



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:47 AM UTC

PDB ID : 9JDQ / pdb_00009jdq
Title : Crystal structure of reductase EA
Authors : Tang, J.; Liuqing, C.
Deposited on : 2024-09-01
Resolution : 1.71 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

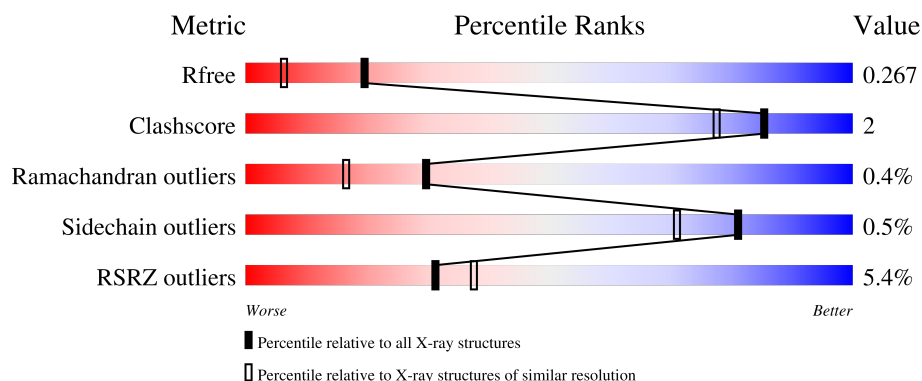
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.71 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	1039 (1.72-1.72)
Clashscore	190562	1049 (1.72-1.72)
Ramachandran outliers	187476	1041 (1.72-1.72)
Sidechain outliers	187428	1041 (1.72-1.72)
RSRZ outliers	180081	1039 (1.72-1.72)

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	256	6% 91% 6%
1	B	256	5% 91% 7%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4314 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	249	Total	C	N	O	S	0	0	0
			1922	1218	322	378	4			
1	B	249	Total	C	N	O	S	0	0	0
			1922	1218	322	378	4			

There are 26 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	MET	-	initiating methionine	UNP Q6BDS0
A	-5	HIS	-	expression tag	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	82	LEU	TRP	conflict	UNP Q6BDS0
A	121	ALA	VAL	conflict	UNP Q6BDS0
A	138	LEU	ALA	conflict	UNP Q6BDS0
A	190	VAL	ALA	conflict	UNP Q6BDS0
A	193	ALA	SER	conflict	UNP Q6BDS0
A	206	HIS	LYS	conflict	UNP Q6BDS0
B	-6	MET	-	initiating methionine	UNP Q6BDS0
B	-5	HIS	-	expression tag	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	82	LEU	TRP	conflict	UNP Q6BDS0
B	121	ALA	VAL	conflict	UNP Q6BDS0
B	138	LEU	ALA	conflict	UNP Q6BDS0
B	190	VAL	ALA	conflict	UNP Q6BDS0
B	193	ALA	SER	conflict	UNP Q6BDS0

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Chain	Residue	Modelled	Actual	Comment	Reference
B	206	HIS	LYS	conflict	UNP Q6BDS0

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	235	Total 235	O 235	0	0
2	B	235	Total 235	O 235	0	0

i

- Molecule 1: Oxidoreductase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	142.75Å 67.67Å 74.55Å 90.00° 117.88° 90.00°	Depositor
Resolution (Å)	19.92 – 1.71 19.92 – 1.71	Depositor EDS
% Data completeness (in resolution range)	99.0 (19.92-1.71) 98.4 (19.92-1.71)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.29 (at 1.71Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.230 , 0.250 0.238 , 0.267	Depositor DCC
R_{free} test set	3286 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	20.7	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.42 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4314	wwPDB-VP
Average B, all atoms (Å ²)	22.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.14% 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	0.65	1/1951 (0.1%)	1.07	2/2635 (0.1%)
1	B	0.64	0/1951	1.06	1/2635 (0.0%)
All	All	0.64	1/3902 (0.0%)	1.06	3/5270 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	0	2
All	All	0	3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	110	ILE	C-N	-5.54	1.26	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	43	ASP	CA-CB-CG	6.61	119.21	112.60
1	A	243	PRO	N-CA-CB	-5.64	98.28	103.25
1	B	68	HIS	CA-CB-CG	5.10	118.90	113.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	176	ARG	Sidechain
1	B	176	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	B	241	ARG	Sidechain

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	1922	0	1923	8	0
1	B	1922	0	1923	9	0
2	A	235	0	0	2	0
2	B	235	0	0	1	0
All	All	4314	0	3846	17	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 2.

All (17) 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:A:234:GLU:HG2	2:A:675:HOH:O	2.00	0.61
1:B:137:SER:HA	1:B:182:PRO:HD2	1.89	0.55
1:B:75:LYS:HB2	2:B:571:HOH:O	2.06	0.54
1:B:190:VAL:O	1:B:194:ARG:HG2	2.07	0.54
1:A:225:ASP:HA	2:A:512:HOH:O	2.12	0.50
1:B:40:LYS:NZ	1:B:44:GLU:OE2	2.39	0.49
1:B:194:ARG:NE	1:B:196:GLU:HG3	2.27	0.49
1:B:20:LEU:HD23	1:B:20:LEU:C	2.38	0.48
1:A:32:ALA:O	1:A:58:SER:HA	2.16	0.46
1:B:218:LEU:HD23	1:B:218:LEU:C	2.42	0.45
1:A:30:LEU:HD13	1:A:41:LEU:HD23	1.99	0.44
1:A:80:GLU:O	1:A:130:THR:HA	2.19	0.43
1:A:31:VAL:HG22	1:A:57:LYS:HB2	2.00	0.43
1:B:194:ARG:HG3	1:B:196:GLU:HG2	2.01	0.42
1:A:218:LEU:HD23	1:A:218:LEU:C	2.45	0.42
1:A:194:ARG:HE	1:A:194:ARG:HB2	1.74	0.41
1:B:15:TYR:CE2	1:B:41:LEU:HB2	2.56	0.41

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	247/256 (96%)	238 (96%)	8 (3%)	1 (0%)	30	16
1	B	247/256 (96%)	238 (96%)	8 (3%)	1 (0%)	30	16
All	All	494/512 (96%)	476 (96%)	16 (3%)	2 (0%)	30	16

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	92	ASP
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	203/210 (97%)	202 (100%)	1 (0%)	81	71
1	B	203/210 (97%)	202 (100%)	1 (0%)	81	71
All	All	406/420 (97%)	404 (100%)	2 (0%)	81	71

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

Mol	Chain	Res	Type
1	A	243	PRO

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Mol	Chain	Res	Type
1	B	97	ILE

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 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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	249/256 (97%)	0.38	15 (6%) 27 33	11, 19, 37, 53	0
1	B	249/256 (97%)	0.36	12 (4%) 35 42	11, 19, 36, 54	0
All	All	498/512 (97%)	0.37	27 (5%) 31 37	11, 19, 37, 54	0

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	3.9
1	B	1	MET	3.6
1	A	205	VAL	3.4
1	B	202	SER	3.0
1	A	194	ARG	2.9
1	A	203	LYS	2.9
1	A	202	SER	2.9
1	A	195	GLY	2.9
1	B	193	ALA	2.8
1	A	197	ALA	2.7
1	B	206	HIS	2.6
1	B	194	ARG	2.5
1	B	205	VAL	2.5
1	A	199	PHE	2.5
1	B	198	GLY	2.4
1	B	196	GLU	2.4
1	A	196	GLU	2.3
1	A	248	ALA	2.3
1	A	206	HIS	2.2
1	A	193	ALA	2.2
1	B	197	ALA	2.2
1	A	192	ARG	2.1
1	B	225	ASP	2.0
1	B	182	PRO	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	201	TYR	2.0
1	B	192	ARG	2.0
1	A	75	LYS	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.