

Full wwPDB X-ray Structure Validation Report (i)

May 25, 2020 - 02:07 am BST

PDB ID	:	2BDT
Title	:	Crystal Structure of the Putative Gluconate Kinase from Bacillus halodurans,
		Northeast Structural Genomics Target BhR61
Authors	:	Forouhar, F.; Abashidze, M.; Jayaraman, S.; Janjua, H.; Cooper, B.; Xiao,
		R.; Acton, T.B.; Montelione, G.T.; Tong, L.; Hunt, J.F.; Northeast Structural
		Genomics Consortium (NESG)
Deposited on	:	2005-10-20
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 (i) symbol.

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

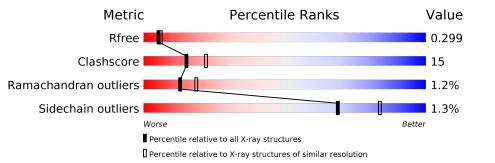
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.11
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25 th 2019)
Refmac	:	5.8.0158
CCP4	:	$7.0.044 (\mathrm{Gargrove})$
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal 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	$egin{array}{c} { m Whole \ archive} \ (\#{ m Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries},{ m resolution\ range}({ m \AA}))$
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 <=5%

Mol	Chain	Length	Quality of chair	n	
1	А	189	62%	29%	• 9%



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1432 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 BH3686.

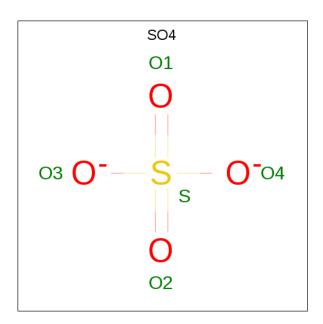
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	А	172	Total 1391	C 888	N 236	O 262	${ m S} { m 3}$	$\frac{\mathrm{Se}}{2}$	0	0	0

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MSE	MET	MODIFIED RESIDUE	UNP Q9K6P2
A	40	MSE	MET	MODIFIED RESIDUE	UNP Q9K6P2
A	128	MSE	MET	MODIFIED RESIDUE	UNP Q9K6P2
A	177	MSE	-	SEE REMARK 999	UNP Q9K6P2
A	178	ALA	-	CLONING ARTIFACT	UNP Q9K6P2
A	179	GLY	-	CLONING ARTIFACT	UNP Q9K6P2
A	180	ASP	-	CLONING ARTIFACT	UNP Q9K6P2
A	181	PRO	-	CLONING ARTIFACT	UNP Q9K6P2
A	182	LEU	-	CLONING ARTIFACT	UNP Q9K6P2
A	183	GLU	-	CLONING ARTIFACT	UNP Q9K6P2
A	184	HIS	-	EXPRESSION TAG	UNP Q9K6P2
A	185	HIS	-	EXPRESSION TAG	UNP Q9K6P2
A	186	HIS	-	EXPRESSION TAG	UNP Q9K6P2
A	187	HIS	-	EXPRESSION TAG	UNP Q9K6P2
A	188	HIS	-	EXPRESSION TAG	UNP Q9K6P2
А	189	HIS	-	EXPRESSION TAG	UNP Q9K6P2

• Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	А	1	Total 5	0 4	S 1	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	А	36	Total O 36 36	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.

- Chain A:
 62%
 29%
 9%

 1
 62%
 9%
 9%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 10%
 1
- Molecule 1: BH3686



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants	43.67Å 43.67Å 198.85Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.81 - 2.40	Depositor
Resolution (A)	42.66 - 1.75	EDS
% Data completeness	85.7 (32.81-2.40)	Depositor
(in resolution range)	75.8 (42.66 - 1.75)	EDS
R _{merge}	0.08	Depositor
R_{sym}	0.07	Depositor
$< I/\sigma(I) > 1$	4.18 (at 1.75Å)	Xtriage
Refinement program	CNS 1.1, XTALVIEW	Depositor
D D.	0.233 , 0.287	Depositor
R, R_{free}	0.248 , 0.299	DCC
R_{free} test set	2678 reflections $(9.45%)$	wwPDB-VP
Wilson B-factor (Å ²)	20.2	Xtriage
Anisotropy	0.027	Xtriage
Bulk solvent $k_{sol}(e/Å^3), B_{sol}(Å^2)$	0.35, 46.1	EDS
L-test for $twinning^2$	$ \langle L \rangle = 0.46, \langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	1432	wwPDB-VP
Average B, all atoms $(Å^2)$	27.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 8.05% of the height of the origin peak. No significant pseudotranslation is detected.

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.



 $^{^1 {\}rm Intensities}$ estimated from amplitudes.

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: SO4

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		
	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	А	0.36	0/1415	0.51	0/1915	

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 (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	А	1391	0	1396	42	0
2	А	5	0	0	0	0
3	А	36	0	0	1	0
All	All	1432	0	1396	42	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 15.

All (42) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic}\\ {\rm distance}~({\rm \AA}) \end{array}$	Clash overlap (Å)	
1:A:41:VAL:HG13	1:A:45:TYR:HD1	1.51	0.75	

Continued on next page...



Continued from previous page								
Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å) 0.74					
1:A:113:GLU:O	1:A:116:LEU:HB3	1.87						
1:A:33:GLU:O	1:A:36:ILE:HG22	1.87	0.74					
1:A:152:THR:HA	1:A:155:LEU:HD23	1.91	0.70					
1:A:152:1HK.HA 1:A:21:ARG:HH11	1:A:161:ASN:HD21	1.43	0.68					
1:A:111:ASN:HB3	1:A:101:ASN:HD21 1:A:114:GLU:HG2	1.43	0.64					
1:A:47:PRO:HG2	1:A:50:GLU:HG3	1.79	0.62					
1:A:116:LEU:HD21	1:A:117:ARG:NH2	2.19	0.62					
1:A:173:PHE:C	1:A:175:PHE:H	$\frac{2.19}{2.08}$	0.57					
1:A:173:PHE:O	1:A:175:PHE:N	2.08	0.55					
1:A:173:PHE:O	1:A:175:PHE:N 1:A:131:ARG:O							
		2.07	0.54					
1:A:110:THR:O	1:A:153:SER:HB3	2.08	0.53					
1:A:131:ARG:HA	1:A:134:GLU:HG3	1.90	0.53					
1:A:34:GLY:HA3	1:A:80:TYR:CD2	2.43	0.53					
1:A:158:THR:HG23	1:A:159:ASN:ND2	2.24	0.52					
1:A:150:TYR:CE1	1:A:163:ILE:HG23	2.45	0.52					
1:A:121:LEU:HD12	1:A:121:LEU:N	2.25	0.51					
1:A:109:TRP:O	1:A:151:ASN:HA	2.11	0.50					
1:A:5:TYR:CE1	1:A:104:ARG:HD2	2.46	0.49					
1:A:150:TYR:HE1	1:A:163:ILE:HG23	1.77	0.49					
1:A:120:ALA:C	1:A:121:LEU:HD12	2.34	0.48					
1:A:83:PHE:HB3	1:A:84:PRO:HD2	1.95	0.48					
1:A:111:ASN:HB3	1:A:114:GLU:CG	2.44	0.48					
1:A:116:LEU:HD21	1:A:117:ARG:HH21	1.79	0.47					
1:A:104:ARG:HH21	1:A:104:ARG:HG2	1.78	0.47					
1:A:38:ASN:O	1:A:41:VAL:HG12	2.14	0.47					
1:A:6:ILE:HD11	1:A:90:LEU:HD23	1.97	0.47					
1:A:94:VAL:HG23	1:A:95:GLN:N	2.30	0.46					
1:A:1:MSE:HB2	1:A:100:ASP:O	2.16	0.46					
1:A:161:ASN:O	1:A:165:LYS:HB2	2.17	0.45					
1:A:34:GLY:HA3	1:A:80:TYR:CG	2.52	0.44					
1:A:119:ASP:C	1:A:121:LEU:H	2.20	0.44					
1:A:154:HIS:HB2	3:A:202:HOH:O	2.16	0.44					
1:A:47:PRO:HG2	1:A:50:GLU:CG	2.47	0.43					
1:A:13:VAL:HG21	1:A:108:LEU:O	2.19	0.43					
1:A:2:LYS:N	1:A:2:LYS:HD3	2.34	0.42					
1:A:138:GLU:O	1:A:142:LYS:HG2	2.19	0.42					
1:A:173:PHE:C	1:A:175:PHE:N	2.72	0.42					
1:A:117:ARG:HA	1:A:117:ARG:HD3	1.85	0.41					
1:A:122:ARG:HG3	1:A:123:LYS:N	2.35	0.41					
1:A:110:THR:C	1:A:153:SER:HB3	2.40	0.41					
1:A:41:VAL:HG13	1:A:45:TYR:CD1	2.42	0.41					

Continued from previous page...



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	А	168/189~(89%)	159~(95%)	7~(4%)	2(1%)	13 19	

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type	
1	А	174	ILE	
1	А	123	LYS	

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	А	152/163~(93%)	150~(99%)	2(1%)	69	84	

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	А	118	ARG
1	А	147	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:



Mol	Chain	Res	Type
1	А	25	GLN
1	А	38	ASN
1	А	61	ASN
1	А	68	ASN
1	А	74	ASN
1	А	92	GLN
1	А	159	ASN
1	А	161	ASN

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)

1 ligand is modelled in this entry.

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	e Chain	ain Res Linl	Link	B	ond leng	\mathbf{gths}	B	ond ang	gles
						Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
	2	SO4	A	190	-	$4,\!4,\!4$	0.24	0	6,6,6	0.07	0

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 (i)

6.1 Protein, DNA and RNA chains (i)

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

6.2 Non-standard residues in protein, DNA, RNA chains (i)

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

6.3 Carbohydrates (i)

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

6.4 Ligands (i)

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

6.5 Other polymers (i)

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

