



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 04:35 AM UTC

PDB ID : 5QLR / pdb_00005qlr
Title : Group deposition of library data - Crystal Structure of EcDsbA after initial refinement with no ligand modelled (structure D10_1)
Authors : Ilyichova, O.V.; Bentley, M.R.; Doak, B.C.; Scanlon, M.J.
Deposited on : 2019-01-27
Resolution : 1.97 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

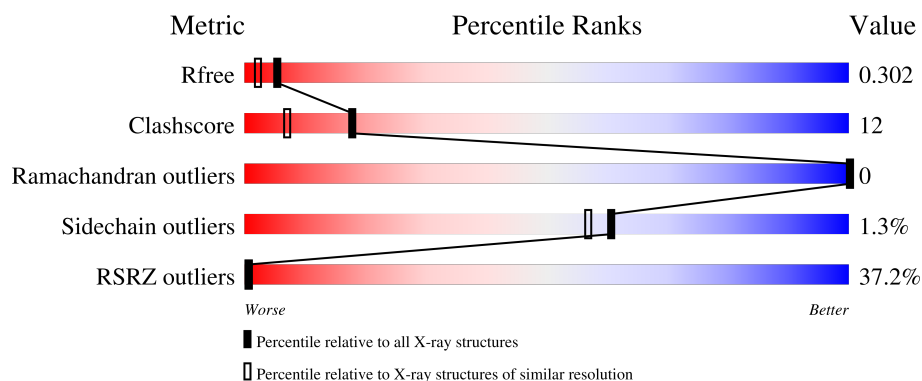
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.97 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	1506 (1.98-1.98)
Clashscore	190562	1534 (1.98-1.98)
Ramachandran outliers	187476	1518 (1.98-1.98)
Sidechain outliers	187428	1518 (1.98-1.98)
RSRZ outliers	180081	1506 (1.98-1.98)

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	189	13% 85% 14% ..
1	B	189	61% 70% 26% ...

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3153 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.

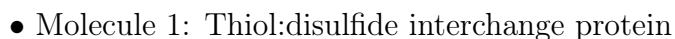
- Molecule 1 is a protein called Thiol:disulfide interchange protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	188	Total	C	N	O	S	0	0	0
			1478	946	242	282	8			
1	B	188	Total	C	N	O	S	0	0	0
			1478	946	242	282	8			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	134	Total	O	0	0
			134	134		
2	B	63	Total	O	0	0
			63	63		

- Molecule 1: Thiol:disulfide interchange protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	117.44Å 64.55Å 74.47Å 90.00° 125.83° 90.00°	Depositor
Resolution (Å)	34.75 – 1.97 34.75 – 1.97	Depositor EDS
% Data completeness (in resolution range)	97.7 (34.75-1.97) 97.7 (34.75-1.97)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 1.97Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.240 , 0.302 0.246 , 0.302	Depositor DCC
R_{free} test set	953 reflections (2.98%)	wwPDB-VP
Wilson B-factor (Å ²)	35.7	Xtriage
Anisotropy	0.402	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.7	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	0.94	EDS
Total number of atoms	3153	wwPDB-VP
Average B, all atoms (Å ²)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.64	0/1510	0.91	1/2042 (0.0%)
1	B	0.64	0/1510	1.15	9/2042 (0.4%)
All	All	0.64	0/3020	1.03	10/4084 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	14	LYS	CA-C-N	-10.90	108.21	119.99
1	B	14	LYS	C-N-CA	-10.90	108.21	119.99
1	B	128	SER	CA-C-N	-6.75	111.94	122.67
1	B	128	SER	C-N-CA	-6.75	111.94	122.67
1	B	132	LYS	CB-CA-C	-6.41	100.73	110.92
1	B	130	VAL	N-CA-C	-5.57	104.08	111.05
1	B	142	ALA	N-CA-C	5.36	116.93	111.14
1	A	8	GLN	N-CA-C	-5.20	106.98	113.38
1	B	128	SER	N-CA-C	-5.16	103.23	110.50
1	B	13	GLU	N-CA-C	-5.08	105.74	112.34

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	1478	0	1449	24	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	1478	0	1449	51	0
2	A	134	0	0	9	0
2	B	63	0	0	17	0
All	All	3153	0	2898	72	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 12.

All (72) 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:139:GLU:O	2:B:201:HOH:O	1.85	0.93
1:B:2:GLN:OE1	2:B:202:HOH:O	1.86	0.92
1:B:2:GLN:NE2	2:B:206:HOH:O	2.07	0.87
1:A:15:PRO:HB3	1:A:158:LYS:HG3	1.60	0.82
1:B:128:SER:O	2:B:203:HOH:O	1.98	0.82
1:A:187:GLU:OE1	2:A:201:HOH:O	1.98	0.80
1:B:104:SER:OG	2:B:204:HOH:O	2.02	0.77
1:B:92:LEU:O	2:B:205:HOH:O	2.06	0.74
1:B:129:PHE:CG	1:B:132:LYS:HG3	2.26	0.69
1:A:5:ASP:OD1	2:A:202:HOH:O	2.10	0.69
1:B:129:PHE:CE2	2:B:212:HOH:O	2.47	0.68
1:B:28:PHE:HB3	2:B:205:HOH:O	1.97	0.64
1:B:3:TYR:HB3	1:B:9:TYR:HE2	1.62	0.64
1:B:143:ALA:N	2:B:201:HOH:O	1.98	0.64
1:B:129:PHE:CZ	2:B:212:HOH:O	2.52	0.63
1:A:40:LEU:HD21	1:A:171:MET:HE2	1.81	0.63
1:A:50:LEU:HD13	1:A:54:VAL:HG11	1.82	0.61
1:A:139:GLU:OE2	2:A:203:HOH:O	2.17	0.58
1:A:34:TYR:CE1	1:A:38:GLU:HG3	2.40	0.57
1:A:51:PRO:O	2:A:204:HOH:O	2.17	0.57
1:B:126:TRP:O	2:B:203:HOH:O	2.17	0.57
1:B:20:PRO:HG2	1:B:23:LEU:HD22	1.91	0.53
1:B:12:LEU:C	1:B:14:LYS:H	2.17	0.52
1:A:1:ALA:N	2:A:209:HOH:O	2.40	0.52
1:A:24:GLU:HG2	2:A:264:HOH:O	2.10	0.50
1:B:46:VAL:HB	1:B:56:MET:HE1	1.92	0.50
1:A:38:GLU:O	1:B:100:GLN:NE2	2.44	0.50
1:B:129:PHE:CD1	1:B:132:LYS:HG3	2.47	0.50
1:B:24:GLU:OE1	1:B:43:SER:OG	2.29	0.49
1:B:12:LEU:C	1:B:14:LYS:N	2.68	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:148:ARG:NH2	2:A:214:HOH:O	2.46	0.48
1:A:98:LYS:HG2	1:B:35:GLN:HG2	1.95	0.48
1:B:14:LYS:HD2	1:B:145:VAL:HA	1.94	0.48
1:B:12:LEU:HB3	1:B:14:LYS:HE2	1.94	0.48
1:B:131:VAL:HB	2:B:203:HOH:O	2.13	0.47
1:A:98:LYS:O	1:B:35:GLN:HG3	2.15	0.47
1:B:100:GLN:HB3	1:B:103:ARG:NH2	2.29	0.46
1:A:70:LYS:NZ	2:A:210:HOH:O	2.42	0.46
1:B:8:GLN:C	1:B:162:ASN:HB3	2.41	0.46
1:B:50:LEU:HB3	1:B:54:VAL:CG1	2.46	0.46
1:B:109:ARG:O	1:B:113:ILE:HG12	2.15	0.45
1:B:129:PHE:HA	1:B:132:LYS:H	1.81	0.45
1:A:24:GLU:HG3	2:A:303:HOH:O	2.17	0.45
1:A:7:LYS:HA	1:A:7:LYS:HD2	1.77	0.45
1:B:120:GLU:HG3	1:B:121:GLU:N	2.32	0.45
1:A:184:TYR:OH	1:A:188:LYS:NZ	2.50	0.44
1:B:4:GLU:HB3	1:B:7:LYS:HB2	1.99	0.44
1:B:30:CYS:HA	1:B:31:PRO:HD3	1.86	0.44
1:B:92:LEU:C	2:B:205:HOH:O	2.57	0.43
1:B:87:LYS:NZ	2:B:215:HOH:O	2.52	0.43
1:B:171:MET:O	1:B:175:VAL:HG23	2.19	0.43
1:B:12:LEU:HA	1:B:12:LEU:HD23	1.61	0.43
1:B:159:TYR:HE2	1:B:188:LYS:NZ	2.17	0.43
1:A:39:VAL:HG11	1:A:171:MET:HE1	2.01	0.43
1:A:50:LEU:HD13	1:A:54:VAL:CG1	2.47	0.43
1:A:91:PRO:HB2	1:A:111:VAL:HG13	2.00	0.43
1:B:9:TYR:N	1:B:162:ASN:HB3	2.34	0.42
1:B:14:LYS:O	1:B:14:LYS:HG2	2.18	0.42
1:B:129:PHE:CD2	1:B:132:LYS:HG3	2.54	0.42
1:B:134:LEU:HD12	1:B:134:LEU:HA	1.85	0.42
1:B:12:LEU:HD13	1:B:14:LYS:CE	2.49	0.42
1:B:140:LYS:C	2:B:201:HOH:O	2.62	0.42
1:A:34:TYR:CD1	1:A:38:GLU:HG3	2.55	0.42
1:B:51:PRO:O	1:B:54:VAL:HG12	2.20	0.42
1:B:152:ALA:HA	2:B:221:HOH:O	2.19	0.42
1:A:55:LYS:HB2	1:A:55:LYS:HE2	1.83	0.41
1:B:164:GLN:H	1:B:164:GLN:CD	2.29	0.41
1:B:35:GLN:OE1	1:B:39:VAL:HG21	2.21	0.41
1:B:147:LEU:HA	2:B:207:HOH:O	2.20	0.41
1:A:30:CYS:HA	1:A:31:PRO:HD3	1.93	0.40
1:B:90:VAL:O	1:B:94:GLU:HG3	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:145:VAL:C	1:B:146:GLN:HG2	2.46	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	186/189 (98%)	184 (99%)	2 (1%)	0	100	100
1	B	186/189 (98%)	180 (97%)	6 (3%)	0	100	100
All	All	372/378 (98%)	364 (98%)	8 (2%)	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	Percentiles	
1	A	158/159 (99%)	157 (99%)	1 (1%)	78	76
1	B	158/159 (99%)	155 (98%)	3 (2%)	50	44
All	All	316/318 (99%)	312 (99%)	4 (1%)	61	57

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	54	VAL
1	B	4	GLU
1	B	14	LYS
1	B	146	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	32	HIS
1	B	114	ASN
1	B	137	GLN
1	B	162	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	188/189 (99%)	0.77	24 (12%) 7 11	23, 34, 62, 104	0
1	B	188/189 (99%)	2.52	116 (61%) 0 0	36, 57, 104, 125	0
All	All	376/378 (99%)	1.65	140 (37%) 1 1	23, 44, 96, 125	0

All (140) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	1	ALA	10.0
1	B	129	PHE	9.2
1	B	170	ASN	7.4
1	B	168	THR	7.3
1	B	2	GLN	6.8
1	A	51	PRO	6.3
1	B	54	VAL	6.1
1	B	9	TYR	5.8
1	B	169	SER	5.6
1	B	171	MET	5.4
1	B	3	TYR	5.0
1	B	6	GLY	5.0
1	B	162	ASN	4.9
1	B	51	PRO	4.8
1	A	54	VAL	4.7
1	B	90	VAL	4.7
1	B	167	ASP	4.7
1	B	165	GLY	4.6
1	B	184	TYR	4.6
1	B	11	THR	4.5
1	B	56	MET	4.4
1	B	157	GLY	4.3
1	A	53	GLY	4.2
1	B	44	ASP	4.2

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Mol	Chain	Res	Type	RSRZ
1	B	12	LEU	4.2
1	B	47	LYS	4.2
1	B	156	ASN	4.0
1	B	14	LYS	4.0
1	B	63	PHE	4.0
1	B	159	TYR	3.9
1	B	154	PHE	3.9
1	B	130	VAL	3.8
1	B	15	PRO	3.8
1	A	146	GLN	3.8
1	B	128	SER	3.7
1	B	20	PRO	3.7
1	B	50	LEU	3.7
1	B	147	LEU	3.7
1	B	186	SER	3.7
1	B	19	ALA	3.6
1	B	17	ALA	3.6
1	A	157	GLY	3.6
1	B	103	ARG	3.5
1	B	131	VAL	3.5
1	B	13	GLU	3.5
1	B	23	LEU	3.5
1	B	155	VAL	3.5
1	B	145	VAL	3.4
1	B	166	MET	3.4
1	B	173	VAL	3.4
1	B	135	VAL	3.4
1	B	153	MET	3.4
1	A	168	THR	3.3
1	B	4	GLU	3.3
1	B	32	HIS	3.3
1	B	182	VAL	3.3
1	B	5	ASP	3.2
1	A	15	PRO	3.2
1	B	10	THR	3.2
1	B	62	ASN	3.2
1	A	52	GLU	3.2
1	B	65	GLY	3.1
1	B	164	GLN	3.1
1	B	34	TYR	3.1
1	B	55	LYS	3.1
1	B	16	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	136	ALA	3.1
1	B	152	ALA	3.1
1	B	174	PHE	3.0
1	A	167	ASP	3.0
1	B	185	LEU	2.9
1	A	158	LYS	2.9
1	B	150	VAL	2.9
1	B	48	LYS	2.9
1	B	158	LYS	2.9
1	B	187	GLU	2.9
1	B	117	ILE	2.9
1	B	134	LEU	2.9
1	B	61	VAL	2.8
1	B	7	LYS	2.8
1	A	50	LEU	2.8
1	A	164	GLN	2.8
1	B	142	ALA	2.8
1	B	161	LEU	2.8
1	B	43	SER	2.7
1	B	66	GLY	2.7
1	B	188	LYS	2.7
1	A	16	VAL	2.7
1	B	46	VAL	2.7
1	A	148	ARG	2.7
1	B	133	SER	2.7
1	B	120	GLU	2.7
1	A	165	GLY	2.6
1	B	53	GLY	2.6
1	A	169	SER	2.6
1	B	52	GLU	2.6
1	B	94	GLU	2.6
1	B	57	THR	2.6
1	B	25	PHE	2.5
1	B	64	MET	2.5
1	B	41	HIS	2.5
1	B	132	LYS	2.5
1	A	19	ALA	2.5
1	A	100	GLN	2.5
1	A	18	GLY	2.5
1	B	146	GLN	2.5
1	B	143	ALA	2.5
1	B	179	ALA	2.5

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Mol	Chain	Res	Type	RSRZ
1	B	49	LYS	2.5
1	B	148	ARG	2.4
1	B	70	LYS	2.4
1	B	93	PHE	2.4
1	A	6	GLY	2.4
1	B	81	ALA	2.4
1	B	18	GLY	2.4
1	B	22	VAL	2.4
1	A	17	ALA	2.3
1	A	145	VAL	2.3
1	B	144	ASP	2.3
1	B	68	LEU	2.3
1	B	181	THR	2.3
1	B	105	ALA	2.3
1	B	89	THR	2.3
1	B	91	PRO	2.2
1	B	39	VAL	2.2
1	B	8	GLN	2.2
1	B	127	ASN	2.2
1	B	177	GLN	2.2
1	B	86	ASP	2.2
1	B	77	ALA	2.2
1	A	20	PRO	2.1
1	B	163	PRO	2.1
1	B	172	ASP	2.1
1	B	183	LYS	2.1
1	A	12	LEU	2.1
1	B	29	PHE	2.0
1	B	45	ASN	2.0
1	B	40	LEU	2.0
1	B	79	ALA	2.0
1	B	59	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.