Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 05:32 AM GMT

PDB ID	:	2R6O
Title	:	Crystal structure of putative diguanylate cyclase/phosphodiesterase from Thiobacillus denitrificans
Authors	:	Chang, C.; Xu, X.; Zheng, H.; Savchenko, A.; Edwards, A.M.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on	:	2007-09-06
Resolution	:	1.80 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

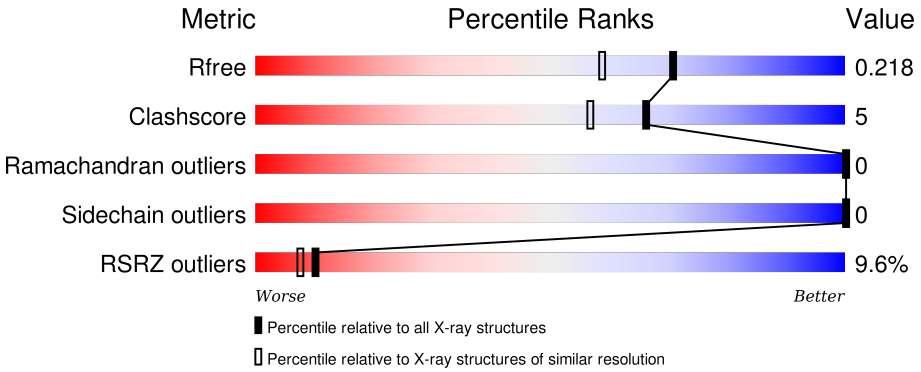
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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 <=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	294	7% 79% 9% 12%
1	B	294	9% 76% 6% 18%

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	MG	B	803	-	-	-	X

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4346 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 Putative diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains).

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	258	Total	C	N	O	S	Se	0	12	0
			2054	1287	363	394	5	5			
1	B	242	Total	C	N	O	S	Se	0	10	0
			1908	1194	344	361	5	4			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	465	MSE	-	EXPRESSION TAG	UNP Q3SJE6
A	466	GLY	-	EXPRESSION TAG	UNP Q3SJE6
A	467	SER	-	EXPRESSION TAG	UNP Q3SJE6
A	468	SER	-	EXPRESSION TAG	UNP Q3SJE6
A	469	HIS	-	EXPRESSION TAG	UNP Q3SJE6
A	470	HIS	-	EXPRESSION TAG	UNP Q3SJE6
A	471	HIS	-	EXPRESSION TAG	UNP Q3SJE6
A	472	HIS	-	EXPRESSION TAG	UNP Q3SJE6
A	473	HIS	-	EXPRESSION TAG	UNP Q3SJE6
A	474	HIS	-	EXPRESSION TAG	UNP Q3SJE6
A	475	SER	-	EXPRESSION TAG	UNP Q3SJE6
A	476	SER	-	EXPRESSION TAG	UNP Q3SJE6
A	477	GLY	-	EXPRESSION TAG	UNP Q3SJE6
A	478	ARG	-	EXPRESSION TAG	UNP Q3SJE6
A	479	GLU	-	EXPRESSION TAG	UNP Q3SJE6
A	480	ASN	-	EXPRESSION TAG	UNP Q3SJE6
A	481	LEU	-	EXPRESSION TAG	UNP Q3SJE6
A	482	TYR	-	EXPRESSION TAG	UNP Q3SJE6
A	483	PHE	-	EXPRESSION TAG	UNP Q3SJE6
A	484	GLN	-	EXPRESSION TAG	UNP Q3SJE6
A	485	GLY	-	EXPRESSION TAG	UNP Q3SJE6
A	486	HIS	-	EXPRESSION TAG	UNP Q3SJE6
B	465	MSE	-	EXPRESSION TAG	UNP Q3SJE6
B	466	GLY	-	EXPRESSION TAG	UNP Q3SJE6

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Chain	Residue	Modelled	Actual	Comment	Reference
B	467	SER	-	EXPRESSION TAG	UNP Q3SJE6
B	468	SER	-	EXPRESSION TAG	UNP Q3SJE6
B	469	HIS	-	EXPRESSION TAG	UNP Q3SJE6
B	470	HIS	-	EXPRESSION TAG	UNP Q3SJE6
B	471	HIS	-	EXPRESSION TAG	UNP Q3SJE6
B	472	HIS	-	EXPRESSION TAG	UNP Q3SJE6
B	473	HIS	-	EXPRESSION TAG	UNP Q3SJE6
B	474	HIS	-	EXPRESSION TAG	UNP Q3SJE6
B	475	SER	-	EXPRESSION TAG	UNP Q3SJE6
B	476	SER	-	EXPRESSION TAG	UNP Q3SJE6
B	477	GLY	-	EXPRESSION TAG	UNP Q3SJE6
B	478	ARG	-	EXPRESSION TAG	UNP Q3SJE6
B	479	GLU	-	EXPRESSION TAG	UNP Q3SJE6
B	480	ASN	-	EXPRESSION TAG	UNP Q3SJE6
B	481	LEU	-	EXPRESSION TAG	UNP Q3SJE6
B	482	TYR	-	EXPRESSION TAG	UNP Q3SJE6
B	483	PHE	-	EXPRESSION TAG	UNP Q3SJE6
B	484	GLN	-	EXPRESSION TAG	UNP Q3SJE6
B	485	GLY	-	EXPRESSION TAG	UNP Q3SJE6
B	486	HIS	-	EXPRESSION TAG	UNP Q3SJE6

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	3	Total Cl 3 3	0	0

- Molecule 4 is water.

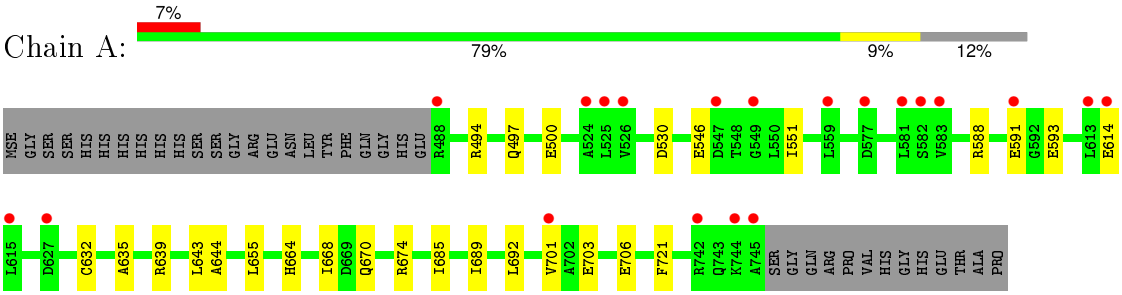
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	202	Total O 202 202	0	0
4	B	176	Total O 176 176	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

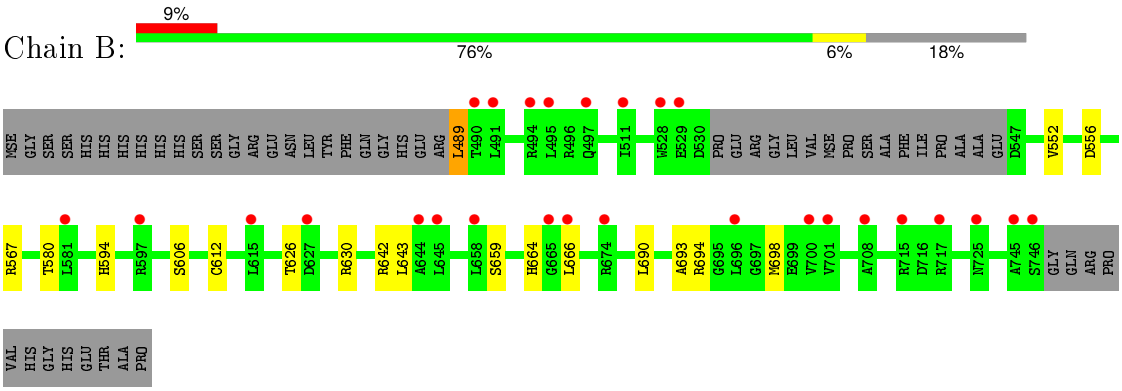
- Molecule 1: Putative diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains)

Chain A:



- Molecule 1: Putative diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains)

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	50.05Å 63.14Å 173.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.70 – 1.80 27.70 – 1.80	Depositor EDS
% Data completeness (in resolution range)	97.2 (27.70-1.80) 97.2 (27.70-1.80)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.92 (at 1.80Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.188 , 0.218 0.187 , 0.218	Depositor DCC
R_{free} test set	2554 reflections (5.34%)	DCC
Wilson B-factor (Å^2)	26.8	Xtriage
Anisotropy	0.594	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 42.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 50343 reflections	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4346	wwPDB-VP
Average B, all atoms (Å^2)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.13% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, CL

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	0.53	0/2112	0.65	0/2855
1	B	0.58	1/1956 (0.1%)	0.63	0/2642
All	All	0.56	1/4068 (0.0%)	0.64	0/5497

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	489	LEU	N-CA	11.06	1.68	1.46

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	2054	0	2059	23	0
1	B	1908	0	1914	17	0
2	A	1	0	0	0	0
2	B	2	0	0	0	0
3	A	3	0	0	0	0
4	A	202	0	0	1	0
4	B	176	0	0	4	0
All	All	4346	0	3973	39	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 (39) 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:489:LEU:N	1:B:489:LEU:CA	1.68	1.52
1:B:552:VAL:HG13	1:B:594:HIS:CD2	2.12	0.84
1:B:643:LEU:H	1:B:664:HIS:HD2	1.32	0.75
1:A:643:LEU:H	1:A:664:HIS:HD2	1.32	0.75
1:B:698:MSE:HE2	4:B:206:HOH:O	1.89	0.73
1:B:698:MSE:CE	4:B:206:HOH:O	2.40	0.70
1:A:643:LEU:H	1:A:664:HIS:CD2	2.11	0.68
1:A:655:LEU:HD21	1:A:692:LEU:HD11	1.89	0.54
1:A:546:GLU:O	1:A:588[A]:ARG:NH1	2.40	0.54
1:A:674[A]:ARG:NE	1:A:706:GLU:OE2	2.40	0.54
1:A:588[B]:ARG:HD3	1:A:591[B]:GLU:CD	2.31	0.50
1:A:655:LEU:HD21	1:A:692:LEU:CD1	2.40	0.50
1:B:642:ARG:NH1	4:B:221:HOH:O	2.42	0.50
1:A:655:LEU:CD2	1:A:692:LEU:HD11	2.42	0.50
1:A:588[B]:ARG:HD3	1:A:591[B]:GLU:OE2	2.12	0.50
1:B:626:THR:O	1:B:630[B]:ARG:HG3	2.12	0.50
1:B:580:THR:HG22	1:B:612:CYS:HA	1.95	0.49
1:A:588[B]:ARG:CD	1:A:591[B]:GLU:OE1	2.62	0.48
1:A:494:ARG:NH2	1:A:530:ASP:OD2	2.42	0.48
1:A:703:GLU:OE2	4:A:1:HOH:O	2.20	0.47
1:A:635:ALA:O	1:A:639:ARG:HG2	2.15	0.47
1:B:666[A]:LEU:HD12	1:B:693:ALA:HB2	1.97	0.47
1:B:567:ARG:HG2	1:B:606:SER:O	2.16	0.45
1:B:489:LEU:N	1:B:489:LEU:CB	2.70	0.45
1:A:551:ILE:HG21	1:A:588[A]:ARG:HD3	1.98	0.45
1:A:497:GLN:HA	1:A:500:GLU:HG2	1.98	0.45
1:A:668:ILE:HG12	1:A:689:ILE:HG21	1.97	0.44
1:B:698:MSE:HE3	4:B:206:HOH:O	2.12	0.44
1:A:701:VAL:HG22	1:A:721:PHE:HB2	2.00	0.43
1:B:556:ASP:OD1	1:B:594:HIS:NE2	2.51	0.42
1:A:614[B]:GLU:OE1	1:A:644:ALA:HB3	2.18	0.42
1:A:670[B]:GLN:OE1	1:A:674[B]:ARG:HD3	2.19	0.42
1:A:685:ILE:HG12	1:B:659[B]:SER:OG	2.20	0.42
1:B:552:VAL:HG13	1:B:594:HIS:NE2	2.34	0.42
1:A:593:GLU:HA	1:A:632:CYS:SG	2.60	0.42
1:A:588[B]:ARG:HG3	1:A:591[B]:GLU:OE1	2.19	0.41
1:B:690:LEU:O	1:B:694:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:556:ASP:CG	1:B:594:HIS:HE2	2.24	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	268/294 (91%)	264 (98%)	4 (2%)	0	100	100
1	B	248/294 (84%)	244 (98%)	4 (2%)	0	100	100
All	All	516/588 (88%)	508 (98%)	8 (2%)	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	220/236 (93%)	220 (100%)	0	100	100
1	B	202/236 (86%)	202 (100%)	0	100	100
All	All	422/472 (89%)	422 (100%)	0	100	100

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

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	664	HIS
1	B	664	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

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 6 ligands modelled in this entry, 6 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

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	253/294 (86%)	0.52	20 (7%) 15 12	22, 27, 39, 46	0
1	B	238/294 (80%)	0.75	27 (11%) 7 5	22, 30, 42, 48	0
All	All	491/588 (83%)	0.64	47 (9%) 10 7	22, 28, 40, 48	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	528	TRP	7.5
1	A	745	ALA	4.6
1	B	490	THR	4.4
1	B	746	SER	4.3
1	B	666[A]	LEU	4.0
1	A	524	ALA	3.6
1	B	745	ALA	3.4
1	B	645	LEU	3.3
1	A	581	LEU	3.2
1	B	491	LEU	3.2
1	B	708	ALA	3.2
1	A	583	VAL	3.1
1	B	597[A]	ARG	3.1
1	A	525	LEU	3.0
1	B	696	LEU	3.0
1	A	613	LEU	2.9
1	A	744	LYS	2.8
1	B	615	LEU	2.7
1	B	725	ASN	2.5
1	B	665	GLY	2.5
1	A	488	ARG	2.5
1	B	495	LEU	2.5
1	B	658	LEU	2.5
1	B	581	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	547	ASP	2.4
1	A	591[A]	GLU	2.4
1	B	529	GLU	2.3
1	B	715	ARG	2.3
1	A	549	GLY	2.3
1	A	559[A]	LEU	2.3
1	A	614[A]	GLU	2.2
1	A	701	VAL	2.2
1	B	717	ARG	2.2
1	A	742	ARG	2.2
1	B	674	ARG	2.2
1	B	644	ALA	2.2
1	A	615	LEU	2.2
1	B	700	VAL	2.2
1	B	701	VAL	2.2
1	A	582	SER	2.1
1	A	577[A]	ASP	2.1
1	A	526	VAL	2.1
1	A	627[A]	ASP	2.1
1	B	497	GLN	2.1
1	B	627	ASP	2.0
1	B	494	ARG	2.0
1	B	511	ILE	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95^{th} 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	LLDF	B-factors(Å^2)	Q<0.9
2	MG	B	803	1/1	0.98	0.24	3.47	38,38,38,38	0
3	CL	A	806	1/1	0.99	0.11	-0.22	25,25,25,25	0
2	MG	B	802	1/1	0.99	0.09	-2.14	23,23,23,23	0
2	MG	A	801	1/1	0.98	0.06	-6.99	20,20,20,20	0
3	CL	A	804	1/1	0.97	0.04	-	30,30,30,30	0
3	CL	A	805	1/1	0.99	0.08	-	24,24,24,24	0

6.5 Other polymers (i)

There are no such residues in this entry.