



Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 10:51 pm BST

PDB ID : 3D6W
Title : LytTr DNA-binding domain of putative methyl-accepting/DNA response regulator from *Bacillus cereus*.
Authors : Osipiuk, J.; Evdokimova, E.; Kudritska, M.; Savchenko, A.; Edwards, A.M.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2008-05-20
Resolution : 2.40 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

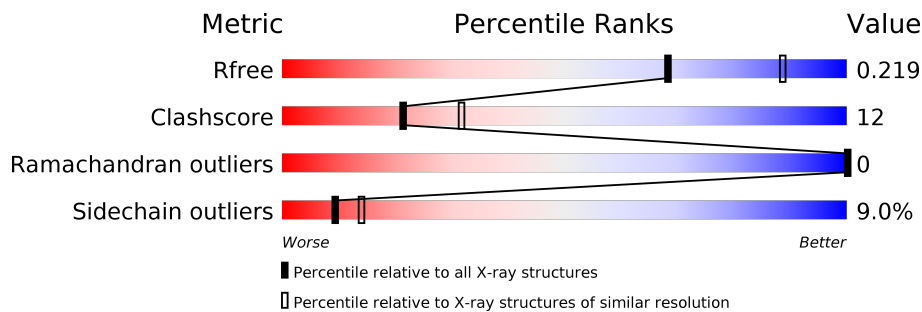
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	130704	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)

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 on 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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	111	80% (green), 16% (yellow), 4% (orange), 0% (red), 0% (grey)
1	B	111	68% (green), 25% (yellow), 5% (orange), 0% (red), 0% (grey)

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	FMT	B	305	-	-	X	-

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 1866 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 Methyl-accepting/DNA response regulator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	109	889	578	146	162	1	2	0	0	0
1	B	109	889	578	146	162	1	2	0	0	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	215	GLY	-	EXPRESSION TAG	UNP Q73A38
A	216	SER	-	EXPRESSION TAG	UNP Q73A38
B	215	GLY	-	EXPRESSION TAG	UNP Q73A38
B	216	SER	-	EXPRESSION TAG	UNP Q73A38

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

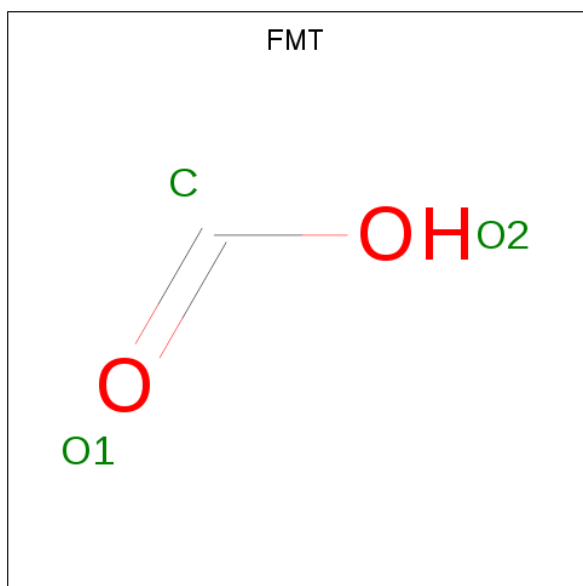
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



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

- Molecule 4 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



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

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	42	Total 42	O 42	0	0
5	B	34	Total 34	O 34	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 the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. 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. 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: Methyl-accepting/DNA response regulator

Chain A: 



- Molecule 1: Methyl-accepting/DNA response regulator

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 42 2 2	Depositor
Cell constants a, b, c, α , β , γ	88.78Å 88.78Å 74.42Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.00 – 2.40 47.99 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (48.00-2.40) 99.9 (47.99-2.40)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.87 (at 2.39Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.182 , 0.209 0.189 , 0.219	Depositor DCC
R_{free} test set	582 reflections (4.79%)	wwPDB-VP
Wilson B-factor (Å ²)	52.1	Xtrriage
Anisotropy	0.131	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	1866	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.04% 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: FMT, MG, EDO

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	0.84	0/911	0.84	1/1229 (0.1%)
1	B	0.78	1/911 (0.1%)	0.79	0/1229
All	All	0.81	1/1822 (0.1%)	0.81	1/2458 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	160	LYS	CD-CE	5.11	1.64	1.51

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	LEU	CA-CB-CG	5.89	128.85	115.30

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	889	0	886	14	0
1	B	889	0	886	30	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	A	4	0	6	1	0
4	A	3	0	1	0	0
4	B	3	0	1	3	0
5	A	42	0	0	3	0
5	B	34	0	0	0	0
All	All	1866	0	1780	43	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 12.

All (43) 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:189:LEU:HD11	1:B:197:ARG:HG2	1.39	1.01
1:B:114:THR:HG21	4:B:305:FMT:O2	1.68	0.92
1:A:146:THR:CG2	5:A:25:HOH:O	2.17	0.92
1:A:146:THR:HG22	5:A:25:HOH:O	1.75	0.85
1:B:189:LEU:HD11	1:B:197:ARG:CG	2.07	0.83
1:B:114:THR:HG21	4:B:305:FMT:C	2.09	0.82
1:B:183:ASP:OD1	1:B:187:THR:CG2	2.32	0.78
1:B:125:LYS:NZ	1:B:142:GLU:OE1	2.16	0.78
1:B:184:THR:HG22	1:B:186:SER:H	1.50	0.77
1:B:183:ASP:OD1	1:B:187:THR:HG22	1.87	0.74
1:B:114:THR:CG2	4:B:305:FMT:O2	2.40	0.67
1:B:186:SER:O	1:B:202:GLN:HA	1.95	0.67
1:B:186:SER:HB3	1:B:202:GLN:HG3	1.82	0.61
1:B:122:PRO:HG2	1:B:125:LYS:HG3	1.84	0.60
1:A:110:VAL:HG22	1:A:123:PHE:HE1	1.67	0.60
1:B:164:ILE:HD12	1:B:211:LEU:CD2	2.32	0.59
1:A:142:GLU:HG2	5:A:75:HOH:O	2.03	0.58
1:B:111:THR:HG22	1:B:118:TRP:HB3	1.87	0.57
1:B:184:THR:CG2	1:B:185:HIS:N	2.69	0.56
1:B:184:THR:HG23	1:B:185:HIS:N	2.20	0.56
1:B:114:THR:HG23	1:B:115:THR:N	2.21	0.56
1:B:164:ILE:HD12	1:B:211:LEU:HD22	1.87	0.55
1:A:110:VAL:HG22	1:A:123:PHE:CE1	2.42	0.55
1:B:114:THR:CG2	1:B:115:THR:N	2.71	0.54
1:B:133:ASP:O	1:B:134:LYS:HB2	2.07	0.53
1:A:116:ASP:OD1	1:A:116:ASP:N	2.43	0.52
1:B:164:ILE:CD1	1:B:211:LEU:HD22	2.39	0.51
1:B:119:ILE:HD12	1:B:143:LEU:CD1	2.44	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:111:THR:CG2	1:A:118:TRP:HB3	2.44	0.47
1:A:112:LEU:HD22	1:A:138:VAL:HB	1.96	0.47
1:B:184:THR:CG2	1:B:186:SER:H	2.24	0.47
1:A:153:GLU:OE2	1:B:210:LYS:HE3	2.15	0.46
1:A:111:THR:HG22	1:A:118:TRP:HB3	1.98	0.46
1:B:119:ILE:HD12	1:B:143:LEU:HD13	1.99	0.45
1:B:190:LEU:O	1:B:197:ARG:HA	2.16	0.45
1:A:112:LEU:HB3	1:A:145:GLY:HA3	1.99	0.43
1:B:164:ILE:HD12	1:B:211:LEU:HD23	2.00	0.43
1:B:157:LEU:C	1:B:157:LEU:HD12	2.38	0.43
1:A:107:LYS:HG2	3:A:303:EDO:C2	2.48	0.43
1:B:149:TYR:HB2	1:B:154:PHE:CE2	2.54	0.43
1:A:141:GLU:OE2	1:A:176:HIS:HE1	2.03	0.42
1:B:111:THR:CG2	1:B:118:TRP:HB3	2.50	0.42
1:A:112:LEU:N	1:A:112:LEU:HD23	2.35	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	107/111 (96%)	105 (98%)	2 (2%)	0	100	100
1	B	107/111 (96%)	106 (99%)	1 (1%)	0	100	100
All	All	214/222 (96%)	211 (99%)	3 (1%)	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	100/99 (101%)	93 (93%)	7 (7%)	15	24
1	B	100/99 (101%)	89 (89%)	11 (11%)	6	8
All	All	200/198 (101%)	182 (91%)	18 (9%)	9	14

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	114	THR
1	A	125	LYS
1	A	134	LYS
1	A	143	LEU
1	A	146	THR
1	A	162	SER
1	A	203	SER
1	B	114	THR
1	B	132	LYS
1	B	135	LYS
1	B	157	LEU
1	B	162	SER
1	B	178	LYS
1	B	184	THR
1	B	187	THR
1	B	197	ARG
1	B	203	SER
1	B	212	LEU

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

Mol	Chain	Res	Type
1	A	152	GLN
1	A	175	ASN
1	B	175	ASN
1	B	185	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 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	FMT	B	305	-	0,2,2	0.00	-	0,1,1	0.00	-
4	FMT	A	304	-	0,2,2	0.00	-	0,1,1	0.00	-
3	EDO	A	303	-	3,3,3	0.75	0	2,2,2	0.37	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
3	EDO	A	303	-	-	1/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	303	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	305	FMT	3	0
3	A	303	EDO	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

6.1 Protein, DNA and RNA chains

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers

Unable to reproduce the depositors R factor - this section is therefore empty.