



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 07:18 AM UTC

PDB ID : 7W6B / pdb_00007w6b
Title : Crystal Structure of PitA from pilus islet-2 of Streptococcus oralis
Authors : Yadav, R.K.; Krishnan, V.
Deposited on : 2021-12-01
Resolution : 2.98 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
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

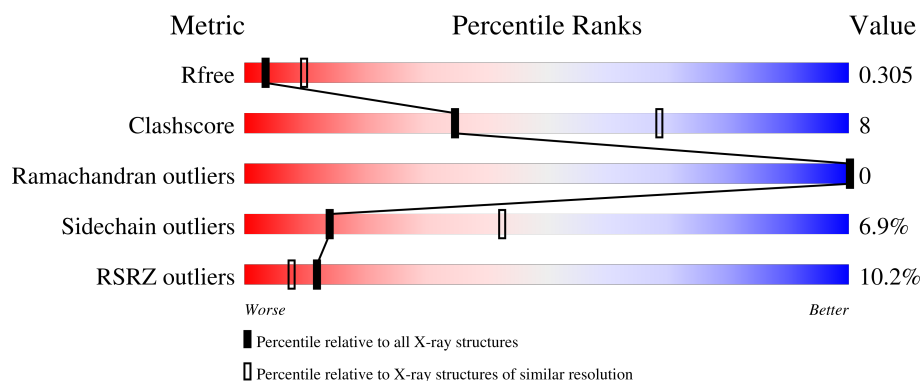
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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	3580 (3.00-2.96)
Clashscore	190562	3904 (3.00-2.96)
Ramachandran outliers	187476	3761 (3.00-2.96)
Sidechain outliers	187428	3764 (3.00-2.96)
RSRZ outliers	180081	3579 (3.00-2.96)

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	793	10% 79% 17% ..

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	IOD	A	911	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 5925 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 von Willebrand factor type A domain protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	782	Total	C	N	O	S	0	0	0
			5877	3635	1022	1216	4			

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	15	Total	I	0	0
			15	15		

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	31	Total	O	0	0
			31	31		

4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	52.27Å 422.93Å 48.39Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	51.93 – 2.98 51.93 – 2.98	Depositor EDS
% Data completeness (in resolution range)	90.1 (51.93-2.98) 90.1 (51.93-2.98)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 3.01Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.253 , 0.305 0.254 , 0.305	Depositor DCC
R_{free} test set	1068 reflections (4.63%)	wwPDB-VP
Wilson B-factor (Å ²)	59.0	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 74.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	5925	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% 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: CA, IOD, MG

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	0.61	0/5973	1.19	12/8118 (0.1%)

There are no bond length outliers.

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	788	THR	CA-CB-OG1	-7.37	98.55	109.60
1	A	492	ASN	CB-CA-C	7.09	117.56	110.33
1	A	762	THR	CA-CB-OG1	-6.43	99.96	109.60
1	A	555	ASN	CA-CB-CG	6.42	119.02	112.60
1	A	722	VAL	CA-C-O	-5.86	115.59	121.45
1	A	769	ASP	CB-CA-C	-5.49	101.18	110.19
1	A	723	PHE	N-CA-C	5.34	119.55	112.72
1	A	757	THR	CB-CA-C	5.09	116.83	109.45
1	A	591	THR	CA-CB-OG1	-5.09	101.97	109.60
1	A	699	LYS	N-CA-C	-5.07	101.75	108.74
1	A	698	ASN	N-CA-C	-5.02	107.19	113.72
1	A	447	ALA	N-CA-C	-5.01	106.67	112.89

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	5877	0	5528	86	0
2	A	1	0	0	0	0
3	A	15	0	0	7	0
4	A	1	0	0	0	0
5	A	31	0	0	0	0
All	All	5925	0	5528	86	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 8.

All (86) 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:611:LYS:NZ	1:A:707:ASN:CG	1.70	1.46
1:A:551:ASN:OD1	3:A:911:IOD:I	2.24	1.26
1:A:611:LYS:HZ2	1:A:707:ASN:CG	1.41	1.06
1:A:81:VAL:HG23	1:A:233:MET:HE2	1.46	0.94
1:A:81:VAL:CG2	1:A:233:MET:HE2	1.97	0.94
1:A:611:LYS:CE	1:A:707:ASN:CG	2.47	0.88
1:A:684:ASN:O	1:A:684:ASN:OD1	2.00	0.79
1:A:717:LYS:HE2	1:A:730:PHE:CG	2.23	0.74
1:A:727:LEU:HA	3:A:912:IOD:I	2.60	0.72
1:A:622:GLU:OE1	1:A:654:ARG:HD2	1.88	0.72
1:A:331:PRO:HG3	1:A:479:ILE:CG2	2.20	0.71
1:A:738:ASP:OD1	1:A:739:ALA:N	2.23	0.70
1:A:735:ASN:HA	1:A:764:GLY:O	1.93	0.68
1:A:331:PRO:HG3	1:A:479:ILE:HG22	1.78	0.65
1:A:81:VAL:HG23	1:A:233:MET:CE	2.25	0.65
1:A:717:LYS:HE2	1:A:730:PHE:CD2	2.32	0.65
1:A:41:PRO:HG2	1:A:69:LEU:HG	1.80	0.64
1:A:644:ILE:HG21	1:A:665:LEU:HD21	1.81	0.61
1:A:606:SER:HB3	1:A:666:SER:HA	1.83	0.61
1:A:525:SER:O	3:A:911:IOD:I	2.91	0.59
1:A:644:ILE:HB	1:A:665:LEU:HD23	1.86	0.58
1:A:257:ASP:OD1	1:A:258:ALA:N	2.31	0.58
1:A:722:VAL:CG2	1:A:725:ASN:HD22	2.16	0.58
1:A:536:LYS:HE3	1:A:569:GLY:O	2.05	0.57
1:A:607:LEU:HD23	1:A:665:LEU:HD12	1.86	0.57
1:A:809:LYS:O	1:A:814:LYS:HE3	2.06	0.56
1:A:141:GLY:HA3	1:A:254:MET:SD	2.45	0.55
1:A:81:VAL:HG21	1:A:233:MET:HE2	1.85	0.55
1:A:722:VAL:HA	3:A:915:IOD:I	2.76	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:411:LEU:CD1	1:A:469:LYS:HD2	2.37	0.54
1:A:123:ILE:HD11	1:A:199:VAL:HG21	1.89	0.54
1:A:714:SER:HA	1:A:776:ILE:O	2.08	0.54
1:A:532:VAL:HG22	1:A:543:GLN:HA	1.89	0.53
1:A:688:VAL:HG22	1:A:707:ASN:OD1	2.09	0.53
1:A:644:ILE:CG2	1:A:665:LEU:HD21	2.41	0.51
1:A:606:SER:HB3	1:A:667:TYR:H	1.77	0.50
1:A:791:GLU:HG2	1:A:796:SER:OG	2.12	0.50
1:A:64:ASP:HB3	1:A:431:VAL:HB	1.94	0.50
1:A:606:SER:CB	1:A:666:SER:HA	2.41	0.50
1:A:613:LEU:HD21	1:A:623:PHE:CE2	2.47	0.50
1:A:619:LEU:HB3	1:A:657:LYS:HD2	1.95	0.49
1:A:563:PHE:HA	3:A:905:IOD:I	2.82	0.48
1:A:57:ASP:O	1:A:437:THR:HA	2.13	0.48
1:A:90:MET:HA	1:A:105:ARG:HD2	1.94	0.48
1:A:611:LYS:HE3	1:A:707:ASN:CG	2.37	0.48
1:A:385:VAL:HB	1:A:431:VAL:HG13	1.96	0.48
1:A:747:THR:HG22	1:A:760:GLN:OE1	2.15	0.47
1:A:750:ALA:HB1	1:A:776:ILE:HD11	1.96	0.46
1:A:589:VAL:N	1:A:596:SER:O	2.48	0.46
1:A:768:ILE:CD1	1:A:776:ILE:HG21	2.46	0.46
1:A:811:ASP:OD1	1:A:814:LYS:HE2	2.16	0.46
1:A:465:LEU:O	1:A:494:THR:HA	2.16	0.45
1:A:659:LYS:O	1:A:660:ARG:HB2	2.16	0.45
1:A:177:SER:OG	1:A:180:ASP:OD2	2.34	0.45
1:A:247:LEU:HD12	1:A:305:ILE:O	2.18	0.45
1:A:513:THR:OG1	1:A:517:THR:HG21	2.17	0.45
1:A:606:SER:HB3	1:A:667:TYR:N	2.32	0.44
1:A:43:THR:HG1	1:A:487:LYS:HZ3	1.59	0.43
1:A:752:VAL:HG22	1:A:776:ILE:HD12	2.00	0.43
1:A:145:ASN:HA	1:A:172:TYR:HA	1.99	0.43
1:A:67:SER:O	1:A:68:LYS:HG3	2.18	0.43
1:A:85:ASP:HB2	1:A:248:SER:HA	2.01	0.43
1:A:737:ARG:O	1:A:785:SER:HB2	2.19	0.43
1:A:483:GLN:O	1:A:484:THR:C	2.62	0.42
1:A:574:LEU:HB3	1:A:586:ILE:HG21	2.00	0.42
1:A:722:VAL:HG21	1:A:725:ASN:HD22	1.84	0.42
1:A:184:THR:N	1:A:228:LEU:HD21	2.34	0.42
1:A:93:GLN:HA	1:A:104:SER:HA	2.01	0.42
1:A:125:THR:HG21	1:A:351:THR:HB	2.00	0.42
1:A:457:ALA:HB2	1:A:465:LEU:HD23	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:807:GLU:H	1:A:807:GLU:HG2	1.80	0.42
1:A:47:LYS:HA	1:A:62:SER:O	2.19	0.41
1:A:95:VAL:HG22	1:A:308:ARG:HD3	2.01	0.41
1:A:78:LEU:HD23	1:A:241:LYS:CB	2.50	0.41
1:A:519:ILE:HD13	1:A:582:PHE:HE2	1.84	0.41
1:A:354:ILE:HA	1:A:479:ILE:HG12	2.02	0.41
1:A:551:ASN:CG	3:A:911:IOD:I	3.22	0.41
1:A:684:ASN:OD1	1:A:684:ASN:C	2.63	0.41
1:A:737:ARG:HG3	3:A:903:IOD:I	2.91	0.41
1:A:688:VAL:HG13	1:A:707:ASN:OD1	2.20	0.41
1:A:523:GLN:HE22	1:A:554:LYS:HG3	1.84	0.41
1:A:613:LEU:HD23	1:A:613:LEU:HA	1.87	0.41
1:A:759:LEU:HD12	1:A:759:LEU:HA	1.91	0.41
1:A:768:ILE:HD12	1:A:776:ILE:HG21	2.02	0.41
1:A:306:LYS:HG2	1:A:316:ILE:HD12	2.02	0.40
1:A:503:VAL:HA	1:A:504:PRO:HD3	1.87	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	780/793 (98%)	737 (94%)	43 (6%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	622/697 (89%)	579 (93%)	43 (7%)	14	42

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	THR
1	A	137	VAL
1	A	169	MET
1	A	170	THR
1	A	183	ASN
1	A	242	LYS
1	A	316	ILE
1	A	353	LYS
1	A	394	ILE
1	A	411	LEU
1	A	431	VAL
1	A	451	LYS
1	A	453	GLU
1	A	513	THR
1	A	516	ARG
1	A	548	THR
1	A	560	THR
1	A	584	LYS
1	A	587	LYS
1	A	606	SER
1	A	608	THR
1	A	611	LYS
1	A	613	LEU
1	A	617	ASN
1	A	619	LEU
1	A	621	LYS
1	A	624	ARG
1	A	631	SER
1	A	645	THR
1	A	647	VAL
1	A	662	ARG
1	A	697	LEU
1	A	709	LYS
1	A	723	PHE
1	A	725	ASN

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Mol	Chain	Res	Type
1	A	749	THR
1	A	752	VAL
1	A	755	LYS
1	A	757	THR
1	A	776	ILE
1	A	788	THR
1	A	791	GLU
1	A	792	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	287	ASN
1	A	338	ASN
1	A	360	HIS
1	A	523	GLN
1	A	549	ASN
1	A	558	ASN
1	A	562	ASN
1	A	684	ASN
1	A	725	ASN
1	A	735	ASN
1	A	753	ASN

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 ⓘ

Of 17 ligands modelled in this entry, 17 are monoatomic - leaving 0 for Mogul analysis.

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.

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 ⓘ

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	782/793 (98%)	0.72	80 (10%) 12 8	11, 89, 178, 238	0

All (80) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	166	TYR	5.4
1	A	252	ALA	5.3
1	A	473	VAL	4.3
1	A	724	ALA	4.2
1	A	692	ASN	3.8
1	A	347	PHE	3.7
1	A	266	TYR	3.6
1	A	723	PHE	3.5
1	A	67	SER	3.5
1	A	159	LEU	3.4
1	A	822	LYS	3.4
1	A	459	GLY	3.3
1	A	248	SER	3.3
1	A	350	ILE	3.3
1	A	250	GLY	3.3
1	A	315	SER	3.3
1	A	351	THR	3.2
1	A	678	GLU	3.2
1	A	682	SER	3.0
1	A	202	MET	3.0
1	A	194	ALA	2.9
1	A	195	ALA	2.9
1	A	679	GLU	2.9
1	A	307	PHE	2.9
1	A	251	PHE	2.9
1	A	45	LEU	2.8
1	A	192	ALA	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	681	ALA	2.8
1	A	281	TRP	2.8
1	A	208	ASN	2.8
1	A	522	ASP	2.8
1	A	480	GLY	2.8
1	A	616	GLU	2.7
1	A	477	TYR	2.7
1	A	727	LEU	2.7
1	A	279	TRP	2.7
1	A	69	LEU	2.7
1	A	618	ASN	2.7
1	A	792	GLU	2.7
1	A	291	LEU	2.7
1	A	199	VAL	2.6
1	A	302	PHE	2.6
1	A	247	LEU	2.6
1	A	394	ILE	2.6
1	A	134	LEU	2.5
1	A	619	LEU	2.5
1	A	615	ALA	2.5
1	A	469	LYS	2.5
1	A	86	LEU	2.5
1	A	73	THR	2.5
1	A	820	ASN	2.5
1	A	277	PRO	2.4
1	A	346	SER	2.4
1	A	162	PRO	2.4
1	A	75	THR	2.4
1	A	685	GLY	2.4
1	A	460	SER	2.4
1	A	311	ASN	2.3
1	A	206	GLY	2.3
1	A	71	THR	2.3
1	A	309	TYR	2.3
1	A	168	ARG	2.3
1	A	796	SER	2.3
1	A	382	PHE	2.2
1	A	375	LEU	2.2
1	A	126	ILE	2.2
1	A	157	TRP	2.2
1	A	280	PHE	2.2
1	A	376	PRO	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	84	ALA	2.2
1	A	798	GLY	2.1
1	A	151	TYR	2.1
1	A	187	GLY	2.1
1	A	633	ASP	2.1
1	A	164	TRP	2.1
1	A	273	ILE	2.1
1	A	684	ASN	2.0
1	A	197	THR	2.0
1	A	479	ILE	2.0
1	A	257	ASP	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](#)

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(Å ²)	Q<0.9
2	MG	A	901	1/1	0.71	0.16	104,104,104,104	0
3	IOD	A	916	1/1	0.85	0.12	79,79,79,79	1
3	IOD	A	913	1/1	0.91	0.13	97,97,97,97	1
3	IOD	A	912	1/1	0.93	0.08	94,94,94,94	1
3	IOD	A	905	1/1	0.93	0.07	66,66,66,66	1
3	IOD	A	911	1/1	0.93	0.07	60,60,60,60	1
3	IOD	A	907	1/1	0.94	0.11	83,83,83,83	0
4	CA	A	917	1/1	0.94	0.06	104,104,104,104	0
3	IOD	A	910	1/1	0.95	0.10	67,67,67,67	1
3	IOD	A	909	1/1	0.95	0.08	93,93,93,93	1
3	IOD	A	906	1/1	0.96	0.09	61,61,61,61	1
3	IOD	A	915	1/1	0.97	0.07	55,55,55,55	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	IOD	A	914	1/1	0.98	0.10	77,77,77,77	1
3	IOD	A	904	1/1	0.98	0.04	57,57,57,57	1
3	IOD	A	902	1/1	0.98	0.04	64,64,64,64	1
3	IOD	A	903	1/1	0.98	0.04	66,66,66,66	1
3	IOD	A	908	1/1	0.99	0.06	54,54,54,54	1

6.5 Other polymers [i](#)

There are no such residues in this entry.