O5-C1-C2	-2.29	107.75	111.29
6	C	404	NAG	C2-N2-C7	2.17	125.81	122.90
6	B	402	NAG	O5-C1-C2	-2.07	108.09	111.29
6	A	802	NAG	O5-C1-C2	-2.03	108.15	111.29

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	403	NAG	C1-C2-N2-C7
6	C	404	NAG	C3-C2-N2-C7
6	B	402	NAG	C1-C2-N2-C7
6	A	802	NAG	O5-C5-C6-O6

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	C	402	NAG	2	0
6	C	403	NAG	1	0
6	C	404	NAG	2	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.

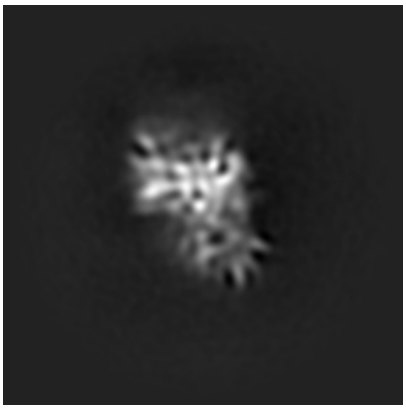
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-46921. These allow visual inspection of the internal detail of the map and identification of artifacts.

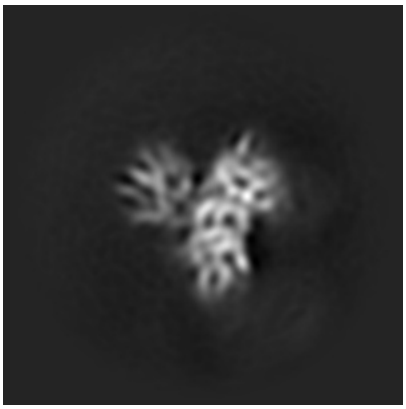
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

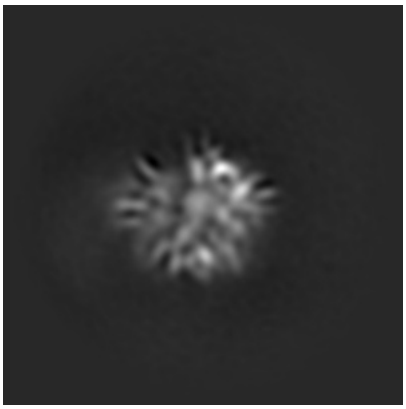
6.1.1 Primary map



X

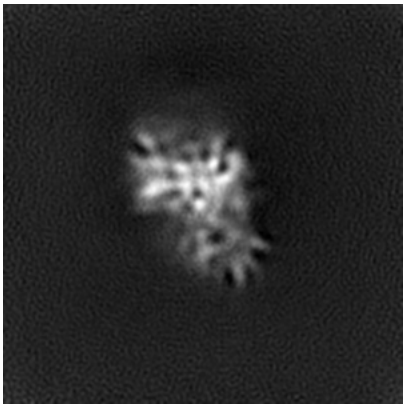


Y

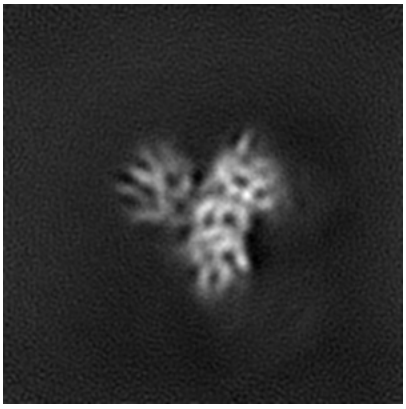


Z

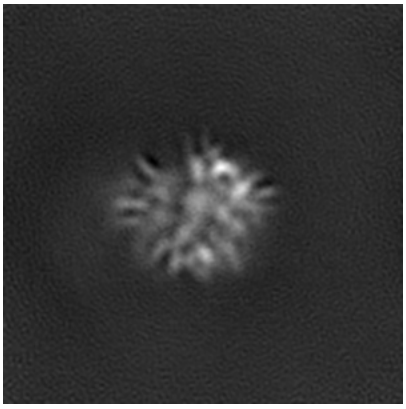
6.1.2 Raw map



X



Y



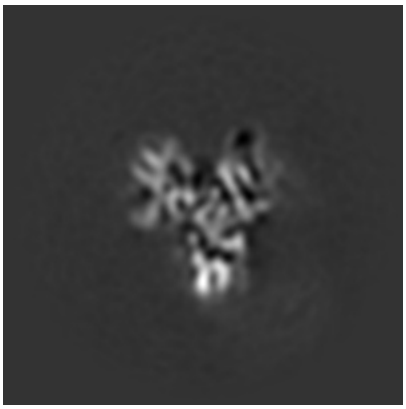
Z

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

6.2 Central slices (i)

6.2.1 Primary map

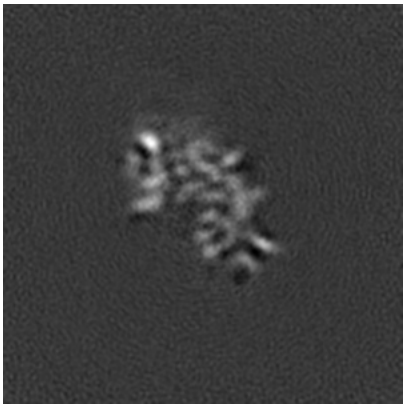
X Index: 80



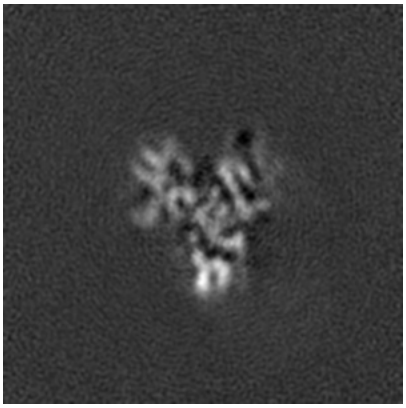
Y Index: 80

Z Index: 80

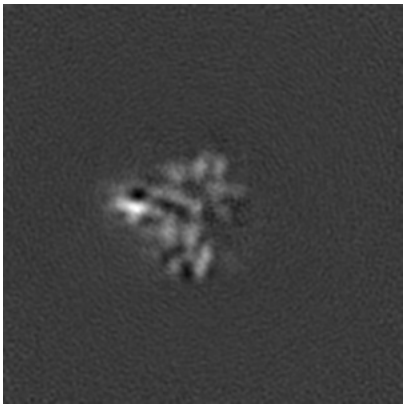
6.2.2 Raw map



X Index: 80



Y Index: 80

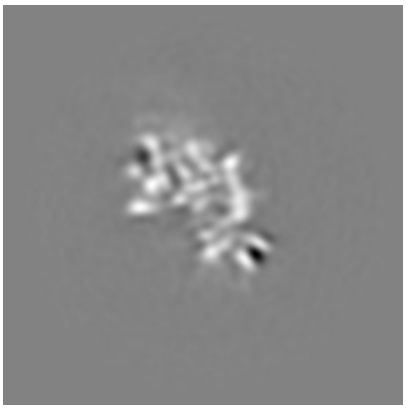


Z Index: 80

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

6.3 Largest variance slices (i)

6.3.1 Primary map

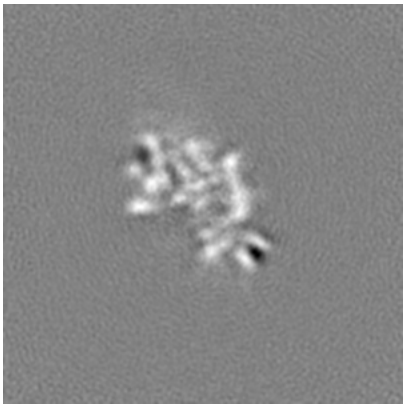


X Index: 78

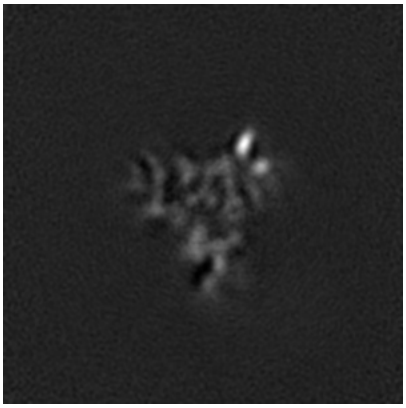
Y Index: 84

Z Index: 96

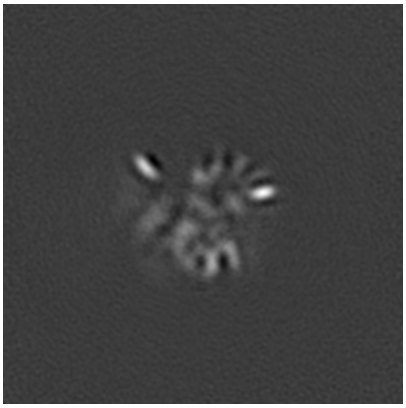
6.3.2 Raw map



X Index: 78



Y Index: 84

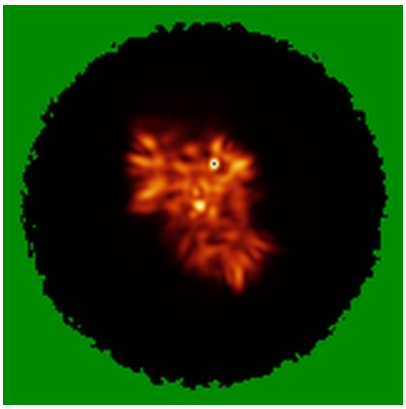


Z Index: 96

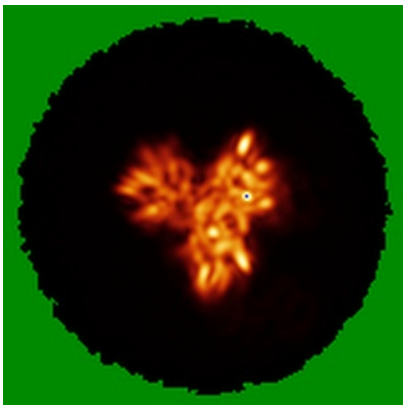
The images above show the largest variance slices of the map in three orthogonal directions.

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

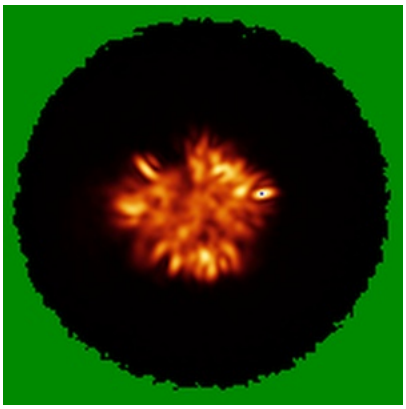
6.4.1 Primary map



X

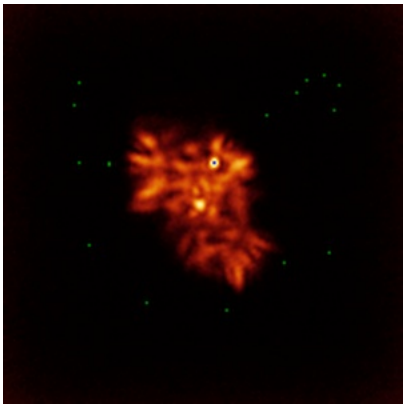


Y

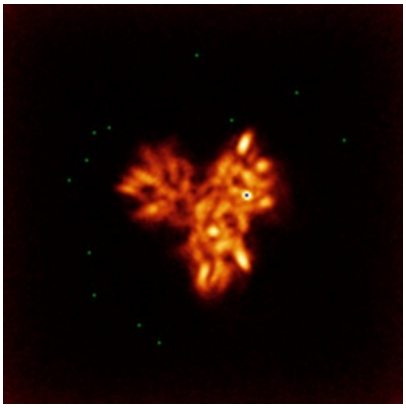


Z

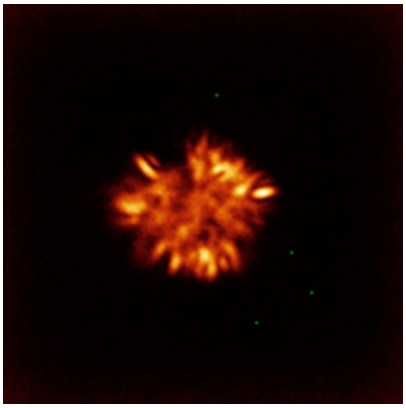
6.4.2 Raw map



X



Y

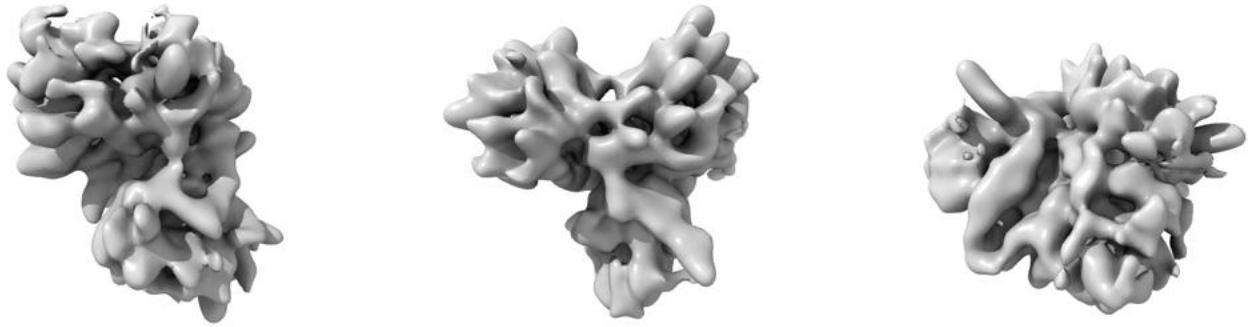


Z

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 0.0625. 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.

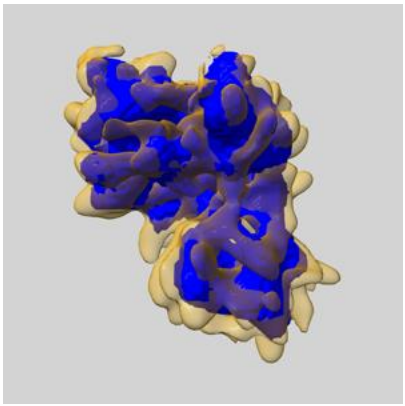
6.6 Mask visualisation (i)

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

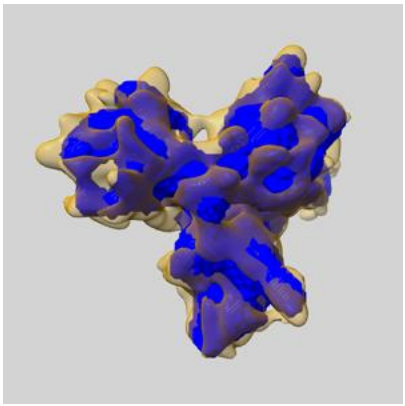
A mask typically either:

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

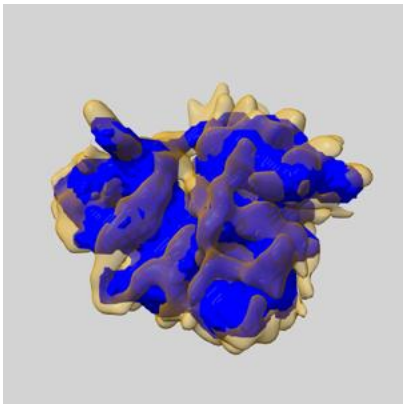
6.6.1 emd_46921_msk_1.map (i)



X



Y

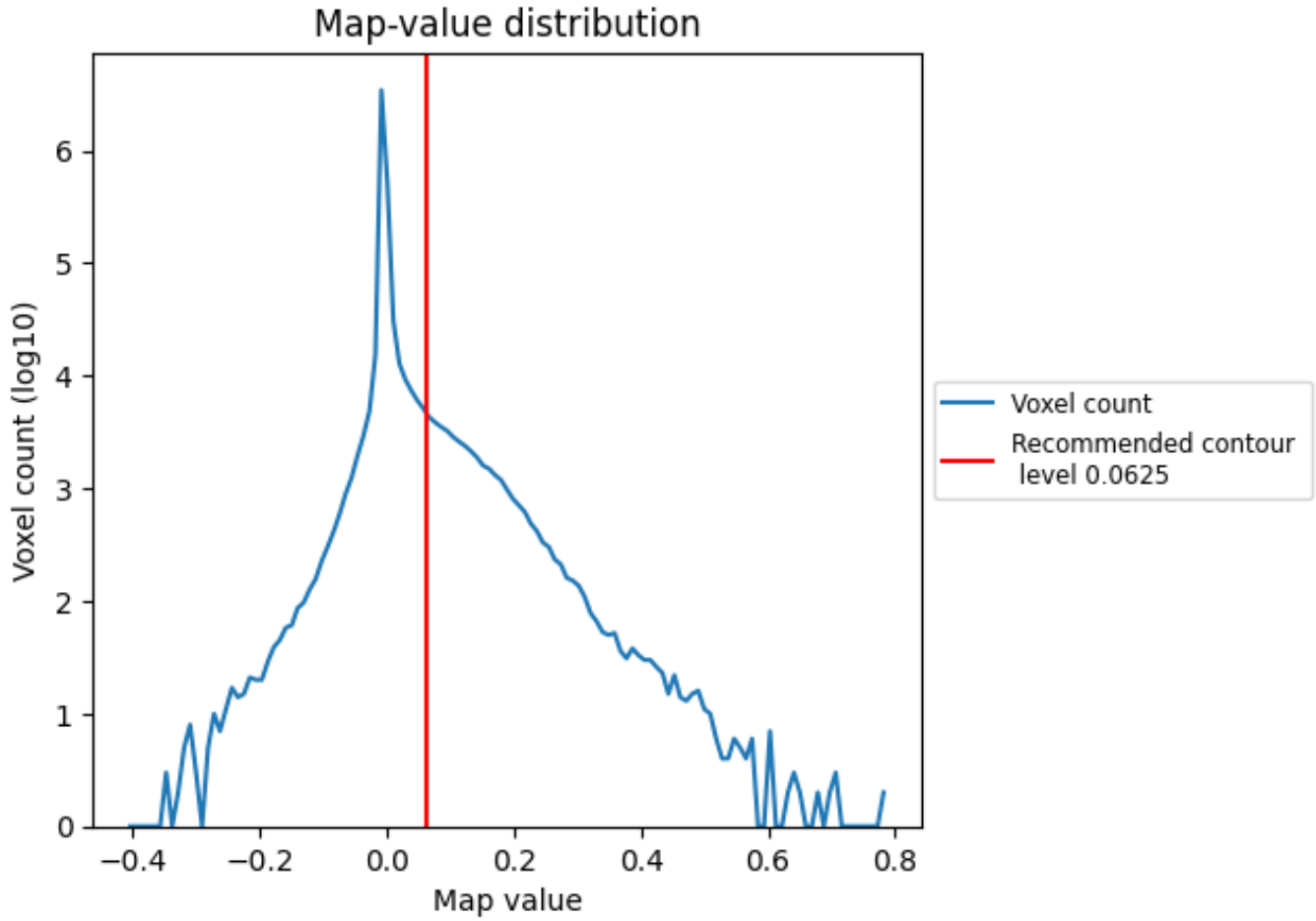


Z

7 Map analysis

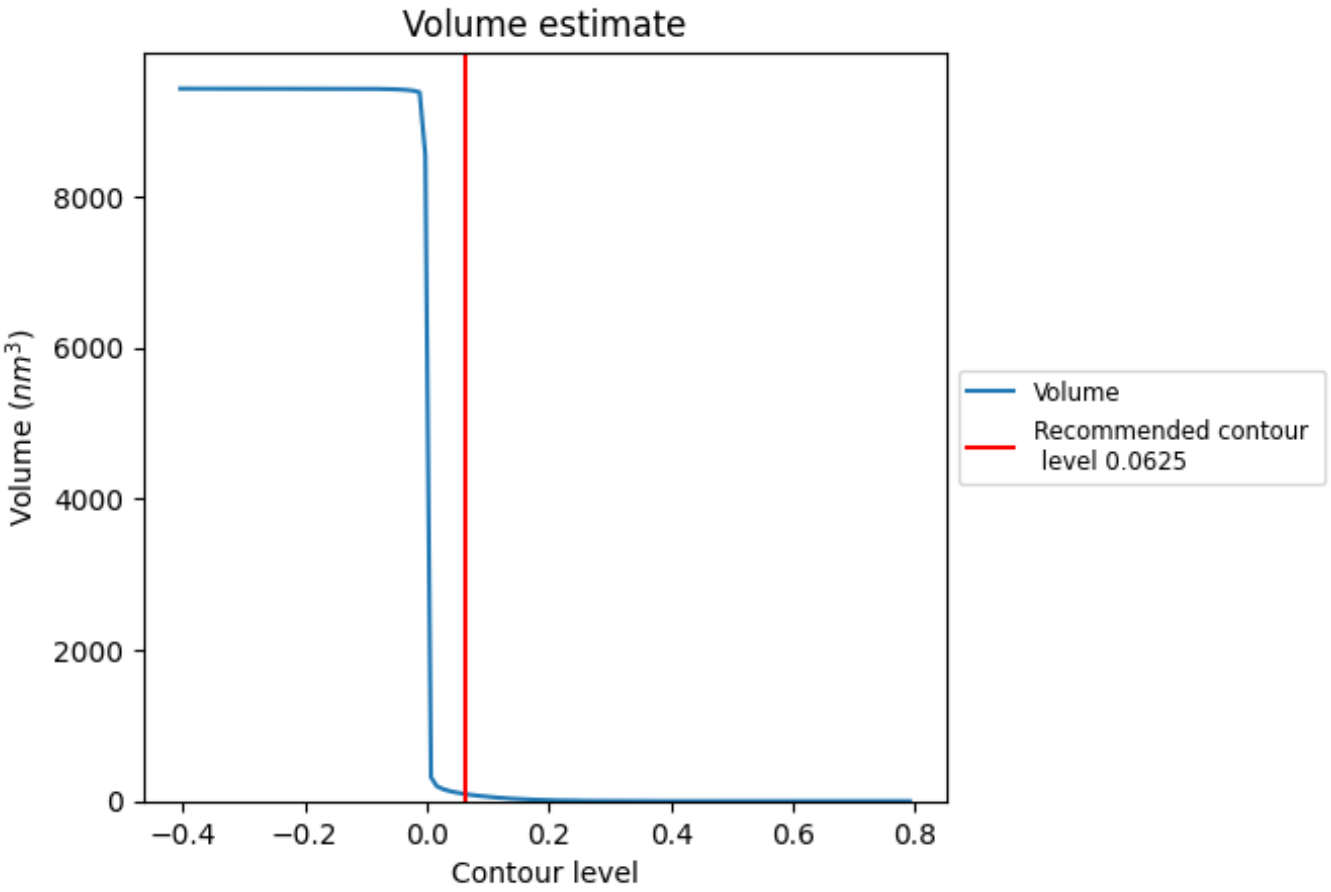
This section contains the results of statistical analysis of the map.

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.

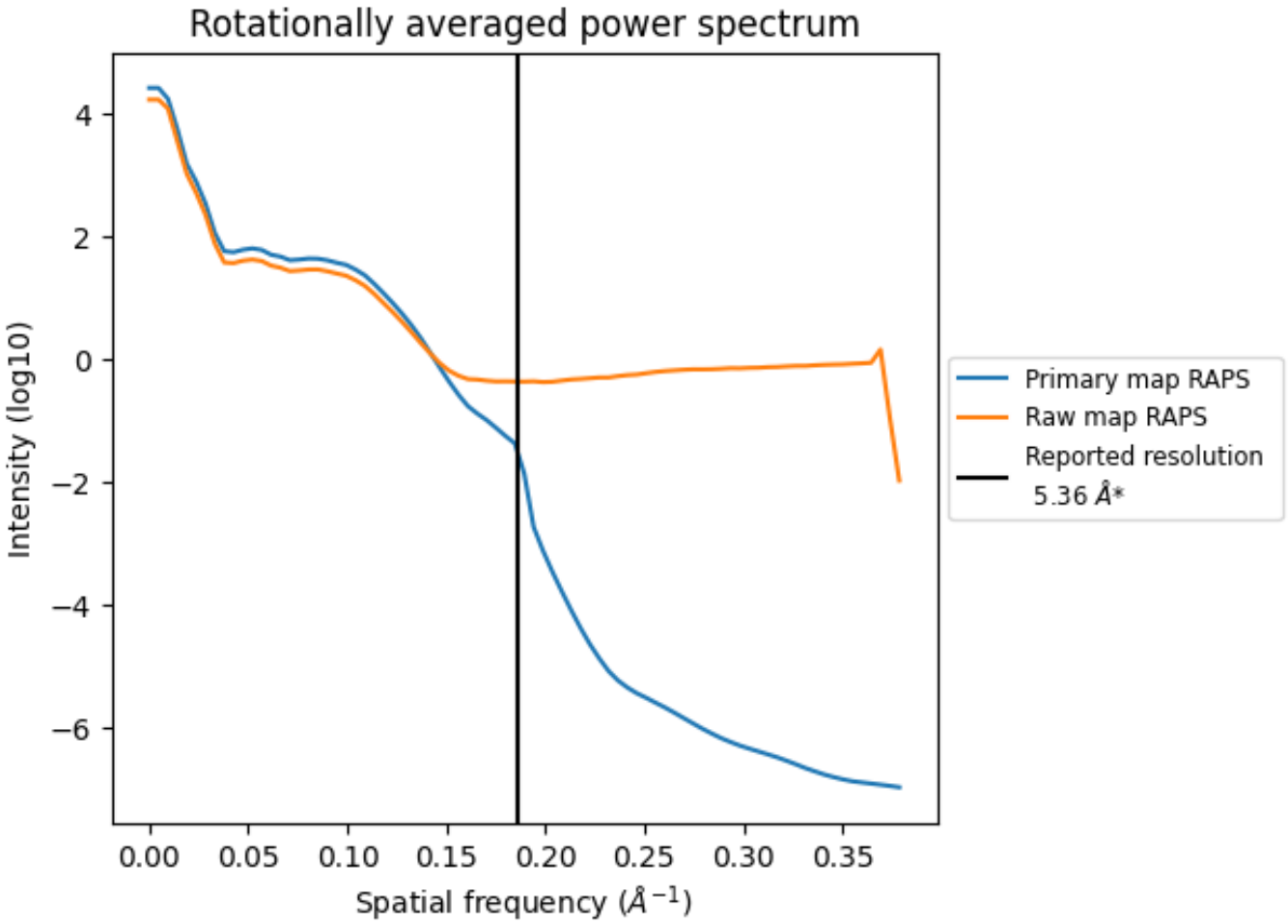
7.2 Volume estimate



The volume at the recommended contour level is 94 nm^3; this corresponds to an approximate mass of 85 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)

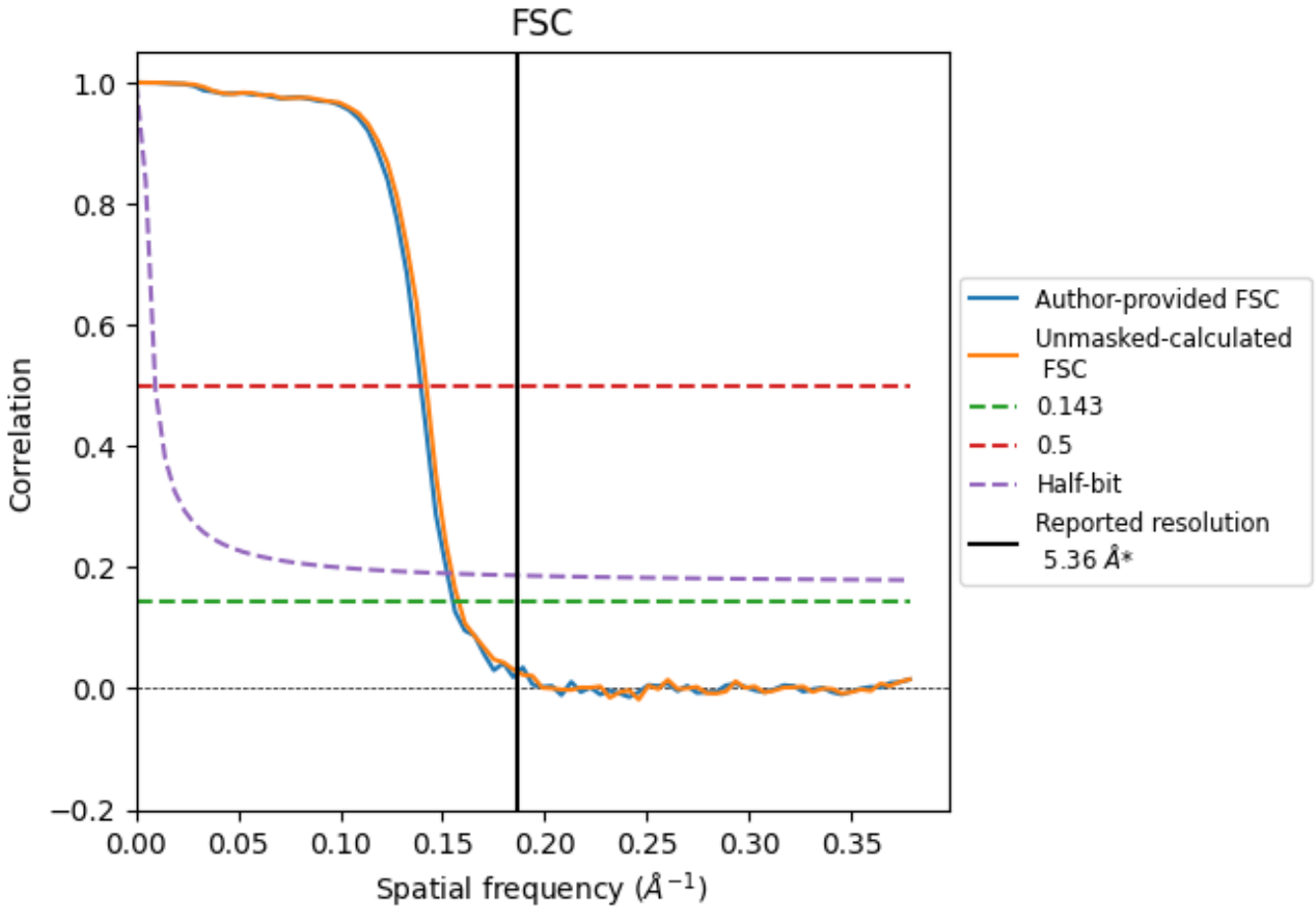


*Reported resolution corresponds to spatial frequency of 0.187 Å^{-1}

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 0.187 $Å^{-1}$

8.2 Resolution estimates (i)

Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	5.36	-	-
Author-provided FSC curve	6.44	7.17	6.56
Unmasked-calculated*	6.33	7.03	6.46

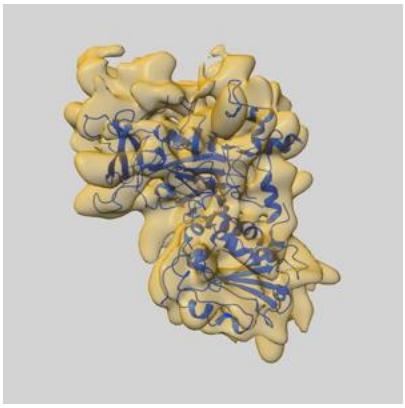
*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from author-provided FSC intersecting FSC 0.143 CUT-OFF 6.44 differs from the reported value 5.36 by more than 10 %

The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 6.33 differs from the reported value 5.36 by more than 10 %

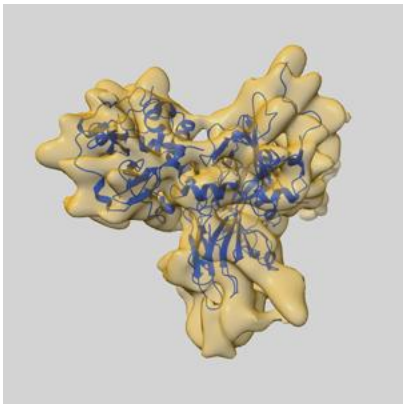
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-46921 and PDB model 9DIY. Per-residue inclusion information can be found in section 3 on page 7.

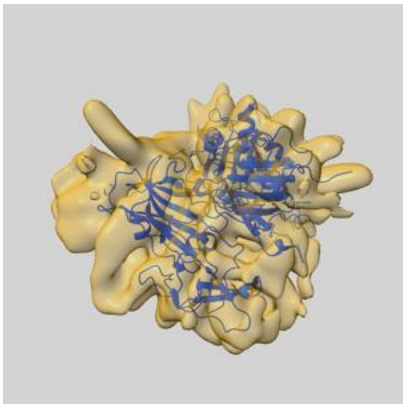
9.1 Map-model overlay



X



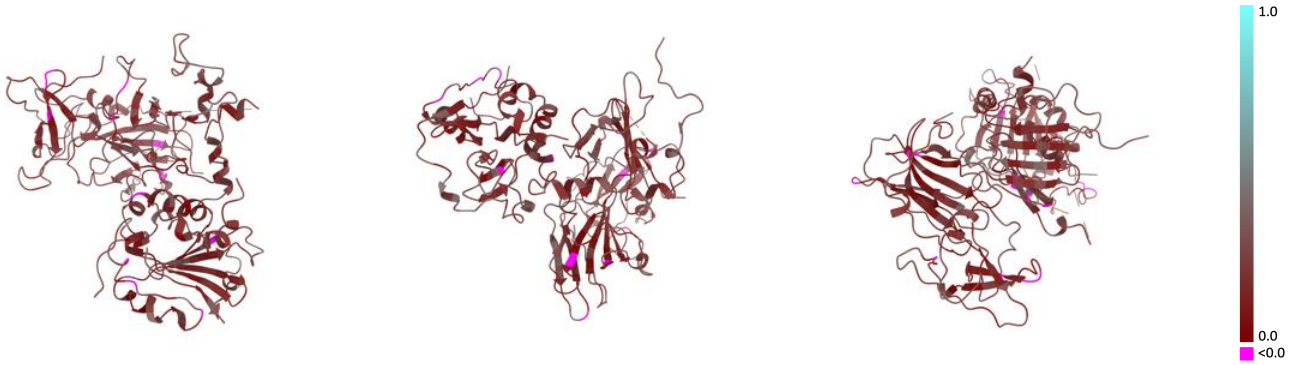
Y



Z

The images above show the 3D surface view of the map at the recommended contour level 0.0625 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.

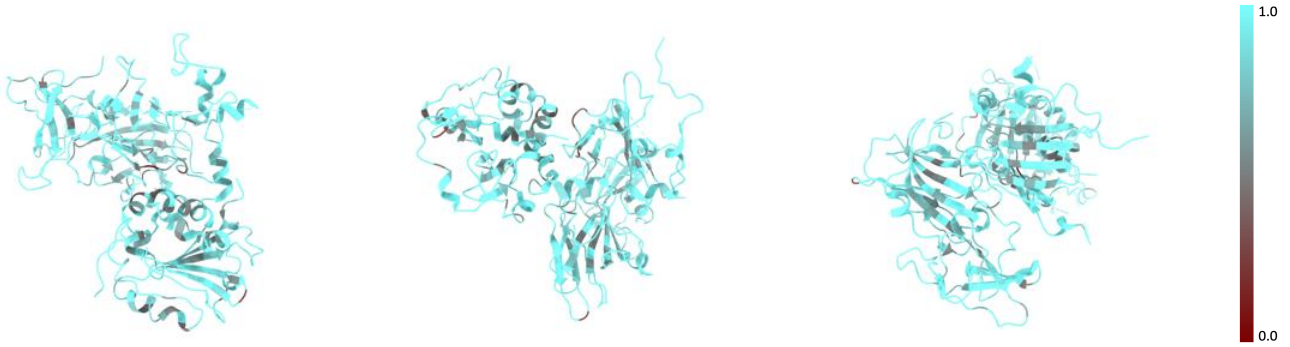
9.2 Q-score mapped to coordinate model (i)



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.

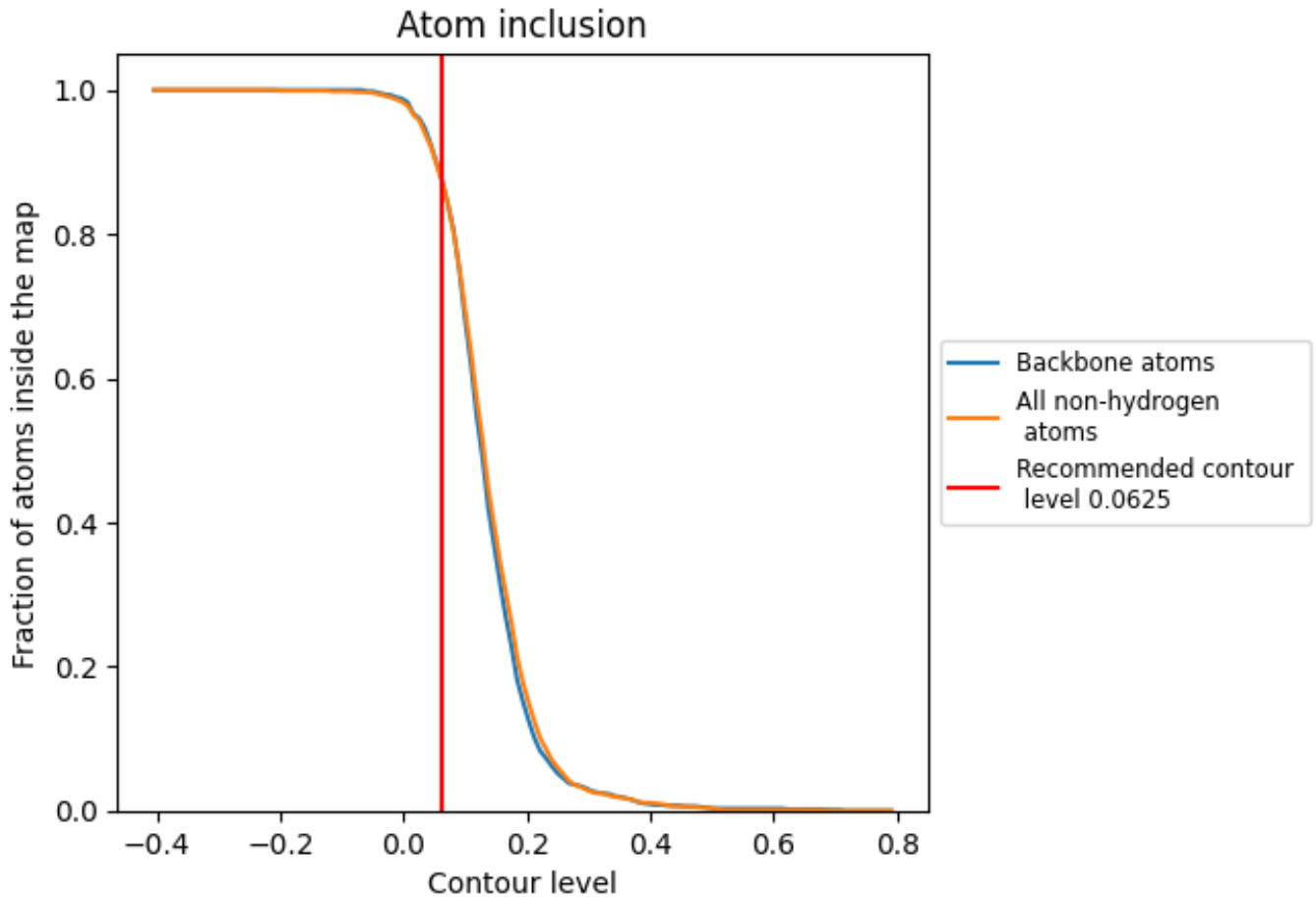
9.3 Atom inclusion mapped to coordinate model (i)



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 (0.0625).

9.4 Atom inclusion (i)



At the recommended contour level, 88% of all backbone atoms, 87% 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 (0.0625) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.8740	0.2180
A	0.8860	0.2240
B	0.8990	0.2000
C	0.8770	0.2350
D	1.0000	0.3320
E	0.9740	0.3560