

Full wwPDB X-ray Structure Validation Report (i)

Oct 17, 2023 – 07:52 AM EDT

PDB ID : 1VFH

Title : Crystal structure of alanine racemase from D-cycloserine producing Strepto-

myces lavendulae

Authors: Noda, M.; Matoba, Y.; Kumagai, T.; Sugiyama, M.

Deposited on : 2004-04-13

Resolution : 2.00 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 types of validation reports are described at http://www.wwpdb.org/validation/2017/FAQs#types.

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

MolProbity: 4.02b-467

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

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)

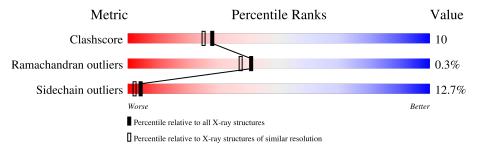
Validation Pipeline (wwPDB-VP) : 2.36

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 2.00 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 $(\#\text{Entries})$	Similar resolution $(\#\text{Entries, resolution range}(\text{\AA}))$
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)

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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain		
1	A	386	74%	21%	



2 Entry composition (i)

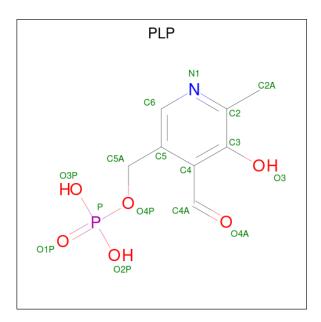
There are 3 unique types of molecules in this entry. The entry contains 2940 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 alanine racemase.

Mol	Chain	Residues		At	oms			ZeroOcc	AltConf	Trace
1	A	382	Total 2851	C 1778	N 528	O 535	S 10	0	0	0

• Molecule 2 is PYRIDOXAL-5'-PHOSPHATE (three-letter code: PLP) (formula: C₈H₁₀NO₆P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf		
2	Λ	1	Total	С	N	Ο	Р	0	0
	Α	1	15	8	1	5	1	0	U

• Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	74	Total O 74 74	0	0

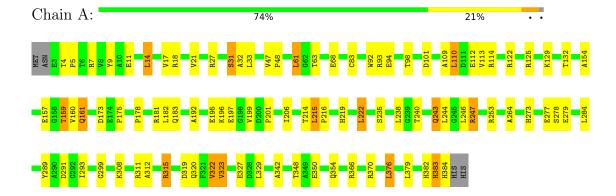


3 Residue-property plots (i)

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.

Note EDS was not executed.

• Molecule 1: alanine racemase





4 Data and refinement statistics (i)

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

Property	Value	Source	
Space group	C 1 2 1	Depositor	
Cell constants	83.98Å 63.38Å 85.95Å	Depositor	
a, b, c, α , β , γ	90.00° 120.14° 90.00°	Depositor	
Resolution (Å)	30.00 - 2.00	Depositor	
% Data completeness	92.6 (30.00-2.00)	Depositor	
(in resolution range)	32.0 (80.00 2.00)		
R_{merge}	0.11	Depositor	
R_{sym}	0.09	Depositor	
Refinement program	X-PLOR 3.851	Depositor	
R, R_{free}	0.197 , 0.252	Depositor	
Estimated twinning fraction	No twinning to report.	Xtriage	
Total number of atoms	2940	wwPDB-VP	
Average B, all atoms (Å ²)	32.0	wwPDB-VP	



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: KCX, PLP

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).

Mal	Chain	Bond	lengths	Bo	nd angles
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5
1	A	0.30	0/2902	0.56	1/3960 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	${f Z}$	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	33	LEU	CA-CB-CG	5.06	126.94	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)	$\mathbf{H}(\mathbf{added})$	Clashes	Symm-Clashes
1	A	2851	0	2791	56	0
2	A	15	0	6	0	0
3	A	74	0	0	2	0
All	All	2940	0	2797	56	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 10.

All (56) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.



Atom 1	Atom 2	Interatomic	Clash
Atom-1	Atom-2	${\rm distance}(\mathring{\rm A})$	overlap (Å)
1:A:159:THR:HG23	1:A:160:VAL:HG13	1.52	0.89
1:A:94:GLU:O	1:A:98:THR:HG23	1.87	0.75
1:A:379:LEU:H	1:A:382:HIS:CD2	2.08	0.71
1:A:161:GLN:O	1:A:161:GLN:HG3	1.90	0.69
1:A:247:ARG:HG2	1:A:247:ARG:HH21	1.57	0.69
1:A:11:GLU:HG2	1:A:376:LEU:HD11	1.80	0.63
1:A:114:ARG:HD3	1:A:154:ALA:CB	2.29	0.62
1:A:264:ALA:HB2	1:A:278:SER:HA	1.80	0.62
1:A:14:LEU:O	1:A:18:ARG:HG3	1.99	0.62
1:A:247:ARG:HG2	1:A:247:ARG:NH2	2.15	0.62
1:A:284:LEU:HD11	1:A:320:GLN:HE21	1.66	0.60
1:A:159:THR:CG2	1:A:160:VAL:HG13	2.29	0.59
1:A:11:GLU:CG	1:A:376:LEU:HD11	2.32	0.58
1:A:114:ARG:HD3	1:A:154:ALA:HB2	1.85	0.58
1:A:7:ARG:HH22	1:A:291:ASP:CG	2.08	0.57
1:A:132:THR:O	1:A:183:GLN:HG2	2.05	0.57
1:A:173:ASP:O	1:A:175:PRO:HD3	2.06	0.56
1:A:68:GLU:HG2	3:A:512:HOH:O	2.06	0.56
1:A:7:ARG:NH2	1:A:291:ASP:OD1	2.38	0.56
1:A:31:SER:OG	1:A:219:HIS:HB3	2.05	0.55
1:A:289:TYR:HA	1:A:293:ILE:O	2.06	0.55
1:A:240:THR:OG1	1:A:243:GLN:HG3	2.07	0.55
1:A:196:LYS:N	1:A:196:LYS:HD3	2.22	0.54
1:A:47:VAL:HB	1:A:48:PRO:HD3	1.89	0.54
1:A:216:PRO:HA	1:A:219:HIS:CE1	2.43	0.54
1:A:32:ALA:O	1:A:222:LEU:HD23	2.08	0.54
1:A:350:GLU:O	1:A:354:GLN:HG2	2.07	0.54
1:A:63:THR:O	1:A:83:CYS:HA	2.09	0.52
1:A:342:ALA:HB2	1:A:348:THR:HG21	1.91	0.51
1:A:299:GLY:HA2	1:A:312:ALA:O	2.11	0.51
1:A:192:ALA:O	1:A:196:LYS:HG2	2.11	0.51
1:A:154:ALA:O	1:A:157:GLU:HG2	2.10	0.51
1:A:273:HIS:ND1	1:A:315:ARG:HD3	2.26	0.50
1:A:157:GLU:CG	1:A:159:THR:HB	2.41	0.50
1:A:178:PRO:O	1:A:182:LEU:HG	2.13	0.49
1:A:157:GLU:HG3	1:A:159:THR:HB	1.93	0.49
1:A:199:VAL:HG12	1:A:201:PRO:HD3	1.95	0.49
1:A:92:TRP:NE1	1:A:112:GLU:OE2	2.45	0.47
1:A:17:VAL:O	1:A:21:VAL:HG13	2.16	0.46
1:A:18:ARG:CZ	1:A:18:ARG:HB3	2.44	0.46
1:A:195:GLU:HA	1:A:199:VAL:O	2.15	0.46
1:A:114:ARG:HD3	1:A:154:ALA:HB1	1.96	0.46
1.11.1111111111111111111111111111111111	1.11.101.111111111111111111111111111111	1.50	

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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
1:A:182:LEU:N	1:A:182:LEU:HD23	2.32	0.45
1:A:110:LEU:O	1:A:114:ARG:HG3	2.17	0.44
1:A:11:GLU:CD	1:A:253:ARG:HH12	2.19	0.44
1:A:214:THR:C	1:A:215:LEU:HD13	2.38	0.44
1:A:114:ARG:HD2	1:A:159:THR:HG21	2.02	0.42
1:A:5:PRO:HG2	1:A:9:TYR:HB3	2.02	0.41
1:A:61:LEU:HD12	1:A:61:LEU:HA	1.92	0.41
1:A:238:LEU:O	1:A:244:LEU:HD11	2.21	0.41
1:A:247:ARG:HG3	3:A:573:HOH:O	2.20	0.41
1:A:109:ALA:O	1:A:113:VAL:HG12	2.20	0.41
1:A:322:VAL:HG23	1:A:323:VAL:N	2.36	0.41
1:A:383:HIS:CD2	1:A:383:HIS:H	2.39	0.41
1:A:264:ALA:CB	1:A:278:SER:HA	2.50	0.40
1:A:114:ARG:HG2	1:A:159:THR:HG21	2.02	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	379/386 (98%)	367 (97%)	11 (3%)	1 (0%)	41 37

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type		
1	A	206	ILE		

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	276/280 (99%)	241 (87%)	35 (13%)	4 2	

All (35) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type	
1	A	4	THR	
1	A	14	LEU	
1	A	27	ARG	
1	A	31	SER	
1	A A	61	LEU	
1	A	93	ARG	
1	A	101	ASP	
1	A A A A A	110	LEU	
1	A	122	ARG	
1	A	125	ARG THR	
1	A	159	THR	
1	A	161	GLN	
1	A	181	ARG	
1	A	197	GLU	
1	A	215	LEU	
1	A	222	LEU	
1	A	235	SER	
1	A A	243	GLN	
1	A	246	LEU	
1	A A	247	ARG	
1	A	277	GLU	
1	A	279	GLU	
1	A	308	LYS	
1	A A	311	ARG	
1	A	315	ARG	
1	A	319	ASP	
1	A A	322	VAL	
1	A	323	VAL	
1	A	327	GLU	
1	A	329	LEU	
1	A	366	ARG	
1	A	370	ARG	
1	A	376	LEU	
1	A	383	HIS	

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Mol	Chain	Res	Type		
1	A	384	HIS		

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type		
1	A	78	GLN		
1	A	266	HIS		
1	A	320	GLN		
1	A	382	HIS		
1	A	383	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)

1 non-standard protein/DNA/RNA residue 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	ol Type	Chain	Res	Link	B	Bond lengths			Bond angles		
	Type	Chain	nes	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2	
1	KCX	A	129	1	9,11,12	2.21	2 (22%)	5,12,14	1.47	1 (20%)	

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
1	KCX	A	129	1	-	1/9/10/12	-

All (2) bond length outliers are listed below:



Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	Ideal(Å)
1	A	129	KCX	CX-NZ	6.00	1.45	1.35
1	A	129	KCX	OQ1-CX	2.07	1.25	1.21

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$Ideal(^{o})$
1	A	129	KCX	OQ1-CX-NZ	-2.74	120.71	124.96

There are no chirality outliers.

All (1) torsion outliers are listed below:

\mathbf{Mol}	Chain	Res	Type	Atoms
1	A	129	KCX	CG-CD-CE-NZ

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides 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	1 Type	Chain	Res	Link	Bond lengths			Bond angles		
	Type			Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	PLP	A	401	1	15,15,16	2.00	6 (40%)	20,22,23	1.35	4 (20%)

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
2	PLP	A	401	1	-	0/6/6/8	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
2	A	401	PLP	C4A-C4	3.80	1.59	1.51
2	A	401	PLP	C2-N1	3.59	1.40	1.33
2	A	401	PLP	C3-C2	-3.09	1.37	1.40
2	A	401	PLP	C6-C5	-2.29	1.33	1.37
2	A	401	PLP	P-O3P	-2.27	1.46	1.54
2	A	401	PLP	P-O2P	-2.18	1.46	1.54

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\mathrm{Ideal}(^{o})$
2	A	401	PLP	C6-N1-C2	2.58	123.95	119.17
2	A	401	PLP	C3-C2-N1	-2.54	117.49	120.77
2	A	401	PLP	C5-C6-N1	-2.45	119.74	123.82
2	A	401	PLP	C6-C5-C4	2.44	120.08	118.16

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.

