



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 12:42 AM UTC

PDB ID : 3MSD / pdb_00003msd
Title : Enzyme-Substrate interactions of IXT6, the intracellular xylanase of *G. stearothermophilus*.
Authors : Solomon, V.; Zolotnitsky, G.; Alhadeff, R.; Shoham, Y.; Shoham, G.
Deposited on : 2010-04-29
Resolution : 1.58 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

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>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

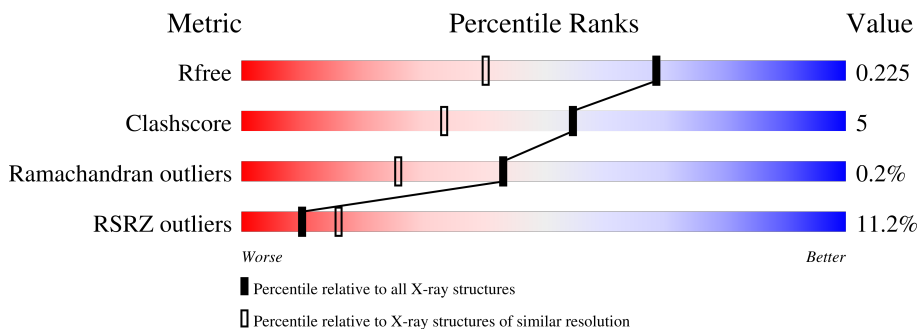
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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}	180053	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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 ≥ 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	331	
1	B	331	
2	C	2	
2	D	2	

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6250 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 Intra-cellular xylanase ixt6.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	330	2813	1796	497	507	13	0	14	0
1	B	328	2745	1755	483	495	12	0	7	0

- Molecule 2 is an oligosaccharide called beta-D-xylopyranose-(1-4)-beta-D-xylopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
			Total	C	O			
2	C	2	19	10	9	0	0	0
2	D	2	19	10	9	0	0	0

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0

- Molecule 5 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 4 2 2	0	0

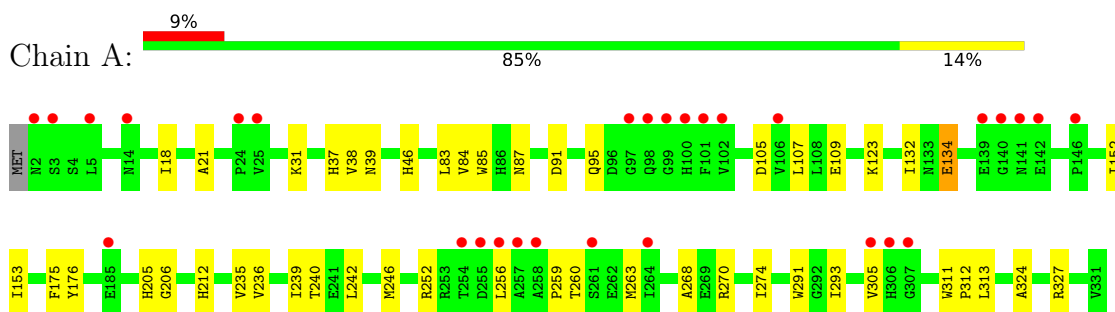
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	351	Total O 351 351	0	0
6	B	285	Total O 285 285	0	0

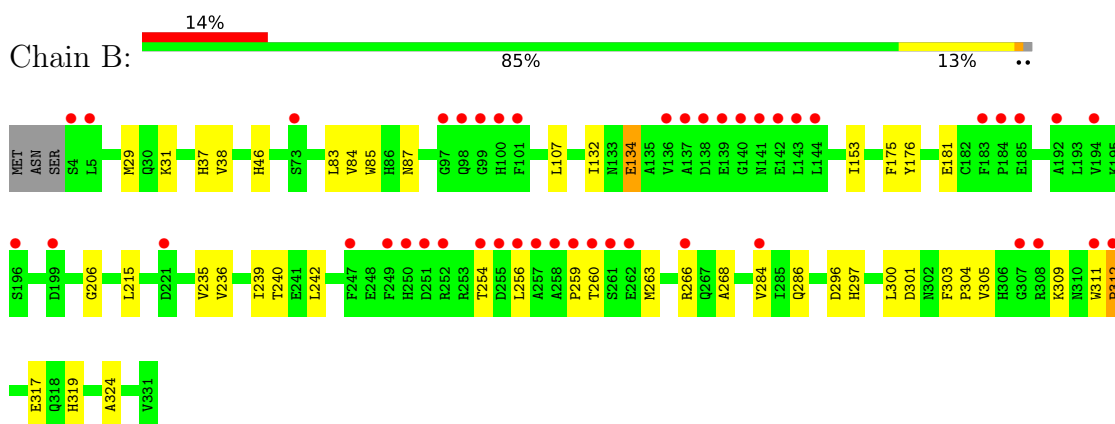
3 Residue-property plots [i](#)

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 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: Intra-cellular xylanase ixt6



- Molecule 1: Intra-cellular xylanase ixt6



- Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose



- Molecule 2: beta-D-xylopyranose-(1-4)-beta-D-xylopyranose



4 Data and refinement statistics i

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	169.26Å 80.99Å 79.28Å 90.00° 91.95° 90.00°	Depositor
Resolution (Å)	39.48 – 1.58 39.48 – 1.58	Depositor EDS
% Data completeness (in resolution range)	(Not available) (39.48-1.58) 94.6 (39.48-1.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 1.58Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.197 , 0.209 0.213 , 0.225	Depositor DCC
R_{free} test set	7251 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtrriage
Anisotropy	0.644	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 41.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.014 for -h,-k,l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6250	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.65% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, ACT, XYP, NA

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	0.36	0/2889	0.91	15/3909 (0.4%)
1	B	0.34	0/2822	0.91	12/3822 (0.3%)
All	All	0.35	0/5711	0.91	27/7731 (0.3%)

There are no bond length outliers.

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	240	THR	N-CA-C	9.21	124.65	113.41
1	B	240	THR	N-CA-C	8.87	124.23	113.41
1	A	239	ILE	N-CA-C	-8.35	95.45	108.23
1	B	46	HIS	N-CA-C	8.22	122.98	113.19
1	B	37	HIS	N-CA-C	8.00	123.95	114.04
1	B	239	ILE	N-CA-C	-7.89	95.42	107.73
1	A	46	HIS	N-CA-C	7.56	122.19	113.19
1	A	37	HIS	N-CA-C	7.46	123.29	114.04
1	A	176	TYR	N-CA-C	-7.18	96.82	108.52
1	B	176	TYR	N-CA-C	-6.57	97.81	108.52
1	B	83	LEU	N-CA-C	6.20	119.23	111.24
1	B	242	LEU	N-CA-C	5.68	118.56	110.10
1	A	134	GLU	N-CA-C	5.65	119.22	111.54
1	B	312	PRO	N-CA-C	5.64	122.82	114.80
1	A	242	LEU	N-CA-C	5.55	118.37	110.10
1	A	38	VAL	N-CA-C	5.55	117.80	109.20
1	A	83	LEU	N-CA-C	5.50	118.34	111.24
1	B	31	LYS	N-CA-C	5.41	117.60	111.11
1	B	175	PHE	N-CA-C	5.36	118.30	109.72
1	A	152	ILE	N-CA-C	5.33	115.54	110.53
1	B	38	VAL	N-CA-C	5.28	117.30	109.17
1	B	134	GLU	N-CA-C	5.25	118.64	111.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	175	PHE	N-CA-C	5.20	118.04	109.72
1	A	312	PRO	N-CA-C	5.15	123.51	114.75
1	A	212	HIS	N-CA-C	-5.05	99.77	108.56
1	A	313	LEU	N-CA-C	5.05	117.94	109.96
1	A	31	LYS	N-CA-C	5.05	117.17	111.11

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	2813	0	2704	26	0
1	B	2745	0	2635	27	0
2	C	19	0	0	1	0
2	D	19	0	0	1	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	4	0	3	0	0
6	A	351	0	0	3	0
6	B	285	0	0	0	0
All	All	6250	0	5358	53	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 (53) 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:260:THR:H	1:B:263:MET:HE3	1.15	1.09
1:A:260:THR:H	1:A:263[A]:MET:HE3	1.19	1.07
1:B:256:LEU:HD23	1:B:263:MET:HE1	1.63	0.79
1:B:260:THR:N	1:B:263:MET:HE3	1.98	0.75

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:260:THR:N	1:A:263[A]:MET:HE3	2.00	0.72
1:A:105:ASP:O	1:A:109:GLU:HG3	1.90	0.71
1:A:18:ILE:H	1:A:39:ASN:HD21	1.41	0.68
1:B:236:VAL:HG13	1:B:286[A]:GLN:OE1	1.95	0.65
1:A:256:LEU:HD13	1:A:263[A]:MET:HE1	1.80	0.64
1:B:301:ASP:OD1	1:B:309[B]:LYS:HD2	1.99	0.63
1:B:259:PRO:HD3	1:B:311:TRP:CE2	2.38	0.58
1:B:296:ASP:OD2	1:B:319:HIS:HE1	1.87	0.57
1:A:18:ILE:H	1:A:39:ASN:ND2	2.02	0.55
1:A:252:ARG:HD2	1:A:305:VAL:CG2	2.38	0.54
1:A:260:THR:HG23	1:A:263[A]:MET:HE3	1.90	0.53
1:A:270:ARG:O	1:A:274[B]:ILE:HG13	2.08	0.53
1:A:84:VAL:HB	1:A:132:ILE:HD13	1.91	0.52
1:A:260:THR:HG23	1:A:263[A]:MET:CE	2.40	0.52
1:A:246:MET:HB3	1:A:263[B]:MET:HE2	1.92	0.52
1:A:107:LEU:HD23	1:A:153:ILE:HG13	1.91	0.52
1:B:260:THR:HG23	1:B:263:MET:CE	2.41	0.51
1:B:84:VAL:HB	1:B:132:ILE:HD13	1.93	0.51
1:B:254:THR:HG22	1:B:305:VAL:HG11	1.95	0.49
1:B:301:ASP:CG	1:B:309[B]:LYS:HD2	2.38	0.48
1:B:215:LEU:HD22	1:B:266:ARG:HG3	1.96	0.48
1:B:134:GLU:OE2	2:D:1:XYP:O1	2.31	0.48
1:B:29:MET:HE1	1:B:297[B]:HIS:ND1	2.28	0.48
1:A:85:TRP:CE2	1:A:87:ASN:HB2	2.50	0.47
1:A:268:ALA:HA	1:A:324:ALA:HA	1.97	0.47
1:B:300:LEU:HD12	1:B:312:PRO:HG3	1.97	0.47
1:A:134:GLU:OE2	2:C:1:XYP:O1	2.33	0.46
1:B:85:TRP:CE2	1:B:87:ASN:HB2	2.50	0.46
1:A:123[B]:LYS:HB2	1:A:123[B]:LYS:NZ	2.31	0.46
1:B:266:ARG:O	1:B:266:ARG:HD2	2.16	0.46
1:B:256:LEU:HD23	1:B:263:MET:CE	2.42	0.44
1:B:309[B]:LYS:NZ	1:B:317:GLU:OE2	2.51	0.44
1:A:206:GLY:HA2	1:A:235:VAL:HB	1.99	0.44
1:A:205:HIS:O	1:A:236[A]:VAL:HG22	2.17	0.43
1:B:107:LEU:HD23	1:B:153:ILE:HG13	2.00	0.43
1:A:327[A]:ARG:NH2	6:A:978:HOH:O	2.51	0.43
1:B:284:VAL:C	1:B:286[A]:GLN:HE22	2.26	0.43
1:B:181:GLU:CD	1:B:181:GLU:H	2.26	0.43
1:B:254:THR:CG2	1:B:305:VAL:HG11	2.48	0.43
1:A:259:PRO:HD3	1:A:311:TRP:CE2	2.53	0.43
1:A:123[A]:LYS:HE3	6:A:718:HOH:O	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:21:ALA:HB2	1:A:291:TRP:CE3	2.54	0.42
1:B:206:GLY:HA2	1:B:235:VAL:HB	2.01	0.42
1:B:256:LEU:HD12	1:B:256:LEU:N	2.35	0.42
1:A:91:ASP:O	1:A:95:GLN:HG3	2.20	0.41
1:B:303:PHE:CD1	1:B:304:PRO:HA	2.54	0.41
1:B:268:ALA:HA	1:B:324:ALA:HA	2.03	0.41
1:A:18:ILE:N	1:A:39:ASN:HD21	2.15	0.41
1:A:123[A]:LYS:NZ	6:A:1136:HOH:O	2.54	0.41

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	342/331 (103%)	332 (97%)	9 (3%)	1 (0%)	36	20
1	B	333/331 (101%)	324 (97%)	9 (3%)	0	100	100
All	All	675/662 (102%)	656 (97%)	18 (3%)	1 (0%)	43	28

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	ILE

5.3.2 Protein sidechains [i](#)

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

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](#)

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	XYP	C	1	2	10,10,10	0.54	0	14,14,14	0.63	0
2	XYP	C	2	2	9,9,10	0.68	0	10,12,14	0.32	0
2	XYP	D	1	2	10,10,10	0.54	0	14,14,14	0.54	0
2	XYP	D	2	2	9,9,10	0.66	0	10,12,14	0.37	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
2	XYP	C	1	2	-	-	0/1/1/1
2	XYP	C	2	2	-	-	0/1/1/1
2	XYP	D	1	2	-	-	0/1/1/1
2	XYP	D	2	2	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

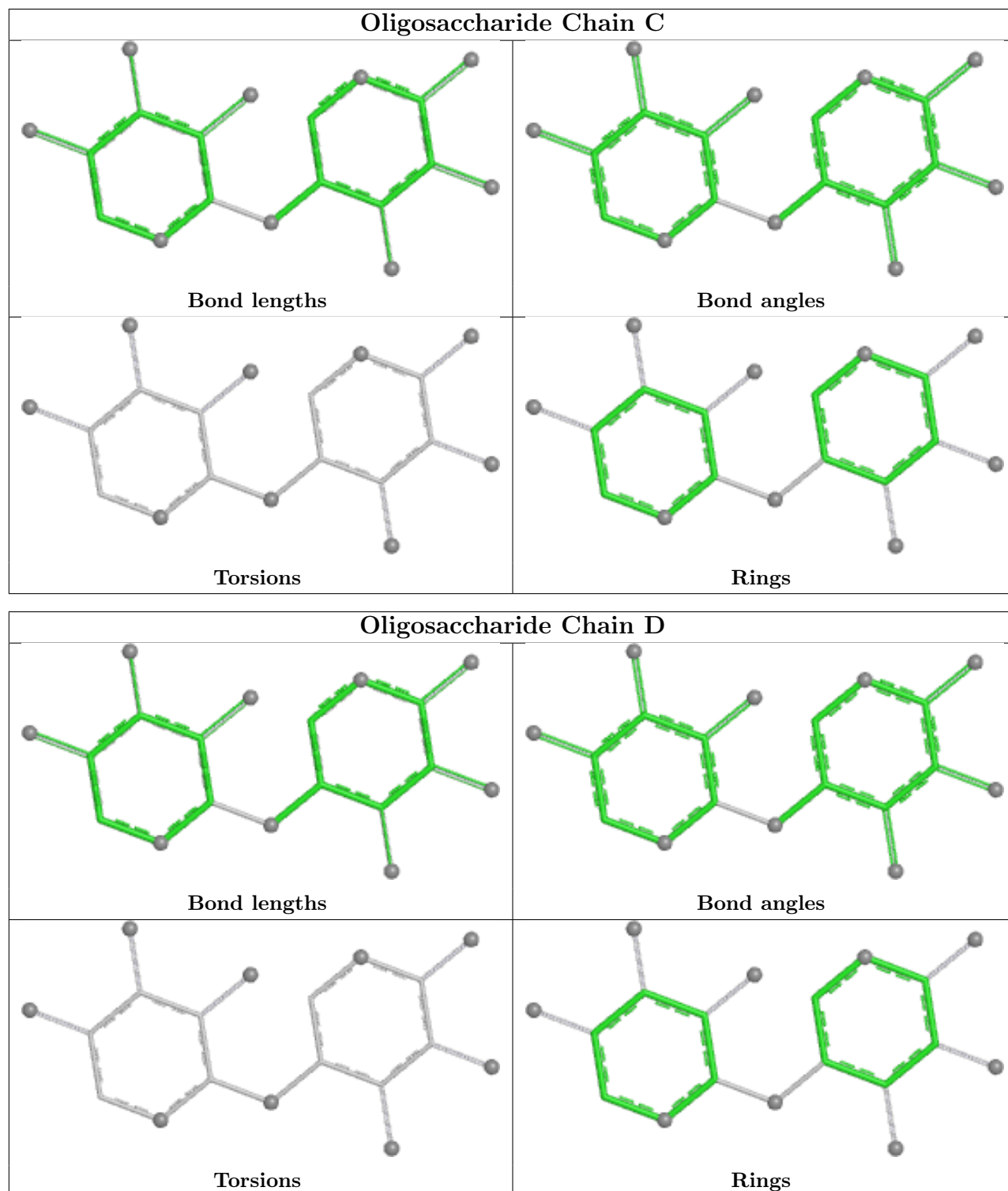
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	1	XYP	1	0
2	D	1	XYP	1	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.



5.6 Ligand geometry

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	ACT	A	337	-	3,3,3	1.04	0	3,3,3	0.82	0
3	GOL	B	481	-	5,5,5	0.76	0	5,5,5	0.43	0
3	GOL	A	482	-	5,5,5	0.78	0	5,5,5	0.43	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
3	GOL	B	481	-	-	2/4/4/4	-
3	GOL	A	482	-	-	2/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	482	GOL	O1-C1-C2-C3
3	B	481	GOL	O1-C1-C2-C3
3	A	482	GOL	O1-C1-C2-O2
3	B	481	GOL	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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, 95th 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 ²)	Q<0.9
1	A	330/331 (99%)	0.53	29 (8%) 15 24	9, 21, 35, 50	14 (4%)
1	B	328/331 (99%)	0.89	45 (13%) 6 11	9, 24, 38, 48	7 (2%)
All	All	658/662 (99%)	0.71	74 (11%) 10 16	9, 22, 38, 50	21 (3%)

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	99	GLY	7.9
1	B	249	PHE	7.8
1	A	2	ASN	5.9
1	B	256	LEU	5.2
1	B	183	PHE	4.9
1	A	3	SER	4.8
1	B	258	ALA	4.5
1	A	256	LEU	4.4
1	A	99	GLY	4.1
1	B	4	SER	3.9
1	A	305	VAL	3.8
1	B	97	GLY	3.8
1	B	257	ALA	3.7
1	B	100	HIS	3.5
1	B	142	GLU	3.4
1	B	262	GLU	3.4
1	A	5	LEU	3.4
1	B	254	THR	3.3
1	A	255	ASP	3.3
1	B	140	GLY	3.3
1	B	185	GLU	3.3
1	B	101	PHE	3.2
1	B	143	LEU	3.2
1	A	307	GLY	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	5	LEU	3.2
1	A	146	PRO	3.2
1	B	137	ALA	3.1
1	A	100	HIS	3.0
1	B	250	HIS	3.0
1	A	139	GLU	3.0
1	A	257	ALA	2.9
1	B	136	VAL	2.9
1	B	266	ARG	2.9
1	A	24	PRO	2.9
1	B	138	ASP	2.9
1	B	141	ASN	2.8
1	A	254	THR	2.8
1	A	101	PHE	2.8
1	B	247	PHE	2.8
1	B	307	GLY	2.7
1	B	192	ALA	2.7
1	B	184	PRO	2.7
1	A	25	VAL	2.6
1	A	140	GLY	2.6
1	A	141	ASN	2.6
1	B	308	ARG	2.5
1	A	261	SER	2.5
1	B	251	ASP	2.4
1	B	98	GLN	2.4
1	B	261[A]	SER	2.4
1	A	97	GLY	2.4
1	B	194	VAL	2.4
1	B	199	ASP	2.3
1	B	311	TRP	2.3
1	B	73[A]	SER	2.3
1	B	259	PRO	2.3
1	B	196	SER	2.3
1	A	106	VAL	2.2
1	B	260	THR	2.2
1	A	102	VAL	2.2
1	A	142	GLU	2.2
1	A	306	HIS	2.2
1	B	144	LEU	2.1
1	B	139	GLU	2.1
1	B	312	PRO	2.1
1	B	221	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	255	ASP	2.1
1	A	98	GLN	2.0
1	A	185	GLU	2.0
1	A	264	ILE	2.0
1	A	14	ASN	2.0
1	B	252	ARG	2.0
1	A	258	ALA	2.0
1	B	284	VAL	2.0

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](#)

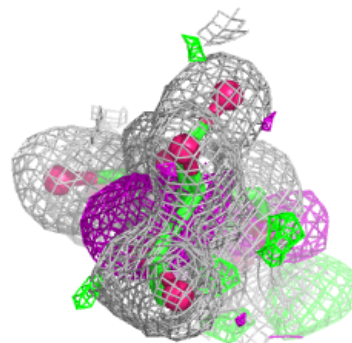
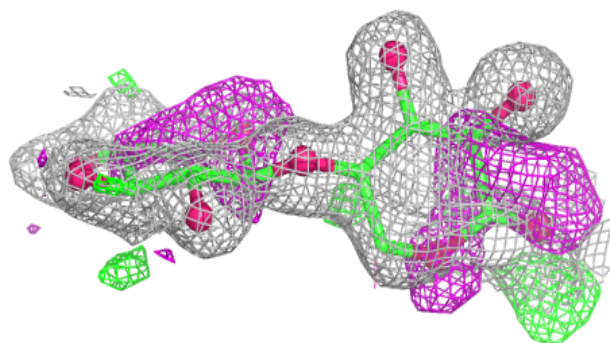
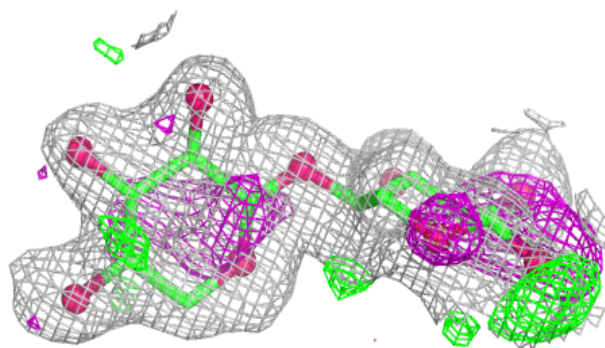
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	XYP	C	2	9/10	0.83	0.14	33,35,37,39	0
2	XYP	C	1	10/10	0.84	0.15	22,32,35,37	0
2	XYP	D	1	10/10	0.84	0.18	23,33,37,40	0
2	XYP	D	2	9/10	0.84	0.14	30,34,35,38	0

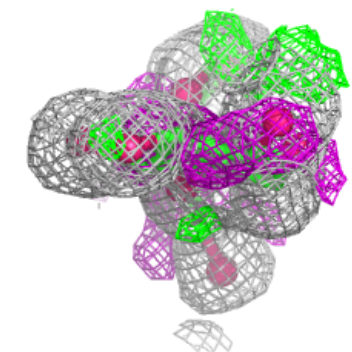
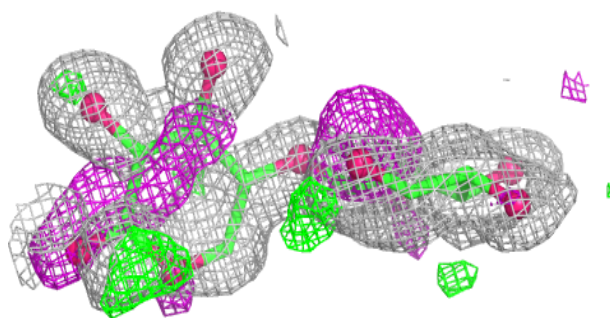
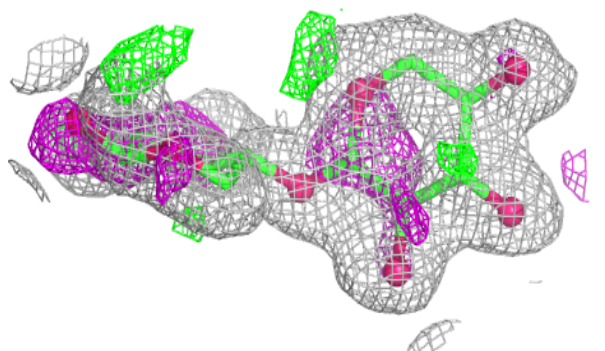
The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Chain C:

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

**Electron density around Chain D:**

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



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, 95th 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 ²)	Q<0.9
3	GOL	A	482	6/6	0.75	0.22	51,55,55,56	0
3	GOL	B	481	6/6	0.75	0.19	55,56,56,57	0
5	ACT	A	337	4/4	0.91	0.16	28,31,31,32	0
4	NA	B	402	1/1	0.97	0.06	29,29,29,29	0
4	NA	A	401	1/1	0.98	0.07	22,22,22,22	0

6.5 Other polymers [i](#)

There are no such residues in this entry.