Full wwPDB EM Validation Report

Feb 19, 2024 – 06:23 PM JST

PDB ID	:	8IFN
EMDB ID	:	EMD-35422
Title	:	MERS-CoV spike trimer in complex with nanobody VHH-T148
Authors	:	Wang, X.; Tian, L.
Deposited on	:	2023-02-19
Resolution	:	2.81 Å(reported)

This is a Full wwPDB EM Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/EMValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

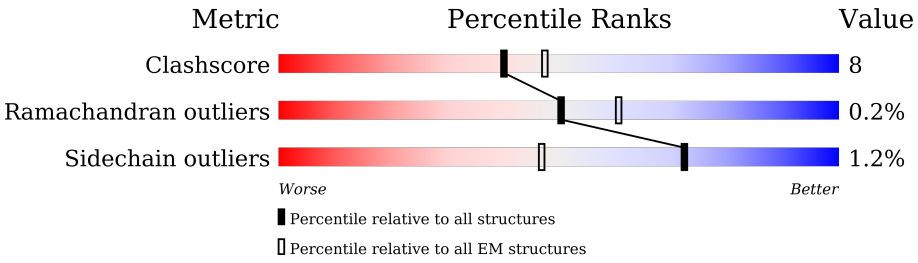
EMDB validation analysis	:	0.0.1.dev70
Mogul	:	1.8.5 (274361), CSD as541be (2020)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
MapQ	:	1.9.13
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.81 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	158937	4297
Ramachandran outliers	154571	4023
Sidechain outliers	154315	3826

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the EM map (all-atom inclusion < 40%). The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	B	1347	72% 15% 12%
1	C	1347	72% 15% 12%
1	E	1347	71% 16% 12%
2	A	135	6% 75% 20% 5%
2	D	135	5% 74% 21% 5%
2	F	135	5% 75% 20% 5%
3	G	4	100%
3	H	4	100%

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Mol	Chain	Length	Quality of chain
3	I	4	100%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 30441 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	B	1180	Total	C	N	O	S	0	0
			9124	5793	1513	1767	51		
1	C	1180	Total	C	N	O	S	0	0
			9124	5793	1513	1767	51		
1	E	1180	Total	C	N	O	S	0	0
			9124	5793	1513	1767	51		

There are 168 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	748	SER	ARG	conflict	UNP R9UQ53
B	751	GLY	ARG	conflict	UNP R9UQ53
B	1020	GLN	ARG	conflict	UNP R9UQ53
B	1060	PRO	VAL	conflict	UNP R9UQ53
B	1061	PRO	LEU	conflict	UNP R9UQ53
B	1208	GLN	HIS	conflict	UNP R9UQ53
B	1291	SER	-	insertion	UNP R9UQ53
B	1292	ARG	-	insertion	UNP R9UQ53
B	1293	GLU	-	insertion	UNP R9UQ53
B	1294	ASN	-	insertion	UNP R9UQ53
B	1295	LEU	-	insertion	UNP R9UQ53
B	1297	PHE	-	insertion	UNP R9UQ53
B	1298	GLN	-	insertion	UNP R9UQ53
B	1299	GLY	-	insertion	UNP R9UQ53
B	1300	GLY	-	insertion	UNP R9UQ53
B	1301	GLY	TYR	conflict	UNP R9UQ53
B	1302	SER	ASN	conflict	UNP R9UQ53
B	1303	ALA	LYS	conflict	UNP R9UQ53
B	1304	GLY	TRP	conflict	UNP R9UQ53
B	1305	SER	PRO	conflict	UNP R9UQ53
B	1306	GLY	TRP	conflict	UNP R9UQ53
B	1309	PRO	TRP	conflict	UNP R9UQ53
B	1310	GLU	LEU	conflict	UNP R9UQ53
B	1311	ALA	GLY	conflict	UNP R9UQ53

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1312	PRO	PHE	conflict	UNP R9UQ53
B	1313	ARG	ILE	conflict	UNP R9UQ53
B	1314	ASP	ALA	conflict	UNP R9UQ53
B	1316	GLN	LEU	conflict	UNP R9UQ53
B	1317	ALA	VAL	conflict	UNP R9UQ53
B	1318	TYR	ALA	conflict	UNP R9UQ53
B	1319	VAL	LEU	conflict	UNP R9UQ53
B	1320	ARG	ALA	conflict	UNP R9UQ53
B	1321	LYS	LEU	conflict	UNP R9UQ53
B	1322	ASP	CYS	conflict	UNP R9UQ53
B	1323	GLY	VAL	conflict	UNP R9UQ53
B	1324	GLU	PHE	conflict	UNP R9UQ53
B	1325	TRP	PHE	conflict	UNP R9UQ53
B	1326	VAL	ILE	conflict	UNP R9UQ53
B	1328	LEU	CYS	conflict	UNP R9UQ53
B	1329	SER	CYS	conflict	UNP R9UQ53
B	1331	PHE	GLY	conflict	UNP R9UQ53
B	1332	LEU	CYS	conflict	UNP R9UQ53
B	1334	HIS	-	expression tag	UNP R9UQ53
B	1335	HIS	-	expression tag	UNP R9UQ53
B	1336	HIS	-	expression tag	UNP R9UQ53
B	1337	HIS	-	expression tag	UNP R9UQ53
B	1338	HIS	-	expression tag	UNP R9UQ53
B	1339	HIS	-	expression tag	UNP R9UQ53
B	1340	TRP	-	expression tag	UNP R9UQ53
B	1341	SER	-	expression tag	UNP R9UQ53
B	1342	HIS	-	expression tag	UNP R9UQ53
B	1343	PRO	-	expression tag	UNP R9UQ53
B	1344	GLN	-	expression tag	UNP R9UQ53
B	1345	PHE	-	expression tag	UNP R9UQ53
B	1346	GLU	-	expression tag	UNP R9UQ53
B	1347	LYS	-	expression tag	UNP R9UQ53
C	748	SER	ARG	conflict	UNP R9UQ53
C	751	GLY	ARG	conflict	UNP R9UQ53
C	1020	GLN	ARG	conflict	UNP R9UQ53
C	1060	PRO	VAL	conflict	UNP R9UQ53
C	1061	PRO	LEU	conflict	UNP R9UQ53
C	1208	GLN	HIS	conflict	UNP R9UQ53
C	1291	SER	-	insertion	UNP R9UQ53
C	1292	ARG	-	insertion	UNP R9UQ53
C	1293	GLU	-	insertion	UNP R9UQ53
C	1294	ASN	-	insertion	UNP R9UQ53

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1295	LEU	-	insertion	UNP R9UQ53
C	1297	PHE	-	insertion	UNP R9UQ53
C	1298	GLN	-	insertion	UNP R9UQ53
C	1299	GLY	-	insertion	UNP R9UQ53
C	1300	GLY	-	insertion	UNP R9UQ53
C	1301	GLY	TYR	conflict	UNP R9UQ53
C	1302	SER	ASN	conflict	UNP R9UQ53
C	1303	ALA	LYS	conflict	UNP R9UQ53
C	1304	GLY	TRP	conflict	UNP R9UQ53
C	1305	SER	PRO	conflict	UNP R9UQ53
C	1306	GLY	TRP	conflict	UNP R9UQ53
C	1309	PRO	TRP	conflict	UNP R9UQ53
C	1310	GLU	LEU	conflict	UNP R9UQ53
C	1311	ALA	GLY	conflict	UNP R9UQ53
C	1312	PRO	PHE	conflict	UNP R9UQ53
C	1313	ARG	ILE	conflict	UNP R9UQ53
C	1314	ASP	ALA	conflict	UNP R9UQ53
C	1316	GLN	LEU	conflict	UNP R9UQ53
C	1317	ALA	VAL	conflict	UNP R9UQ53
C	1318	TYR	ALA	conflict	UNP R9UQ53
C	1319	VAL	LEU	conflict	UNP R9UQ53
C	1320	ARG	ALA	conflict	UNP R9UQ53
C	1321	LYS	LEU	conflict	UNP R9UQ53
C	1322	ASP	CYS	conflict	UNP R9UQ53
C	1323	GLY	VAL	conflict	UNP R9UQ53
C	1324	GLU	PHE	conflict	UNP R9UQ53
C	1325	TRP	PHE	conflict	UNP R9UQ53
C	1326	VAL	ILE	conflict	UNP R9UQ53
C	1328	LEU	CYS	conflict	UNP R9UQ53
C	1329	SER	CYS	conflict	UNP R9UQ53
C	1331	PHE	GLY	conflict	UNP R9UQ53
C	1332	LEU	CYS	conflict	UNP R9UQ53
C	1334	HIS	-	expression tag	UNP R9UQ53
C	1335	HIS	-	expression tag	UNP R9UQ53
C	1336	HIS	-	expression tag	UNP R9UQ53
C	1337	HIS	-	expression tag	UNP R9UQ53
C	1338	HIS	-	expression tag	UNP R9UQ53
C	1339	HIS	-	expression tag	UNP R9UQ53
C	1340	TRP	-	expression tag	UNP R9UQ53
C	1341	SER	-	expression tag	UNP R9UQ53
C	1342	HIS	-	expression tag	UNP R9UQ53
C	1343	PRO	-	expression tag	UNP R9UQ53

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1344	GLN	-	expression tag	UNP R9UQ53
C	1345	PHE	-	expression tag	UNP R9UQ53
C	1346	GLU	-	expression tag	UNP R9UQ53
C	1347	LYS	-	expression tag	UNP R9UQ53
E	748	SER	ARG	conflict	UNP R9UQ53
E	751	GLY	ARG	conflict	UNP R9UQ53
E	1020	GLN	ARG	conflict	UNP R9UQ53
E	1060	PRO	VAL	conflict	UNP R9UQ53
E	1061	PRO	LEU	conflict	UNP R9UQ53
E	1208	GLN	HIS	conflict	UNP R9UQ53
E	1291	SER	-	insertion	UNP R9UQ53
E	1292	ARG	-	insertion	UNP R9UQ53
E	1293	GLU	-	insertion	UNP R9UQ53
E	1294	ASN	-	insertion	UNP R9UQ53
E	1295	LEU	-	insertion	UNP R9UQ53
E	1297	PHE	-	insertion	UNP R9UQ53
E	1298	GLN	-	insertion	UNP R9UQ53
E	1299	GLY	-	insertion	UNP R9UQ53
E	1300	GLY	-	insertion	UNP R9UQ53
E	1301	GLY	TYR	conflict	UNP R9UQ53
E	1302	SER	ASN	conflict	UNP R9UQ53
E	1303	ALA	LYS	conflict	UNP R9UQ53
E	1304	GLY	TRP	conflict	UNP R9UQ53
E	1305	SER	PRO	conflict	UNP R9UQ53
E	1306	GLY	TRP	conflict	UNP R9UQ53
E	1309	PRO	TRP	conflict	UNP R9UQ53
E	1310	GLU	LEU	conflict	UNP R9UQ53
E	1311	ALA	GLY	conflict	UNP R9UQ53
E	1312	PRO	PHE	conflict	UNP R9UQ53
E	1313	ARG	ILE	conflict	UNP R9UQ53
E	1314	ASP	ALA	conflict	UNP R9UQ53
E	1316	GLN	LEU	conflict	UNP R9UQ53
E	1317	ALA	VAL	conflict	UNP R9UQ53
E	1318	TYR	ALA	conflict	UNP R9UQ53
E	1319	VAL	LEU	conflict	UNP R9UQ53
E	1320	ARG	ALA	conflict	UNP R9UQ53
E	1321	LYS	LEU	conflict	UNP R9UQ53
E	1322	ASP	CYS	conflict	UNP R9UQ53
E	1323	GLY	VAL	conflict	UNP R9UQ53
E	1324	GLU	PHE	conflict	UNP R9UQ53
E	1325	TRP	PHE	conflict	UNP R9UQ53
E	1326	VAL	ILE	conflict	UNP R9UQ53

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Chain	Residue	Modelled	Actual	Comment	Reference
E	1328	LEU	CYS	conflict	UNP R9UQ53
E	1329	SER	CYS	conflict	UNP R9UQ53
E	1331	PHE	GLY	conflict	UNP R9UQ53
E	1332	LEU	CYS	conflict	UNP R9UQ53
E	1334	HIS	-	expression tag	UNP R9UQ53
E	1335	HIS	-	expression tag	UNP R9UQ53
E	1336	HIS	-	expression tag	UNP R9UQ53
E	1337	HIS	-	expression tag	UNP R9UQ53
E	1338	HIS	-	expression tag	UNP R9UQ53
E	1339	HIS	-	expression tag	UNP R9UQ53
E	1340	TRP	-	expression tag	UNP R9UQ53
E	1341	SER	-	expression tag	UNP R9UQ53
E	1342	HIS	-	expression tag	UNP R9UQ53
E	1343	PRO	-	expression tag	UNP R9UQ53
E	1344	GLN	-	expression tag	UNP R9UQ53
E	1345	PHE	-	expression tag	UNP R9UQ53
E	1346	GLU	-	expression tag	UNP R9UQ53
E	1347	LYS	-	expression tag	UNP R9UQ53

- Molecule 2 is a protein called VHH-T148.

Mol	Chain	Residues	Atoms					AltConf	Trace
2	A	128	Total	C	N	O	S	0	0
			973	609	160	197	7		
2	D	128	Total	C	N	O	S	0	0
			973	609	160	197	7		
2	F	128	Total	C	N	O	S	0	0
			973	609	160	197	7		

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.

Mol	Chain	Residues	Atoms				AltConf	Trace
3	G	4	Total	C	N	O	0	0
			50	28	2	20		
3	H	4	Total	C	N	O	0	0
			50	28	2	20		

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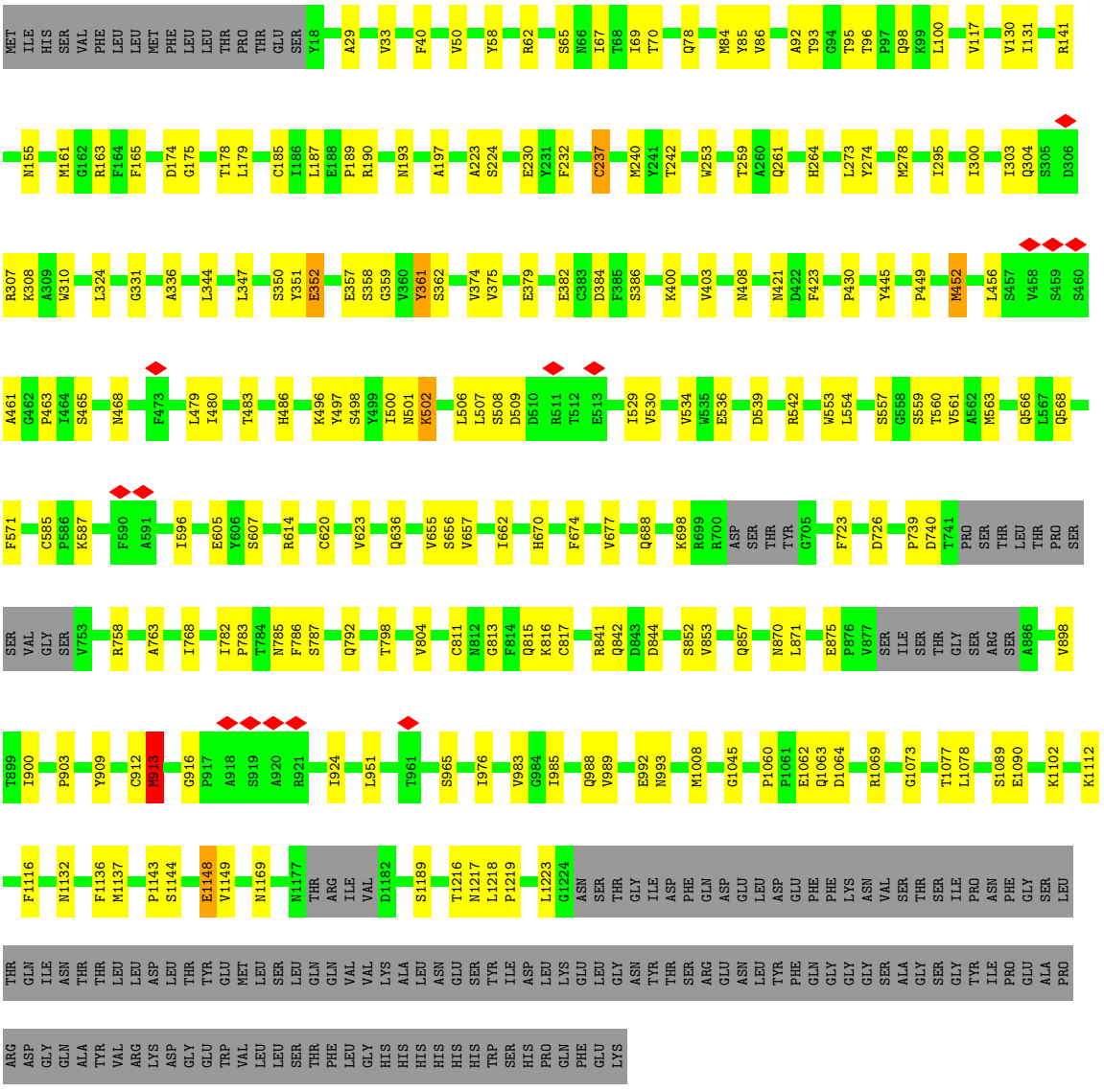
Mol	Chain	Residues	Atoms				AltConf	Trace
3	I	4	Total	C	N	O	0	0
			50	28	2	20		

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and atom inclusion in map density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red diamond above a residue indicates a poor fit to the EM map for this residue (all-atom inclusion < 40%). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

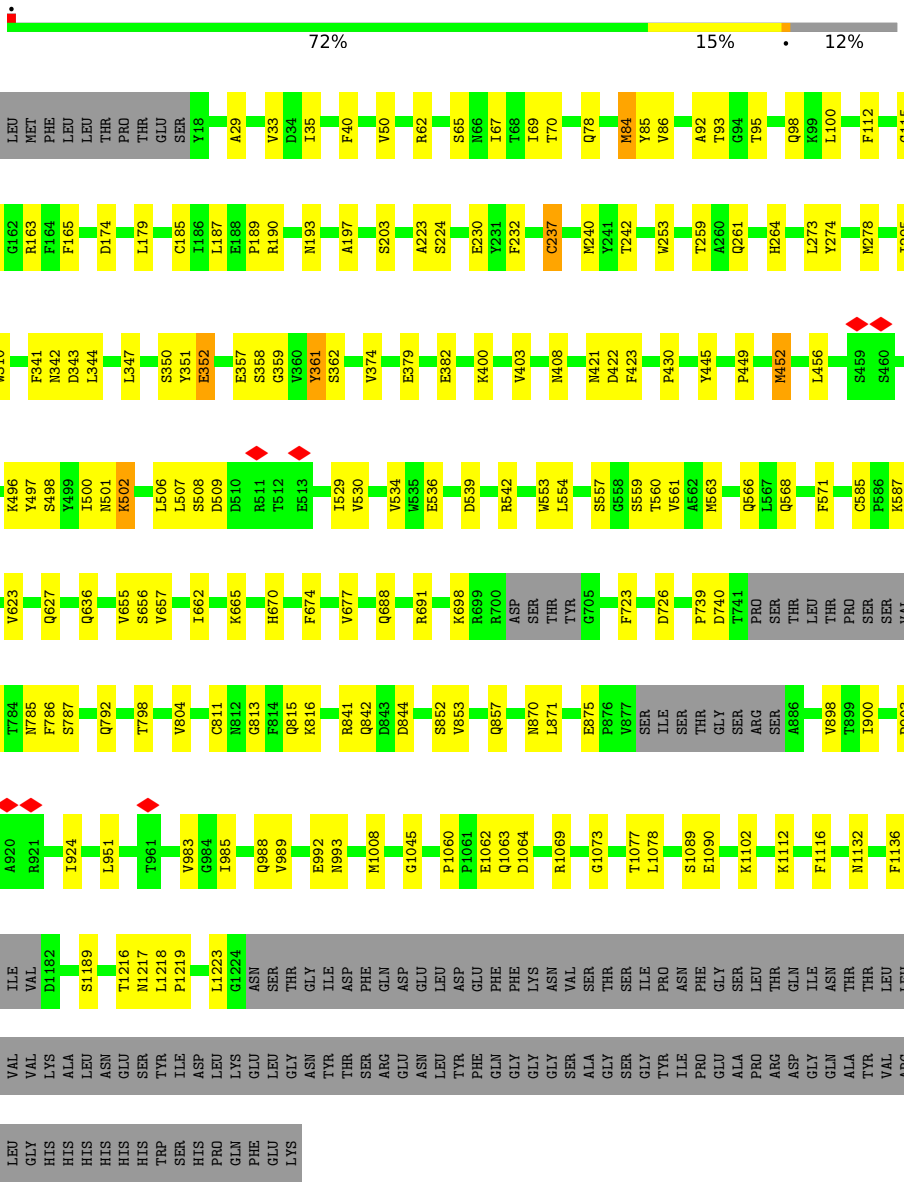
• Molecule 1: Spike glycoprotein

Chain B:



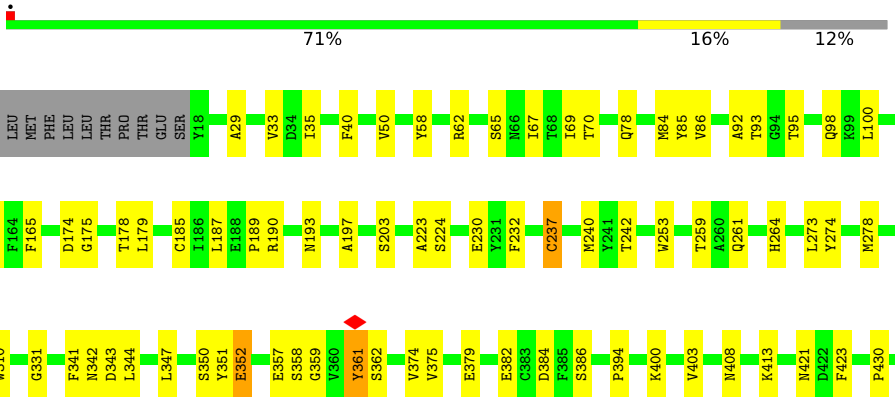
• Molecule 1: Spike glycoprotein

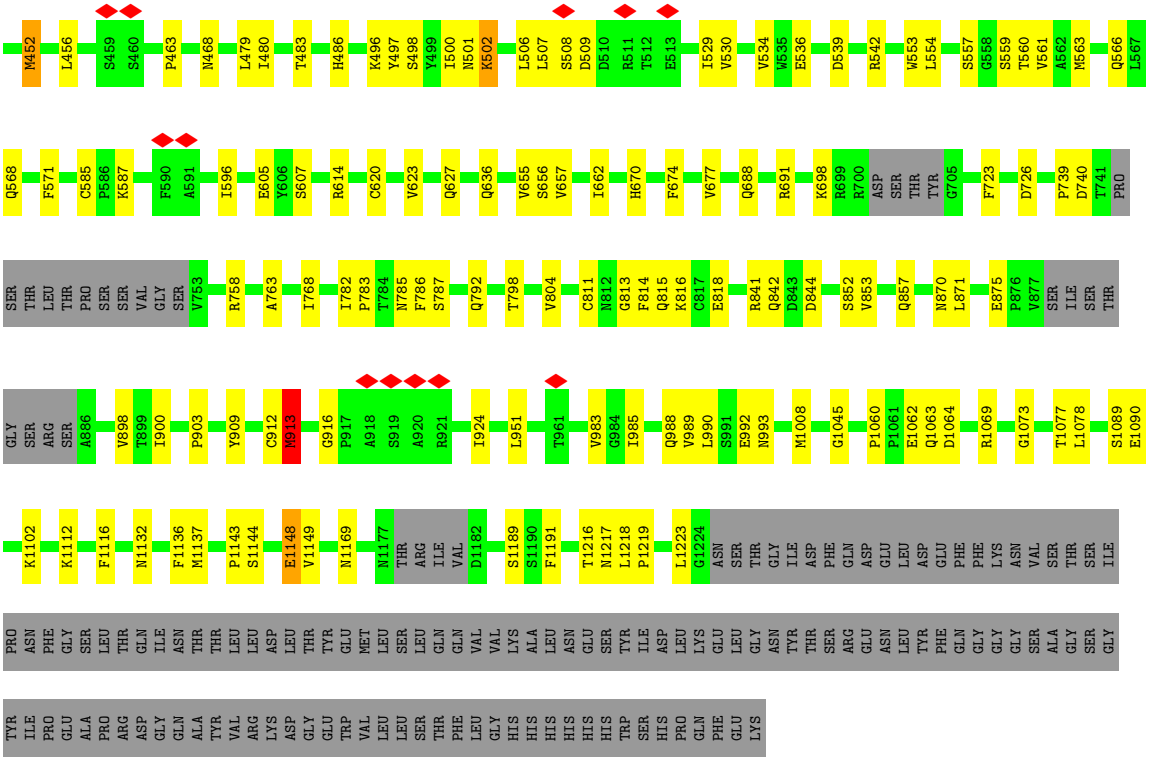
Chain C:



• Molecule 1: Spike glycoprotein

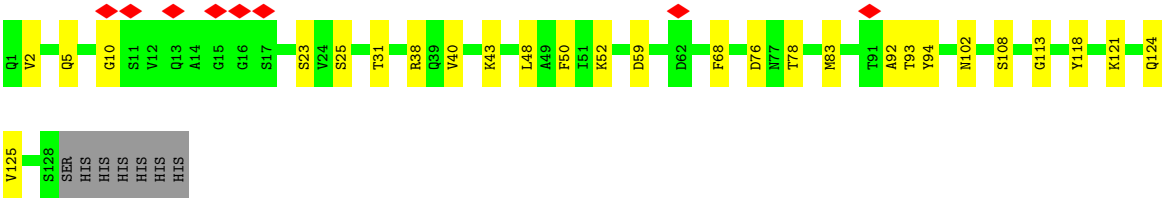
Chain E:





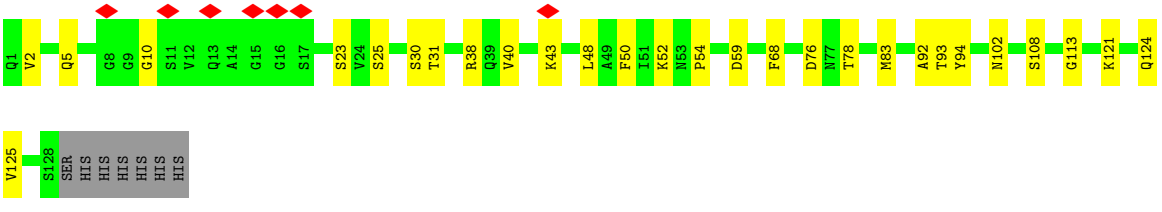
• Molecule 2: VHH-T148

Chain A:



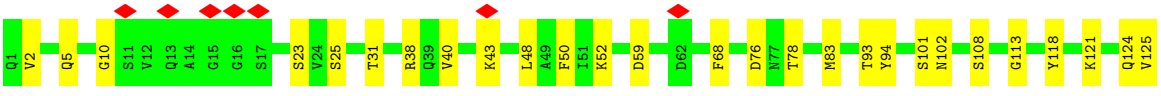
• Molecule 2: VHH-T148

Chain D:



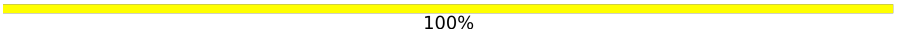
• Molecule 2: VHH-T148

Chain F:



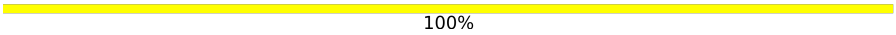
• Molecule 3: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain G:



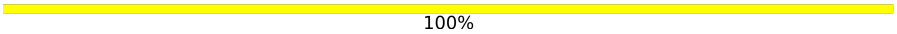
• Molecule 3: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain H:



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

Chain I:



4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	216306	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	NONE	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ($e^-/Å^2$)	50	Depositor
Minimum defocus (nm)	1500	Depositor
Maximum defocus (nm)	1800	Depositor
Magnification	Not provided	
Image detector	GATAN K3 (6k x 4k)	Depositor
Maximum map value	0.143	Depositor
Minimum map value	-0.067	Depositor
Average map value	0.000	Depositor
Map value standard deviation	0.003	Depositor
Recommended contour level	0.0116	Depositor
Map size (Å)	303.1, 303.1, 303.1	wwPDB
Map dimensions	280, 280, 280	wwPDB
Map angles (°)	90.0, 90.0, 90.0	wwPDB
Pixel spacing (Å)	1.0825, 1.0825, 1.0825	Depositor

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: BMA, MAN, 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	B	0.47	0/9336	0.57	6/12701 (0.0%)
1	C	0.47	0/9336	0.57	6/12701 (0.0%)
1	E	0.47	0/9336	0.57	6/12701 (0.0%)
2	A	0.35	0/994	0.50	0/1346
2	D	0.35	0/994	0.50	0/1346
2	F	0.34	0/994	0.50	0/1346
All	All	0.46	0/30990	0.56	18/42141 (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
1	B	0	3
1	C	0	3
1	E	0	3
All	All	0	9

There are no bond length outliers.

All (18) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	E	913	MET	CA-CB-CG	9.47	129.40	113.30
1	C	913	MET	CA-CB-CG	9.44	129.35	113.30
1	B	913	MET	CA-CB-CG	9.44	129.34	113.30
1	C	237	CYS	CA-CB-SG	9.00	130.21	114.00
1	B	237	CYS	CA-CB-SG	8.99	130.19	114.00
1	E	237	CYS	CA-CB-SG	8.99	130.19	114.00
1	E	913	MET	CB-CG-SD	8.63	138.31	112.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	913	MET	CB-CG-SD	8.62	138.25	112.40
1	C	913	MET	CB-CG-SD	8.62	138.25	112.40
1	E	185	CYS	CA-CB-SG	7.99	128.38	114.00
1	C	185	CYS	CA-CB-SG	7.99	128.38	114.00
1	B	185	CYS	CA-CB-SG	7.98	128.36	114.00
1	B	913	MET	CG-SD-CE	6.18	110.09	100.20
1	E	913	MET	CG-SD-CE	6.18	110.08	100.20
1	C	913	MET	CG-SD-CE	6.14	110.03	100.20
1	B	620	CYS	CA-CB-SG	5.75	124.36	114.00
1	E	620	CYS	CA-CB-SG	5.75	124.35	114.00
1	C	620	CYS	CA-CB-SG	5.74	124.33	114.00

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	1148	GLU	Peptide
1	B	237	CYS	Peptide
1	B	361	TYR	Peptide
1	C	1148	GLU	Peptide
1	C	237	CYS	Peptide
1	C	361	TYR	Peptide
1	E	1148	GLU	Peptide
1	E	237	CYS	Peptide
1	E	361	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	B	9124	0	8818	137	0
1	C	9124	0	8818	138	0
1	E	9124	0	8818	141	0
2	A	973	0	916	17	0
2	D	973	0	916	17	0
2	F	973	0	916	17	0
3	G	50	0	43	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	50	0	43	2	0
3	I	50	0	43	3	0
All	All	30441	0	29331	451	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.

All (451) 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:C:483:THR:HG22	1:C:568:GLN:HG2	1.65	0.79
1:B:483:THR:HG22	1:B:568:GLN:HG2	1.65	0.78
1:C:506:LEU:HB2	1:C:553:TRP:HB2	1.66	0.78
1:E:483:THR:HG22	1:E:568:GLN:HG2	1.65	0.78
1:E:95:THR:HA	1:E:303:ILE:HD12	1.66	0.77
1:B:506:LEU:HB2	1:B:553:TRP:HB2	1.66	0.77
1:E:506:LEU:HB2	1:E:553:TRP:HB2	1.66	0.77
1:B:95:THR:HA	1:B:303:ILE:HD12	1.67	0.77
1:B:804:VAL:HG11	1:B:1078:LEU:HD11	1.67	0.76
1:C:804:VAL:HG11	1:C:1078:LEU:HD11	1.67	0.76
1:E:804:VAL:HG11	1:E:1078:LEU:HD11	1.68	0.75
1:C:95:THR:HA	1:C:303:ILE:HD12	1.67	0.75
1:B:655:VAL:HB	1:C:913:MET:SD	2.28	0.74
1:B:913:MET:SD	1:E:655:VAL:HB	2.27	0.74
1:C:655:VAL:HB	1:E:913:MET:SD	2.27	0.73
1:E:92:ALA:O	1:E:304:GLN:NE2	2.18	0.73
1:B:816:LYS:NZ	1:B:1064:ASP:OD1	2.20	0.73
1:E:816:LYS:NZ	1:E:1064:ASP:OD1	2.21	0.72
1:C:816:LYS:NZ	1:C:1064:ASP:OD1	2.20	0.72
1:B:496:LYS:HD3	1:B:560:THR:HG21	1.72	0.72
1:B:92:ALA:O	1:B:304:GLN:NE2	2.18	0.71
1:B:423:PHE:HD1	1:B:480:ILE:HG12	1.55	0.71
1:C:92:ALA:O	1:C:304:GLN:NE2	2.18	0.71
1:B:841:ARG:NH1	1:B:1090:GLU:OE1	2.22	0.70
1:E:496:LYS:HD3	1:E:560:THR:HG21	1.71	0.70
1:C:496:LYS:HD3	1:C:560:THR:HG21	1.72	0.70
1:C:423:PHE:HD1	1:C:480:ILE:HG12	1.55	0.70
3:H:1:NAG:HO4	3:H:2:NAG:C1	2.04	0.70
1:E:423:PHE:HD1	1:E:480:ILE:HG12	1.55	0.70
1:E:382:GLU:HB2	2:F:31:THR:HG21	1.73	0.70
1:C:507:LEU:HD23	1:C:509:ASP:H	1.58	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:507:LEU:HD23	1:B:509:ASP:H	1.58	0.68
1:B:785:ASN:OD1	1:B:786:PHE:N	2.27	0.68
1:E:507:LEU:HD23	1:E:509:ASP:H	1.58	0.68
1:E:841:ARG:NH1	1:E:1090:GLU:OE1	2.22	0.68
1:E:785:ASN:OD1	1:E:786:PHE:N	2.27	0.68
1:E:33:VAL:HG22	1:E:100:LEU:HD12	1.77	0.67
1:C:785:ASN:OD1	1:C:786:PHE:N	2.27	0.67
1:B:501:ASN:ND2	1:B:559:SER:OG	2.29	0.65
1:C:33:VAL:HG22	1:C:100:LEU:HD12	1.77	0.65
1:B:33:VAL:HG22	1:B:100:LEU:HD12	1.77	0.65
1:B:253:TRP:HB3	1:B:278:MET:SD	2.37	0.65
1:E:501:ASN:ND2	1:E:559:SER:OG	2.29	0.65
1:C:501:ASN:ND2	1:C:559:SER:OG	2.29	0.65
1:E:253:TRP:HB3	1:E:278:MET:SD	2.37	0.65
1:C:841:ARG:NH1	1:C:1090:GLU:OE1	2.22	0.65
1:C:253:TRP:HB3	1:C:278:MET:SD	2.37	0.64
1:B:480:ILE:HB	1:B:571:PHE:HB2	1.80	0.63
3:G:1:NAG:C4	3:G:2:NAG:C1	2.76	0.63
3:H:1:NAG:C4	3:H:2:NAG:C1	2.76	0.62
1:C:480:ILE:HB	1:C:571:PHE:HB2	1.80	0.62
1:E:605:GLU:OE2	1:E:614:ARG:NE	2.30	0.62
3:I:1:NAG:C4	3:I:2:NAG:C1	2.76	0.62
1:C:605:GLU:OE2	1:C:614:ARG:NE	2.30	0.62
1:E:480:ILE:HB	1:E:571:PHE:HB2	1.80	0.62
3:G:1:NAG:HO4	3:G:2:NAG:C1	2.08	0.61
1:C:141:ARG:HD3	1:C:308:LYS:HD3	1.83	0.61
1:E:989:VAL:O	1:E:993:ASN:HB2	2.01	0.60
2:A:52:LYS:HG3	2:A:102:ASN:OD1	2.01	0.60
1:B:989:VAL:O	1:B:993:ASN:HB2	2.01	0.60
1:C:989:VAL:O	1:C:993:ASN:HB2	2.01	0.60
1:E:898:VAL:HG12	1:E:900:ILE:HG23	1.83	0.60
2:F:52:LYS:HG3	2:F:102:ASN:OD1	2.01	0.60
1:B:605:GLU:OE2	1:B:614:ARG:NE	2.30	0.60
1:B:1218:LEU:HD12	1:B:1219:PRO:HD2	1.84	0.60
1:C:1218:LEU:HD12	1:C:1219:PRO:HD2	1.84	0.60
1:E:141:ARG:HD3	1:E:308:LYS:HD3	1.83	0.60
1:E:423:PHE:CD1	1:E:480:ILE:HG12	2.36	0.60
1:C:300:ILE:HD13	1:C:310:TRP:HE1	1.67	0.60
1:E:300:ILE:HD13	1:E:310:TRP:HE1	1.67	0.60
1:E:1218:LEU:HD12	1:E:1219:PRO:HD2	1.84	0.60
1:C:423:PHE:CD1	1:C:480:ILE:HG12	2.36	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:983:VAL:O	1:E:985:ILE:N	2.35	0.59
1:C:898:VAL:HG12	1:C:900:ILE:HG23	1.83	0.59
1:B:300:ILE:HD13	1:B:310:TRP:HE1	1.67	0.59
1:B:898:VAL:HG12	1:B:900:ILE:HG23	1.83	0.59
1:C:983:VAL:O	1:C:985:ILE:N	2.35	0.59
1:B:141:ARG:HD3	1:B:308:LYS:HD3	1.83	0.59
1:B:423:PHE:CD1	1:B:480:ILE:HG12	2.36	0.59
1:C:259:THR:OG1	1:C:264:HIS:NE2	2.31	0.59
1:C:1045:GLY:HA3	1:C:1069:ARG:HH21	1.68	0.59
2:D:52:LYS:HG3	2:D:102:ASN:OD1	2.01	0.59
1:C:50:VAL:HG22	1:C:78:GLN:NE2	2.18	0.59
1:B:983:VAL:O	1:B:985:ILE:N	2.35	0.59
1:B:1045:GLY:HA3	1:B:1069:ARG:HH21	1.68	0.58
1:E:357:GLU:HG3	1:E:358:SER:H	1.68	0.58
1:C:347:LEU:HD12	1:C:361:TYR:CD2	2.38	0.58
1:E:347:LEU:HD12	1:E:361:TYR:CD2	2.38	0.58
1:B:50:VAL:HG22	1:B:78:GLN:NE2	2.18	0.58
1:B:449:PRO:HG2	1:B:452:MET:HE1	1.85	0.58
1:E:50:VAL:HG22	1:E:78:GLN:NE2	2.18	0.58
1:C:449:PRO:HG2	1:C:452:MET:HE1	1.85	0.57
1:C:636:GLN:OE1	1:E:62:ARG:NH1	2.37	0.57
1:B:347:LEU:HD12	1:B:361:TYR:CD2	2.38	0.57
1:E:1045:GLY:HA3	1:E:1069:ARG:HH21	1.68	0.57
1:B:1102:LYS:NZ	1:B:1116:PHE:O	2.38	0.57
1:C:357:GLU:HG3	1:C:358:SER:H	1.68	0.57
1:B:985:ILE:HD13	1:B:1169:ASN:HB3	1.86	0.57
1:C:361:TYR:HB3	1:C:362:SER:O	2.04	0.57
1:B:62:ARG:NH1	1:E:636:GLN:OE1	2.38	0.57
1:C:1102:LYS:NZ	1:C:1116:PHE:O	2.38	0.57
1:C:985:ILE:HD13	1:C:1169:ASN:HB3	1.86	0.57
1:E:361:TYR:HB3	1:E:362:SER:O	2.04	0.57
1:B:382:GLU:HB2	2:A:31:THR:HG21	1.87	0.57
1:E:423:PHE:CE2	1:E:430:PRO:HB3	2.40	0.57
1:E:1102:LYS:NZ	1:E:1116:PHE:O	2.38	0.57
3:I:1:NAG:HO4	3:I:2:NAG:C1	2.12	0.57
1:B:361:TYR:HB3	1:B:362:SER:O	2.04	0.56
1:B:636:GLN:OE1	1:C:62:ARG:NH1	2.38	0.56
1:B:357:GLU:HG3	1:B:358:SER:H	1.68	0.56
1:C:163:ARG:HH21	1:C:189:PRO:HD3	1.70	0.56
1:B:223:ALA:O	1:B:224:SER:OG	2.24	0.56
1:C:423:PHE:CE2	1:C:430:PRO:HB3	2.40	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:449:PRO:HG2	1:E:452:MET:HE1	1.88	0.56
1:C:40:PHE:HD2	1:C:86:VAL:HG13	1.71	0.56
1:E:985:ILE:HD13	1:E:1169:ASN:HB3	1.86	0.56
1:E:40:PHE:HD2	1:E:86:VAL:HG13	1.71	0.56
1:B:40:PHE:HD2	1:B:86:VAL:HG13	1.71	0.55
1:B:423:PHE:CE2	1:B:430:PRO:HB3	2.40	0.55
1:E:223:ALA:O	1:E:224:SER:OG	2.24	0.55
1:C:1008:MET:SD	1:C:1137:MET:HG2	2.47	0.55
1:B:723:PHE:HB3	1:B:763:ALA:HB2	1.89	0.55
1:C:674:PHE:O	1:C:677:VAL:HG22	2.06	0.55
1:B:1008:MET:SD	1:B:1137:MET:HG2	2.47	0.55
1:C:223:ALA:O	1:C:224:SER:OG	2.24	0.55
1:E:723:PHE:HB3	1:E:763:ALA:HB2	1.89	0.55
1:E:674:PHE:O	1:E:677:VAL:HG22	2.06	0.55
2:A:68:PHE:CE1	2:A:83:MET:HG3	2.42	0.54
2:D:40:VAL:HG23	2:D:43:LYS:HB2	1.89	0.54
1:E:163:ARG:HH21	1:E:189:PRO:HD3	1.70	0.54
1:B:163:ARG:HH21	1:B:189:PRO:HD3	1.70	0.54
1:C:853:VAL:HG13	1:C:951:LEU:HD22	1.90	0.54
1:B:498:SER:HB3	1:B:534:VAL:HG23	1.89	0.54
1:E:1008:MET:SD	1:E:1137:MET:HG2	2.47	0.54
2:F:68:PHE:CE1	2:F:83:MET:HG3	2.42	0.54
1:B:875:GLU:N	1:B:875:GLU:OE1	2.40	0.54
1:B:674:PHE:O	1:B:677:VAL:HG22	2.06	0.54
1:E:498:SER:HB3	1:E:534:VAL:HG23	1.89	0.54
1:E:875:GLU:OE1	1:E:875:GLU:N	2.40	0.54
1:B:740:ASP:OD1	1:B:758:ARG:NH1	2.41	0.54
1:B:853:VAL:HG13	1:B:951:LEU:HD22	1.90	0.54
1:C:723:PHE:HB3	1:C:763:ALA:HB2	1.89	0.54
2:D:68:PHE:CE1	2:D:83:MET:HG3	2.42	0.54
2:A:40:VAL:HG23	2:A:43:LYS:HB2	1.89	0.53
1:C:382:GLU:HB2	2:D:31:THR:HG21	1.90	0.53
1:C:740:ASP:OD1	1:C:758:ARG:NH1	2.41	0.53
1:C:498:SER:HB3	1:C:534:VAL:HG23	1.89	0.53
1:E:740:ASP:OD1	1:E:758:ARG:NH1	2.41	0.53
2:F:40:VAL:HG23	2:F:43:LYS:HB2	1.89	0.53
1:C:875:GLU:OE1	1:C:875:GLU:N	2.40	0.53
1:B:421:ASN:OD1	1:B:483:THR:HG23	2.09	0.53
1:E:352:GLU:OE1	1:E:352:GLU:HA	2.09	0.53
1:E:853:VAL:HG13	1:E:951:LEU:HD22	1.90	0.53
1:C:403:VAL:HG11	1:E:261:GLN:HG3	1.91	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:421:ASN:OD1	1:E:483:THR:HG23	2.09	0.53
1:B:261:GLN:HG3	1:E:403:VAL:HG11	1.90	0.52
1:B:403:VAL:HG11	1:C:261:GLN:HG3	1.90	0.52
1:C:912:CYS:O	1:C:916:GLY:HA2	2.10	0.52
1:B:179:LEU:HD12	1:B:242:THR:HG23	1.92	0.52
1:E:179:LEU:HD12	1:E:242:THR:HG23	1.92	0.52
1:E:1216:THR:HG23	1:E:1217:ASN:H	1.75	0.52
1:B:909:TYR:CG	1:E:677:VAL:HG12	2.45	0.52
1:B:912:CYS:O	1:B:916:GLY:HA2	2.10	0.52
1:C:421:ASN:OD1	1:C:483:THR:HG23	2.09	0.52
1:B:657:VAL:HG13	1:B:677:VAL:HG11	1.92	0.52
1:B:688:GLN:OE1	1:B:688:GLN:N	2.41	0.52
1:B:1216:THR:HG23	1:B:1217:ASN:H	1.75	0.51
1:E:688:GLN:OE1	1:E:688:GLN:N	2.41	0.51
1:B:259:THR:OG1	1:B:264:HIS:NE2	2.31	0.51
1:C:352:GLU:HA	1:C:352:GLU:OE1	2.09	0.51
1:B:352:GLU:OE1	1:B:352:GLU:HA	2.09	0.51
1:C:179:LEU:HD12	1:C:242:THR:HG23	1.92	0.51
1:E:58:TYR:OH	1:E:331:GLY:O	2.19	0.51
2:D:2:VAL:HA	2:D:25:SER:O	2.11	0.51
1:E:912:CYS:O	1:E:916:GLY:HA2	2.10	0.51
1:E:657:VAL:HG13	1:E:677:VAL:HG11	1.92	0.51
1:C:657:VAL:HG13	1:C:677:VAL:HG11	1.92	0.50
1:C:677:VAL:HG12	1:E:909:TYR:CG	2.45	0.50
1:C:1216:THR:HG23	1:C:1217:ASN:H	1.75	0.50
1:E:85:TYR:CE1	1:E:295:ILE:HG13	2.47	0.50
2:A:2:VAL:HA	2:A:25:SER:O	2.11	0.50
1:C:811:CYS:O	1:C:813:GLY:N	2.43	0.50
1:C:842:GLN:HE21	1:C:1089:SER:HB2	1.76	0.50
1:B:811:CYS:O	1:B:813:GLY:N	2.43	0.50
2:F:2:VAL:HA	2:F:25:SER:O	2.11	0.50
1:B:677:VAL:HG12	1:C:909:TYR:CG	2.46	0.50
2:A:108:SER:OG	2:A:113:GLY:HA2	2.12	0.50
1:E:117:VAL:HG12	1:E:278:MET:HE1	1.94	0.50
1:E:502:LYS:HB2	1:E:557:SER:OG	2.12	0.50
1:C:502:LYS:HB2	1:C:557:SER:OG	2.12	0.50
2:F:118:TYR:HE1	3:I:2:NAG:HO6	1.57	0.49
1:B:502:LYS:HB2	1:B:557:SER:OG	2.12	0.49
1:C:85:TYR:CE1	1:C:295:ILE:HG13	2.46	0.49
1:B:842:GLN:HE21	1:B:1089:SER:HB2	1.77	0.49
1:C:117:VAL:HG12	1:C:278:MET:HE1	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:108:SER:OG	2:D:113:GLY:HA2	2.12	0.49
1:E:811:CYS:O	1:E:813:GLY:N	2.43	0.49
1:B:85:TYR:CE1	1:B:295:ILE:HG13	2.47	0.49
1:E:374:VAL:HG11	1:E:596:ILE:HG13	1.95	0.49
1:B:988:GLN:O	1:B:992:GLU:HG2	2.13	0.49
1:E:842:GLN:HE21	1:E:1089:SER:HB2	1.77	0.49
1:E:988:GLN:O	1:E:992:GLU:HG2	2.13	0.49
2:F:108:SER:OG	2:F:113:GLY:HA2	2.12	0.49
1:B:1218:LEU:HD23	1:B:1223:LEU:HD23	1.95	0.48
1:C:688:GLN:OE1	1:C:688:GLN:N	2.41	0.48
1:C:785:ASN:HD21	1:C:787:SER:HB2	1.78	0.48
1:B:347:LEU:HD12	1:B:361:TYR:CE2	2.48	0.48
1:B:374:VAL:HG11	1:B:596:ILE:HG13	1.95	0.48
1:B:384:ASP:OD1	1:B:386:SER:OG	2.26	0.48
1:E:785:ASN:HD21	1:E:787:SER:HB2	1.78	0.48
1:E:1218:LEU:HD23	1:E:1223:LEU:HD23	1.95	0.48
1:B:739:PRO:O	1:B:758:ARG:NH1	2.47	0.48
1:C:374:VAL:HG11	1:C:596:ILE:HG13	1.95	0.48
1:C:988:GLN:O	1:C:992:GLU:HG2	2.13	0.48
1:E:347:LEU:HD12	1:E:361:TYR:CE2	2.48	0.48
1:B:117:VAL:HG12	1:B:278:MET:HE1	1.94	0.48
1:C:1218:LEU:HD23	1:C:1223:LEU:HD23	1.95	0.48
2:D:76:ASP:HB3	2:D:78:THR:HG22	1.95	0.48
1:C:347:LEU:HD12	1:C:361:TYR:CE2	2.48	0.48
1:B:785:ASN:HD21	1:B:787:SER:HB2	1.78	0.48
2:A:76:ASP:HB3	2:A:78:THR:HG22	1.95	0.48
1:E:130:VAL:HG11	1:E:307:ARG:HD3	1.96	0.48
1:B:163:ARG:HH11	1:B:165:PHE:HE2	1.62	0.47
2:F:76:ASP:HB3	2:F:78:THR:HG22	1.95	0.47
1:B:350:SER:O	1:B:351:TYR:HB2	2.15	0.47
1:E:350:SER:O	1:E:351:TYR:HB2	2.15	0.47
1:E:496:LYS:HD2	1:E:534:VAL:O	2.14	0.47
1:B:496:LYS:HD2	1:B:534:VAL:O	2.14	0.47
1:B:501:ASN:OD1	1:B:557:SER:OG	2.22	0.47
1:C:40:PHE:CE2	1:C:131:ILE:HG21	2.50	0.47
1:C:496:LYS:HD2	1:C:534:VAL:O	2.14	0.47
1:C:1216:THR:HG23	1:C:1217:ASN:N	2.30	0.47
1:E:40:PHE:CE2	1:E:131:ILE:HG21	2.50	0.47
1:E:536:GLU:HB2	1:E:539:ASP:OD1	2.15	0.47
1:B:130:VAL:HG11	1:B:307:ARG:HD3	1.96	0.47
1:E:1060:PRO:HA	1:E:1063:GLN:HB3	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:40:PHE:CE2	1:B:131:ILE:HG21	2.50	0.47
1:B:983:VAL:O	1:B:985:ILE:HG13	2.15	0.47
1:C:536:GLU:HB2	1:C:539:ASP:OD1	2.15	0.47
1:E:163:ARG:HH11	1:E:165:PHE:HE2	1.63	0.47
1:C:1060:PRO:HA	1:C:1063:GLN:HB3	1.96	0.46
1:B:985:ILE:HB	1:B:1189:SER:HB3	1.97	0.46
1:C:350:SER:O	1:C:351:TYR:HB2	2.15	0.46
1:B:58:TYR:OH	1:B:331:GLY:O	2.19	0.46
1:B:1216:THR:HG23	1:B:1217:ASN:N	2.30	0.46
1:E:903:PRO:HA	1:E:924:ILE:HG12	1.98	0.46
1:C:174:ASP:OD2	1:C:224:SER:OG	2.33	0.46
1:E:259:THR:OG1	1:E:264:HIS:NE2	2.31	0.46
1:E:1216:THR:HG23	1:E:1217:ASN:N	2.30	0.46
1:B:536:GLU:HB2	1:B:539:ASP:OD1	2.15	0.46
1:C:502:LYS:HA	1:C:502:LYS:HD3	1.62	0.46
1:E:174:ASP:OD2	1:E:224:SER:OG	2.33	0.46
1:B:67:ILE:HG22	1:B:69:ILE:HG12	1.98	0.46
1:B:486:HIS:ND1	1:B:566:GLN:OE1	2.49	0.46
1:B:1060:PRO:HA	1:B:1063:GLN:HB3	1.96	0.46
1:C:67:ILE:HG22	1:C:69:ILE:HG12	1.98	0.46
1:C:130:VAL:HG11	1:C:307:ARG:HD3	1.96	0.46
1:C:497:TYR:HB2	1:C:561:VAL:O	2.16	0.46
1:E:983:VAL:O	1:E:985:ILE:HG13	2.15	0.46
1:C:163:ARG:HH11	1:C:165:PHE:HE2	1.62	0.46
1:C:983:VAL:O	1:C:985:ILE:HG13	2.15	0.46
1:E:739:PRO:O	1:E:758:ARG:NH1	2.47	0.46
1:B:903:PRO:HA	1:B:924:ILE:HG12	1.98	0.46
1:C:259:THR:HG1	1:C:264:HIS:CD2	2.31	0.46
1:E:155:ASN:HB3	1:E:161:MET:CE	2.46	0.46
1:E:175:GLY:O	1:E:178:THR:OG1	2.27	0.46
1:B:174:ASP:OD2	1:B:224:SER:OG	2.33	0.46
1:E:1073:GLY:O	1:E:1077:THR:HG23	2.16	0.46
1:B:29:ALA:HB1	1:B:193:ASN:HB2	1.98	0.45
1:B:155:ASN:HB3	1:B:161:MET:CE	2.46	0.45
1:B:175:GLY:O	1:B:178:THR:OG1	2.27	0.45
1:E:67:ILE:HG22	1:E:69:ILE:HG12	1.98	0.45
1:E:497:TYR:HB2	1:E:561:VAL:O	2.16	0.45
1:C:29:ALA:HB1	1:C:193:ASN:HB2	1.98	0.45
1:C:155:ASN:HB3	1:C:161:MET:CE	2.46	0.45
1:C:1073:GLY:O	1:C:1077:THR:HG23	2.16	0.45
1:C:486:HIS:ND1	1:C:566:GLN:OE1	2.49	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:357:GLU:O	1:B:359:GLY:N	2.49	0.45
1:C:163:ARG:HH21	1:C:189:PRO:CD	2.30	0.45
1:B:1073:GLY:O	1:B:1077:THR:HG23	2.16	0.45
1:C:985:ILE:HB	1:C:1189:SER:HB3	1.98	0.45
2:D:5:GLN:HE22	2:D:121:LYS:HE3	1.82	0.45
1:E:985:ILE:HB	1:E:1189:SER:HB3	1.97	0.45
1:C:903:PRO:HA	1:C:924:ILE:HG12	1.98	0.45
1:C:739:PRO:O	1:C:758:ARG:NH1	2.47	0.45
1:E:486:HIS:ND1	1:E:566:GLN:OE1	2.49	0.45
1:B:542:ARG:HA	1:B:554:LEU:O	2.17	0.45
1:E:384:ASP:OD1	1:E:386:SER:OG	2.26	0.45
2:F:5:GLN:HE22	2:F:121:LYS:HE3	1.82	0.45
1:E:542:ARG:HA	1:E:554:LEU:O	2.17	0.45
1:E:29:ALA:HB1	1:E:193:ASN:HB2	1.98	0.44
1:B:449:PRO:HB3	1:B:497:TYR:CE2	2.52	0.44
1:B:497:TYR:HB2	1:B:561:VAL:O	2.16	0.44
2:A:5:GLN:HE22	2:A:121:LYS:HE3	1.82	0.44
2:D:50:PHE:CE2	2:D:59:ASP:HB3	2.53	0.44
1:B:1062:GLU:OE1	1:B:1062:GLU:N	2.51	0.44
2:A:48:LEU:HD13	2:A:68:PHE:HE2	1.83	0.44
1:C:408:ASN:HA	1:C:585:CYS:O	2.17	0.44
1:C:449:PRO:HB3	1:C:497:TYR:CE2	2.52	0.44
2:F:50:PHE:CE2	2:F:59:ASP:HB3	2.53	0.44
1:E:449:PRO:HB3	1:E:497:TYR:CE2	2.52	0.44
1:E:798:THR:HG23	1:E:1132:ASN:HD22	1.83	0.44
1:B:798:THR:HG23	1:B:1132:ASN:HD22	1.83	0.44
1:B:408:ASN:HA	1:B:585:CYS:O	2.17	0.44
2:A:50:PHE:CE2	2:A:59:ASP:HB3	2.52	0.44
1:E:400:LYS:HD3	1:E:445:TYR:OH	2.18	0.44
1:E:408:ASN:HA	1:E:585:CYS:O	2.17	0.44
1:B:163:ARG:HH21	1:B:189:PRO:CD	2.30	0.44
1:B:456:LEU:HB3	1:B:479:LEU:HD21	2.00	0.44
1:E:463:PRO:O	1:E:468:ASN:ND2	2.51	0.44
1:C:798:THR:HG23	1:C:1132:ASN:HD22	1.83	0.43
2:D:94:TYR:CE1	2:D:125:VAL:HG11	2.53	0.43
1:E:259:THR:HG1	1:E:264:HIS:HE2	1.62	0.43
1:E:456:LEU:HB3	1:E:479:LEU:HD21	2.00	0.43
1:E:507:LEU:HD23	1:E:508:SER:N	2.33	0.43
1:E:187:LEU:HB3	1:E:232:PHE:CD1	2.53	0.43
1:E:357:GLU:O	1:E:359:GLY:N	2.49	0.43
1:B:187:LEU:HB3	1:B:232:PHE:CD1	2.53	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:502:LYS:HD3	1:B:502:LYS:HA	1.62	0.43
1:C:400:LYS:HD3	1:C:445:TYR:OH	2.18	0.43
1:C:542:ARG:HA	1:C:554:LEU:O	2.17	0.43
1:C:662:ILE:O	1:C:670:HIS:HA	2.19	0.43
2:D:48:LEU:HD13	2:D:68:PHE:HE2	1.83	0.43
1:E:501:ASN:OD1	1:E:557:SER:OG	2.21	0.43
2:F:48:LEU:HD13	2:F:68:PHE:HE2	1.83	0.43
1:B:463:PRO:O	1:B:468:ASN:ND2	2.51	0.43
1:B:623:VAL:HG22	1:C:65:SER:OG	2.19	0.43
1:C:84:MET:HE2	1:C:84:MET:HB3	1.90	0.43
1:C:456:LEU:HB3	1:C:479:LEU:HD21	2.00	0.43
1:B:65:SER:OG	1:E:623:VAL:HG22	2.19	0.43
1:B:357:GLU:HG3	1:B:358:SER:N	2.34	0.43
2:A:94:TYR:CE1	2:A:125:VAL:HG11	2.53	0.43
1:C:357:GLU:HG3	1:C:358:SER:N	2.34	0.43
1:B:400:LYS:HD3	1:B:445:TYR:OH	2.18	0.43
1:C:70:THR:HG23	1:C:352:GLU:OE1	2.19	0.43
1:C:357:GLU:O	1:C:359:GLY:N	2.49	0.43
1:C:870:ASN:O	1:C:871:LEU:HD23	2.19	0.43
1:E:783:PRO:HB3	1:E:1143:PRO:HB2	2.01	0.43
1:E:163:ARG:HH21	1:E:189:PRO:CD	2.30	0.43
1:C:463:PRO:O	1:C:468:ASN:ND2	2.51	0.43
1:E:662:ILE:O	1:E:670:HIS:HA	2.18	0.43
1:B:507:LEU:HD23	1:B:508:SER:N	2.34	0.43
1:B:529:ILE:HG13	1:B:530:VAL:N	2.34	0.43
2:A:118:TYR:HE1	3:G:2:NAG:HO6	1.65	0.43
2:F:10:GLY:O	2:F:125:VAL:HG23	2.19	0.43
2:F:94:TYR:CE1	2:F:125:VAL:HG11	2.53	0.43
1:B:857:GLN:HG2	1:E:768:ILE:HB	2.01	0.42
1:C:623:VAL:HG22	1:E:65:SER:OG	2.19	0.42
1:C:187:LEU:HB3	1:C:232:PHE:CD1	2.53	0.42
1:E:502:LYS:HD3	1:E:502:LYS:HA	1.61	0.42
1:C:65:SER:O	1:C:67:ILE:HG12	2.19	0.42
1:C:783:PRO:HB3	1:C:1143:PRO:HB2	2.00	0.42
1:C:456:LEU:HD23	1:C:456:LEU:HA	1.82	0.42
1:E:70:THR:HG23	1:E:352:GLU:OE1	2.19	0.42
1:B:870:ASN:O	1:B:871:LEU:HD23	2.19	0.42
1:C:500:ILE:HD11	1:C:530:VAL:HG21	2.02	0.42
1:E:1062:GLU:OE1	1:E:1062:GLU:N	2.50	0.42
1:B:70:THR:HG23	1:B:352:GLU:OE1	2.19	0.42
1:B:768:ILE:HB	1:C:857:GLN:HG2	2.01	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:665:LYS:HE3	1:C:665:LYS:HB2	1.89	0.42
1:E:35:ILE:HD11	1:E:203:SER:HB3	2.02	0.42
1:C:529:ILE:HG13	1:C:530:VAL:N	2.34	0.42
1:E:65:SER:O	1:E:67:ILE:HG12	2.19	0.42
1:E:273:LEU:HD23	1:E:274:TYR:CZ	2.55	0.42
1:E:870:ASN:O	1:E:871:LEU:HD23	2.19	0.42
1:B:65:SER:O	1:B:67:ILE:HG12	2.19	0.42
2:A:10:GLY:O	2:A:125:VAL:HG23	2.19	0.42
1:E:500:ILE:HD11	1:E:530:VAL:HG21	2.02	0.42
1:B:783:PRO:HB3	1:B:1143:PRO:HB2	2.00	0.42
1:C:507:LEU:HD23	1:C:508:SER:N	2.34	0.42
1:B:273:LEU:HD23	1:B:274:TYR:CZ	2.55	0.42
1:B:662:ILE:O	1:B:670:HIS:HA	2.19	0.42
1:B:726:ASP:OD1	1:B:726:ASP:N	2.53	0.42
1:B:976:ILE:HD13	1:B:976:ILE:HA	1.93	0.42
1:C:273:LEU:HD23	1:C:274:TYR:CZ	2.55	0.42
1:C:344:LEU:HD23	1:C:347:LEU:HD22	2.02	0.42
1:E:190:ARG:HD3	1:E:230:GLU:O	2.20	0.42
1:E:344:LEU:HD23	1:E:347:LEU:HD22	2.02	0.42
1:E:627:GLN:OE1	1:E:627:GLN:N	2.51	0.42
1:C:93:THR:HG22	1:C:98:GLN:OE1	2.20	0.41
1:C:408:ASN:HB3	1:C:587:LYS:HG2	2.02	0.41
1:E:50:VAL:HG22	1:E:78:GLN:HE21	1.85	0.41
1:E:529:ILE:HG13	1:E:530:VAL:N	2.34	0.41
1:B:456:LEU:HA	1:B:456:LEU:HD23	1.81	0.41
1:E:501:ASN:O	1:E:502:LYS:HE2	2.20	0.41
1:B:815:GLN:OE1	1:B:815:GLN:HA	2.20	0.41
1:C:343:ASP:OD1	1:C:691:ARG:NH2	2.49	0.41
1:C:627:GLN:OE1	1:C:627:GLN:N	2.51	0.41
1:E:189:PRO:HB2	1:E:197:ALA:HB2	2.03	0.41
1:E:815:GLN:OE1	1:E:815:GLN:HA	2.20	0.41
1:E:792:GLN:HA	1:E:1136:PHE:O	2.20	0.41
2:A:38:ARG:HE	2:A:48:LEU:HD21	1.86	0.41
1:C:785:ASN:HD22	1:C:1144:SER:HB3	1.86	0.41
1:C:1062:GLU:OE1	1:C:1062:GLU:N	2.50	0.41
2:D:5:GLN:HB2	2:D:23:SER:OG	2.21	0.41
2:D:40:VAL:HG12	2:D:92:ALA:HB2	2.03	0.41
1:E:343:ASP:OD1	1:E:691:ARG:NH2	2.49	0.41
1:E:375:VAL:HG22	1:E:607:SER:HB3	2.03	0.41
1:E:782:ILE:HA	1:E:783:PRO:HD3	1.92	0.41
1:B:782:ILE:HA	1:B:783:PRO:HD3	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:792:GLN:HA	1:B:1136:PHE:O	2.20	0.41
1:C:341:PHE:CD2	1:C:342:ASN:HB2	2.56	0.41
1:C:726:ASP:OD1	1:C:726:ASP:N	2.53	0.41
1:E:93:THR:HG22	1:E:98:GLN:OE1	2.20	0.41
1:B:500:ILE:HD11	1:B:530:VAL:HG21	2.01	0.41
1:C:190:ARG:HD3	1:C:230:GLU:O	2.20	0.41
1:C:422:ASP:HB3	1:C:481:LEU:HB2	2.03	0.41
1:E:785:ASN:HD22	1:E:1144:SER:HB3	1.86	0.41
2:F:5:GLN:HB2	2:F:23:SER:OG	2.21	0.41
1:B:190:ARG:HD3	1:B:230:GLU:O	2.20	0.41
1:B:375:VAL:HG22	1:B:607:SER:HB3	2.03	0.41
1:B:785:ASN:HD22	1:B:1144:SER:HB3	1.86	0.41
1:C:768:ILE:HB	1:E:857:GLN:HG2	2.02	0.41
1:C:792:GLN:HA	1:C:1136:PHE:O	2.20	0.41
2:D:38:ARG:HE	2:D:48:LEU:HD21	1.86	0.41
1:B:50:VAL:HG22	1:B:78:GLN:HE21	1.85	0.41
1:B:93:THR:HG23	1:B:96:THR:HG23	2.02	0.41
1:B:344:LEU:HD23	1:B:347:LEU:HD22	2.02	0.41
2:A:40:VAL:HG12	2:A:92:ALA:HB2	2.03	0.41
1:C:452:MET:HE3	1:C:452:MET:HB2	1.74	0.41
1:C:501:ASN:O	1:C:502:LYS:HE2	2.20	0.41
1:C:815:GLN:HA	1:C:815:GLN:OE1	2.20	0.41
1:E:990:LEU:HD21	1:E:1191:PHE:CD2	2.56	0.41
2:F:38:ARG:HE	2:F:48:LEU:HD21	1.86	0.41
1:B:189:PRO:HB2	1:B:197:ALA:HB2	2.02	0.41
1:C:35:ILE:HD11	1:C:203:SER:HB3	2.02	0.41
1:C:50:VAL:HG22	1:C:78:GLN:HE21	1.85	0.41
1:E:341:PHE:CD2	1:E:342:ASN:HB2	2.56	0.41
1:E:408:ASN:HB3	1:E:587:LYS:HG2	2.02	0.40
2:D:30:SER:O	2:D:54:PRO:HG3	2.21	0.40
2:F:93:THR:HA	2:F:124:GLN:HA	2.03	0.40
1:B:408:ASN:HB3	1:B:587:LYS:HG2	2.02	0.40
1:B:461:ALA:O	1:B:465:SER:OG	2.34	0.40
1:B:811:CYS:HB3	1:B:817:CYS:HB3	1.98	0.40
2:A:93:THR:HA	2:A:124:GLN:HA	2.03	0.40
1:C:691:ARG:HH21	1:C:691:ARG:HD2	1.76	0.40
2:D:10:GLY:O	2:D:125:VAL:HG23	2.19	0.40
1:E:394:PRO:O	1:E:447:SER:N	2.53	0.40
1:E:413:LYS:HG2	2:F:101:SER:OG	2.22	0.40
1:B:93:THR:HG22	1:B:98:GLN:OE1	2.20	0.40
1:B:324:LEU:O	1:B:336:ALA:HA	2.22	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:5:GLN:HB2	2:A:23:SER:OG	2.21	0.40
1:E:814:PHE:O	1:E:818:GLU:HG3	2.22	0.40
1:E:990:LEU:O	1:E:993:ASN:N	2.49	0.40
1:B:501:ASN:O	1:B:502:LYS:HE2	2.20	0.40
1:C:112:PHE:CZ	1:C:115:GLY:HA2	2.57	0.40
1:C:189:PRO:HB2	1:C:197:ALA:HB2	2.02	0.40
1:C:501:ASN:OD1	1:C:557:SER:OG	2.21	0.40
2:D:93:THR:HA	2:D:124:GLN:HA	2.03	0.40
1:E:300:ILE:HD13	1:E:310:TRP:NE1	2.36	0.40
1:E:726:ASP:OD1	1:E:726:ASP:N	2.53	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	1170/1347 (87%)	1091 (93%)	77 (7%)	2 (0%)	47 76
1	C	1170/1347 (87%)	1091 (93%)	77 (7%)	2 (0%)	47 76
1	E	1170/1347 (87%)	1090 (93%)	78 (7%)	2 (0%)	47 76
2	A	126/135 (93%)	124 (98%)	2 (2%)	0	100 100
2	D	126/135 (93%)	124 (98%)	2 (2%)	0	100 100
2	F	126/135 (93%)	123 (98%)	3 (2%)	0	100 100
All	All	3888/4446 (87%)	3643 (94%)	239 (6%)	6 (0%)	50 76

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	1149	VAL
1	C	1149	VAL

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Mol	Chain	Res	Type
1	E	1149	VAL
1	B	1148	GLU
1	C	1148	GLU
1	E	1148	GLU

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all EM entries.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	B	1013/1163 (87%)	999 (99%)	14 (1%)	67 89
1	C	1013/1163 (87%)	1000 (99%)	13 (1%)	69 90
1	E	1013/1163 (87%)	1000 (99%)	13 (1%)	69 90
2	A	105/112 (94%)	105 (100%)	0	100 100
2	D	105/112 (94%)	105 (100%)	0	100 100
2	F	105/112 (94%)	105 (100%)	0	100 100
All	All	3354/3825 (88%)	3314 (99%)	40 (1%)	72 91

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	84	MET
1	B	240	MET
1	B	352	GLU
1	B	379	GLU
1	B	452	MET
1	B	502	LYS
1	B	563	MET
1	B	656	SER
1	B	698	LYS
1	B	844	ASP
1	B	852	SER
1	B	913	MET
1	B	965	SER
1	B	1112	LYS

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	84	MET
1	C	240	MET
1	C	352	GLU
1	C	379	GLU
1	C	452	MET
1	C	502	LYS
1	C	563	MET
1	C	656	SER
1	C	698	LYS
1	C	844	ASP
1	C	852	SER
1	C	913	MET
1	C	1112	LYS
1	E	84	MET
1	E	240	MET
1	E	352	GLU
1	E	379	GLU
1	E	452	MET
1	E	502	LYS
1	E	563	MET
1	E	656	SER
1	E	698	LYS
1	E	844	ASP
1	E	852	SER
1	E	913	MET
1	E	1112	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	1146	HIS
1	C	1146	HIS
1	E	1146	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

12 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	$\#\|Z\|>2$
3	NAG	G	1	1,3	14,14,15	0.34	0	17,19,21	0.43	0
3	NAG	G	2	3	14,14,15	0.52	0	17,19,21	0.36	0
3	BMA	G	3	3	11,11,12	0.84	0	15,15,17	1.51	2 (13%)
3	MAN	G	4	3	11,11,12	0.63	0	15,15,17	1.39	2 (13%)
3	NAG	H	1	1,3	14,14,15	0.34	0	17,19,21	0.42	0
3	NAG	H	2	3	14,14,15	0.54	0	17,19,21	0.38	0
3	BMA	H	3	3	11,11,12	0.85	0	15,15,17	1.50	2 (13%)
3	MAN	H	4	3	11,11,12	0.62	0	15,15,17	1.40	2 (13%)
3	NAG	I	1	1,3	14,14,15	0.32	0	17,19,21	0.43	0
3	NAG	I	2	3	14,14,15	0.53	0	17,19,21	0.38	0
3	BMA	I	3	3	11,11,12	0.84	0	15,15,17	1.51	2 (13%)
3	MAN	I	4	3	11,11,12	0.61	0	15,15,17	1.39	2 (13%)

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
3	NAG	G	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	G	2	3	-	1/6/23/26	0/1/1/1
3	BMA	G	3	3	-	0/2/19/22	0/1/1/1
3	MAN	G	4	3	-	0/2/19/22	0/1/1/1
3	NAG	H	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	H	2	3	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	H	3	3	-	0/2/19/22	0/1/1/1
3	MAN	H	4	3	-	0/2/19/22	0/1/1/1
3	NAG	I	1	1,3	-	1/6/23/26	0/1/1/1
3	NAG	I	2	3	-	1/6/23/26	0/1/1/1
3	BMA	I	3	3	-	0/2/19/22	0/1/1/1
3	MAN	I	4	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	G	3	BMA	C1-C2-C3	4.07	114.66	109.67
3	I	3	BMA	C1-C2-C3	4.06	114.66	109.67
3	H	3	BMA	C1-C2-C3	4.02	114.61	109.67
3	H	4	MAN	C1-O5-C5	3.66	117.15	112.19
3	G	4	MAN	C1-O5-C5	3.61	117.08	112.19
3	I	4	MAN	C1-O5-C5	3.58	117.04	112.19
3	I	4	MAN	O2-C2-C3	-2.45	105.22	110.14
3	G	4	MAN	O2-C2-C3	-2.42	105.28	110.14
3	H	4	MAN	O2-C2-C3	-2.41	105.31	110.14
3	I	3	BMA	O5-C1-C2	2.19	114.15	110.77
3	G	3	BMA	O5-C1-C2	2.18	114.14	110.77
3	H	3	BMA	O5-C1-C2	2.18	114.13	110.77

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	H	2	NAG	O5-C5-C6-O6
3	I	2	NAG	O5-C5-C6-O6
3	G	2	NAG	O5-C5-C6-O6
3	I	1	NAG	C4-C5-C6-O6
3	G	1	NAG	C4-C5-C6-O6
3	H	1	NAG	C4-C5-C6-O6

There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	I	2	NAG	3	0

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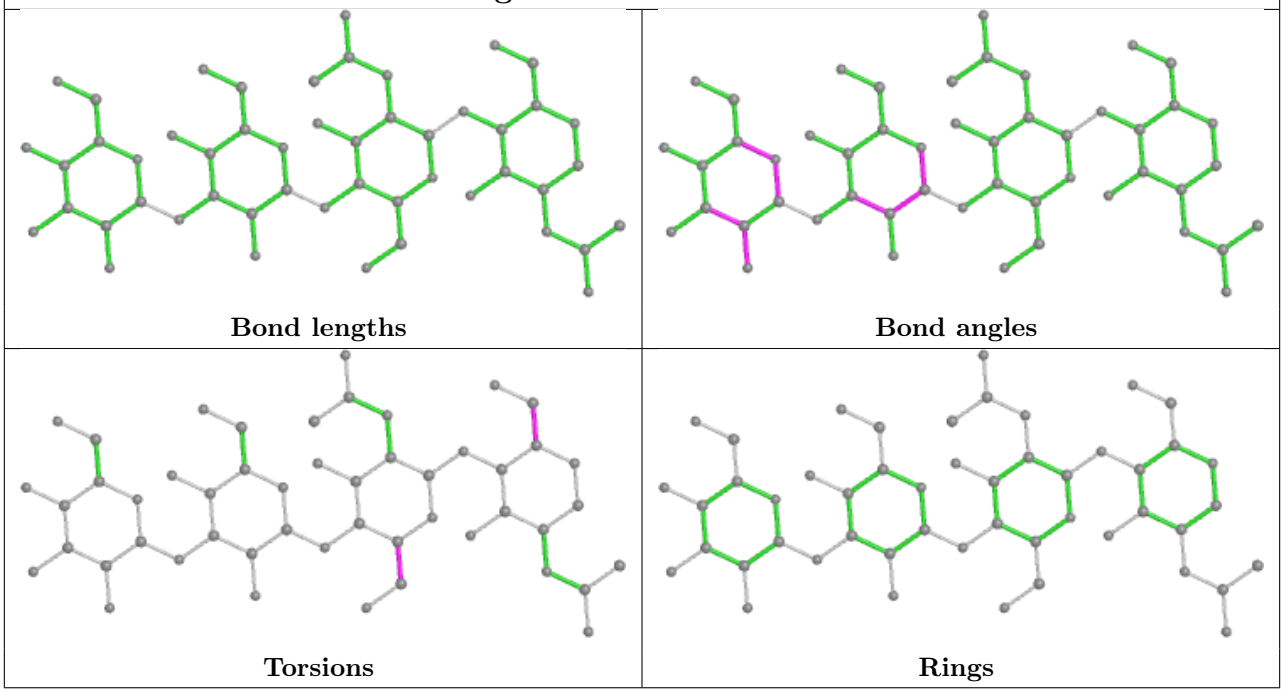
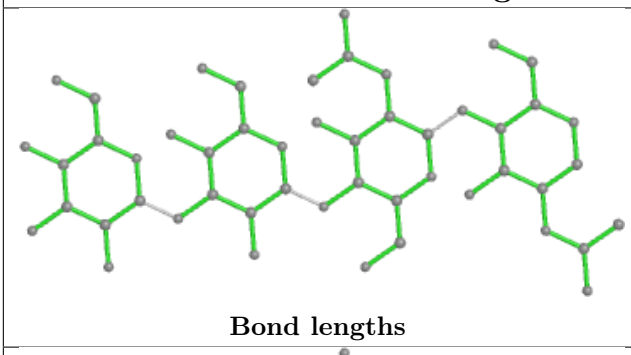
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	G	1	NAG	2	0
3	H	1	NAG	2	0
3	G	2	NAG	3	0
3	I	1	NAG	2	0
3	H	2	NAG	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.

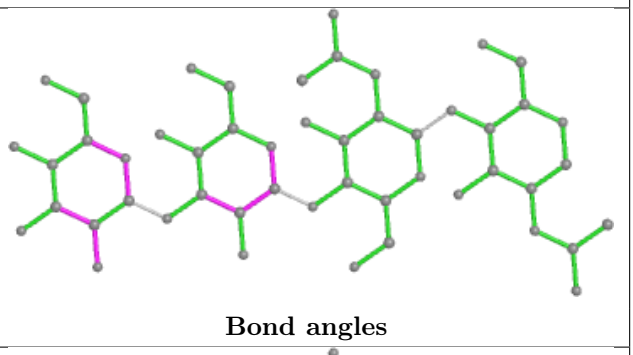
Oligosaccharide Chain G



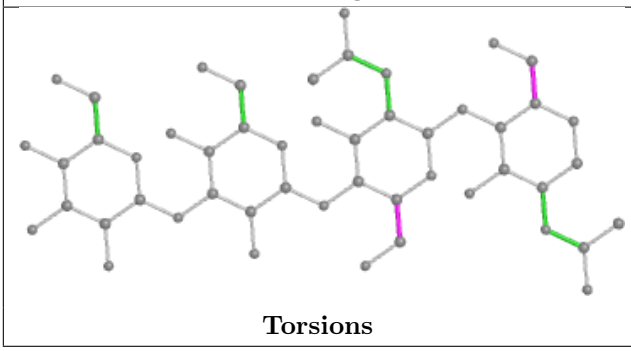
Oligosaccharide Chain H



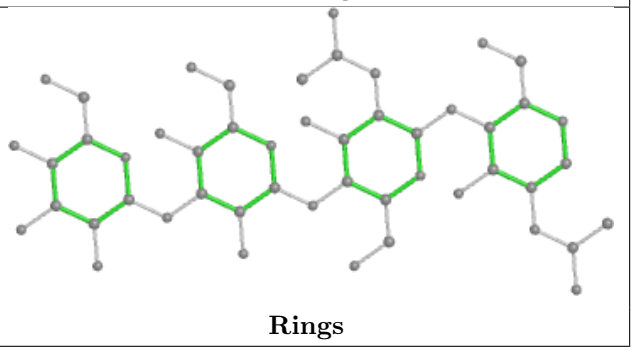
Bond lengths



Bond angles

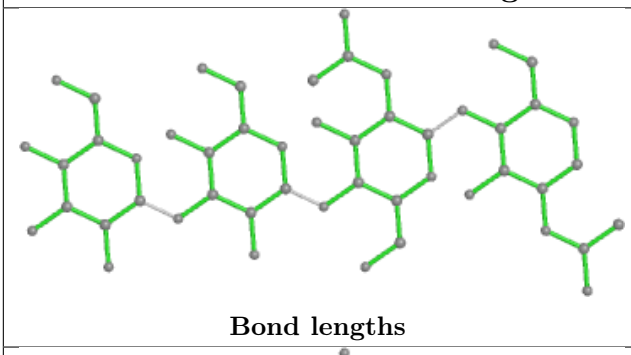


Torsions

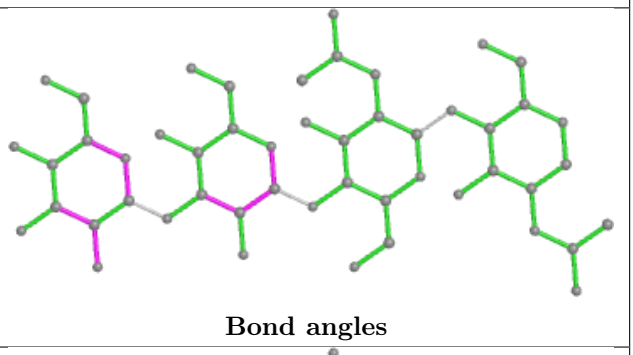


Rings

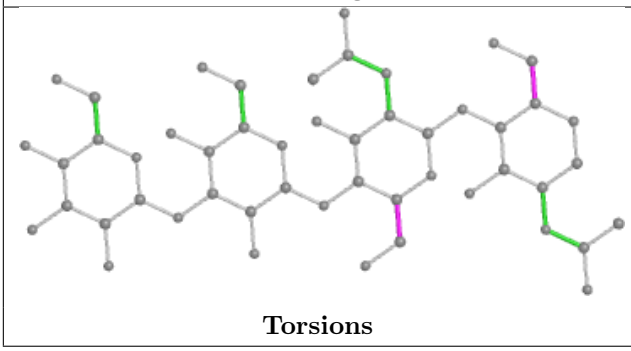
Oligosaccharide Chain I



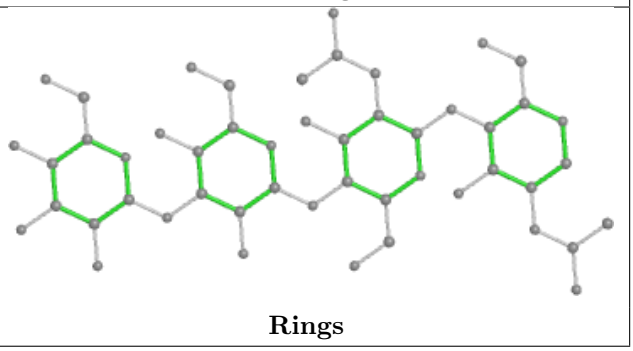
Bond lengths



Bond angles



Torsions



Rings

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.

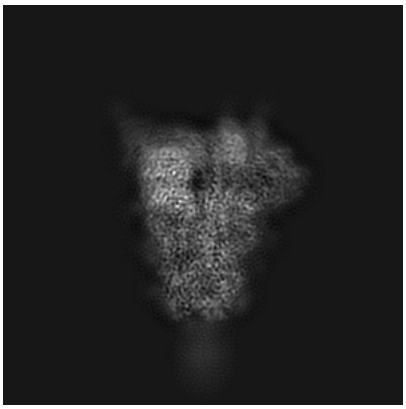
6 Map visualisation

This section contains visualisations of the EMDB entry EMD-35422. These allow visual inspection of the internal detail of the map and identification of artifacts.

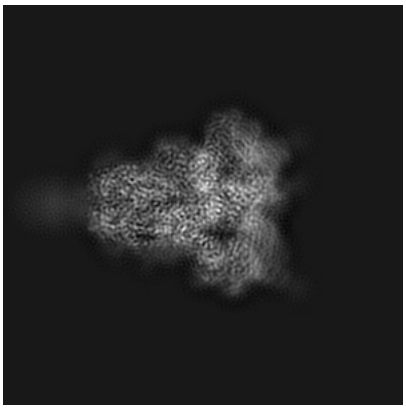
Images derived from a raw map, generated by summing the deposited half-maps, are presented below the corresponding image components of the primary map to allow further visual inspection and comparison with those of the primary map.

6.1 Orthogonal projections

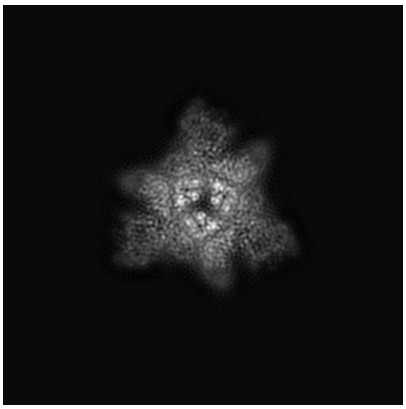
6.1.1 Primary map



X

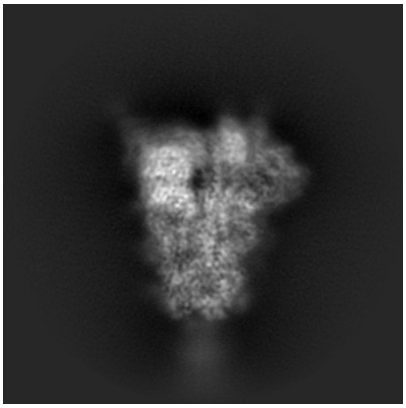


Y

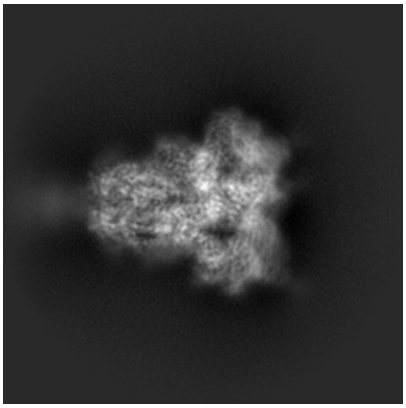


Z

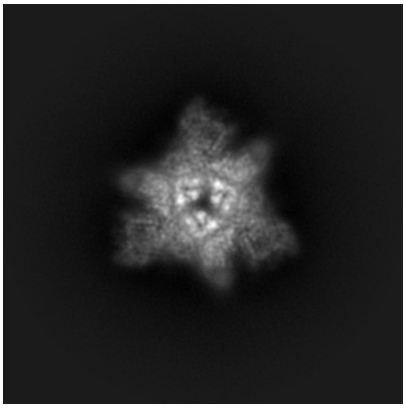
6.1.2 Raw map



X



Y

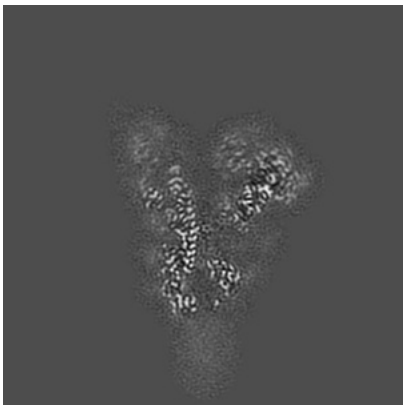


Z

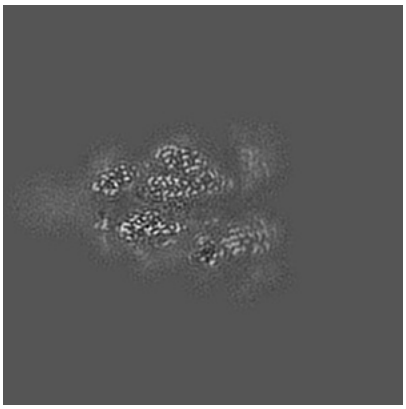
The images above show the map projected in three orthogonal directions.

6.2 Central slices (i)

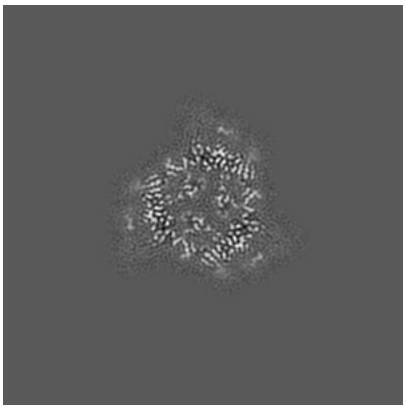
6.2.1 Primary map



X Index: 140

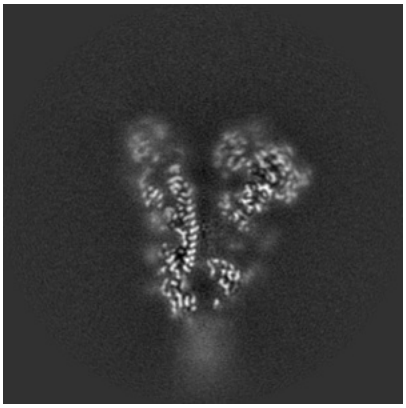


Y Index: 140

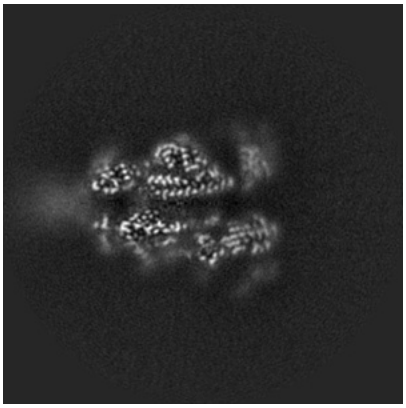


Z Index: 140

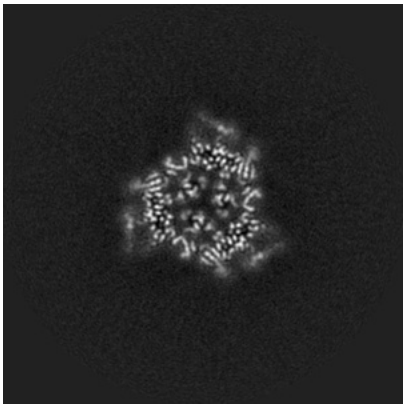
6.2.2 Raw map



X Index: 140



Y Index: 140



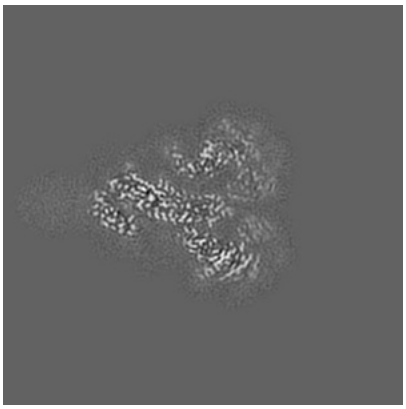
Z Index: 140

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

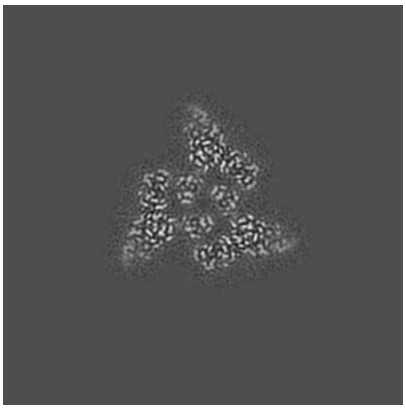
6.3 Largest variance slices (i)

6.3.1 Primary map

X Index: 149

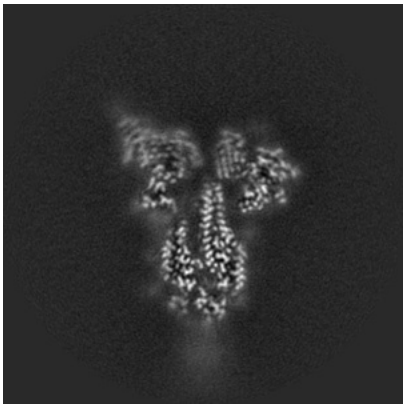


Y Index: 127

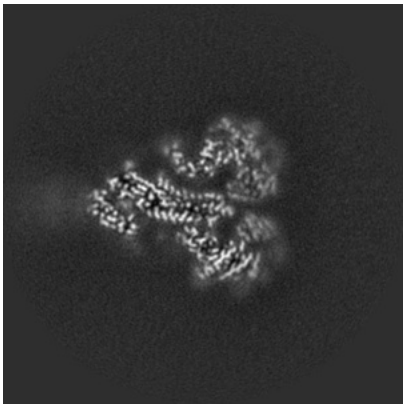


Z Index: 146

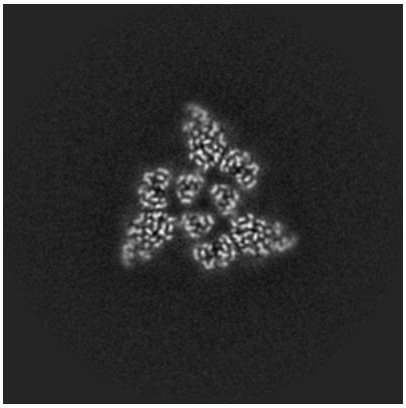
6.3.2 Raw map



X Index: 149



Y Index: 127

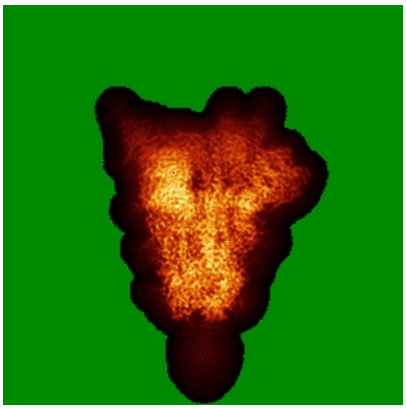


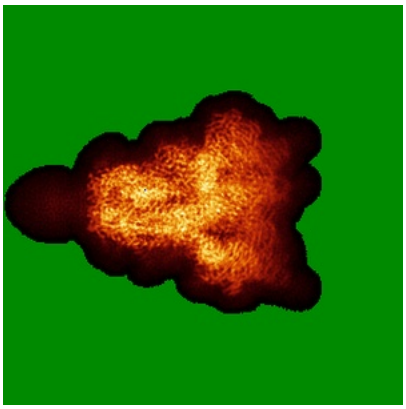
Z Index: 146

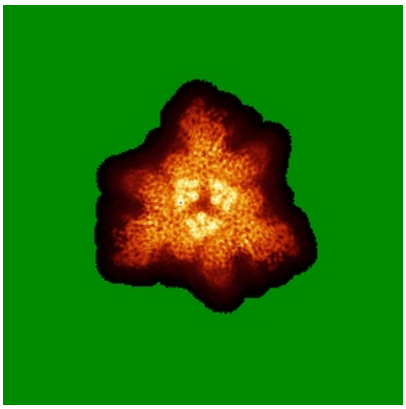
The images above show the largest variance slices of the map in three orthogonal directions.

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

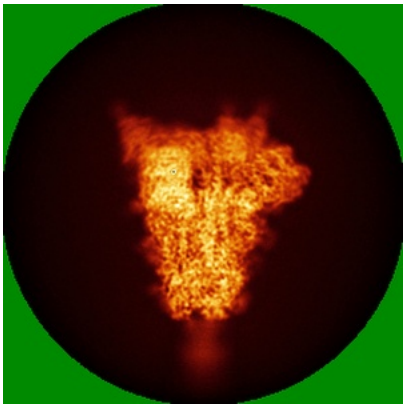
6.4.1 Primary map

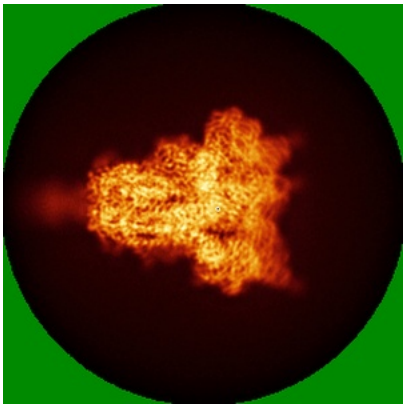

X

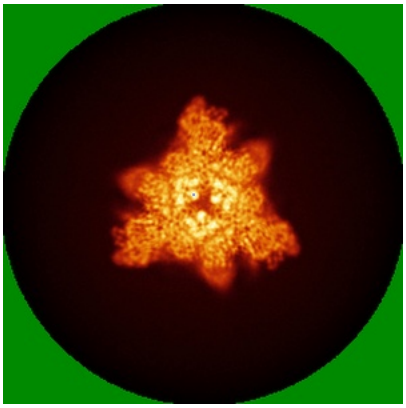

Y


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 0.0116. 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.

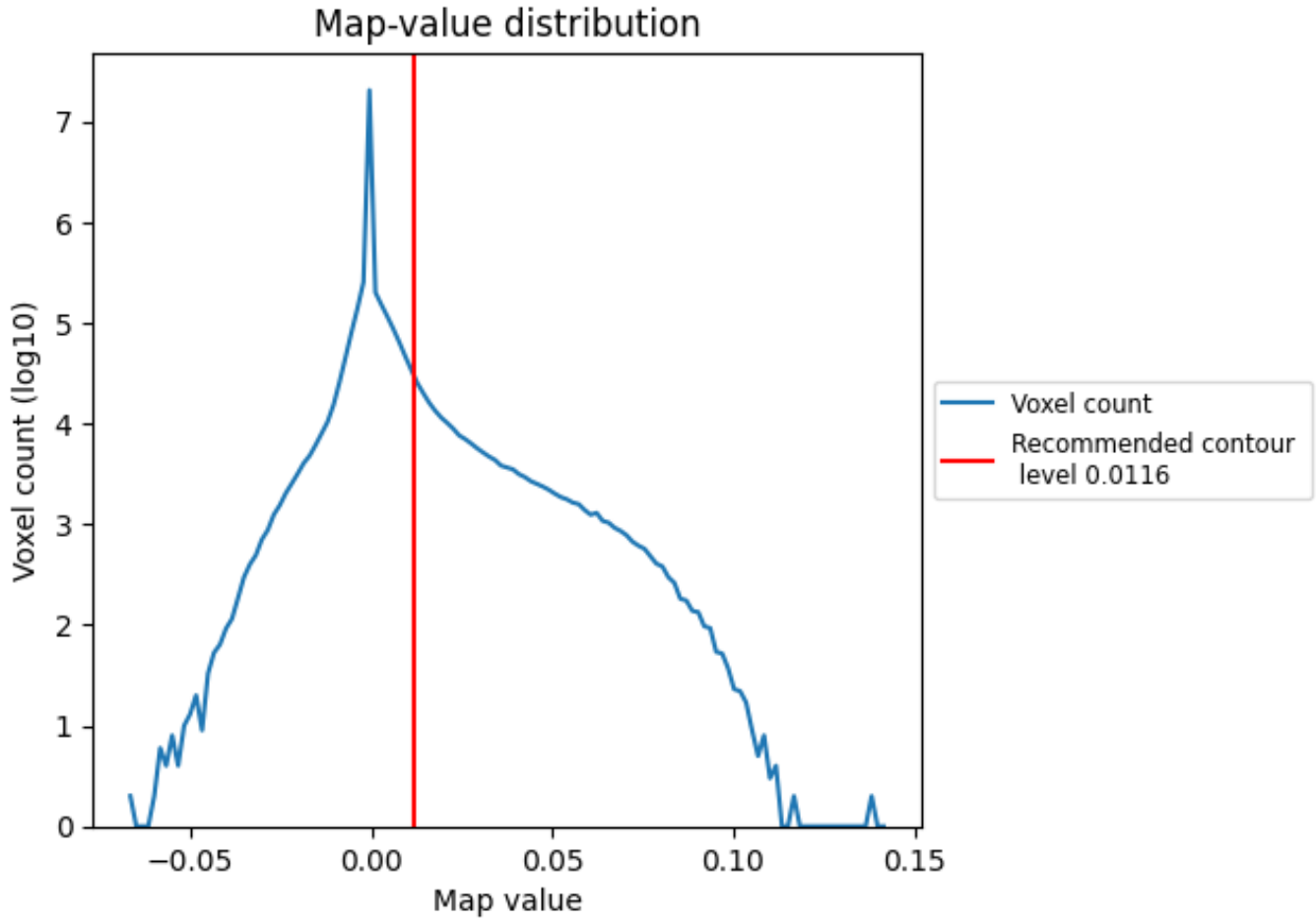
6.6 Mask visualisation (i)

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

7 Map analysis

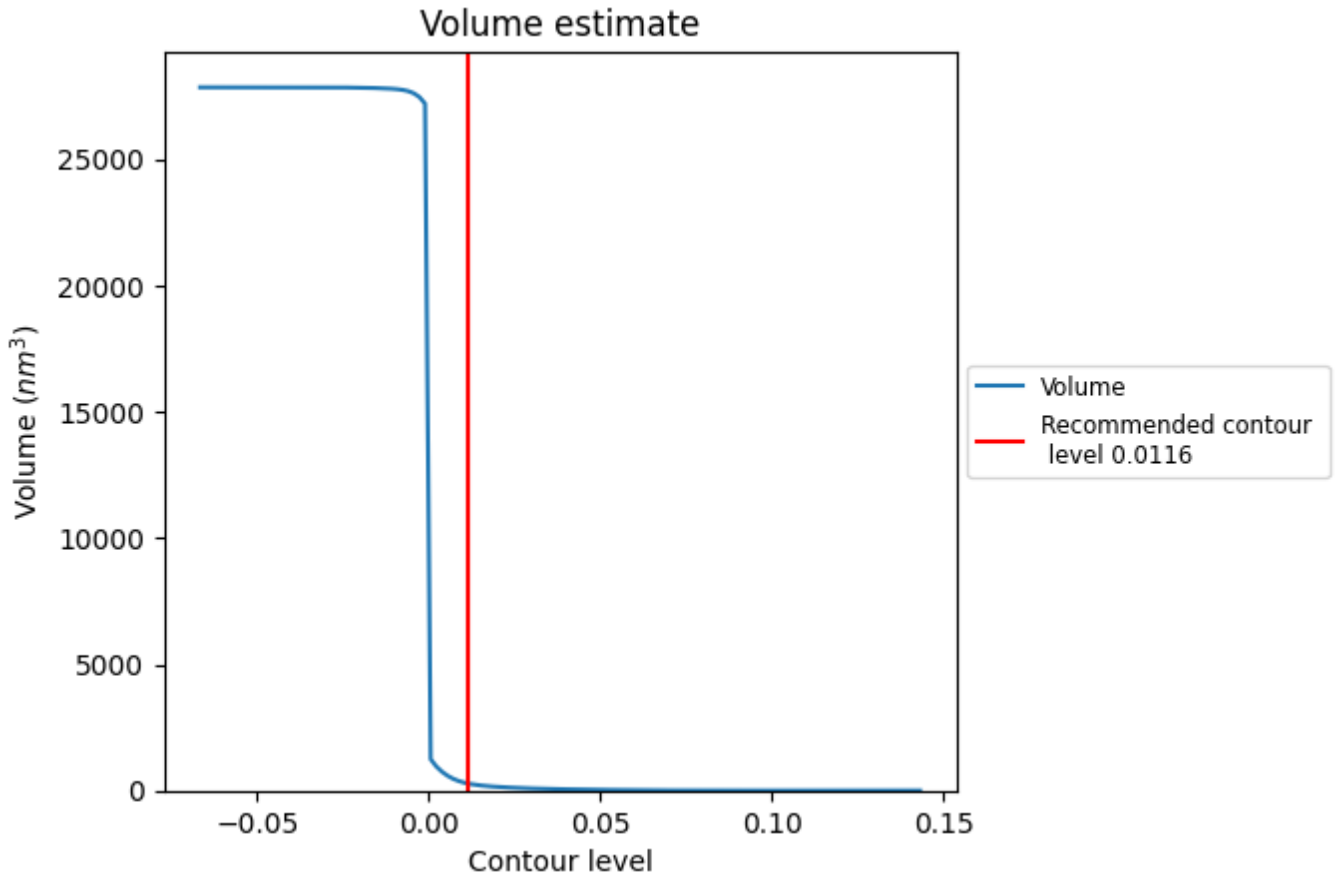
This section contains the results of statistical analysis of the map.

7.1 Map-value distribution



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

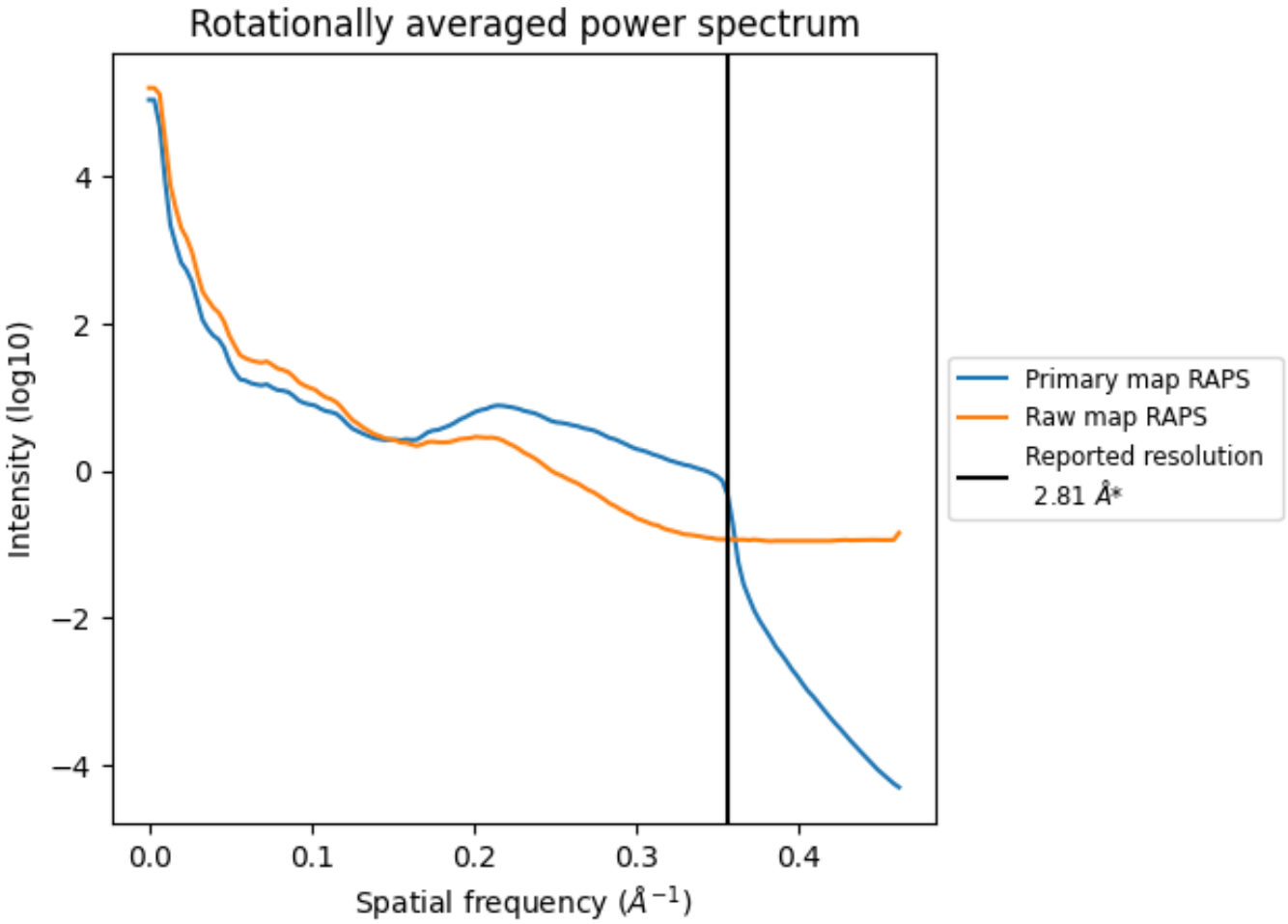
7.2 Volume estimate



The volume at the recommended contour level is 277 nm^3; this corresponds to an approximate mass of 251 kDa.

The volume estimate graph shows how the enclosed volume varies with the contour level. The recommended contour level is shown as a vertical line and the intersection between the line and the curve gives the volume of the enclosed surface at the given level.

7.3 Rotationally averaged power spectrum (i)

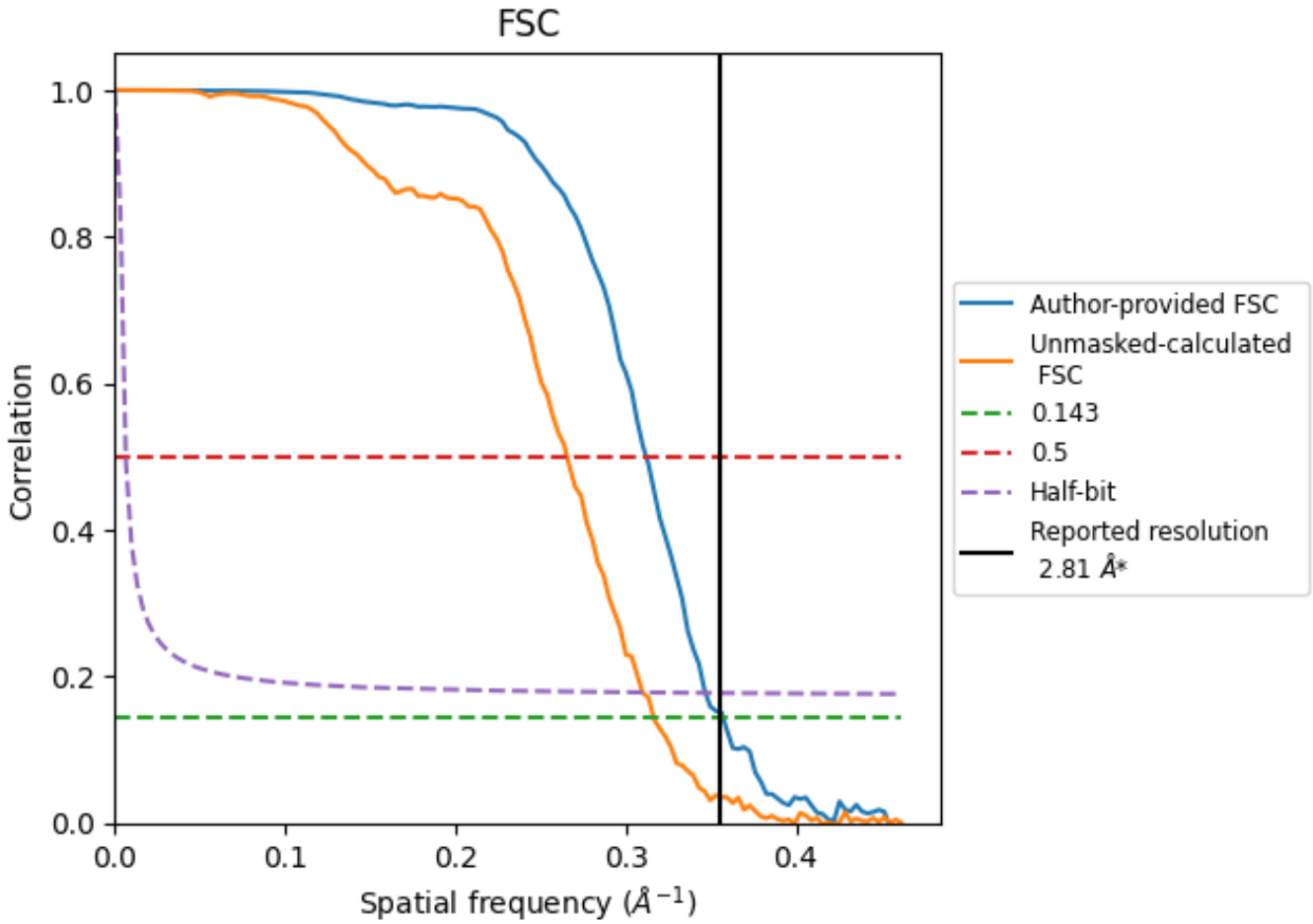


*Reported resolution corresponds to spatial frequency of 0.356 Å^{-1}

8 Fourier-Shell correlation

Fourier-Shell Correlation (FSC) is the most commonly used method to estimate the resolution of single-particle and subtomogram-averaged maps. The shape of the curve depends on the imposed symmetry, mask and whether or not the two 3D reconstructions used were processed from a common reference. The reported resolution is shown as a black line. A curve is displayed for the half-bit criterion in addition to lines showing the 0.143 gold standard cut-off and 0.5 cut-off.

8.1 FSC



*Reported resolution corresponds to spatial frequency of 0.356 Å^{-1}

8.2 Resolution estimates (i)

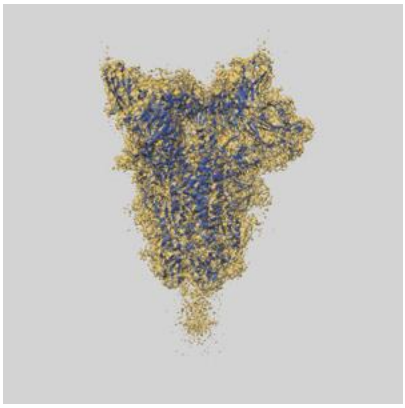
Resolution estimate (Å)	Estimation criterion (FSC cut-off)		
	0.143	0.5	Half-bit
Reported by author	2.81	-	-
Author-provided FSC curve	2.80	3.20	2.88
Unmasked-calculated*	3.16	3.77	3.23

*Resolution estimate based on FSC curve calculated by comparison of deposited half-maps. The value from deposited half-maps intersecting FSC 0.143 CUT-OFF 3.16 differs from the reported value 2.81 by more than 10 %

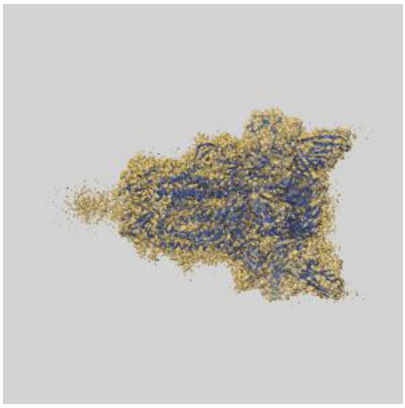
9 Map-model fit

This section contains information regarding the fit between EMDB map EMD-35422 and PDB model 8IFN. Per-residue inclusion information can be found in section 3 on page 10.

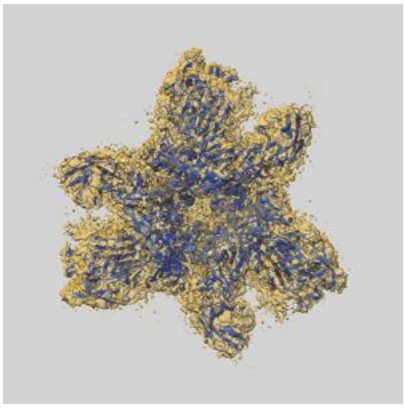
9.1 Map-model overlay



X



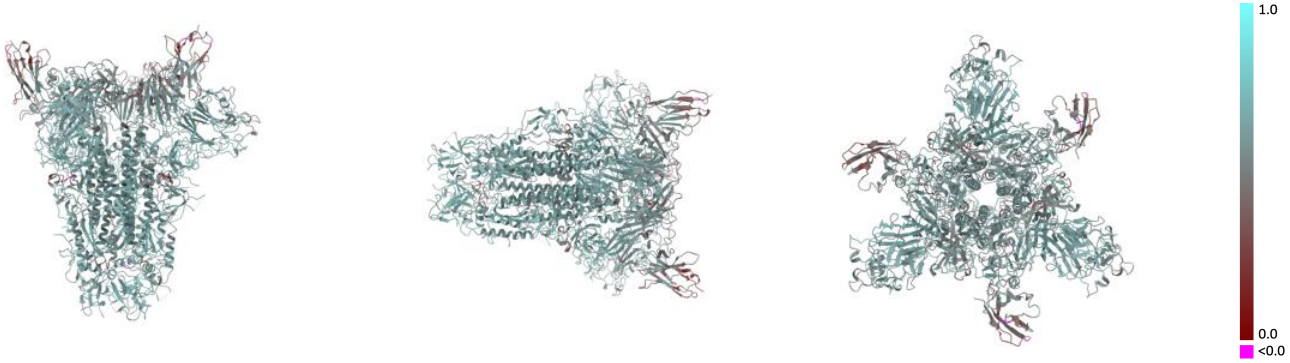
Y



Z

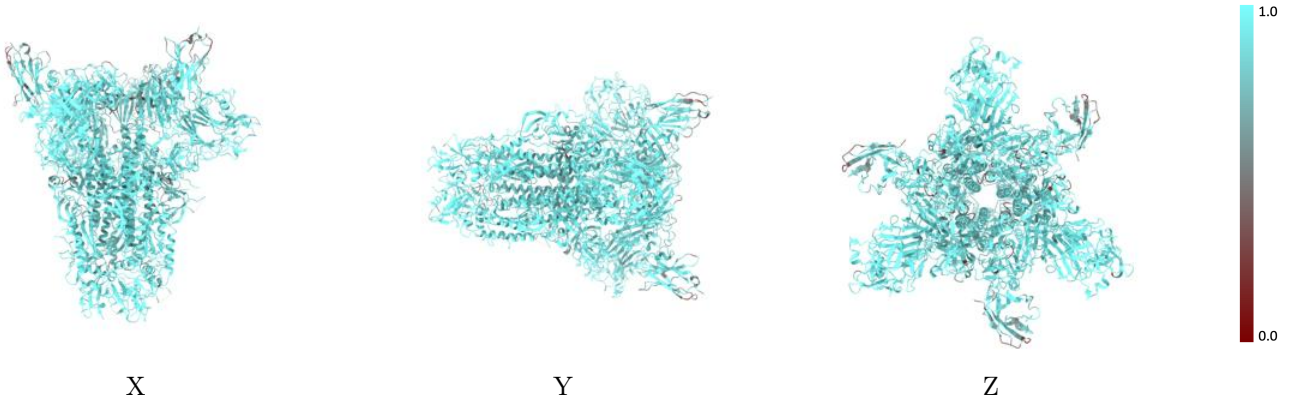
The images above show the 3D surface view of the map at the recommended contour level 0.0116 at 50% transparency in yellow overlaid with a ribbon representation of the model coloured in blue. These images allow for the visual assessment of the quality of fit between the atomic model and the map.

9.2 Q-score mapped to coordinate model (i)



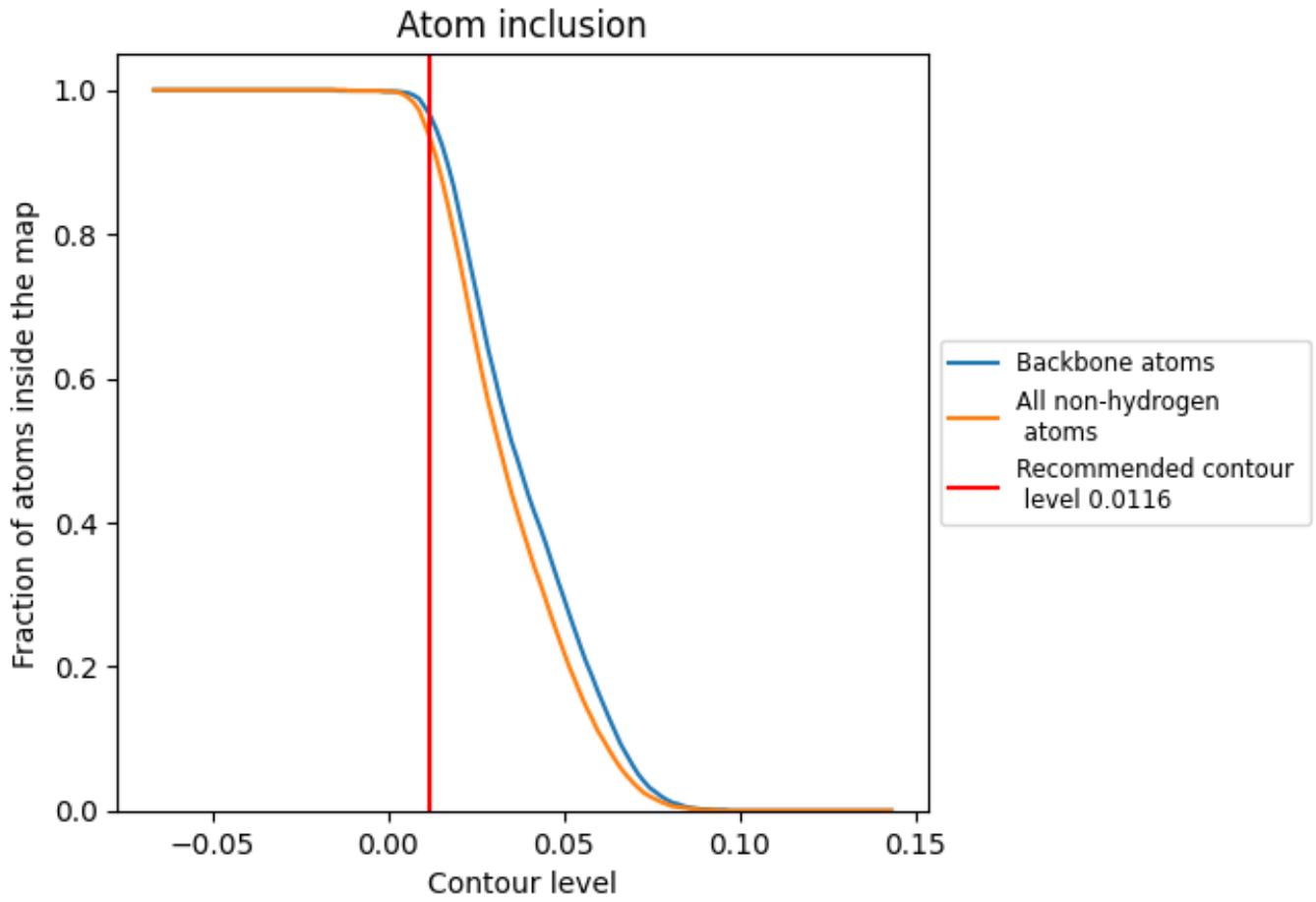
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (0.0116).

9.4 Atom inclusion (i)



At the recommended contour level, 97% of all backbone atoms, 94% 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 (0.0116) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	0.9380	0.5770
A	0.8150	0.4580
B	0.9510	0.5900
C	0.9510	0.5900
D	0.8200	0.4480
E	0.9510	0.5900
F	0.8210	0.4560
G	0.9400	0.5340
H	0.9400	0.5030
I	0.9400	0.5260