



## wwPDB EM Validation Summary Report ⓘ

Mar 29, 2026 – 12:19 AM UTC

PDB ID : 7WPF / pdb\_00007wpf  
EMDB ID : EMD-32685  
Title : SARS-CoV-2 Omicron Variant S Trimer complexed with three JMB2002 Fab  
Authors : Yin, W.; Xu, Y.; Xu, P.; Cao, X.; Wu, C.; Gu, C.; He, X.; Wang, X.; Huang, S.; Yuan, Q.; Wu, K.; Hu, W.; Huang, Z.; Liu, J.; Wang, Z.; Jia, F.; Xia, K.; Liu, P.; Wang, X.; Song, B.; Zheng, J.; Jiang, H.; Cheng, X.; Jiang, Y.; Deng, S.J.; Xu, H.E.  
Deposited on : 2022-01-23  
Resolution : 2.92 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](mailto: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>.

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

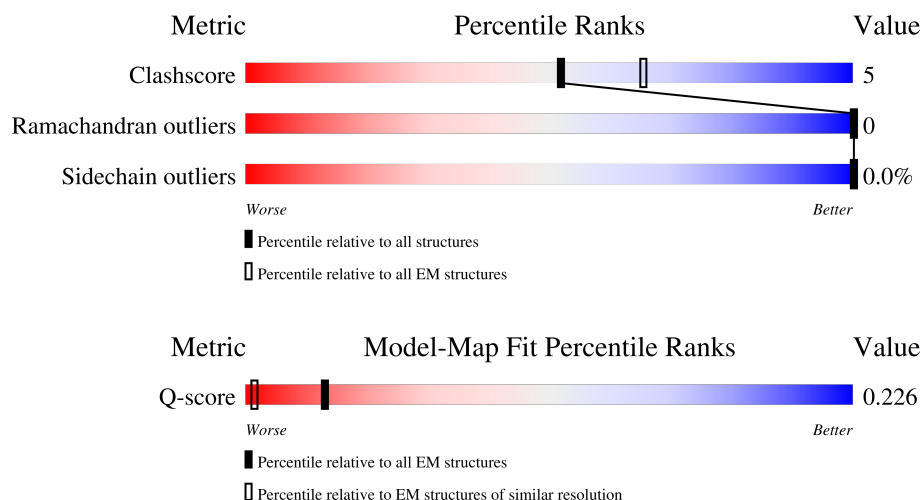
EMDB validation analysis : 0.0.1.dev132  
Mogul : 2022.3.0, CSD as543be (2022)  
MolProbity : 4-5-2 with Phenix2.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
EM percentile statistics : 202505.v01 (Using data in the EMDB archive up until May 2025)  
MapQ : 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 2.92 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	13007 ( 2.42 - 3.42 )

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  $\geq 3$ , 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	1205	<div> <div>6%</div> <div>76%</div> <div>9%</div> <div>15%</div> </div>
1	B	1205	<div> <div>10%</div> <div>76%</div> <div>9%</div> <div>15%</div> </div>
1	C	1205	<div> <div>•</div> <div>77%</div> <div>8%</div> <div>15%</div> </div>
2	R	237	<div> <div>68%</div> <div>85%</div> <div>10%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
2	U	237	<div>62%</div> <div>79%16%5%</div>
2	X	237	<div>60%</div> <div>81%14%5%</div>
3	S	214	<div>66%</div> <div>89%11%</div>
3	V	214	<div>51%</div> <div>79%21%</div>
3	Y	214	<div>62%</div> <div>81%18%</div>
4	T	133	<div>65%</div> <div>72%18%10%</div>
4	W	133	<div>77%</div> <div>77%14%10%</div>
4	Z	133	<div>64%</div> <div>78%12%10%</div>
5	D	2	<div>100%</div>
5	E	2	<div>50%</div> <div>100%</div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 36202 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 Spike glycoprotein.

Mol	Chain	Residues	Atoms					AltConf	Trace
1	A	1024	Total	C	N	O	S	0	0
			7676	4919	1276	1447	34		
1	B	1023	Total	C	N	O	S	0	0
			7672	4920	1276	1442	34		
1	C	1022	Total	C	N	O	S	0	0
			7700	4958	1275	1432	35		

There are 132 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	67	VAL	ALA	variant	UNP P0DTC2
A	?	-	HIS	deletion	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	95	ILE	THR	variant	UNP P0DTC2
A	142	ASP	GLY	variant	UNP P0DTC2
A	?	-	VAL	deletion	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	?	-	TYR	deletion	UNP P0DTC2
A	?	-	ASN	deletion	UNP P0DTC2
A	210A	ILE	LEU	variant	UNP P0DTC2
A	210D	GLU	-	insertion	UNP P0DTC2
A	210E	PRO	-	insertion	UNP P0DTC2
A	210F	GLU	-	insertion	UNP P0DTC2
A	339	ASP	GLY	variant	UNP P0DTC2
A	371	LEU	SER	variant	UNP P0DTC2
A	373	PRO	SER	variant	UNP P0DTC2
A	375	PHE	SER	variant	UNP P0DTC2
A	417	ASN	LYS	variant	UNP P0DTC2
A	440	LYS	ASN	variant	UNP P0DTC2
A	446	SER	GLY	variant	UNP P0DTC2
A	477	ASN	SER	variant	UNP P0DTC2
A	478	LYS	THR	variant	UNP P0DTC2
A	484	ALA	GLU	variant	UNP P0DTC2
A	493	ARG	GLN	engineered mutation	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
A	496	SER	GLY	variant	UNP P0DTC2
A	498	ARG	GLN	variant	UNP P0DTC2
A	501	TYR	ASN	variant	UNP P0DTC2
A	505	HIS	TYR	variant	UNP P0DTC2
A	547	LYS	THR	variant	UNP P0DTC2
A	614	GLY	ASP	variant	UNP P0DTC2
A	655	TYR	HIS	variant	UNP P0DTC2
A	679	LYS	ASN	variant	UNP P0DTC2
A	681	HIS	PRO	variant	UNP P0DTC2
A	682	GLY	ARG	engineered mutation	UNP P0DTC2
A	683	SER	ARG	engineered mutation	UNP P0DTC2
A	685	SER	ARG	engineered mutation	UNP P0DTC2
A	764	LYS	ASN	variant	UNP P0DTC2
A	796	TYR	ASP	variant	UNP P0DTC2
A	856	LYS	ASN	variant	UNP P0DTC2
A	954	HIS	GLN	variant	UNP P0DTC2
A	969	LYS	ASN	variant	UNP P0DTC2
A	981	PHE	LEU	variant	UNP P0DTC2
A	986	PRO	LYS	engineered mutation	UNP P0DTC2
A	987	PRO	VAL	engineered mutation	UNP P0DTC2
B	67	VAL	ALA	variant	UNP P0DTC2
B	?	-	HIS	deletion	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	95	ILE	THR	variant	UNP P0DTC2
B	142	ASP	GLY	variant	UNP P0DTC2
B	?	-	VAL	deletion	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	?	-	TYR	deletion	UNP P0DTC2
B	?	-	ASN	deletion	UNP P0DTC2
B	210A	ILE	LEU	variant	UNP P0DTC2
B	210D	GLU	-	insertion	UNP P0DTC2
B	210E	PRO	-	insertion	UNP P0DTC2
B	210F	GLU	-	insertion	UNP P0DTC2
B	339	ASP	GLY	variant	UNP P0DTC2
B	371	LEU	SER	variant	UNP P0DTC2
B	373	PRO	SER	variant	UNP P0DTC2
B	375	PHE	SER	variant	UNP P0DTC2
B	417	ASN	LYS	variant	UNP P0DTC2
B	440	LYS	ASN	variant	UNP P0DTC2
B	446	SER	GLY	variant	UNP P0DTC2
B	477	ASN	SER	variant	UNP P0DTC2
B	478	LYS	THR	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
B	484	ALA	GLU	variant	UNP P0DTC2
B	493	ARG	GLN	engineered mutation	UNP P0DTC2
B	496	SER	GLY	variant	UNP P0DTC2
B	498	ARG	GLN	variant	UNP P0DTC2
B	501	TYR	ASN	variant	UNP P0DTC2
B	505	HIS	TYR	variant	UNP P0DTC2
B	547	LYS	THR	variant	UNP P0DTC2
B	614	GLY	ASP	variant	UNP P0DTC2
B	655	TYR	HIS	variant	UNP P0DTC2
B	679	LYS	ASN	variant	UNP P0DTC2
B	681	HIS	PRO	variant	UNP P0DTC2
B	682	GLY	ARG	engineered mutation	UNP P0DTC2
B	683	SER	ARG	engineered mutation	UNP P0DTC2
B	685	SER	ARG	engineered mutation	UNP P0DTC2
B	764	LYS	ASN	variant	UNP P0DTC2
B	796	TYR	ASP	variant	UNP P0DTC2
B	856	LYS	ASN	variant	UNP P0DTC2
B	954	HIS	GLN	variant	UNP P0DTC2
B	969	LYS	ASN	variant	UNP P0DTC2
B	981	PHE	LEU	variant	UNP P0DTC2
B	986	PRO	LYS	engineered mutation	UNP P0DTC2
B	987	PRO	VAL	engineered mutation	UNP P0DTC2
C	67	VAL	ALA	variant	UNP P0DTC2
C	?	-	HIS	deletion	UNP P0DTC2
C	?	-	VAL	deletion	UNP P0DTC2
C	95	ILE	THR	variant	UNP P0DTC2
C	142	ASP	GLY	variant	UNP P0DTC2
C	?	-	VAL	deletion	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	?	-	TYR	deletion	UNP P0DTC2
C	?	-	ASN	deletion	UNP P0DTC2
C	210A	ILE	LEU	variant	UNP P0DTC2
C	210D	GLU	-	insertion	UNP P0DTC2
C	210E	PRO	-	insertion	UNP P0DTC2
C	210F	GLU	-	insertion	UNP P0DTC2
C	339	ASP	GLY	variant	UNP P0DTC2
C	371	LEU	SER	variant	UNP P0DTC2
C	373	PRO	SER	variant	UNP P0DTC2
C	375	PHE	SER	variant	UNP P0DTC2
C	417	ASN	LYS	variant	UNP P0DTC2
C	440	LYS	ASN	variant	UNP P0DTC2
C	446	SER	GLY	variant	UNP P0DTC2

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Chain	Residue	Modelled	Actual	Comment	Reference
C	477	ASN	SER	variant	UNP P0DTC2
C	478	LYS	THR	variant	UNP P0DTC2
C	484	ALA	GLU	variant	UNP P0DTC2
C	493	ARG	GLN	engineered mutation	UNP P0DTC2
C	496	SER	GLY	variant	UNP P0DTC2
C	498	ARG	GLN	variant	UNP P0DTC2
C	501	TYR	ASN	variant	UNP P0DTC2
C	505	HIS	TYR	variant	UNP P0DTC2
C	547	LYS	THR	variant	UNP P0DTC2
C	614	GLY	ASP	variant	UNP P0DTC2
C	655	TYR	HIS	variant	UNP P0DTC2
C	679	LYS	ASN	variant	UNP P0DTC2
C	681	HIS	PRO	variant	UNP P0DTC2
C	682	GLY	ARG	engineered mutation	UNP P0DTC2
C	683	SER	ARG	engineered mutation	UNP P0DTC2
C	685	SER	ARG	engineered mutation	UNP P0DTC2
C	764	LYS	ASN	variant	UNP P0DTC2
C	796	TYR	ASP	variant	UNP P0DTC2
C	856	LYS	ASN	variant	UNP P0DTC2
C	954	HIS	GLN	variant	UNP P0DTC2
C	969	LYS	ASN	variant	UNP P0DTC2
C	981	PHE	LEU	variant	UNP P0DTC2
C	986	PRO	LYS	engineered mutation	UNP P0DTC2
C	987	PRO	VAL	engineered mutation	UNP P0DTC2

- Molecule 2 is a protein called JMB2002 Fab heavy chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	R	225	Total	C	N	O	S	0	0
			1659	1047	271	334	7		
2	U	225	Total	C	N	O	S	0	0
			1648	1038	269	334	7		
2	X	225	Total	C	N	O	S	0	0
			1656	1046	271	332	7		

- Molecule 3 is a protein called JMB2002 Fab light chain.

Mol	Chain	Residues	Atoms					AltConf	Trace
3	S	213	Total	C	N	O	S	0	0
			1622	1013	271	333	5		
3	V	213	Total	C	N	O	S	0	0
			1630	1019	272	334	5		

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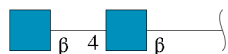
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Mol	Chain	Residues	Atoms					AltConf	Trace
3	Y	213	Total	C	N	O	S	0	0
			1622	1017	269	331	5		

- Molecule 4 is a protein called Anti-Fab nanobody.

Mol	Chain	Residues	Atoms					AltConf	Trace
4	T	120	Total	C	N	O	S	0	0
			925	574	163	184	4		
4	W	120	Total	C	N	O	S	0	0
			925	574	163	184	4		
4	Z	120	Total	C	N	O	S	0	0
			921	572	162	183	4		

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



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

- Molecule 6 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).





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

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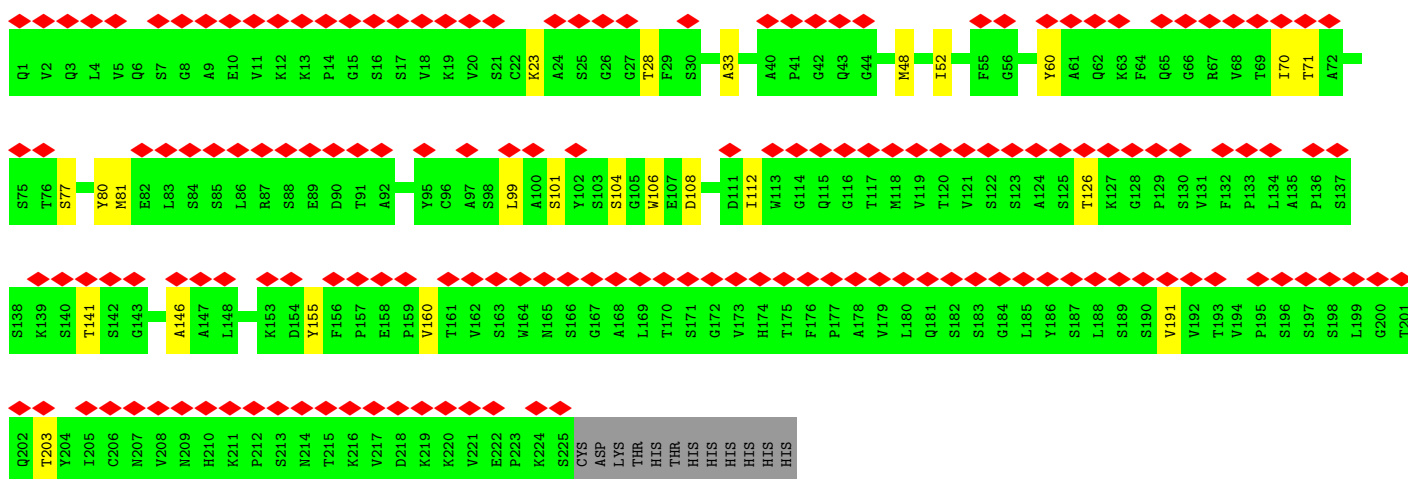
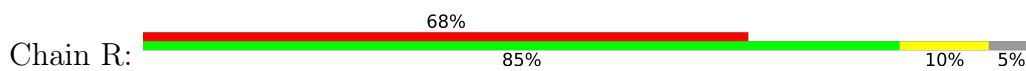
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Mol	Chain	Residues	Atoms				AltConf
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C	N	O	0
			14	8	1	5	
6	B	1	Total	C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

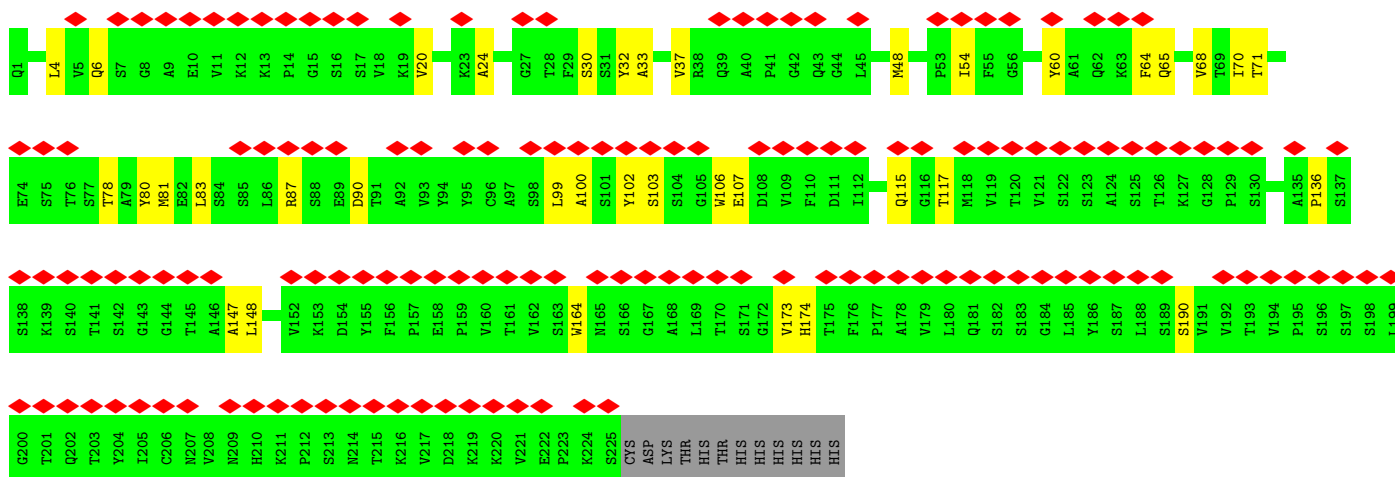
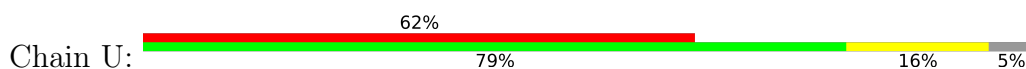




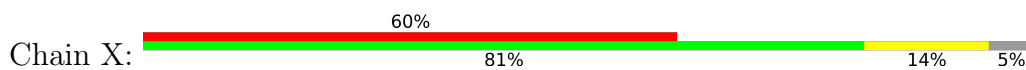
- Molecule 2: JMB2002 Fab heavy chain

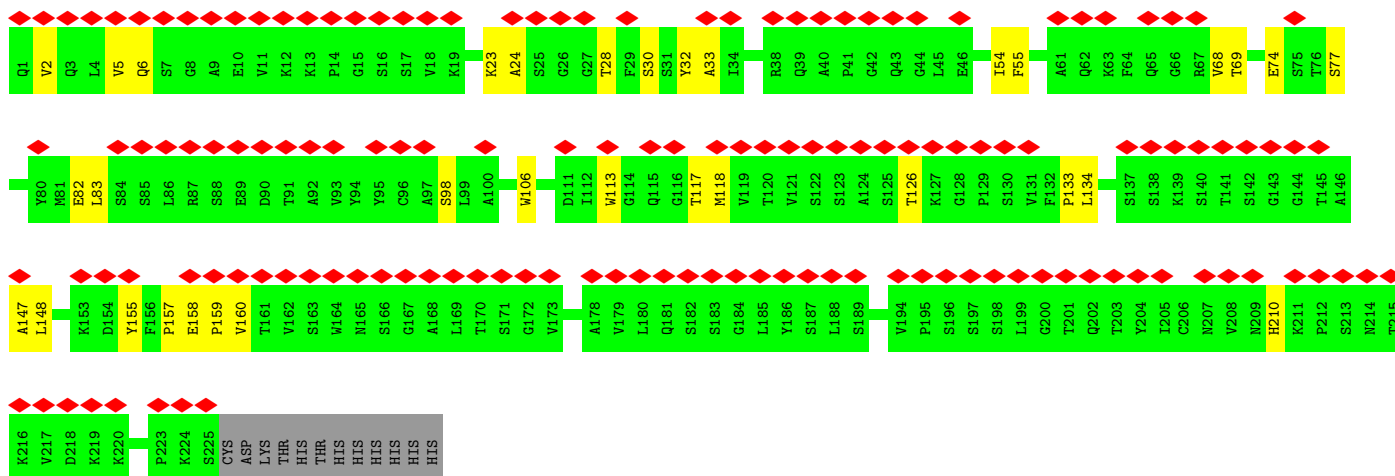


- Molecule 2: JMB2002 Fab heavy chain

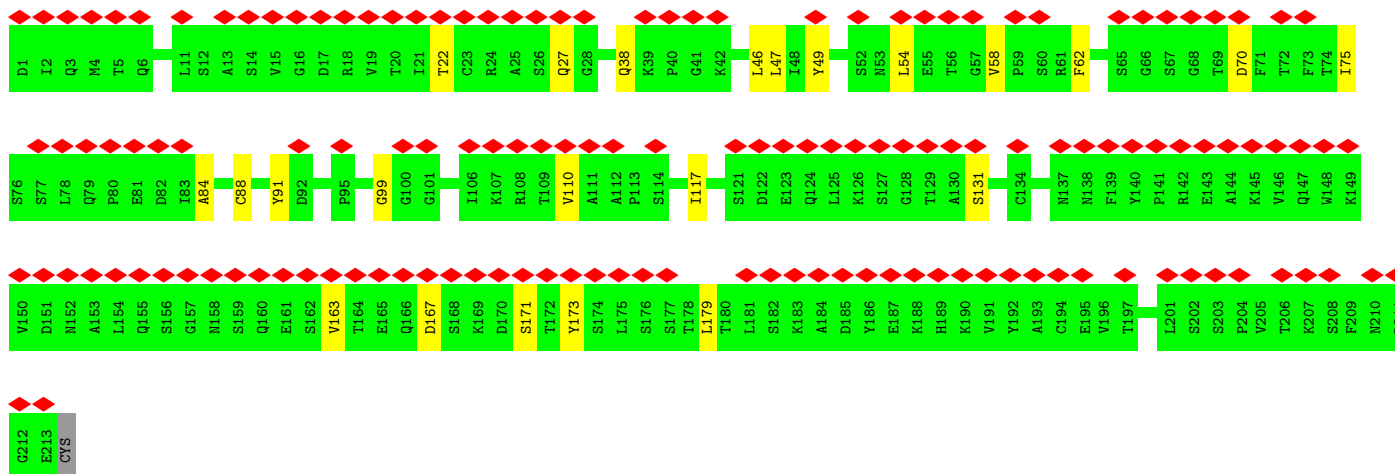
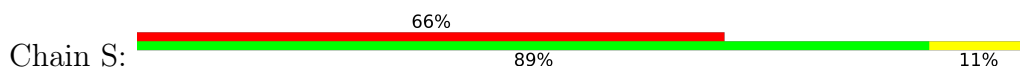


- Molecule 2: JMB2002 Fab heavy chain

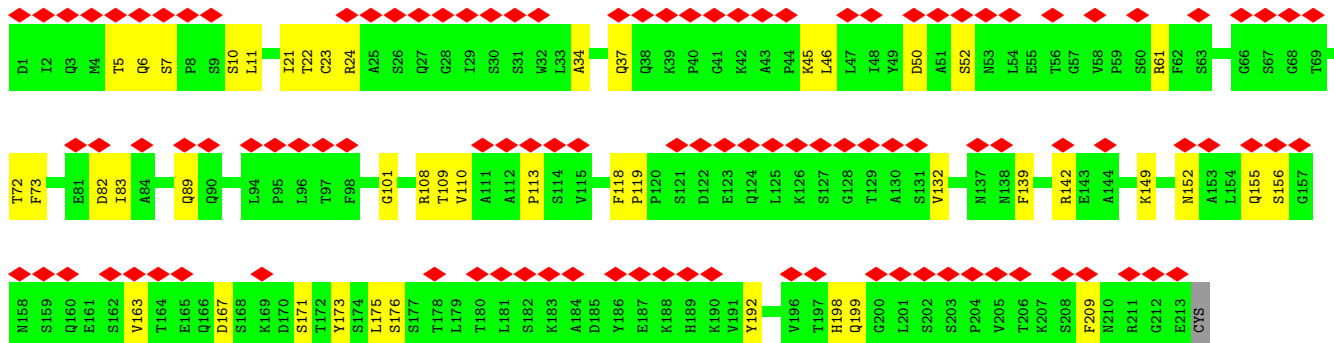
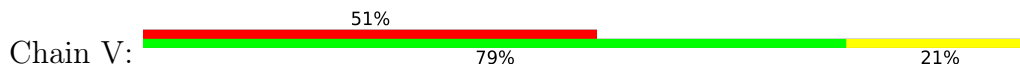




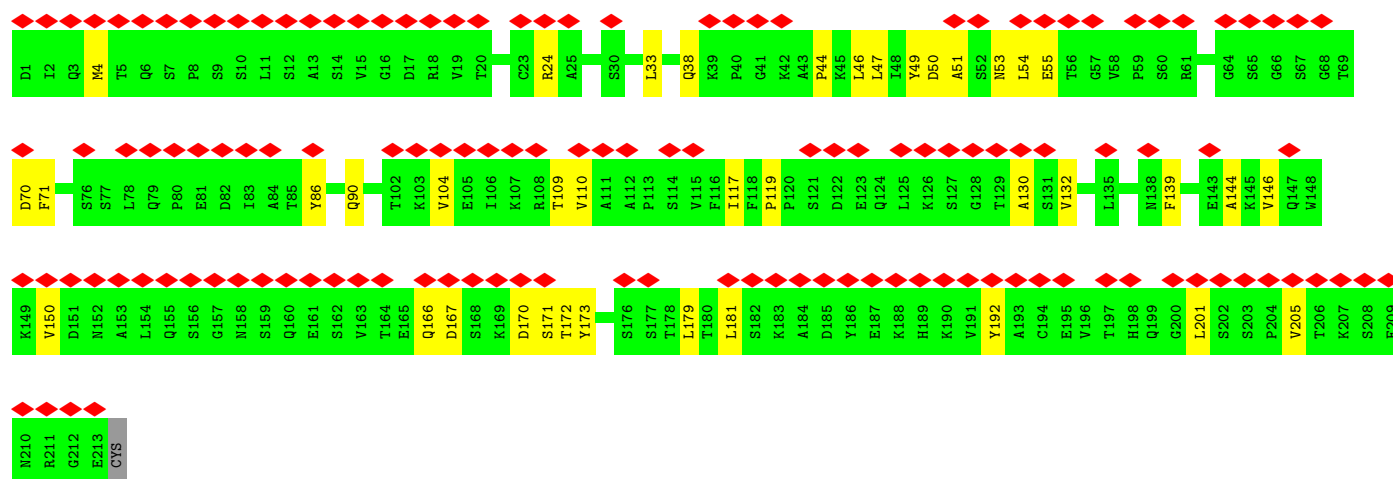
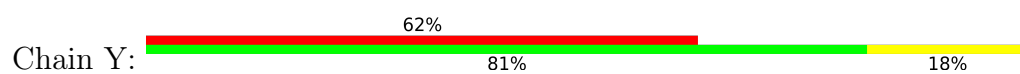
- Molecule 3: JMB2002 Fab light chain



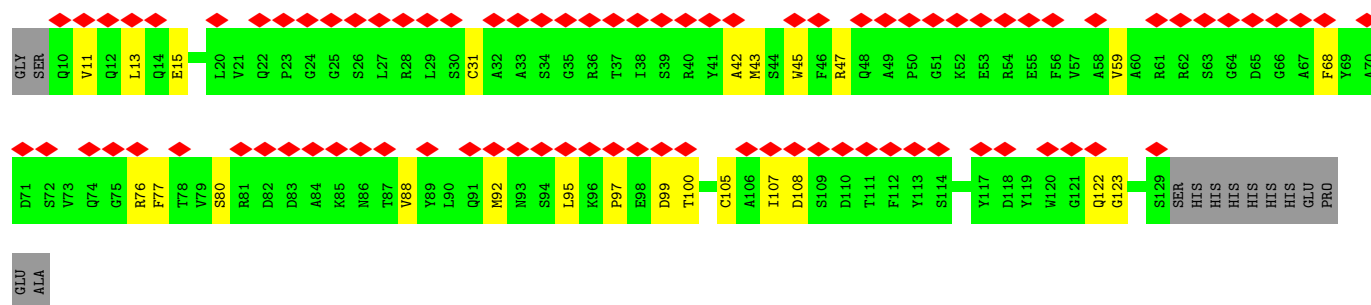
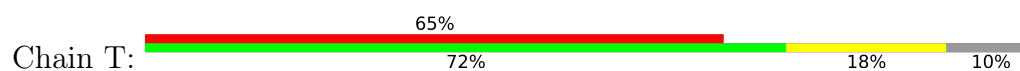
- Molecule 3: JMB2002 Fab light chain



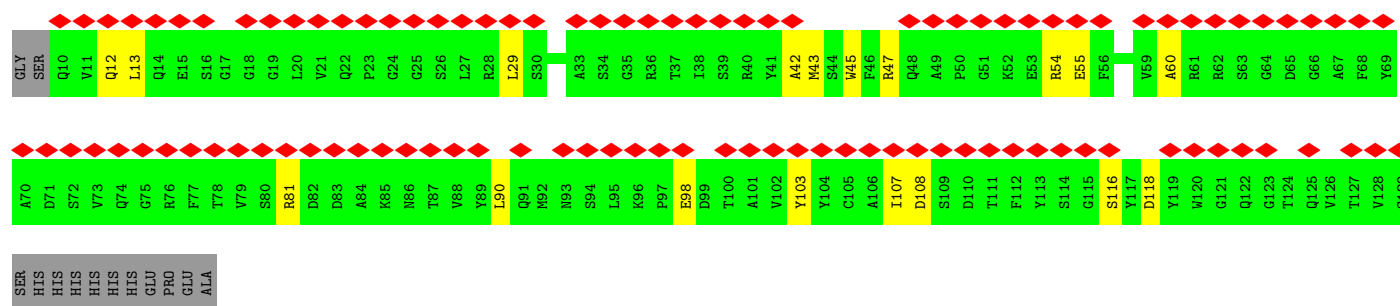
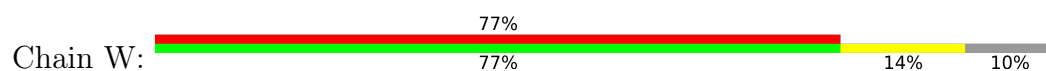
- Molecule 3: JMB2002 Fab light chain



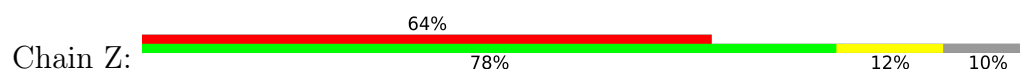
• Molecule 4: Anti-Fab nanobody

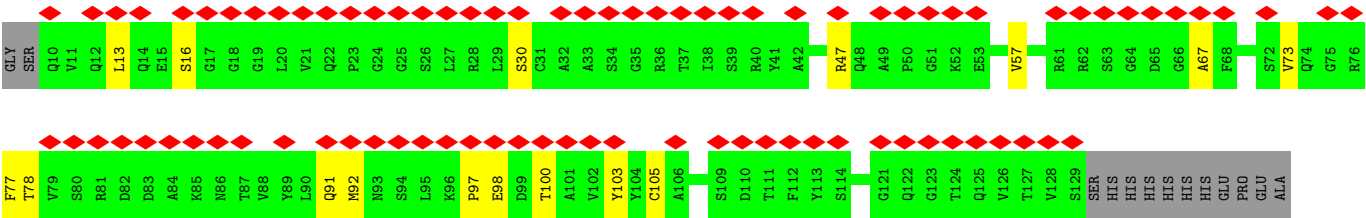


• Molecule 4: Anti-Fab nanobody



• Molecule 4: Anti-Fab nanobody





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



- Molecule 5: 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	434893	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	50	Depositor
Minimum defocus (nm)	12000	Depositor
Maximum defocus (nm)	22000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	2.452	Depositor
Minimum map value	-0.031	Depositor
Average map value	0.001	Depositor
Map value standard deviation	0.021	Depositor
Recommended contour level	0.02	Depositor
Map size ( $\text{\AA}$ )	395.52, 395.52, 395.52	wwPDB
Map dimensions	480, 480, 480	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	0.824, 0.824, 0.824	Depositor

## 5 Model quality

### 5.1 Standard geometry

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	A	0.13	0/7857	0.35	0/10738
1	B	0.13	0/7853	0.35	0/10731
1	C	0.13	0/7884	0.35	0/10767
2	R	0.14	0/1698	0.55	4/2314 (0.2%)
2	U	0.13	0/1686	0.50	2/2298 (0.1%)
2	X	0.15	0/1695	0.55	2/2310 (0.1%)
3	S	0.12	0/1656	0.41	1/2251 (0.0%)
3	V	0.14	0/1665	0.42	0/2262
3	Y	0.15	0/1657	0.46	1/2253 (0.0%)
4	T	0.18	0/944	0.53	0/1276
4	W	0.16	0/944	0.42	0/1276
4	Z	0.17	0/940	0.49	1/1271 (0.1%)
All	All	0.14	0/36479	0.40	11/49747 (0.0%)

There are no bond length outliers.

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	U	103	SER	CA-C-N	11.13	142.38	123.91
2	U	103	SER	C-N-CA	11.13	142.38	123.91
4	Z	67	ALA	N-CA-C	5.91	117.20	108.86
2	R	126	THR	OG1-CB-CG2	5.63	120.57	109.30
2	X	28	THR	OG1-CB-CG2	5.59	120.49	109.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts ⓘ

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	7676	0	7180	69	0
1	B	7672	0	7194	78	0
1	C	7700	0	7271	62	0
2	R	1659	0	1624	14	0
2	U	1648	0	1601	29	0
2	X	1656	0	1622	25	0
3	S	1622	0	1566	13	0
3	V	1630	0	1575	34	0
3	Y	1622	0	1566	25	0
4	T	925	0	870	22	0
4	W	925	0	870	17	0
4	Z	921	0	864	10	0
5	D	28	0	25	0	0
5	E	28	0	25	0	0
6	A	154	0	143	1	0
6	B	168	0	156	4	0
6	C	168	0	156	1	0
All	All	36202	0	34308	377	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 5.

The worst 5 of 377 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:1134:ASN:ND2	6:B:1304:NAG:C1	2.35	0.89
3:S:49:TYR:O	3:S:91:TYR:OH	2.02	0.76
1:A:983:ARG:HG2	1:C:390:LEU:HD21	1.65	0.76
1:A:802:PHE:CD2	1:A:882:ILE:HD13	2.21	0.76
2:X:30:SER:HB2	2:X:54:ILE:HD12	1.68	0.76

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	A	1008/1205 (84%)	973 (96%)	35 (4%)	0	100	100
1	B	1007/1205 (84%)	971 (96%)	36 (4%)	0	100	100
1	C	1006/1205 (84%)	960 (95%)	46 (5%)	0	100	100
2	R	223/237 (94%)	210 (94%)	13 (6%)	0	100	100
2	U	223/237 (94%)	216 (97%)	7 (3%)	0	100	100
2	X	223/237 (94%)	210 (94%)	13 (6%)	0	100	100
3	S	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
3	V	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
3	Y	211/214 (99%)	205 (97%)	6 (3%)	0	100	100
4	T	118/133 (89%)	109 (92%)	9 (8%)	0	100	100
4	W	118/133 (89%)	109 (92%)	9 (8%)	0	100	100
4	Z	118/133 (89%)	111 (94%)	7 (6%)	0	100	100
All	All	4677/5367 (87%)	4484 (96%)	193 (4%)	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	801/1053 (76%)	800 (100%)	1 (0%)	88	97
1	B	801/1053 (76%)	801 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	C	802/1053 (76%)	802 (100%)	0	100	100
2	R	187/200 (94%)	187 (100%)	0	100	100
2	U	184/200 (92%)	184 (100%)	0	100	100
2	X	186/200 (93%)	186 (100%)	0	100	100
3	S	184/187 (98%)	184 (100%)	0	100	100
3	V	185/187 (99%)	185 (100%)	0	100	100
3	Y	183/187 (98%)	183 (100%)	0	100	100
4	T	96/107 (90%)	96 (100%)	0	100	100
4	W	96/107 (90%)	96 (100%)	0	100	100
4	Z	95/107 (89%)	95 (100%)	0	100	100
All	All	3800/4641 (82%)	3799 (100%)	1 (0%)	100	100

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

Mol	Chain	Res	Type
1	A	195	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 33 such sidechains are listed below:

Mol	Chain	Res	Type
3	S	198	HIS
2	U	59	ASN
3	Y	166	GLN
1	B	370	ASN
1	B	125	ASN

### 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

4 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	$\# Z  > 2$
5	NAG	D	1	1,5	14,14,15	0.21	0	17,19,21	0.44	0
5	NAG	D	2	5	14,14,15	0.20	0	17,19,21	0.45	0
5	NAG	E	1	1,5	14,14,15	0.32	0	17,19,21	0.43	0
5	NAG	E	2	5	14,14,15	0.20	0	17,19,21	0.45	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	D	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	D	2	5	-	0/6/23/26	0/1/1/1
5	NAG	E	1	1,5	-	0/6/23/26	0/1/1/1
5	NAG	E	2	5	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

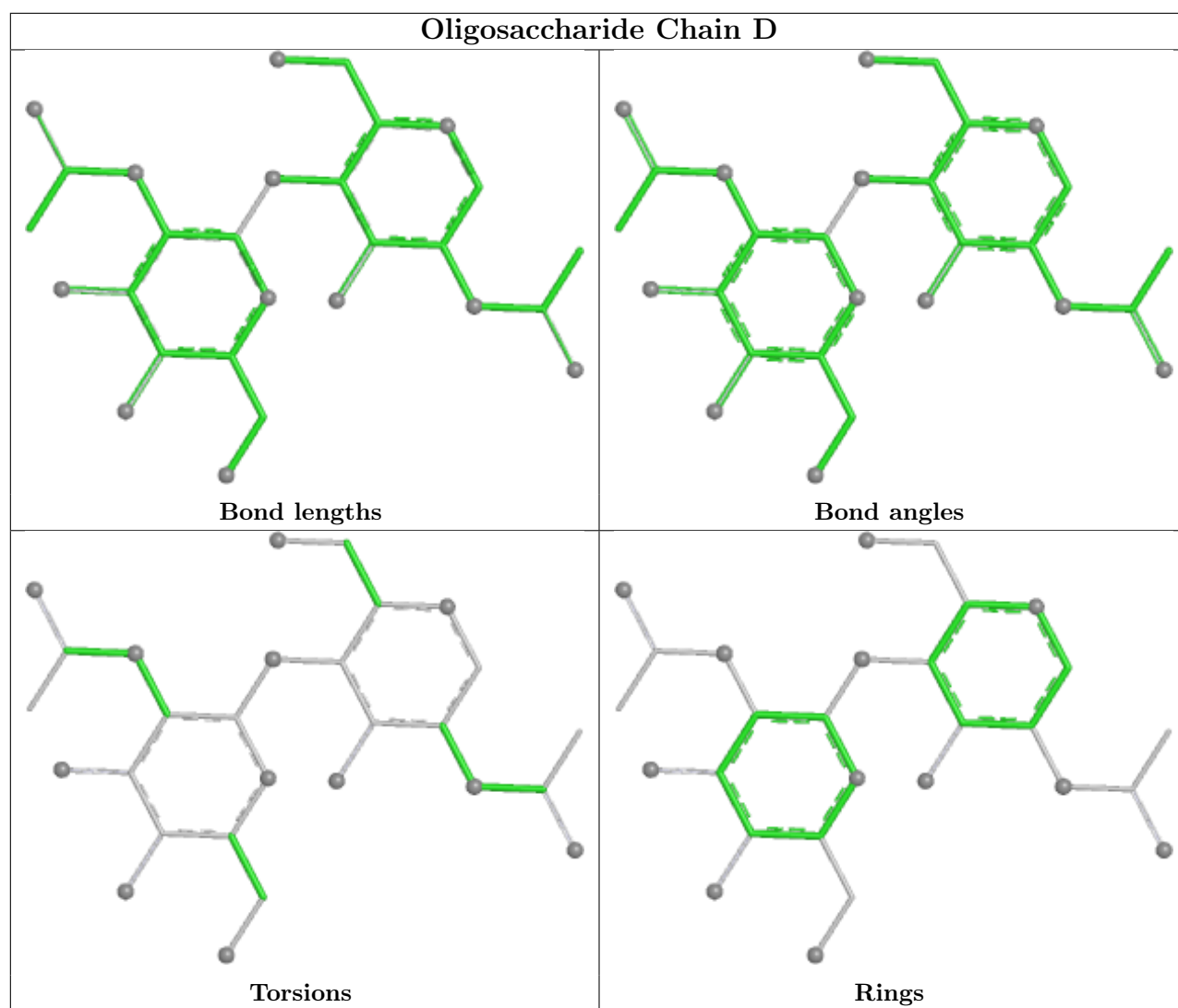
There are no chirality outliers.

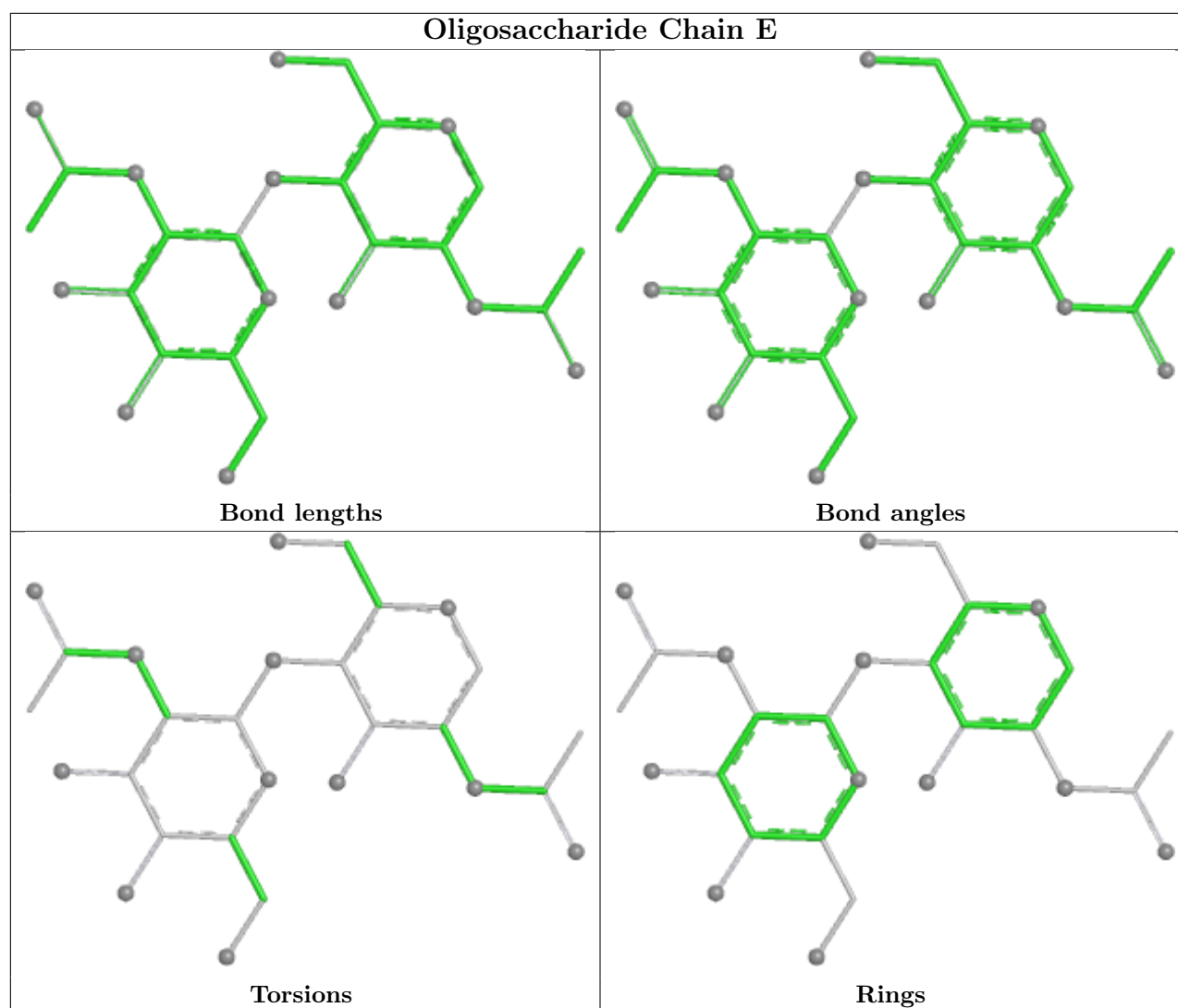
There are no torsion outliers.

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](#)

35 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
6	NAG	A	1311	1	14,14,15	0.19	0	17,19,21	0.43	0
6	NAG	B	1302	1	14,14,15	0.26	0	17,19,21	0.45	0
6	NAG	C	1308	1	14,14,15	0.22	0	17,19,21	0.39	0



Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
6	NAG	A	1309	1	14,14,15	0.20	0	17,19,21	0.41	0
6	NAG	A	1307	1	14,14,15	0.21	0	17,19,21	0.35	0
6	NAG	A	1301	1	14,14,15	0.37	0	17,19,21	0.54	0
6	NAG	B	1304	-	14,14,15	0.21	0	17,19,21	0.43	0
6	NAG	B	1306	1	14,14,15	0.25	0	17,19,21	0.46	0
6	NAG	B	1310	1	14,14,15	0.19	0	17,19,21	0.41	0
6	NAG	C	1306	1	14,14,15	0.27	0	17,19,21	0.50	0
6	NAG	C	1310	1	14,14,15	0.23	0	17,19,21	0.45	0
6	NAG	B	1307	1	14,14,15	0.24	0	17,19,21	0.49	0
6	NAG	A	1304	1	14,14,15	0.20	0	17,19,21	0.44	0
6	NAG	B	1312	1	14,14,15	0.21	0	17,19,21	0.44	0
6	NAG	C	1312	1	14,14,15	0.21	0	17,19,21	0.43	0
6	NAG	A	1303	1	14,14,15	0.21	0	17,19,21	0.43	0
6	NAG	B	1311	1	14,14,15	0.20	0	17,19,21	0.44	0
6	NAG	B	1309	1	14,14,15	0.23	0	17,19,21	0.49	0
6	NAG	A	1306	1	14,14,15	0.23	0	17,19,21	0.46	0
6	NAG	C	1302	1	14,14,15	0.24	0	17,19,21	0.44	0
6	NAG	C	1303	1	14,14,15	0.23	0	17,19,21	0.49	0
6	NAG	A	1305	1	14,14,15	0.25	0	17,19,21	0.50	0
6	NAG	B	1308	1	14,14,15	0.21	0	17,19,21	0.38	0
6	NAG	C	1304	1	14,14,15	0.21	0	17,19,21	0.43	0
6	NAG	A	1310	1	14,14,15	0.20	0	17,19,21	0.45	0
6	NAG	C	1307	1	14,14,15	0.22	0	17,19,21	0.44	0
6	NAG	C	1311	1	14,14,15	0.24	0	17,19,21	0.45	0
6	NAG	B	1301	1	14,14,15	0.25	0	17,19,21	0.78	1 (5%)
6	NAG	C	1305	1	14,14,15	0.27	0	17,19,21	0.49	0
6	NAG	B	1305	1	14,14,15	0.21	0	17,19,21	0.41	0
6	NAG	C	1309	1	14,14,15	0.32	0	17,19,21	0.57	0
6	NAG	A	1308	1	14,14,15	0.24	0	17,19,21	0.43	0
6	NAG	C	1301	1	14,14,15	0.22	0	17,19,21	0.44	0
6	NAG	B	1303	1	14,14,15	0.22	0	17,19,21	0.43	0
6	NAG	A	1302	1	14,14,15	0.22	0	17,19,21	0.44	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	1311	1	-	2/6/23/26	0/1/1/1
6	NAG	B	1302	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1308	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	A	1309	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1307	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1301	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1304	-	-	0/6/23/26	0/1/1/1
6	NAG	B	1306	1	-	1/6/23/26	0/1/1/1
6	NAG	B	1310	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1306	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1310	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1307	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1304	1	-	1/6/23/26	0/1/1/1
6	NAG	B	1312	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1312	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1311	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1309	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1306	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1302	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1305	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1308	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1304	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1310	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1307	1	-	1/6/23/26	0/1/1/1
6	NAG	C	1311	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1301	1	-	2/6/23/26	0/1/1/1
6	NAG	C	1305	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1305	1	-	1/6/23/26	0/1/1/1
6	NAG	C	1309	1	-	2/6/23/26	0/1/1/1
6	NAG	A	1308	1	-	0/6/23/26	0/1/1/1
6	NAG	C	1301	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1303	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1302	1	-	0/6/23/26	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(°)
6	B	1301	NAG	C1-O5-C5	2.86	116.02	112.19

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	C	1307	NAG	O5-C5-C6-O6
6	A	1304	NAG	O5-C5-C6-O6
6	B	1305	NAG	O5-C5-C6-O6
6	A	1311	NAG	C1-C2-N2-C7
6	B	1312	NAG	C1-C2-N2-C7

There are no ring outliers.

3 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	1301	NAG	1	0
6	B	1304	NAG	4	0
6	C	1312	NAG	1	0

## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

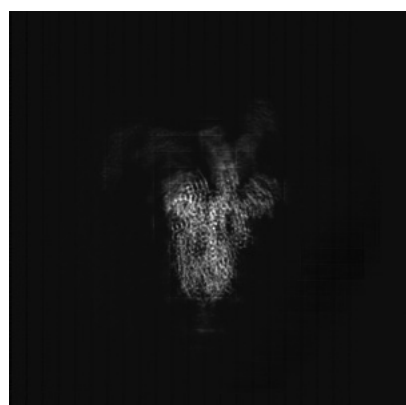
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-32685. These allow visual inspection of the internal detail of the map and identification of artifacts.

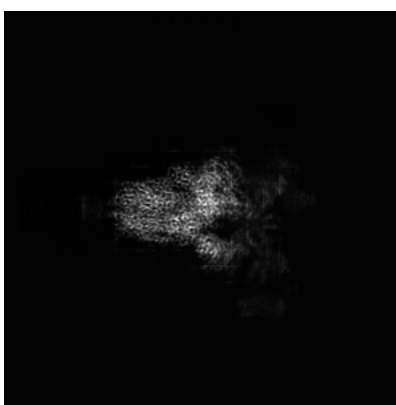
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

### 6.1 Orthogonal projections [i](#)

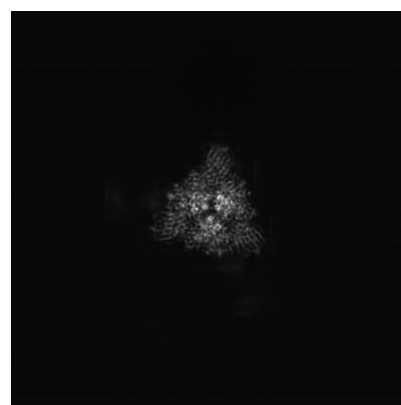
#### 6.1.1 Primary map



X



Y



Z

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

### 6.2 Central slices [i](#)

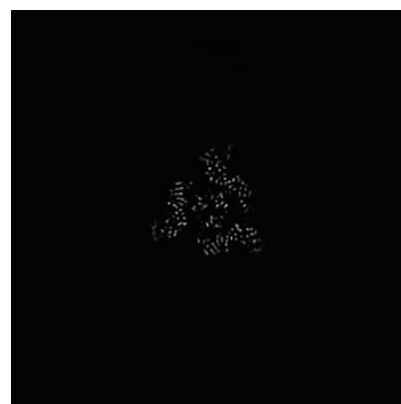
#### 6.2.1 Primary map



X Index: 240



Y Index: 240



Z Index: 240

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: 249



Y Index: 242

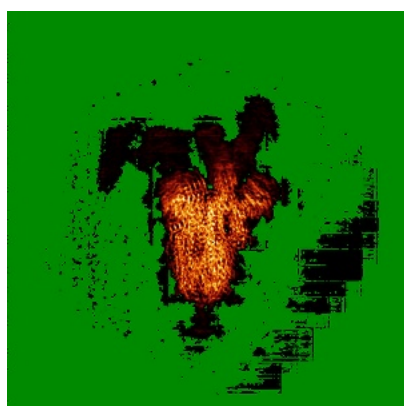


Z Index: 243

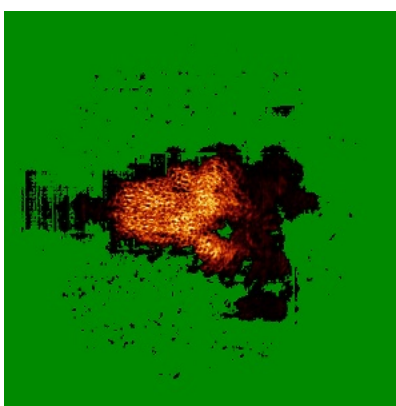
The images above show the largest variance slices of the map in three orthogonal directions.

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

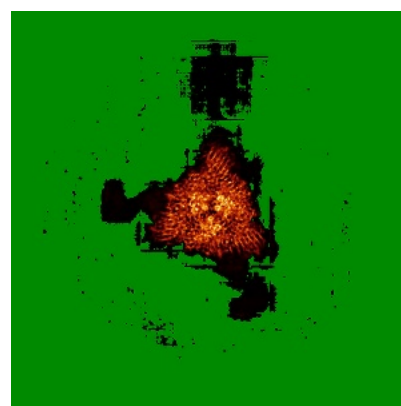
### 6.4.1 Primary map



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

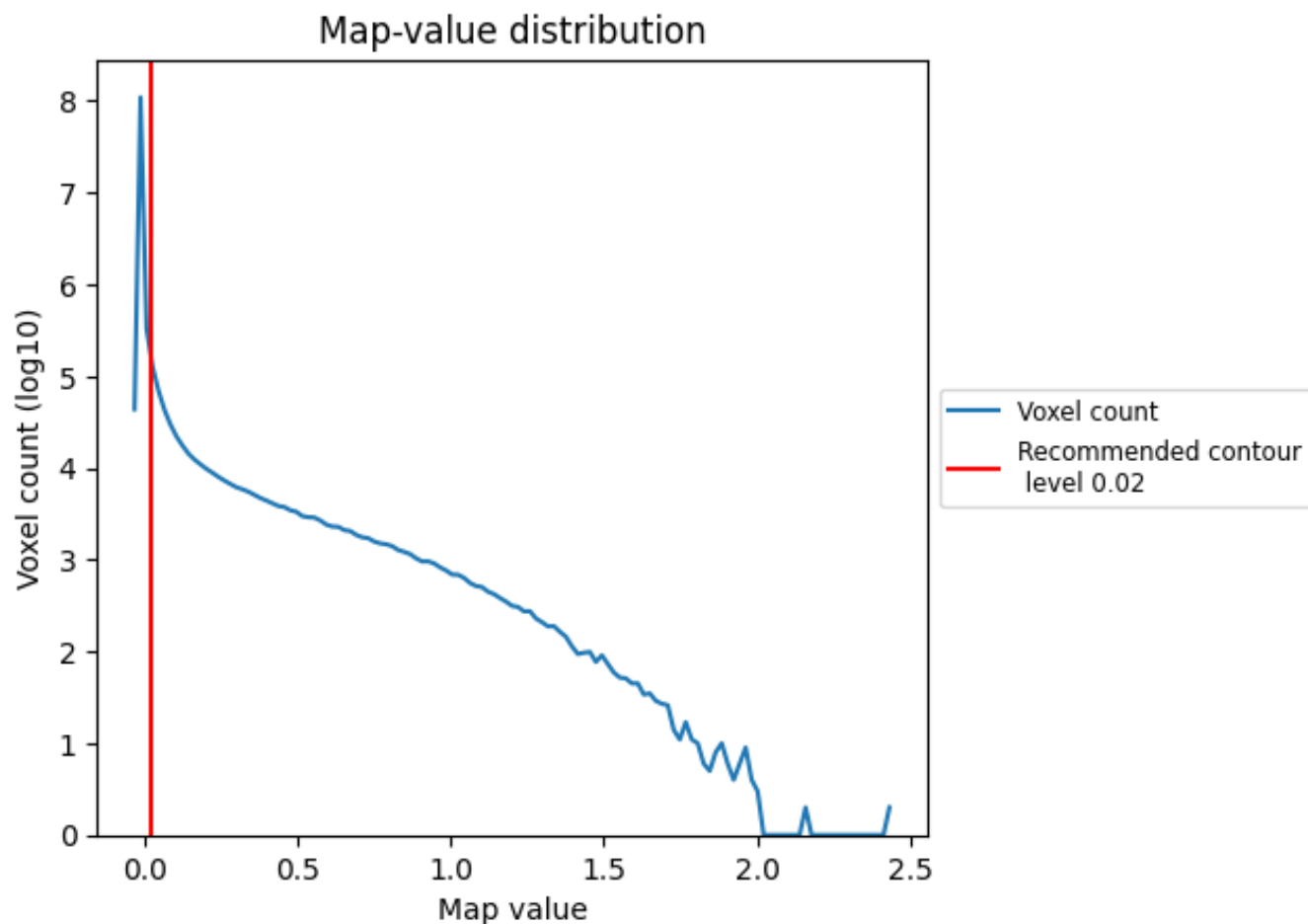
## 6.6 Mask visualisation [i](#)

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

## 7 Map analysis [i](#)

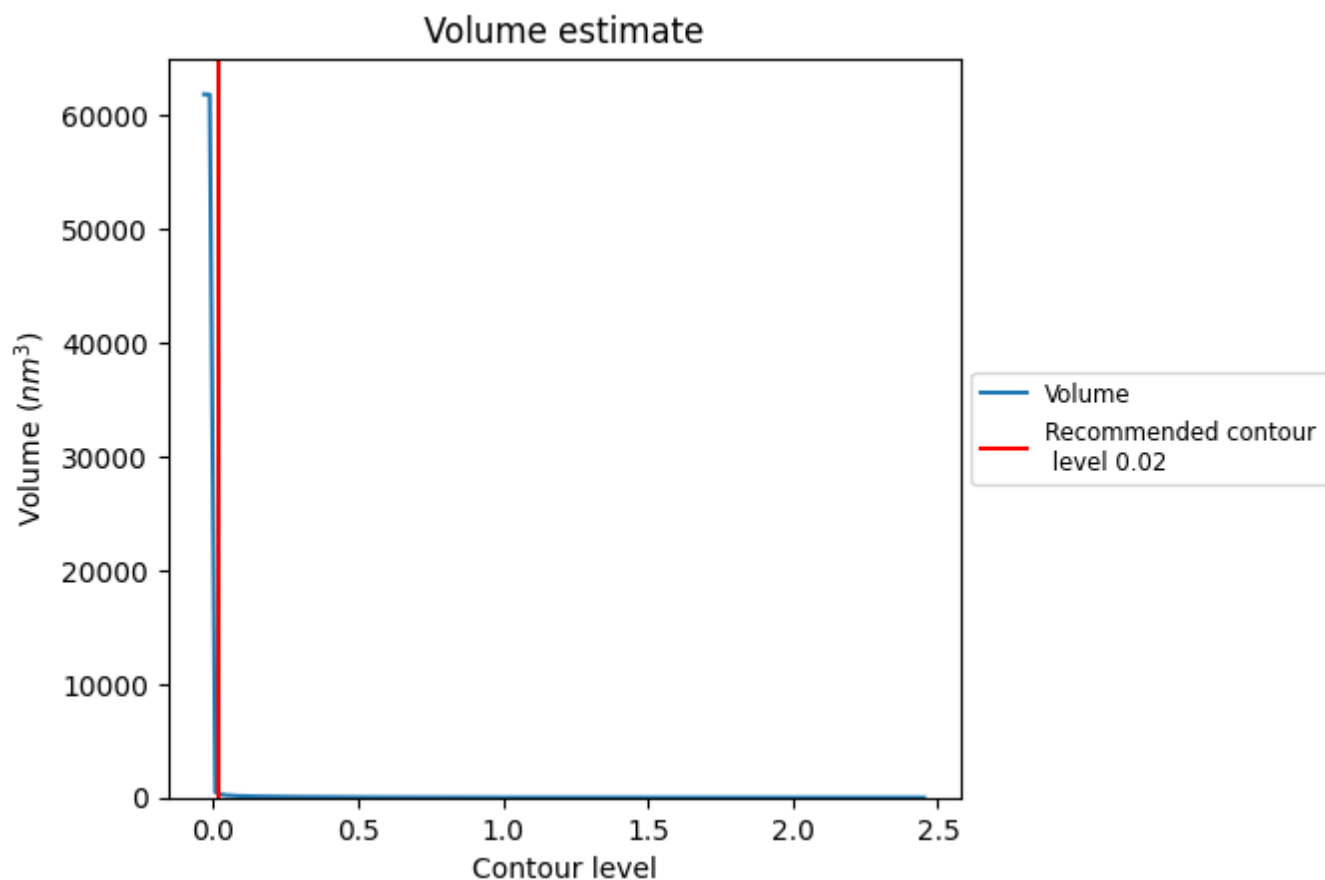
This section contains the results of statistical analysis of the map.

### 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](#)

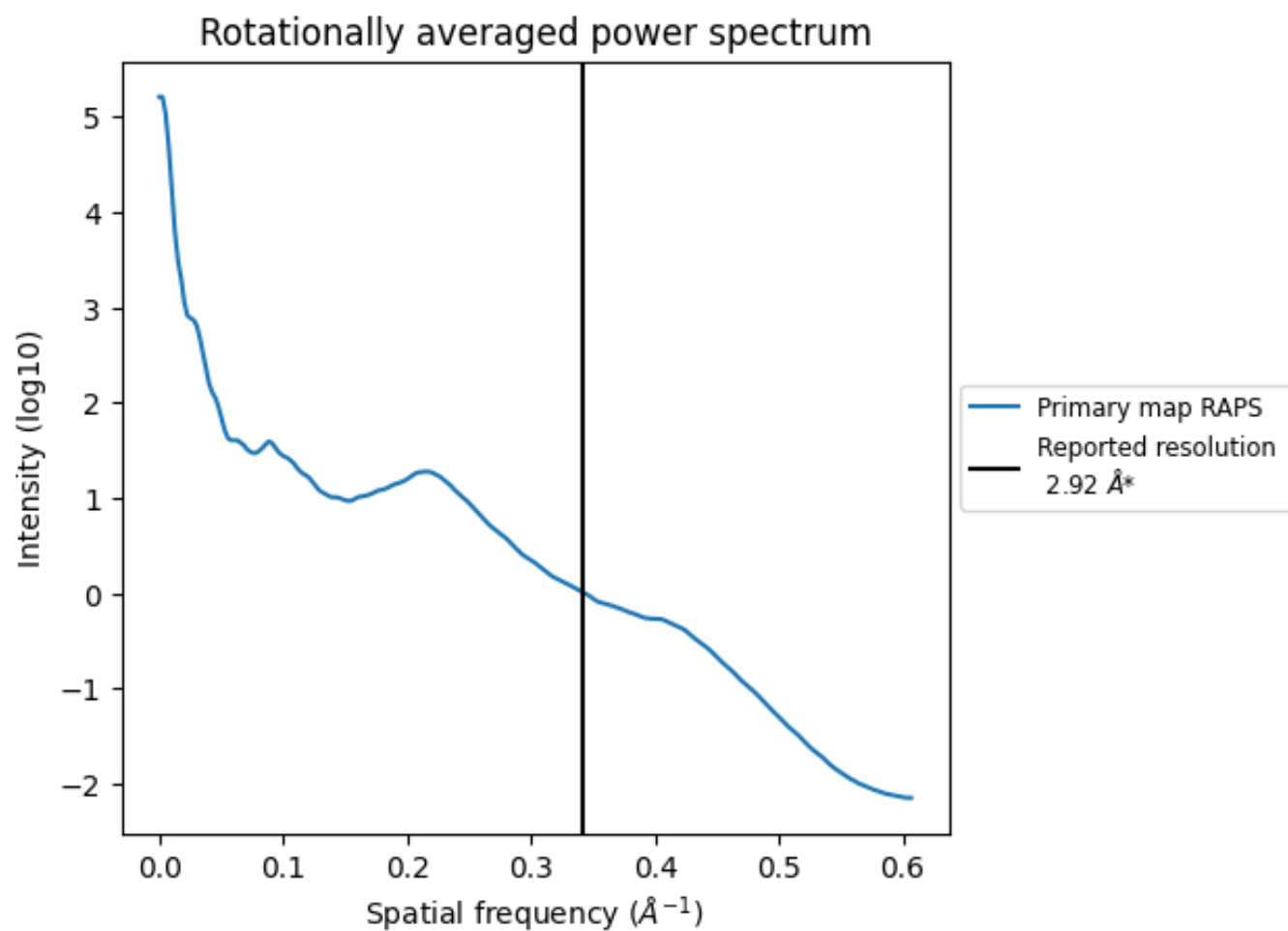


The volume at the recommended contour level is 343  $\text{nm}^3$ ; this corresponds to an approximate mass of 310 kDa.

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 0.342 Å<sup>-1</sup>

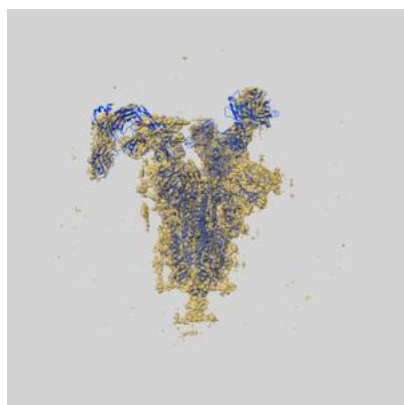
## 8 Fourier-Shell correlation

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

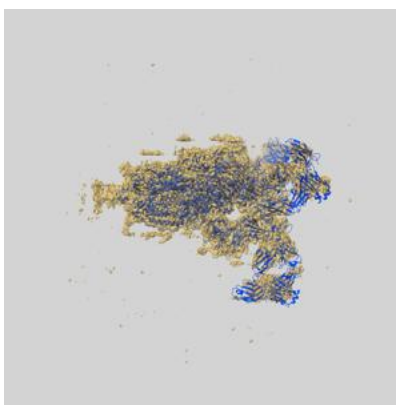
## 9 Map-model fit [i](#)

This section contains information regarding the fit between EMDB map EMD-32685 and PDB model 7WPF. Per-residue inclusion information can be found in section [3](#) on page [11](#).

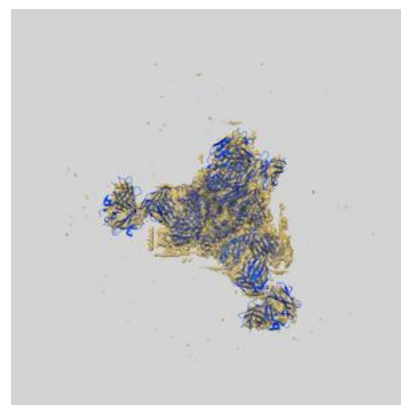
### 9.1 Map-model overlay [i](#)



X



Y



Z

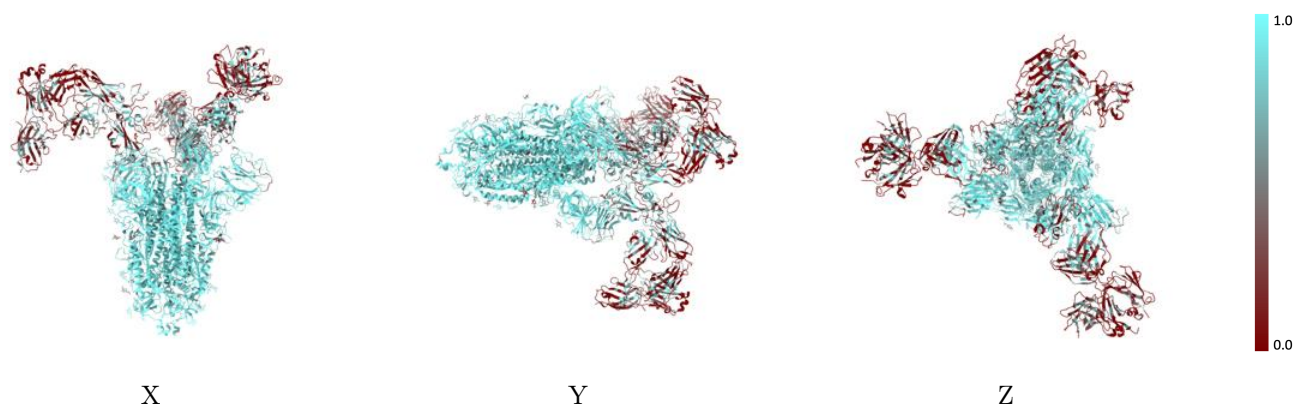
The images above show the 3D surface view of the map at the recommended contour level 0.02 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

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



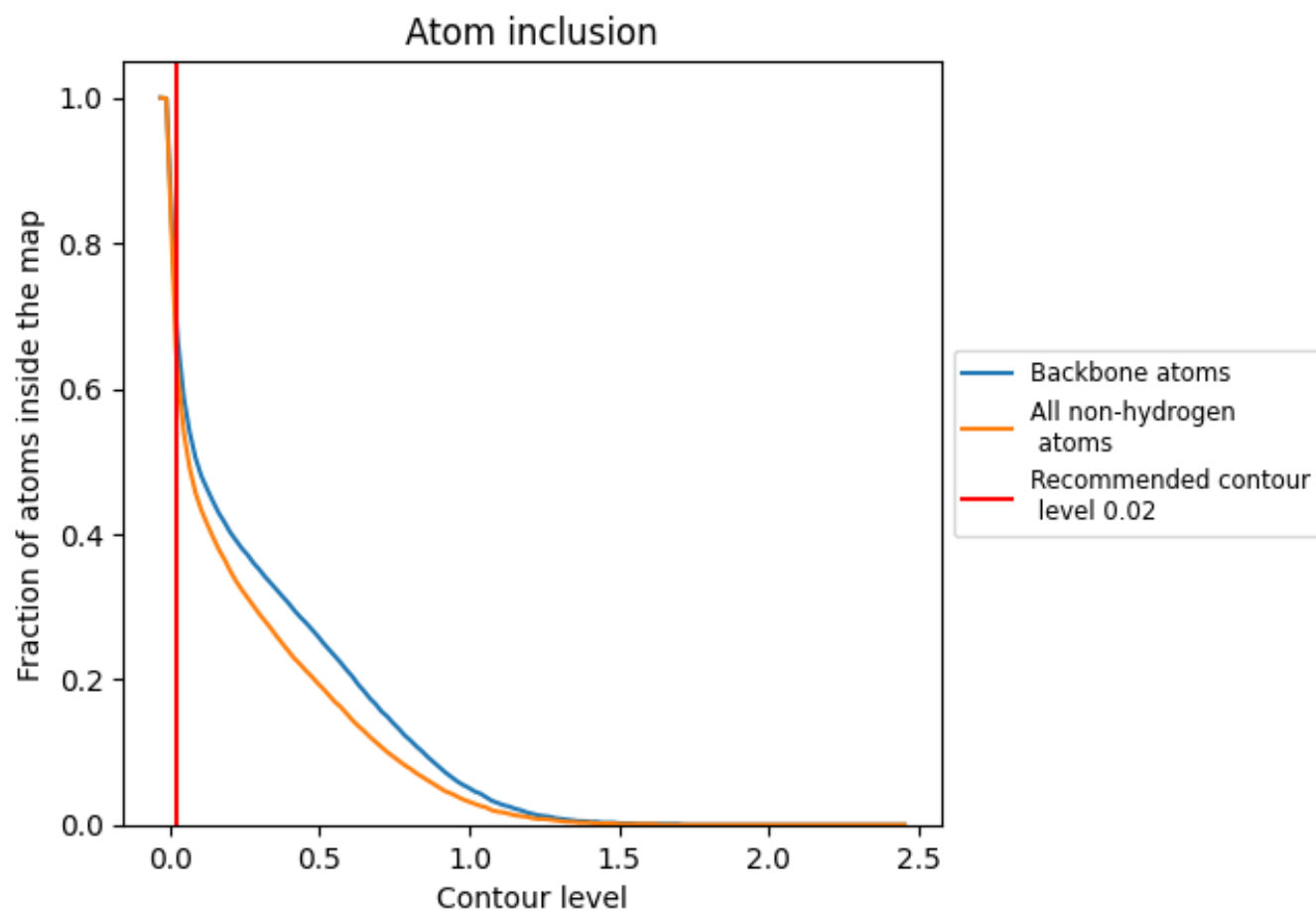
The images above show the model with each residue coloured according to its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.02).

## 9.4 Atom inclusion [i](#)



At the recommended contour level, 70% of all backbone atoms, 66% 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 (0.02) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	<div></div> 0.6560	<div></div> 0.2260
A	<div></div> 0.8410	<div></div> 0.3480
B	<div></div> 0.8090	<div></div> 0.3390
C	<div></div> 0.8820	<div></div> 0.3920
D	<div></div> 0.8930	<div></div> 0.3810
E	<div></div> 0.6070	<div></div> 0.2750
R	<div></div> 0.2640	<div></div> -0.0310
S	<div></div> 0.2730	<div></div> -0.0430
T	<div></div> 0.2500	<div></div> -0.0350
U	<div></div> 0.3200	<div></div> -0.0260
V	<div></div> 0.4480	<div></div> 0.0210
W	<div></div> 0.1290	<div></div> -0.0450
X	<div></div> 0.3210	<div></div> -0.0140
Y	<div></div> 0.3530	<div></div> -0.0200
Z	<div></div> 0.2680	<div></div> -0.0310

1.0

0.0

<0.0