



Full wwPDB X-ray Structure Validation Report ⓘ

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PDB ID : 7E28 / pdb_00007e28
Title : Crystal structure of SDR family NAD(P)-dependent oxidoreductase from Exiguobacterium
Authors : Chen, L.; Tang, J.; Yuan, S.
Deposited on : 2021-02-05
Resolution : 1.83 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

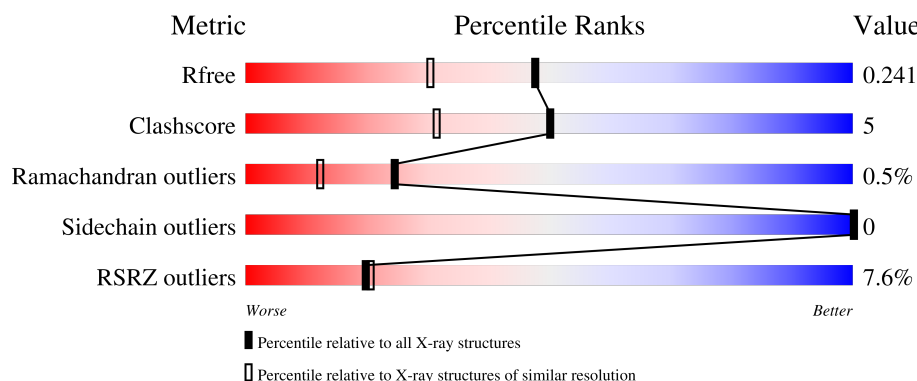
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.83 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}	180053	1296 (1.84-1.84)
Clashscore	190562	1329 (1.84-1.84)
Ramachandran outliers	187476	1318 (1.84-1.84)
Sidechain outliers	187428	1318 (1.84-1.84)
RSRZ outliers	180081	1296 (1.84-1.84)

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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	255	7% 81% 7% 12%
1	B	255	7% 76% 12% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3575 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 Oxidoreductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	224	Total	C	N	O	S	0	0	0
			1735	1105	291	336	3			
1	B	226	Total	C	N	O	S	0	0	0
			1742	1108	291	340	3			

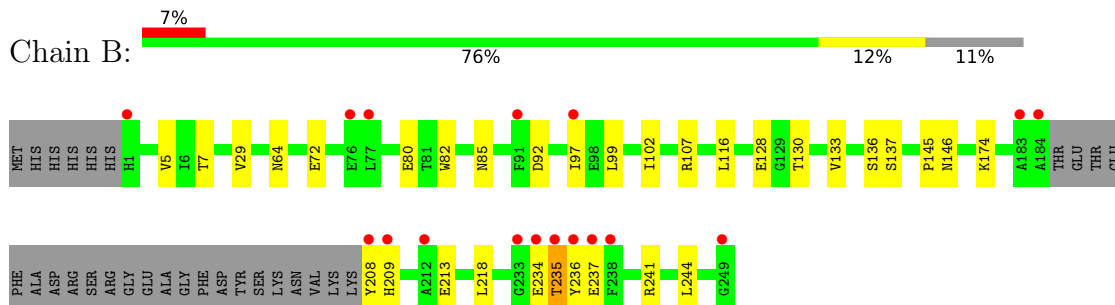
There are 14 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	MET	-	initiating methionine	UNP Q6BDS0
A	-4	HIS	-	expression tag	UNP Q6BDS0
A	-3	HIS	-	expression tag	UNP Q6BDS0
A	-2	HIS	-	expression tag	UNP Q6BDS0
A	-1	HIS	-	expression tag	UNP Q6BDS0
A	0	HIS	-	expression tag	UNP Q6BDS0
A	1	HIS	-	expression tag	UNP Q6BDS0
B	-5	MET	-	initiating methionine	UNP Q6BDS0
B	-4	HIS	-	expression tag	UNP Q6BDS0
B	-3	HIS	-	expression tag	UNP Q6BDS0
B	-2	HIS	-	expression tag	UNP Q6BDS0
B	-1	HIS	-	expression tag	UNP Q6BDS0
B	0	HIS	-	expression tag	UNP Q6BDS0
B	1	HIS	-	expression tag	UNP Q6BDS0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	56	Total	O	0	0
			56	56		
2	B	42	Total	O	0	0
			42	42		

- Molecule 1: Oxidoreductase



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	86.99Å 134.97Å 81.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.49 – 1.83 43.49 – 1.83	Depositor EDS
% Data completeness (in resolution range)	98.8 (43.49-1.83) 98.9 (43.49-1.83)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 1.83Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.231 , 0.264 (Not available) , 0.241	Depositor DCC
R_{free} test set	2000 reflections (4.69%)	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.539	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 29.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	3575	wwPDB-VP
Average B, all atoms (Å ²)	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.54% 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

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	0.36	0/1762	0.54	0/2382
1	B	0.36	0/1769	0.59	2/2392 (0.1%)
All	All	0.36	0/3531	0.56	2/4774 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	GLU	CA-C-N	5.90	132.81	121.54
1	B	234	GLU	C-N-CA	5.90	132.81	121.54

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	1735	0	1740	13	0
1	B	1742	0	1746	24	0
2	A	56	0	0	3	0
2	B	42	0	0	2	1
All	All	3575	0	3486	37	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 5.

All (37) 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:208:TYR:N	1:B:237:GLU:OE1	1.90	1.04
1:A:128:GLU:HG3	1:A:174:LYS:HD2	1.64	0.80
1:B:97:ILE:HG23	1:B:102:ILE:HG12	1.66	0.77
1:B:208:TYR:CA	1:B:237:GLU:OE1	2.36	0.72
1:A:214:MET:HE1	1:A:231:VAL:HG21	1.78	0.66
1:B:133:VAL:HG11	1:B:218:LEU:HD11	1.80	0.62
1:B:235:THR:O	1:B:236:TYR:HB3	2.02	0.59
1:A:128:GLU:H	1:A:128:GLU:CD	2.12	0.57
1:B:241:ARG:HD3	1:B:244:LEU:HD11	1.89	0.54
1:B:5:VAL:HG22	1:B:29:VAL:HB	1.90	0.53
1:B:208:TYR:CD1	1:B:237:GLU:OE2	2.63	0.52
1:A:46:LYS:HE2	1:A:52:SER:O	2.09	0.51
1:A:105:MET:HE3	1:A:153:THR:HG21	1.94	0.50
1:B:107:ARG:NH2	2:B:303:HOH:O	2.35	0.50
1:A:7:THR:O	1:A:85:ASN:HB3	2.12	0.49
1:B:208:TYR:HB3	1:B:213:GLU:OE1	2.13	0.49
1:A:208:TYR:OH	2:A:301:HOH:O	1.98	0.48
1:B:128:GLU:HG2	1:B:174:LYS:HD3	1.95	0.48
1:B:7:THR:O	1:B:85:ASN:HB3	2.14	0.47
1:B:145:PRO:O	1:B:146:ASN:HB2	2.15	0.46
1:A:32:ALA:HB3	1:A:38:LEU:HD21	1.98	0.46
1:B:97:ILE:CG2	1:B:102:ILE:HG12	2.42	0.46
1:A:133:VAL:HG11	1:A:218:LEU:HD11	1.98	0.46
1:B:208:TYR:CE1	1:B:237:GLU:OE2	2.69	0.45
1:A:214:MET:HE3	2:A:340:HOH:O	2.15	0.45
2:A:336:HOH:O	1:B:64:ASN:HB3	2.16	0.45
1:B:72:GLU:OE1	2:B:301:HOH:O	2.21	0.44
1:B:80:GLU:O	1:B:130:THR:HA	2.18	0.44
1:B:82:TRP:CZ2	1:B:116:LEU:HD22	2.54	0.43
1:A:10:SER:HB2	1:A:37:GLU:OE1	2.19	0.43
1:B:99:LEU:HD23	1:B:99:LEU:HA	1.82	0.43
1:A:133:VAL:HG11	1:A:218:LEU:CD1	2.50	0.42
1:B:136:SER:OG	1:B:137:SER:N	2.52	0.41
1:B:208:TYR:HA	1:B:237:GLU:OE1	2.16	0.41
1:B:97:ILE:HG23	1:B:102:ILE:CG1	2.43	0.41
1:A:105:MET:HE3	1:A:153:THR:CG2	2.51	0.41
1:B:208:TYR:HB3	1:B:209:HIS:H	1.81	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)
2:B:337:HOH:O	2:B:337:HOH:O[3_555]	2.08	0.12

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	218/255 (86%)	216 (99%)	2 (1%)	0	100	100
1	B	222/255 (87%)	214 (96%)	6 (3%)	2 (1%)	14	4
All	All	440/510 (86%)	430 (98%)	8 (2%)	2 (0%)	24	12

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	235	THR
1	B	92	ASP

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	184/209 (88%)	184 (100%)	0	100	100
1	B	184/209 (88%)	184 (100%)	0	100	100
All	All	368/418 (88%)	368 (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. All (6) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	85	ASN
1	A	125	HIS
1	A	146	ASN
1	A	169	GLN
1	A	246	ASN
1	B	64	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	224/255 (87%)	0.35	17 (7%) 20 20	22, 31, 51, 97	0
1	B	226/255 (88%)	0.50	17 (7%) 20 21	22, 32, 55, 115	0
All	All	450/510 (88%)	0.43	34 (7%) 20 20	22, 32, 54, 115	0

All (34) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	208	TYR	9.4
1	B	208	TYR	6.0
1	B	236	TYR	5.5
1	A	184	ALA	4.9
1	B	184	ALA	4.7
1	B	235	THR	4.0
1	B	1	HIS	3.7
1	B	237	GLU	3.7
1	A	91	PHE	3.6
1	B	209	HIS	3.5
1	B	91	PHE	3.3
1	B	77	LEU	3.2
1	B	233	GLY	3.2
1	B	76	GLU	3.1
1	B	249	GLY	3.0
1	A	209	HIS	3.0
1	A	128	GLU	2.9
1	A	97	ILE	2.9
1	A	171	GLY	2.8
1	B	97	ILE	2.8
1	A	0	HIS	2.5
1	B	183	ALA	2.5
1	B	234	GLU	2.5
1	A	2	LYS	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	23	GLY	2.4
1	A	11	SER	2.3
1	A	98	GLU	2.2
1	A	37	GLU	2.1
1	A	248	ALA	2.1
1	A	75	LYS	2.1
1	B	238	PHE	2.1
1	B	212	ALA	2.1
1	A	64	ASN	2.0
1	A	236	TYR	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.