



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 09:32 PM UTC

PDB ID : 4CU7 / pdb_00004cu7
Title : Unravelling the multiple functions of the architecturally intricate *Streptococcus pneumoniae* beta-galactosidase, BgaA
Authors : Singh, A.K.; Pluvinae, B.; Higgins, M.A.; Dalia, A.B.; Flynn, M.; Lloyd, A.R.; Weiser, J.N.; Stubbs, K.A.; Boraston, A.B.; King, S.J.
Deposited on : 2014-03-17
Resolution : 2.20 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

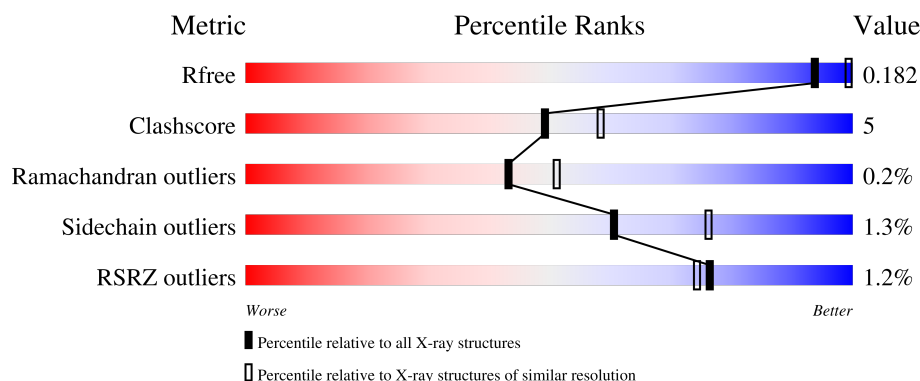
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	849	

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
4	EDO	A	2000	-	-	X	-

2 Entry composition [i](#)

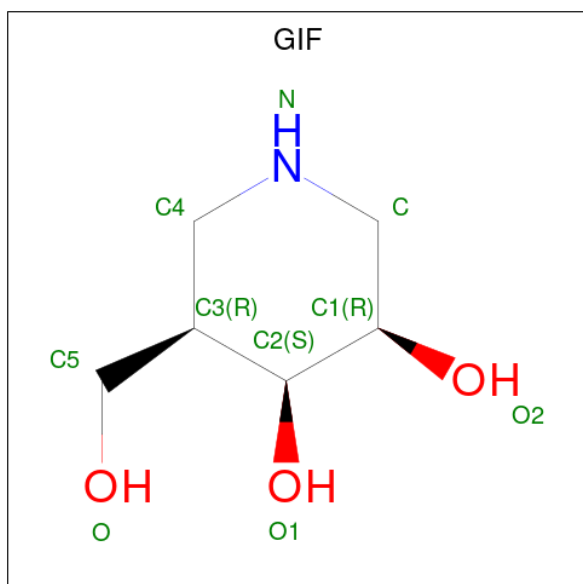
There are 5 unique types of molecules in this entry. The entry contains 8206 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 BETA-GALACTOSIDASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	848	7072	4442	1262	1360	8	9	31	0

- Molecule 2 is D-galacto-isofagomine (CCD ID: GIF) (formula: C₆H₁₃NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	10	6	1	3	0	0

- Molecule 3 is SULFATE ION (CCD ID: 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	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: 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 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0
4	A	1	Total C O 4 2 2	0	0

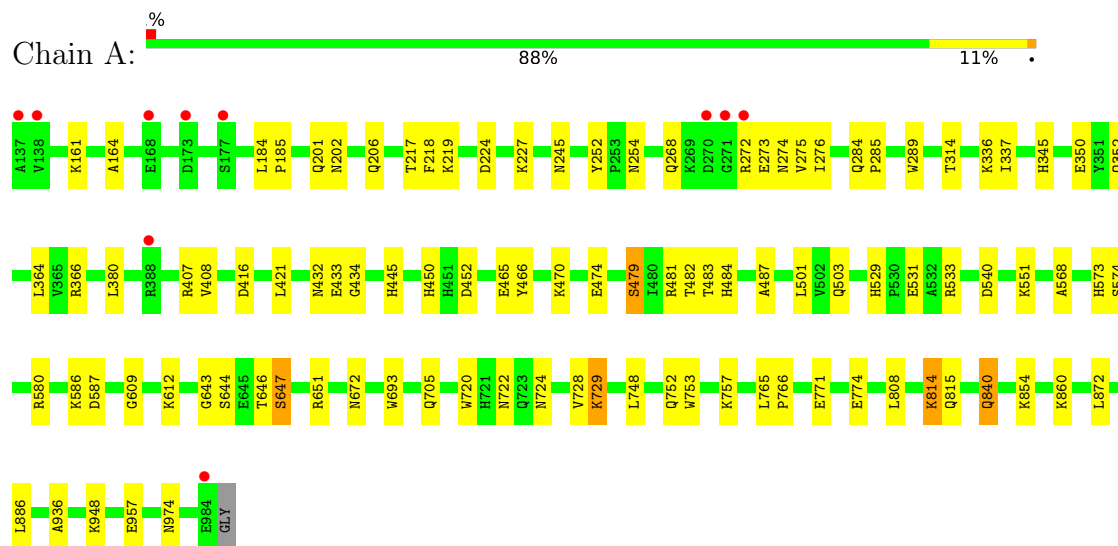
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	984	Total O 984 984	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: BETA-GALACTOSIDASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 2 2	Depositor
Cell constants a, b, c, α , β , γ	116.78Å 116.78Å 219.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	116.78 – 2.20 116.78 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.5 (116.78-2.20) 99.5 (116.78-2.20)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.31 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.151 , 0.182 0.151 , 0.182	Depositor DCC
R_{free} test set	3928 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	19.5	Xtriage
Anisotropy	0.046	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8206	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, SO4, GIF

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	0.76	2/7236 (0.0%)	0.86	8/9787 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	814	LYS	CE-NZ	-10.60	1.17	1.49
1	A	854	LYS	CE-NZ	-5.09	1.34	1.49

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	765	LEU	C-N-CD	6.33	134.52	120.60
1	A	479	SER	N-CA-C	5.70	117.51	108.79
1	A	840[A]	GLN	CA-C-N	5.55	125.56	119.90
1	A	840[A]	GLN	C-N-CA	5.55	125.56	119.90
1	A	840[B]	GLN	CA-C-N	5.55	125.56	119.90
1	A	840[B]	GLN	C-N-CA	5.55	125.56	119.90
1	A	646	THR	CA-C-N	5.35	131.75	121.54
1	A	646	THR	C-N-CA	5.35	131.75	121.54

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	647	SER	Mainchain

5.2 Too-close contacts ⓘ

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	7072	0	6786	69	0
2	A	10	0	13	0	0
3	A	40	0	0	3	0
4	A	100	0	150	23	0
5	A	984	0	0	15	0
All	All	8206	0	6949	76	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 (76) 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:433[A]:GLU:OE1	4:A:2000:EDO:H11	1.56	1.03
1:A:433[A]:GLU:OE1	4:A:2000:EDO:C1	2.11	0.98
1:A:201:GLN:HE21	1:A:724:ASN:HD21	1.11	0.95
4:A:2000:EDO:C2	5:A:3434:HOH:O	2.16	0.93
1:A:529:HIS:HD2	1:A:531:GLU:H	1.10	0.91
1:A:245:ASN:HD21	1:A:274:ASN:HD22	1.20	0.89
1:A:529:HIS:CD2	1:A:531:GLU:H	1.98	0.78
4:A:2000:EDO:H21	5:A:3434:HOH:O	1.81	0.74
1:A:540:ASP:OD1	1:A:580[A]:ARG:NH1	2.21	0.74
1:A:573:HIS:HD2	5:A:3242:HOH:O	1.71	0.73
1:A:693:TRP:HE1	1:A:752:GLN:HE21	1.35	0.71
1:A:268:GLN:H	1:A:274:ASN:HD21	1.39	0.70
1:A:432:ASN:HB2	4:A:2000:EDO:H21	1.73	0.70
1:A:433[A]:GLU:OE1	4:A:2000:EDO:H12	1.92	0.70
1:A:774[B]:GLU:HG3	5:A:3755:HOH:O	1.92	0.69
4:A:2000:EDO:H22	5:A:3434:HOH:O	1.90	0.66
4:A:2013:EDO:H22	5:A:3714:HOH:O	1.96	0.65
1:A:814:LYS:HA	4:A:2018:EDO:H11	1.79	0.64

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:470[B]:LYS:O	1:A:474[B]:GLU:HG2	1.96	0.64
1:A:479:SER:HB3	1:A:501:LEU:HB2	1.80	0.62
1:A:366:ARG:HH12	4:A:2010:EDO:H11	1.65	0.61
4:A:2005:EDO:H11	5:A:3085:HOH:O	2.01	0.59
1:A:268:GLN:H	1:A:274:ASN:ND2	2.01	0.58
1:A:609:GLY:H	4:A:2017:EDO:H12	1.70	0.57
1:A:724:ASN:H	4:A:2013:EDO:H12	1.70	0.56
1:A:345:HIS:HE1	3:A:1993:SO4:O2	1.89	0.55
4:A:2013:EDO:C2	5:A:3714:HOH:O	2.54	0.55
1:A:808:LEU:H	4:A:2006:EDO:H21	1.71	0.55
1:A:748:LEU:C	1:A:748:LEU:HD23	2.32	0.55
1:A:529:HIS:HD2	1:A:531:GLU:N	1.92	0.54
1:A:201:GLN:HE21	1:A:724:ASN:ND2	1.93	0.53
1:A:957:GLU:OE1	5:A:3958:HOH:O	2.19	0.53
1:A:217:THR:HG22	1:A:275:VAL:HG22	1.92	0.52
1:A:872:LEU:H	1:A:974[A]:ASN:HD22	1.55	0.52
1:A:184:LEU:HB3	1:A:185:PRO:HA	1.92	0.52
1:A:314:THR:O	1:A:551:LYS:HE2	2.10	0.51
1:A:337[B]:ILE:HD12	1:A:380:LEU:HD12	1.93	0.51
1:A:224:ASP:HA	1:A:227:LYS:HG3	1.92	0.51
1:A:948:LYS:HD3	4:A:2009:EDO:H12	1.95	0.49
1:A:219:LYS:HG3	1:A:273:GLU:HA	1.94	0.48
1:A:408:VAL:HB	1:A:416:ASP:HB3	1.95	0.48
1:A:533:ARG:NE	3:A:1992:SO4:O1	2.32	0.48
1:A:609:GLY:N	4:A:2017:EDO:H12	2.29	0.48
1:A:433[B]:GLU:HB2	4:A:2012:EDO:H11	1.96	0.48
1:A:729:LYS:C	1:A:729:LYS:HD2	2.38	0.48
4:A:2005:EDO:C1	5:A:3085:HOH:O	2.60	0.47
1:A:218:PHE:CE1	1:A:276:ILE:HD11	2.49	0.47
1:A:722:ASN:HD22	4:A:2005:EDO:H12	1.80	0.46
1:A:434:GLY:O	4:A:2012:EDO:H22	2.16	0.46
1:A:272[B]:ARG:HG3	1:A:273:GLU:N	2.30	0.46
1:A:815[A]:GLN:H	4:A:2018:EDO:C1	2.29	0.46
1:A:284:GLN:HB3	1:A:285:PRO:HA	1.98	0.45
1:A:540:ASP:HB3	5:A:3534:HOH:O	2.17	0.45
1:A:161:LYS:HB3	1:A:164:ALA:HB2	1.98	0.45
1:A:482:THR:HG21	1:A:487:ALA:HB2	1.99	0.44
1:A:672[B]:ASN:OD1	5:A:3667:HOH:O	2.21	0.43
1:A:421[B]:LEU:C	1:A:421[B]:LEU:HD23	2.42	0.43
1:A:771:GLU:OE2	5:A:3753:HOH:O	2.21	0.43
1:A:643:GLY:O	1:A:705:GLN:HA	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:720:TRP:HB2	1:A:728:VAL:HG21	2.00	0.43
1:A:568:ALA:HA	1:A:574:SER:HB2	2.01	0.43
1:A:352:GLN:HB2	1:A:364:LEU:HD23	2.00	0.43
1:A:289:TRP:CD2	1:A:450:HIS:CE1	3.06	0.43
1:A:252:TYR:CE2	1:A:254:ASN:HB3	2.54	0.43
1:A:350:GLU:HB3	1:A:407:ARG:HB2	2.02	0.42
1:A:481:ARG:HE	1:A:503:GLN:NE2	2.17	0.42
1:A:466:TYR:CZ	4:A:2011:EDO:H12	2.55	0.42
1:A:587:ASP:HB3	5:A:3566:HOH:O	2.20	0.41
1:A:936:ALA:HA	3:A:1991:SO4:O2	2.20	0.41
1:A:202:ASN:HA	1:A:206:GLN:HG3	2.03	0.41
1:A:748:LEU:O	1:A:752:GLN:HG2	2.20	0.41
1:A:840[A]:GLN:HG2	5:A:3781:HOH:O	2.19	0.41
1:A:483:THR:HA	1:A:484:HIS:HA	1.79	0.41
1:A:445:HIS:HB3	1:A:753:TRP:CE3	2.56	0.41
1:A:586[B]:LYS:HA	1:A:586[B]:LYS:HD2	1.84	0.41
1:A:465:GLU:OE1	1:A:465:GLU:HA	2.20	0.41

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	878/849 (103%)	861 (98%)	15 (2%)	2 (0%)	43 51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	647	SER
1	A	766	PRO

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	741/715 (104%)	732 (99%)	9 (1%)	63	78

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	336	LYS
1	A	452	ASP
1	A	612	LYS
1	A	644	SER
1	A	651	ARG
1	A	729	LYS
1	A	757	LYS
1	A	860	LYS
1	A	886	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	201	GLN
1	A	274	ASN
1	A	308	HIS
1	A	312	ASN
1	A	485	ASN
1	A	503	GLN
1	A	529	HIS
1	A	573	HIS
1	A	675	GLN
1	A	752	GLN
1	A	823	GLN
1	A	917	GLN
1	A	958	GLN

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

34 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	EDO	A	2000	-	3,3,3	0.29	0	2,2,2	0.72	0
4	EDO	A	2011	-	3,3,3	0.38	0	2,2,2	0.58	0
4	EDO	A	1994	-	3,3,3	0.36	0	2,2,2	0.66	0
4	EDO	A	2014	-	3,3,3	0.34	0	2,2,2	1.13	0
4	EDO	A	2008	-	3,3,3	0.30	0	2,2,2	0.90	0
4	EDO	A	2003	-	3,3,3	0.37	0	2,2,2	0.63	0
3	SO4	A	1986	-	4,4,4	0.39	0	6,6,6	0.38	0
3	SO4	A	1987	-	4,4,4	0.40	0	6,6,6	0.54	0
4	EDO	A	2006	-	3,3,3	0.46	0	2,2,2	0.45	0
4	EDO	A	2007	-	3,3,3	0.47	0	2,2,2	0.80	0
3	SO4	A	1991	-	4,4,4	0.71	0	6,6,6	0.72	0
3	SO4	A	1992	-	4,4,4	1.00	0	6,6,6	0.18	0
3	SO4	A	1988	-	4,4,4	0.53	0	6,6,6	0.53	0
3	SO4	A	1993	-	4,4,4	1.09	0	6,6,6	0.14	0
4	EDO	A	2015	-	3,3,3	0.46	0	2,2,2	0.38	0
3	SO4	A	1990	-	4,4,4	0.47	0	6,6,6	0.31	0
4	EDO	A	2017	-	3,3,3	0.62	0	2,2,2	0.51	0
4	EDO	A	2018	-	3,3,3	0.55	0	2,2,2	0.76	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	EDO	A	2009	-	3,3,3	0.42	0	2,2,2	0.59	0
4	EDO	A	1996	-	3,3,3	0.57	0	2,2,2	0.37	0
4	EDO	A	2013	-	3,3,3	0.39	0	2,2,2	0.83	0
4	EDO	A	2005	-	3,3,3	0.38	0	2,2,2	0.54	0
4	EDO	A	1995	-	3,3,3	0.43	0	2,2,2	0.41	0
4	EDO	A	2010	-	3,3,3	0.34	0	2,2,2	0.81	0
4	EDO	A	1998	-	3,3,3	0.34	0	2,2,2	0.53	0
4	EDO	A	2012	-	3,3,3	0.33	0	2,2,2	0.70	0
2	GIF	A	1985	-	10,10,10	1.10	1 (10%)	9,13,13	2.09	1 (11%)
4	EDO	A	2001	-	3,3,3	0.52	0	2,2,2	0.23	0
4	EDO	A	2002	-	3,3,3	0.50	0	2,2,2	0.28	0
4	EDO	A	2004	-	3,3,3	0.24	0	2,2,2	1.31	0
4	EDO	A	2016	-	3,3,3	0.50	0	2,2,2	0.94	0
4	EDO	A	1999	-	3,3,3	0.43	0	2,2,2	0.43	0
3	SO4	A	1989	-	4,4,4	0.44	0	6,6,6	0.41	0
4	EDO	A	1997	-	3,3,3	0.31	0	2,2,2	0.71	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	2000	-	-	0/1/1/1	-
4	EDO	A	2011	-	-	0/1/1/1	-
4	EDO	A	1994	-	-	0/1/1/1	-
4	EDO	A	2014	-	-	1/1/1/1	-
4	EDO	A	2008	-	-	1/1/1/1	-
4	EDO	A	2003	-	-	1/1/1/1	-
4	EDO	A	2006	-	-	1/1/1/1	-
4	EDO	A	2007	-	-	0/1/1/1	-
4	EDO	A	2015	-	-	1/1/1/1	-
4	EDO	A	2017	-	-	1/1/1/1	-
4	EDO	A	2018	-	-	0/1/1/1	-
4	EDO	A	2009	-	-	1/1/1/1	-
4	EDO	A	1996	-	-	0/1/1/1	-
4	EDO	A	2013	-	-	1/1/1/1	-
4	EDO	A	2005	-	-	1/1/1/1	-
4	EDO	A	2010	-	-	0/1/1/1	-
4	EDO	A	1995	-	-	0/1/1/1	-
4	EDO	A	1998	-	-	0/1/1/1	-
4	EDO	A	2012	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	GIF	A	1985	-	-	0/2/16/16	0/1/1/1
4	EDO	A	2001	-	-	1/1/1/1	-
4	EDO	A	2002	-	-	1/1/1/1	-
4	EDO	A	2004	-	-	1/1/1/1	-
4	EDO	A	2016	-	-	1/1/1/1	-
4	EDO	A	1999	-	-	1/1/1/1	-
4	EDO	A	1997	-	-	1/1/1/1	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1985	GIF	C1-C2	2.05	1.55	1.52

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1985	GIF	C4-N-C	5.88	118.60	111.78

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	2009	EDO	O1-C1-C2-O2
4	A	1997	EDO	O1-C1-C2-O2
4	A	2014	EDO	O1-C1-C2-O2
4	A	2005	EDO	O1-C1-C2-O2
4	A	2006	EDO	O1-C1-C2-O2
4	A	1999	EDO	O1-C1-C2-O2
4	A	2003	EDO	O1-C1-C2-O2
4	A	2016	EDO	O1-C1-C2-O2
4	A	2004	EDO	O1-C1-C2-O2
4	A	2008	EDO	O1-C1-C2-O2
4	A	2017	EDO	O1-C1-C2-O2
4	A	2001	EDO	O1-C1-C2-O2
4	A	2015	EDO	O1-C1-C2-O2
4	A	2002	EDO	O1-C1-C2-O2
4	A	2013	EDO	O1-C1-C2-O2

There are no ring outliers.

13 monomers are involved in 26 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	2000	EDO	7	0
4	A	2011	EDO	1	0
4	A	2006	EDO	1	0
3	A	1991	SO4	1	0
3	A	1992	SO4	1	0
3	A	1993	SO4	1	0
4	A	2017	EDO	2	0
4	A	2018	EDO	2	0
4	A	2009	EDO	1	0
4	A	2013	EDO	3	0
4	A	2005	EDO	3	0
4	A	2010	EDO	1	0
4	A	2012	EDO	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 [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	848/849 (99%)	-0.69	10 (1%) 76 74	5, 16, 36, 58	36 (4%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	272[A]	ARG	4.8
1	A	137	ALA	4.3
1	A	138	VAL	3.4
1	A	173	ASP	3.4
1	A	270	ASP	3.1
1	A	168[A]	GLU	2.9
1	A	388[A]	ARG	2.4
1	A	984	GLU	2.2
1	A	271	GLY	2.2
1	A	177	SER	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](#)

There are no oligosaccharides in this entry.

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($\text{\AA}^2$)	Q<0.9
4	EDO	A	2007	4/4	0.69	0.22	43,50,51,53	0
4	EDO	A	1994	4/4	0.73	0.22	58,58,59,61	0
4	EDO	A	2003	4/4	0.77	0.24	54,55,55,58	0
4	EDO	A	2015	4/4	0.79	0.23	65,65,70,71	0
4	EDO	A	2010	4/4	0.83	0.20	52,52,56,56	0
4	EDO	A	2017	4/4	0.83	0.13	29,29,30,30	0
4	EDO	A	2004	4/4	0.85	0.17	41,44,45,46	0
4	EDO	A	2005	4/4	0.85	0.19	39,43,45,46	0
4	EDO	A	2006	4/4	0.86	0.14	49,50,53,56	0
4	EDO	A	2013	4/4	0.86	0.15	33,38,39,44	0
4	EDO	A	2008	4/4	0.86	0.16	37,42,44,50	0
4	EDO	A	2009	4/4	0.86	0.13	36,39,39,45	0
3	SO4	A	1991	5/5	0.88	0.39	29,30,31,31	0
4	EDO	A	2018	4/4	0.88	0.14	29,29,30,33	0
4	EDO	A	2014	4/4	0.89	0.15	32,37,39,42	0
4	EDO	A	2011	4/4	0.91	0.14	47,48,50,52	0
3	SO4	A	1989	5/5	0.91	0.14	55,57,58,61	0
4	EDO	A	2000	4/4	0.91	0.13	30,32,38,44	0
4	EDO	A	1997	4/4	0.92	0.14	40,42,44,47	0
3	SO4	A	1993	5/5	0.92	0.34	31,32,33,34	0
3	SO4	A	1988	5/5	0.93	0.16	36,42,48,49	0
4	EDO	A	2002	4/4	0.93	0.10	25,32,32,32	0
4	EDO	A	2012	4/4	0.94	0.14	36,39,39,41	0
4	EDO	A	2016	4/4	0.94	0.08	24,24,26,28	0
3	SO4	A	1992	5/5	0.94	0.35	30,31,32,33	0
4	EDO	A	2001	4/4	0.94	0.08	20,22,23,26	0
4	EDO	A	1999	4/4	0.95	0.09	45,47,48,51	0
4	EDO	A	1998	4/4	0.95	0.09	25,28,30,32	0
3	SO4	A	1987	5/5	0.96	0.11	45,46,47,52	0
3	SO4	A	1990	5/5	0.96	0.12	41,46,47,50	0
3	SO4	A	1986	5/5	0.98	0.06	28,29,31,32	0
4	EDO	A	1996	4/4	0.98	0.07	18,18,19,19	0
4	EDO	A	1995	4/4	0.99	0.03	13,14,15,15	0
2	GIF	A	1985	10/10	0.99	0.04	11,12,13,13	0

6.5 Other polymers ⓘ

There are no such residues in this entry.