Full wwPDB X-ray Structure Validation Report ⓘ

Jun 3, 2020 – 02:28 pm BST

PDB ID	:	1B4B
Title	:	STRUCTURE OF THE OLIGOMERIZATION DOMAIN OF THE ARGININE REPRESSOR FROM BACILLUS STEAROTHERMOPHILUS
Authors	:	Ni, J.; Sakanyan, V.; Charlier, D.; Glansdorff, N.; Van Duyne, G.D.
Deposited on	:	1998-12-18
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 following versions of software and data (see references ⓘ) were used in the production of this report:

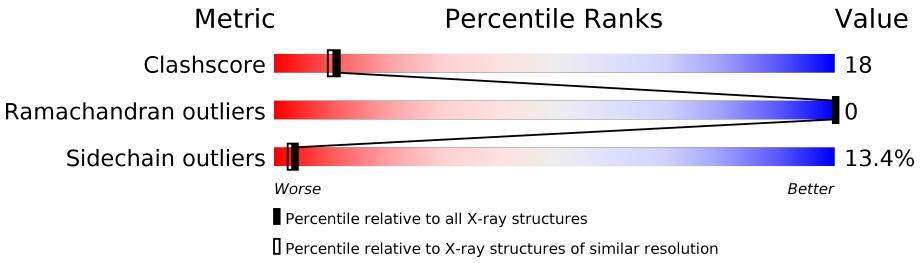
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

1 Overall quality at a glance

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))
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (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 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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	71	73% 23% .
1	B	71	59% 30% 11%
1	C	71	58% 38% .

2 Entry composition

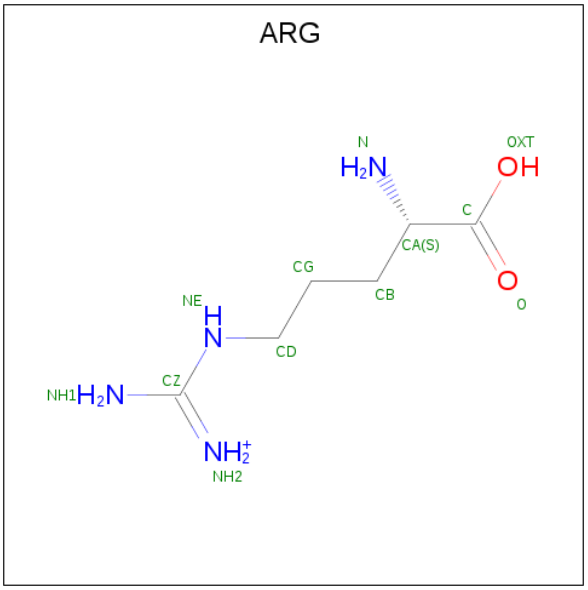
There are 3 unique types of molecules in this entry. The entry contains 1835 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ARGININE REPRESSOR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	71	Total	C	N	O	S	0	0	0
			533	338	89	102	4			
1	B	71	Total	C	N	O	S	0	0	0
			533	338	89	102	4			
1	C	71	Total	C	N	O	S	0	0	0
			533	338	89	102	4			

- Molecule 2 is ARGININE (three-letter code: ARG) (formula: $C_6H_{15}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			12	6	4	2		
2	B	1	Total	C	N	O	0	0
			12	6	4	2		
2	B	1	Total	C	N	O	0	0
			12	6	4	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	63	Total O 63 63	0	0
3	B	75	Total O 75 75	0	0
3	C	62	Total O 62 62	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.

Note EDS was not executed.

- Molecule 1: ARGININE REPRESSOR

Chain A:

- Molecule 1: ARGININE REPRESSOR

Chain B:

- Molecule 1: ARGININE REPRESSOR

Chain C:

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α, β, γ	82.00Å 82.00Å 67.20Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.20	Depositor
% Data completeness (in resolution range)	95.0 (8.00-2.20)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.218 , 0.266	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	1835	wwPDB-VP
Average B, all atoms (Å^2)	27.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

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	0.38	0/538	0.60	0/730
1	B	0.37	0/538	0.66	0/730
1	C	0.34	0/538	0.60	0/730
All	All	0.37	0/1614	0.62	0/2190

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	533	0	557	19	0
1	B	533	0	557	28	0
1	C	533	0	557	27	0
2	A	12	0	15	4	0
2	B	24	0	27	6	0
3	A	63	0	0	2	0
3	B	75	0	0	4	1
3	C	62	0	0	1	0
All	All	1835	0	1713	60	1

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 18.

All (60) 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:C:83:VAL:HG23	1:C:106:ILE:HD11	1.48	0.96
1:B:90:THR:HG21	1:C:133:ARG:HA	1.53	0.90
1:B:104:HIS:CD2	2:B:1:ARG:HH11	2.01	0.77
1:C:83:VAL:CG2	1:C:106:ILE:HD11	2.15	0.76
1:A:104:HIS:CD2	2:A:1:ARG:HH11	2.03	0.75
2:B:150:ARG:HH11	1:C:104:HIS:CD2	2.08	0.72
1:A:104:HIS:HD2	2:A:1:ARG:HH11	1.38	0.71
1:B:81:VAL:HG13	1:B:149:LEU:HA	1.74	0.70
2:B:150:ARG:HH11	1:C:104:HIS:HD2	1.40	0.68
1:B:85:ILE:HD11	1:B:99:LEU:HD23	1.76	0.68
1:A:133:ARG:HA	1:C:90:THR:HG21	1.76	0.66
1:B:104:HIS:HD2	2:B:1:ARG:HH11	1.42	0.66
1:B:133:ARG:HD2	3:B:161:HOH:O	1.98	0.64
1:C:139:LYS:HE2	3:C:204:HOH:O	1.97	0.63
1:A:133:ARG:O	1:C:90:THR:HG21	1.99	0.63
1:A:140:LYS:O	1:A:144:GLN:HG3	2.00	0.61
1:B:90:THR:CG2	1:C:133:ARG:HA	2.30	0.61
1:B:104:HIS:HD2	2:B:1:ARG:HD2	1.65	0.60
1:A:122:ILE:HD11	1:C:127:THR:HG22	1.85	0.59
1:B:116:ASP:HB3	3:B:188:HOH:O	2.05	0.56
1:A:106:ILE:HG22	1:A:110:LEU:HD22	1.86	0.56
1:B:144:GLN:HG3	3:B:216:HOH:O	2.05	0.56
1:B:83:VAL:HG11	1:B:102:ASN:OD1	2.06	0.55
1:A:109:LEU:HD12	3:A:155:HOH:O	2.06	0.55
1:B:95:VAL:HG11	1:C:120:GLY:HA3	1.89	0.55
1:B:97:ARG:HH22	1:C:111:ASP:HB3	1.75	0.52
1:A:144:GLN:O	1:A:148:MET:HG3	2.11	0.51
1:C:144:GLN:O	1:C:148:MET:HG3	2.11	0.51
1:C:141:VAL:O	1:C:145:LEU:HG	2.12	0.49
1:A:79:ALA:HB1	3:A:150:HOH:O	2.11	0.49
1:B:127:THR:HG22	1:C:122:ILE:HD11	1.95	0.48
1:B:139:LYS:HD2	1:B:143:ASN:HD21	1.79	0.48
1:B:96:LEU:HD12	1:B:97:ARG:N	2.29	0.47
1:A:104:HIS:HD2	2:A:1:ARG:HD2	1.80	0.47
1:B:144:GLN:O	1:B:148:MET:HG3	2.15	0.46
1:B:113:LEU:HD12	1:B:113:LEU:HA	1.82	0.46
1:A:133:ARG:NH2	1:C:88:ASP:OD1	2.49	0.45
1:A:88:ASP:OD1	1:B:133:ARG:NH2	2.49	0.45
1:B:81:VAL:HG22	3:B:167:HOH:O	2.17	0.45
2:B:150:ARG:NH1	1:C:104:HIS:CD2	2.82	0.45
1:A:90:THR:HG21	1:B:133:ARG:O	2.17	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:80:LEU:HD22	1:C:84:PHE:HB2	1.98	0.45
1:A:113:LEU:HD13	1:A:115:TRP:CZ2	2.53	0.44
1:C:94:LEU:HB2	1:C:130:ILE:HB	1.99	0.44
1:B:85:ILE:HD12	1:B:98:THR:C	2.38	0.43
1:A:109:LEU:O	1:A:113:LEU:HG	2.19	0.43
1:C:115:TRP:CH2	1:C:144:GLN:HB3	2.54	0.42
1:C:137:ASP:O	1:C:141:VAL:HG23	2.18	0.42
1:B:110:LEU:HD23	1:B:110:LEU:HA	1.91	0.42
1:B:93:LEU:HG	1:B:129:LEU:HD11	2.01	0.42
1:B:81:VAL:HG13	1:B:149:LEU:HD12	2.01	0.42
1:A:133:ARG:O	1:C:90:THR:CG2	2.65	0.41
1:A:133:ARG:HH22	1:C:88:ASP:CG	2.23	0.41
1:B:97:ARG:NH1	1:B:126:ASP:OD1	2.54	0.41
1:B:129:LEU:HB2	1:C:122:ILE:HG13	2.02	0.41
1:C:117:GLU:HB3	1:C:137:ASP:HB3	2.03	0.41
2:A:1:ARG:O	1:C:124:GLY:HA3	2.21	0.40
1:A:84:PHE:CZ	1:A:87:LEU:HB2	2.56	0.40
1:B:123:CYS:HG	1:B:128:CYS:HG	1.68	0.40
1:C:107:GLY:HA3	1:C:123:CYS:SG	2.61	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:B:153:HOH:O	3:B:217:HOH:O[7_556]	0.29	1.91

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	69/71 (97%)	68 (99%)	1 (1%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	69/71 (97%)	68 (99%)	1 (1%)	0	100	100
1	C	69/71 (97%)	68 (99%)	1 (1%)	0	100	100
All	All	207/213 (97%)	204 (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	61/61 (100%)	55 (90%)	6 (10%)	8	7
1	B	61/61 (100%)	50 (82%)	11 (18%)	1	1
1	C	61/61 (100%)	53 (87%)	8 (13%)	4	3
All	All	183/183 (100%)	158 (86%)	25 (14%)	4	3

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	LEU
1	A	90	THR
1	A	97	ARG
1	A	110	LEU
1	A	128	CYS
1	A	129	LEU
1	B	81	VAL
1	B	90	THR
1	B	93	LEU
1	B	96	LEU
1	B	106	ILE
1	B	112	ASN
1	B	113	LEU
1	B	116	ASP
1	B	133	ARG
1	B	140	LYS

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Mol	Chain	Res	Type
1	B	149	LEU
1	C	80	LEU
1	C	87	LEU
1	C	90	THR
1	C	109	LEU
1	C	113	LEU
1	C	133	ARG
1	C	136	LYS
1	C	147	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	104	HIS
1	B	104	HIS
1	B	143	ASN
1	C	104	HIS
1	C	112	ASN
1	C	143	ASN
1	C	144	GLN

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)

3 ligands are modelled in this entry.

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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.