



## Full wwPDB EM Validation Report ⓘ

Nov 13, 2022 – 08:44 AM EST

PDB ID : 6WTS  
EMDB ID : EMD-21898  
Title : CryoEM structure of the *C. sordellii* lethal toxin TcsL in complex with SEMA6A  
Authors : Kucharska, I.; Rubinstein, J.L.; Julien, J.P.  
Deposited on : 2020-05-03  
Resolution : 3.30 Å (reported)  
Based on initial model : 6C0B

This is a Full wwPDB EM Validation 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.dev43  
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 : 1.9.9  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.31.2

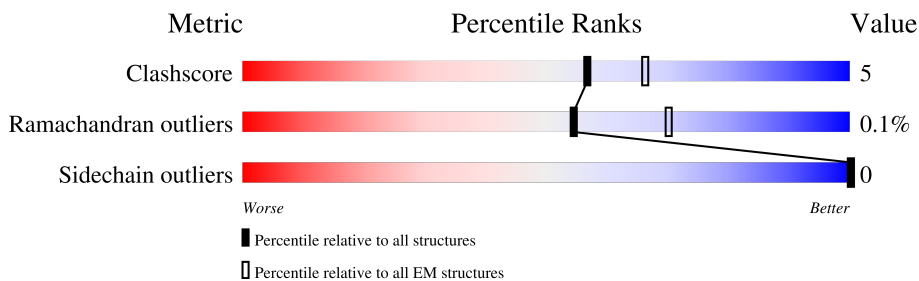
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*ELECTRON MICROSCOPY*

The reported resolution of this entry is 3.30 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	EM structures (#Entries)
Clashscore	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  $\geq 3$ , 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	564	
1	B	564	
2	C	552	
3	D	2	
3	E	2	
3	F	2	

## 2 Entry composition i

There are 4 unique types of molecules in this entry. The entry contains 9863 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 SEMA6A.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
1	A	536	Total	C	N	O	S	0	0
			4170	2657	709	773	31		
1	B	532	Total	C	N	O	S	0	0
			3964	2537	675	721	31		

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	17	GLU	-	expression tag	UNP Q9H2E6
A	18	THR	-	expression tag	UNP Q9H2E6
A	571	GLY	-	expression tag	UNP Q9H2E6
A	572	SER	-	expression tag	UNP Q9H2E6
A	573	TRP	-	expression tag	UNP Q9H2E6
A	574	SER	-	expression tag	UNP Q9H2E6
A	575	HIS	-	expression tag	UNP Q9H2E6
A	576	PRO	-	expression tag	UNP Q9H2E6
A	577	GLN	-	expression tag	UNP Q9H2E6
A	578	PHE	-	expression tag	UNP Q9H2E6
A	579	GLU	-	expression tag	UNP Q9H2E6
A	580	LYS	-	expression tag	UNP Q9H2E6
B	17	GLU	-	expression tag	UNP Q9H2E6
B	18	THR	-	expression tag	UNP Q9H2E6
B	571	GLY	-	expression tag	UNP Q9H2E6
B	572	SER	-	expression tag	UNP Q9H2E6
B	573	TRP	-	expression tag	UNP Q9H2E6
B	574	SER	-	expression tag	UNP Q9H2E6
B	575	HIS	-	expression tag	UNP Q9H2E6
B	576	PRO	-	expression tag	UNP Q9H2E6
B	577	GLN	-	expression tag	UNP Q9H2E6
B	578	PHE	-	expression tag	UNP Q9H2E6
B	579	GLU	-	expression tag	UNP Q9H2E6
B	580	LYS	-	expression tag	UNP Q9H2E6

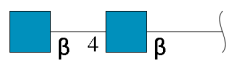
- Molecule 2 is a protein called TcsL.

Mol	Chain	Residues	Atoms					AltConf	Trace
			Total	C	N	O	S		
2	C	219	1589	1043	251	291	4	0	0

There are 32 discrepancies between the modelled and reference sequences:

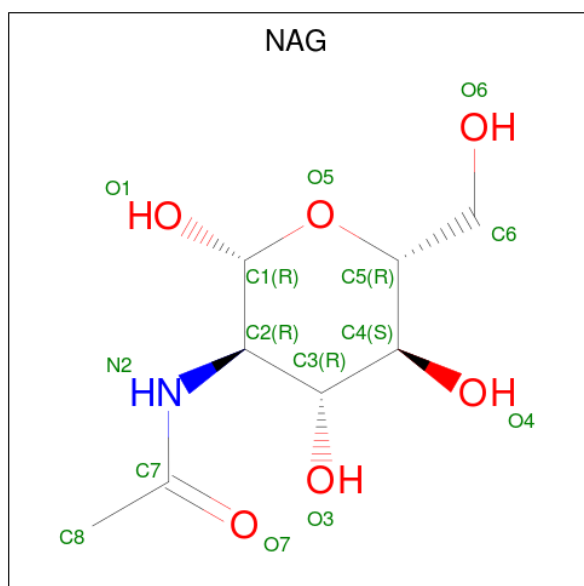
Chain	Residue	Modelled	Actual	Comment	Reference
C	1268	SER	-	expression tag	UNP V5T923
C	1269	ALA	-	expression tag	UNP V5T923
C	1270	TRP	-	expression tag	UNP V5T923
C	1271	SER	-	expression tag	UNP V5T923
C	1272	HIS	-	expression tag	UNP V5T923
C	1273	PRO	-	expression tag	UNP V5T923
C	1274	GLN	-	expression tag	UNP V5T923
C	1275	PHE	-	expression tag	UNP V5T923
C	1276	GLU	-	expression tag	UNP V5T923
C	1277	LYS	-	expression tag	UNP V5T923
C	1278	GLU	-	expression tag	UNP V5T923
C	1279	ASN	-	expression tag	UNP V5T923
C	1280	LEU	-	expression tag	UNP V5T923
C	1281	TYR	-	expression tag	UNP V5T923
C	1282	PHE	-	expression tag	UNP V5T923
C	1283	GLN	-	expression tag	UNP V5T923
C	1284	GLY	-	expression tag	UNP V5T923
C	1805	GLY	-	expression tag	UNP V5T923
C	1806	SER	-	expression tag	UNP V5T923
C	1807	GLU	-	expression tag	UNP V5T923
C	1808	ASN	-	expression tag	UNP V5T923
C	1809	LEU	-	expression tag	UNP V5T923
C	1810	TYR	-	expression tag	UNP V5T923
C	1811	PHE	-	expression tag	UNP V5T923
C	1812	GLN	-	expression tag	UNP V5T923
C	1813	GLY	-	expression tag	UNP V5T923
C	1814	HIS	-	expression tag	UNP V5T923
C	1815	HIS	-	expression tag	UNP V5T923
C	1816	HIS	-	expression tag	UNP V5T923
C	1817	HIS	-	expression tag	UNP V5T923
C	1818	HIS	-	expression tag	UNP V5T923
C	1819	HIS	-	expression tag	UNP V5T923

- Molecule 3 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
			Total	C	N	O		
3	D	2	Total	C	N	O	0	0
			28	16	2	10		
3	E	2	Total	C	N	O	0	0
			28	16	2	10		
3	F	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).

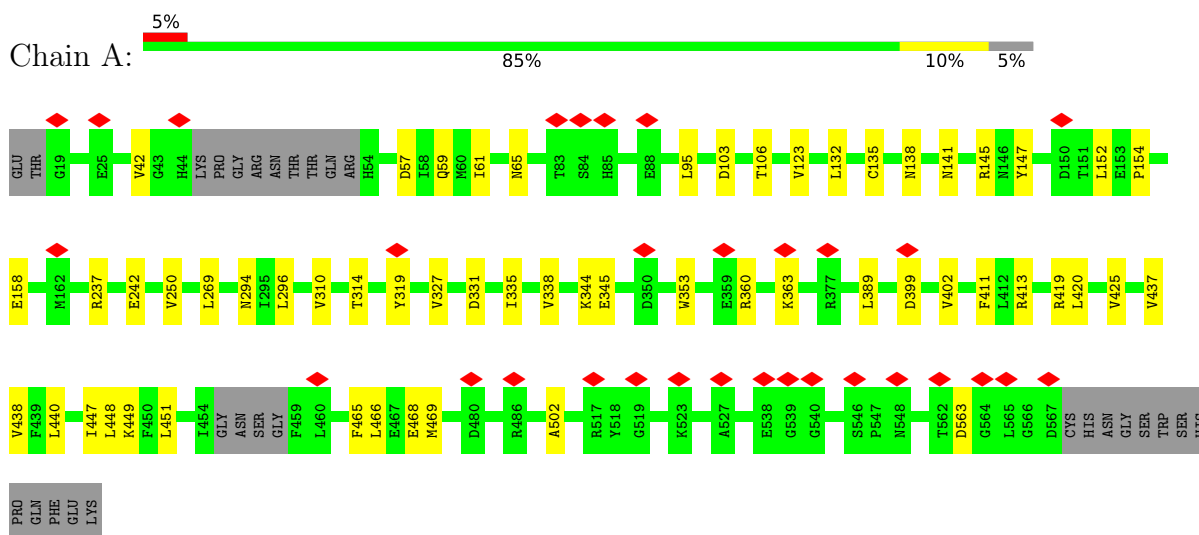


Mol	Chain	Residues	Atoms				AltConf
			Total	C	N	O	
4	A	1	Total	C	N	O	0
			28	16	2	10	
4	A	1	Total	C	N	O	0
			28	16	2	10	
4	B	1	Total	C	N	O	0
			28	16	2	10	
4	B	1	Total	C	N	O	0
			28	16	2	10	

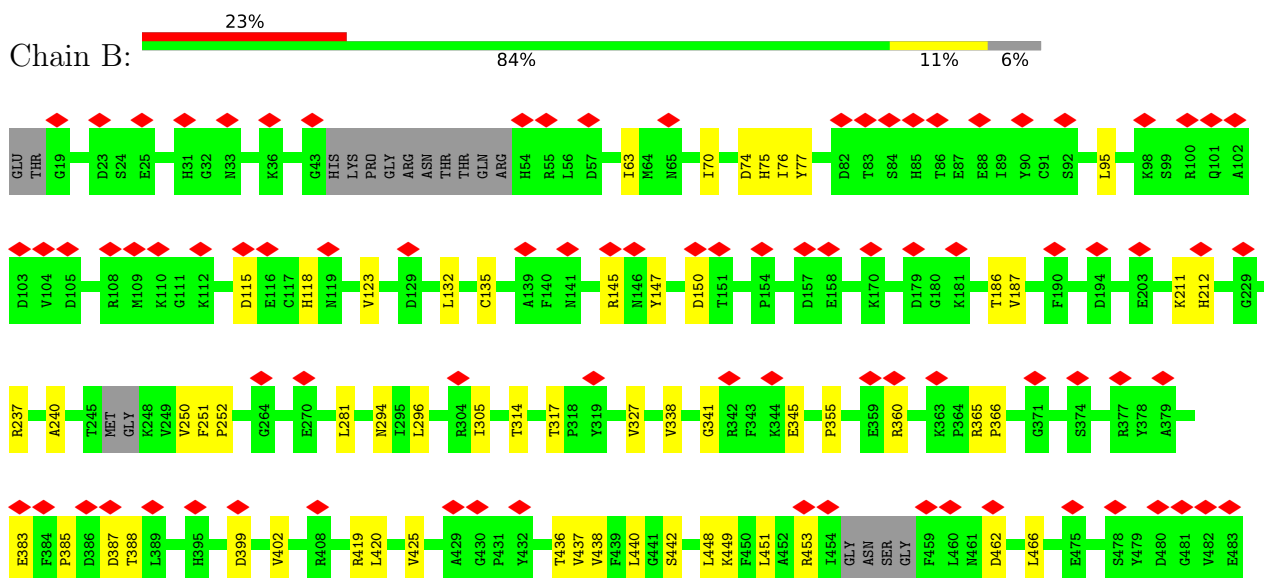
### 3 Residue-property plots [i](#)

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: SEMA6A



#### • Molecule 1: SEMA6A





MAGE  
MAGE

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

Chain F:

100%

MAGE  
MAGE



## 4 Experimental information

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, C1	Depositor
Number of particles used	179188	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE CORRECTION	Depositor
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose ( $e^-/\text{\AA}^2$ )	45.24	Depositor
Minimum defocus (nm)	Not provided	
Maximum defocus (nm)	Not provided	
Magnification	Not provided	
Image detector	OTHER	Depositor
Maximum map value	16.825	Depositor
Minimum map value	-12.241	Depositor
Average map value	0.000	Depositor
Map value standard deviation	1.000	Depositor
Recommended contour level	2.3	Depositor
Map size ( $\text{\AA}$ )	125.659996, 120.509995, 148.31999	wwPDB
Map dimensions	144, 117, 122	wwPDB
Map angles ( $^\circ$ )	90.0, 90.0, 90.0	wwPDB
Pixel spacing ( $\text{\AA}$ )	1.03, 1.03, 1.03	Depositor

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAG

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.25	0/4270	0.43	0/5786
1	B	0.24	0/4059	0.41	0/5523
2	C	0.25	0/1615	0.48	0/2196
All	All	0.25	0/9944	0.43	0/13505

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	A	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	363	LYS	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	A	4170	0	4009	31	0
1	B	3964	0	3670	33	0
2	C	1589	0	1428	33	0
3	D	28	0	25	0	0
3	E	28	0	25	0	0
3	F	28	0	25	0	0
4	A	28	0	26	1	0
4	B	28	0	26	0	0
All	All	9863	0	9234	97	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.

All (97) 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:123:VAL:HB	1:B:135:CYS:HB2	1.71	0.73
1:B:338:VAL:HG11	1:B:402:VAL:HG22	1.75	0.69
2:C:1495:ARG:HB2	2:C:1507:ILE:HG12	1.77	0.67
1:A:338:VAL:HG11	1:A:402:VAL:HG22	1.79	0.62
1:A:314:THR:HG22	1:A:327:VAL:HG22	1.82	0.61
2:C:1437:ILE:HD11	2:C:1497:ILE:HD13	1.81	0.61
1:A:319:TYR:HA	1:A:419:ARG:HH12	1.67	0.59
1:A:123:VAL:HB	1:A:135:CYS:HB2	1.84	0.59
1:A:345:GLU:OE2	1:A:360:ARG:NH2	2.37	0.58
2:C:1540:LEU:HD22	2:C:1552:LEU:HD11	1.86	0.58
1:A:65:ASN:OD1	4:A:606:NAG:N2	2.38	0.57
1:B:314:THR:HG22	1:B:327:VAL:HG22	1.87	0.57
1:B:341:GLY:O	1:B:365:ARG:NH2	2.37	0.57
2:C:1483:LEU:HD21	2:C:1527:LEU:HD21	1.88	0.56
1:B:240:ALA:HB2	1:B:251:PHE:HD2	1.70	0.56
1:B:237:ARG:NH1	1:B:296:LEU:O	2.39	0.55
2:C:1466:ASP:HB3	2:C:1469:THR:OG1	2.07	0.55
2:C:1495:ARG:NE	2:C:1497:ILE:HD11	2.22	0.54
1:A:237:ARG:NH1	1:A:296:LEU:O	2.38	0.54
1:B:150:ASP:OD1	1:B:150:ASP:N	2.40	0.54
1:B:186:THR:OG1	1:B:187:VAL:N	2.40	0.52
2:C:1589:ILE:HG13	2:C:1591:ILE:HG13	1.91	0.52
1:A:95:LEU:HD12	1:A:152:LEU:HD22	1.90	0.52
2:C:1434:ILE:O	2:C:1437:ILE:HG22	2.10	0.51
2:C:1409:LEU:HB3	2:C:1412:ILE:HD12	1.93	0.51
1:A:425:VAL:HG22	1:A:438:VAL:HG13	1.91	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:THR:OG1	1:B:419:ARG:NH1	2.42	0.51
1:B:383:GLU:N	1:B:383:GLU:OE1	2.44	0.50
1:A:451:LEU:HB2	1:A:466:LEU:HD11	1.92	0.50
1:A:61:ILE:HD13	1:A:502:ALA:HB2	1.94	0.50
2:C:1429:LEU:HB2	2:C:1462:TYR:HB2	1.94	0.49
2:C:1547:THR:OG1	2:C:1548:ASN:OD1	2.27	0.49
1:B:420:LEU:HD13	1:B:440:LEU:HD13	1.94	0.49
2:C:1539:SER:O	2:C:1556:TYR:N	2.46	0.49
1:B:442:SER:H	1:B:487:ILE:HD12	1.78	0.49
2:C:1530:ASN:HD22	2:C:1537:LYS:HE3	1.77	0.49
1:A:132:LEU:N	1:A:147:TYR:O	2.45	0.49
2:C:1551:LYS:HD2	2:C:1608:ASP:HB2	1.95	0.48
1:B:76:ILE:HD12	1:B:95:LEU:HD13	1.96	0.48
1:B:252:PRO:HB2	1:B:281:LEU:HD12	1.96	0.48
1:A:103:ASP:HA	1:A:106:THR:HG22	1.95	0.48
1:B:250:VAL:O	1:B:294:ASN:HB3	2.13	0.48
1:B:74:ASP:O	1:B:75:HIS:ND1	2.46	0.48
2:C:1532:PHE:HB3	2:C:1537:LYS:HA	1.96	0.47
2:C:1432:ASN:N	2:C:1432:ASN:OD1	2.40	0.47
1:B:345:GLU:OE1	1:B:360:ARG:NH2	2.48	0.47
1:B:115:ASP:O	1:B:118:HIS:ND1	2.39	0.47
1:B:145:ARG:HD2	1:B:147:TYR:CZ	2.50	0.46
2:C:1506:PHE:HB3	2:C:1547:THR:HG22	1.96	0.46
1:A:145:ARG:HD2	1:A:147:TYR:CZ	2.50	0.46
2:C:1505:LEU:HG	2:C:1506:PHE:HD2	1.80	0.46
1:B:366:PRO:HG3	1:B:388:THR:HG23	1.98	0.46
1:A:145:ARG:HD3	1:A:154:PRO:HB3	1.98	0.46
1:A:335:ILE:O	1:A:338:VAL:HG12	2.17	0.45
2:C:1474:PHE:CE2	2:C:1483:LEU:HD23	2.52	0.45
2:C:1540:LEU:HB2	2:C:1552:LEU:HD21	1.98	0.45
2:C:1553:ASN:OD1	2:C:1554:GLY:N	2.48	0.45
1:B:70:ILE:HB	1:B:77:TYR:HB2	1.98	0.45
1:B:451:LEU:HB2	1:B:466:LEU:HD11	1.98	0.45
2:C:1499:MET:HB3	2:C:1500:PRO:HD3	1.98	0.45
1:A:420:LEU:HD13	1:A:440:LEU:HD13	1.98	0.44
1:A:138:ASN:HB3	1:A:141:ASN:O	2.18	0.44
1:A:420:LEU:HD21	1:A:448:LEU:HD22	2.00	0.44
1:A:447:ILE:HB	1:A:469:MET:HG2	1.99	0.44
2:C:1418:ILE:HG22	2:C:1425:TYR:HB2	1.99	0.44
2:C:1498:TYR:CD2	2:C:1500:PRO:HD2	2.53	0.43
1:A:310:VAL:HG22	1:A:331:ASP:HA	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:211:LYS:HG2	1:B:212:HIS:ND1	2.34	0.43
2:C:1540:LEU:HA	2:C:1555:VAL:HA	2.01	0.43
1:B:425:VAL:HG22	1:B:438:VAL:HG13	2.01	0.43
2:C:1544:ILE:HG23	2:C:1550:ILE:HG12	2.00	0.43
1:A:242:GLU:HA	1:A:353:TRP:NE1	2.34	0.43
1:B:63:ILE:HD13	1:B:493:ASP:HB2	2.00	0.43
1:A:57:ASP:O	1:A:59:GLN:NE2	2.40	0.42
1:B:453:ARG:NH1	1:B:462:ASP:O	2.52	0.42
1:B:437:VAL:HG11	1:B:449:LYS:HE3	2.02	0.42
1:A:344:LYS:HE3	1:A:399:ASP:HA	2.02	0.41
2:C:1497:ILE:HD12	2:C:1497:ILE:N	2.34	0.41
1:A:411:PHE:CE2	1:A:413:ARG:HG2	2.56	0.41
1:A:269:LEU:HD12	1:A:389:LEU:HB3	2.02	0.41
2:C:1495:ARG:HE	2:C:1507:ILE:HD11	1.86	0.41
1:B:76:ILE:HB	1:B:95:LEU:HB3	2.01	0.41
1:B:132:LEU:HD23	1:B:132:LEU:HA	1.90	0.41
1:A:563:ASP:N	1:A:563:ASP:OD1	2.54	0.41
1:B:420:LEU:HD21	1:B:448:LEU:HD22	2.01	0.41
1:B:305:ILE:HD12	1:B:436:THR:HG21	2.03	0.41
2:C:1437:ILE:O	2:C:1437:ILE:HG13	2.20	0.41
2:C:1494:ILE:HD11	2:C:1516:ILE:HD13	2.03	0.41
1:A:250:VAL:O	1:A:294:ASN:HB3	2.20	0.40
1:B:355:PRO:HB3	1:B:399:ASP:OD2	2.21	0.40
1:A:437:VAL:HG11	1:A:449:LYS:HE3	2.02	0.40
1:B:385:PRO:HB2	1:B:387:ASP:OD1	2.21	0.40
1:A:465:PHE:HZ	1:A:468:GLU:HB2	1.85	0.40
1:A:145:ARG:NH1	1:A:158:GLU:OE1	2.55	0.40
2:C:1437:ILE:HG12	2:C:1495:ARG:NH1	2.37	0.40
2:C:1495:ARG:HH21	2:C:1507:ILE:HD11	1.86	0.40
2:C:1562:VAL:HG13	2:C:1566:LEU:HD12	2.04	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	A	530/564 (94%)	510 (96%)	19 (4%)	1 (0%)	47	77
1	B	524/564 (93%)	509 (97%)	15 (3%)	0	100	100
2	C	211/552 (38%)	196 (93%)	15 (7%)	0	100	100
All	All	1265/1680 (75%)	1215 (96%)	49 (4%)	1 (0%)	54	81

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	42	VAL

### 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	A	445/494 (90%)	445 (100%)	0	100	100
1	B	393/494 (80%)	393 (100%)	0	100	100
2	C	145/515 (28%)	145 (100%)	0	100	100
All	All	983/1503 (65%)	983 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

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

6 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	D	1	3,1	14,14,15	0.23	0	17,19,21	0.46	0
3	NAG	D	2	3	14,14,15	0.27	0	17,19,21	0.43	0
3	NAG	E	1	3,1	14,14,15	0.24	0	17,19,21	0.50	0
3	NAG	E	2	3	14,14,15	0.25	0	17,19,21	0.44	0
3	NAG	F	1	3,1	14,14,15	0.37	0	17,19,21	0.59	0
3	NAG	F	2	3	14,14,15	0.17	0	17,19,21	0.52	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
3	NAG	D	1	3,1	-	4/6/23/26	0/1/1/1
3	NAG	D	2	3	-	3/6/23/26	0/1/1/1
3	NAG	E	1	3,1	-	3/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	F	2	3	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (16) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	E	2	NAG	O5-C5-C6-O6
3	F	2	NAG	O5-C5-C6-O6

*Continued on next page...*

*Continued from previous page...*

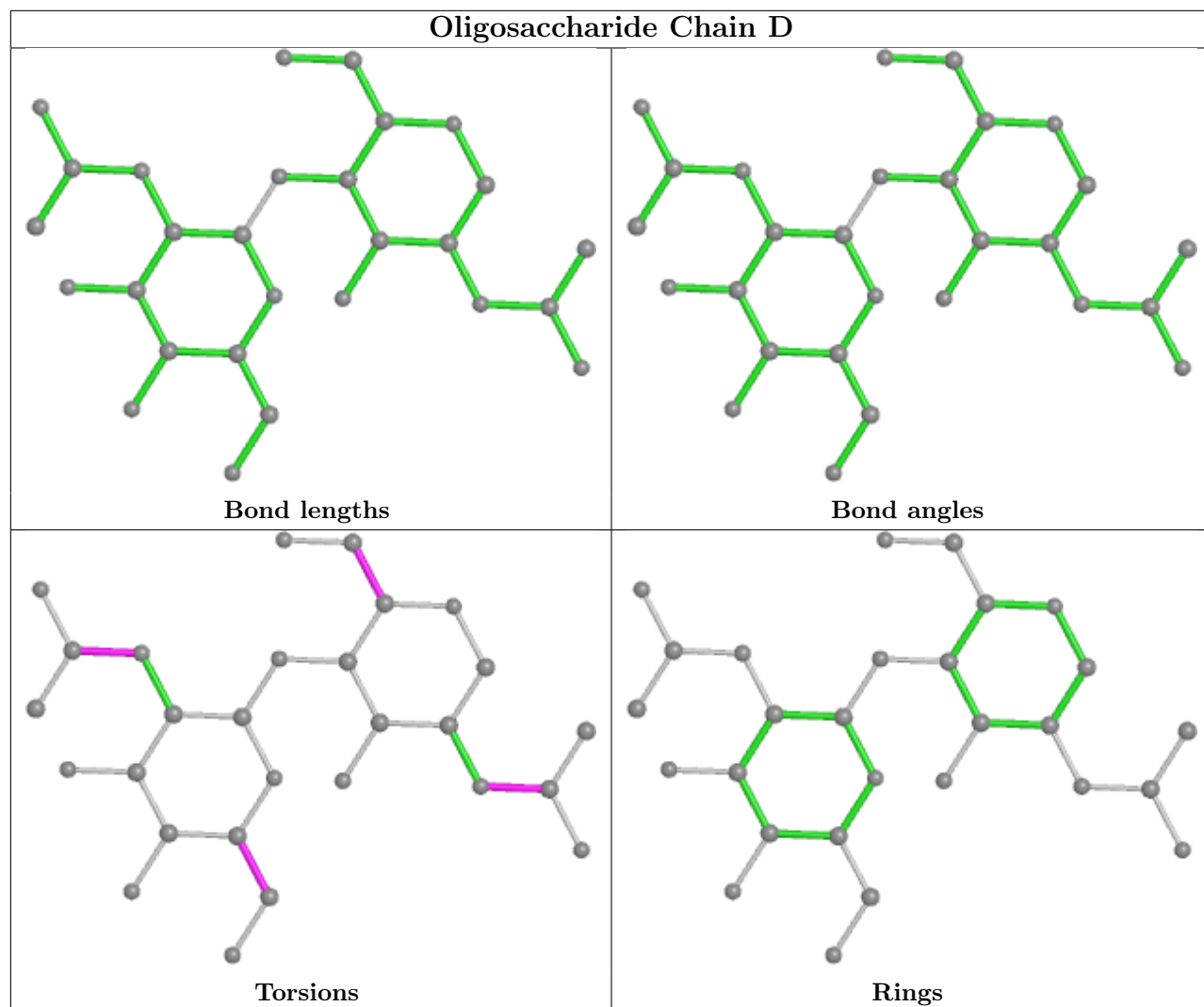
Mol	Chain	Res	Type	Atoms
3	E	2	NAG	C4-C5-C6-O6
3	D	1	NAG	C8-C7-N2-C2
3	D	1	NAG	O7-C7-N2-C2
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
3	E	1	NAG	C8-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
3	F	1	NAG	O5-C5-C6-O6
3	F	2	NAG	C4-C5-C6-O6
3	F	1	NAG	C4-C5-C6-O6
3	D	1	NAG	O5-C5-C6-O6
3	E	1	NAG	O5-C5-C6-O6
3	D	2	NAG	C4-C5-C6-O6
3	D	1	NAG	C4-C5-C6-O6

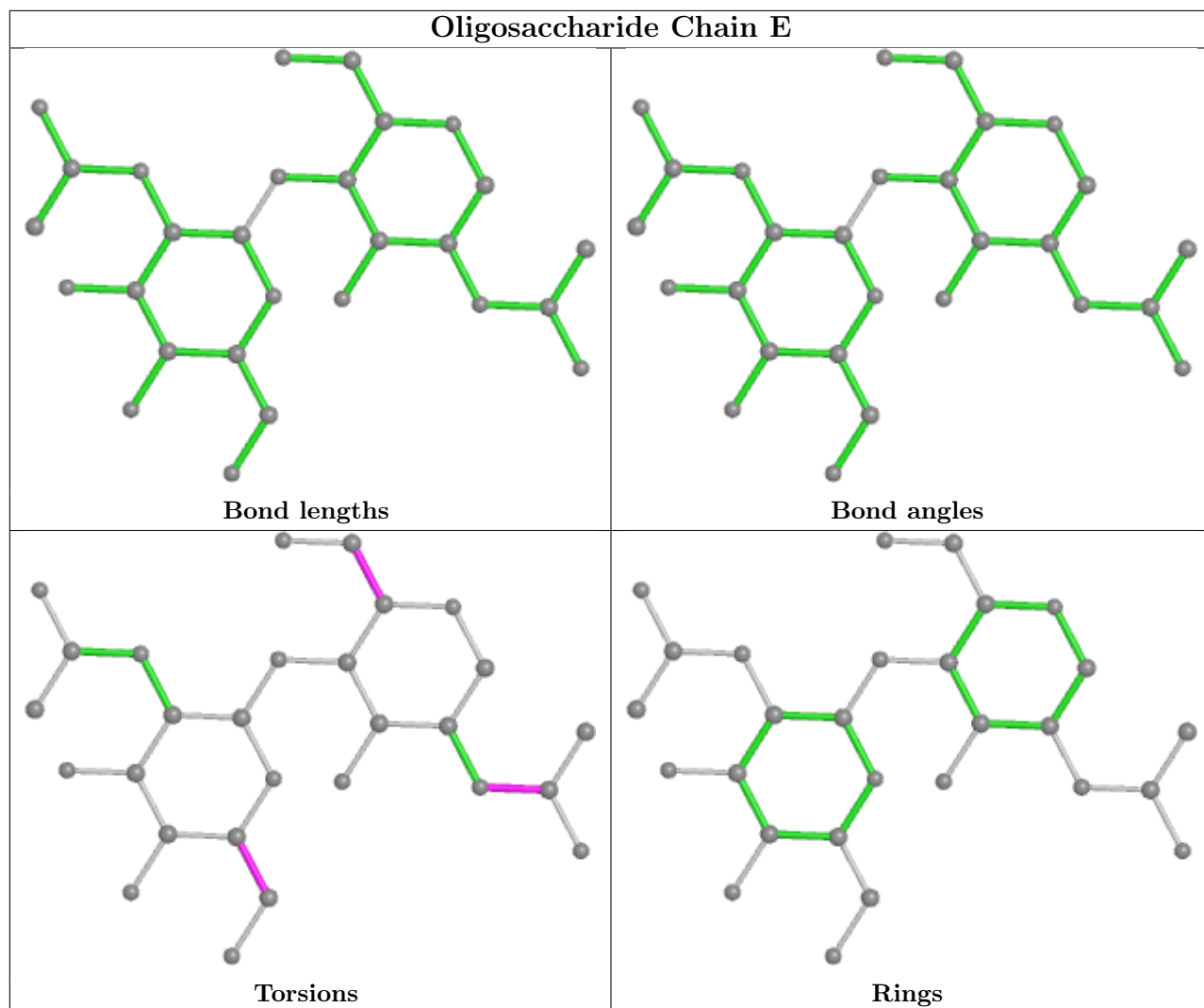
There are no ring outliers.

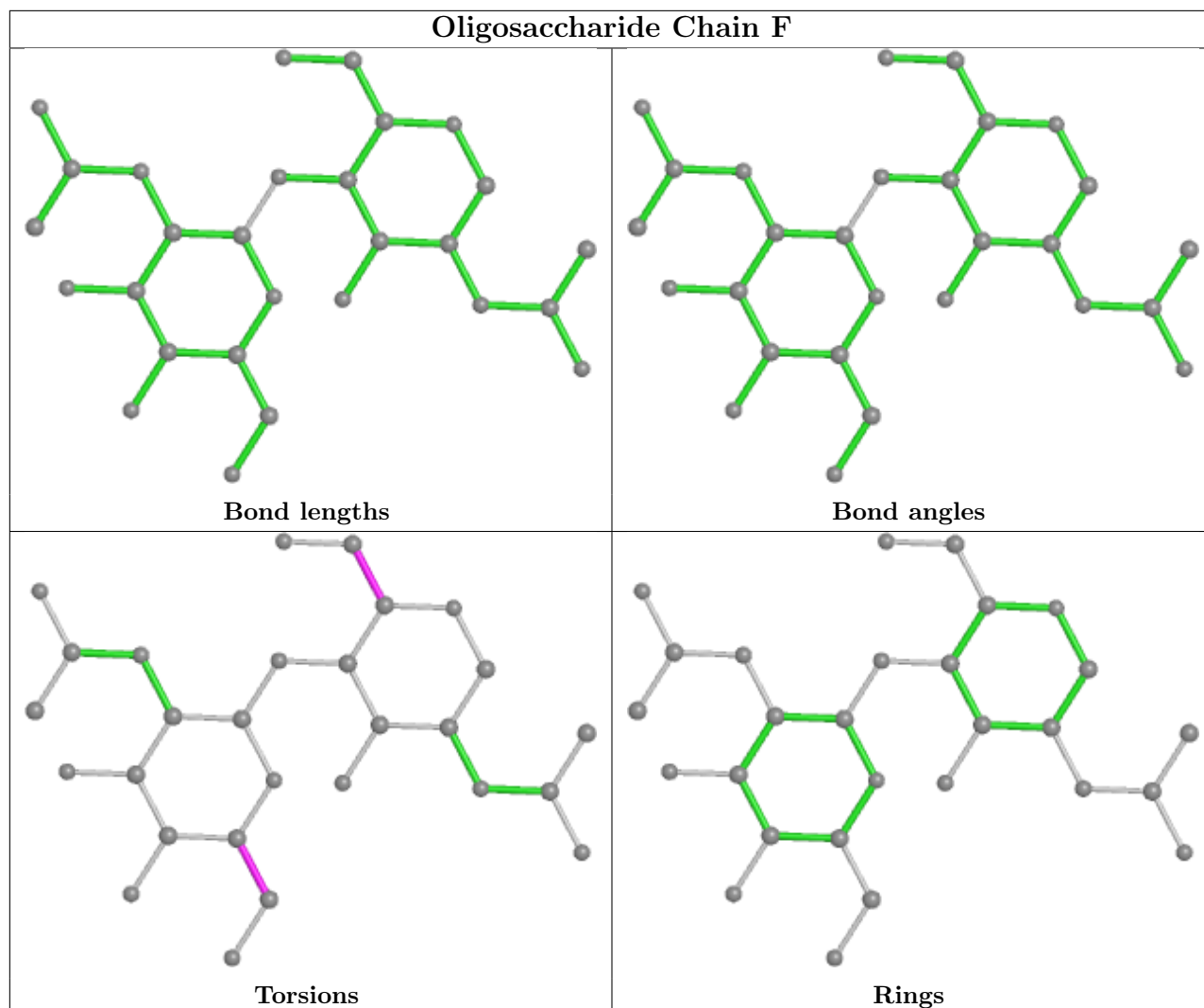
No monomer is involved in short contacts.

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









## 5.6 Ligand geometry [i](#)

4 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	$\# Z  > 2$
4	NAG	A	605	1	14,14,15	0.26	0	17,19,21	0.45	0
4	NAG	A	606	1	14,14,15	0.40	0	17,19,21	0.53	0
4	NAG	B	1303	1	14,14,15	0.22	0	17,19,21	0.41	0
4	NAG	B	1304	1	14,14,15	0.30	0	17,19,21	0.49	0

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	A	605	1	-	3/6/23/26	0/1/1/1
4	NAG	A	606	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1303	1	-	2/6/23/26	0/1/1/1
4	NAG	B	1304	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	606	NAG	O5-C5-C6-O6
4	B	1303	NAG	O5-C5-C6-O6
4	B	1304	NAG	O5-C5-C6-O6
4	A	606	NAG	C4-C5-C6-O6
4	A	605	NAG	C8-C7-N2-C2
4	A	605	NAG	O7-C7-N2-C2
4	B	1304	NAG	C4-C5-C6-O6
4	B	1303	NAG	C4-C5-C6-O6
4	A	605	NAG	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	606	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.

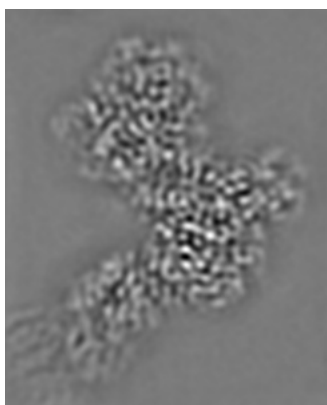
## 6 Map visualisation [i](#)

This section contains visualisations of the EMDB entry EMD-21898. These allow visual inspection of the internal detail of the map and identification of artifacts.

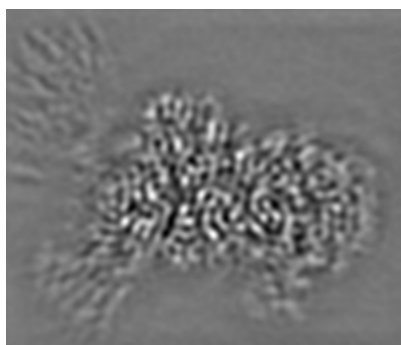
No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

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

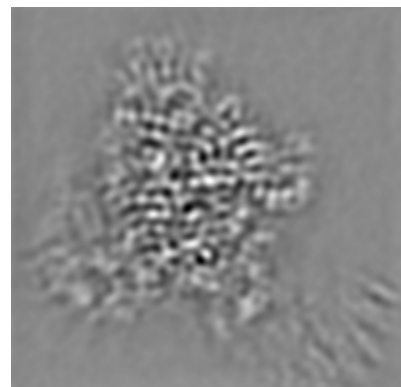
#### 6.1.1 Primary map



X



Y

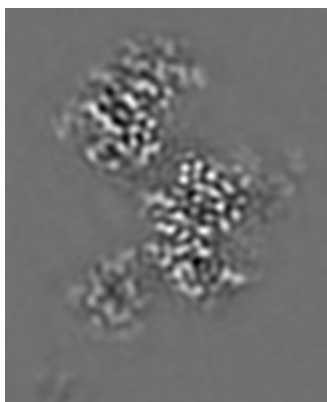


Z

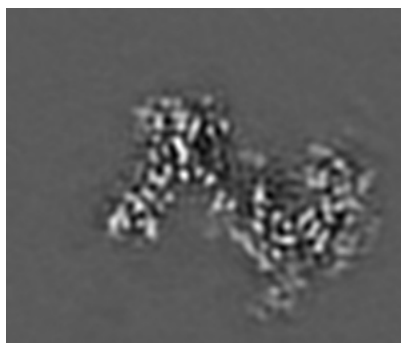
The images above show the map projected in three orthogonal directions.

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

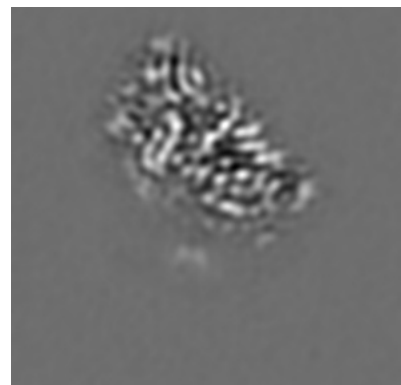
#### 6.2.1 Primary map



X Index: 61



Y Index: 58

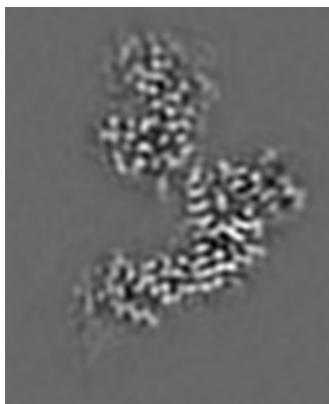


Z Index: 72

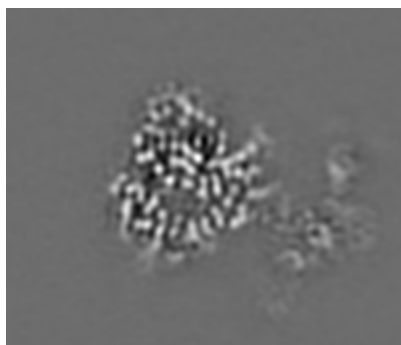
The images above show central slices of the map in three orthogonal directions.

## 6.3 Largest variance slices [i](#)

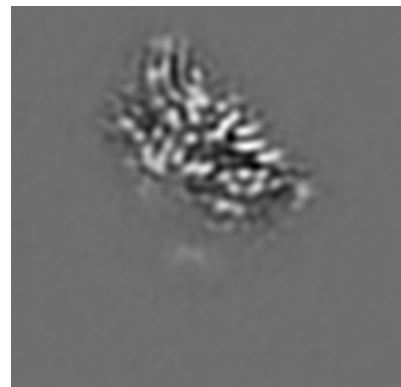
### 6.3.1 Primary map



X Index: 45



Y Index: 68

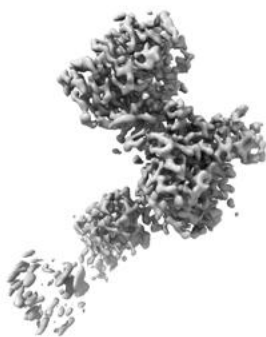


Z Index: 71

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

## 6.4 Orthogonal surface views [i](#)

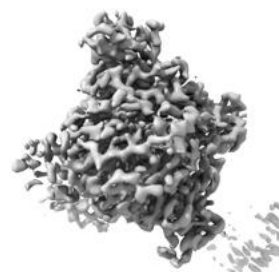
### 6.4.1 Primary map



X



Y



Z

The images above show the 3D surface view of the map at the recommended contour level 2.3. These images, in conjunction with the slice images, may facilitate assessment of whether an appropriate contour level has been provided.

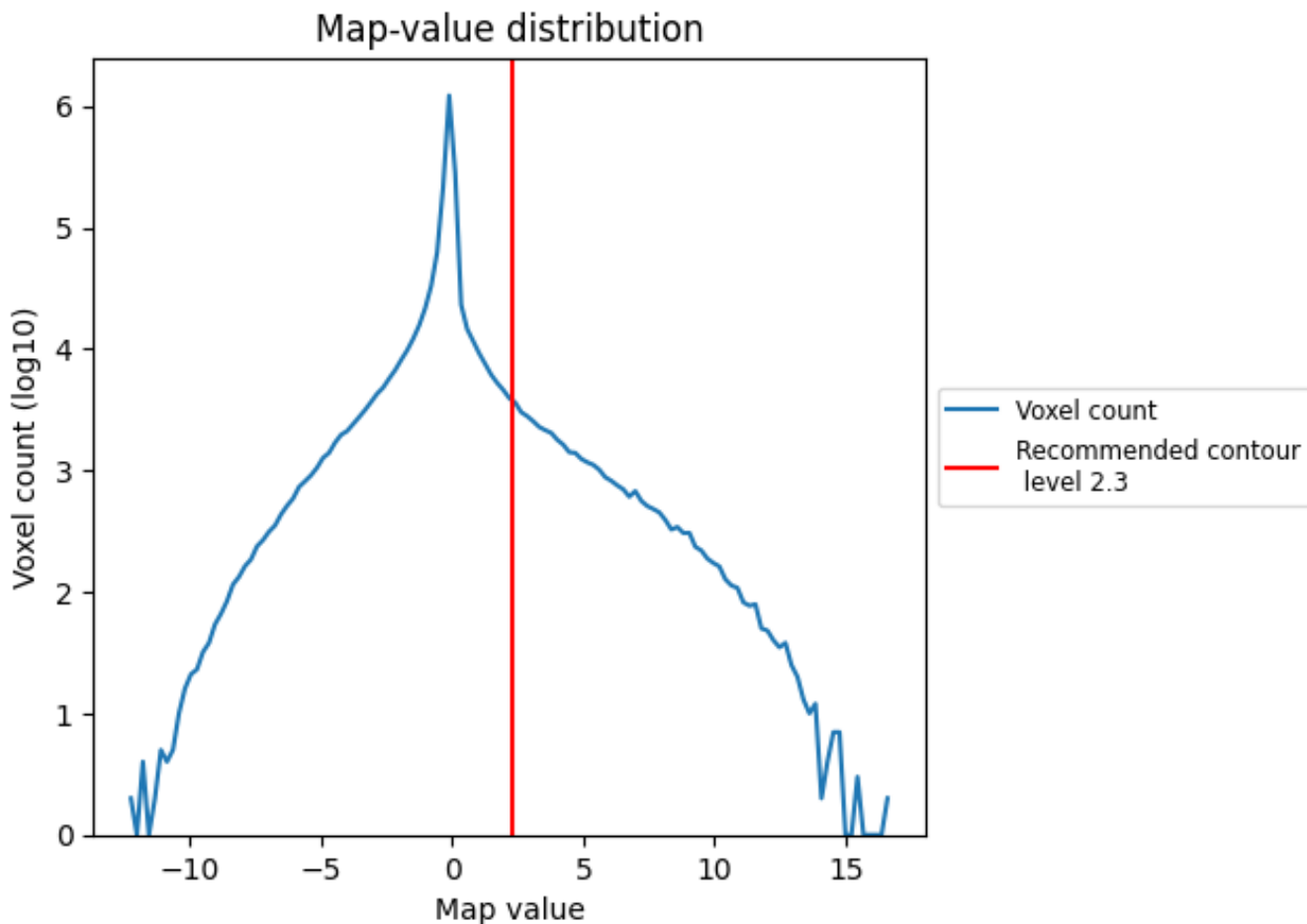
## 6.5 Mask visualisation

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.

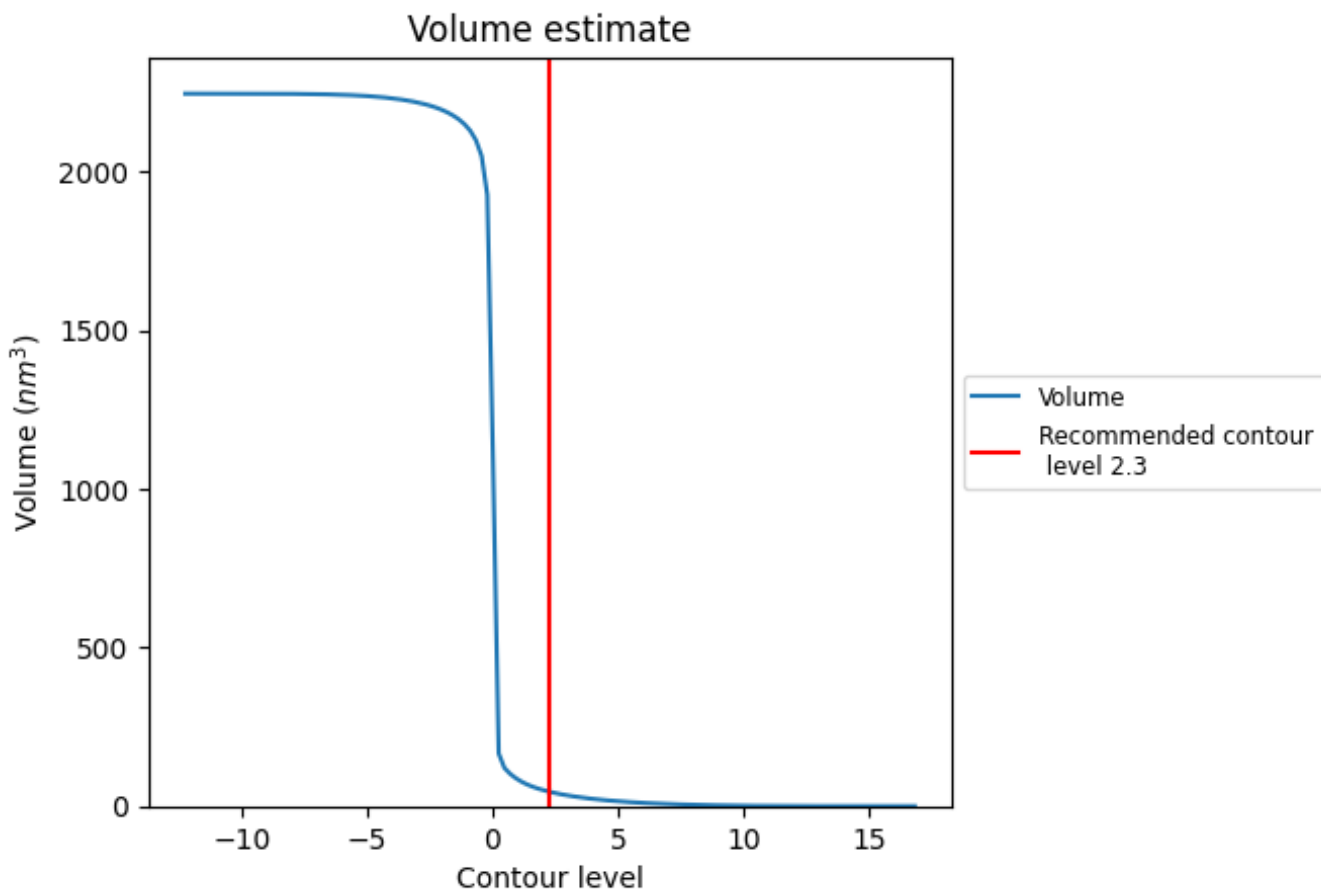
### 7.1 Map-value distribution [i](#)



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 45 nm<sup>3</sup>; this corresponds to an approximate mass of 40 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 [\(i\)](#)

This section was not generated. The rotationally averaged power spectrum is only generated for cubic maps.

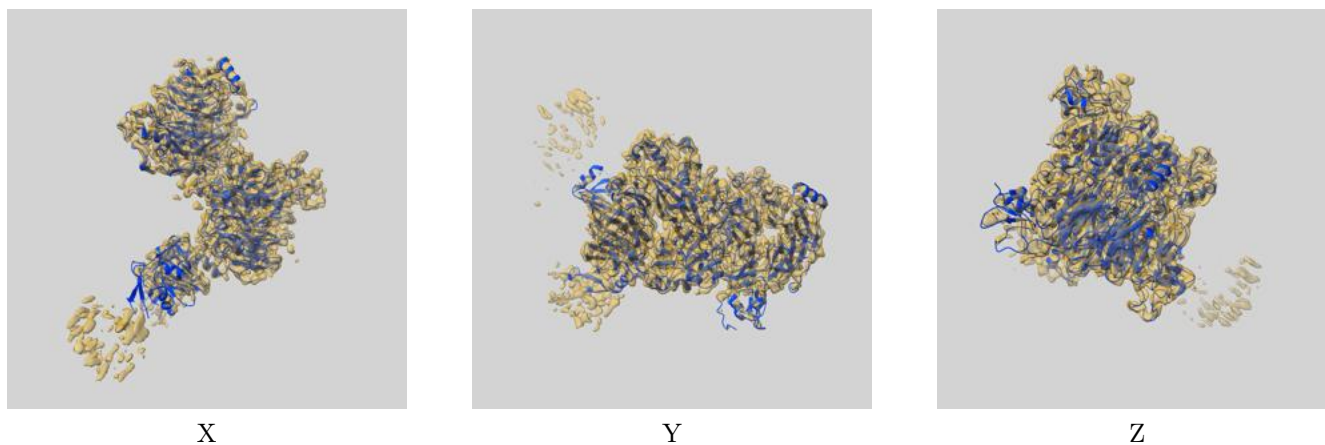
## 8 Fourier-Shell correlation

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

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

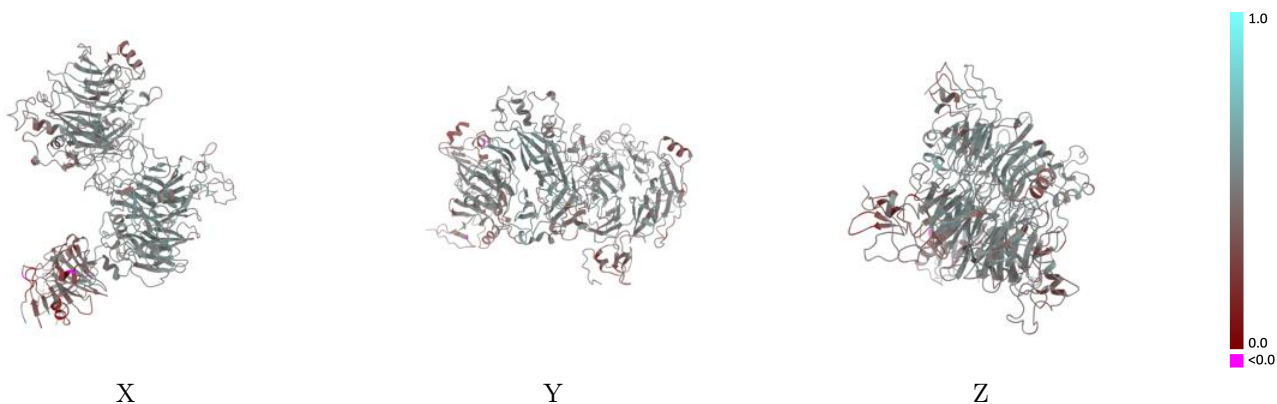
This section contains information regarding the fit between EMDB map EMD-21898 and PDB model 6WTS. Per-residue inclusion information can be found in section [3](#) on page [6](#).

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



The images above show the 3D surface view of the map at the recommended contour level 2.3 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 [\(i\)](#)



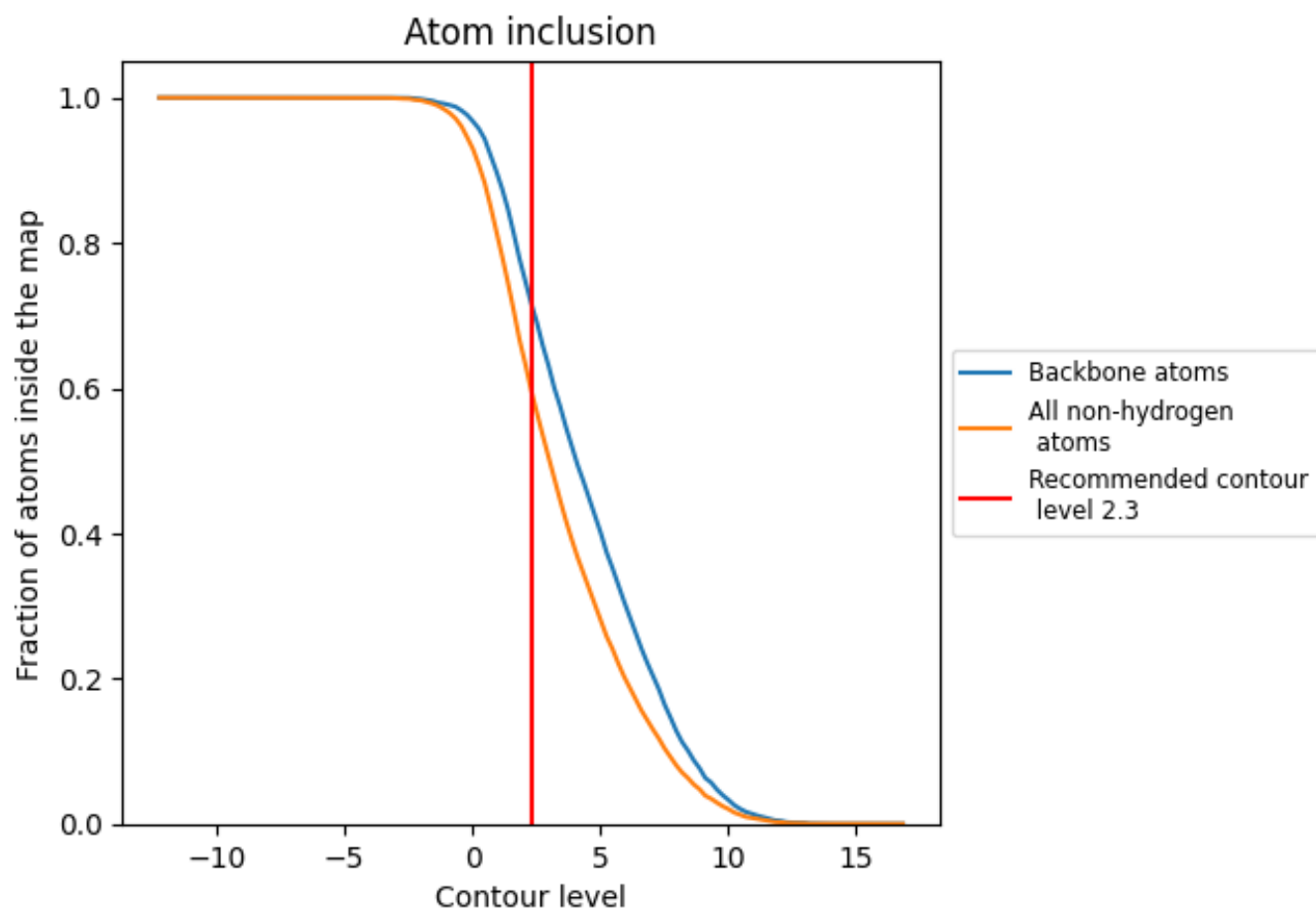
The images above show the model with each residue coloured according its Q-score. This shows their resolvability in the map with higher Q-score values reflecting better resolvability. Please note: Q-score is calculating the resolvability of atoms, and thus high values are only expected at resolutions 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 (2.3).















## 9.4 Atom inclusion [i](#)



At the recommended contour level, 72% of all backbone atoms, 60% of all non-hydrogen atoms, are inside the map.

## 9.5 Map-model fit summary [i](#)

The table lists the average atom inclusion at the recommended contour level (2.3) and Q-score for the entire model and for each chain.

Chain	Atom inclusion	Q-score
All	 0.5958	 0.4630
A	 0.6971	 0.5010
B	 0.5701	 0.4630
C	 0.3934	 0.3650
D	 0.6786	 0.4790
E	 0.6429	 0.4660
F	 0.5714	 0.4650

