



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 20, 2020 – 07:34 AM EST

PDB ID : 6NQY
Title : Flagellar protein FcpA from *Leptospira biflexa* / ab-centered monoclinic form
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Deposited on : 2019-01-22
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.0 (224370), CSD as540be (2019)
Xtriage (Phenix) : 1.13
EDS : 2.4
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.4

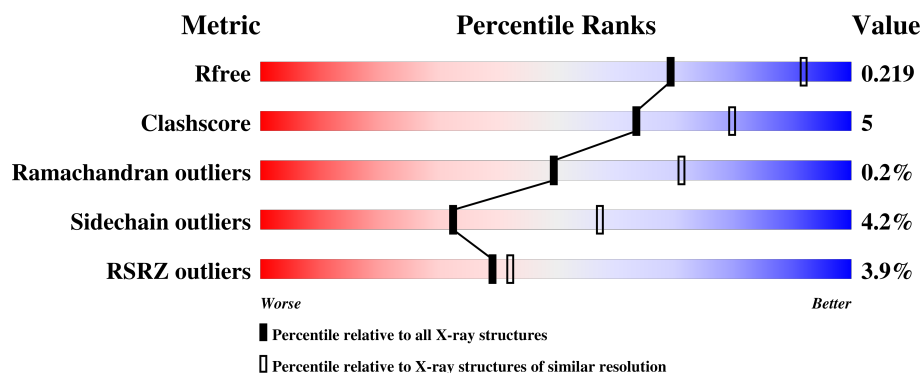
1 Overall quality at a glance

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}	111664	4155 (2.50-2.50)
Clashscore	122126	4827 (2.50-2.50)
Ramachandran outliers	120053	4735 (2.50-2.50)
Sidechain outliers	120020	4737 (2.50-2.50)
RSRZ outliers	108989	4058 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	269	<div> <div>3%</div> <div>77%</div> <div>8%</div> <div>15%</div> </div>
1	B	269	<div> <div>4%</div> <div>76%</div> <div>7%</div> <div>16%</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
2	GOL	B	403	-	-	X	-
3	IOD	A	405[B]	-	-	X	-
3	IOD	B	405	-	-	X	-

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 4101 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.

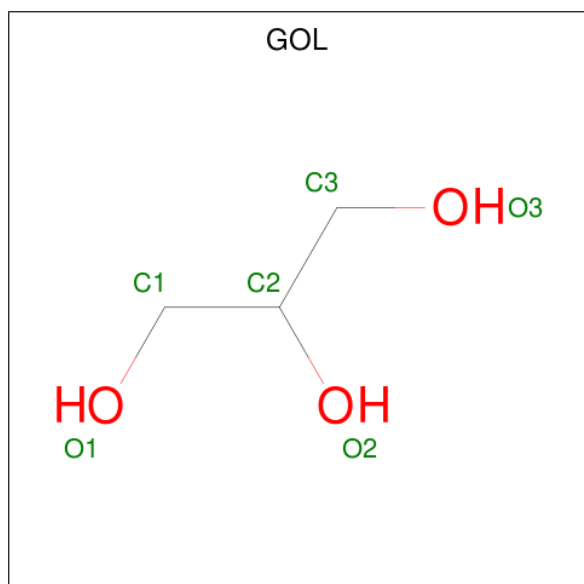
- Molecule 1 is a protein called Flagellar coiling protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	0	1	0
			1946	1241	338	362	5			
1	B	227	Total	C	N	O	S	0	0	0
			1929	1231	335	359	4			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	32	GLY	-	expression tag	UNP B0STJ8
A	33	SER	-	expression tag	UNP B0STJ8
B	32	GLY	-	expression tag	UNP B0STJ8
B	33	SER	-	expression tag	UNP B0STJ8

- Molecule 2 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).

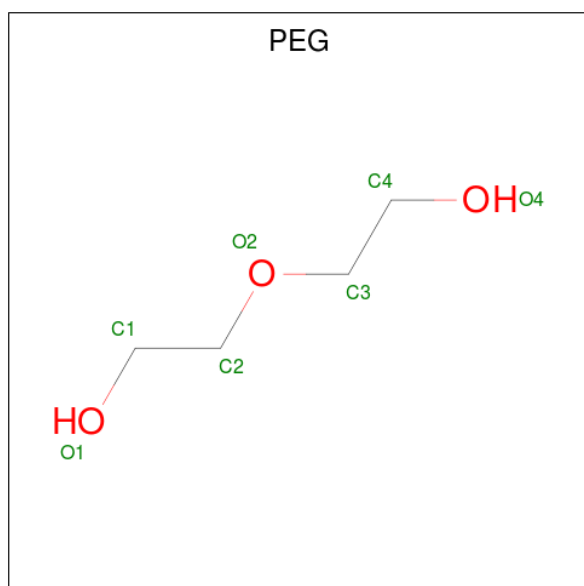


Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0
2	B	1	Total C O 6 3 3	0	0

- Molecule 3 is IODIDE ION (three-letter code: IOD) (formula: I).

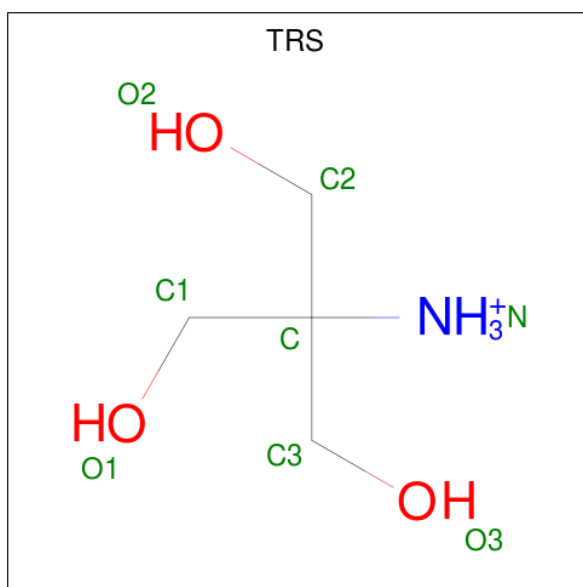
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	13	Total I 13 13	0	0
3	A	16	Total I 18 18	0	2

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C O 7 4 3	0	0

- Molecule 5 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	N	O	0	0
			8	4	1	3		
5	B	1	Total	C	N	O	0	0
			8	4	1	3		
5	B	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	74	Total	O	0	0
			74	74		
6	B	65	Total	O	0	1
			66	66		

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	82.32Å 99.59Å 106.69Å 90.00° 91.95° 90.00°	Depositor
Resolution (Å)	40.29 – 2.50 41.14 – 2.50	Depositor EDS
% Data completeness (in resolution range)	98.2 (40.29-2.50) 98.2 (41.14-2.50)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.17 (at 2.51Å)	Xtriage
Refinement program	BUSTER 2.10.3	Depositor
R, R_{free}	0.196 , 0.221 0.203 , 0.219	Depositor DCC
R_{free} test set	1489 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	64.4	Xtriage
Anisotropy	0.206	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 62.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4101	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% 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: GOL, TRS, PEG, IOD

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	0.52	0/1992	0.65	0/2684
1	B	0.51	0/1975	0.64	0/2661
All	All	0.51	0/3967	0.65	0/5345

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	1946	0	1881	12	0
1	B	1929	0	1871	21	0
2	A	6	0	8	1	0
2	B	18	0	24	10	0
3	A	18	0	0	5	0
3	B	13	0	0	7	0
4	B	7	0	10	1	0
5	B	24	0	36	3	0
6	A	74	0	0	1	0
6	B	66	0	0	1	0
All	All	4101	0	3830	36	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 (36) 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:76:PRO:HD3	2:B:403:GOL:H2	1.45	0.95
1:B:145:ARG:NH2	3:B:411:IOD:I	2.87	0.77
3:B:405:IOD:I	3:B:415:IOD:I	3.50	0.69
1:B:199:SER:HB3	2:B:403:GOL:H32	1.75	0.67
2:A:401:GOL:H12	3:A:405[B]:IOD:I	2.65	0.67
1:B:201:ILE:HD13	1:B:217:LEU:HD13	1.81	0.62
1:B:187:PRO:HB2	3:B:408:IOD:I	2.70	0.61
1:B:231:PRO:HB3	3:B:406:IOD:I	2.71	0.60
1:B:151:ARG:HG3	2:B:404:GOL:H32	1.85	0.58
1:B:76:PRO:HA	2:B:401:GOL:H12	1.87	0.56
1:A:161:LYS:HD3	1:A:207:LEU:HD12	1.88	0.55
1:A:66:ILE:HG23	1:A:230:TYR:HE1	1.73	0.54
1:A:231:PRO:HB3	3:A:403:IOD:I	2.81	0.51
1:B:76:PRO:CD	2:B:403:GOL:H2	2.30	0.50
1:A:187:PRO:HB2	3:A:414:IOD:I	2.83	0.48
3:B:416:IOD:I	6:B:543:HOH:O	2.90	0.48
1:A:226:ASN:O	1:A:229:GLU:HG2	2.13	0.47
1:B:69:GLN:HE21	1:B:231:PRO:HD3	1.80	0.47
1:B:154:TYR:HD2	2:B:404:GOL:H31	1.80	0.46
1:B:263:LYS:HE2	3:B:413:IOD:I	2.86	0.46
1:A:157:LYS:HD2	3:A:405[B]:IOD:I	2.86	0.46
1:B:151:ARG:HA	2:B:404:GOL:H12	1.97	0.45
1:A:69:GLN:HE21	1:A:231:PRO:HD3	1.81	0.45
1:B:120:TRP:CD1	5:B:418:TRS:H22	2.52	0.45
1:B:76:PRO:HD3	2:B:403:GOL:C2	2.30	0.44
1:B:114:ILE:HG13	2:B:403:GOL:H31	1.99	0.44
1:B:191:ARG:HG2	5:B:420:TRS:H21	2.00	0.43
1:B:120:TRP:HD1	5:B:418:TRS:H22	1.84	0.42
1:B:224:ASP:HB3	1:B:225:ASP:H	1.53	0.42
1:A:212:GLN:HG2	6:A:514:HOH:O	2.20	0.42
1:B:202:MET:HB2	2:B:403:GOL:O2	2.20	0.42
1:A:77:ASP:HB2	3:A:407:IOD:I	2.90	0.41
1:A:157:LYS:HB3	1:A:157:LYS:HE3	1.95	0.41
1:A:192:LEU:O	1:A:196:VAL:HG23	2.21	0.41
1:B:115:MET:CB	4:B:402:PEG:H32	2.51	0.41
1:A:139:TYR:HD1	3:B:405:IOD:I	2.75	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	228/269 (85%)	223 (98%)	4 (2%)	1 (0%)	36	57
1	B	225/269 (84%)	222 (99%)	3 (1%)	0	100	100
All	All	453/538 (84%)	445 (98%)	7 (2%)	1 (0%)	49	71

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	253	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	205/248 (83%)	196 (96%)	9 (4%)	31	55
1	B	204/248 (82%)	196 (96%)	8 (4%)	35	61
All	All	409/496 (82%)	392 (96%)	17 (4%)	32	57

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	A	95	PHE
1	A	162	GLN
1	A	177	GLU
1	A	185	GLU

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Mol	Chain	Res	Type
1	A	224	ASP
1	A	230	TYR
1	A	246	MET
1	A	274	LEU
1	B	69	GLN
1	B	177	GLU
1	B	185	GLU
1	B	191	ARG
1	B	217	LEU
1	B	224	ASP
1	B	230	TYR
1	B	274	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	69	GLN
1	B	69	GLN
1	B	285	HIS

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](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 39 ligands modelled in this entry, 31 are monoatomic - leaving 8 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	$\# Z > 2$
2	GOL	A	401	-	5,5,5	0.12	0	5,5,5	0.52	0
2	GOL	B	401	-	5,5,5	0.23	0	5,5,5	0.26	0
4	PEG	B	402	-	6,6,6	0.37	0	5,5,5	0.30	0
2	GOL	B	403	-	5,5,5	0.22	0	5,5,5	0.87	0
2	GOL	B	404	-	5,5,5	0.06	0	5,5,5	0.37	0
5	TRS	B	418	-	7,7,7	0.52	0	9,9,9	0.61	0
5	TRS	B	419	-	7,7,7	0.40	0	9,9,9	0.45	0
5	TRS	B	420	-	7,7,7	0.37	0	9,9,9	0.48	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	GOL	A	401	-	-	0/4/4/4	-
2	GOL	B	401	-	-	0/4/4/4	-
4	PEG	B	402	-	-	3/4/4/4	-
2	GOL	B	403	-	-	2/4/4/4	-
2	GOL	B	404	-	-	0/4/4/4	-
5	TRS	B	418	-	-	3/9/9/9	-
5	TRS	B	419	-	-	0/9/9/9	-
5	TRS	B	420	-	-	3/9/9/9	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (11) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	420	TRS	C2-C-C1-O1
5	B	420	TRS	C3-C-C1-O1
5	B	420	TRS	N-C-C1-O1
5	B	418	TRS	C1-C-C3-O3
5	B	418	TRS	C2-C-C3-O3

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Mol	Chain	Res	Type	Atoms
5	B	418	TRS	N-C-C3-O3
2	B	403	GOL	O1-C1-C2-C3
4	B	402	PEG	C4-C3-O2-C2
4	B	402	PEG	C1-C2-O2-C3
2	B	403	GOL	O1-C1-C2-O2
4	B	402	PEG	O2-C3-C4-O4

There are no ring outliers.

7 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	GOL	1	0
2	B	401	GOL	1	0
4	B	402	PEG	1	0
2	B	403	GOL	6	0
2	B	404	GOL	3	0
5	B	418	TRS	2	0
5	B	420	TRS	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 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	229/269 (85%)	0.18	8 (3%) 44 47	50, 75, 113, 154	0
1	B	227/269 (84%)	0.25	10 (4%) 34 37	52, 76, 138, 163	0
All	All	456/538 (84%)	0.21	18 (3%) 39 42	50, 75, 131, 163	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	66	ILE	5.2
1	B	279	ASP	4.9
1	B	290	ILE	3.6
1	A	91	LEU	3.5
1	A	88	LEU	3.4
1	B	286	ILE	3.3
1	A	279	ASP	3.0
1	B	65	GLU	3.0
1	B	66	ILE	2.6
1	B	283	TYR	2.6
1	B	179	LYS	2.6
1	A	252	GLY	2.6
1	A	95	PHE	2.4
1	A	132	LYS	2.4
1	B	251	LYS	2.4
1	A	65	GLU	2.3
1	B	248	LYS	2.1
1	B	269	LEU	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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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	GOL	B	404	6/6	0.72	0.17	100,102,103,105	0
5	TRS	B	418	8/8	0.73	0.31	92,96,98,99	0
5	TRS	B	420	8/8	0.74	0.35	119,121,123,124	0
3	IOD	A	410	1/1	0.75	0.07	133,133,133,133	1
5	TRS	B	419	8/8	0.75	0.25	107,112,118,122	0
2	GOL	B	401	6/6	0.76	0.35	85,90,93,97	0
3	IOD	B	414	1/1	0.80	0.11	107,107,107,107	1
2	GOL	A	401	6/6	0.83	0.26	88,89,90,90	0
4	PEG	B	402	7/7	0.83	0.18	77,78,83,84	0
2	GOL	B	403	6/6	0.85	0.34	72,78,79,80	0
3	IOD	A	414	1/1	0.86	0.20	131,131,131,131	1
3	IOD	A	415	1/1	0.87	0.25	109,109,109,109	1
3	IOD	B	412	1/1	0.88	0.11	109,109,109,109	1
3	IOD	A	416[B]	1/1	0.88	0.19	91,91,91,91	1
3	IOD	B	417	1/1	0.88	0.12	94,94,94,94	1
3	IOD	A	416[A]	1/1	0.88	0.19	153,153,153,153	1
3	IOD	A	412	1/1	0.91	0.12	95,95,95,95	1
3	IOD	B	409	1/1	0.91	0.06	115,115,115,115	1
3	IOD	A	411	1/1	0.91	0.10	105,105,105,105	1
3	IOD	B	408	1/1	0.92	0.15	87,87,87,87	1
3	IOD	A	413	1/1	0.93	0.29	97,97,97,97	1
3	IOD	A	406	1/1	0.93	0.12	84,84,84,84	1
3	IOD	A	409	1/1	0.93	0.19	85,85,85,85	1
3	IOD	B	416	1/1	0.93	0.14	85,85,85,85	1
3	IOD	B	413	1/1	0.94	0.19	95,95,95,95	1
3	IOD	B	407	1/1	0.95	0.20	102,102,102,102	1
3	IOD	A	408	1/1	0.95	0.08	82,82,82,82	1
3	IOD	B	415	1/1	0.96	0.12	67,67,67,67	1
3	IOD	B	410	1/1	0.96	0.14	112,112,112,112	1
3	IOD	A	407	1/1	0.97	0.14	69,69,69,69	1
3	IOD	A	403	1/1	0.97	0.18	80,80,80,80	1
3	IOD	A	417	1/1	0.97	0.20	75,75,75,75	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	IOD	A	405[B]	1/1	0.98	0.12	91,91,91,91	1
3	IOD	B	411	1/1	0.98	0.13	69,69,69,69	1
3	IOD	A	405[A]	1/1	0.98	0.12	76,76,76,76	1
3	IOD	A	404	1/1	0.99	0.14	75,75,75,75	1
3	IOD	B	405	1/1	0.99	0.14	65,65,65,65	1
3	IOD	B	406	1/1	0.99	0.18	86,86,86,86	1
3	IOD	A	402	1/1	0.99	0.21	68,68,68,68	1

6.5 Other polymers [i](#)

There are no such residues in this entry.