



wwPDB EM Validation Summary Report ⓘ

Oct 20, 2024 – 11:11 AM EDT

PDB ID : 7K0C
EMDB ID : EMD-22591
Title : Structure of Secretory IgM Core
Authors : Kumar, N.; Arthur, C.P.; Ciferri, C.; Matsumoto, M.L.
Deposited on : 2020-09-04
Resolution : 3.30 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.dev113
Mogul : 2022.3.0, CSD as543be (2022)
MolProbity : 4.02b-467
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) : 2.39

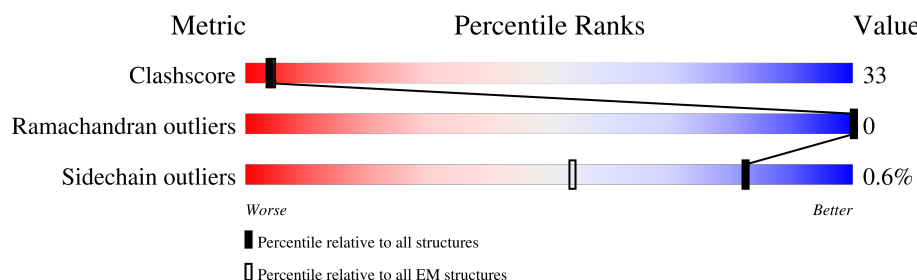
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY




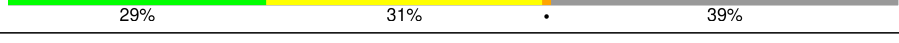
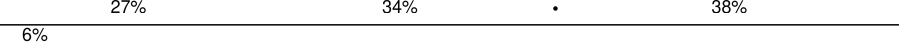
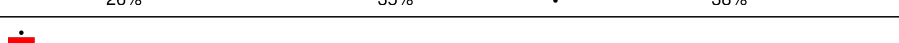
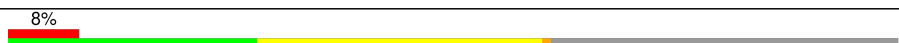

The reported resolution of this entry is 3.30 Å.

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.





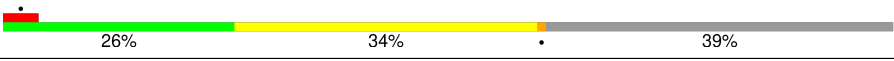
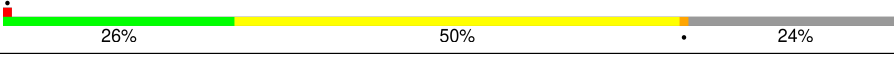

Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	210492	15764
Ramachandran outliers	207382	16835
Sidechain outliers	206894	16415

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 $\leq 5\%$. 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	C	591	
2	A	369	
2	B	369	
2	E	369	
2	F	369	
2	G	369	
2	H	369	
2	I	369	

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Mol	Chain	Length	Quality of chain
2	J	369	
2	K	369	
2	L	369	
3	D	137	
4	M	2	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 22540 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 Polymeric immunoglobulin receptor.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	C	534	Total	C	N	O	S	0	0
			4109	2588	709	792	20		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	586	HIS	-	expression tag	UNP P01833
C	587	HIS	-	expression tag	UNP P01833
C	588	HIS	-	expression tag	UNP P01833
C	589	HIS	-	expression tag	UNP P01833
C	590	HIS	-	expression tag	UNP P01833
C	591	HIS	-	expression tag	UNP P01833

- Molecule 2 is a protein called Immunoglobulin heavy constant mu.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	227	Total	C	N	O	S	0	0
			1764	1111	299	346	8		
2	B	227	Total	C	N	O	S	0	0
			1764	1111	299	346	8		
2	K	225	Total	C	N	O	S	0	0
			1748	1103	297	340	8		
2	L	224	Total	C	N	O	S	0	0
			1737	1097	293	339	8		
2	I	224	Total	C	N	O	S	0	0
			1743	1100	296	339	8		
2	J	221	Total	C	N	O	S	0	0
			1723	1087	292	336	8		
2	E	224	Total	C	N	O	S	0	0
			1742	1100	296	338	8		
2	H	230	Total	C	N	O	S	0	0
			1785	1124	301	351	9		
2	G	230	Total	C	N	O	S	0	0
			1786	1124	302	351	9		

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Mol	Chain	Residues	Atoms					AltConf	Trace
2	F	228	Total	C	N	O	S	0	0
			1773	1116	299	349	9		

There are 180 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	208	ASP	-	expression tag	UNP P01871
A	209	TYR	-	expression tag	UNP P01871
A	210	LYS	-	expression tag	UNP P01871
A	211	ASP	-	expression tag	UNP P01871
A	212	ASP	-	expression tag	UNP P01871
A	213	ASP	-	expression tag	UNP P01871
A	214	ASP	-	expression tag	UNP P01871
A	215	LYS	-	expression tag	UNP P01871
A	216	LEU	-	expression tag	UNP P01871
A	217	GLU	-	expression tag	UNP P01871
A	218	VAL	-	expression tag	UNP P01871
A	219	LEU	-	expression tag	UNP P01871
A	220	PHE	-	expression tag	UNP P01871
A	221	GLN	-	expression tag	UNP P01871
A	222	GLY	-	expression tag	UNP P01871
A	223	PRO	-	expression tag	UNP P01871
A	224	GLY	-	expression tag	UNP P01871
A	225	SER	-	expression tag	UNP P01871
B	208	ASP	-	expression tag	UNP P01871
B	209	TYR	-	expression tag	UNP P01871
B	210	LYS	-	expression tag	UNP P01871
B	211	ASP	-	expression tag	UNP P01871
B	212	ASP	-	expression tag	UNP P01871
B	213	ASP	-	expression tag	UNP P01871
B	214	ASP	-	expression tag	UNP P01871
B	215	LYS	-	expression tag	UNP P01871
B	216	LEU	-	expression tag	UNP P01871
B	217	GLU	-	expression tag	UNP P01871
B	218	VAL	-	expression tag	UNP P01871
B	219	LEU	-	expression tag	UNP P01871
B	220	PHE	-	expression tag	UNP P01871
B	221	GLN	-	expression tag	UNP P01871
B	222	GLY	-	expression tag	UNP P01871
B	223	PRO	-	expression tag	UNP P01871
B	224	GLY	-	expression tag	UNP P01871
B	225	SER	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
K	208	ASP	-	expression tag	UNP P01871
K	209	TYR	-	expression tag	UNP P01871
K	210	LYS	-	expression tag	UNP P01871
K	211	ASP	-	expression tag	UNP P01871
K	212	ASP	-	expression tag	UNP P01871
K	213	ASP	-	expression tag	UNP P01871
K	214	ASP	-	expression tag	UNP P01871
K	215	LYS	-	expression tag	UNP P01871
K	216	LEU	-	expression tag	UNP P01871
K	217	GLU	-	expression tag	UNP P01871
K	218	VAL	-	expression tag	UNP P01871
K	219	LEU	-	expression tag	UNP P01871
K	220	PHE	-	expression tag	UNP P01871
K	221	GLN	-	expression tag	UNP P01871
K	222	GLY	-	expression tag	UNP P01871
K	223	PRO	-	expression tag	UNP P01871
K	224	GLY	-	expression tag	UNP P01871
K	225	SER	-	expression tag	UNP P01871
L	208	ASP	-	expression tag	UNP P01871
L	209	TYR	-	expression tag	UNP P01871
L	210	LYS	-	expression tag	UNP P01871
L	211	ASP	-	expression tag	UNP P01871
L	212	ASP	-	expression tag	UNP P01871
L	213	ASP	-	expression tag	UNP P01871
L	214	ASP	-	expression tag	UNP P01871
L	215	LYS	-	expression tag	UNP P01871
L	216	LEU	-	expression tag	UNP P01871
L	217	GLU	-	expression tag	UNP P01871
L	218	VAL	-	expression tag	UNP P01871
L	219	LEU	-	expression tag	UNP P01871
L	220	PHE	-	expression tag	UNP P01871
L	221	GLN	-	expression tag	UNP P01871
L	222	GLY	-	expression tag	UNP P01871
L	223	PRO	-	expression tag	UNP P01871
L	224	GLY	-	expression tag	UNP P01871
L	225	SER	-	expression tag	UNP P01871
I	208	ASP	-	expression tag	UNP P01871
I	209	TYR	-	expression tag	UNP P01871
I	210	LYS	-	expression tag	UNP P01871
I	211	ASP	-	expression tag	UNP P01871
I	212	ASP	-	expression tag	UNP P01871
I	213	ASP	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
I	214	ASP	-	expression tag	UNP P01871
I	215	LYS	-	expression tag	UNP P01871
I	216	LEU	-	expression tag	UNP P01871
I	217	GLU	-	expression tag	UNP P01871
I	218	VAL	-	expression tag	UNP P01871
I	219	LEU	-	expression tag	UNP P01871
I	220	PHE	-	expression tag	UNP P01871
I	221	GLN	-	expression tag	UNP P01871
I	222	GLY	-	expression tag	UNP P01871
I	223	PRO	-	expression tag	UNP P01871
I	224	GLY	-	expression tag	UNP P01871
I	225	SER	-	expression tag	UNP P01871
J	208	ASP	-	expression tag	UNP P01871
J	209	TYR	-	expression tag	UNP P01871
J	210	LYS	-	expression tag	UNP P01871
J	211	ASP	-	expression tag	UNP P01871
J	212	ASP	-	expression tag	UNP P01871
J	213	ASP	-	expression tag	UNP P01871
J	214	ASP	-	expression tag	UNP P01871
J	215	LYS	-	expression tag	UNP P01871
J	216	LEU	-	expression tag	UNP P01871
J	217	GLU	-	expression tag	UNP P01871
J	218	VAL	-	expression tag	UNP P01871
J	219	LEU	-	expression tag	UNP P01871
J	220	PHE	-	expression tag	UNP P01871
J	221	GLN	-	expression tag	UNP P01871
J	222	GLY	-	expression tag	UNP P01871
J	223	PRO	-	expression tag	UNP P01871
J	224	GLY	-	expression tag	UNP P01871
J	225	SER	-	expression tag	UNP P01871
E	208	ASP	-	expression tag	UNP P01871
E	209	TYR	-	expression tag	UNP P01871
E	210	LYS	-	expression tag	UNP P01871
E	211	ASP	-	expression tag	UNP P01871
E	212	ASP	-	expression tag	UNP P01871
E	213	ASP	-	expression tag	UNP P01871
E	214	ASP	-	expression tag	UNP P01871
E	215	LYS	-	expression tag	UNP P01871
E	216	LEU	-	expression tag	UNP P01871
E	217	GLU	-	expression tag	UNP P01871
E	218	VAL	-	expression tag	UNP P01871
E	219	LEU	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
E	220	PHE	-	expression tag	UNP P01871
E	221	GLN	-	expression tag	UNP P01871
E	222	GLY	-	expression tag	UNP P01871
E	223	PRO	-	expression tag	UNP P01871
E	224	GLY	-	expression tag	UNP P01871
E	225	SER	-	expression tag	UNP P01871
H	208	ASP	-	expression tag	UNP P01871
H	209	TYR	-	expression tag	UNP P01871
H	210	LYS	-	expression tag	UNP P01871
H	211	ASP	-	expression tag	UNP P01871
H	212	ASP	-	expression tag	UNP P01871
H	213	ASP	-	expression tag	UNP P01871
H	214	ASP	-	expression tag	UNP P01871
H	215	LYS	-	expression tag	UNP P01871
H	216	LEU	-	expression tag	UNP P01871
H	217	GLU	-	expression tag	UNP P01871
H	218	VAL	-	expression tag	UNP P01871
H	219	LEU	-	expression tag	UNP P01871
H	220	PHE	-	expression tag	UNP P01871
H	221	GLN	-	expression tag	UNP P01871
H	222	GLY	-	expression tag	UNP P01871
H	223	PRO	-	expression tag	UNP P01871
H	224	GLY	-	expression tag	UNP P01871
H	225	SER	-	expression tag	UNP P01871
G	208	ASP	-	expression tag	UNP P01871
G	209	TYR	-	expression tag	UNP P01871
G	210	LYS	-	expression tag	UNP P01871
G	211	ASP	-	expression tag	UNP P01871
G	212	ASP	-	expression tag	UNP P01871
G	213	ASP	-	expression tag	UNP P01871
G	214	ASP	-	expression tag	UNP P01871
G	215	LYS	-	expression tag	UNP P01871
G	216	LEU	-	expression tag	UNP P01871
G	217	GLU	-	expression tag	UNP P01871
G	218	VAL	-	expression tag	UNP P01871
G	219	LEU	-	expression tag	UNP P01871
G	220	PHE	-	expression tag	UNP P01871
G	221	GLN	-	expression tag	UNP P01871
G	222	GLY	-	expression tag	UNP P01871
G	223	PRO	-	expression tag	UNP P01871
G	224	GLY	-	expression tag	UNP P01871
G	225	SER	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
F	208	ASP	-	expression tag	UNP P01871
F	209	TYR	-	expression tag	UNP P01871
F	210	LYS	-	expression tag	UNP P01871
F	211	ASP	-	expression tag	UNP P01871
F	212	ASP	-	expression tag	UNP P01871
F	213	ASP	-	expression tag	UNP P01871
F	214	ASP	-	expression tag	UNP P01871
F	215	LYS	-	expression tag	UNP P01871
F	216	LEU	-	expression tag	UNP P01871
F	217	GLU	-	expression tag	UNP P01871
F	218	VAL	-	expression tag	UNP P01871
F	219	LEU	-	expression tag	UNP P01871
F	220	PHE	-	expression tag	UNP P01871
F	221	GLN	-	expression tag	UNP P01871
F	222	GLY	-	expression tag	UNP P01871
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F	225	SER	-	expression tag	UNP P01871

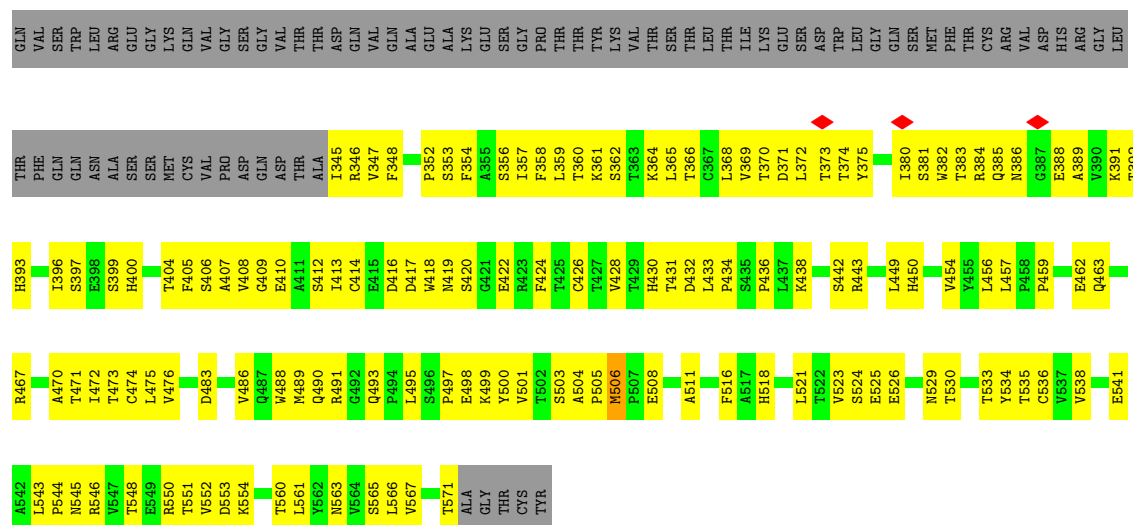
- Molecule 3 is a protein called Immunoglobulin J chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	D	104	Total	C	N	O	S	0	0
			838	521	148	162	7		

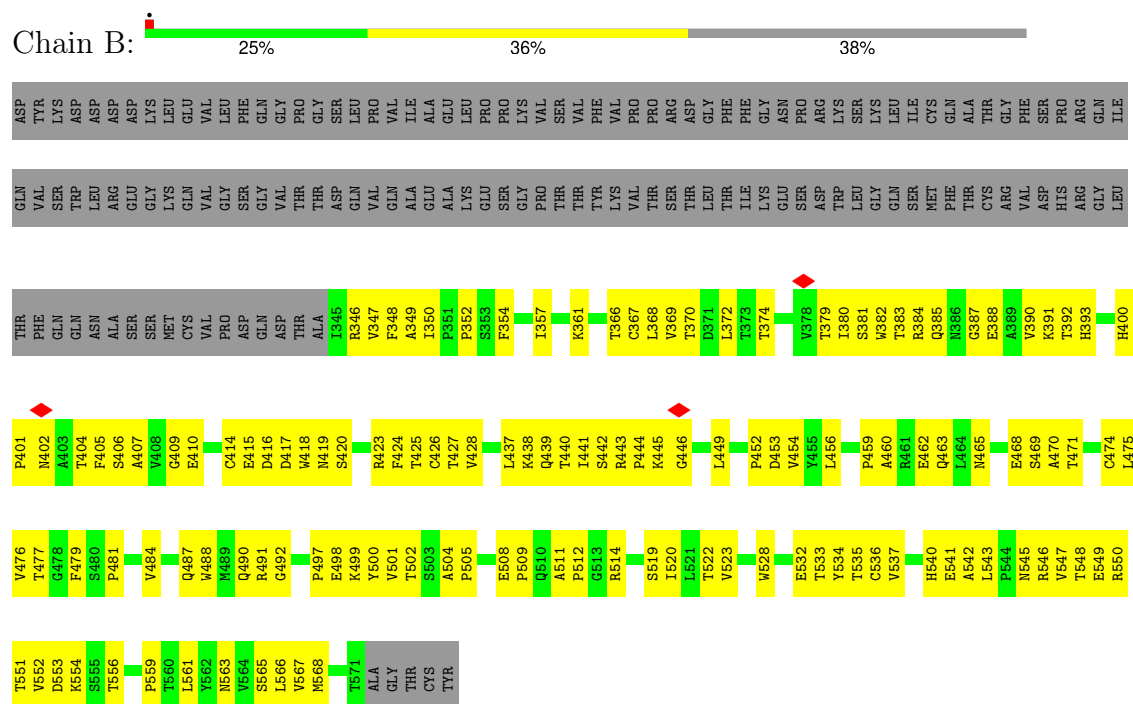
- Molecule 4 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



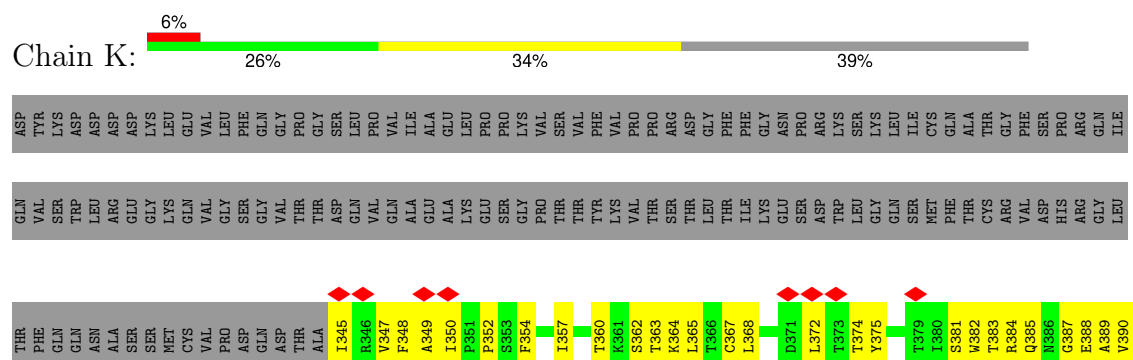
Mol	Chain	Residues	Atoms				AltConf	Trace
4	M	2	Total	C	N	O	0	0
			28	16	2	10		

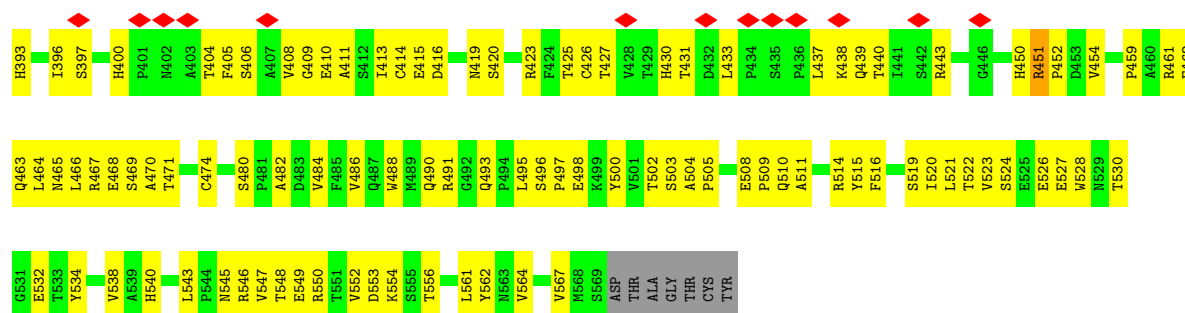


• Molecule 2: Immunoglobulin heavy constant mu

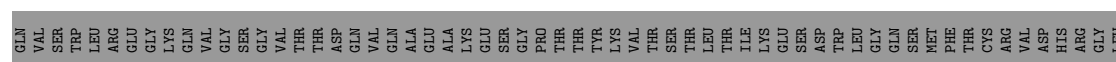
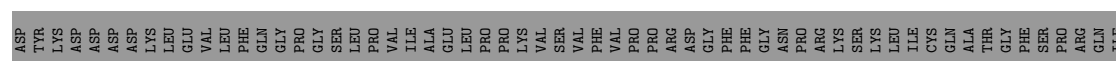
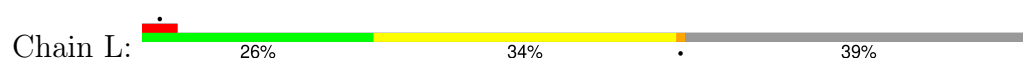


• Molecule 2: Immunoglobulin heavy constant mu

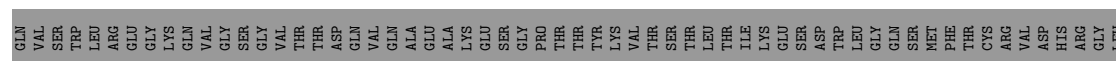
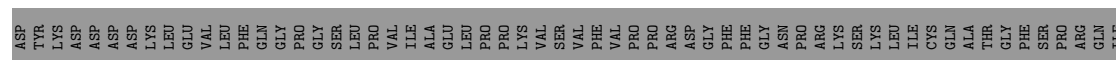
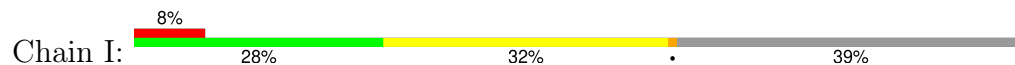


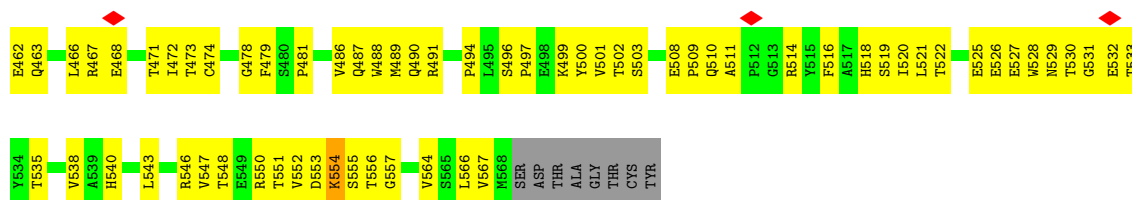


• Molecule 2: Immunoglobulin heavy constant mu

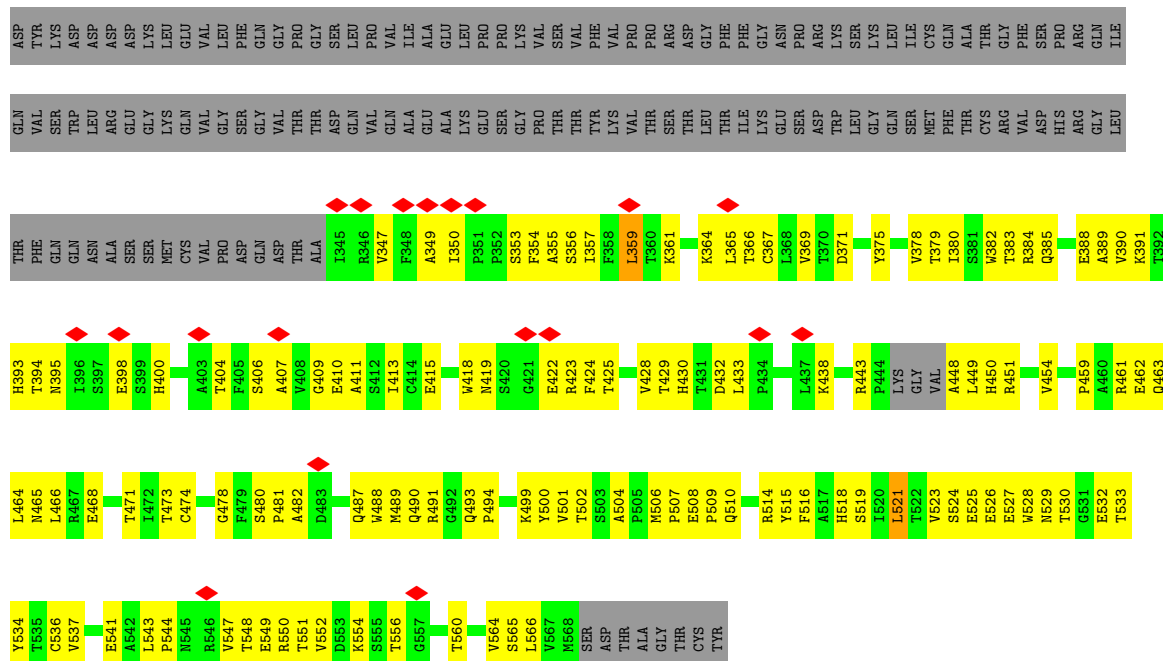
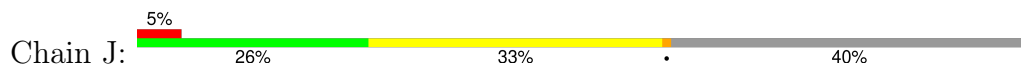


• Molecule 2: Immunoglobulin heavy constant mu

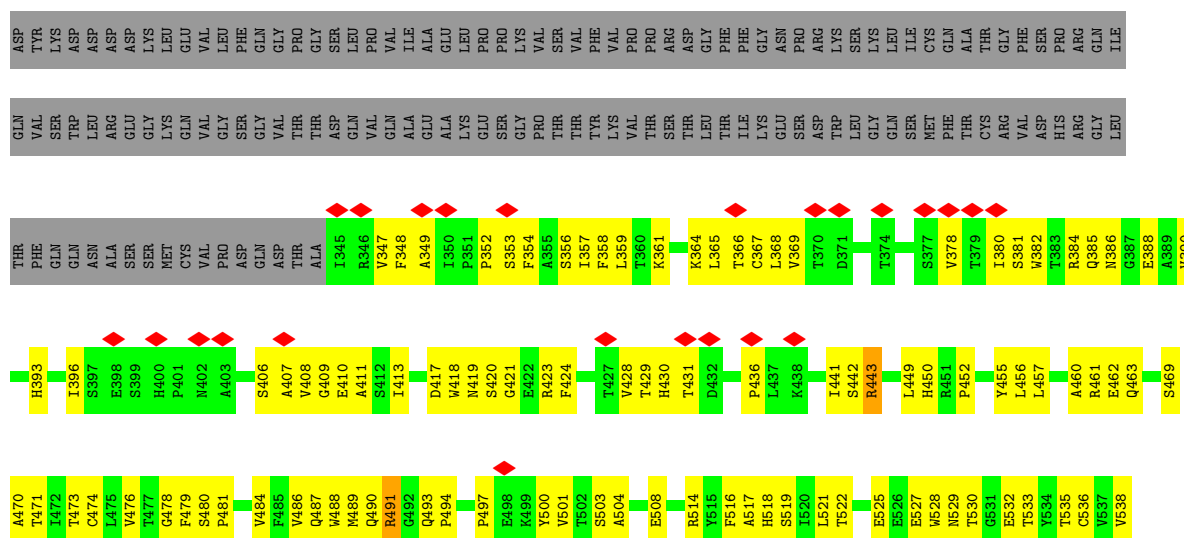
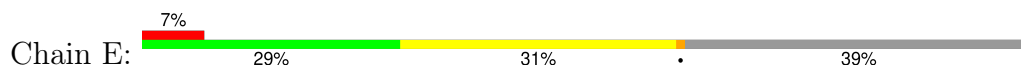




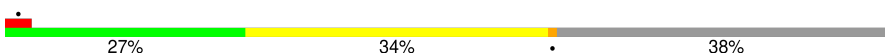
• Molecule 2: Immunoglobulin heavy constant mu

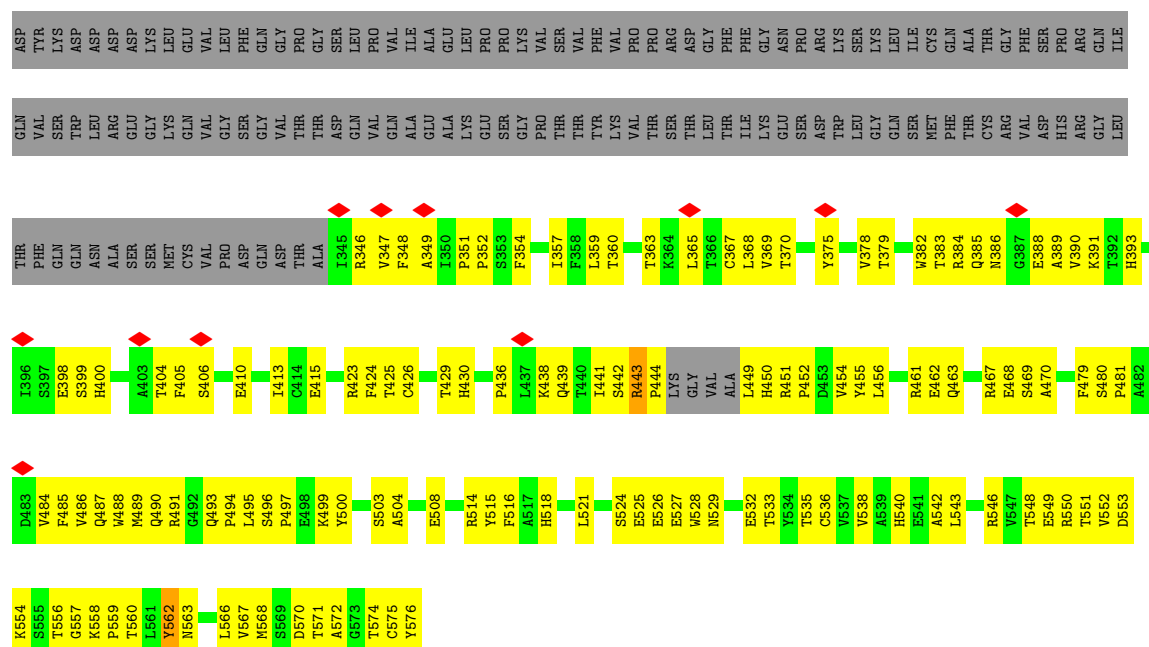


• Molecule 2: Immunoglobulin heavy constant mu



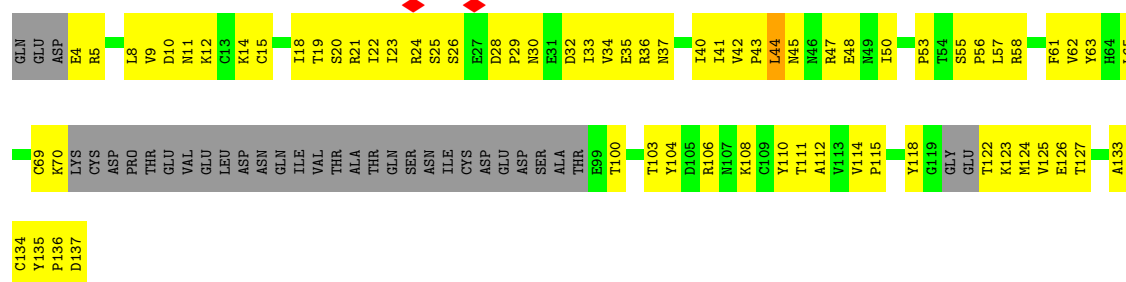


Chain F: 



• Molecule 3: Immunoglobulin J chain

Chain D: 



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

Chain M: 



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	244123	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 ($e^-/\text{\AA}^2$)	1.02	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	165000	Depositor
Image detector	GATAN K2 SUMMIT (4k x 4k)	Depositor
Maximum map value	42.554	Depositor
Minimum map value	-24.536	Depositor
Average map value	-0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	4.5	Depositor
Map size (Å)	480.00003, 480.00003, 480.00003	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.2, 1.2, 1.2	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: 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	C	0.44	0/4198	0.61	1/5708 (0.0%)
2	A	0.51	1/1809 (0.1%)	0.64	1/2478 (0.0%)
2	B	0.47	0/1809	0.63	1/2478 (0.0%)
2	E	0.38	0/1787	0.56	1/2447 (0.0%)
2	F	0.40	0/1818	0.56	0/2490
2	G	0.41	0/1831	0.63	2/2506 (0.1%)
2	H	0.38	0/1830	0.58	0/2507
2	I	0.35	0/1788	0.57	0/2449
2	J	0.37	0/1767	0.59	2/2420 (0.1%)
2	K	0.42	0/1793	0.57	0/2455
2	L	0.39	0/1782	0.59	1/2442 (0.0%)
3	D	0.56	0/850	0.69	1/1153 (0.1%)
All	All	0.42	1/23062 (0.0%)	0.60	10/31533 (0.0%)

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
2	F	0	1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	506	MET	C-N	7.57	1.48	1.34

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	G	536	CYS	CA-CB-SG	8.12	128.62	114.00
2	G	474	CYS	CA-CB-SG	7.83	128.09	114.00
2	J	359	LEU	CA-CB-CG	6.86	131.08	115.30
1	C	281	LEU	CA-CB-CG	6.39	130.01	115.30
2	J	521	LEU	CB-CG-CD2	-6.39	100.14	111.00

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	F	562	TYR	Peptide

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	C	4109	0	3992	227	0
2	A	1764	0	1725	132	0
2	B	1764	0	1724	123	0
2	E	1742	0	1708	117	0
2	F	1773	0	1721	141	0
2	G	1786	0	1737	149	0
2	H	1785	0	1735	121	0
2	I	1743	0	1708	117	0
2	J	1723	0	1682	119	0
2	K	1748	0	1713	123	0
2	L	1737	0	1697	135	0
3	D	838	0	833	70	0
4	M	28	0	25	1	0
All	All	22540	0	22000	1461	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 33.

The worst 5 of 1461 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:K:562:TYR:OH	2:H:568:MET:SD	2.20	1.00
2:I:564:VAL:HG21	2:J:564:VAL:HG21	1.42	1.00
2:A:374:THR:HG23	2:A:405:PHE:HB3	1.49	0.93
2:L:500:TYR:HA	2:L:521:LEU:HD21	1.46	0.93
1:C:391:TYR:HE1	1:C:394:ARG:HH11	1.16	0.93

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	C	530/591 (90%)	482 (91%)	48 (9%)	0	100	100
2	A	225/369 (61%)	199 (88%)	26 (12%)	0	100	100
2	B	225/369 (61%)	182 (81%)	43 (19%)	0	100	100
2	E	222/369 (60%)	189 (85%)	33 (15%)	0	100	100
2	F	224/369 (61%)	181 (81%)	43 (19%)	0	100	100
2	G	226/369 (61%)	192 (85%)	34 (15%)	0	100	100
2	H	226/369 (61%)	187 (83%)	39 (17%)	0	100	100
2	I	222/369 (60%)	187 (84%)	35 (16%)	0	100	100
2	J	217/369 (59%)	188 (87%)	29 (13%)	0	100	100
2	K	223/369 (60%)	185 (83%)	38 (17%)	0	100	100
2	L	222/369 (60%)	188 (85%)	34 (15%)	0	100	100
3	D	98/137 (72%)	69 (70%)	29 (30%)	0	100	100
All	All	2860/4418 (65%)	2429 (85%)	431 (15%)	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	C	450/501 (90%)	448 (100%)	2 (0%)	89	93
2	A	203/326 (62%)	203 (100%)	0	100	100
2	B	203/326 (62%)	203 (100%)	0	100	100
2	E	200/326 (61%)	197 (98%)	3 (2%)	60	77
2	F	204/326 (63%)	203 (100%)	1 (0%)	86	91
2	G	205/326 (63%)	202 (98%)	3 (2%)	60	77
2	H	205/326 (63%)	204 (100%)	1 (0%)	86	91
2	I	200/326 (61%)	198 (99%)	2 (1%)	73	84
2	J	198/326 (61%)	198 (100%)	0	100	100
2	K	201/326 (62%)	200 (100%)	1 (0%)	86	91
2	L	199/326 (61%)	198 (100%)	1 (0%)	86	91
3	D	99/129 (77%)	97 (98%)	2 (2%)	50	71
All	All	2567/3890 (66%)	2551 (99%)	16 (1%)	82	90

5 of 16 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	461	ARG
2	G	443	ARG
2	E	491	ARG
2	G	423	ARG
2	E	443	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
2	E	540	HIS
3	D	37	ASN
2	F	487	GLN
2	H	518	HIS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
2	G	400	HIS

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 ⓘ

2 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	M	1	3,4	14,14,15	0.77	1 (7%)	17,19,21	0.61	0
4	NAG	M	2	4	14,14,15	0.19	0	17,19,21	0.38	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	M	1	3,4	-	3/6/23/26	0/1/1/1
4	NAG	M	2	4	-	1/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	M	1	NAG	O5-C1	-2.81	1.39	1.43

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

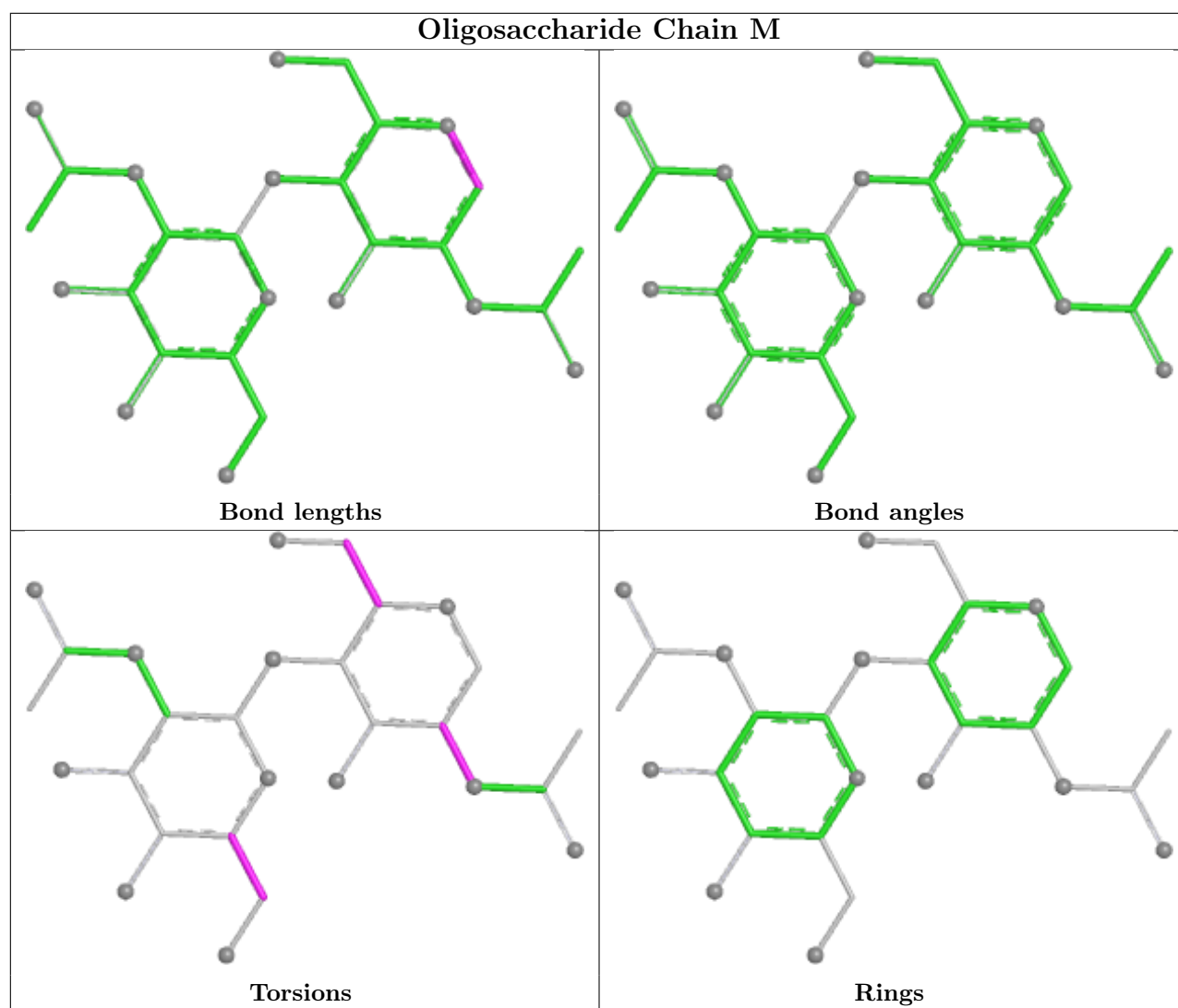
Mol	Chain	Res	Type	Atoms
4	M	1	NAG	O5-C5-C6-O6
4	M	1	NAG	C4-C5-C6-O6
4	M	2	NAG	O5-C5-C6-O6
4	M	1	NAG	C3-C2-N2-C7

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	M	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](#)

There are no ligands in this entry.

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.

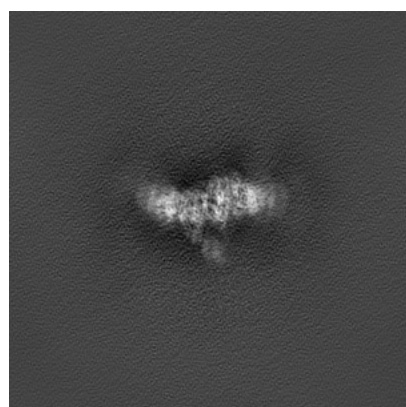
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-22591. These allow visual inspection of the internal detail of the map and identification of artifacts.

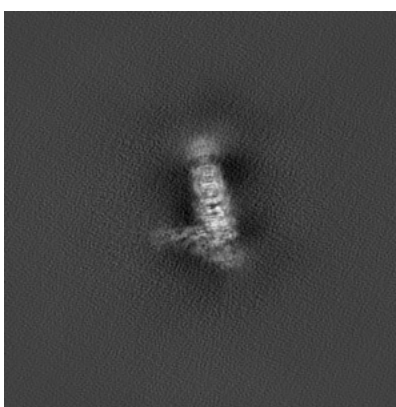
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections [i](#)

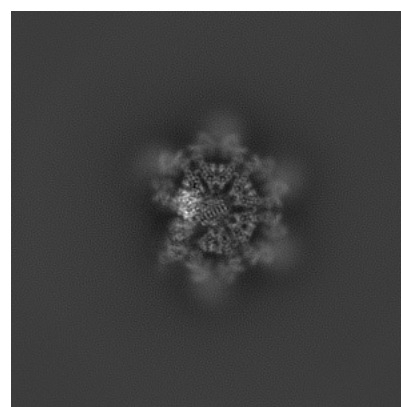
6.1.1 Primary map



X



Y

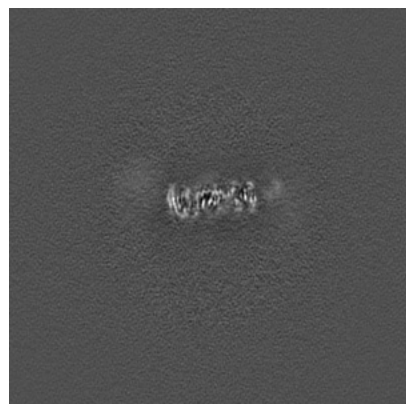


Z

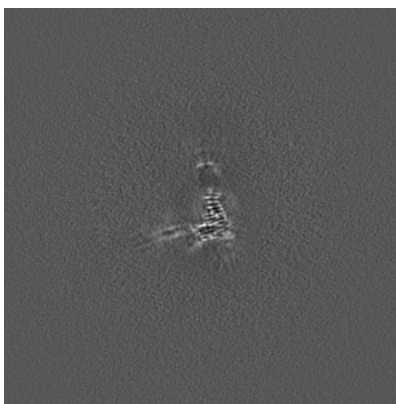
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

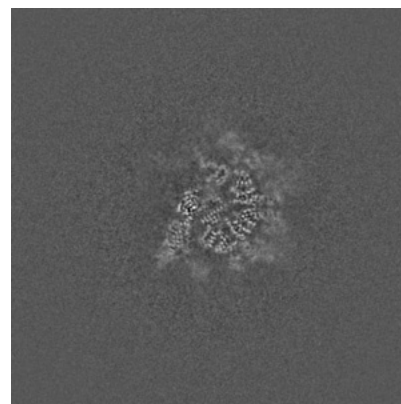
6.2.1 Primary map



X Index: 200



Y Index: 200

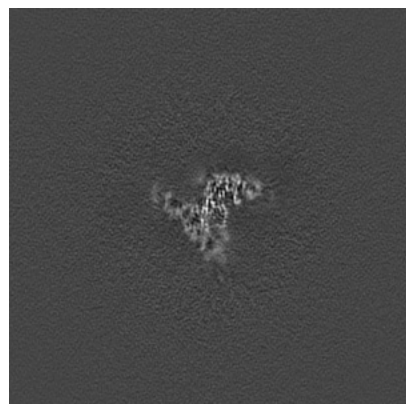


Z Index: 200

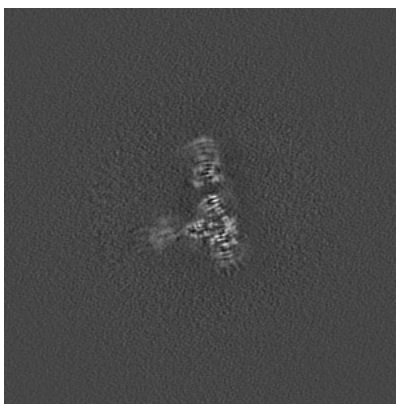
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

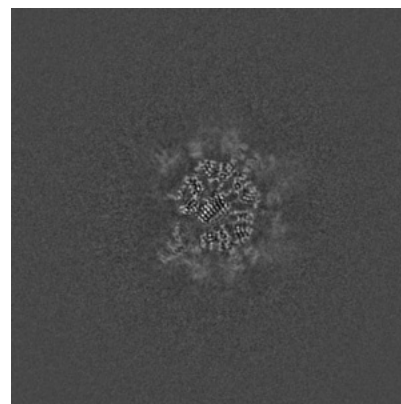
6.3.1 Primary map



X Index: 175



Y Index: 209

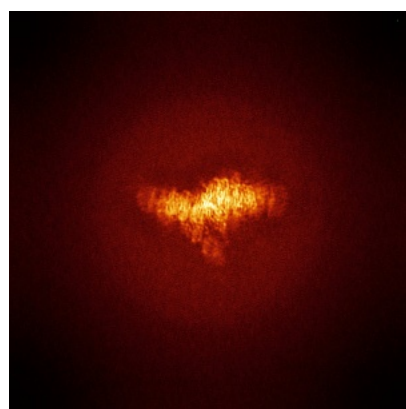


Z Index: 207

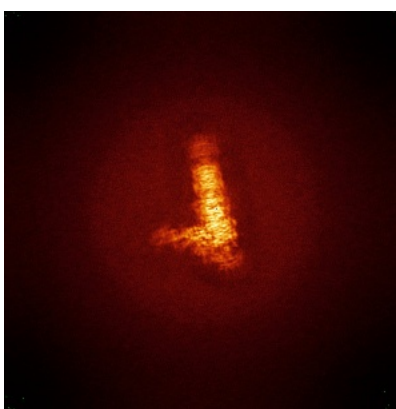
The images above show the largest variance slices of the map in three orthogonal directions.

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

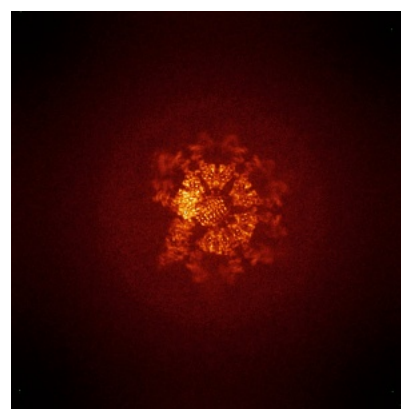
6.4.1 Primary map



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

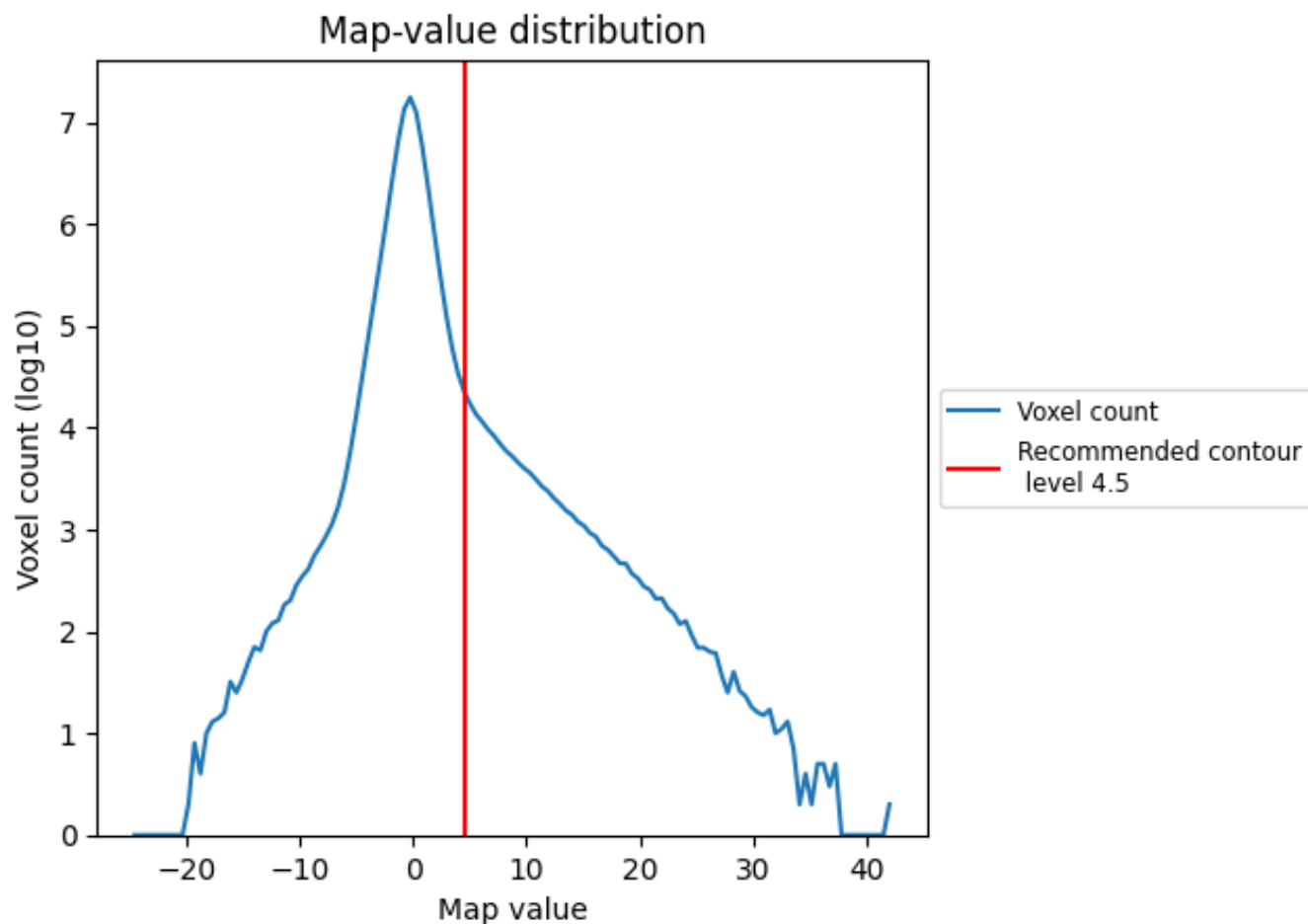
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

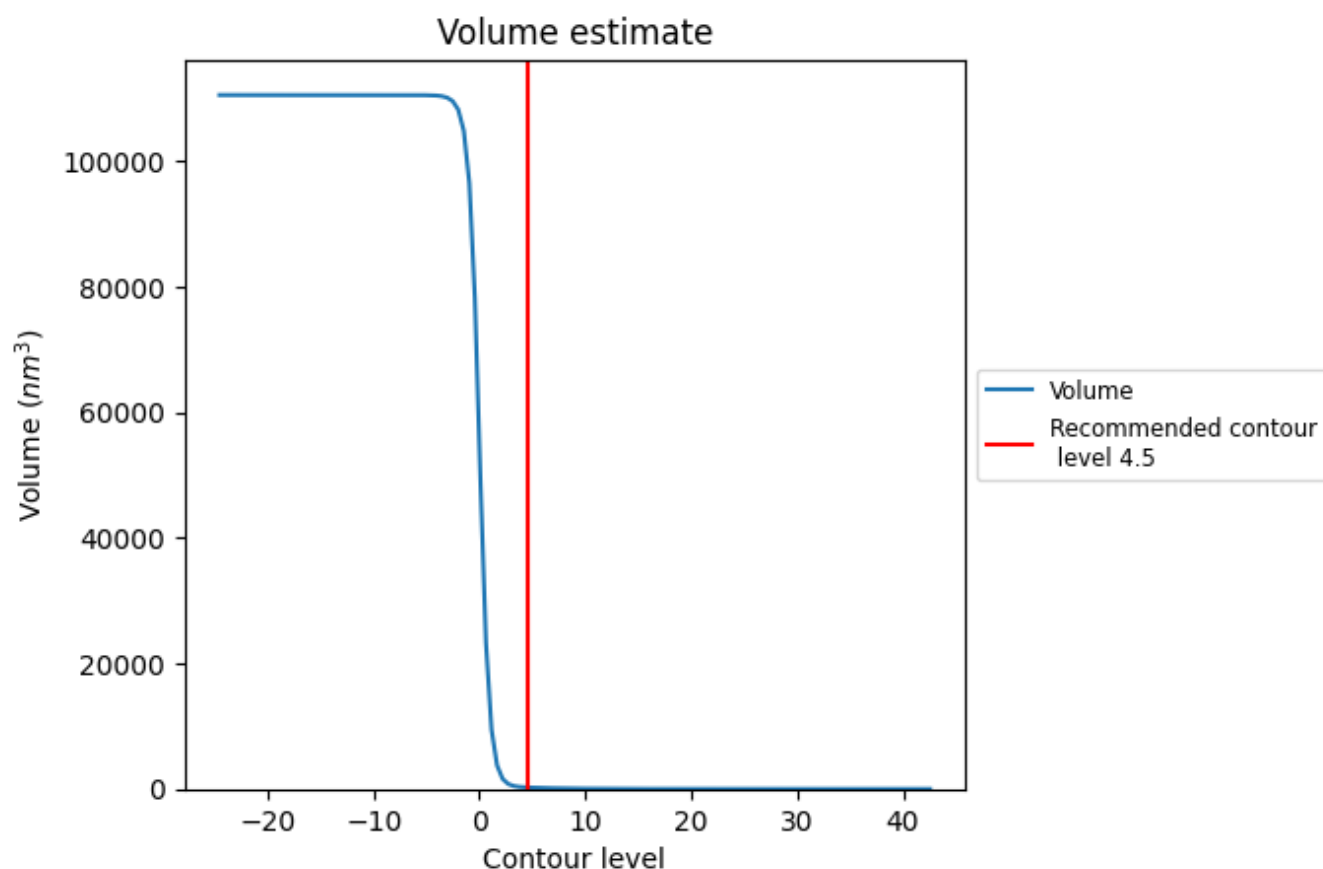
This section contains the results of statistical analysis of the map.

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.

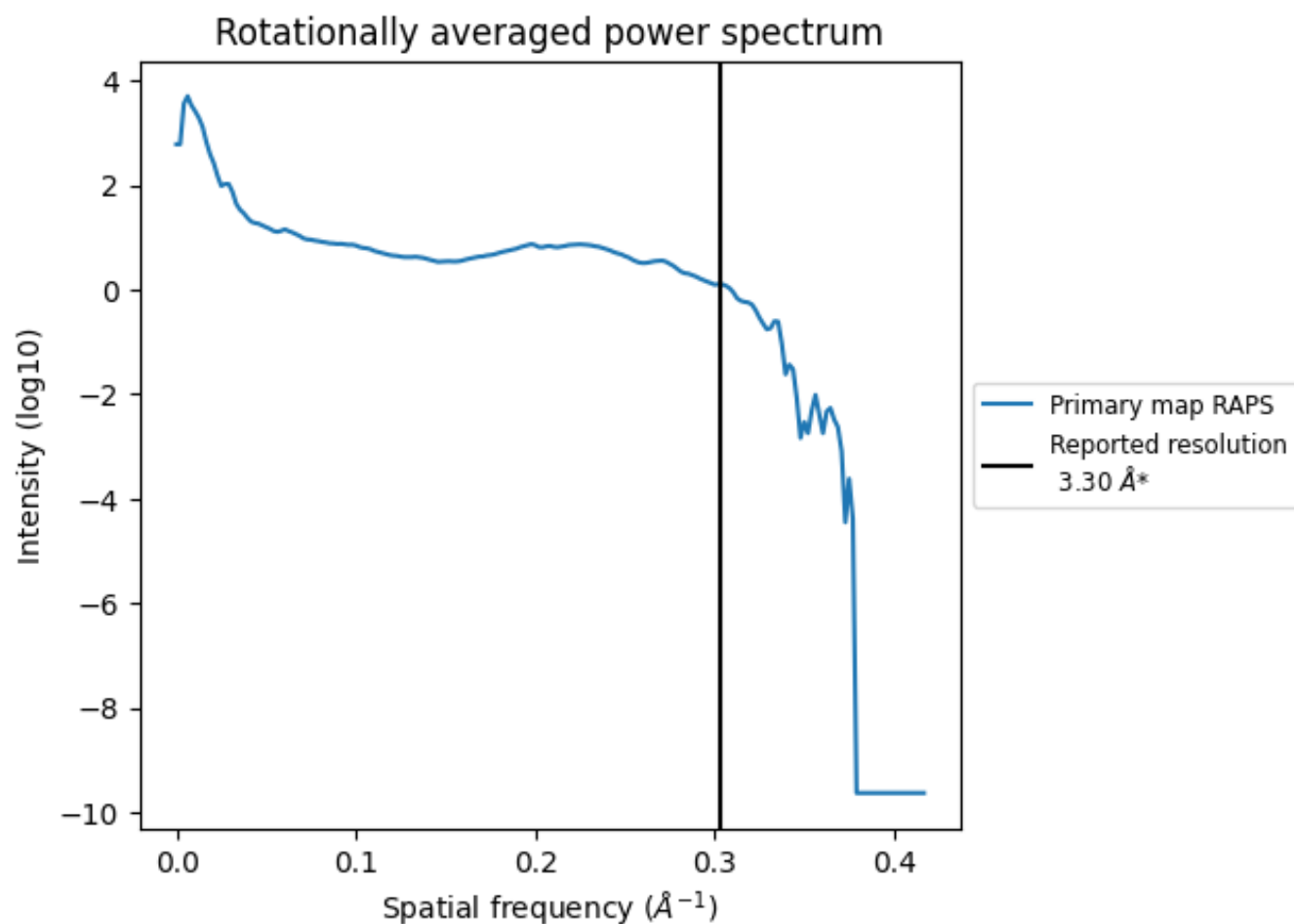
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 241 nm^3 ; this corresponds to an approximate mass of 218 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 0.303 Å⁻¹

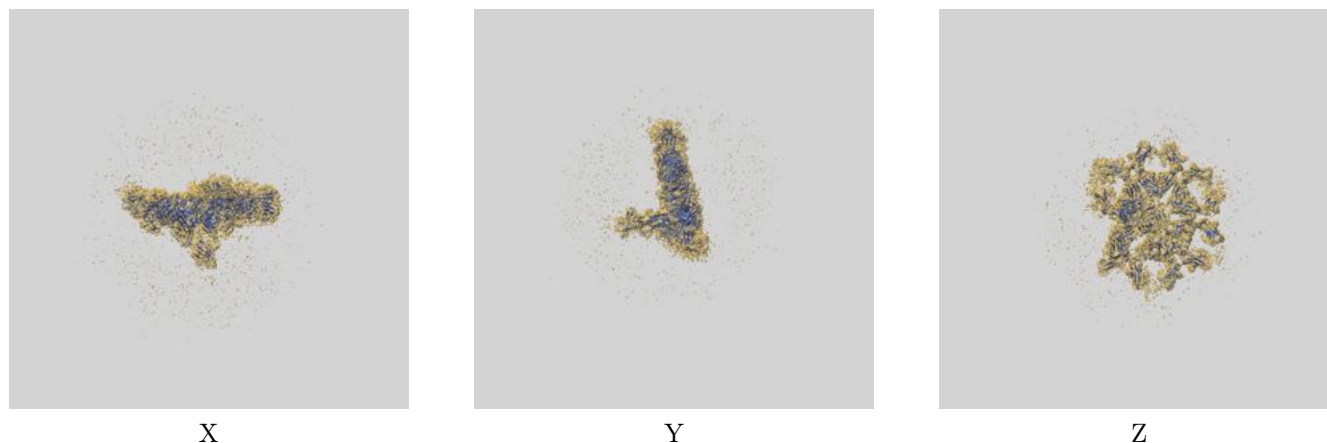
8 Fourier-Shell correlation ⓘ

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

9 Map-model fit [i](#)

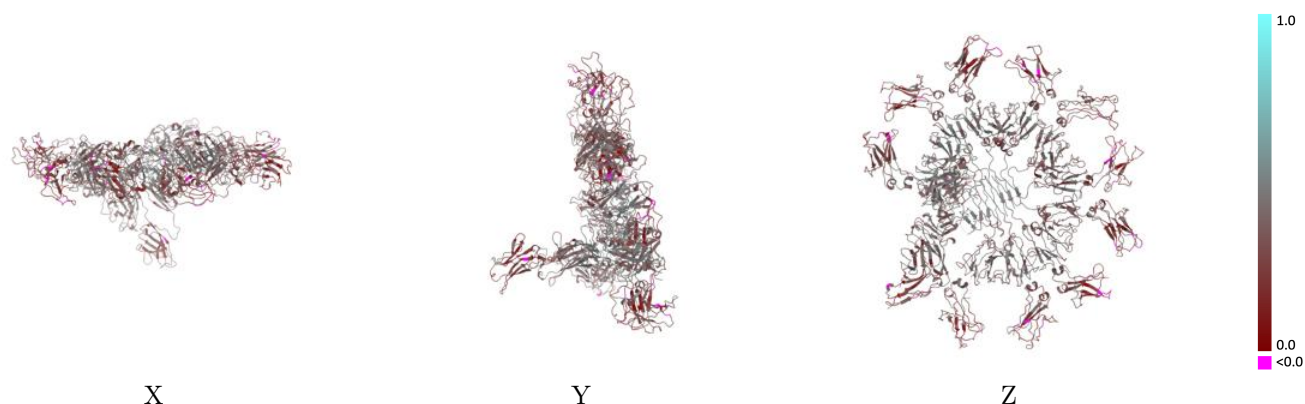
This section contains information regarding the fit between EMDB map EMD-22591 and PDB model 7K0C. Per-residue inclusion information can be found in section [3](#) on page [10](#).

9.1 Map-model overlay [i](#)



The images above show the 3D surface view of the map at the recommended contour level 4.5 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](#)



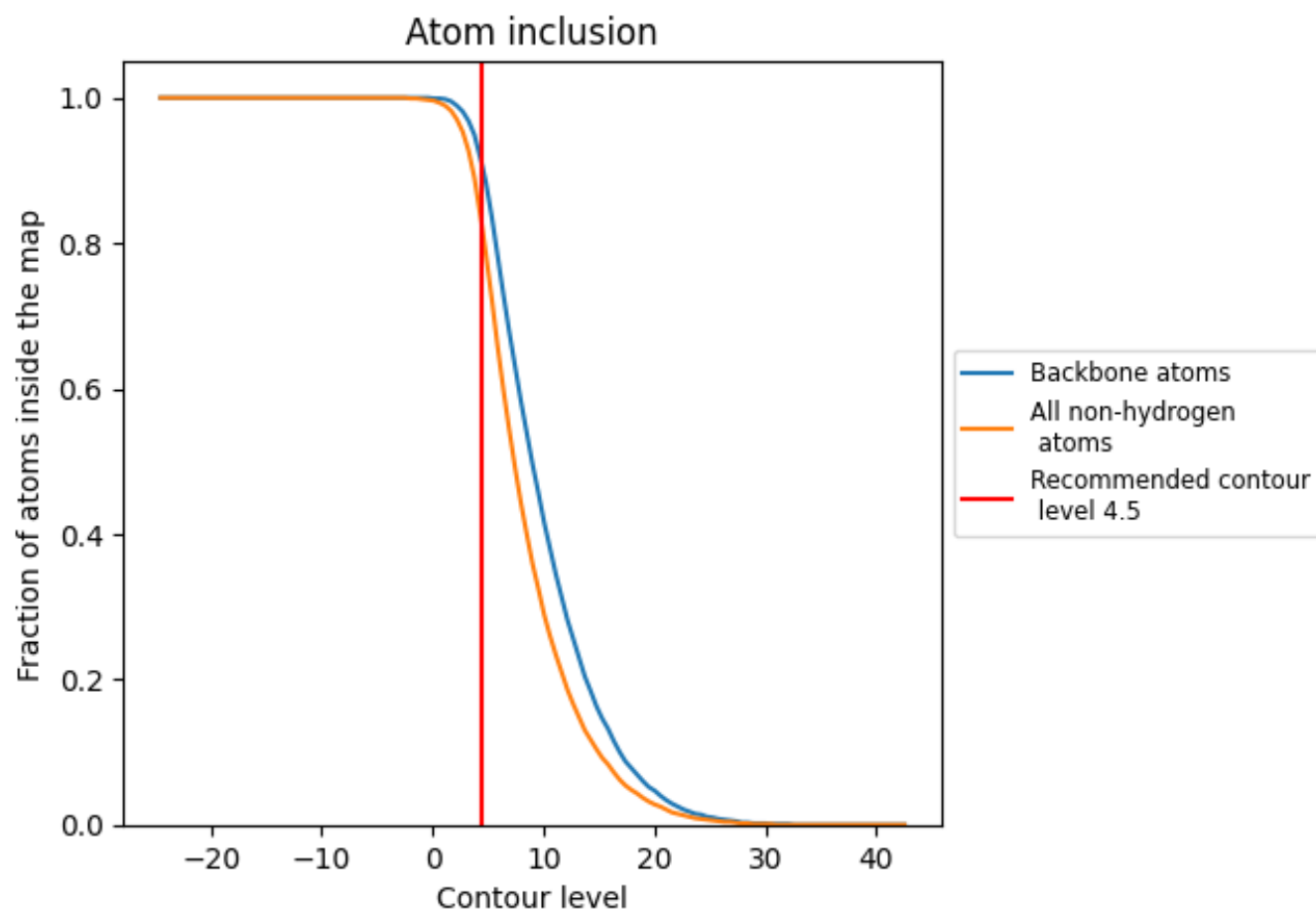
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (4.5).





























9.4 Atom inclusion [i](#)



At the recommended contour level, 90% of all backbone atoms, 82% 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 (4.5) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.8190	 0.3620
A	 0.8990	 0.3980
B	 0.8830	 0.3850
C	 0.8460	 0.3620
D	 0.9080	 0.4390
E	 0.7580	 0.3440
F	 0.8110	 0.3540
G	 0.8010	 0.3610
H	 0.8090	 0.3460
I	 0.7540	 0.3460
J	 0.7820	 0.3330
K	 0.7910	 0.3660
L	 0.7960	 0.3430
M	 0.9290	 0.4010

