

wwPDB X-ray Structure Validation Summary Report (i)

Sep 14, 2023 – 08:15 PM EDT

PDB ID : 2AH6

Title : Crystal structure of a putative cobalamin adenosyltransferase (bh1595) from

bacillus halodurans c-125 at 1.60 A resolution

Authors : Joint Center for Structural Genomics (JCSG)

Deposited on : 2005-07-27

Resolution : 1.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

 $Mol Probity \quad : \quad 4.02b\text{--}467$

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.35.1

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

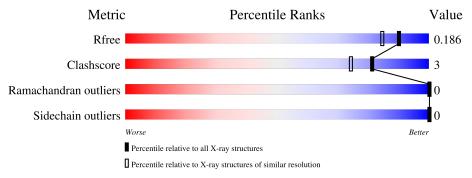
Validation Pipeline (wwPDB-VP) : 2.35.1

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 1.60 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	Similar resolution
Wicorie	(# Entries)	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)

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 <=5%

Mol	Chain	Length	Quality of chain				
1	A	208	68%	•	27%		
1	В	208	75%		• 22%		
1	С	208	75%		• 22%		



2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4371 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 BH1595, unknown conserved protein.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace		
1	Λ	151	Total	С	N	О	S	Se	0	4	0
1	A	191	1212	769	211	229	2	1	0	4	U
1	D	162	Total	С	N	О	S	Se	0	4	0
1	Ъ	102	1303	831	222	247	2	1	0	4	U
1	C	162	Total	С	N	О	S	Se	0	6	0
1		102	1283	818	218	244	2	1	U	0	U

There are 45 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MSE	-	modified residue	UNP Q9KCH6
A	-10	GLY	-	expression tag	UNP Q9KCH6
A	-9	SER	-	expression tag	UNP Q9KCH6
A	-8	ASP	-	expression tag	UNP Q9KCH6
A	-7	LYS	-	expression tag	UNP Q9KCH6
A	-6	ILE	-	expression tag	UNP Q9KCH6
A	-5	HIS	-	expression tag	UNP Q9KCH6
A	-4	HIS	-	expression tag	UNP Q9KCH6
A	-3	HIS	-	expression tag	UNP Q9KCH6
A	-2	HIS	-	expression tag	UNP Q9KCH6
A	-1	HIS	-	expression tag	UNP Q9KCH6
A	0	HIS	-	expression tag	UNP Q9KCH6
A	1	MSE	MET	modified residue	UNP Q9KCH6
A	42	SER	LEU	SEE REMARK 999	UNP Q9KCH6
A	75	MSE	MET	modified residue	UNP Q9KCH6
В	-11	MSE	-	modified residue	UNP Q9KCH6
В	-10	GLY	-	expression tag	UNP Q9KCH6
В	-9	SER	-	expression tag	UNP Q9KCH6
В	-8	ASP	-	expression tag	UNP Q9KCH6
В	-7	LYS	-	expression tag	UNP Q9KCH6
В	-6	ILE	-	expression tag	UNP Q9KCH6
В	-5	HIS	-	expression tag	UNP Q9KCH6
В	-4	HIS	-	expression tag	UNP Q9KCH6

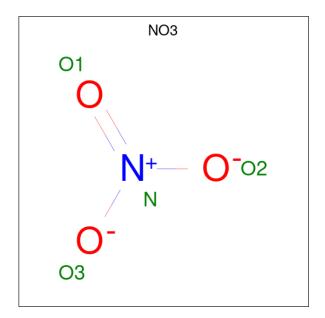
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Chain	Residue	Modelled	Actual	Comment	Reference
В	-3	HIS	-	expression tag	UNP Q9KCH6
В	-2	HIS	-	expression tag	UNP Q9KCH6
В	-1	HIS	-	expression tag	UNP Q9KCH6
В	0	HIS	-	expression tag	UNP Q9KCH6
В	1	MSE	MET	modified residue	UNP Q9KCH6
В	42	SER	LEU	SEE REMARK 999	UNP Q9KCH6
В	75	MSE	MET	modified residue	UNP Q9KCH6
С	-11	MSE	-	modified residue	UNP Q9KCH6
С	-10	GLY	-	expression tag	UNP Q9KCH6
С	-9	SER	-	expression tag	UNP Q9KCH6
С	-8	ASP	ı	expression tag	UNP Q9KCH6
С	-7	LYS	-	expression tag	UNP Q9KCH6
С	-6	ILE	-	expression tag	UNP Q9KCH6
С	-5	HIS	ı	expression tag	UNP Q9KCH6
С	-4	HIS	-	expression tag	UNP Q9KCH6
С	-3	HIS	ı	expression tag	UNP Q9KCH6
С	-2	HIS	-	expression tag	UNP Q9KCH6
С	-1	HIS	ı	expression tag	UNP Q9KCH6
С	0	HIS	-	expression tag	UNP Q9KCH6
С	1	MSE	MET	modified residue	UNP Q9KCH6
С	42	SER	LEU	SEE REMARK 999	UNP Q9KCH6
С	75	MSE	MET	modified residue	UNP Q9KCH6

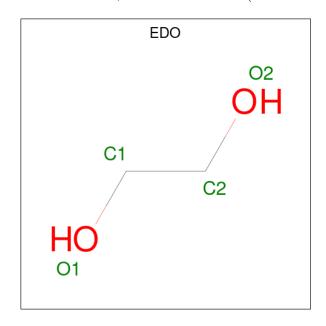
• Molecule 2 is NITRATE ION (three-letter code: NO3) (formula: NO₃).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	В	1	Total N O 4 1 3	0	0
2	С	1	Total N O 4 1 3	0	0
2	С	1	Total N O 4 1 3	0	0

 \bullet Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $\mathrm{C_2H_6O_2}).$



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

• Molecule 4 is water.

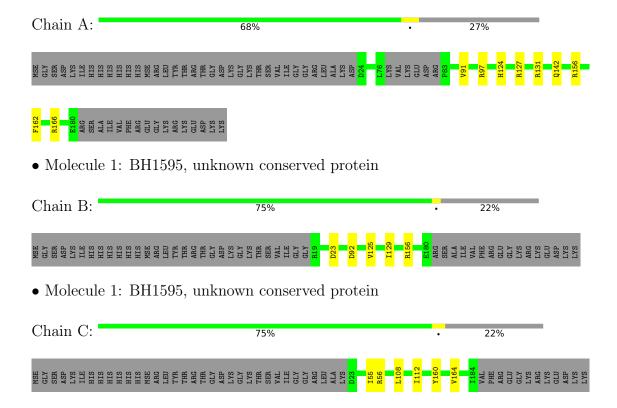
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	179	Total O 179 179	0	0
4	В	206	Total O 206 206	0	0
4	С	164	Total O 164 164	0	0



3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: BH1595, unknown conserved protein





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	53.61Å 84.38Å 113.48Å	Donositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.02 - 1.60	Depositor
rtesolution (A)	29.02 - 1.60	EDS
% Data completeness	99.8 (29.02-1.60)	Depositor
(in resolution range)	99.8 (29.02-1.60)	EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.75 (at 1.60Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
D D.	0.150 , 0.179	Depositor
R, R_{free}	0.162 , 0.186	DCC
R_{free} test set	3503 reflections $(5.11%)$	wwPDB-VP
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.092	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.34, 44.8	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	4371	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 7.24% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $<L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities 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: EDO, NO3

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.77	0/1243	0.81	1/1680 (0.1%)	
1	В	0.80	0/1337	0.83	0/1806	
1	С	0.69	0/1319	0.76	1/1787 (0.1%)	
All	All	0.75	0/3899	0.80	$2/5273 \ (0.0\%)$	

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\operatorname{Observed}(^{o})$	$\operatorname{Ideal}({}^o)$
1	A	97	ARG	NE-CZ-NH1	5.36	122.98	120.30
1	С	56	ARG	NE-CZ-NH1	5.06	122.83	120.30

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	1212	0	1179	11	0
1	В	1303	0	1290	5	0
1	С	1283	0	1241	4	0
2	В	4	0	0	0	0
2	С	8	0	0	0	0
3	В	12	0	18	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	179	0	0	5	0
4	В	206	0	0	2	0
4	С	164	0	0	0	0
All	All	4371	0	3728	20	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 3.

The worst 5 of 20 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:B:92:ASP:OD2	3:B:200:EDO:H22	1.92	0.69
3:B:199:EDO:H22	4:B:302:HOH:O	1.95	0.65
1:C:108:LEU:HD11	1:C:112:ILE:HG12	1.85	0.58
1:A:162:PHE:CD2	1:A:166[B]:ARG:NH1	2.76	0.54
1:C:55:ILE:HD13	1:C:164[B]:VAL:HG13	1.90	0.54

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	Perce	ntiles
1	A	151/208 (73%)	149 (99%)	2 (1%)	0	100	100
1	В	164/208 (79%)	164 (100%)	0	0	100	100
1	С	165/208 (79%)	162 (98%)	3 (2%)	0	100	100
All	All	480/624 (77%)	475 (99%)	5 (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	Perce	ntiles
1	A	126/175~(72%)	126 (100%)	0	100	100
1	В	136/175 (78%)	136 (100%)	0	100	100
1	С	131/175 (75%)	131 (100%)	0	100	100
All	All	393/525 (75%)	393 (100%)	0	100	100

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

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

6 ligands are 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	Tuno	Chain	Res	Link	В	ond len	gths	В	ond ang	gles
MIOI	Type	Cham	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NO3	С	197	-	1,3,3	3.63	1 (100%)	0,3,3	-	-
2	NO3	С	198	-	1,3,3	4.11	1 (100%)	0,3,3	_	-
3	EDO	В	199	-	3,3,3	0.22	0	2,2,2	0.60	0
3	EDO	В	198	-	3,3,3	0.78	0	2,2,2	0.13	0
3	EDO	В	200	-	3,3,3	0.70	0	2,2,2	0.29	0
2	NO3	В	197	-	1,3,3	2.85	1 (100%)	0,3,3	-	-

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	В	200	-	-	1/1/1/1	-
3	EDO	В	199	-	-	0/1/1/1	-
3	EDO	В	198	-	-	0/1/1/1	_

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
2	С	198	NO3	O1-N	4.11	1.43	1.24
2	С	197	NO3	O1-N	3.63	1.40	1.24
2	В	197	NO3	O1-N	2.85	1.37	1.24

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	В	200	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	В	199	EDO	1	0
3	В	200	EDO	2	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 (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.

