



wwPDB EM Validation Summary Report ⓘ

Mar 8, 2026 – 09:44 AM UTC

PDB ID : 7QCU / pdb_00007qcu
EMDB ID : EMD-13899
Title : Structure of the MUCIN-2 Cterminal domains partially deglycosylated.
Authors : Gallego, P.; Hansson, G.C.
Deposited on : 2021-11-25
Resolution : 3.25 Å(reported)

This is a wwPDB EM Validation Summary 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

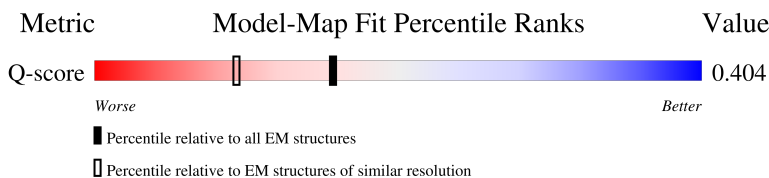
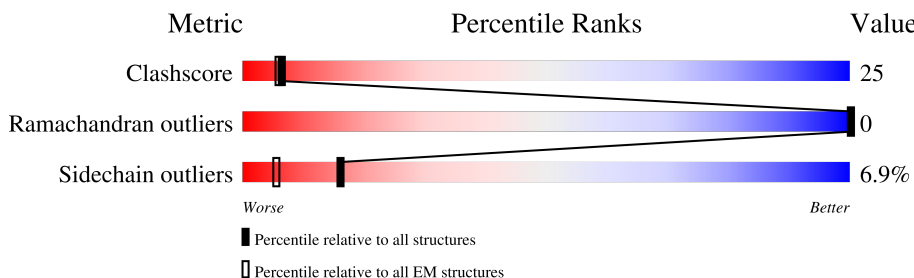
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

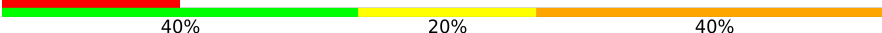
The reported resolution of this entry is 3.25 Å.

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	14599 (2.75 - 3.75)

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	807	
1	B	807	
2	C	5	
2	D	5	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7069 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 Mucin-2.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	443	Total	C	N	O	S	0	0
			3410	2127	564	666	53		
1	B	445	Total	C	N	O	S	0	0
			3423	2134	566	670	53		

There are 66 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	4313	ALA	-	expression tag	UNP Q02817
A	4314	ALA	-	expression tag	UNP Q02817
A	4315	GLN	-	expression tag	UNP Q02817
A	4316	PRO	-	expression tag	UNP Q02817
A	4317	ALA	-	expression tag	UNP Q02817
A	4318	ARG	-	expression tag	UNP Q02817
A	4319	ARG	-	expression tag	UNP Q02817
A	4320	ALA	-	expression tag	UNP Q02817
A	4321	VAL	-	expression tag	UNP Q02817
A	4322	ARG	-	expression tag	UNP Q02817
A	4323	SER	-	expression tag	UNP Q02817
A	4324	SER	-	expression tag	UNP Q02817
A	4325	ARG	-	expression tag	UNP Q02817
A	4326	ARG	-	expression tag	UNP Q02817
A	4327	HIS	-	expression tag	UNP Q02817
A	4328	HIS	-	expression tag	UNP Q02817
A	4329	HIS	-	expression tag	UNP Q02817
A	4330	HIS	-	expression tag	UNP Q02817
A	4331	HIS	-	expression tag	UNP Q02817
A	4332	HIS	-	expression tag	UNP Q02817
A	4333	GLY	-	expression tag	UNP Q02817
A	4334	SER	-	expression tag	UNP Q02817
A	4335	GLY	-	expression tag	UNP Q02817
A	4336	LEU	-	expression tag	UNP Q02817
A	4337	GLU	-	expression tag	UNP Q02817
A	4338	VAL	-	expression tag	UNP Q02817

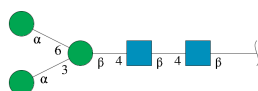
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Chain	Residue	Modelled	Actual	Comment	Reference
A	4339	LEU	-	expression tag	UNP Q02817
A	4340	PHE	-	expression tag	UNP Q02817
A	4341	GLN	-	expression tag	UNP Q02817
A	4342	GLY	-	expression tag	UNP Q02817
A	4343	PRO	-	expression tag	UNP Q02817
A	4344	THR	-	expression tag	UNP Q02817
A	4345	PRO	-	expression tag	UNP Q02817
B	4313	ALA	-	expression tag	UNP Q02817
B	4314	ALA	-	expression tag	UNP Q02817
B	4315	GLN	-	expression tag	UNP Q02817
B	4316	PRO	-	expression tag	UNP Q02817
B	4317	ALA	-	expression tag	UNP Q02817
B	4318	ARG	-	expression tag	UNP Q02817
B	4319	ARG	-	expression tag	UNP Q02817
B	4320	ALA	-	expression tag	UNP Q02817
B	4321	VAL	-	expression tag	UNP Q02817
B	4322	ARG	-	expression tag	UNP Q02817
B	4323	SER	-	expression tag	UNP Q02817
B	4324	SER	-	expression tag	UNP Q02817
B	4325	ARG	-	expression tag	UNP Q02817
B	4326	ARG	-	expression tag	UNP Q02817
B	4327	HIS	-	expression tag	UNP Q02817
B	4328	HIS	-	expression tag	UNP Q02817
B	4329	HIS	-	expression tag	UNP Q02817
B	4330	HIS	-	expression tag	UNP Q02817
B	4331	HIS	-	expression tag	UNP Q02817
B	4332	HIS	-	expression tag	UNP Q02817
B	4333	GLY	-	expression tag	UNP Q02817
B	4334	SER	-	expression tag	UNP Q02817
B	4335	GLY	-	expression tag	UNP Q02817
B	4336	LEU	-	expression tag	UNP Q02817
B	4337	GLU	-	expression tag	UNP Q02817
B	4338	VAL	-	expression tag	UNP Q02817
B	4339	LEU	-	expression tag	UNP Q02817
B	4340	PHE	-	expression tag	UNP Q02817
B	4341	GLN	-	expression tag	UNP Q02817
B	4342	GLY	-	expression tag	UNP Q02817
B	4343	PRO	-	expression tag	UNP Q02817
B	4344	THR	-	expression tag	UNP Q02817
B	4345	PRO	-	expression tag	UNP Q02817

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

cetamido-2-deoxy-beta-D-glucopyranose.

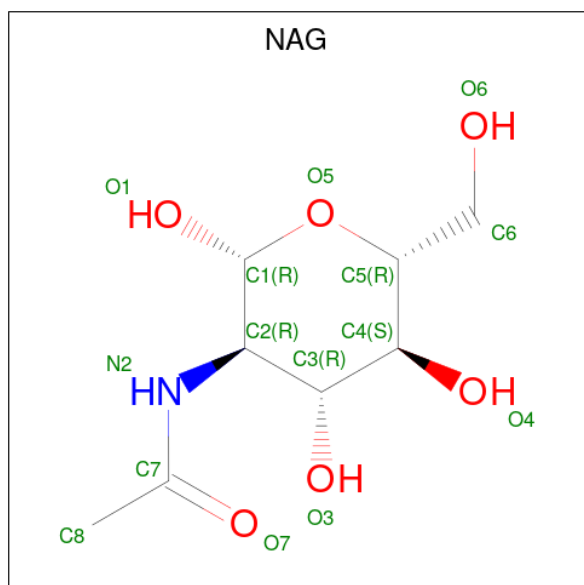


Mol	Chain	Residues	Atoms				AltConf	Trace
2	C	5	Total	C	N	O	0	0
			61	34	2	25		
2	D	5	Total	C	N	O	0	0
			61	34	2	25		

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca) (labeled as "Ligand of Interest" by depositor).

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

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



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

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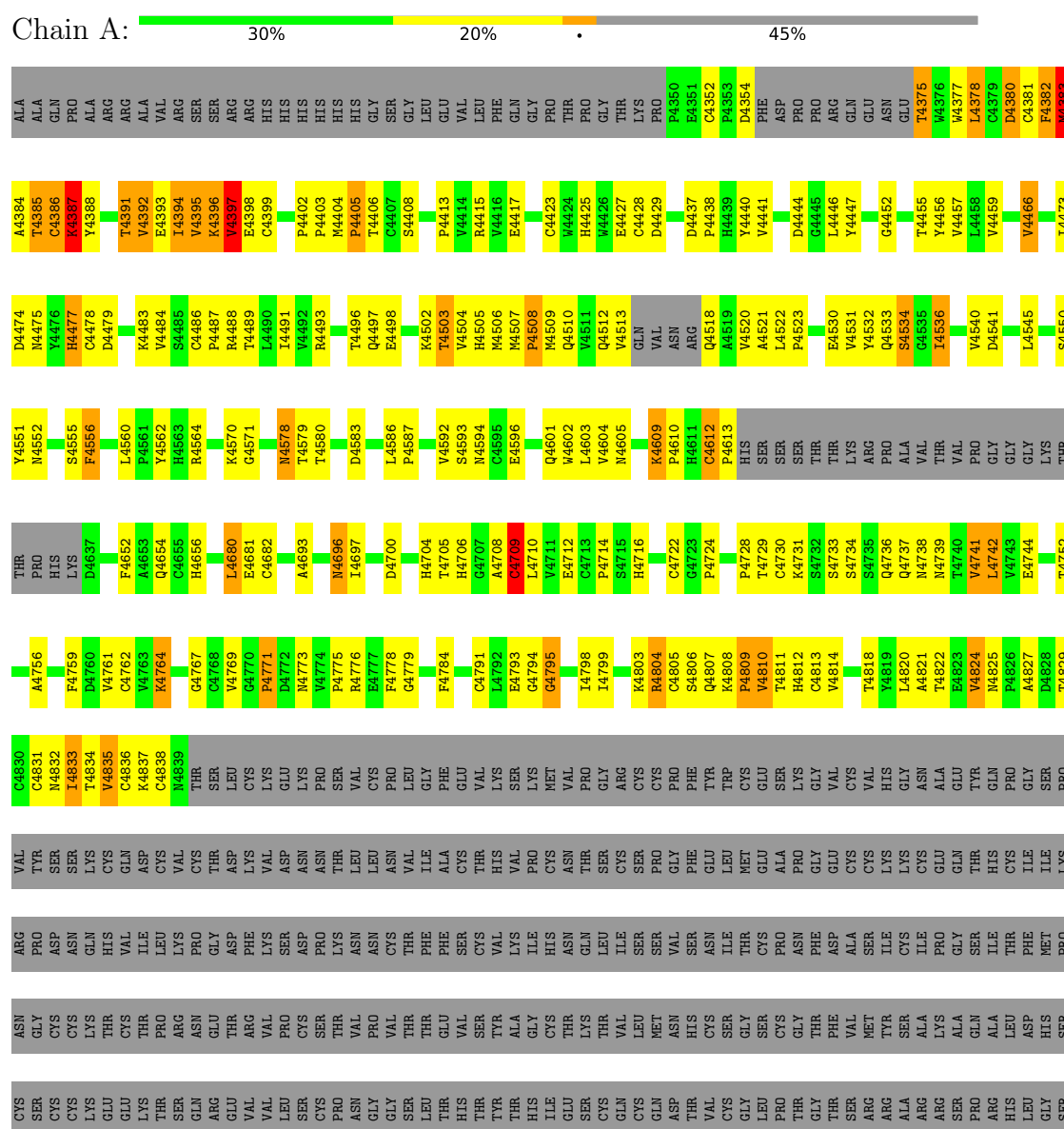
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Mol	Chain	Residues	Atoms				AltConf
4	A	1	Total 14	C 8	N 1	O 5	0
4	A	1	Total 14	C 8	N 1	O 5	0
4	A	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0
4	B	1	Total 14	C 8	N 1	O 5	0

3 Residue-property plots

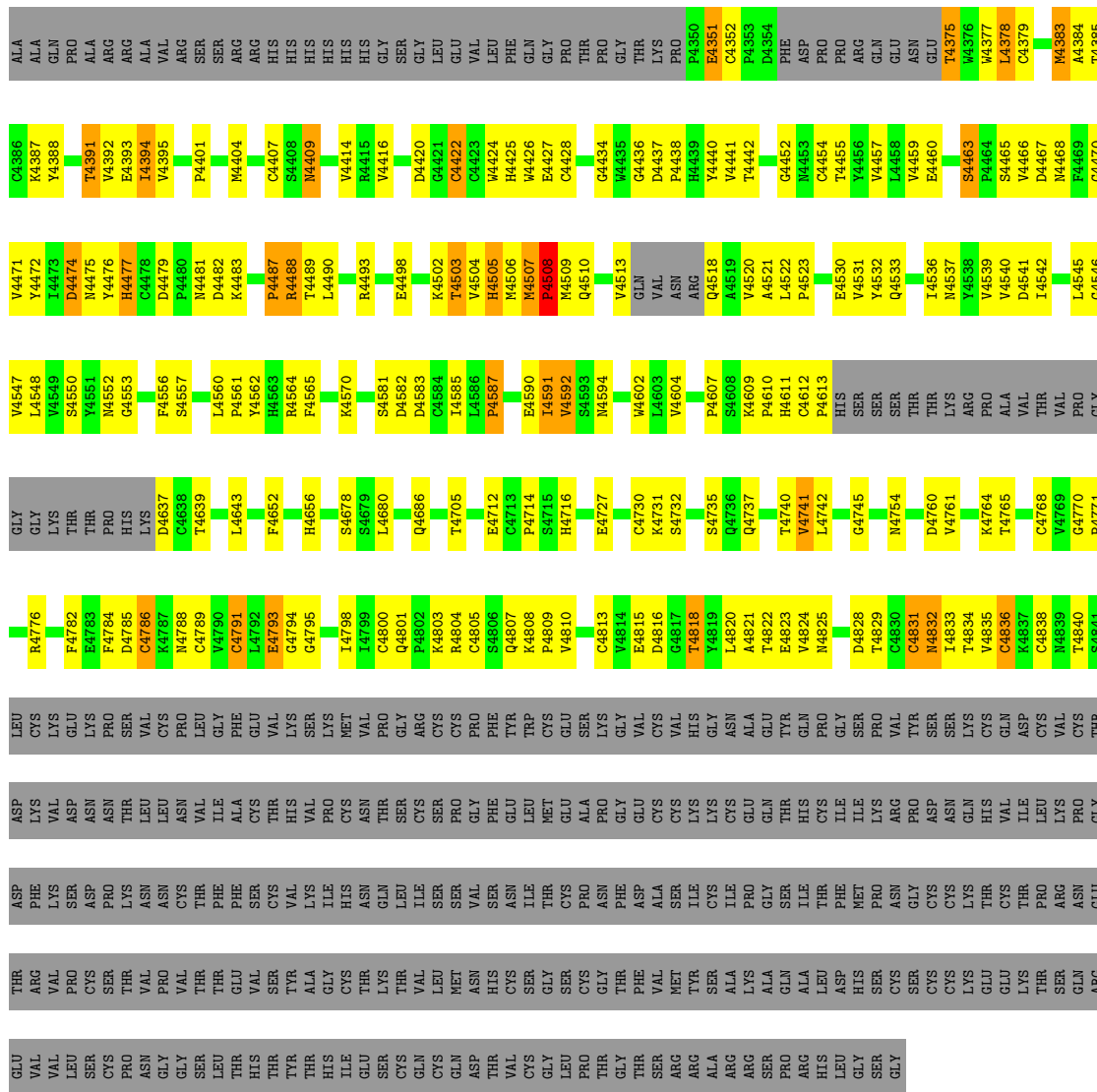
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion 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: Mucin-2



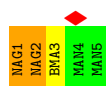
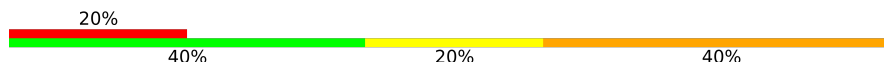
- Molecule 1: Mucin-2

Chain B:



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

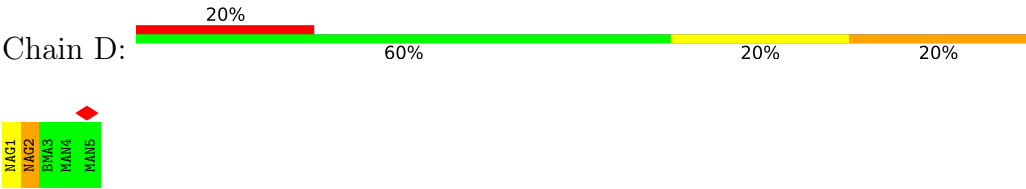
Chain C:



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

nose

Chain D:



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	387288	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	TFS KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/\text{\AA}^2$)	79	Depositor
Minimum defocus (nm)	1200	Depositor
Maximum defocus (nm)	5000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor
Maximum map value	0.512	Depositor
Minimum map value	-0.249	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	0.007	Depositor
Recommended contour level	0.034	Depositor
Map size ($\text{\AA}$)	354.24, 354.24, 354.24	wwPDB
Map dimensions	432, 432, 432	wwPDB
Map angles ($^\circ$)	90.0, 90.0, 90.0	wwPDB
Pixel spacing ($\text{\AA}$)	0.82, 0.82, 0.82	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: BMA, NAG, CA, MAN

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	0.98	10/3503 (0.3%)	1.62	96/4785 (2.0%)
1	B	0.85	2/3516 (0.1%)	1.36	50/4803 (1.0%)
All	All	0.92	12/7019 (0.2%)	1.50	146/9588 (1.5%)

The worst 5 of 12 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	4398	GLU	C-N	15.96	1.52	1.33
1	A	4809	PRO	N-CD	-11.35	1.31	1.47
1	A	4491	ILE	C-O	-7.99	1.15	1.24
1	A	4610	PRO	N-CD	6.01	1.56	1.47
1	A	4562	TYR	C-O	-5.71	1.17	1.24

The worst 5 of 146 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	4552	ASN	CB-CA-C	-13.50	84.85	110.24
1	A	4705	THR	CB-CA-C	-12.71	87.14	110.01
1	A	4744	GLU	CB-CA-C	-11.83	88.15	110.51
1	A	4503	THR	CB-CA-C	-10.61	93.16	110.14
1	B	4375	THR	CA-CB-OG1	-9.84	94.84	109.60

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	3410	0	3126	172	0
1	B	3423	0	3139	183	0
2	C	61	0	52	4	0
2	D	61	0	52	1	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	56	0	52	5	0
4	B	56	0	52	3	0
All	All	7069	0	6473	341	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 25.

The worst 5 of 341 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:4643:LEU:CD1	1:B:4705:THR:HG23	1.33	1.58
1:B:4643:LEU:HD11	1:B:4705:THR:CG2	1.44	1.45
1:A:4503:THR:HG23	1:A:4503:THR:O	1.43	1.13
1:A:4586:LEU:CD2	1:A:4587:PRO:HD2	1.83	1.08
1:B:4824:VAL:HA	1:B:4832:ASN:HB3	1.33	1.07

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	435/807 (54%)	406 (93%)	29 (7%)	0	100	100
1	B	437/807 (54%)	406 (93%)	31 (7%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	872/1614 (54%)	812 (93%)	60 (7%)	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	395/719 (55%)	367 (93%)	28 (7%)	13	39
1	B	397/719 (55%)	370 (93%)	27 (7%)	14	41
All	All	792/1438 (55%)	737 (93%)	55 (7%)	16	41

5 of 55 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	4378	LEU
1	B	4505	HIS
1	B	4840	THR
1	B	4818	THR
1	B	4394	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 19 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	4694	GLN
1	B	4801	GLN
1	B	4825	ASN
1	B	4704	HIS
1	B	4412	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

10 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$
2	NAG	C	1	1,2	14,14,15	0.49	0	17,19,21	1.76	4 (23%)
2	NAG	C	2	2	14,14,15	0.32	0	17,19,21	0.89	1 (5%)
2	BMA	C	3	2	11,11,12	0.18	0	15,15,17	0.54	0
2	MAN	C	4	2	11,11,12	0.21	0	15,15,17	0.57	0
2	MAN	C	5	2	11,11,12	0.20	0	15,15,17	0.56	0
2	NAG	D	1	1,2	14,14,15	0.43	0	17,19,21	2.16	7 (41%)
2	NAG	D	2	2	14,14,15	0.81	1 (7%)	17,19,21	0.99	1 (5%)
2	BMA	D	3	2	11,11,12	0.20	0	15,15,17	0.54	0
2	MAN	D	4	2	11,11,12	0.20	0	15,15,17	0.54	0
2	MAN	D	5	2	11,11,12	0.21	0	15,15,17	0.51	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
2	NAG	C	1	1,2	-	3/6/23/26	0/1/1/1
2	NAG	C	2	2	-	5/6/23/26	0/1/1/1
2	BMA	C	3	2	-	1/2/19/22	0/1/1/1
2	MAN	C	4	2	-	0/2/19/22	0/1/1/1
2	MAN	C	5	2	-	0/2/19/22	0/1/1/1
2	NAG	D	1	1,2	-	4/6/23/26	0/1/1/1
2	NAG	D	2	2	-	2/6/23/26	0/1/1/1
2	BMA	D	3	2	-	1/2/19/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	D	4	2	-	0/2/19/22	0/1/1/1
2	MAN	D	5	2	-	1/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	2	NAG	O5-C1	2.60	1.48	1.43

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	1	NAG	C4-C3-C2	4.29	117.31	111.02
2	C	1	NAG	C3-C4-C5	4.27	117.97	110.23
2	D	2	NAG	C1-O5-C5	3.77	117.25	112.19
2	D	1	NAG	C2-N2-C7	3.72	127.89	122.90
2	D	1	NAG	O5-C1-C2	3.59	116.85	111.29

There are no chirality outliers.

5 of 17 torsion outliers are listed below:

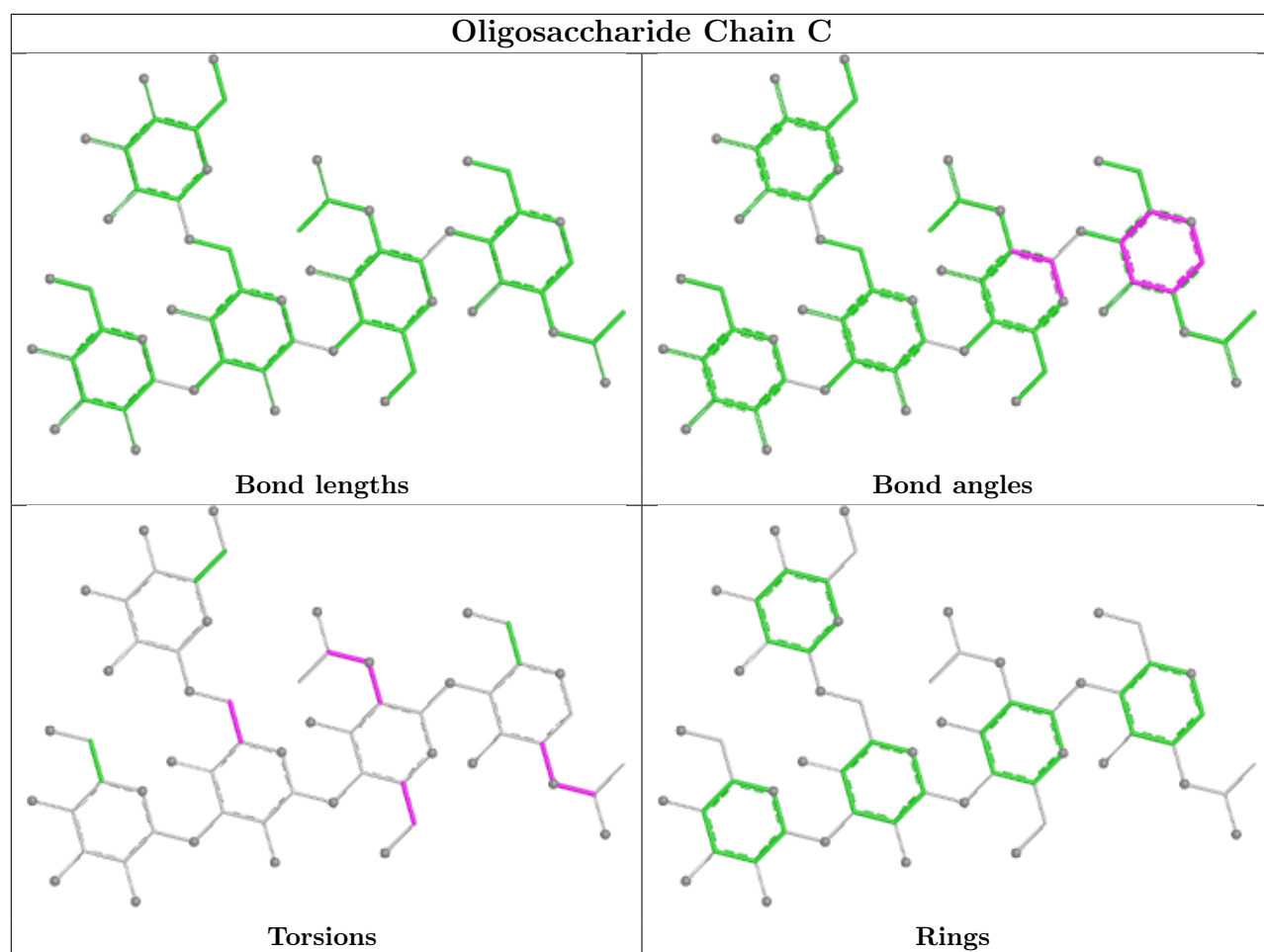
Mol	Chain	Res	Type	Atoms
2	C	1	NAG	C3-C2-N2-C7
2	C	2	NAG	C1-C2-N2-C7
2	C	2	NAG	C8-C7-N2-C2
2	C	2	NAG	O7-C7-N2-C2
2	D	1	NAG	C3-C2-N2-C7

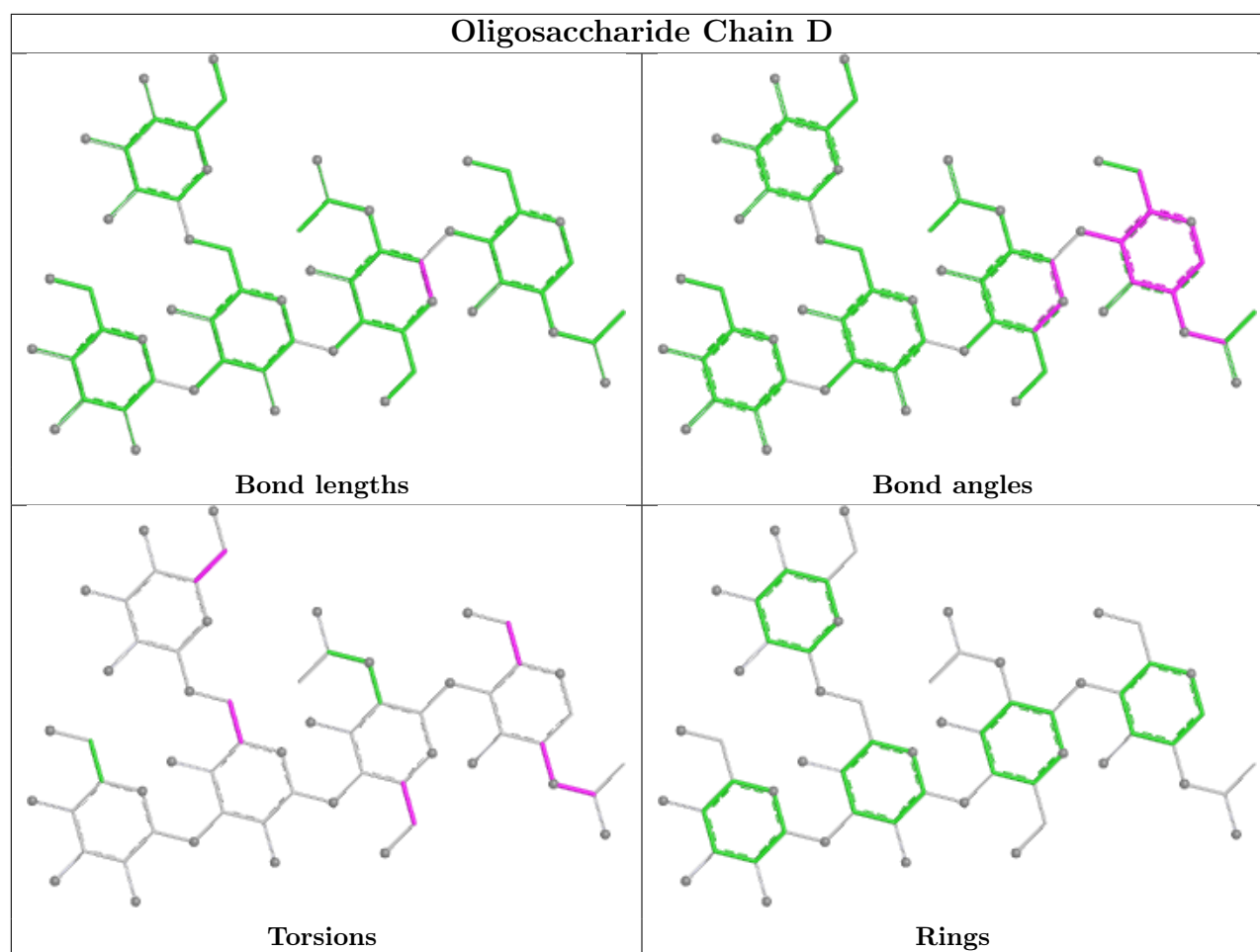
There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	NAG	1	0
2	C	2	NAG	3	0
2	C	3	BMA	1	0
2	D	2	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 10 ligands modelled in this entry, 2 are monoatomic - leaving 8 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	A	5203	1	14,14,15	0.53	0	17,19,21	1.58	2 (11%)
4	NAG	B	5203	1	14,14,15	0.30	0	17,19,21	0.55	0
4	NAG	A	5202	1	14,14,15	0.74	1 (7%)	17,19,21	2.60	3 (17%)
4	NAG	A	5204	1	14,14,15	0.32	0	17,19,21	0.77	1 (5%)
4	NAG	A	5205	1	14,14,15	0.30	0	17,19,21	0.65	0
4	NAG	B	5204	1	14,14,15	0.28	0	17,19,21	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	NAG	B	5202	1	14,14,15	0.30	0	17,19,21	0.70	0
4	NAG	B	5205	1	14,14,15	0.30	0	17,19,21	0.72	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
4	NAG	A	5203	1	-	4/6/23/26	0/1/1/1
4	NAG	B	5203	1	-	2/6/23/26	0/1/1/1
4	NAG	A	5202	1	-	4/6/23/26	0/1/1/1
4	NAG	A	5204	1	-	2/6/23/26	0/1/1/1
4	NAG	A	5205	1	-	3/6/23/26	0/1/1/1
4	NAG	B	5204	1	-	3/6/23/26	0/1/1/1
4	NAG	B	5202	1	-	2/6/23/26	0/1/1/1
4	NAG	B	5205	1	-	2/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	5202	NAG	O5-C5	-2.06	1.39	1.43

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	5202	NAG	C1-O5-C5	8.83	124.02	112.19
4	A	5202	NAG	O5-C5-C6	-4.29	99.32	107.66
4	A	5203	NAG	C1-C2-N2	4.24	117.12	110.43
4	A	5202	NAG	O5-C1-C2	-2.72	107.08	111.29
4	A	5203	NAG	C1-O5-C5	-2.45	108.90	112.19

There are no chirality outliers.

5 of 22 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	5202	NAG	C8-C7-N2-C2
4	A	5202	NAG	O7-C7-N2-C2
4	A	5203	NAG	C8-C7-N2-C2
4	A	5203	NAG	O7-C7-N2-C2

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Mol	Chain	Res	Type	Atoms
4	A	5205	NAG	C1-C2-N2-C7

There are no ring outliers.

4 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	5203	NAG	1	0
4	A	5202	NAG	1	0
4	A	5205	NAG	4	0
4	B	5204	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.

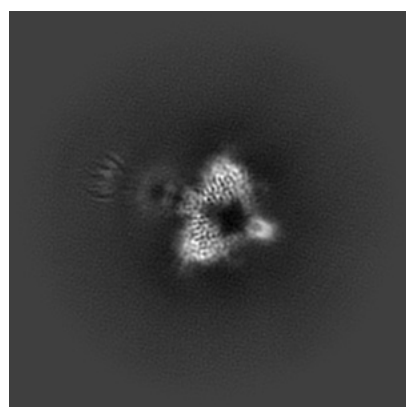
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-13899. These allow visual inspection of the internal detail of the map and identification of artifacts.

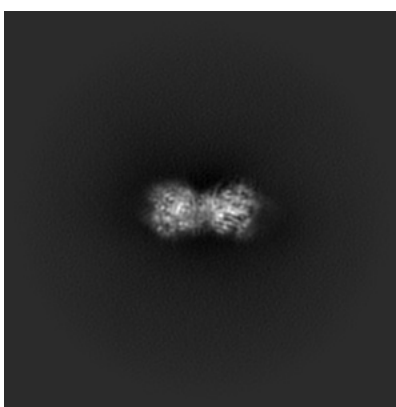
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

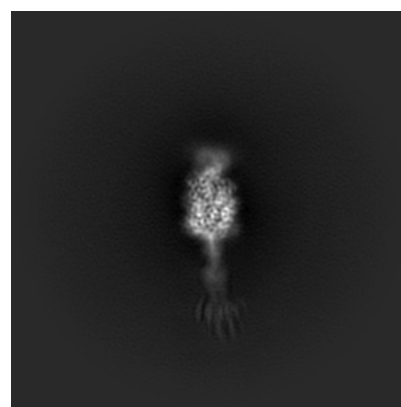
6.1.1 Primary map



X



Y

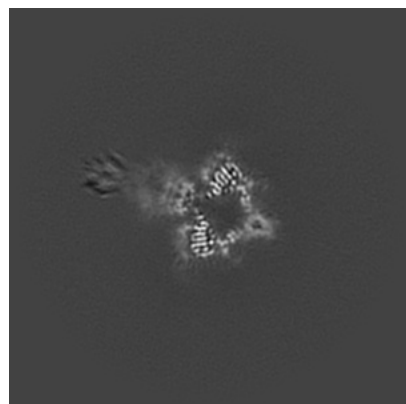


Z

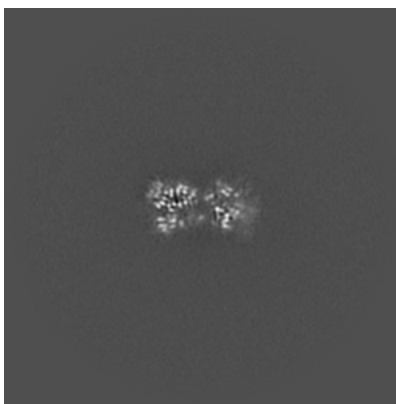
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

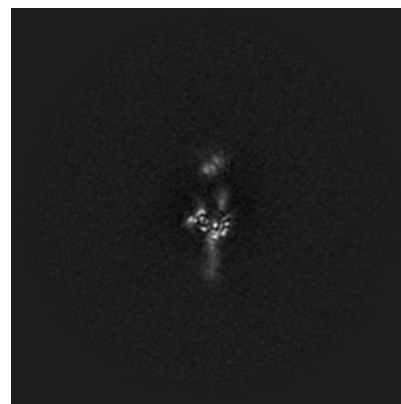
6.2.1 Primary map



X Index: 216



Y Index: 216

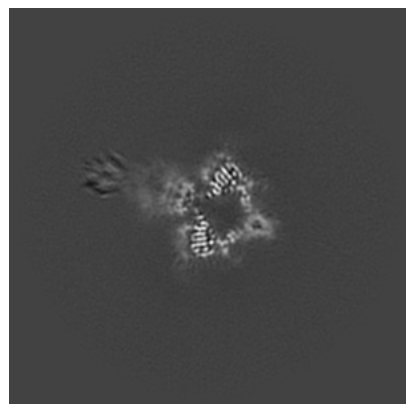


Z Index: 216

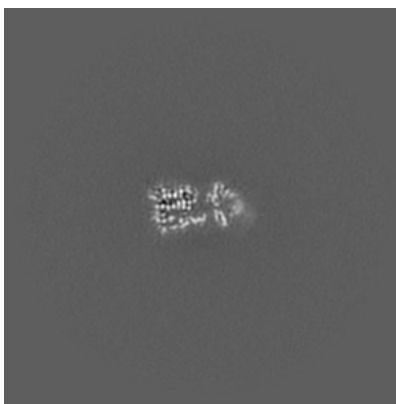
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

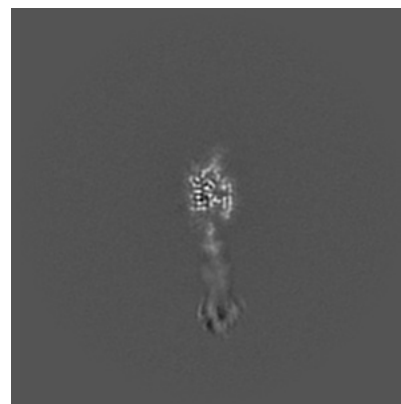
6.3.1 Primary map



X Index: 216



Y Index: 211

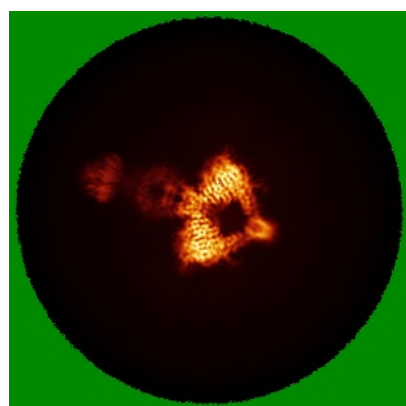


Z Index: 242

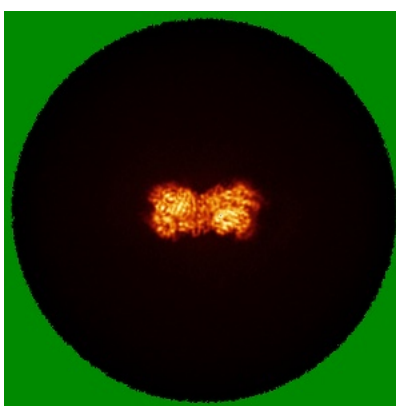
The images above show the largest variance slices of the map in three orthogonal directions.

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

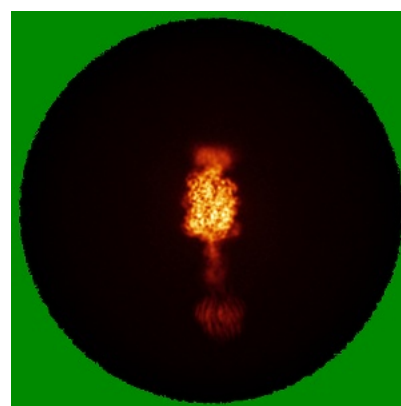
6.4.1 Primary map



X



Y

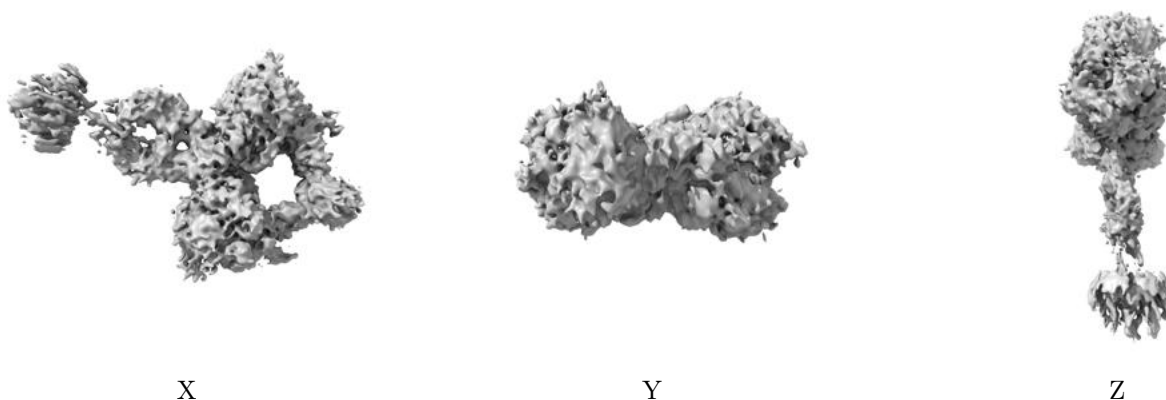


Z

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



The images above show the 3D surface view of the map at the recommended contour level 0.034. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

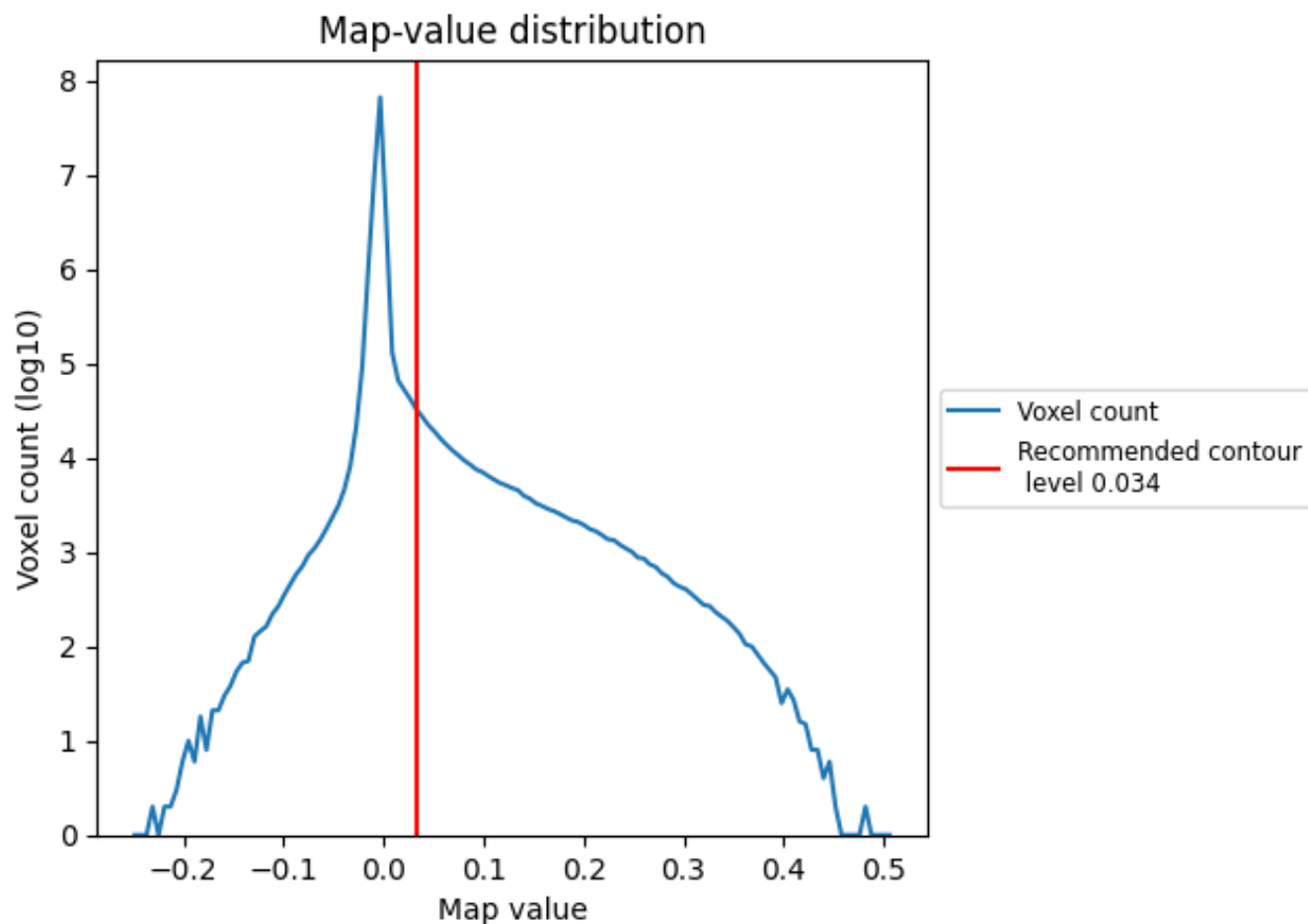
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

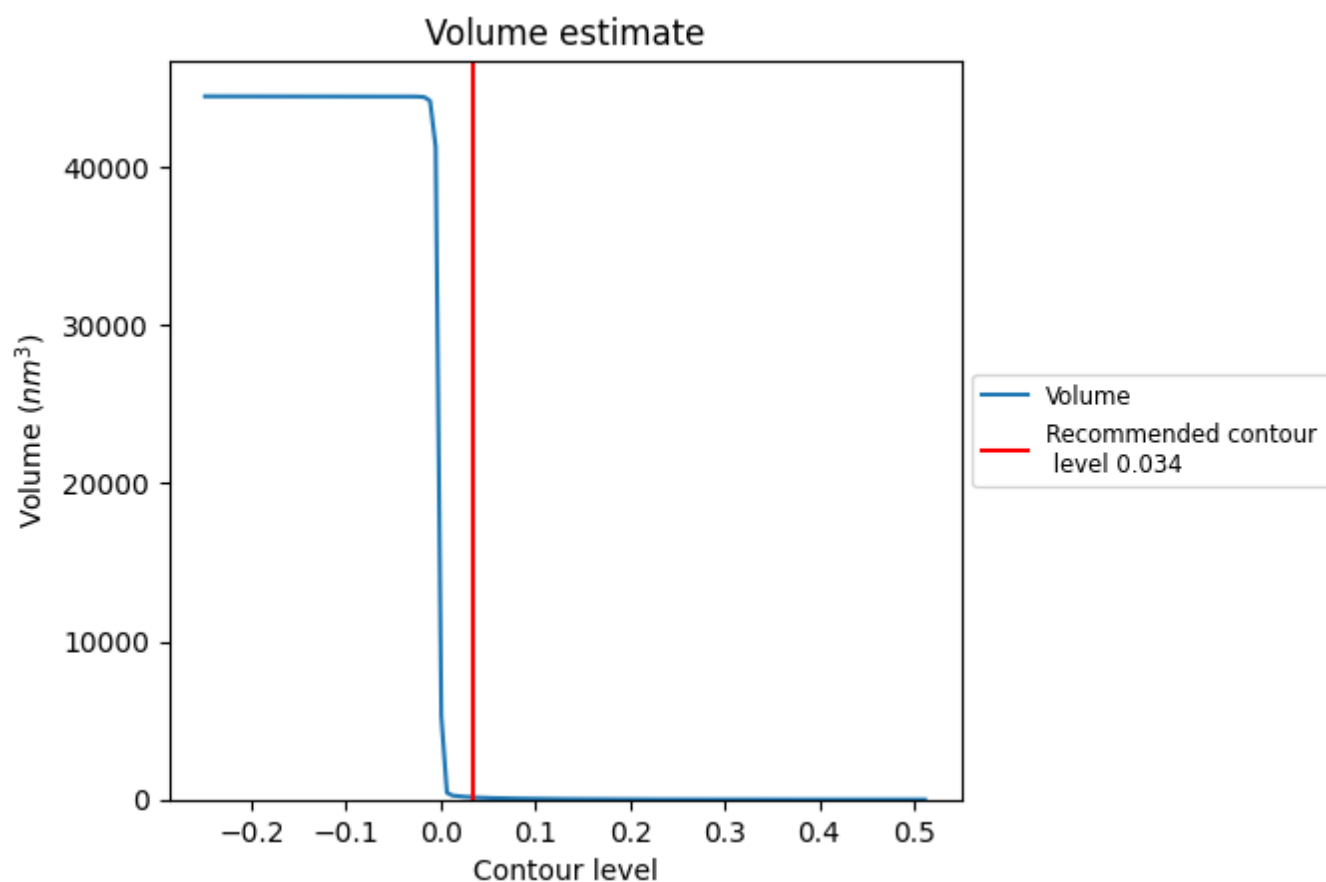
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution [i](#)



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

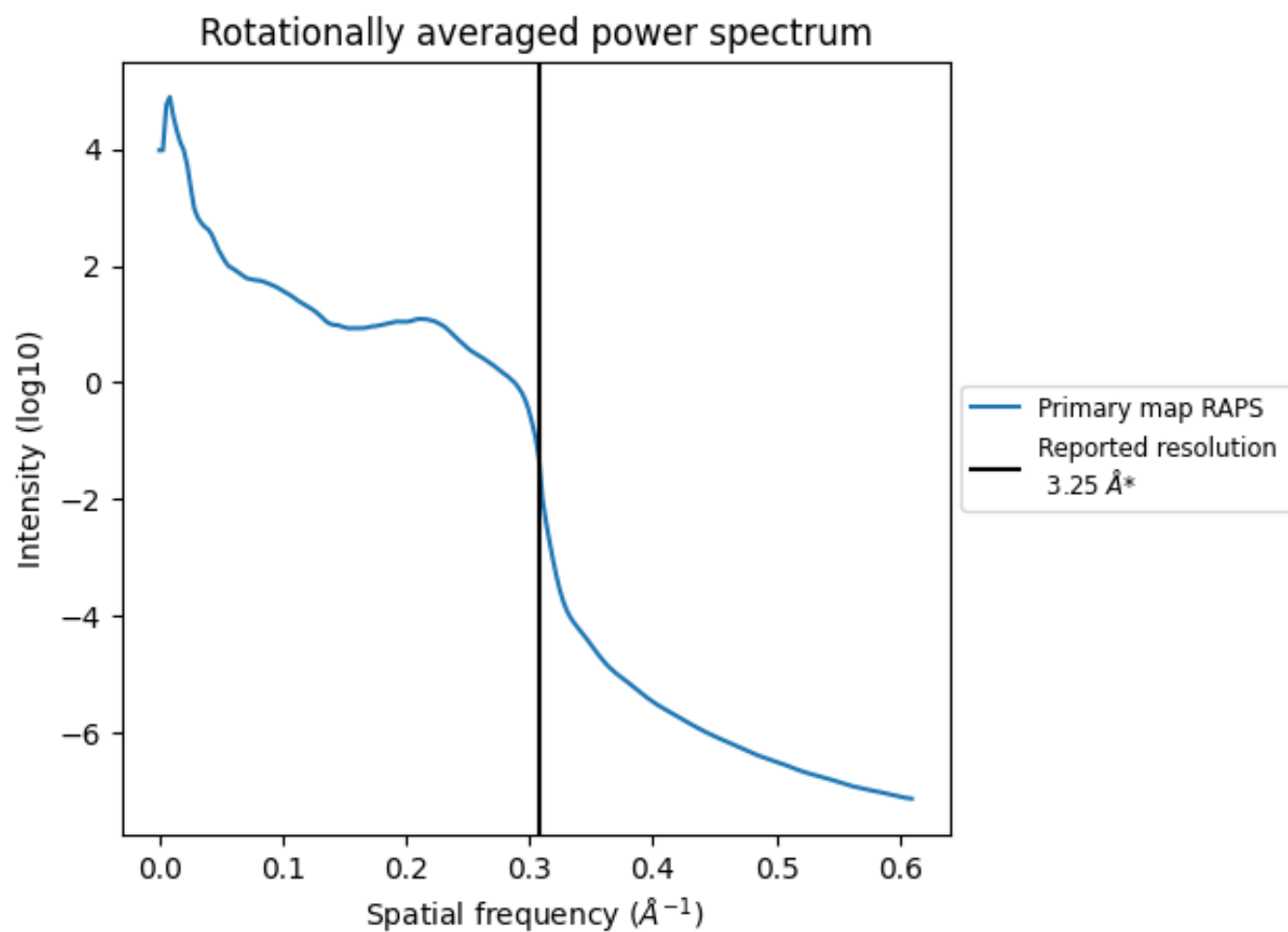
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 144 nm^3 ; this corresponds to an approximate mass of 130 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 0.308 Å⁻¹

8 Fourier-Shell correlation

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

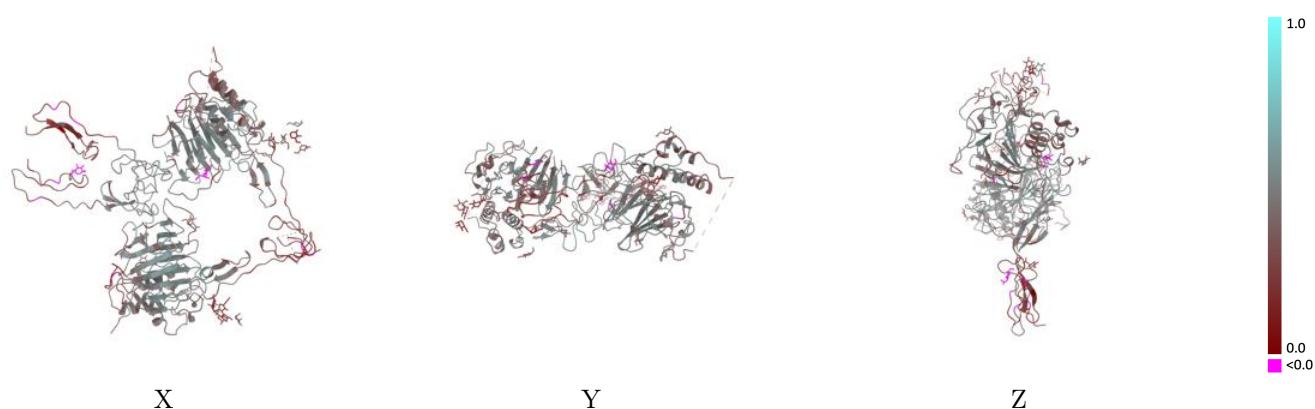
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-13899 and PDB model 7QCU. Per-residue inclusion information can be found in section 3 on page 7.

9.1 Map-model overlay [i](#)

This section was not generated.

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

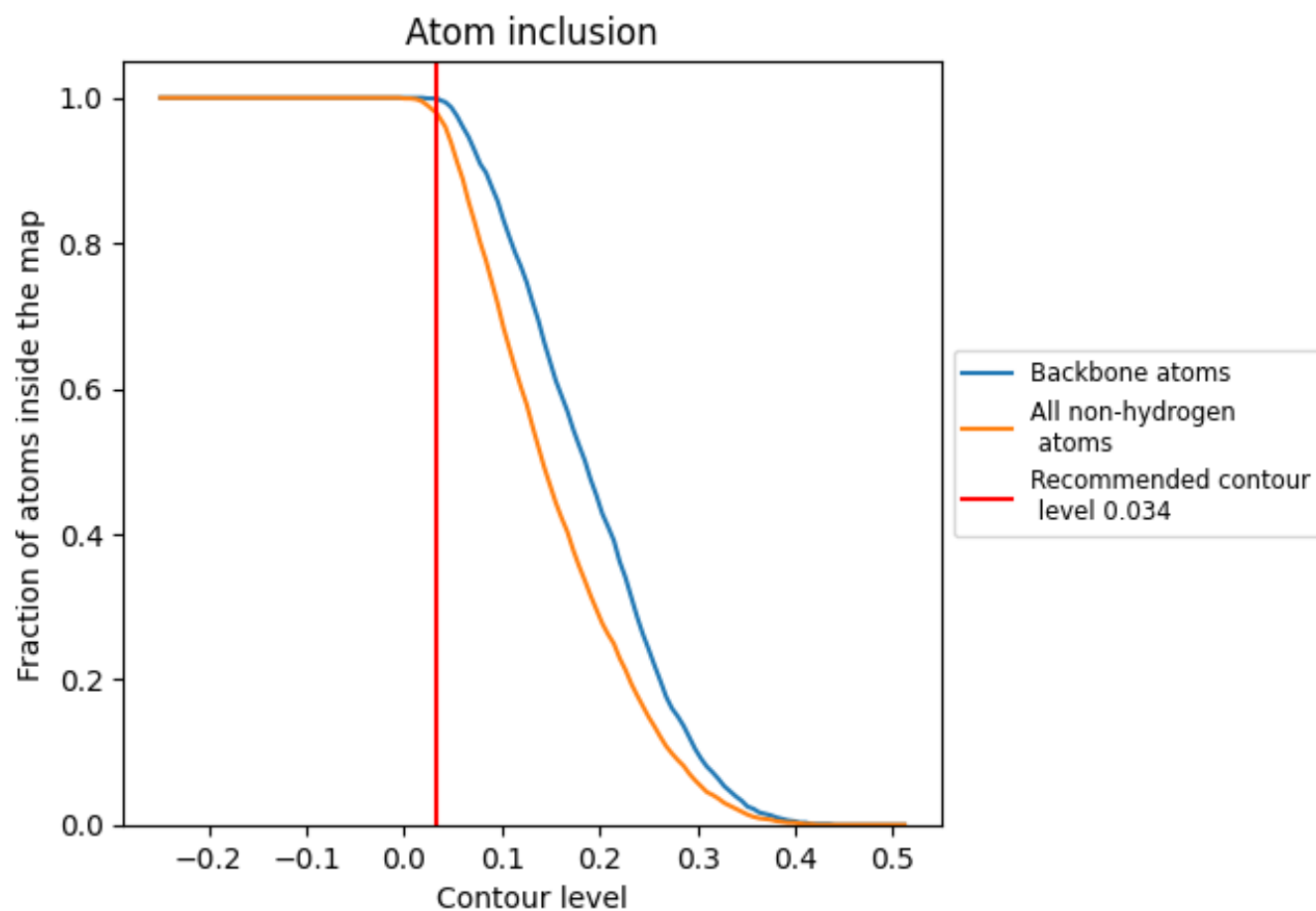


The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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](#)

This section was not generated.

9.4 Atom inclusion [i](#)



At the recommended contour level, 100% of all backbone atoms, 98% 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 (0.034) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9780	0.4040
A	0.9820	0.4060
B	0.9830	0.4060
C	0.7870	0.3060
D	0.6890	0.2180

