



# Full wwPDB X-ray Structure Validation Report ⓘ

Oct 15, 2023 – 08:08 AM EDT

PDB ID : 8EQX  
Title : Co-crystal structure of Chaetomium glucosidase with compound 21  
Authors : Karade, S.S.; Mariuzza, R.A.  
Deposited on : 2022-10-10  
Resolution : 2.50 Å(reported)

This is a Full wwPDB X-ray Structure 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/XrayValidationReportHelp>

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:

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

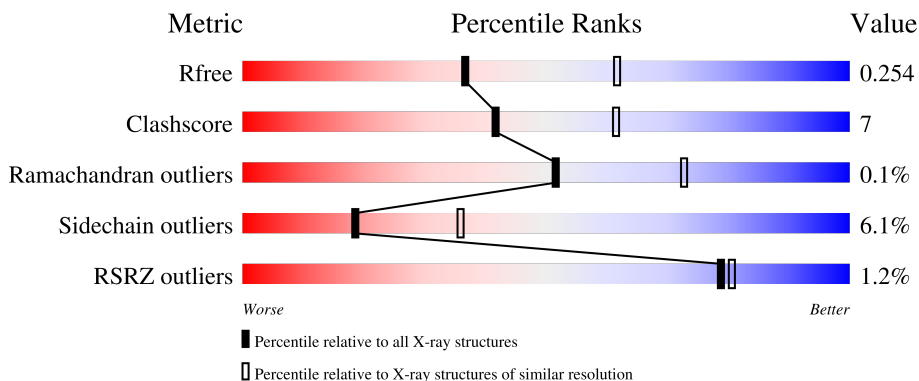
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

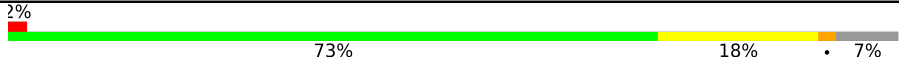

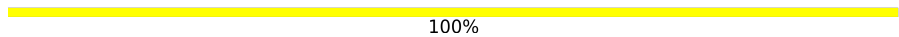
The reported resolution of this entry is 2.50 Å.

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)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower 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 electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	819	 2% 73% 18% • 7%
1	B	819	 80% 13% • 6%
2	C	2	 100%

## 2 Entry composition i

There are 6 unique types of molecules in this entry. The entry contains 12235 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, 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 Chaetomium alpha glucosidase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	765	6004	3850	1013	1128	13	0	1	0
1	B	767	6014	3859	1015	1127	13	0	0	0

There are 78 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	initiating methionine	UNP G0SFD1
A	0	GLY	-	expression tag	UNP G0SFD1
A	1	ILE	-	expression tag	UNP G0SFD1
A	2	LEU	-	expression tag	UNP G0SFD1
A	3	PRO	-	expression tag	UNP G0SFD1
A	4	SER	-	expression tag	UNP G0SFD1
A	5	PRO	-	expression tag	UNP G0SFD1
A	6	GLY	-	expression tag	UNP G0SFD1
A	7	MET	-	expression tag	UNP G0SFD1
A	8	PRO	-	expression tag	UNP G0SFD1
A	9	ALA	-	expression tag	UNP G0SFD1
A	10	LEU	-	expression tag	UNP G0SFD1
A	11	LEU	-	expression tag	UNP G0SFD1
A	12	SER	-	expression tag	UNP G0SFD1
A	13	LEU	-	expression tag	UNP G0SFD1
A	14	VAL	-	expression tag	UNP G0SFD1
A	15	SER	-	expression tag	UNP G0SFD1
A	16	LEU	-	expression tag	UNP G0SFD1
A	17	LEU	-	expression tag	UNP G0SFD1
A	18	SER	-	expression tag	UNP G0SFD1
A	19	VAL	-	expression tag	UNP G0SFD1
A	20	LEU	-	expression tag	UNP G0SFD1
A	21	LEU	-	expression tag	UNP G0SFD1
A	22	MET	-	expression tag	UNP G0SFD1
A	23	GLY	-	expression tag	UNP G0SFD1

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Chain	Residue	Modelled	Actual	Comment	Reference
A	24	CYS	-	expression tag	UNP G0SFD1
A	25	VAL	-	expression tag	UNP G0SFD1
A	26	ALA	-	expression tag	UNP G0SFD1
A	27	GLU	-	expression tag	UNP G0SFD1
A	28	THR	-	expression tag	UNP G0SFD1
A	29	GLY	-	expression tag	UNP G0SFD1
A	810	SER	-	expression tag	UNP G0SFD1
A	811	GLY	-	expression tag	UNP G0SFD1
A	812	HIS	-	expression tag	UNP G0SFD1
A	813	HIS	-	expression tag	UNP G0SFD1
A	814	HIS	-	expression tag	UNP G0SFD1
A	815	HIS	-	expression tag	UNP G0SFD1
A	816	HIS	-	expression tag	UNP G0SFD1
A	817	HIS	-	expression tag	UNP G0SFD1
B	-1	MET	-	initiating methionine	UNP G0SFD1
B	0	GLY	-	expression tag	UNP G0SFD1
B	1	ILE	-	expression tag	UNP G0SFD1
B	2	LEU	-	expression tag	UNP G0SFD1
B	3	PRO	-	expression tag	UNP G0SFD1
B	4	SER	-	expression tag	UNP G0SFD1
B	5	PRO	-	expression tag	UNP G0SFD1
B	6	GLY	-	expression tag	UNP G0SFD1
B	7	MET	-	expression tag	UNP G0SFD1
B	8	PRO	-	expression tag	UNP G0SFD1
B	9	ALA	-	expression tag	UNP G0SFD1
B	10	LEU	-	expression tag	UNP G0SFD1
B	11	LEU	-	expression tag	UNP G0SFD1
B	12	SER	-	expression tag	UNP G0SFD1
B	13	LEU	-	expression tag	UNP G0SFD1
B	14	VAL	-	expression tag	UNP G0SFD1
B	15	SER	-	expression tag	UNP G0SFD1
B	16	LEU	-	expression tag	UNP G0SFD1
B	17	LEU	-	expression tag	UNP G0SFD1
B	18	SER	-	expression tag	UNP G0SFD1
B	19	VAL	-	expression tag	UNP G0SFD1
B	20	LEU	-	expression tag	UNP G0SFD1
B	21	LEU	-	expression tag	UNP G0SFD1
B	22	MET	-	expression tag	UNP G0SFD1
B	23	GLY	-	expression tag	UNP G0SFD1
B	24	CYS	-	expression tag	UNP G0SFD1
B	25	VAL	-	expression tag	UNP G0SFD1
B	26	ALA	-	expression tag	UNP G0SFD1

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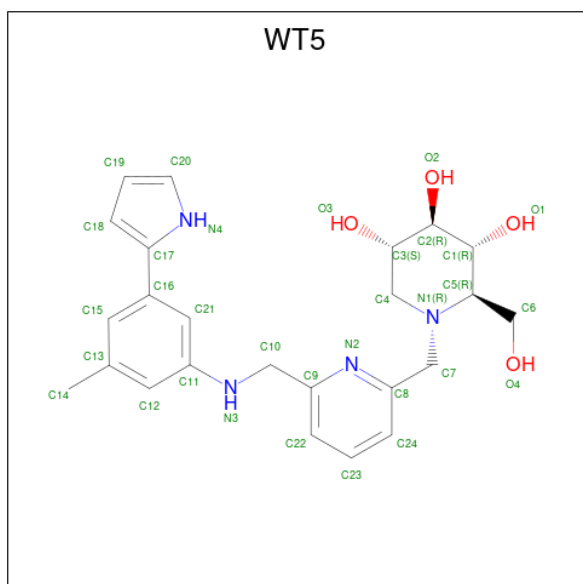
Chain	Residue	Modelled	Actual	Comment	Reference
B	27	GLU	-	expression tag	UNP G0SFD1
B	28	THR	-	expression tag	UNP G0SFD1
B	29	GLY	-	expression tag	UNP G0SFD1
B	810	SER	-	expression tag	UNP G0SFD1
B	811	GLY	-	expression tag	UNP G0SFD1
B	812	HIS	-	expression tag	UNP G0SFD1
B	813	HIS	-	expression tag	UNP G0SFD1
B	814	HIS	-	expression tag	UNP G0SFD1
B	815	HIS	-	expression tag	UNP G0SFD1
B	816	HIS	-	expression tag	UNP G0SFD1
B	817	HIS	-	expression tag	UNP G0SFD1

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



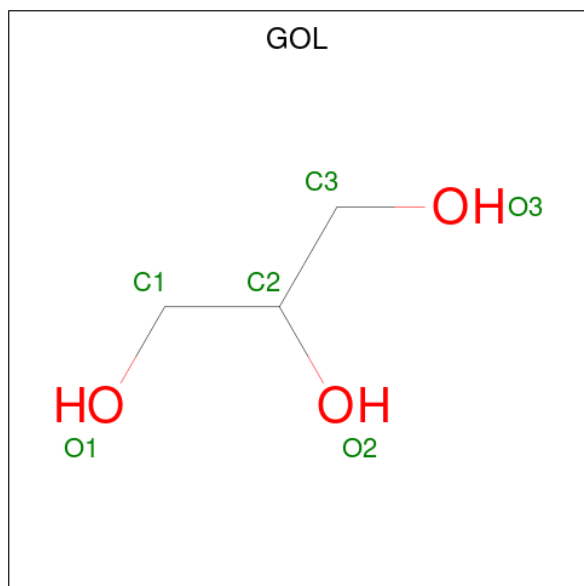
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	2	28	16	2	10	0	0	0

- Molecule 3 is (2R,3R,4R,5S)-2-(hydroxymethyl)-1-{{6-({[(5M)-3-methyl-5-(1H-pyrrol-2-yl)phenyl]amino}methyl)pyridin-2-yl]methyl}piperidine-3,4,5-triol (three-letter code: WT5) (formula: C<sub>24</sub>H<sub>30</sub>N<sub>4</sub>O<sub>4</sub>) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
3	A	1	32	24	4	4	0	0
3	A	1	32	24	4	4	0	0
3	B	1	32	24	4	4	0	0

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: C<sub>3</sub>H<sub>8</sub>O<sub>3</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
4	A	1	6	3	3	0	0
4	B	1	6	3	3	0	0
4	B	1	6	3	3	0	0
4	B	1	6	3	3	0	0

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	A	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0
5	B	1	Total O S 5 4 1	0	0

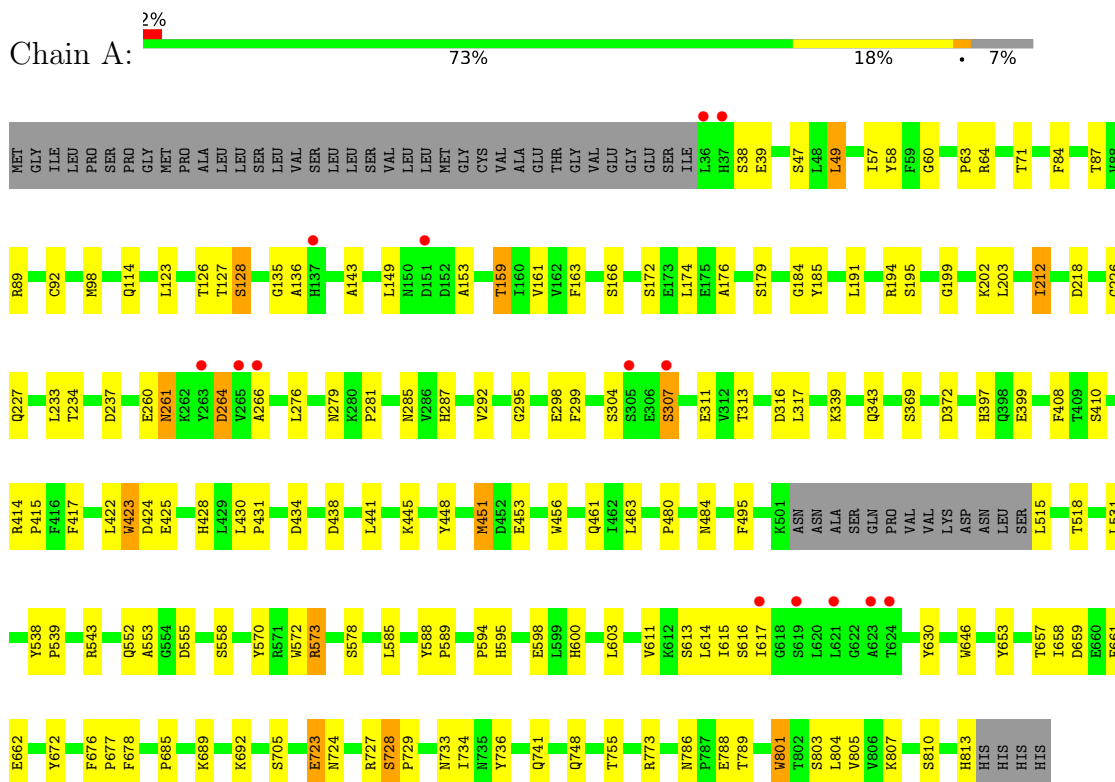
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	11	Total O 11 11	0	0
6	B	18	Total O 18 18	0	0

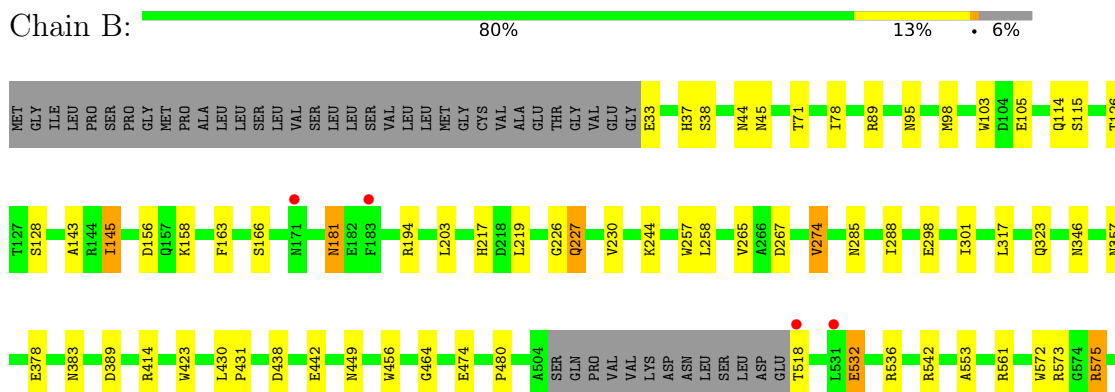
### 3 Residue-property plots

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 electron 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 dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). 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: Chaetomium alpha glucosidase



- Molecule 1: Chaetomium alpha glucosidase







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

Chain C:  100%

MAG1  
MAG2

## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	141.39Å 179.82Å 180.86Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.39 – 2.50 47.35 – 2.50	Depositor EDS
% Data completeness (in resolution range)	97.4 (47.39-2.50) 97.4 (47.35-2.50)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.08 (at 2.51Å)	Xtrriage
Refinement program	REFMAC 5.8.0258	Depositor
R, $R_{free}$	0.191 , 0.253 0.197 , 0.254	Depositor DCC
$R_{free}$ test set	3686 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	60.7	Xtrriage
Anisotropy	0.499	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 36.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.011 for -h,-l,-k	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12235	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	65.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.28% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 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, GOL, WT5, SO4

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	0.71	0/6182	0.87	2/8429 (0.0%)
1	B	0.71	0/6190	0.87	4/8443 (0.0%)
All	All	0.71	0/12372	0.87	6/16872 (0.0%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	575	ARG	CG-CD-NE	-6.76	97.60	111.80
1	A	805[A]	VAL	CA-C-O	6.57	133.89	120.10
1	A	805[B]	VAL	CA-C-O	6.57	133.89	120.10
1	B	812	HIS	CA-C-O	-5.67	108.20	120.10
1	B	702	GLU	N-CA-C	5.65	126.26	111.00
1	B	45	ASN	CB-CA-C	5.38	121.17	110.40

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts i

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	6004	0	5583	95	0
1	B	6014	0	5589	68	0
2	C	28	0	25	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	64	0	0	3	0
3	B	32	0	0	0	0
4	A	6	0	8	0	0
4	B	18	0	24	3	0
5	A	25	0	0	1	0
5	B	15	0	0	1	0
6	A	11	0	0	1	0
6	B	18	0	0	0	0
All	All	12235	0	11229	164	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 7.

All (164) 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:A:531:LEU:CB	6:A:1311:HOH:O	1.64	1.26
1:A:202:LYS:HE2	1:A:311:GLU:OE1	1.39	1.19
1:A:555:ASP:OD2	1:A:558:SER:OG	1.81	0.97
1:A:613:SER:O	1:A:617:ILE:HG13	1.70	0.90
1:B:575:ARG:NH1	1:B:598:GLU:OE2	2.05	0.89
1:B:257:TRP:HE1	4:B:1504:GOL:H31	1.37	0.87
1:A:202:LYS:CE	1:A:311:GLU:OE1	2.24	0.84
1:B:702:GLU:O	1:B:713:SER:HA	1.77	0.83
1:B:114:GLN:NE2	1:B:414:ARG:HH12	1.78	0.80
1:A:555:ASP:CG	1:A:558:SER:OG	2.20	0.80
1:B:572:TRP:H	1:B:600:HIS:HD2	1.32	0.77
1:B:553:ALA:O	1:B:573:ARG:NH2	2.20	0.74
1:B:766:ASN:O	1:B:770:THR:HG23	1.93	0.69
1:B:561:ARG:HE	1:B:664:HIS:HD2	1.39	0.68
1:A:39:GLU:HA	1:A:39:GLU:OE2	1.95	0.67
1:A:685:PRO:HG2	1:A:748:GLN:HE22	1.61	0.66
1:B:89:ARG:CZ	1:B:98:MET:CE	2.74	0.65
1:B:723:GLU:O	1:B:794:ARG:NH2	2.28	0.65
1:A:123:LEU:HD11	1:A:159:THR:HG21	1.79	0.64
1:B:786:ASN:HD22	1:B:789:THR:H	1.43	0.64
1:A:553:ALA:O	1:A:573:ARG:NH2	2.30	0.64
1:B:128:SER:O	1:B:143:ALA:HA	1.97	0.64
1:A:728:SER:H	1:A:729:PRO:CD	2.11	0.64
1:A:114:GLN:HB3	1:A:127:THR:OG1	1.99	0.62
1:A:736:TYR:OH	1:A:807:LYS:HE3	2.00	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:181:ASN:HD22	1:B:181:ASN:N	1.98	0.61
1:A:456:TRP:CE2	1:A:480:PRO:HA	2.35	0.61
1:A:135:GLY:CA	1:A:307:SER:OG	2.48	0.61
1:B:542:ARG:HD3	1:B:630:TYR:OH	2.01	0.61
1:A:135:GLY:HA3	1:A:307:SER:OG	2.00	0.60
1:A:64:ARG:HD3	1:A:408:PHE:CE1	2.36	0.60
1:A:555:ASP:OD1	1:A:558:SER:OG	2.19	0.60
1:A:430:LEU:HB2	1:A:431:PRO:HD3	1.84	0.60
1:A:572:TRP:H	1:A:600:HIS:HD2	1.47	0.59
1:A:578:SER:HB2	5:A:1205:SO4:O1	2.01	0.59
1:A:233:LEU:HD22	1:B:265:VAL:HG23	1.84	0.59
1:A:422:LEU:HB3	1:A:484:ASN:HD22	1.69	0.58
1:A:149:LEU:HD11	1:A:295:GLY:HA2	1.86	0.57
1:A:166:SER:HA	1:A:285:ASN:O	2.04	0.57
1:B:203:LEU:HD11	1:B:301:ILE:CG2	2.34	0.57
1:B:89:ARG:CZ	1:B:98:MET:HE1	2.35	0.57
1:B:226:GLY:H	1:B:227:GLN:HE22	1.52	0.56
1:A:428:HIS:O	1:A:431:PRO:HD2	2.05	0.56
1:B:103:TRP:H	1:B:357:ASN:ND2	2.03	0.55
1:B:114:GLN:HE22	1:B:414:ARG:HH22	1.54	0.55
1:B:671:GLY:HA2	1:B:703:LEU:HD21	1.89	0.55
1:A:728:SER:N	1:A:729:PRO:CD	2.71	0.54
1:B:114:GLN:HE22	1:B:414:ARG:HH12	1.55	0.54
1:B:78:ILE:HG23	1:B:78:ILE:O	2.08	0.54
1:A:136:ALA:N	1:A:307:SER:OG	2.39	0.54
1:B:786:ASN:ND2	1:B:788:GLU:H	2.06	0.54
1:B:783:GLU:OE1	1:B:795:THR:HB	2.08	0.53
1:A:57:ILE:HD11	1:A:60:GLY:HA3	1.89	0.53
1:B:578:SER:N	4:B:1502:GOL:O1	2.41	0.53
1:B:37:HIS:CG	1:B:532:GLU:HG2	2.44	0.53
1:B:89:ARG:NH2	1:B:98:MET:CE	2.72	0.53
1:B:733:ASN:HB3	1:B:801:TRP:CG	2.44	0.52
1:B:786:ASN:HD21	1:B:788:GLU:HB2	1.73	0.52
1:A:128:SER:O	1:A:143:ALA:HA	2.09	0.52
1:B:217:HIS:HD2	1:B:219:LEU:H	1.56	0.52
1:B:464:GLY:HA2	5:B:1507:SO4:O3	2.10	0.52
1:A:728:SER:N	1:A:729:PRO:HD3	2.24	0.51
1:B:727:ARG:O	1:B:728:SER:HB3	2.10	0.51
1:A:434:ASP:OD2	1:A:807:LYS:HD3	2.11	0.51
1:A:264:ASP:OD1	1:A:266:ALA:HB3	2.10	0.51
3:A:1203:WT5:C6	3:A:1203:WT5:C8	2.86	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:GLU:C	1:A:261:ASN:HD22	2.14	0.50
1:A:195:SER:O	1:A:199:GLY:N	2.45	0.50
1:A:685:PRO:CG	1:A:748:GLN:HE22	2.24	0.50
1:B:578:SER:CB	4:B:1502:GOL:O1	2.60	0.50
3:A:1203:WT5:C6	3:A:1203:WT5:C24	2.90	0.49
1:B:575:ARG:NH1	1:B:598:GLU:CD	2.66	0.49
1:A:646:TRP:CD2	1:A:689:LYS:HD3	2.47	0.49
1:B:103:TRP:H	1:B:357:ASN:HD21	1.60	0.49
1:A:453:GLU:O	1:A:543:ARG:HD3	2.12	0.49
1:A:313:THR:O	1:A:316:ASP:HB2	2.12	0.49
1:A:448:TYR:HD1	1:A:451:MET:CE	2.25	0.49
1:A:261:ASN:HD22	1:A:261:ASN:N	2.11	0.49
1:A:658:ILE:HD13	1:A:662:GLU:HA	1.95	0.48
1:B:346:ASN:N	1:B:346:ASN:OD1	2.42	0.48
1:B:430:LEU:HB2	1:B:431:PRO:HD3	1.96	0.48
1:B:166:SER:HA	1:B:285:ASN:O	2.13	0.48
1:A:456:TRP:CD2	1:A:480:PRO:HA	2.49	0.48
1:A:417:PHE:CZ	3:A:1201:WT5:C24	2.97	0.47
1:A:653:TYR:CD2	1:A:677:PRO:HG2	2.49	0.47
1:A:659:ASP:HB3	1:A:661:PHE:H	1.79	0.47
1:A:801:TRP:O	1:A:804:LEU:HB2	2.14	0.47
1:B:766:ASN:O	1:B:770:THR:CG2	2.61	0.47
1:A:184:GLY:HA3	1:A:227:GLN:HG3	1.96	0.47
1:A:339:LYS:HD3	1:A:810:SER:O	2.15	0.47
1:B:226:GLY:H	1:B:227:GLN:NE2	2.12	0.47
1:B:230:VAL:HA	1:B:288:ILE:O	2.14	0.47
1:B:378:GLU:HG2	1:B:389:ASP:O	2.14	0.47
1:A:49:LEU:O	1:A:63:PRO:HA	2.15	0.47
1:A:191:LEU:HD12	1:A:203:LEU:HD23	1.95	0.47
1:B:572:TRP:N	1:B:600:HIS:HD2	2.06	0.47
1:A:423:TRP:H	1:A:484:ASN:ND2	2.13	0.46
1:B:217:HIS:HE1	1:B:267:ASP:O	1.97	0.46
1:A:212:ILE:HD11	1:A:226:GLY:O	2.15	0.46
1:A:234:THR:HA	1:A:285:ASN:OD1	2.14	0.46
1:B:588:TYR:CD1	1:B:673:ILE:HG13	2.50	0.46
1:A:733:ASN:HB3	1:A:801:TRP:CG	2.51	0.46
1:B:156:ASP:O	1:B:158:LYS:NZ	2.47	0.46
1:B:561:ARG:HE	1:B:664:HIS:CD2	2.28	0.46
1:A:786:ASN:ND2	1:A:788:GLU:H	2.14	0.46
1:B:71:THR:HB	1:B:163:PHE:CZ	2.50	0.46
1:A:84:PHE:HA	1:A:87:THR:OG1	2.15	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:685:PRO:HG2	1:A:748:GLN:NE2	2.30	0.45
1:B:456:TRP:CE2	1:B:480:PRO:HA	2.51	0.45
1:B:89:ARG:NE	1:B:98:MET:HE1	2.32	0.45
1:A:728:SER:OG	1:A:729:PRO:HD3	2.17	0.45
1:A:414:ARG:N	1:A:415:PRO:HD2	2.33	0.44
1:B:145:ILE:CD1	1:B:145:ILE:N	2.80	0.44
1:A:179:SER:HB3	1:A:185:TYR:CD2	2.52	0.44
1:A:570:TYR:HB3	1:A:603:LEU:HD23	1.99	0.44
1:B:798:PHE:C	1:B:800:GLY:HA3	2.38	0.44
1:A:585:LEU:N	1:A:585:LEU:HD12	2.33	0.44
1:A:672:TYR:CG	1:A:734:ILE:HG21	2.53	0.44
1:B:114:GLN:HE21	1:B:414:ARG:HH12	1.59	0.43
1:B:532:GLU:O	1:B:536:ARG:HG3	2.18	0.43
1:B:572:TRP:H	1:B:600:HIS:CD2	2.21	0.43
1:B:590:ARG:HB3	1:B:591:PRO:HD2	1.98	0.43
1:B:600:HIS:HA	1:B:655:ASP:OD1	2.18	0.43
1:A:588:TYR:CD1	1:A:589:PRO:HD2	2.53	0.43
1:A:538:TYR:HB3	1:A:539:PRO:HD3	2.01	0.43
1:B:604:MET:CE	1:B:645:HIS:HD2	2.32	0.43
1:A:71:THR:HB	1:A:163:PHE:CZ	2.54	0.43
1:A:441:LEU:HD11	1:A:495:PHE:CE1	2.54	0.43
1:A:786:ASN:HD22	1:A:789:THR:H	1.66	0.43
1:A:614:LEU:HB3	1:A:630:TYR:CE2	2.54	0.42
1:A:149:LEU:HB3	1:A:153:ALA:HB3	2.00	0.42
1:B:691:GLY:HA3	1:B:752:TYR:CZ	2.55	0.42
1:B:590:ARG:HB3	1:B:591:PRO:CD	2.50	0.42
1:A:279:ASN:ND2	1:A:281:PRO:HD3	2.35	0.42
1:A:461:GLN:HE21	1:A:463:LEU:HD21	1.85	0.42
1:B:615:ILE:O	1:B:619:SER:HB3	2.20	0.42
1:A:89:ARG:NH2	1:A:98:MET:HE2	2.35	0.42
1:A:678:PHE:CE1	1:A:741:GLN:HB3	2.54	0.42
1:A:123:LEU:HD11	1:A:159:THR:CG2	2.48	0.42
1:A:594:PRO:HA	1:A:598:GLU:OE1	2.20	0.42
1:A:595:HIS:O	1:A:598:GLU:HG3	2.19	0.42
1:B:181:ASN:N	1:B:181:ASN:ND2	2.65	0.42
1:A:174:LEU:HD23	1:A:287:HIS:CD2	2.55	0.41
1:A:588:TYR:CG	1:A:589:PRO:HD2	2.55	0.41
1:A:174:LEU:HD23	1:A:287:HIS:HD2	1.85	0.41
1:B:258:LEU:HD11	1:B:274:VAL:HG22	2.02	0.41
1:B:588:TYR:CE1	1:B:673:ILE:HG13	2.55	0.41
1:A:58:TYR:CZ	1:A:92:CYS:HA	2.56	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:615:ILE:HG13	1:A:630:TYR:HB3	2.03	0.41
1:B:671:GLY:HA2	1:B:703:LEU:CD2	2.50	0.41
1:A:410:SER:OG	1:A:425:GLU:OE2	2.35	0.41
1:A:552:GLN:HB3	1:A:603:LEU:HD21	2.02	0.41
1:A:723:GLU:O	1:A:724:ASN:C	2.59	0.41
1:A:572:TRP:N	1:A:600:HIS:HD2	2.17	0.41
1:A:176:ALA:HA	1:A:191:LEU:HD23	2.02	0.40
1:A:194:ARG:HA	1:A:199:GLY:O	2.20	0.40
1:A:372:ASP:HA	1:A:399:GLU:HA	2.02	0.40
1:A:724:ASN:HA	1:A:727:ARG:HB2	2.02	0.40
1:B:728:SER:N	1:B:729:PRO:CD	2.84	0.40
1:A:161:VAL:HG11	1:A:299:PHE:CE2	2.57	0.40
1:A:276:LEU:HD13	1:A:292:VAL:CG2	2.51	0.40
1:B:799:THR:N	1:B:800:GLY:HA3	2.36	0.40
1:A:397:HIS:HD2	1:A:399:GLU:OE2	2.05	0.40
1:A:614:LEU:HD23	1:A:614:LEU:HA	1.96	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 X-ray entries followed by that with respect to entries of similar resolution.

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	762/819 (93%)	729 (96%)	32 (4%)	1 (0%)	51 73
1	B	763/819 (93%)	731 (96%)	31 (4%)	1 (0%)	51 73
All	All	1525/1638 (93%)	1460 (96%)	63 (4%)	2 (0%)	51 73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	728	SER
1	B	728	SER



### 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 X-ray entries followed by that with respect to entries of similar resolution.

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	610/707 (86%)	572 (94%)	38 (6%)	18	35
1	B	610/707 (86%)	574 (94%)	36 (6%)	19	37
All	All	1220/1414 (86%)	1146 (94%)	74 (6%)	18	36

All (74) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	38	SER
1	A	47	SER
1	A	49	LEU
1	A	126	THR
1	A	128	SER
1	A	159	THR
1	A	172	SER
1	A	212	ILE
1	A	218	ASP
1	A	237	ASP
1	A	261	ASN
1	A	264	ASP
1	A	298	GLU
1	A	304	SER
1	A	307	SER
1	A	317	LEU
1	A	343	GLN
1	A	369	SER
1	A	423	TRP
1	A	424	ASP
1	A	438	ASP
1	A	445	LYS
1	A	451	MET
1	A	515	LEU
1	A	518	THR
1	A	573	ARG
1	A	611	VAL

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<b>Mol</b>	<b>Chain</b>	<b>Res</b>	<b>Type</b>
1	A	616	SER
1	A	657	THR
1	A	676	PHE
1	A	692	LYS
1	A	705	SER
1	A	723	GLU
1	A	755	THR
1	A	773	ARG
1	A	801	TRP
1	A	803	SER
1	A	813	HIS
1	B	33	GLU
1	B	38	SER
1	B	44	ASN
1	B	95	ASN
1	B	105	GLU
1	B	115	SER
1	B	126	THR
1	B	145	ILE
1	B	181	ASN
1	B	194	ARG
1	B	227	GLN
1	B	244	LYS
1	B	274	VAL
1	B	298	GLU
1	B	317	LEU
1	B	323	GLN
1	B	383	ASN
1	B	423	TRP
1	B	438	ASP
1	B	442	GLU
1	B	449	ASN
1	B	474	GLU
1	B	518	THR
1	B	532	GLU
1	B	586	ASP
1	B	619	SER
1	B	657	THR
1	B	674	SER
1	B	676	PHE
1	B	692	LYS
1	B	711	SER

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Mol	Chain	Res	Type
1	B	725	TYR
1	B	758	ASP
1	B	770	THR
1	B	801	TRP
1	B	810	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	HIS
1	A	85	GLN
1	A	120	GLN
1	A	167	GLN
1	A	231	GLN
1	A	250	GLN
1	A	261	ASN
1	A	323	GLN
1	A	397	HIS
1	A	398	GLN
1	A	461	GLN
1	A	481	HIS
1	A	484	ASN
1	A	600	HIS
1	A	748	GLN
1	A	786	ASN
1	A	793	GLN
1	B	85	GLN
1	B	95	ASN
1	B	114	GLN
1	B	120	GLN
1	B	167	GLN
1	B	181	ASN
1	B	217	HIS
1	B	227	GLN
1	B	323	GLN
1	B	357	ASN
1	B	368	HIS
1	B	398	GLN
1	B	461	GLN
1	B	481	HIS
1	B	484	ASN
1	B	502	ASN

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Mol	Chain	Res	Type
1	B	600	HIS
1	B	639	HIS
1	B	664	HIS
1	B	744	ASN
1	B	748	GLN
1	B	786	ASN
1	B	793	GLN

### 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](#)

2 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	NAG	C	1	1,2	14,14,15	0.94	0	17,19,21	1.50	2 (11%)
2	NAG	C	2	2	14,14,15	0.77	0	17,19,21	1.72	3 (17%)

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
2	NAG	C	1	1,2	-	0/6/23/26	0/1/1/1
2	NAG	C	2	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	2	NAG	C4-C3-C2	-4.13	104.97	111.02
2	C	2	NAG	C1-O5-C5	3.91	117.49	112.19
2	C	1	NAG	C1-O5-C5	3.25	116.60	112.19
2	C	1	NAG	C2-N2-C7	-2.99	118.65	122.90
2	C	2	NAG	C6-C5-C4	-2.38	107.43	113.00

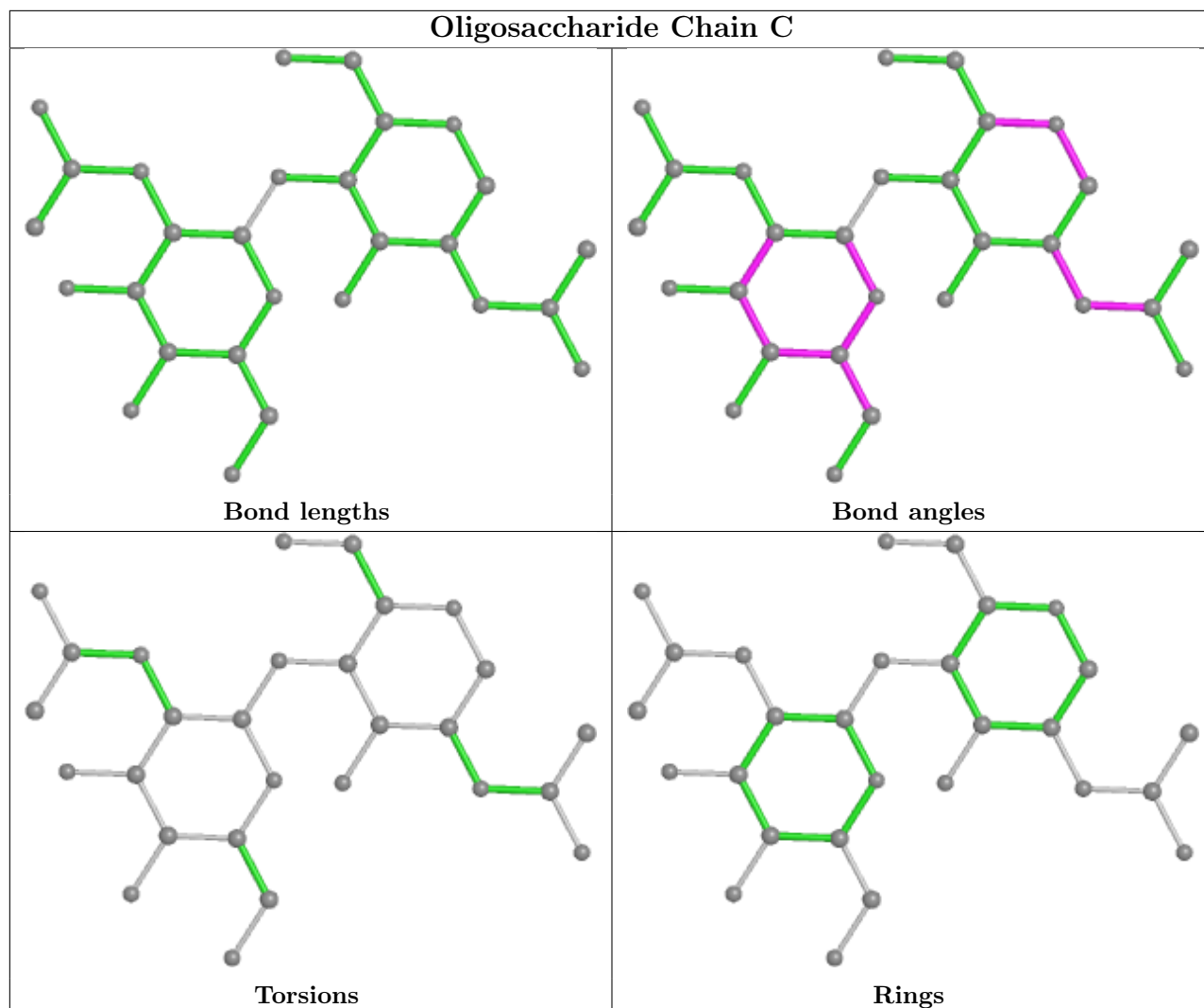
There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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



## 5.6 Ligand geometry [i](#)

15 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	GOL	B	1503	-	5,5,5	0.12	0	5,5,5	0.39	0
5	SO4	B	1506	-	4,4,4	0.22	0	6,6,6	0.15	0
3	WT5	B	1501	-	35,35,35	3.38	10 (28%)	46,49,49	1.62	10 (21%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	SO4	A	1208	-	4,4,4	0.35	0	6,6,6	0.20	0
4	GOL	A	1202	-	5,5,5	0.09	0	5,5,5	0.26	0
5	SO4	A	1204	-	4,4,4	0.35	0	6,6,6	0.10	0
3	WT5	A	1203	-	35,35,35	3.40	9 (25%)	46,49,49	1.87	13 (28%)
3	WT5	A	1201	-	35,35,35	3.30	9 (25%)	46,49,49	1.59	9 (19%)
4	GOL	B	1504	-	5,5,5	0.08	0	5,5,5	0.38	0
5	SO4	A	1207	-	4,4,4	0.29	0	6,6,6	0.12	0
5	SO4	B	1505	-	4,4,4	0.32	0	6,6,6	0.23	0
5	SO4	B	1507	-	4,4,4	0.50	0	6,6,6	0.34	0
5	SO4	A	1205	-	4,4,4	0.32	0	6,6,6	0.09	0
4	GOL	B	1502	-	5,5,5	0.16	0	5,5,5	0.46	0
5	SO4	A	1206	-	4,4,4	0.45	0	6,6,6	0.18	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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GOL	B	1503	-	-	4/4/4/4	-
3	WT5	B	1501	-	-	2/15/35/35	0/4/4/4
4	GOL	A	1202	-	-	4/4/4/4	-
3	WT5	A	1203	-	-	6/15/35/35	0/4/4/4
3	WT5	A	1201	-	-	0/15/35/35	0/4/4/4
4	GOL	B	1504	-	-	4/4/4/4	-
4	GOL	B	1502	-	-	4/4/4/4	-

All (28) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1203	WT5	C7-N1	-17.34	1.18	1.47
3	B	1501	WT5	C7-N1	-16.67	1.19	1.47
3	A	1201	WT5	C7-N1	-16.20	1.20	1.47
3	B	1501	WT5	C3-C2	-6.70	1.42	1.52
3	A	1201	WT5	C3-C2	-6.30	1.43	1.52
3	A	1203	WT5	C3-C2	-5.60	1.44	1.52
3	A	1201	WT5	C2-C1	-3.65	1.43	1.52
3	B	1501	WT5	C2-C1	-3.48	1.43	1.52
3	A	1203	WT5	C2-C1	-3.22	1.44	1.52
3	B	1501	WT5	C17-N4	-2.70	1.29	1.37

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1501	WT5	C8-N2	-2.67	1.30	1.34
3	B	1501	WT5	C4-N1	-2.67	1.43	1.47
3	A	1201	WT5	C17-N4	-2.61	1.29	1.37
3	B	1501	WT5	C5-N1	-2.60	1.42	1.48
3	A	1203	WT5	C4-N1	-2.56	1.43	1.47
3	A	1203	WT5	C5-N1	-2.50	1.42	1.48
3	A	1203	WT5	C16-C17	2.41	1.52	1.48
3	A	1203	WT5	C17-N4	-2.33	1.30	1.37
3	A	1201	WT5	C18-C17	-2.31	1.37	1.40
3	A	1203	WT5	C18-C17	-2.23	1.37	1.40
3	B	1501	WT5	C18-C17	-2.21	1.37	1.40
3	A	1201	WT5	C11-N3	2.19	1.45	1.38
3	A	1201	WT5	C5-N1	-2.17	1.43	1.48
3	B	1501	WT5	C9-N2	-2.13	1.31	1.34
3	A	1201	WT5	C4-N1	-2.12	1.44	1.47
3	A	1201	WT5	C16-C17	2.08	1.52	1.48
3	A	1203	WT5	O2-C2	2.05	1.47	1.43
3	B	1501	WT5	C11-N3	2.04	1.44	1.38

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1203	WT5	C7-C8-N2	4.87	124.18	115.89
3	A	1201	WT5	C18-C17-C16	-4.23	124.82	128.77
3	B	1501	WT5	C18-C17-C16	-4.13	124.91	128.77
3	A	1203	WT5	C10-C9-N2	3.71	123.13	116.61
3	B	1501	WT5	C16-C15-C13	-3.58	118.66	121.28
3	A	1203	WT5	C7-C8-C24	-3.50	114.12	121.24
3	A	1201	WT5	C7-C8-N2	3.27	121.45	115.89
3	A	1201	WT5	C7-N1-C5	-3.19	106.53	112.97
3	A	1203	WT5	C7-N1-C5	3.15	119.33	112.97
3	A	1203	WT5	C7-N1-C4	2.97	116.02	110.31
3	B	1501	WT5	C7-N1-C4	2.92	115.91	110.31
3	A	1203	WT5	C10-C9-C22	-2.87	115.47	121.48
3	A	1203	WT5	C20-N4-C17	2.76	111.68	104.44
3	A	1203	WT5	C4-N1-C5	2.73	116.02	109.69
3	B	1501	WT5	C9-N2-C8	2.68	121.42	118.16
3	A	1203	WT5	C8-C7-N1	2.60	118.18	112.30
3	B	1501	WT5	C21-C16-C15	2.59	122.14	118.31
3	A	1201	WT5	C9-N2-C8	2.57	121.29	118.16
3	B	1501	WT5	C7-C8-N2	2.56	120.25	115.89
3	A	1201	WT5	O1-C1-C2	-2.44	104.72	110.35

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1201	WT5	C10-C9-N2	2.41	120.84	116.61
3	A	1201	WT5	O4-C6-C5	-2.40	106.28	111.42
3	B	1501	WT5	C19-C18-C17	-2.39	105.06	107.02
3	A	1201	WT5	C20-N4-C17	2.22	110.27	104.44
3	B	1501	WT5	C15-C16-C17	-2.22	117.37	120.59
3	A	1203	WT5	C15-C16-C17	-2.22	117.38	120.59
3	A	1203	WT5	C6-C5-C1	-2.19	109.55	112.90
3	A	1201	WT5	C15-C16-C17	-2.18	117.43	120.59
3	A	1203	WT5	C24-C23-C22	-2.17	117.17	120.25
3	B	1501	WT5	C14-C13-C15	-2.16	117.74	120.94
3	A	1203	WT5	C2-C1-C5	-2.12	107.78	111.37
3	B	1501	WT5	C20-N4-C17	2.07	109.88	104.44

There are no chirality outliers.

All (24) torsion outliers are listed below:

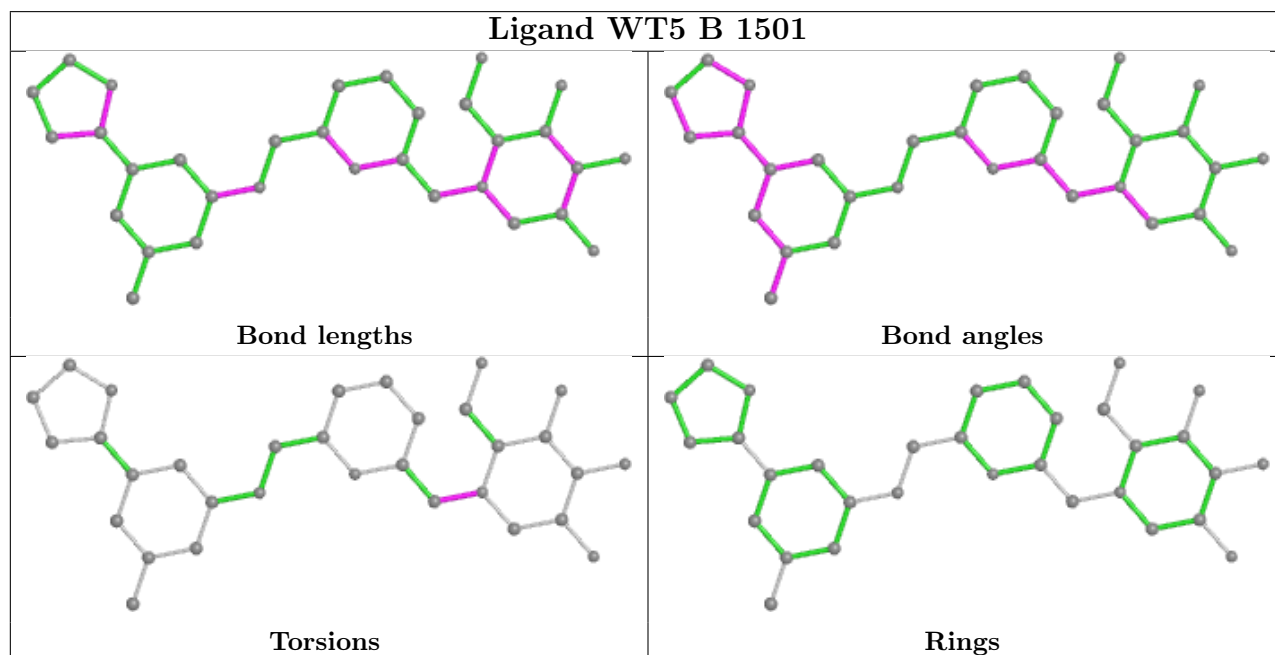
Mol	Chain	Res	Type	Atoms
3	A	1203	WT5	C8-C7-N1-C4
3	A	1203	WT5	C8-C7-N1-C5
3	A	1203	WT5	C15-C16-C17-C18
3	A	1203	WT5	C21-C16-C17-C18
3	A	1203	WT5	C15-C16-C17-N4
3	A	1203	WT5	C21-C16-C17-N4
4	A	1202	GOL	O1-C1-C2-C3
4	A	1202	GOL	C1-C2-C3-O3
4	B	1502	GOL	O1-C1-C2-C3
4	B	1503	GOL	O1-C1-C2-O2
4	B	1503	GOL	O1-C1-C2-C3
4	B	1503	GOL	C1-C2-C3-O3
4	B	1504	GOL	O1-C1-C2-C3
4	B	1504	GOL	C1-C2-C3-O3
4	A	1202	GOL	O1-C1-C2-O2
4	B	1502	GOL	O1-C1-C2-O2
4	B	1503	GOL	O2-C2-C3-O3
3	B	1501	WT5	C8-C7-N1-C4
4	A	1202	GOL	O2-C2-C3-O3
4	B	1504	GOL	O1-C1-C2-O2
4	B	1504	GOL	O2-C2-C3-O3
3	B	1501	WT5	C8-C7-N1-C5
4	B	1502	GOL	O2-C2-C3-O3
4	B	1502	GOL	C1-C2-C3-O3

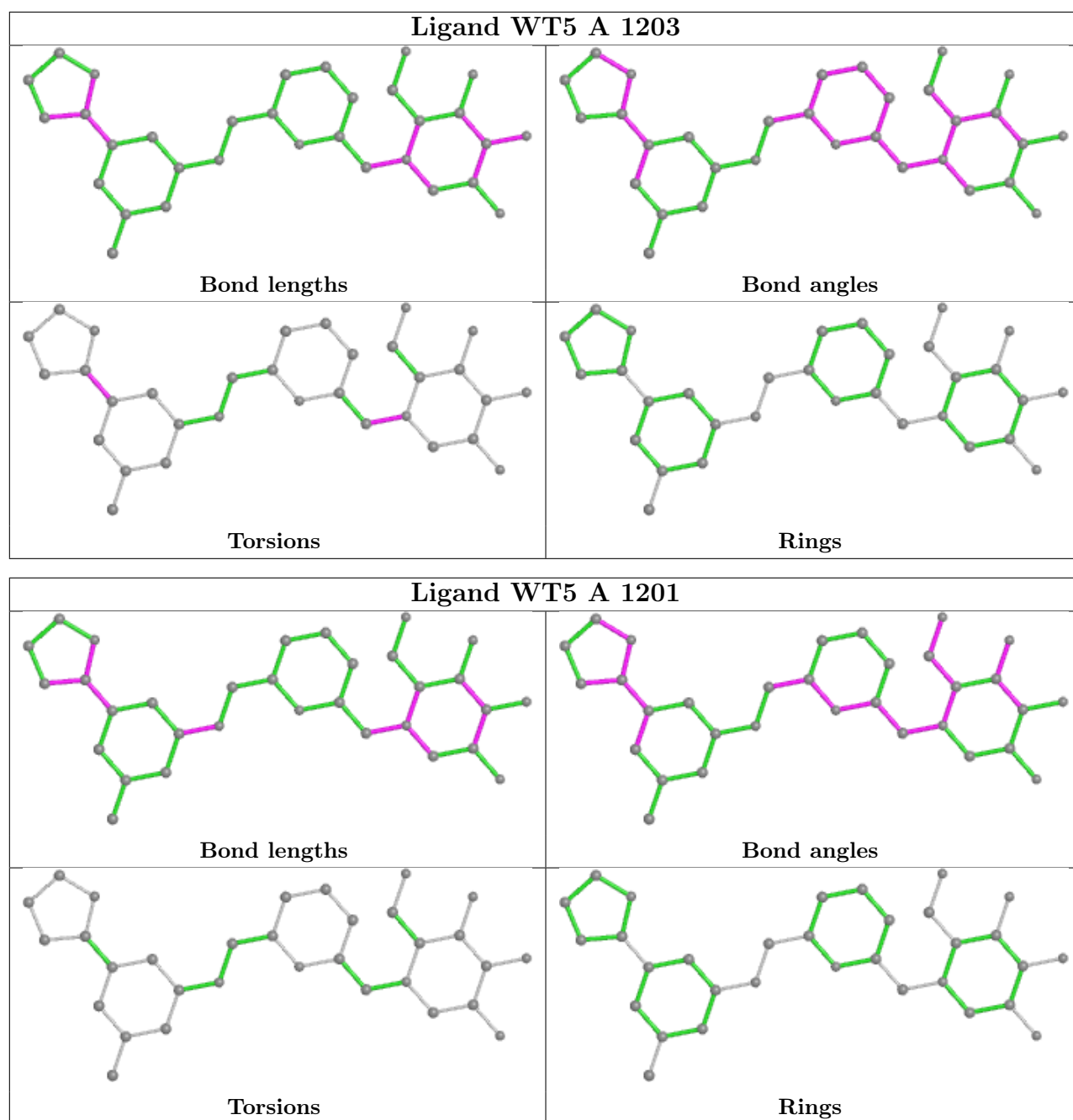
There are no ring outliers.

6 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1203	WT5	2	0
3	A	1201	WT5	1	0
4	B	1504	GOL	1	0
5	B	1507	SO4	1	0
5	A	1205	SO4	1	0
4	B	1502	GOL	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





## 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 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	765/819 (93%)	-0.06	14 (1%) 68 71	43, 68, 98, 143	0
1	B	767/819 (93%)	-0.26	4 (0%) 91 91	44, 60, 82, 122	0
All	All	1532/1638 (93%)	-0.16	18 (1%) 79 80	43, 63, 94, 143	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	621	LEU	3.8
1	A	265	VAL	3.2
1	A	263	TYR	3.1
1	A	36	LEU	3.0
1	B	171	ASN	2.8
1	A	37	HIS	2.6
1	B	531	LEU	2.5
1	B	518	THR	2.5
1	A	266	ALA	2.4
1	B	183	PHE	2.3
1	A	305	SER	2.3
1	A	617	ILE	2.3
1	A	624	THR	2.2
1	A	137	HIS	2.2
1	A	151	ASP	2.2
1	A	307	SER	2.2
1	A	619	SER	2.2
1	A	623	ALA	2.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

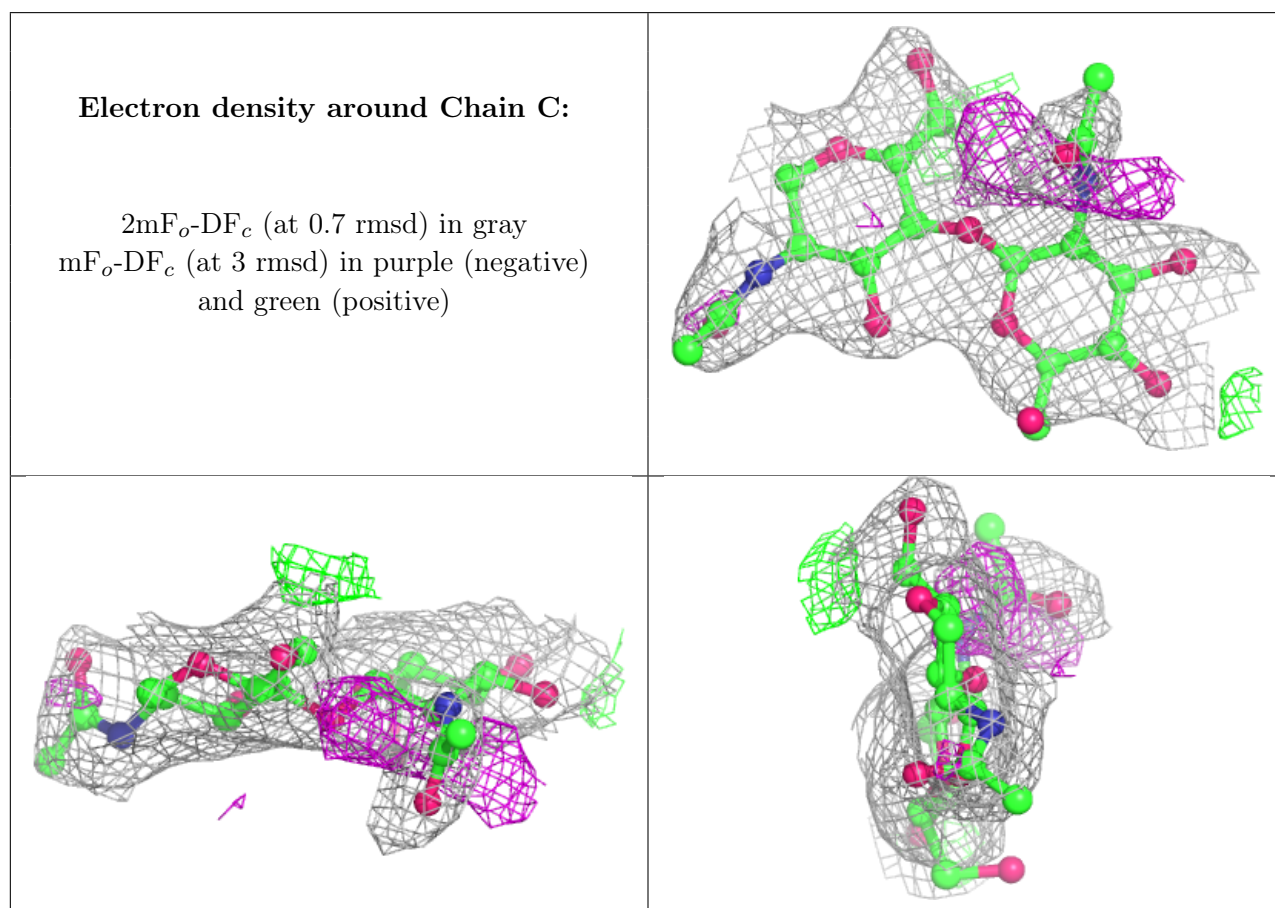
There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	NAG	C	2	14/15	0.84	0.25	69,115,132,137	0
2	NAG	C	1	14/15	0.89	0.21	65,87,97,97	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

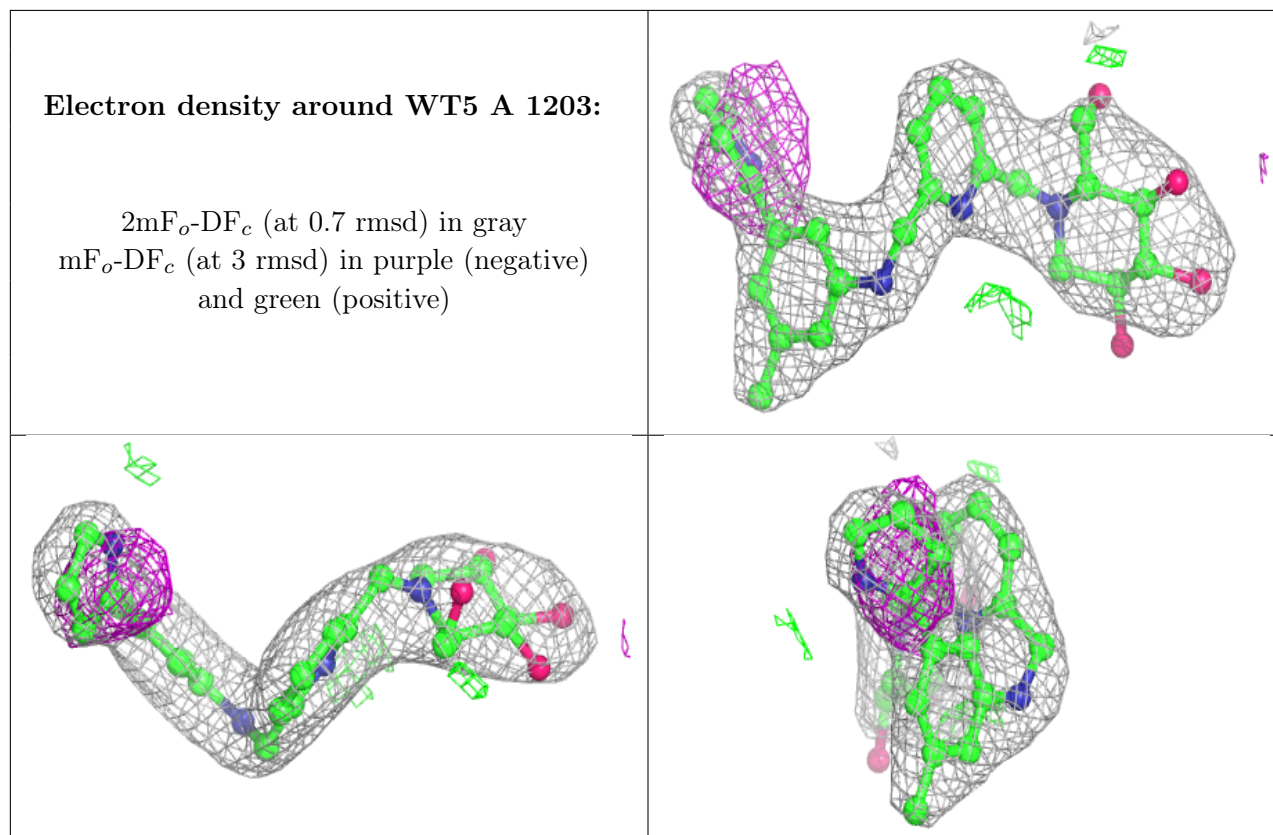


### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
4	GOL	B	1503	6/6	0.84	0.25	66,85,88,90	0
5	SO4	A	1204	5/5	0.88	0.13	120,129,144,161	0
4	GOL	B	1502	6/6	0.89	0.17	83,89,92,97	0
4	GOL	A	1202	6/6	0.91	0.20	87,97,106,113	0
5	SO4	A	1207	5/5	0.91	0.26	83,99,116,121	0
3	WT5	A	1203	32/32	0.92	0.17	49,77,107,112	0
4	GOL	B	1504	6/6	0.94	0.12	86,95,101,107	0
5	SO4	B	1506	5/5	0.94	0.20	64,92,108,116	0
5	SO4	A	1205	5/5	0.96	0.20	106,115,122,132	0
3	WT5	B	1501	32/32	0.96	0.15	41,67,137,143	0
5	SO4	A	1208	5/5	0.96	0.17	76,80,93,99	0
3	WT5	A	1201	32/32	0.96	0.15	42,64,73,75	0
5	SO4	B	1505	5/5	0.97	0.15	66,83,98,98	0
5	SO4	A	1206	5/5	0.98	0.17	55,56,68,84	0
5	SO4	B	1507	5/5	0.99	0.11	52,59,66,78	0

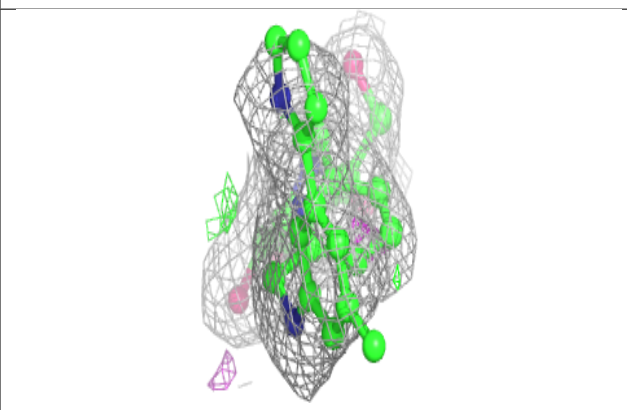
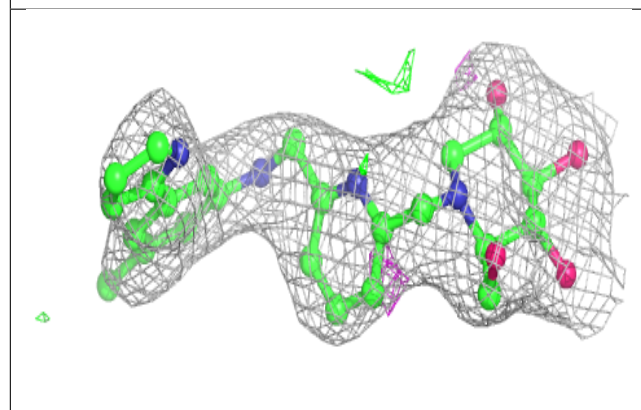
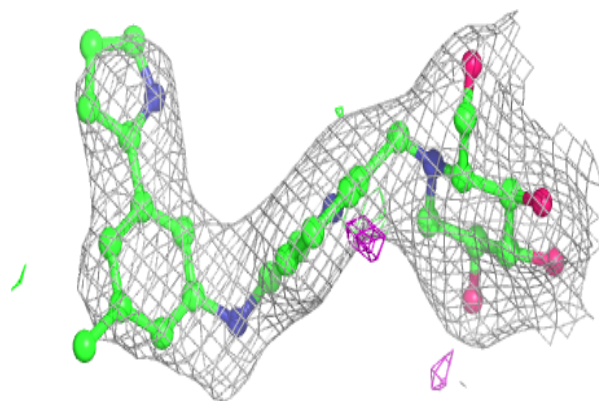
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



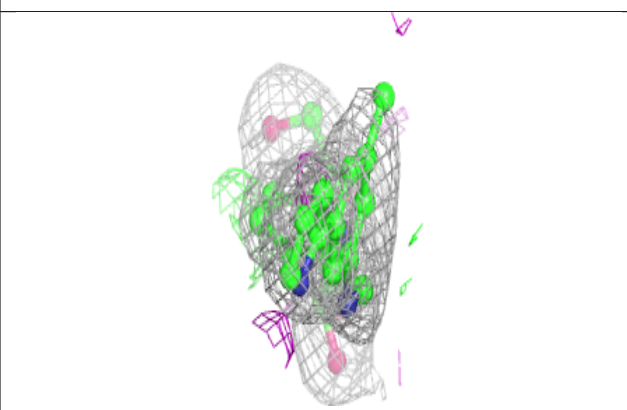
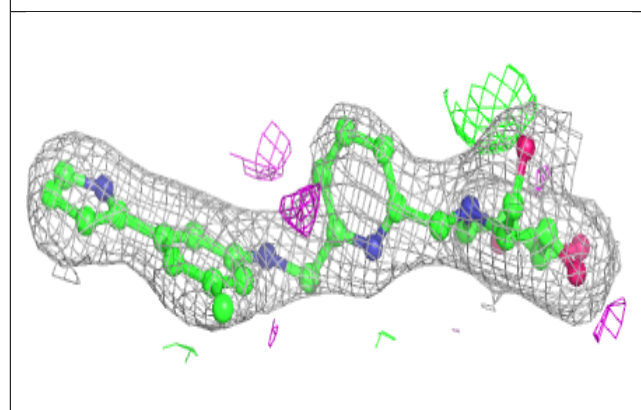
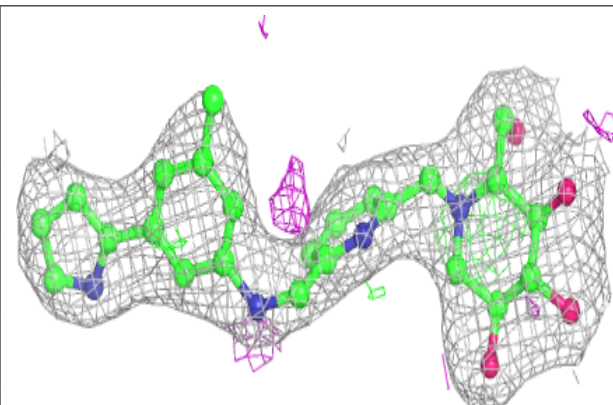


**Electron density around WT5 B 1501:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around WT5 A 1201:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.