



wwPDB EM Validation Summary Report ⓘ

Mar 30, 2026 – 08:06 AM UTC

PDB ID : 7Y0J / pdb_00007y0j
EMDB ID : EMD-33547
Title : Cryo-EM structure of human IgM-Fc in complex with the J chain and the P. falciparum TM284VAR1
Authors : Ji, C.; Xiao, J.
Deposited on : 2022-06-05
Resolution : 3.62 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

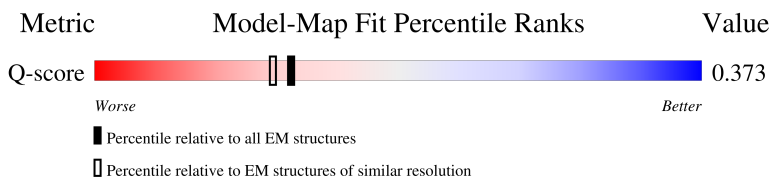
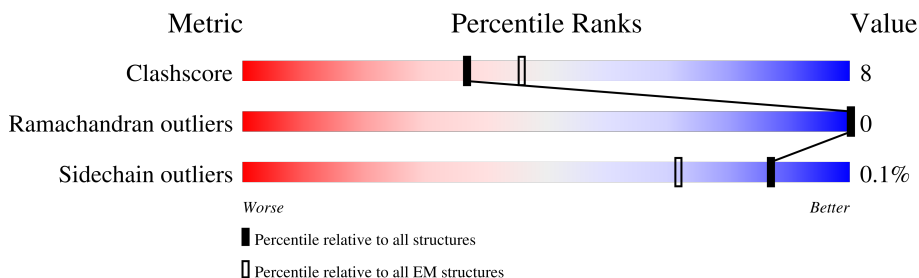
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

ELECTRON MICROSCOPY

The reported resolution of this entry is 3.62 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.



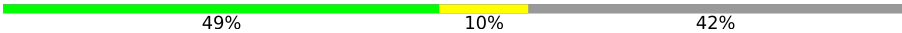
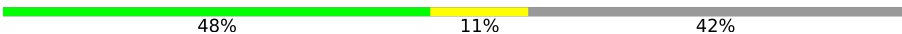
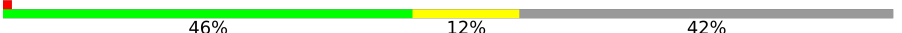
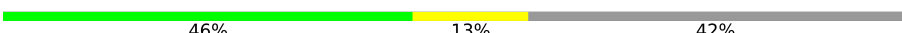
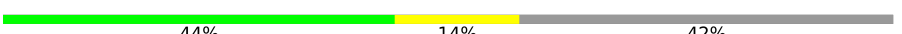
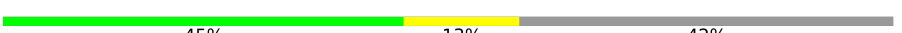
Metric	Whole archive (#Entries)	EM structures (#Entries)	Similar EM resolution (#Entries, resolution range(Å))
Clashscore	229148	23984	-
Ramachandran outliers	224038	23583	-
Sidechain outliers	223484	23102	-
Q-score	-	25397	11773 (3.12 - 4.12)

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	M	2373	 8% . 89%
2	A	383	 49% 12% 39%
2	B	383	 49% 10% 40%
2	C	383	 53% 7% 40%

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Mol	Chain	Length	Quality of chain
2	D	383	 49%10%42%
2	E	383	 48%11%42%
2	F	383	 46%12%42%
2	G	383	 46%13%42%
2	H	383	 44%14%42%
2	K	383	 45%13%42%
2	L	383	 45%15%40%
3	J	136	 71%7%22%
4	I	2	 50%50%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 20717 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 Erythrocyte membrane protein 2 variant TM284var1.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	M	254	Total	C	N	O	S	0	0
			2161	1373	368	406	14		

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
M	2368	HIS	-	expression tag	UNP I1X0L2
M	2369	HIS	-	expression tag	UNP I1X0L2
M	2370	HIS	-	expression tag	UNP I1X0L2
M	2371	HIS	-	expression tag	UNP I1X0L2
M	2372	HIS	-	expression tag	UNP I1X0L2
M	2373	HIS	-	expression tag	UNP I1X0L2

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

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	232	Total	C	N	O	S	0	0
			1798	1132	304	353	9		
2	B	228	Total	C	N	O	S	0	0
			1769	1114	300	347	8		
2	C	230	Total	C	N	O	S	0	0
			1779	1120	302	349	8		
2	D	224	Total	C	N	O	S	0	0
			1743	1100	296	339	8		
2	E	224	Total	C	N	O	S	0	0
			1743	1100	296	339	8		
2	F	221	Total	C	N	O	S	0	0
			1723	1087	292	336	8		
2	G	224	Total	C	N	O	S	0	0
			1742	1100	296	338	8		
2	H	222	Total	C	N	O	S	0	0
			1730	1092	293	337	8		
2	K	223	Total	C	N	O	S	0	0
			1737	1095	295	339	8		

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

There are 350 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	194	ALA	-	expression tag	UNP P01871
A	195	SER	-	expression tag	UNP P01871
A	196	ALA	-	expression tag	UNP P01871
A	197	TRP	-	expression tag	UNP P01871
A	198	SER	-	expression tag	UNP P01871
A	199	HIS	-	expression tag	UNP P01871
A	200	PRO	-	expression tag	UNP P01871
A	201	GLN	-	expression tag	UNP P01871
A	202	PHE	-	expression tag	UNP P01871
A	203	GLU	-	expression tag	UNP P01871
A	204	LYS	-	expression tag	UNP P01871
A	205	GLY	-	expression tag	UNP P01871
A	206	GLY	-	expression tag	UNP P01871
A	207	GLY	-	expression tag	UNP P01871
A	208	SER	-	expression tag	UNP P01871
A	209	GLY	-	expression tag	UNP P01871
A	210	GLY	-	expression tag	UNP P01871
A	211	GLY	-	expression tag	UNP P01871
A	212	SER	-	expression tag	UNP P01871
A	213	GLY	-	expression tag	UNP P01871
A	214	GLY	-	expression tag	UNP P01871
A	215	SER	-	expression tag	UNP P01871
A	216	ALA	-	expression tag	UNP P01871
A	217	TRP	-	expression tag	UNP P01871
A	218	SER	-	expression tag	UNP P01871
A	219	HIS	-	expression tag	UNP P01871
A	220	PRO	-	expression tag	UNP P01871
A	221	GLN	-	expression tag	UNP P01871
A	222	PHE	-	expression tag	UNP P01871
A	223	GLU	-	expression tag	UNP P01871
A	224	LYS	-	expression tag	UNP P01871
A	225	ILE	-	expression tag	UNP P01871
A	226	ASP	-	expression tag	UNP P01871
A	227	THR	-	expression tag	UNP P01871
A	228	THR	-	expression tag	UNP P01871
B	194	ALA	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
B	195	SER	-	expression tag	UNP P01871
B	196	ALA	-	expression tag	UNP P01871
B	197	TRP	-	expression tag	UNP P01871
B	198	SER	-	expression tag	UNP P01871
B	199	HIS	-	expression tag	UNP P01871
B	200	PRO	-	expression tag	UNP P01871
B	201	GLN	-	expression tag	UNP P01871
B	202	PHE	-	expression tag	UNP P01871
B	203	GLU	-	expression tag	UNP P01871
B	204	LYS	-	expression tag	UNP P01871
B	205	GLY	-	expression tag	UNP P01871
B	206	GLY	-	expression tag	UNP P01871
B	207	GLY	-	expression tag	UNP P01871
B	208	SER	-	expression tag	UNP P01871
B	209	GLY	-	expression tag	UNP P01871
B	210	GLY	-	expression tag	UNP P01871
B	211	GLY	-	expression tag	UNP P01871
B	212	SER	-	expression tag	UNP P01871
B	213	GLY	-	expression tag	UNP P01871
B	214	GLY	-	expression tag	UNP P01871
B	215	SER	-	expression tag	UNP P01871
B	216	ALA	-	expression tag	UNP P01871
B	217	TRP	-	expression tag	UNP P01871
B	218	SER	-	expression tag	UNP P01871
B	219	HIS	-	expression tag	UNP P01871
B	220	PRO	-	expression tag	UNP P01871
B	221	GLN	-	expression tag	UNP P01871
B	222	PHE	-	expression tag	UNP P01871
B	223	GLU	-	expression tag	UNP P01871
B	224	LYS	-	expression tag	UNP P01871
B	225	ILE	-	expression tag	UNP P01871
B	226	ASP	-	expression tag	UNP P01871
B	227	THR	-	expression tag	UNP P01871
B	228	THR	-	expression tag	UNP P01871
C	194	ALA	-	expression tag	UNP P01871
C	195	SER	-	expression tag	UNP P01871
C	196	ALA	-	expression tag	UNP P01871
C	197	TRP	-	expression tag	UNP P01871
C	198	SER	-	expression tag	UNP P01871
C	199	HIS	-	expression tag	UNP P01871
C	200	PRO	-	expression tag	UNP P01871
C	201	GLN	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
C	202	PHE	-	expression tag	UNP P01871
C	203	GLU	-	expression tag	UNP P01871
C	204	LYS	-	expression tag	UNP P01871
C	205	GLY	-	expression tag	UNP P01871
C	206	GLY	-	expression tag	UNP P01871
C	207	GLY	-	expression tag	UNP P01871
C	208	SER	-	expression tag	UNP P01871
C	209	GLY	-	expression tag	UNP P01871
C	210	GLY	-	expression tag	UNP P01871
C	211	GLY	-	expression tag	UNP P01871
C	212	SER	-	expression tag	UNP P01871
C	213	GLY	-	expression tag	UNP P01871
C	214	GLY	-	expression tag	UNP P01871
C	215	SER	-	expression tag	UNP P01871
C	216	ALA	-	expression tag	UNP P01871
C	217	TRP	-	expression tag	UNP P01871
C	218	SER	-	expression tag	UNP P01871
C	219	HIS	-	expression tag	UNP P01871
C	220	PRO	-	expression tag	UNP P01871
C	221	GLN	-	expression tag	UNP P01871
C	222	PHE	-	expression tag	UNP P01871
C	223	GLU	-	expression tag	UNP P01871
C	224	LYS	-	expression tag	UNP P01871
C	225	ILE	-	expression tag	UNP P01871
C	226	ASP	-	expression tag	UNP P01871
C	227	THR	-	expression tag	UNP P01871
C	228	THR	-	expression tag	UNP P01871
D	194	ALA	-	expression tag	UNP P01871
D	195	SER	-	expression tag	UNP P01871
D	196	ALA	-	expression tag	UNP P01871
D	197	TRP	-	expression tag	UNP P01871
D	198	SER	-	expression tag	UNP P01871
D	199	HIS	-	expression tag	UNP P01871
D	200	PRO	-	expression tag	UNP P01871
D	201	GLN	-	expression tag	UNP P01871
D	202	PHE	-	expression tag	UNP P01871
D	203	GLU	-	expression tag	UNP P01871
D	204	LYS	-	expression tag	UNP P01871
D	205	GLY	-	expression tag	UNP P01871
D	206	GLY	-	expression tag	UNP P01871
D	207	GLY	-	expression tag	UNP P01871
D	208	SER	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
D	209	GLY	-	expression tag	UNP P01871
D	210	GLY	-	expression tag	UNP P01871
D	211	GLY	-	expression tag	UNP P01871
D	212	SER	-	expression tag	UNP P01871
D	213	GLY	-	expression tag	UNP P01871
D	214	GLY	-	expression tag	UNP P01871
D	215	SER	-	expression tag	UNP P01871
D	216	ALA	-	expression tag	UNP P01871
D	217	TRP	-	expression tag	UNP P01871
D	218	SER	-	expression tag	UNP P01871
D	219	HIS	-	expression tag	UNP P01871
D	220	PRO	-	expression tag	UNP P01871
D	221	GLN	-	expression tag	UNP P01871
D	222	PHE	-	expression tag	UNP P01871
D	223	GLU	-	expression tag	UNP P01871
D	224	LYS	-	expression tag	UNP P01871
D	225	ILE	-	expression tag	UNP P01871
D	226	ASP	-	expression tag	UNP P01871
D	227	THR	-	expression tag	UNP P01871
D	228	THR	-	expression tag	UNP P01871
E	194	ALA	-	expression tag	UNP P01871
E	195	SER	-	expression tag	UNP P01871
E	196	ALA	-	expression tag	UNP P01871
E	197	TRP	-	expression tag	UNP P01871
E	198	SER	-	expression tag	UNP P01871
E	199	HIS	-	expression tag	UNP P01871
E	200	PRO	-	expression tag	UNP P01871
E	201	GLN	-	expression tag	UNP P01871
E	202	PHE	-	expression tag	UNP P01871
E	203	GLU	-	expression tag	UNP P01871
E	204	LYS	-	expression tag	UNP P01871
E	205	GLY	-	expression tag	UNP P01871
E	206	GLY	-	expression tag	UNP P01871
E	207	GLY	-	expression tag	UNP P01871
E	208	SER	-	expression tag	UNP P01871
E	209	GLY	-	expression tag	UNP P01871
E	210	GLY	-	expression tag	UNP P01871
E	211	GLY	-	expression tag	UNP P01871
E	212	SER	-	expression tag	UNP P01871
E	213	GLY	-	expression tag	UNP P01871
E	214	GLY	-	expression tag	UNP P01871
E	215	SER	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
E	216	ALA	-	expression tag	UNP P01871
E	217	TRP	-	expression tag	UNP P01871
E	218	SER	-	expression tag	UNP P01871
E	219	HIS	-	expression tag	UNP P01871
E	220	PRO	-	expression tag	UNP P01871
E	221	GLN	-	expression tag	UNP P01871
E	222	PHE	-	expression tag	UNP P01871
E	223	GLU	-	expression tag	UNP P01871
E	224	LYS	-	expression tag	UNP P01871
E	225	ILE	-	expression tag	UNP P01871
E	226	ASP	-	expression tag	UNP P01871
E	227	THR	-	expression tag	UNP P01871
E	228	THR	-	expression tag	UNP P01871
F	194	ALA	-	expression tag	UNP P01871
F	195	SER	-	expression tag	UNP P01871
F	196	ALA	-	expression tag	UNP P01871
F	197	TRP	-	expression tag	UNP P01871
F	198	SER	-	expression tag	UNP P01871
F	199	HIS	-	expression tag	UNP P01871
F	200	PRO	-	expression tag	UNP P01871
F	201	GLN	-	expression tag	UNP P01871
F	202	PHE	-	expression tag	UNP P01871
F	203	GLU	-	expression tag	UNP P01871
F	204	LYS	-	expression tag	UNP P01871
F	205	GLY	-	expression tag	UNP P01871
F	206	GLY	-	expression tag	UNP P01871
F	207	GLY	-	expression tag	UNP P01871
F	208	SER	-	expression tag	UNP P01871
F	209	GLY	-	expression tag	UNP P01871
F	210	GLY	-	expression tag	UNP P01871
F	211	GLY	-	expression tag	UNP P01871
F	212	SER	-	expression tag	UNP P01871
F	213	GLY	-	expression tag	UNP P01871
F	214	GLY	-	expression tag	UNP P01871
F	215	SER	-	expression tag	UNP P01871
F	216	ALA	-	expression tag	UNP P01871
F	217	TRP	-	expression tag	UNP P01871
F	218	SER	-	expression tag	UNP P01871
F	219	HIS	-	expression tag	UNP P01871
F	220	PRO	-	expression tag	UNP P01871
F	221	GLN	-	expression tag	UNP P01871
F	222	PHE	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
F	223	GLU	-	expression tag	UNP P01871
F	224	LYS	-	expression tag	UNP P01871
F	225	ILE	-	expression tag	UNP P01871
F	226	ASP	-	expression tag	UNP P01871
F	227	THR	-	expression tag	UNP P01871
F	228	THR	-	expression tag	UNP P01871
G	194	ALA	-	expression tag	UNP P01871
G	195	SER	-	expression tag	UNP P01871
G	196	ALA	-	expression tag	UNP P01871
G	197	TRP	-	expression tag	UNP P01871
G	198	SER	-	expression tag	UNP P01871
G	199	HIS	-	expression tag	UNP P01871
G	200	PRO	-	expression tag	UNP P01871
G	201	GLN	-	expression tag	UNP P01871
G	202	PHE	-	expression tag	UNP P01871
G	203	GLU	-	expression tag	UNP P01871
G	204	LYS	-	expression tag	UNP P01871
G	205	GLY	-	expression tag	UNP P01871
G	206	GLY	-	expression tag	UNP P01871
G	207	GLY	-	expression tag	UNP P01871
G	208	SER	-	expression tag	UNP P01871
G	209	GLY	-	expression tag	UNP P01871
G	210	GLY	-	expression tag	UNP P01871
G	211	GLY	-	expression tag	UNP P01871
G	212	SER	-	expression tag	UNP P01871
G	213	GLY	-	expression tag	UNP P01871
G	214	GLY	-	expression tag	UNP P01871
G	215	SER	-	expression tag	UNP P01871
G	216	ALA	-	expression tag	UNP P01871
G	217	TRP	-	expression tag	UNP P01871
G	218	SER	-	expression tag	UNP P01871
G	219	HIS	-	expression tag	UNP P01871
G	220	PRO	-	expression tag	UNP P01871
G	221	GLN	-	expression tag	UNP P01871
G	222	PHE	-	expression tag	UNP P01871
G	223	GLU	-	expression tag	UNP P01871
G	224	LYS	-	expression tag	UNP P01871
G	225	ILE	-	expression tag	UNP P01871
G	226	ASP	-	expression tag	UNP P01871
G	227	THR	-	expression tag	UNP P01871
G	228	THR	-	expression tag	UNP P01871
H	194	ALA	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
H	195	SER	-	expression tag	UNP P01871
H	196	ALA	-	expression tag	UNP P01871
H	197	TRP	-	expression tag	UNP P01871
H	198	SER	-	expression tag	UNP P01871
H	199	HIS	-	expression tag	UNP P01871
H	200	PRO	-	expression tag	UNP P01871
H	201	GLN	-	expression tag	UNP P01871
H	202	PHE	-	expression tag	UNP P01871
H	203	GLU	-	expression tag	UNP P01871
H	204	LYS	-	expression tag	UNP P01871
H	205	GLY	-	expression tag	UNP P01871
H	206	GLY	-	expression tag	UNP P01871
H	207	GLY	-	expression tag	UNP P01871
H	208	SER	-	expression tag	UNP P01871
H	209	GLY	-	expression tag	UNP P01871
H	210	GLY	-	expression tag	UNP P01871
H	211	GLY	-	expression tag	UNP P01871
H	212	SER	-	expression tag	UNP P01871
H	213	GLY	-	expression tag	UNP P01871
H	214	GLY	-	expression tag	UNP P01871
H	215	SER	-	expression tag	UNP P01871
H	216	ALA	-	expression tag	UNP P01871
H	217	TRP	-	expression tag	UNP P01871
H	218	SER	-	expression tag	UNP P01871
H	219	HIS	-	expression tag	UNP P01871
H	220	PRO	-	expression tag	UNP P01871
H	221	GLN	-	expression tag	UNP P01871
H	222	PHE	-	expression tag	UNP P01871
H	223	GLU	-	expression tag	UNP P01871
H	224	LYS	-	expression tag	UNP P01871
H	225	ILE	-	expression tag	UNP P01871
H	226	ASP	-	expression tag	UNP P01871
H	227	THR	-	expression tag	UNP P01871
H	228	THR	-	expression tag	UNP P01871
K	194	ALA	-	expression tag	UNP P01871
K	195	SER	-	expression tag	UNP P01871
K	196	ALA	-	expression tag	UNP P01871
K	197	TRP	-	expression tag	UNP P01871
K	198	SER	-	expression tag	UNP P01871
K	199	HIS	-	expression tag	UNP P01871
K	200	PRO	-	expression tag	UNP P01871
K	201	GLN	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
K	202	PHE	-	expression tag	UNP P01871
K	203	GLU	-	expression tag	UNP P01871
K	204	LYS	-	expression tag	UNP P01871
K	205	GLY	-	expression tag	UNP P01871
K	206	GLY	-	expression tag	UNP P01871
K	207	GLY	-	expression tag	UNP P01871
K	208	SER	-	expression tag	UNP P01871
K	209	GLY	-	expression tag	UNP P01871
K	210	GLY	-	expression tag	UNP P01871
K	211	GLY	-	expression tag	UNP P01871
K	212	SER	-	expression tag	UNP P01871
K	213	GLY	-	expression tag	UNP P01871
K	214	GLY	-	expression tag	UNP P01871
K	215	SER	-	expression tag	UNP P01871
K	216	ALA	-	expression tag	UNP P01871
K	217	TRP	-	expression tag	UNP P01871
K	218	SER	-	expression tag	UNP P01871
K	219	HIS	-	expression tag	UNP P01871
K	220	PRO	-	expression tag	UNP P01871
K	221	GLN	-	expression tag	UNP P01871
K	222	PHE	-	expression tag	UNP P01871
K	223	GLU	-	expression tag	UNP P01871
K	224	LYS	-	expression tag	UNP P01871
K	225	ILE	-	expression tag	UNP P01871
K	226	ASP	-	expression tag	UNP P01871
K	227	THR	-	expression tag	UNP P01871
K	228	THR	-	expression tag	UNP P01871
L	194	ALA	-	expression tag	UNP P01871
L	195	SER	-	expression tag	UNP P01871
L	196	ALA	-	expression tag	UNP P01871
L	197	TRP	-	expression tag	UNP P01871
L	198	SER	-	expression tag	UNP P01871
L	199	HIS	-	expression tag	UNP P01871
L	200	PRO	-	expression tag	UNP P01871
L	201	GLN	-	expression tag	UNP P01871
L	202	PHE	-	expression tag	UNP P01871
L	203	GLU	-	expression tag	UNP P01871
L	204	LYS	-	expression tag	UNP P01871
L	205	GLY	-	expression tag	UNP P01871
L	206	GLY	-	expression tag	UNP P01871
L	207	GLY	-	expression tag	UNP P01871
L	208	SER	-	expression tag	UNP P01871

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Chain	Residue	Modelled	Actual	Comment	Reference
L	209	GLY	-	expression tag	UNP P01871
L	210	GLY	-	expression tag	UNP P01871
L	211	GLY	-	expression tag	UNP P01871
L	212	SER	-	expression tag	UNP P01871
L	213	GLY	-	expression tag	UNP P01871
L	214	GLY	-	expression tag	UNP P01871
L	215	SER	-	expression tag	UNP P01871
L	216	ALA	-	expression tag	UNP P01871
L	217	TRP	-	expression tag	UNP P01871
L	218	SER	-	expression tag	UNP P01871
L	219	HIS	-	expression tag	UNP P01871
L	220	PRO	-	expression tag	UNP P01871
L	221	GLN	-	expression tag	UNP P01871
L	222	PHE	-	expression tag	UNP P01871
L	223	GLU	-	expression tag	UNP P01871
L	224	LYS	-	expression tag	UNP P01871
L	225	ILE	-	expression tag	UNP P01871
L	226	ASP	-	expression tag	UNP P01871
L	227	THR	-	expression tag	UNP P01871
L	228	THR	-	expression tag	UNP P01871

- Molecule 3 is a protein called Immunoglobulin J chain.

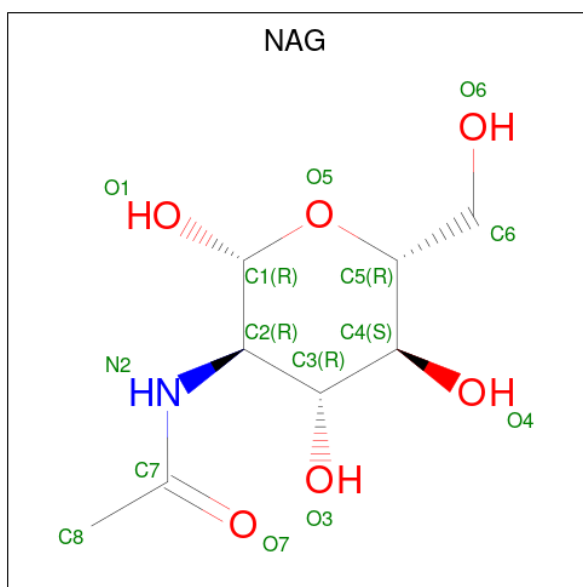
Mol	Chain	Residues	Atoms					AltConf	Trace
3	J	106	Total	C	N	O	S	0	0
			851	528	150	166	7		

- 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	I	2	Total	C	N	O		0	0
			28	16	2	10			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				AltConf
5	A	1	Total	C	N	O	0
			14	8	1	5	
5	B	1	Total	C	N	O	0
			14	8	1	5	
5	C	1	Total	C	N	O	0
			14	8	1	5	
5	D	1	Total	C	N	O	0
			14	8	1	5	
5	E	1	Total	C	N	O	0
			14	8	1	5	
5	F	1	Total	C	N	O	0
			14	8	1	5	
5	G	1	Total	C	N	O	0
			14	8	1	5	
5	H	1	Total	C	N	O	0
			14	8	1	5	
5	K	1	Total	C	N	O	0
			14	8	1	5	
5	L	1	Total	C	N	O	0
			14	8	1	5	



ASP	ASP	ASN	LYS	THR	ILE
GLU	ASP	ARG	ARG	TYR	ASN
PRO	LEU	GLN	GLN	GLN	LYS
PHE	GLY	ASP	TYR	PHE	ASP
HIS	ASN	GLY	LEU	LEU	ILE
HIS	LYS	ARG	ARG	ARG	SER
HIS	CYS	SER	SER	TRP	ALA
HIS	ASP	LEU	LEU	PHE	LYS
HIS	CYS	ASN	GLN	GLU	LEU
HIS	LYS	HIS	HIS	GLY	ARG
	GLN	GLN	TRP	TRP	LYS
	ILE	TYR	ILE	ILE	LEU
	LYS	ASN	LYS	LYS	LEU
	PRO	MET	LYS	LYS	ASP
	LYS	ASN	PHE	PHE	ILE
	ARG	PHE	CYS	CYS	VAL
	HIS	LYS	THR	THR	GLY
	PRO	GLY	GLY	GLN	PRO
	LYS	GLN	GLN	GLN	LYS
	GLU	ALA	LEU	LEU	ALA
	VAL	ALA	LEU	LEU	ALA
	ASN	GLN	GLY	TYR	PRO
	PRO	GLY	MET	ASP	ARG
	GLU	LYS	LYS	ASP	LYS
	GLU	ALA	VAL	VAL	TRP
	PRO	THR	GLN	GLN	LYS
	ALA	GLN	THR	THR	TYR
	ASN	TYR	LYS	LYS	ASN
	SER	ILE	CYS	CYS	LYS
	GLU	ASP	SER	SER	ALA
	PRO	ASP	ASP	ASP	HIS
	LYS	LYS	ALA	VAL	VAL
	TYR	CYS	ASN	ASN	TRP
	ILE	ASN	CYS	CYS	HIS
	VAL	SER	ASN	ASN	ALA
	PRO	LYS	ARG	ARG	MET
	LEU	CYS	ASP	ASP	LEU
	VAL	ASP	GLY	GLY	CYS
	PRO	CYS	THR	THR	GLY
	GLN	LEU	ILE	ILE	TYR
	LYS	ILE	ILE	ILE	ARG
	PRO	LYS	SER	SER	LYS
	THR	TYR	LEU	LEU	GLY
	PRO	ILE	PRO	PRO	GLY
	PRO	ASP	GLY	GLY	THR
	GLY	ARG	CYS	CYS	THR
	VAL	GLY	GLY	GLY	ILE
	PRO	LYS	SER	SER	THR
	PRO	GLY	CYS	CYS	THR
	PRO	TRP	THR	VAL	ASP
	PRO	ASN	GLN	GLY	CYS
	PRO	ILE	TYR	TYR	ASN
	PRO	TYR	LYS	LYS	VAL
	LEU	ASP	ASN	ASN	PRO
	PRO	SER	THR	THR	ASP
	THR	LEU	ILE	ILE	GLY
	PRO	GLY	THR	THR	TYR
	SER	ASN	ARG	ARG	GLY

- Molecule 2: Immunoglobulin heavy constant mu

Chain A: 49% 12% 39%

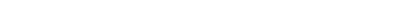
R443	GLY	ALA	LYS	ALA
V454	GLN	SER	LEU	SER
P458	SER	ILE	ILE	ALA
C474	MET	CYS	GLN	THR
L475	PHE	ALA	ALA	HIS
V476	THR	THR	THR	PRO
T477	CYS	GLY	GLY	GLN
G478	ARG	ARG	PRO	LYS
F479	ASP	ASP	SER	GLU
S480	HIS	HIS	PRO	LYS
V486	GLY	GLY	GLN	GLY
Q487	LEU	ILE	ILE	GLY
W488	THR	GLN	GLN	SER
M489	PHE	VAL	VAL	GLY
Y500	GLN	SER	TRP	GLY
P505	ASN	TRP	LEU	SER
B514	ALA	ARG	GLY	GLY
Y515	SER	GLY	GLY	SER
L521	MET	LYS	LYS	ALA
T533	CYS	GLN	GLN	TRP
Y534	VAL	VAL	VAL	SER
T535	PRO	GLY	GLY	HIS
Y536	ASP	SER	PRO	PRO
V538	GLN	GLY	GLN	GLN
A539	ASP	ASP	VAL	THR
H540	THR	THR	GLN	THR
L543	ALA	ILE	ALA	ILE
P544	T360	GLU	ALA	ALA
M545	L365	LYS	LEU	GLU
R546	L366	GLU	LEU	PRO
T551	T367	SER	PRO	PRO
V552	C367	GLY	LYS	LYS
D553	W382	PRO	VAL	VAL
T556	T383	THR	THR	SER
G557	R384	THR	THR	PHE
K558	E388	LYS	VAL	VAL
P559	D417	THR	THR	PRO
T560	W418	SER	THR	ARG
T564	N419	THR	LEU	GLY
S565	S420	THR	THR	PHE
L566	V428	ILE	ILE	PHE
T571	T429	GLY	GLY	GLY
A572	H430	LYS	ASN	ASN
Y576	R438	SER	SER	ARG
		ASP	ASP	ARG
		TRP	TRP	SER
		LEU	LEU	LYS

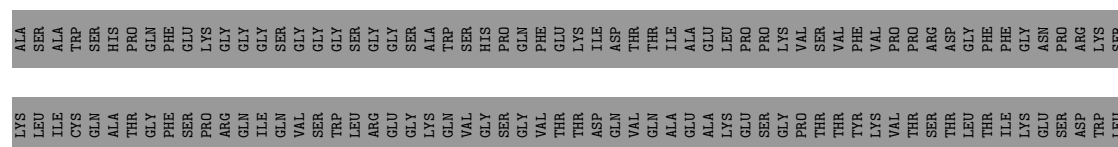
- Molecule 2: Immunoglobulin heavy constant mu

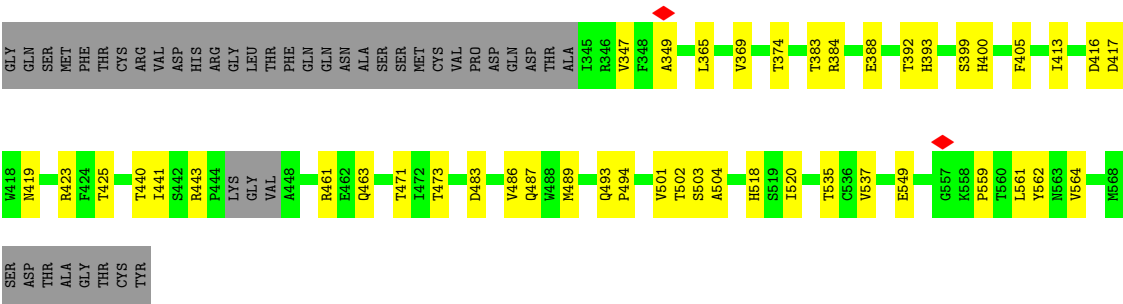
Chain B: 49% 10% 40%

C426	C427	C428	C429	C430	C431	C432	C433	C438	C439	C461	C462	C463	C467	C468	C469	C490	C510	C532	C537	C540	C549	C569	C565	C568	C572	GLY	THR	CYS	TYR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY	THR	GLY
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- Molecule 2: Immunoglobulin heavy constant mu

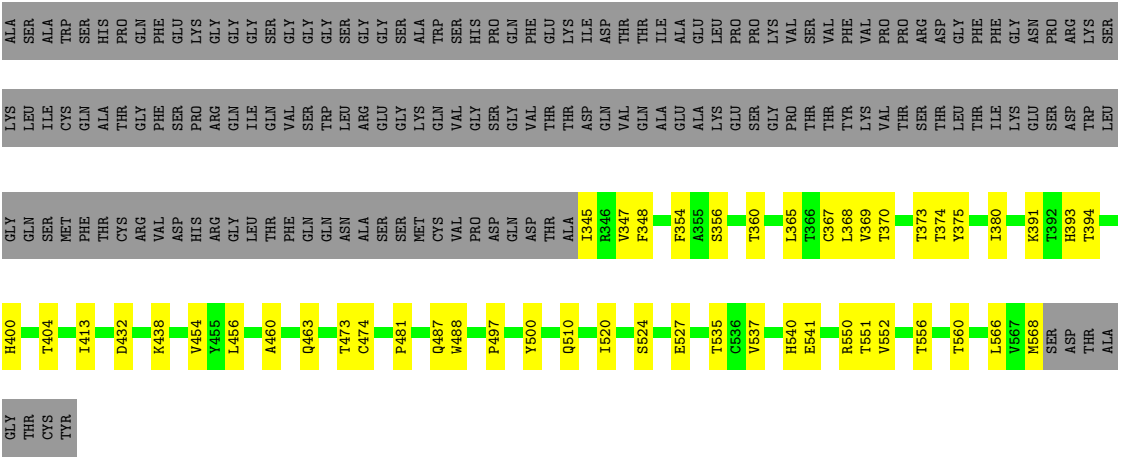
Chain C:  53% 7% 40%





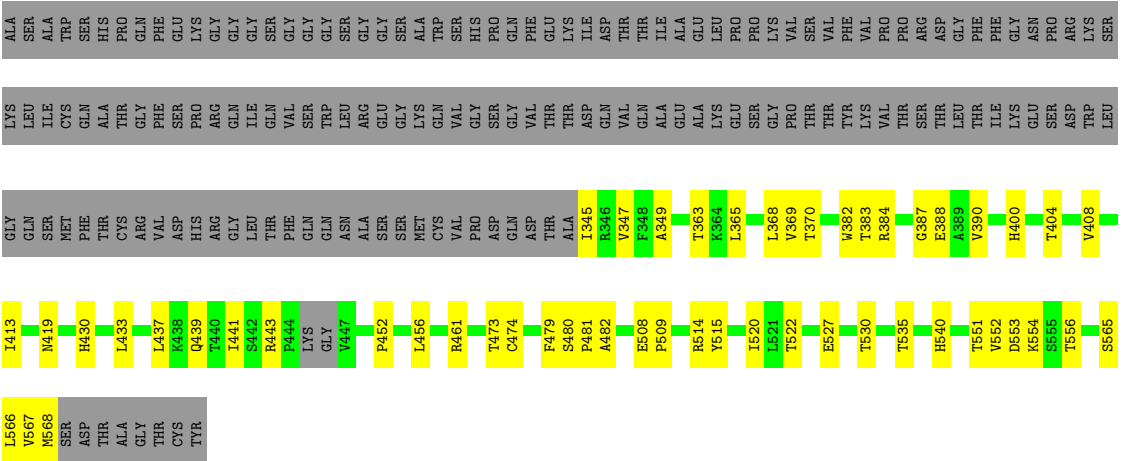
● Molecule 2: Immunoglobulin heavy constant mu

Chain G: 46% 13% 42%



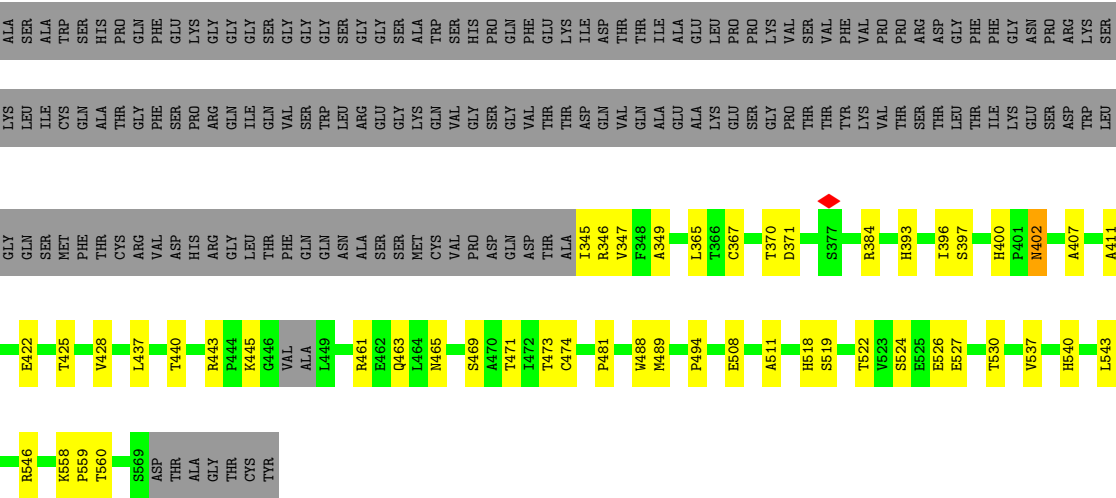
● Molecule 2: Immunoglobulin heavy constant mu

Chain H: 44% 14% 42%

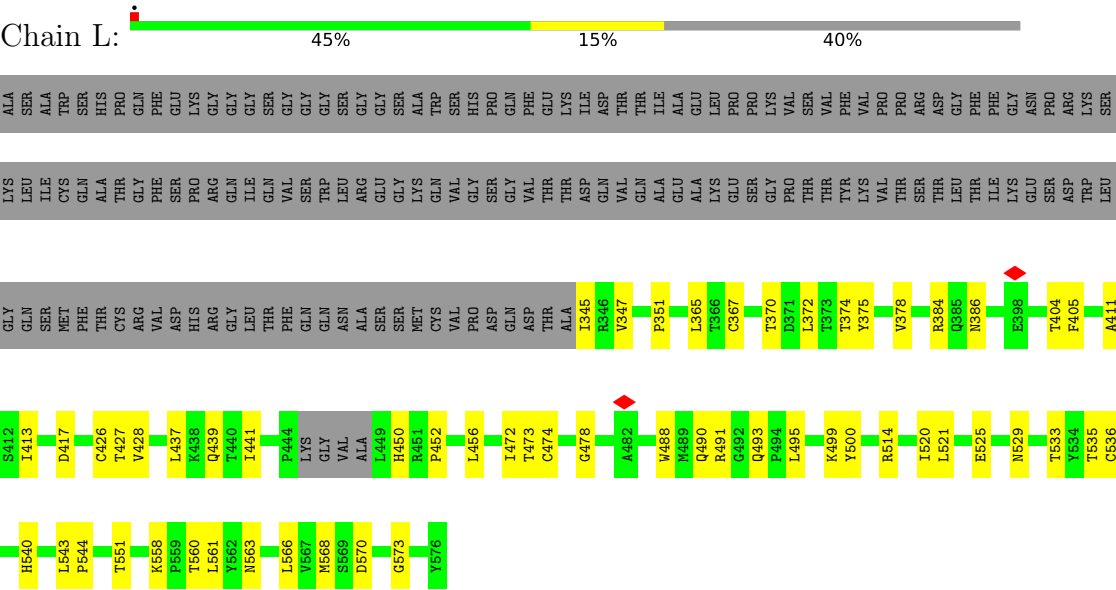


● Molecule 2: Immunoglobulin heavy constant mu

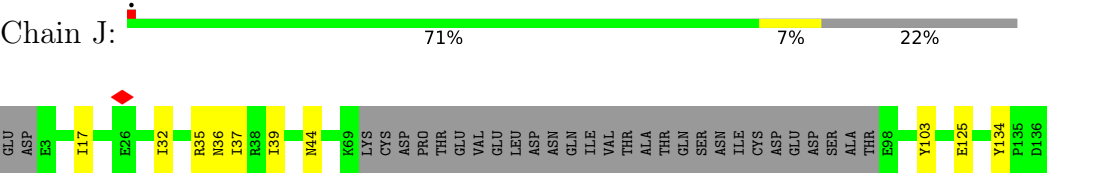
Chain K: 45% 13% 42%



● Molecule 2: Immunoglobulin heavy constant mu



● Molecule 3: Immunoglobulin J chain



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



4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	849826	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 ($e^-/\text{\AA}^2$)	59.74	Depositor
Minimum defocus (nm)	1000	Depositor
Maximum defocus (nm)	2000	Depositor
Magnification	Not provided	
Image detector	GATAN K2 QUANTUM (4k x 4k)	Depositor
Maximum map value	2.736	Depositor
Minimum map value	-1.778	Depositor
Average map value	0.002	Depositor
Map value standard deviation	0.041	Depositor
Recommended contour level	0.13	Depositor
Map size (Å)	340.0, 340.0, 340.0	wwPDB
Map dimensions	400, 400, 400	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	0.85, 0.85, 0.85	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	M	0.16	0/2207	0.41	0/2968
2	A	0.13	0/1844	0.38	0/2526
2	B	0.14	0/1814	0.36	0/2485
2	C	0.14	0/1824	0.37	0/2498
2	D	0.14	0/1788	0.35	0/2449
2	E	0.13	0/1788	0.39	0/2449
2	F	0.13	0/1767	0.38	0/2420
2	G	0.13	0/1787	0.35	0/2447
2	H	0.13	0/1774	0.37	0/2430
2	K	0.14	0/1781	0.38	0/2437
2	L	0.13	0/1818	0.39	0/2490
3	J	0.14	0/864	0.42	0/1173
All	All	0.14	0/21056	0.38	0/28772

There are no bond length outliers.

There are no bond angle outliers.

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	M	2161	0	2110	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	1798	0	1753	32	0
2	B	1769	0	1729	27	0
2	C	1779	0	1739	16	0
2	D	1743	0	1708	27	0
2	E	1743	0	1710	28	0
2	F	1723	0	1682	28	0
2	G	1742	0	1708	30	0
2	H	1730	0	1691	31	0
2	K	1737	0	1698	30	0
2	L	1773	0	1722	38	0
3	J	851	0	844	10	0
4	I	28	0	25	0	0
5	A	14	0	13	1	0
5	B	14	0	13	2	0
5	C	14	0	13	0	0
5	D	14	0	13	0	0
5	E	14	0	13	0	0
5	F	14	0	13	0	0
5	G	14	0	13	1	0
5	H	14	0	13	1	0
5	K	14	0	13	2	0
5	L	14	0	13	2	0
All	All	20717	0	20249	310	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 8.

The worst 5 of 310 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:M:1629:ILE:HG22	1:M:1706:ARG:HD3	1.67	0.77
2:G:556:THR:O	2:H:461:ARG:NH2	2.24	0.71
2:C:367:CYS:HB3	2:C:380:ILE:HD11	1.73	0.70
2:K:402:ASN:O	2:K:402:ASN:ND2	2.22	0.69
2:G:391:LYS:NZ	2:G:394:THR:OG1	2.26	0.68

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	M	244/2373 (10%)	234 (96%)	10 (4%)	0	100	100
2	A	230/383 (60%)	217 (94%)	13 (6%)	0	100	100
2	B	226/383 (59%)	215 (95%)	11 (5%)	0	100	100
2	C	228/383 (60%)	214 (94%)	14 (6%)	0	100	100
2	D	222/383 (58%)	211 (95%)	11 (5%)	0	100	100
2	E	222/383 (58%)	210 (95%)	12 (5%)	0	100	100
2	F	217/383 (57%)	203 (94%)	14 (6%)	0	100	100
2	G	222/383 (58%)	214 (96%)	8 (4%)	0	100	100
2	H	218/383 (57%)	208 (95%)	10 (5%)	0	100	100
2	K	219/383 (57%)	210 (96%)	9 (4%)	0	100	100
2	L	224/383 (58%)	211 (94%)	13 (6%)	0	100	100
3	J	102/136 (75%)	92 (90%)	10 (10%)	0	100	100
All	All	2574/6339 (41%)	2439 (95%)	135 (5%)	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	M	240/2195 (11%)	240 (100%)	0	100	100
2	A	206/331 (62%)	206 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	203/331 (61%)	202 (100%)	1 (0%)	81	78
2	C	204/331 (62%)	204 (100%)	0	100	100
2	D	200/331 (60%)	200 (100%)	0	100	100
2	E	200/331 (60%)	200 (100%)	0	100	100
2	F	198/331 (60%)	198 (100%)	0	100	100
2	G	200/331 (60%)	200 (100%)	0	100	100
2	H	199/331 (60%)	199 (100%)	0	100	100
2	K	200/331 (60%)	198 (99%)	2 (1%)	68	72
2	L	204/331 (62%)	204 (100%)	0	100	100
3	J	100/128 (78%)	100 (100%)	0	100	100
All	All	2354/5633 (42%)	2351 (100%)	3 (0%)	87	87

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

Mol	Chain	Res	Type
2	B	510	GLN
2	K	402	ASN
2	K	465	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
2	G	510	GLN
2	H	510	GLN
2	H	465	ASN
2	H	529	ASN
2	C	463	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

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	I	1	4,3	14,14,15	0.47	0	17,19,21	0.71	1 (5%)
4	NAG	I	2	4	14,14,15	0.46	0	17,19,21	0.48	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	I	1	4,3	-	2/6/23/26	0/1/1/1
4	NAG	I	2	4	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	I	1	NAG	C1-O5-C5	2.23	115.17	112.19

There are no chirality outliers.

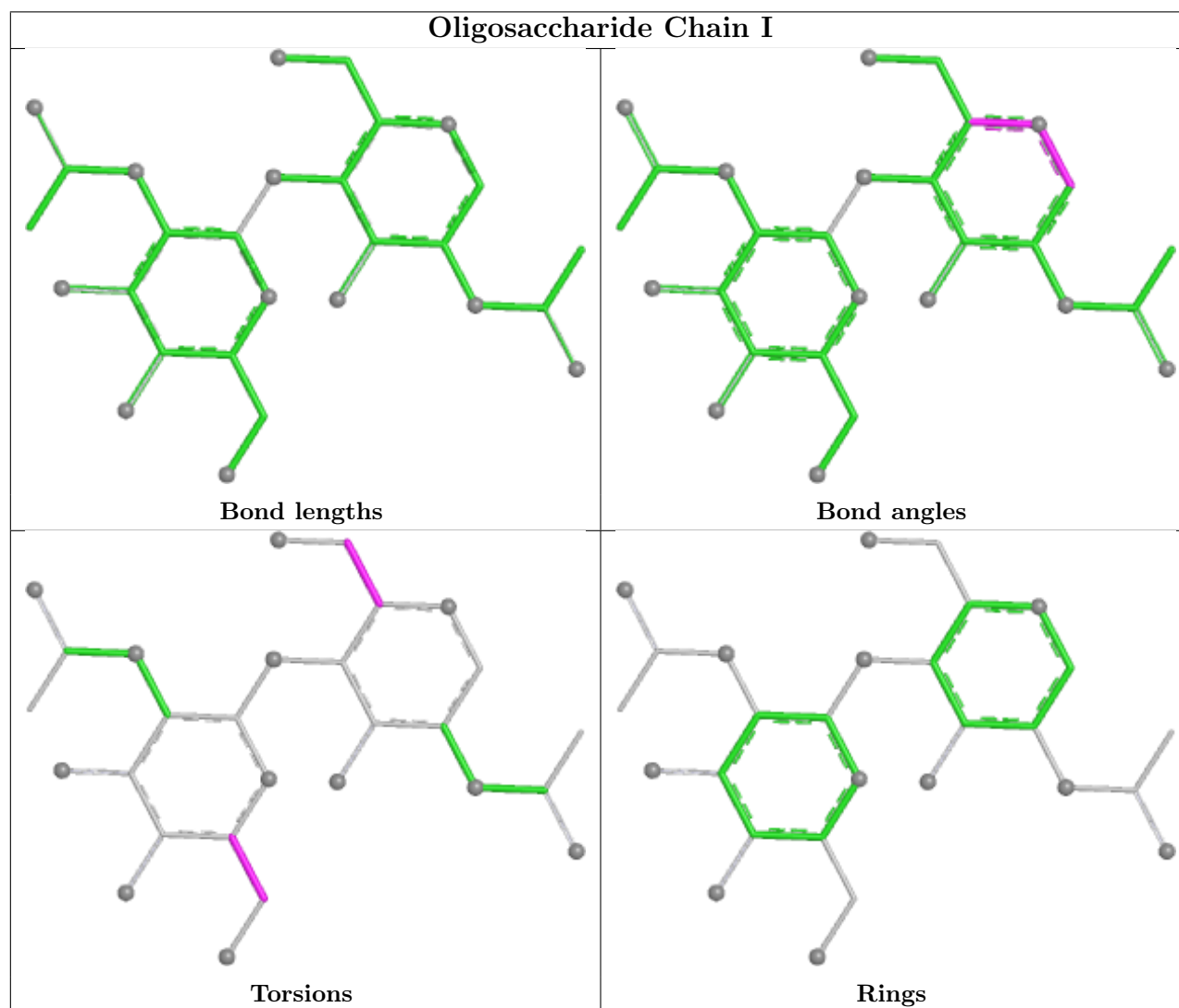
All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	I	2	NAG	O5-C5-C6-O6
4	I	2	NAG	C4-C5-C6-O6
4	I	1	NAG	O5-C5-C6-O6
4	I	1	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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](#)

10 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	$\# Z > 2$
5	NAG	B	601	2	14,14,15	0.28	0	17,19,21	0.50	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	NAG	D	601	2	14,14,15	0.26	0	17,19,21	0.45	0
5	NAG	F	601	2	14,14,15	0.34	0	17,19,21	0.47	0
5	NAG	E	601	2	14,14,15	0.28	0	17,19,21	0.45	0
5	NAG	C	601	2	14,14,15	0.17	0	17,19,21	0.40	0
5	NAG	H	601	2	14,14,15	0.42	0	17,19,21	0.43	0
5	NAG	A	601	2	14,14,15	0.37	0	17,19,21	0.50	0
5	NAG	K	601	2	14,14,15	0.27	0	17,19,21	0.36	0
5	NAG	G	601	2	14,14,15	0.26	0	17,19,21	0.42	0
5	NAG	L	601	2	14,14,15	0.33	0	17,19,21	0.49	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
5	NAG	B	601	2	-	0/6/23/26	0/1/1/1
5	NAG	D	601	2	-	1/6/23/26	0/1/1/1
5	NAG	F	601	2	-	2/6/23/26	0/1/1/1
5	NAG	E	601	2	-	2/6/23/26	0/1/1/1
5	NAG	C	601	2	-	4/6/23/26	0/1/1/1
5	NAG	H	601	2	-	2/6/23/26	0/1/1/1
5	NAG	A	601	2	-	3/6/23/26	0/1/1/1
5	NAG	K	601	2	-	4/6/23/26	0/1/1/1
5	NAG	G	601	2	-	1/6/23/26	0/1/1/1
5	NAG	L	601	2	-	1/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 20 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	E	601	NAG	C4-C5-C6-O6
5	K	601	NAG	O5-C5-C6-O6
5	F	601	NAG	O5-C5-C6-O6
5	H	601	NAG	O5-C5-C6-O6
5	E	601	NAG	O5-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	601	NAG	2	0
5	H	601	NAG	1	0
5	A	601	NAG	1	0
5	K	601	NAG	2	0
5	G	601	NAG	1	0
5	L	601	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.

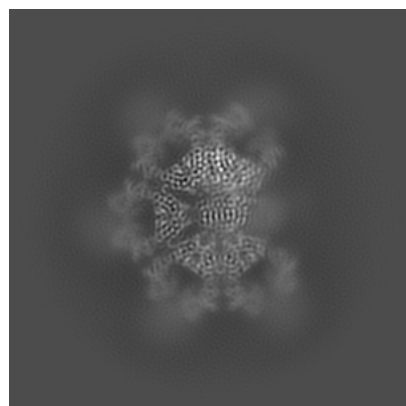
6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-33547. These allow visual inspection of the internal detail of the map and identification of artifacts.

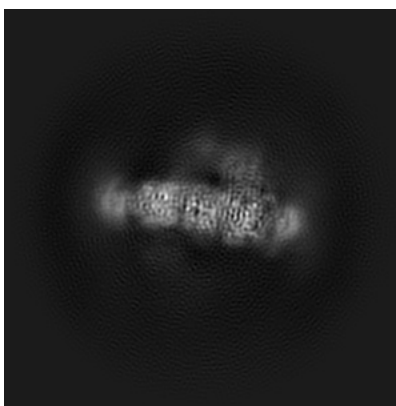
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections [i](#)

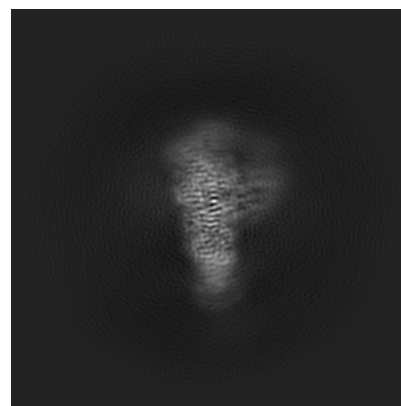
6.1.1 Primary map



X

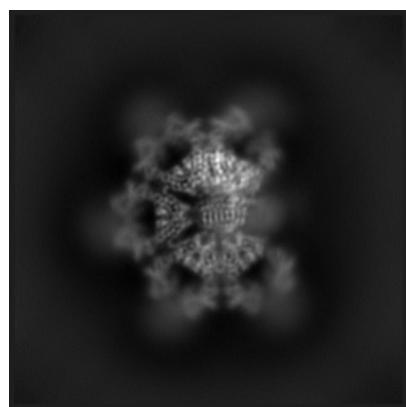


Y

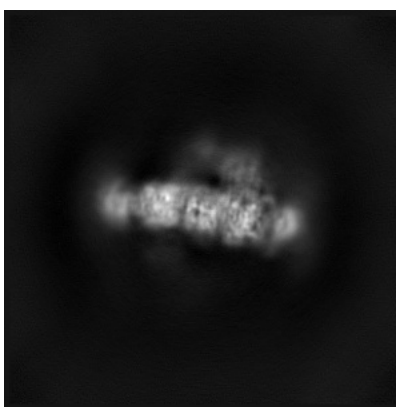


Z

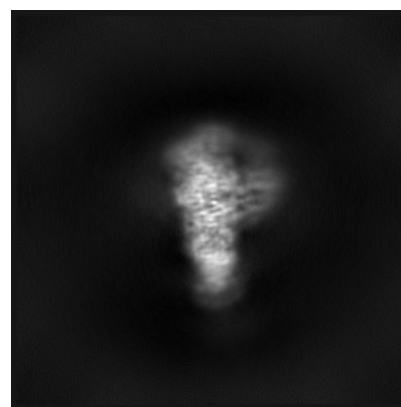
6.1.2 Raw map



X



Y

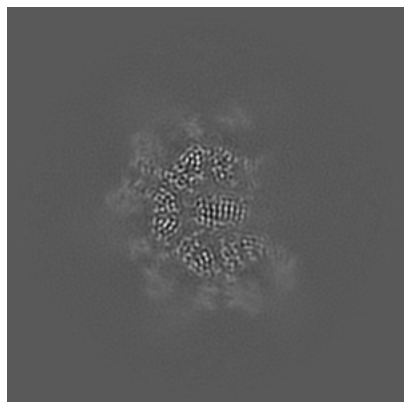


Z

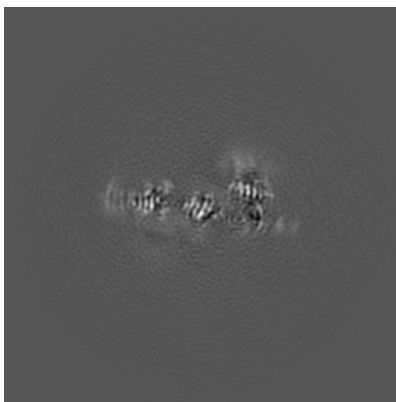
The images above show the map projected in three orthogonal directions.

6.2 Central slices [i](#)

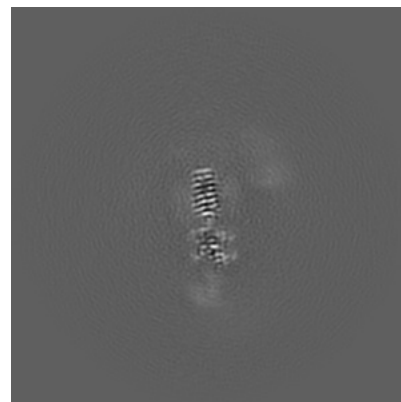
6.2.1 Primary map



X Index: 200

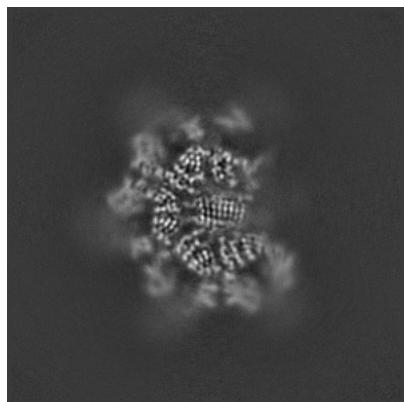


Y Index: 200

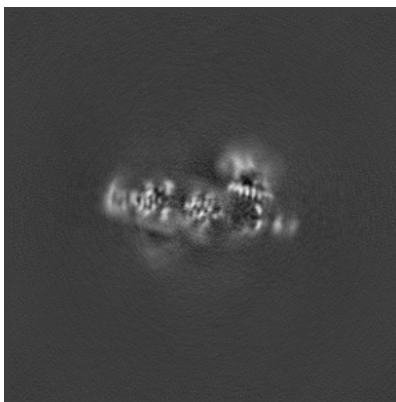


Z Index: 200

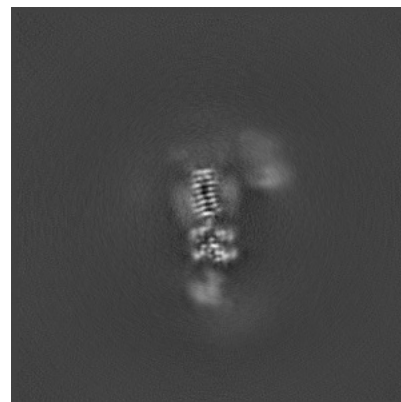
6.2.2 Raw map



X Index: 200



Y Index: 200

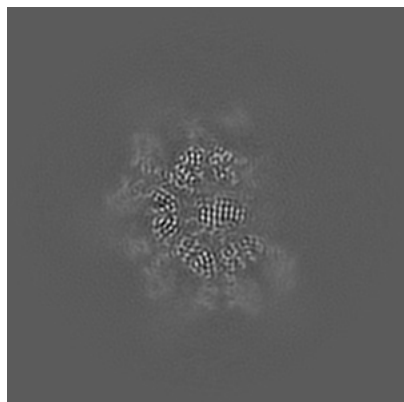


Z Index: 200

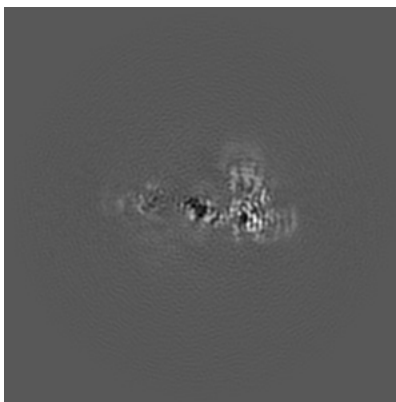
The images above show central slices of the map in three orthogonal directions.

6.3 Largest variance slices [i](#)

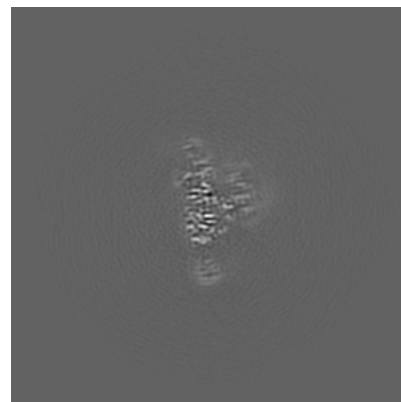
6.3.1 Primary map



X Index: 202

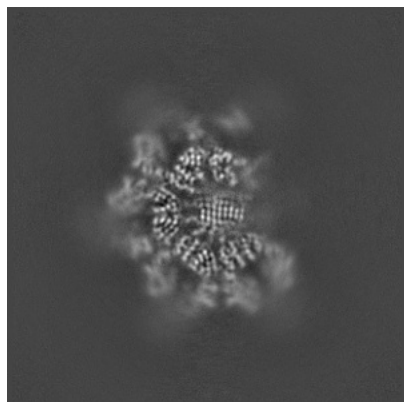


Y Index: 209

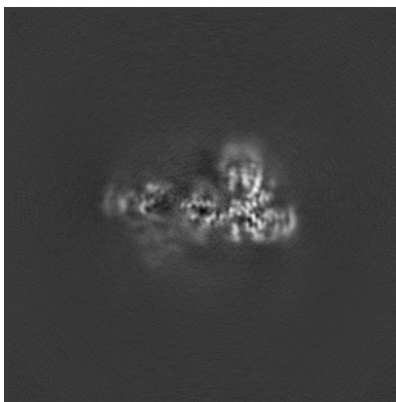


Z Index: 243

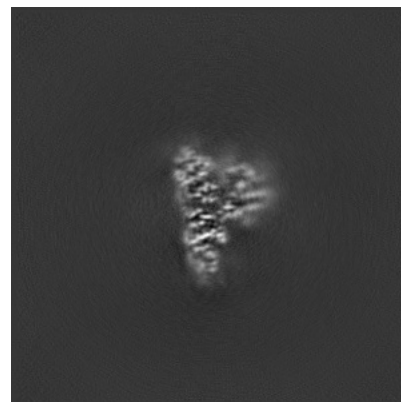
6.3.2 Raw map



X Index: 202



Y Index: 208

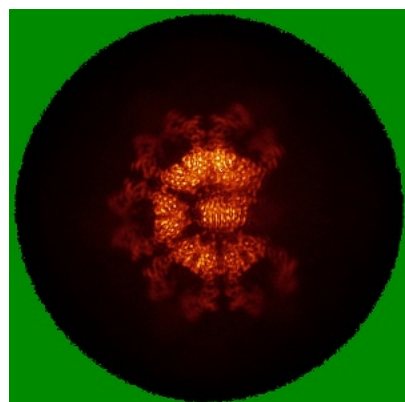


Z Index: 236

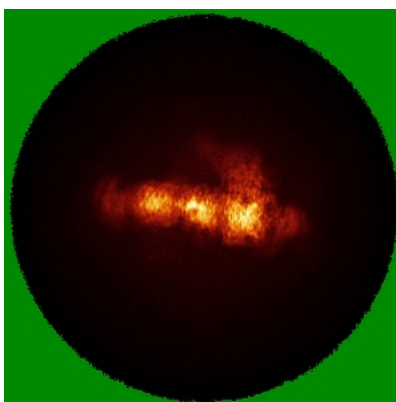
The images above show the largest variance slices of the map in three orthogonal directions.

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

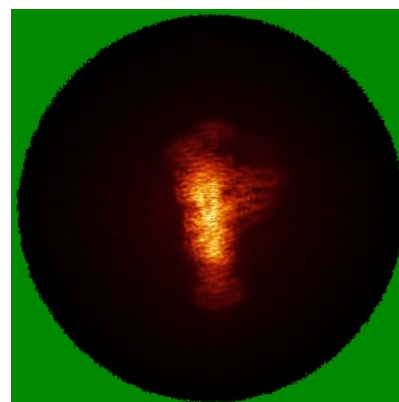
6.4.1 Primary map



X

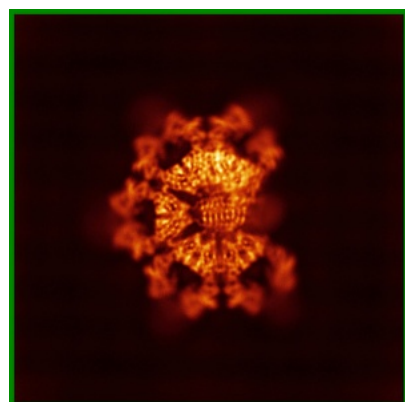


Y

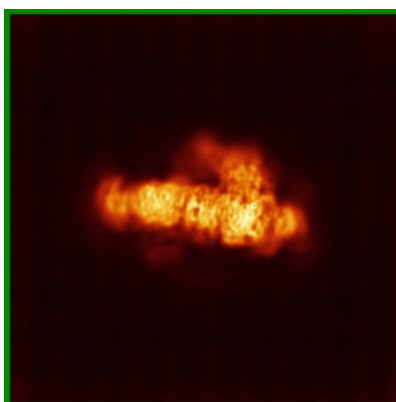


Z

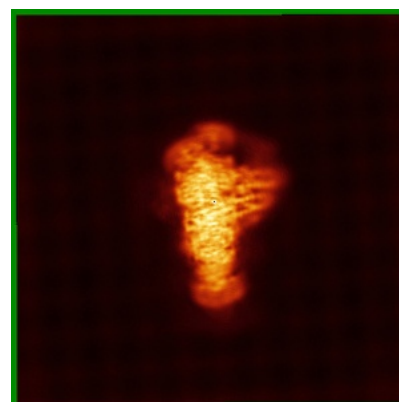
6.4.2 Raw map



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 0.13. 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.

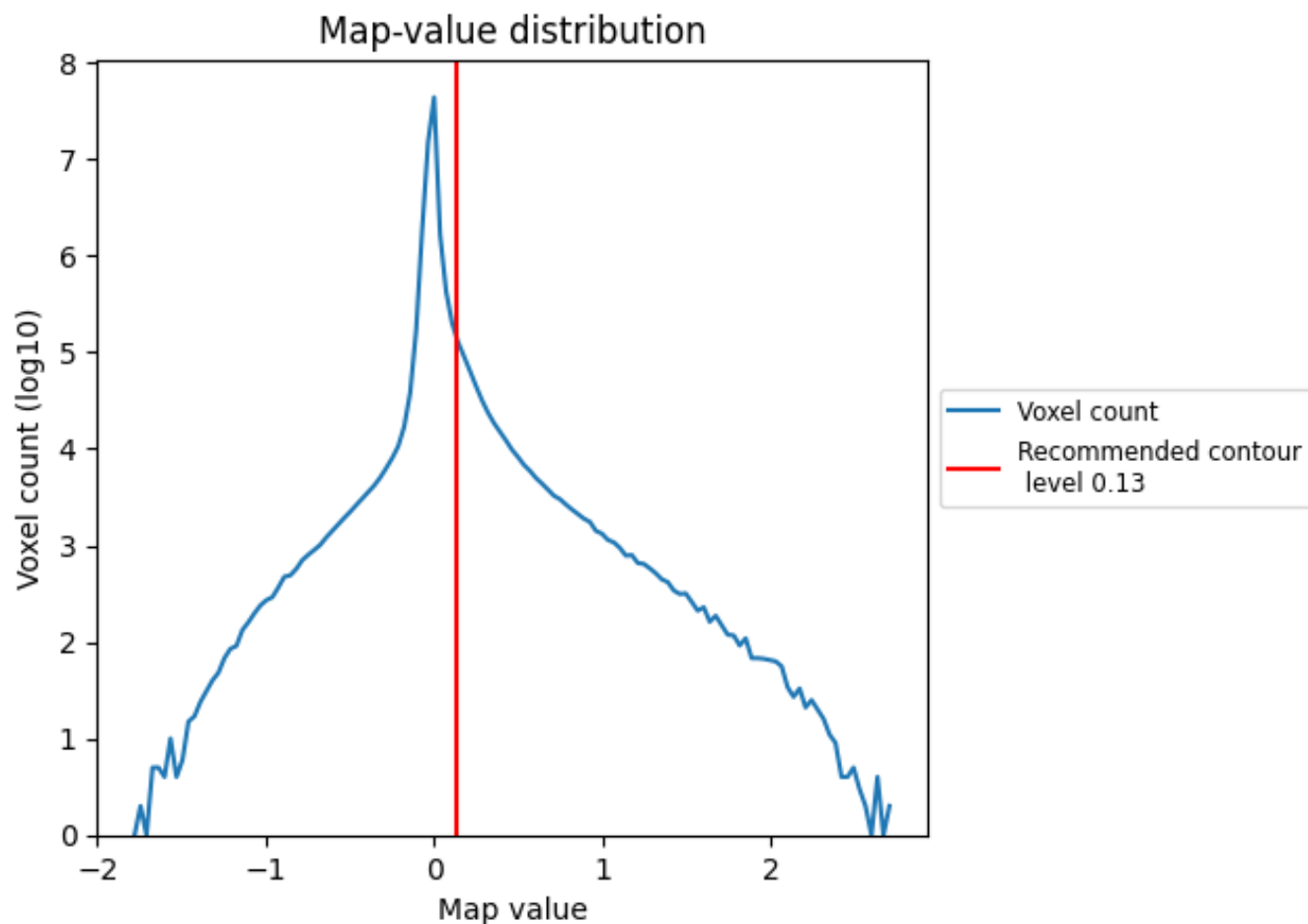
6.6 Mask visualisation [i](#)

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

7 Map analysis [i](#)

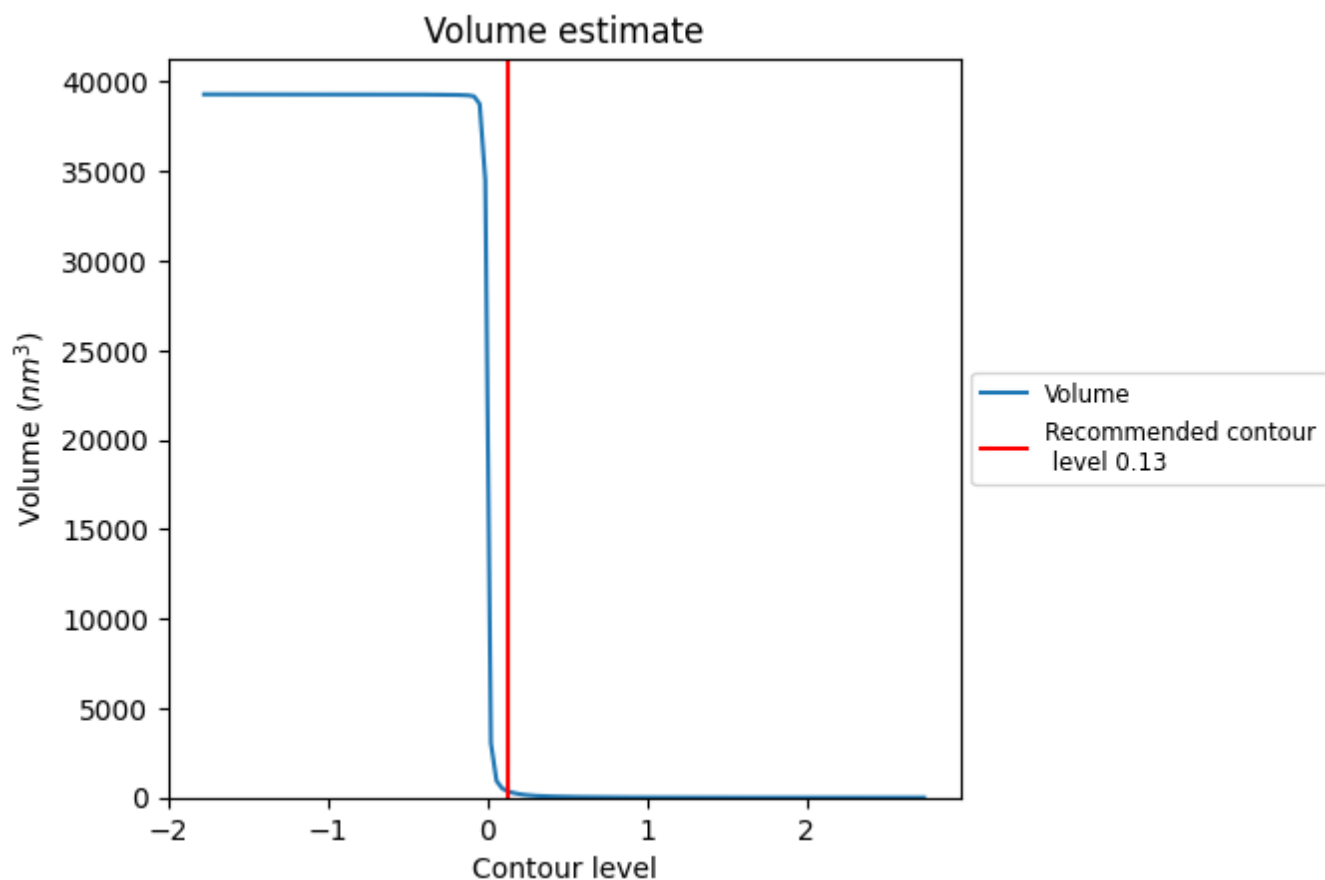
This section contains the results of statistical analysis of the map.

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.

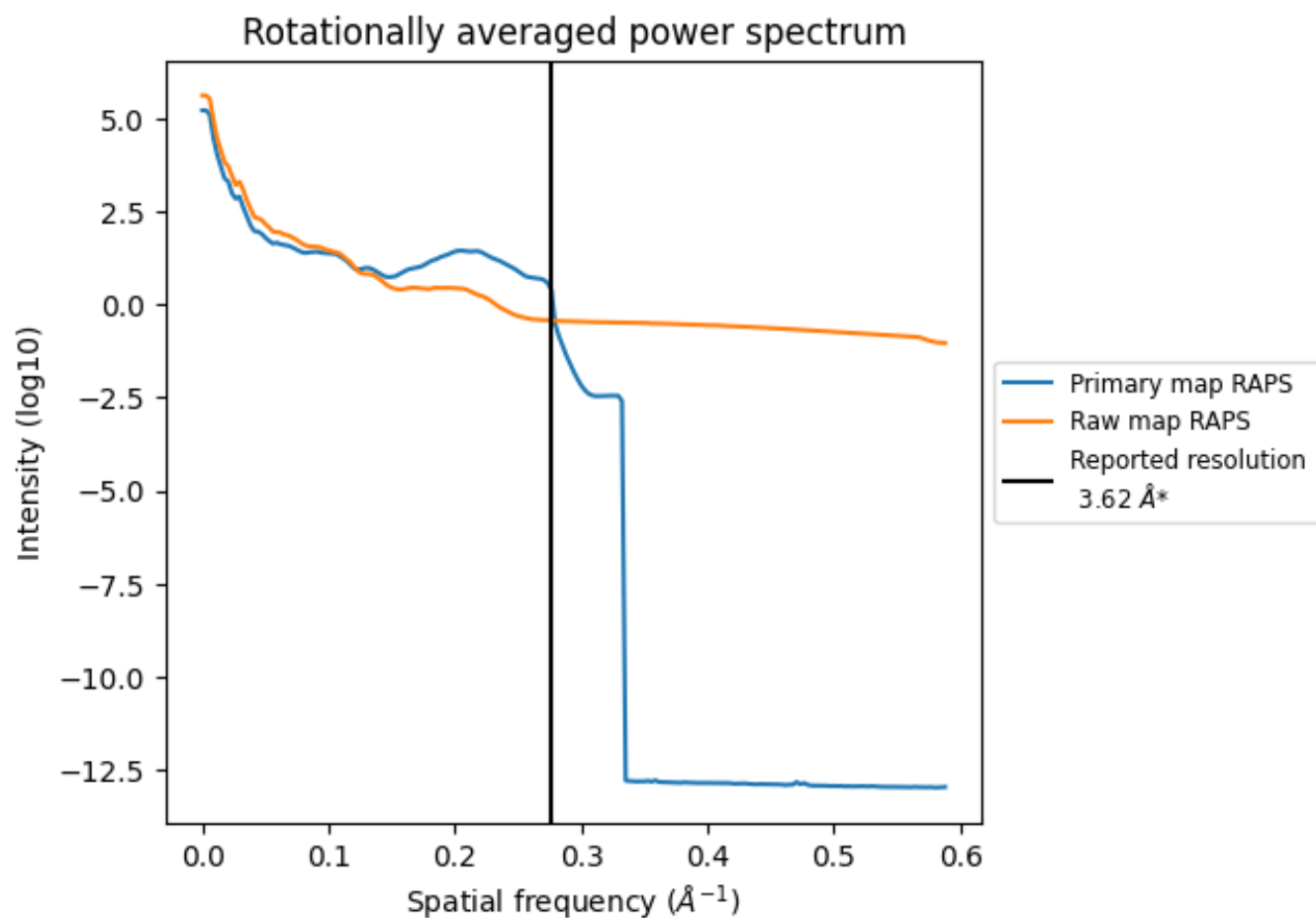
7.2 Volume estimate [i](#)



The volume at the recommended contour level is 344 nm^3 ; this corresponds to an approximate mass of 310 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 ⓘ

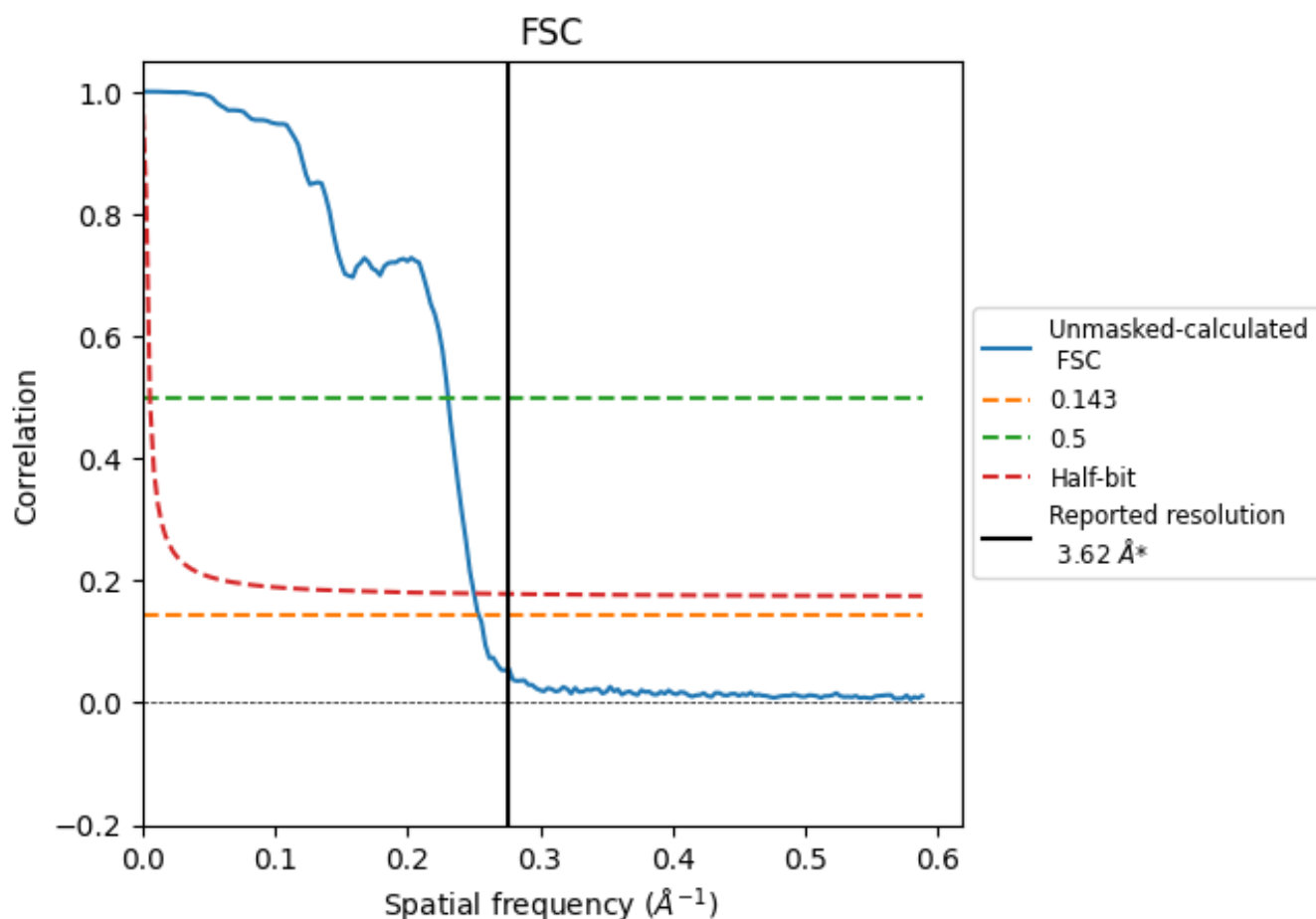


*Reported resolution corresponds to spatial frequency of 0.276 Å⁻¹

8 Fourier-Shell correlation [i](#)

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 [i](#)



*Reported resolution corresponds to spatial frequency of 0.276 Å⁻¹

8.2 Resolution estimates [i](#)

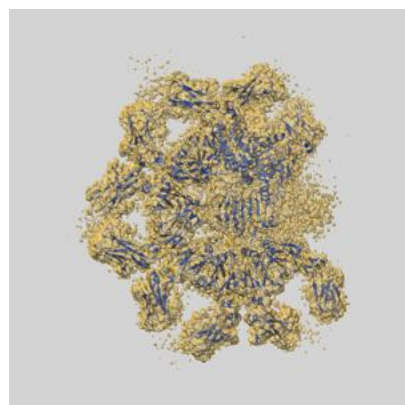
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	3.62	-	-
Author-provided FSC curve	-	-	-
Unmasked-calculated*	3.94	4.34	4.00

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

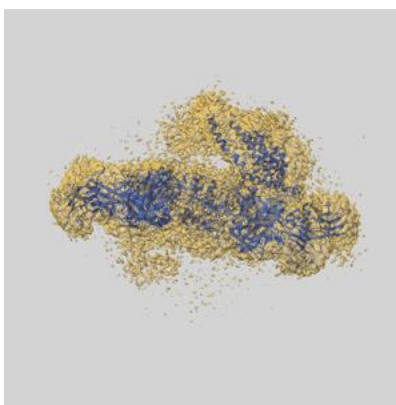
9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-33547 and PDB model 7Y0J. Per-residue inclusion information can be found in section [3](#) on page [15](#).

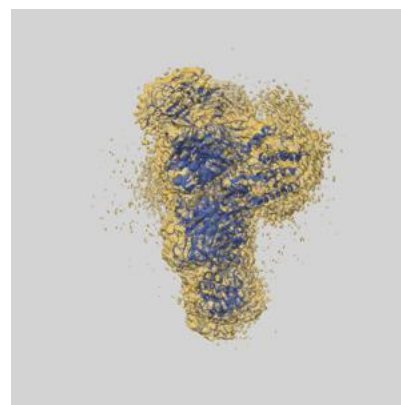
9.1 Map-model overlay [i](#)



X



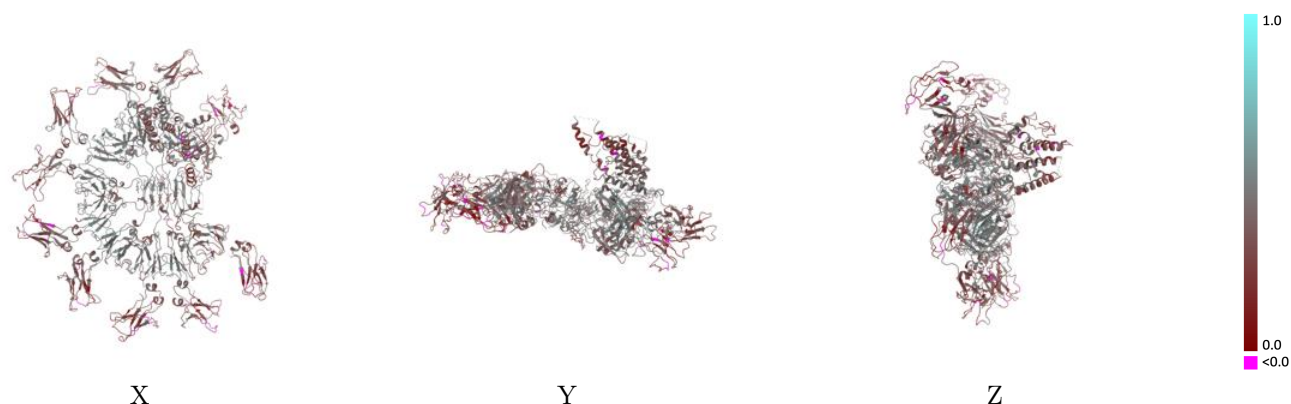
Y



Z

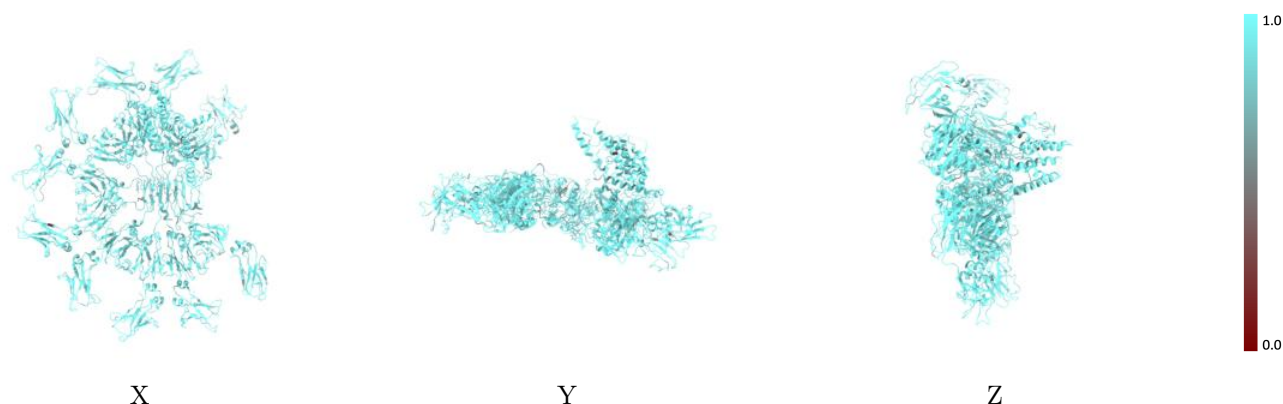
The images above show the 3D surface view of the map at the recommended contour level 0.13 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



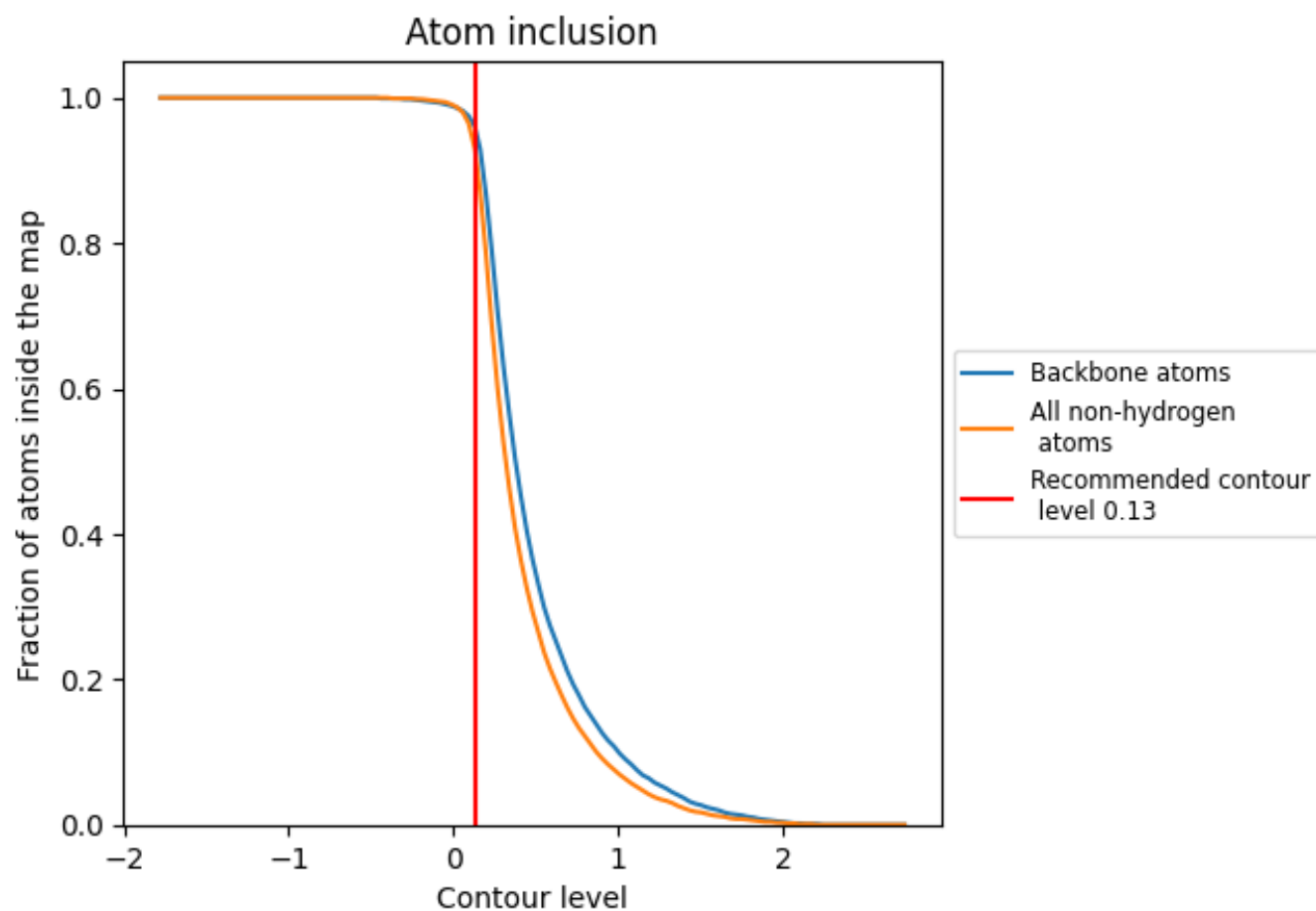
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions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

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



The images above show the model with each residue coloured according to its atom inclusion. This shows to what extent they are inside the map at the recommended contour level (0.13).

9.4 Atom inclusion [i](#)



At the recommended contour level, 96% of all backbone atoms, 93% 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 (0.13) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9290	0.3730
A	0.9210	0.3490
B	0.9450	0.4090
C	0.9380	0.4170
D	0.9440	0.4030
E	0.9320	0.3740
F	0.9310	0.3770
G	0.9330	0.3830
H	0.9390	0.3580
I	0.9640	0.3540
J	0.9010	0.4060
K	0.9180	0.3510
L	0.9010	0.3120
M	0.9270	0.3620

1.0

0.0

<0.0