



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 9, 2024 – 09:44 AM EST

PDB ID : 5TA0
Title : Crystal structure of BuGH86E322Q in complex with neoagarooctaose
Authors : Pluvinae, B.; Boraston, A.B.; Abbott, W.D.
Deposited on : 2016-09-09
Resolution : 1.40 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.003 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.39

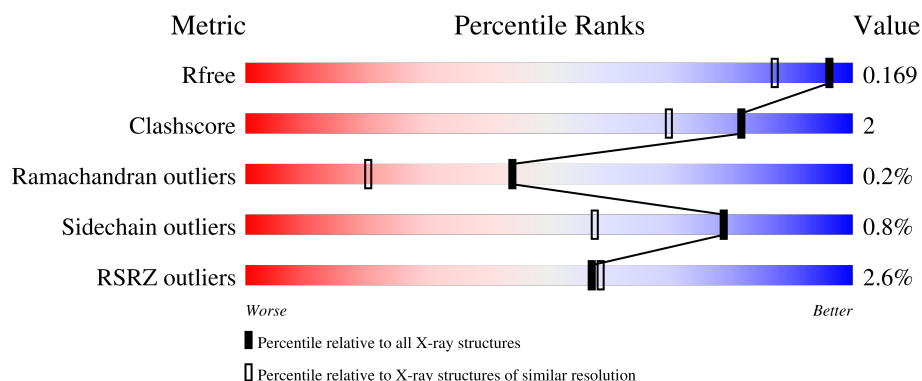
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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}	164625	2247 (1.40-1.40)
Clashscore	180529	2446 (1.40-1.40)
Ramachandran outliers	177936	2398 (1.40-1.40)
Sidechain outliers	177891	2397 (1.40-1.40)
RSRZ outliers	164620	2246 (1.40-1.40)

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	649	<div> <div>0%</div> <div>92%</div> <div>5%</div> <div>•</div> </div>
1	B	649	<div> <div>4%</div> <div>89%</div> <div>5%</div> <div>• 5%</div> </div>
2	C	5	<div> <div>40%</div> <div>40%</div> <div>20%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	701	-	-	X	-

2 Entry composition [i](#)

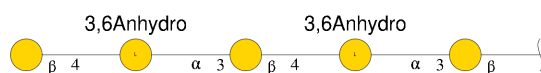
There are 7 unique types of molecules in this entry. The entry contains 12263 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Glycoside Hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	626	Total	C	N	O	S	0	39	0
			5405	3442	915	1014	34			
1	B	615	Total	C	N	O	S	0	38	0
			5274	3357	889	994	34			

- Molecule 2 is an oligosaccharide called beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
2	C	5	Total	C	O	0	0	0
			54	30	24			

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	2	Total	Ca	0	0
			2	2		
6	B	2	Total	Ca	0	0
			2	2		

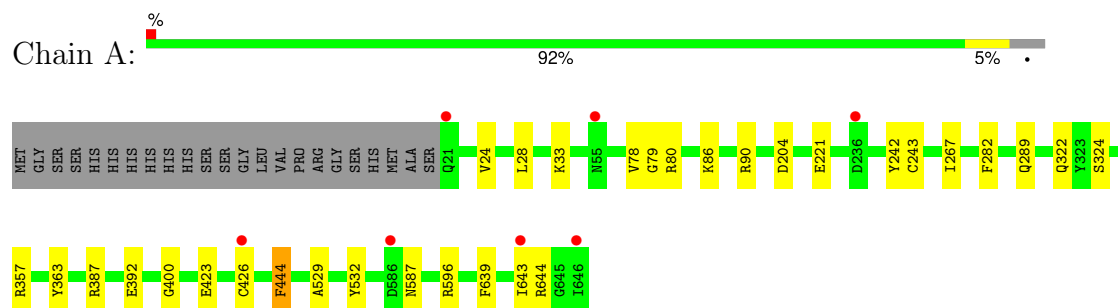
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	693	Total 693	O 693	0	2
7	B	619	Total 619	O 619	0	2

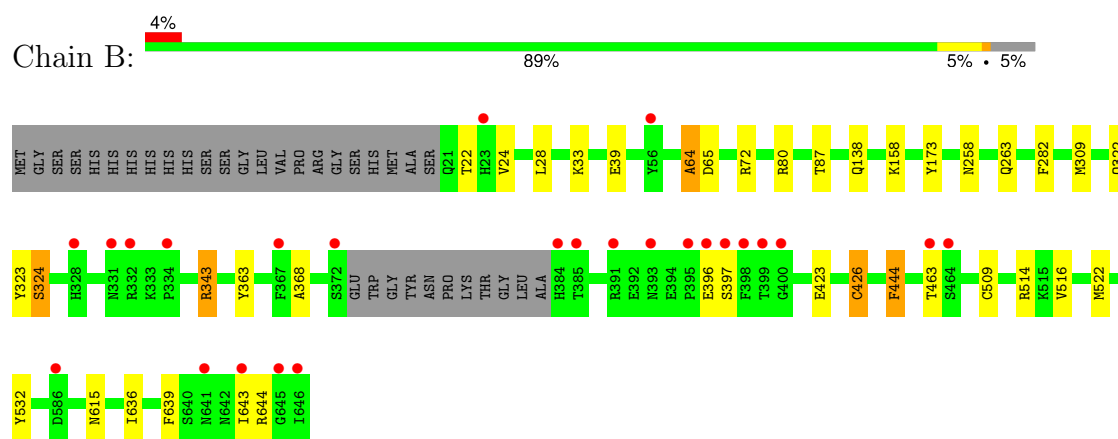
3 Residue-property plots [i](#)

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.

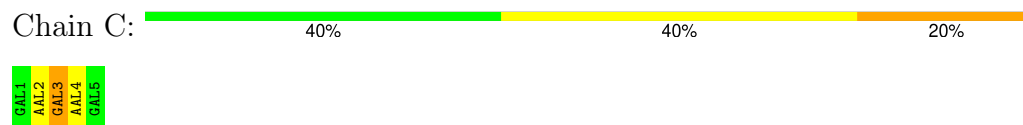
• Molecule 1: Glycoside Hydrolase



• Molecule 1: Glycoside Hydrolase



• Molecule 2: beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose-(1-4)-3,6-anhydro-alpha-L-galactopyranose-(1-3)-beta-D-galactopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	60.72Å 73.54Å 83.19Å 85.87° 86.20° 71.87°	Depositor
Resolution (Å)	82.88 – 1.40 82.88 – 1.40	Depositor EDS
% Data completeness (in resolution range)	95.7 (82.88-1.40) 95.7 (82.88-1.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.61 (at 1.40Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.142 , 0.162 0.151 , 0.169	Depositor DCC
R_{free} test set	12815 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	10.9	Xtriage
Anisotropy	0.022	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 40.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12263	wwPDB-VP
Average B, all atoms (Å ²)	14.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.64% 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: CA, GOL, EDO, GAL, SO4, AAL

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	0.50	0/5534	0.73	6/7468 (0.1%)
1	B	2.08	4/5397 (0.1%)	1.13	14/7285 (0.2%)
All	All	1.51	4/10931 (0.0%)	0.95	20/14753 (0.1%)

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	138[A]	GLN	CD-NE2	75.19	3.20	1.32
1	B	138[B]	GLN	CD-NE2	75.19	3.20	1.32
1	B	138[A]	GLN	CD-OE1	73.42	2.85	1.24
1	B	138[B]	GLN	CD-OE1	73.42	2.85	1.24

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	138[A]	GLN	OE1-CD-NE2	-34.16	43.33	121.90
1	B	138[B]	GLN	OE1-CD-NE2	-34.16	43.33	121.90
1	B	138[A]	GLN	CG-CD-OE1	-26.63	68.34	121.60
1	B	138[B]	GLN	CG-CD-OE1	-26.63	68.34	121.60
1	B	138[A]	GLN	CG-CD-NE2	-25.00	56.70	116.70
1	B	138[B]	GLN	CG-CD-NE2	-25.00	56.70	116.70
1	B	64[A]	ALA	C-N-CA	8.96	144.09	121.70
1	B	64[B]	ALA	C-N-CA	8.96	144.09	121.70
1	B	343	ARG	NE-CZ-NH1	6.93	123.77	120.30
1	B	514	ARG	NE-CZ-NH1	6.87	123.74	120.30
1	A	596	ARG	NE-CZ-NH2	-5.97	117.32	120.30
1	B	282	PHE	CB-CG-CD1	5.84	124.89	120.80
1	A	596	ARG	NE-CZ-NH1	5.74	123.17	120.30
1	B	72	ARG	NE-CZ-NH1	-5.39	117.61	120.30
1	A	282	PHE	CB-CG-CD1	5.38	124.57	120.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	387	ARG	NE-CZ-NH2	-5.27	117.66	120.30
1	B	444	PHE	CB-CG-CD1	5.26	124.48	120.80
1	A	444	PHE	CB-CG-CD1	5.16	124.41	120.80
1	A	357	ARG	NE-CZ-NH2	-5.13	117.73	120.30
1	B	72	ARG	NE-CZ-NH2	5.06	122.83	120.30

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	5405	0	5232	16	0
1	B	5274	0	5064	30	0
2	C	54	0	44	1	0
3	A	20	0	0	2	0
3	B	20	0	0	0	0
4	A	68	0	102	4	0
4	B	52	0	78	4	0
5	A	24	0	32	2	0
5	B	30	0	40	3	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	693	0	0	6	0
7	B	619	0	0	10	0
All	All	12263	0	10592	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 2.

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:24:VAL:HG13	1:B:426[B]:CYS:SG	1.72	1.28
1:B:64[B]:ALA:O	7:B:801:HOH:O	1.83	0.94

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289[B]:GLN:NE2	7:A:801:HOH:O	2.05	0.90
1:A:24[A]:VAL:HG13	1:A:426[A]:CYS:SG	2.24	0.78
1:B:24:VAL:CG1	1:B:426[B]:CYS:SG	2.66	0.74
1:B:423[A]:GLU:OE2	1:B:644:ARG:NH1	2.25	0.70
1:B:636[B]:ILE:HD11	7:B:822:HOH:O	1.92	0.70
5:B:722:GOL:H31	7:B:1171:HOH:O	1.91	0.69
5:A:729:GOL:H32	7:A:1255:HOH:O	1.92	0.69
1:A:33[B]:LYS:NZ	3:A:701:SO4:O4	2.25	0.67
1:A:24[A]:VAL:HG12	1:A:444:PHE:HZ	1.62	0.64
1:B:80:ARG:HH22	1:B:322:GLN:HE21	1.48	0.61
1:A:639[B]:PHE:CE1	1:A:643:ILE:HD11	2.36	0.61
1:B:39[B]:GLU:OE2	7:B:802:HOH:O	2.16	0.60
1:B:509:CYS:HB3	7:B:1323:HOH:O	2.02	0.60
1:A:24[A]:VAL:HG12	1:A:444:PHE:CZ	2.40	0.56
1:B:639[B]:PHE:CE1	1:B:643:ILE:HD11	2.41	0.56
1:A:80:ARG:HH22	1:A:322:GLN:HE21	1.54	0.55
1:A:242:TYR:O	1:A:243[B]:CYS:HB2	2.09	0.52
3:A:701:SO4:O2	1:B:33:LYS:NZ	2.32	0.52
1:B:368:ALA:HB3	7:B:825:HOH:O	2.11	0.50
1:B:396:GLU:HA	1:B:397:SER:HB3	1.93	0.50
4:B:711:EDO:H22	7:B:1110:HOH:O	2.12	0.49
1:B:258:ASN:O	1:B:263[B]:GLN:HG2	2.12	0.49
1:A:529:ALA:O	4:A:710:EDO:H12	2.13	0.49
1:A:221[B]:GLU:HG2	1:A:267:ILE:HG21	1.94	0.49
1:A:587:ASN:ND2	7:A:805:HOH:O	2.46	0.49
1:B:516:VAL:HA	4:B:716:EDO:H21	1.95	0.49
7:A:924:HOH:O	2:C:3:GAL:H4	2.13	0.48
1:B:423[A]:GLU:OE2	1:B:644:ARG:NH2	2.47	0.48
4:A:710:EDO:O1	1:B:615:ASN:ND2	2.41	0.47
1:A:86:LYS:HG2	1:A:90[B]:ARG:HD3	1.96	0.47
1:A:80:ARG:NH2	1:A:322:GLN:HE21	2.13	0.46
1:B:80:ARG:NH2	1:B:322:GLN:HE21	2.12	0.46
1:A:423:GLU:OE2	1:A:644:ARG:NH1	2.37	0.46
1:B:463:THR:HG22	7:B:1165:HOH:O	2.16	0.46
1:B:636[B]:ILE:O	1:B:636[B]:ILE:HG13	2.17	0.45
5:A:729:GOL:H31	7:A:835:HOH:O	2.17	0.45
1:A:78:VAL:HB	1:A:79:GLY:HA3	1.98	0.45
4:A:717:EDO:H12	1:B:309:MET:HB3	1.99	0.44
1:B:639[B]:PHE:CD1	1:B:643:ILE:HG12	2.53	0.44
1:B:87:THR:HG22	4:B:709:EDO:H21	2.00	0.44
1:B:24:VAL:HG12	1:B:444:PHE:HZ	1.83	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:392:GLU:HG2	1:A:400:GLY:HA3	2.00	0.43
1:B:323:TYR:O	1:B:324:SER:HB2	2.19	0.43
1:B:158[B]:LYS:NZ	7:B:812:HOH:O	2.49	0.42
4:B:711:EDO:C2	7:B:1110:HOH:O	2.66	0.42
1:B:22:THR:CG2	1:B:426[C]:CYS:SG	3.08	0.42
1:B:423[B]:GLU:HG3	1:B:522:MET:SD	2.60	0.42
1:B:343:ARG:NH2	5:B:722:GOL:O3	2.53	0.41
1:B:343:ARG:NE	5:B:722:GOL:O3	2.54	0.41
4:A:713:EDO:H21	7:A:952:HOH:O	2.20	0.41
1:B:423[A]:GLU:OE2	1:B:644:ARG:CZ	2.69	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all 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	664/649 (102%)	641 (96%)	22 (3%)	1 (0%)	44	20
1	B	650/649 (100%)	628 (97%)	20 (3%)	2 (0%)	37	17
All	All	1314/1298 (101%)	1269 (97%)	42 (3%)	3 (0%)	44	20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	324	SER
1	B	324	SER
1	B	65	ASP

5.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all 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	589/575 (102%)	585 (99%)	4 (1%)	81	61
1	B	569/575 (99%)	562 (99%)	7 (1%)	67	41
All	All	1158/1150 (101%)	1147 (99%)	11 (1%)	79	53

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	28	LEU
1	A	204	ASP
1	A	363	TYR
1	A	532	TYR
1	B	28	LEU
1	B	173	TYR
1	B	363	TYR
1	B	426[A]	CYS
1	B	426[B]	CYS
1	B	426[C]	CYS
1	B	532	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	91	ASN
1	A	545	ASN
1	B	461	ASN
1	B	497	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

5 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	GAL	C	1	2	12,12,12	0.51	0	17,17,17	0.94	0
2	AAL	C	2	2	11,11,12	0.57	0	13,16,18	1.34	1 (7%)
2	GAL	C	3	2	11,11,12	0.49	0	15,15,17	1.54	3 (20%)
2	AAL	C	4	2	11,11,12	0.69	0	13,16,18	1.88	3 (23%)
2	GAL	C	5	2	11,11,12	0.49	0	15,15,17	0.63	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	GAL	C	1	2	-	0/2/22/22	0/1/1/1
2	AAL	C	2	2	-	-	0/3/2/2
2	GAL	C	3	2	-	1/2/19/22	0/1/1/1
2	AAL	C	4	2	-	-	0/3/2/2
2	GAL	C	5	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	AAL	C1-O5-C5	4.34	118.00	112.19
2	C	2	AAL	C1-O5-C5	3.83	117.32	112.19
2	C	3	GAL	O3-C3-C2	-3.40	103.12	110.05

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	4	AAL	O5-C5-C6	-3.36	108.42	113.33
2	C	3	GAL	C1-C2-C3	3.21	114.32	109.64
2	C	3	GAL	O5-C5-C4	-2.08	105.77	110.83
2	C	4	AAL	C1-C2-C3	2.01	112.04	109.29

There are no chirality outliers.

All (1) torsion outliers are listed below:

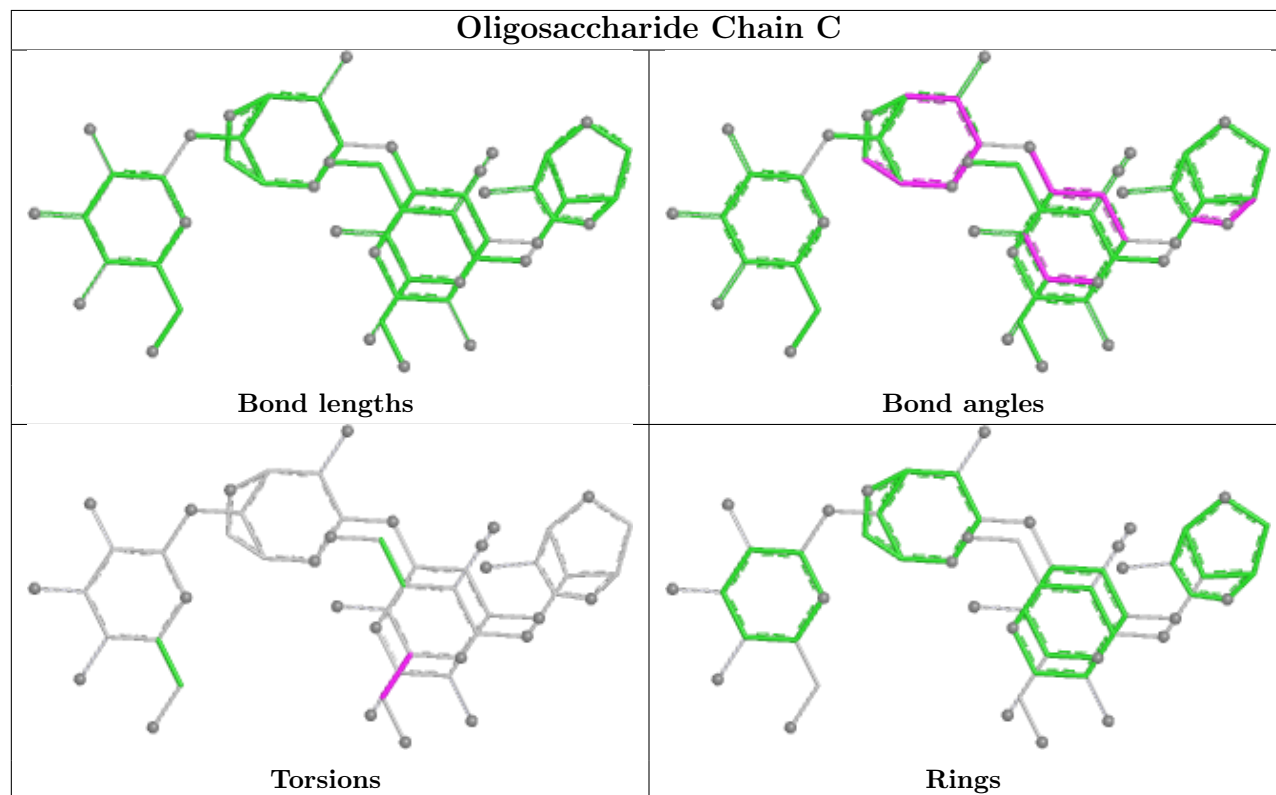
Mol	Chain	Res	Type	Atoms
2	C	3	GAL	O5-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	3	GAL	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 51 ligands modelled in this entry, 4 are monoatomic - leaving 47 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	$\# Z > 2$
4	EDO	A	710	-	3,3,3	0.37	0	2,2,2	0.64	0
4	EDO	A	709	-	3,3,3	0.36	0	2,2,2	0.39	0
3	SO4	A	702	-	4,4,4	0.50	0	6,6,6	0.23	0
5	GOL	B	720	-	5,5,5	0.37	0	5,5,5	0.42	0
5	GOL	B	721	-	5,5,5	0.60	0	5,5,5	1.04	0
4	EDO	A	715	-	3,3,3	0.42	0	2,2,2	0.37	0
4	EDO	A	718	-	3,3,3	0.26	0	2,2,2	0.69	0
4	EDO	B	707	-	3,3,3	0.25	0	2,2,2	0.47	0
5	GOL	B	722	-	5,5,5	0.15	0	5,5,5	0.44	0
4	EDO	A	707	-	3,3,3	0.26	0	2,2,2	0.35	0
5	GOL	A	727	-	5,5,5	0.21	0	5,5,5	0.38	0
4	EDO	A	708	-	3,3,3	0.39	0	2,2,2	0.56	0
3	SO4	B	704	-	4,4,4	0.46	0	6,6,6	0.06	0
4	EDO	B	709	-	3,3,3	0.45	0	2,2,2	0.33	0
4	EDO	B	713	-	3,3,3	0.26	0	2,2,2	1.03	0
4	EDO	B	708	-	3,3,3	0.36	0	2,2,2	0.50	0
4	EDO	A	706	-	3,3,3	0.31	0	2,2,2	0.43	0
4	EDO	B	705	-	3,3,3	0.43	0	2,2,2	0.26	0
5	GOL	B	718	-	5,5,5	0.31	0	5,5,5	0.19	0
4	EDO	B	706	-	3,3,3	0.41	0	2,2,2	0.39	0
4	EDO	B	711	-	3,3,3	0.43	0	2,2,2	0.59	0
5	GOL	A	729	-	5,5,5	0.35	0	5,5,5	0.62	0
5	GOL	B	719	-	5,5,5	0.52	0	5,5,5	0.36	0
4	EDO	A	714	-	3,3,3	0.35	0	2,2,2	0.66	0
4	EDO	A	705	-	3,3,3	0.51	0	2,2,2	0.24	0
4	EDO	B	714	-	3,3,3	0.40	0	2,2,2	0.43	0
4	EDO	B	716	-	3,3,3	0.33	0	2,2,2	0.44	0
4	EDO	B	712	-	3,3,3	0.33	0	2,2,2	0.63	0
4	EDO	A	711	-	3,3,3	0.27	0	2,2,2	0.65	0
4	EDO	A	721	-	3,3,3	0.48	0	2,2,2	0.34	0
3	SO4	A	703	-	4,4,4	0.52	0	6,6,6	0.18	0
3	SO4	B	702	-	4,4,4	0.49	0	6,6,6	0.31	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	B	717	-	3,3,3	0.39	0	2,2,2	0.47	0
4	EDO	A	716	-	3,3,3	0.32	0	2,2,2	0.37	0
5	GOL	A	730	-	5,5,5	0.30	0	5,5,5	0.54	0
4	EDO	A	713	-	3,3,3	0.42	0	2,2,2	0.50	0
4	EDO	A	720	-	3,3,3	0.32	0	2,2,2	0.60	0
4	EDO	A	712	-	3,3,3	0.34	0	2,2,2	1.08	0
4	EDO	B	715	-	3,3,3	0.50	0	2,2,2	0.21	0
4	EDO	A	717	-	3,3,3	0.26	0	2,2,2	0.28	0
3	SO4	B	703	-	4,4,4	0.49	0	6,6,6	0.29	0
5	GOL	A	728	-	5,5,5	0.55	0	5,5,5	0.48	0
3	SO4	A	701	-	4,4,4	0.34	0	6,6,6	0.61	0
4	EDO	B	710	-	3,3,3	0.43	0	2,2,2	0.42	0
3	SO4	B	701	-	4,4,4	0.41	0	6,6,6	0.46	0
3	SO4	A	704	-	4,4,4	0.78	0	6,6,6	0.46	0
4	EDO	A	719	-	3,3,3	0.28	0	2,2,2	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
4	EDO	A	710	-	-	0/1/1/1	-
4	EDO	A	709	-	-	0/1/1/1	-
5	GOL	B	720	-	-	0/4/4/4	-
5	GOL	B	721	-	-	2/4/4/4	-
4	EDO	A	715	-	-	1/1/1/1	-
4	EDO	A	718	-	-	1/1/1/1	-
4	EDO	B	707	-	-	0/1/1/1	-
5	GOL	B	722	-	-	2/4/4/4	-
4	EDO	A	707	-	-	0/1/1/1	-
5	GOL	A	727	-	-	2/4/4/4	-
4	EDO	A	708	-	-	0/1/1/1	-
4	EDO	B	709	-	-	1/1/1/1	-
4	EDO	B	713	-	-	0/1/1/1	-
4	EDO	B	708	-	-	0/1/1/1	-
4	EDO	A	706	-	-	0/1/1/1	-
4	EDO	B	705	-	-	0/1/1/1	-
5	GOL	B	718	-	-	1/4/4/4	-
4	EDO	B	706	-	-	0/1/1/1	-
4	EDO	B	711	-	-	0/1/1/1	-
5	GOL	A	729	-	-	2/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GOL	B	719	-	-	1/4/4/4	-
4	EDO	A	714	-	-	0/1/1/1	-
4	EDO	A	705	-	-	0/1/1/1	-
4	EDO	B	714	-	-	0/1/1/1	-
4	EDO	B	716	-	-	0/1/1/1	-
4	EDO	B	712	-	-	1/1/1/1	-
4	EDO	A	711	-	-	0/1/1/1	-
4	EDO	A	721	-	-	0/1/1/1	-
4	EDO	B	717	-	-	1/1/1/1	-
4	EDO	A	716	-	-	0/1/1/1	-
5	GOL	A	730	-	-	0/4/4/4	-
4	EDO	A	713	-	-	0/1/1/1	-
4	EDO	A	720	-	-	1/1/1/1	-
4	EDO	A	712	-	-	1/1/1/1	-
4	EDO	B	715	-	-	1/1/1/1	-
4	EDO	A	717	-	-	0/1/1/1	-
5	GOL	A	728	-	-	0/4/4/4	-
4	EDO	B	710	-	-	0/1/1/1	-
4	EDO	A	719	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	729	GOL	O1-C1-C2-C3
5	A	727	GOL	O1-C1-C2-C3
5	A	729	GOL	O1-C1-C2-O2
4	A	715	EDO	O1-C1-C2-O2
4	A	718	EDO	O1-C1-C2-O2
4	B	709	EDO	O1-C1-C2-O2
4	B	717	EDO	O1-C1-C2-O2
5	B	721	GOL	O1-C1-C2-O2
5	B	722	GOL	O1-C1-C2-C3
5	B	718	GOL	C1-C2-C3-O3
5	B	719	GOL	C1-C2-C3-O3
4	B	712	EDO	O1-C1-C2-O2
4	B	715	EDO	O1-C1-C2-O2
5	A	727	GOL	O1-C1-C2-O2
5	B	722	GOL	O2-C2-C3-O3

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Mol	Chain	Res	Type	Atoms
4	A	712	EDO	O1-C1-C2-O2
4	A	720	EDO	O1-C1-C2-O2
5	B	721	GOL	O2-C2-C3-O3

There are no ring outliers.

9 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	710	EDO	2	0
5	B	722	GOL	3	0
4	B	709	EDO	1	0
4	B	711	EDO	2	0
5	A	729	GOL	2	0
4	B	716	EDO	1	0
4	A	713	EDO	1	0
4	A	717	EDO	1	0
3	A	701	SO4	2	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 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	626/649 (96%)	-0.34	7 (1%) 77 79	3, 11, 22, 42	39 (6%)
1	B	615/649 (94%)	-0.14	25 (4%) 42 43	3, 11, 28, 52	38 (6%)
All	All	1241/1298 (95%)	-0.24	32 (2%) 57 58	3, 11, 25, 52	77 (6%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	398	PHE	8.4
1	B	399	THR	4.4
1	B	646	ILE	4.3
1	B	385	THR	4.3
1	B	56	TYR	3.6
1	B	397	SER	3.5
1	B	331	ASN	3.4
1	B	400	GLY	3.1
1	B	391[A]	ARG	3.1
1	B	384	HIS	3.1
1	B	396	GLU	2.9
1	A	643	ILE	2.8
1	B	643	ILE	2.8
1	B	464	SER	2.8
1	A	646	ILE	2.7
1	B	334	PRO	2.7
1	B	393	ASN	2.6
1	B	328	HIS	2.5
1	A	586	ASP	2.5
1	B	586	ASP	2.5
1	A	236	ASP	2.5
1	B	463	THR	2.5
1	B	372	SER	2.5
1	B	395	PRO	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	641	ASN	2.3
1	A	55[A]	ASN	2.2
1	B	645	GLY	2.1
1	B	23[A]	HIS	2.1
1	B	332	ARG	2.1
1	B	367	PHE	2.1
1	A	426[A]	CYS	2.1
1	A	21	GLN	2.0

6.2 Non-standard residues in protein, DNA, RNA chains ⓘ

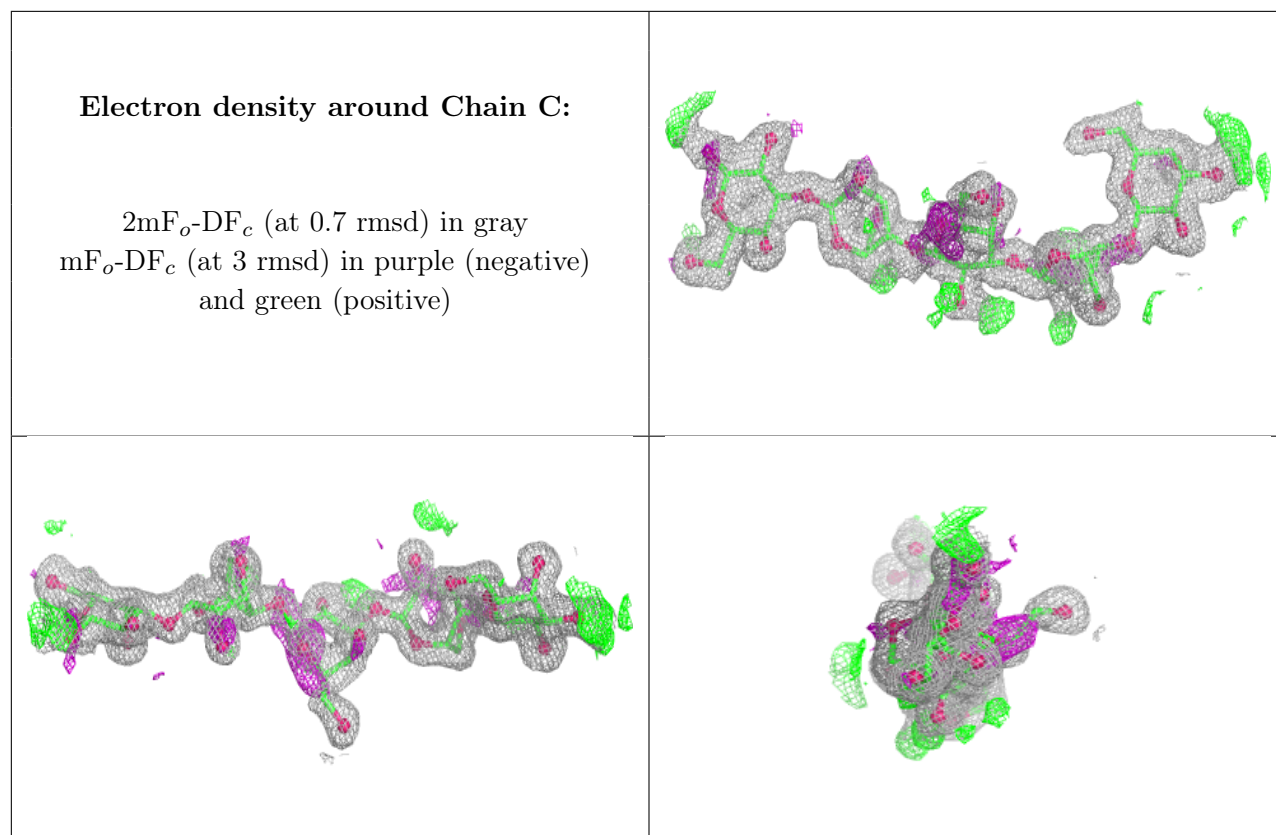
There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

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(\AA^2)	Q<0.9
2	AAL	C	2	10/11	0.90	0.10	18,20,22,23	0
2	GAL	C	3	11/12	0.90	0.12	20,21,24,24	0
2	AAL	C	4	10/11	0.91	0.10	18,19,20,20	0
2	GAL	C	1	12/12	0.92	0.09	17,21,24,25	0
2	GAL	C	5	11/12	0.92	0.09	20,21,24,26	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, 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(\AA^2)	Q<0.9
4	EDO	A	715	4/4	0.69	0.22	38,40,41,43	0
5	GOL	B	722	6/6	0.69	0.22	41,42,44,44	0
4	EDO	B	717	4/4	0.73	0.20	34,37,37,39	0
5	GOL	A	727	6/6	0.74	0.18	31,31,33,36	0
4	EDO	B	715	4/4	0.74	0.20	38,40,41,41	0
4	EDO	B	706	4/4	0.78	0.16	36,36,37,38	0
4	EDO	B	711	4/4	0.78	0.17	26,27,28,30	0
4	EDO	A	720	4/4	0.78	0.21	40,40,41,43	0
4	EDO	B	716	4/4	0.79	0.17	35,36,36,36	0
3	SO4	A	704	5/5	0.80	0.16	20,21,24,24	0
4	EDO	A	714	4/4	0.81	0.16	36,37,37,40	0
4	EDO	A	719	4/4	0.81	0.18	38,38,39,41	0
3	SO4	B	704	5/5	0.82	0.17	63,65,67,70	0
4	EDO	B	705	4/4	0.83	0.17	36,37,37,38	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	EDO	A	709	4/4	0.83	0.18	34,34,36,36	0
4	EDO	B	712	4/4	0.84	0.17	34,36,37,39	0
4	EDO	B	710	4/4	0.85	0.13	24,26,28,31	0
4	EDO	B	713	4/4	0.86	0.19	23,23,23,24	0
5	GOL	B	719	6/6	0.86	0.13	21,24,25,26	0
4	EDO	A	721	4/4	0.86	0.14	31,32,32,32	0
4	EDO	A	708	4/4	0.87	0.13	23,23,24,25	0
5	GOL	A	729	6/6	0.87	0.15	21,30,33,34	0
5	GOL	A	730	6/6	0.87	0.12	23,28,29,31	0
5	GOL	B	718	6/6	0.87	0.12	24,31,34,36	0
4	EDO	B	709	4/4	0.87	0.13	29,29,29,30	0
4	EDO	A	716	4/4	0.87	0.14	18,22,25,29	0
5	GOL	A	728	6/6	0.88	0.11	23,23,23,24	0
3	SO4	A	703	5/5	0.88	0.13	29,33,34,35	0
4	EDO	A	717	4/4	0.88	0.18	22,23,23,24	0
5	GOL	B	721	6/6	0.89	0.14	22,27,29,33	0
4	EDO	A	710	4/4	0.90	0.13	22,23,24,27	0
4	EDO	B	714	4/4	0.91	0.10	22,24,24,24	0
4	EDO	A	713	4/4	0.91	0.11	23,26,27,29	0
3	SO4	A	702	5/5	0.91	0.12	37,37,38,40	0
4	EDO	A	718	4/4	0.91	0.11	19,23,25,27	0
5	GOL	B	720	6/6	0.91	0.10	22,27,27,28	0
3	SO4	B	703	5/5	0.91	0.11	26,27,27,28	0
4	EDO	B	708	4/4	0.91	0.13	16,21,23,27	0
3	SO4	B	702	5/5	0.92	0.10	30,31,37,38	0
4	EDO	A	706	4/4	0.93	0.11	23,23,23,24	0
4	EDO	A	712	4/4	0.93	0.11	18,20,20,21	0
4	EDO	B	707	4/4	0.95	0.09	14,16,17,18	0
4	EDO	A	711	4/4	0.96	0.07	17,18,19,19	0
4	EDO	A	705	4/4	0.97	0.06	13,13,13,14	0
3	SO4	A	701	5/5	0.97	0.08	24,29,31,31	0
4	EDO	A	707	4/4	0.97	0.06	11,13,13,15	0
3	SO4	B	701	5/5	0.98	0.06	20,20,23,24	0
6	CA	A	731	1/1	1.00	0.04	9,9,9,9	0
6	CA	A	732	1/1	1.00	0.04	10,10,10,10	0
6	CA	B	723	1/1	1.00	0.05	10,10,10,10	0
6	CA	B	724	1/1	1.00	0.04	11,11,11,11	0

6.5 Other polymers ⓘ

There are no such residues in this entry.