Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 06:44 PM GMT

PDB ID	:	4ML1
Title	:	Disulfide isomerase (DsbP) from multidrug resistance IncA/C transferable plasmid in oxidized state (P212121 space group)
Authors	:	Premkumar, L.; Kurth, F.; Neyer, S.; Martin, J.L.
Deposited on	:	2013-09-06
Resolution	:	1.98 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

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

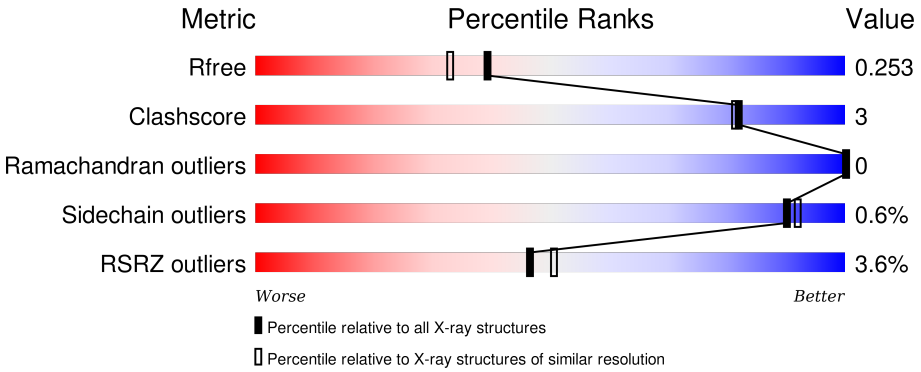
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

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 1.98 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}	91344	8664 (2.00-1.96)
Clashscore	102246	9905 (2.00-1.96)
Ramachandran outliers	100387	9792 (2.00-1.96)
Sidechain outliers	100360	9791 (2.00-1.96)
RSRZ outliers	91569	8679 (2.00-1.96)

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 on the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. 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% 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	217	6% 83% 10% 7%
1	B	217	3% 90% · 6%
1	C	217	% 89% · 7%
1	D	217	4% 84% 9% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 13299 atoms, of which 6334 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 DsbP.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	202	Total	C	H	N	O	S	0	1	0
			3145	989	1579	269	296	12			
1	B	204	Total	C	H	N	O	S	0	0	0
			3167	994	1591	274	296	12			
1	C	202	Total	C	H	N	O	S	0	0	0
			3133	985	1573	269	294	12			
1	D	203	Total	C	H	N	O	S	0	2	0
			3167	996	1591	270	297	13			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	EXPRESSION TAG	UNP A6GV51
A	-1	ASN	-	EXPRESSION TAG	UNP A6GV51
A	0	ALA	-	EXPRESSION TAG	UNP A6GV51
B	-2	SER	-	EXPRESSION TAG	UNP A6GV51
B	-1	ASN	-	EXPRESSION TAG	UNP A6GV51
B	0	ALA	-	EXPRESSION TAG	UNP A6GV51
C	-2	SER	-	EXPRESSION TAG	UNP A6GV51
C	-1	ASN	-	EXPRESSION TAG	UNP A6GV51
C	0	ALA	-	EXPRESSION TAG	UNP A6GV51
D	-2	SER	-	EXPRESSION TAG	UNP A6GV51
D	-1	ASN	-	EXPRESSION TAG	UNP A6GV51
D	0	ALA	-	EXPRESSION TAG	UNP A6GV51

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	143	Total	O	0	0
			143	143		
2	B	177	Total	O	0	0
			177	177		

Continued on next page...

Continued from previous page...

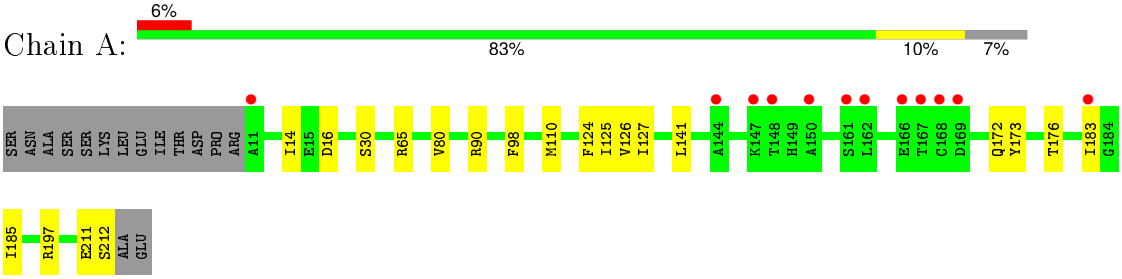
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	195	Total O 195 195	0	0
2	D	172	Total O 172 172	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). 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.

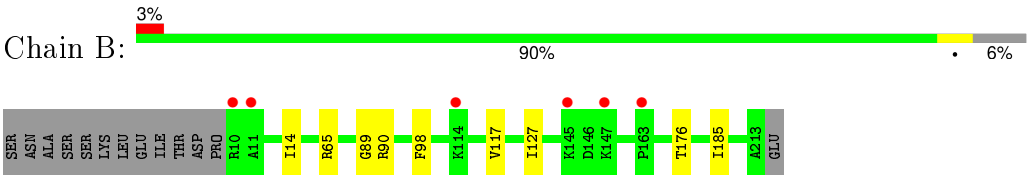
- Molecule 1: DsbP

Chain A:



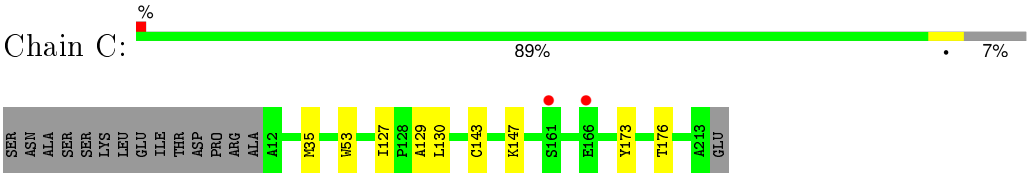
- Molecule 1: DsbP

Chain B:



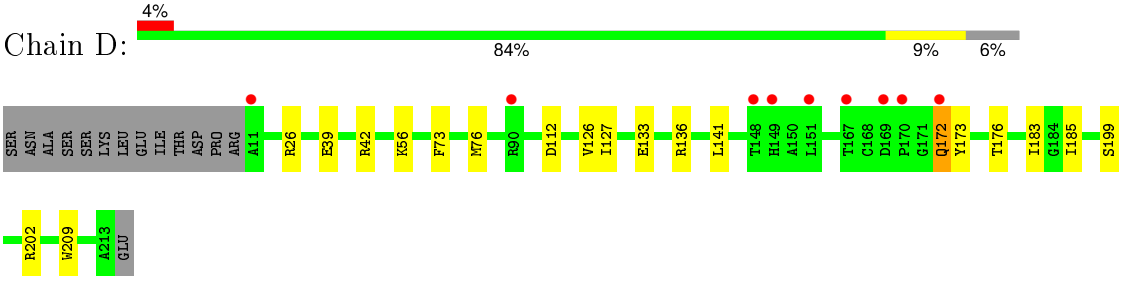
- Molecule 1: DsbP

Chain C:



- Molecule 1: DsbP

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	54.33Å 108.27Å 139.02Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.60 – 1.98 50.60 – 1.98	Depositor EDS
% Data completeness (in resolution range)	99.2 (50.60-1.98) 99.5 (50.60-1.98)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.03 (at 1.98Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.2_1309)	Depositor
R, R_{free}	0.192 , 0.242 0.208 , 0.253	Depositor DCC
R_{free} test set	2938 reflections (5.35%)	DCC
Wilson B-factor (Å^2)	23.6	Xtriage
Anisotropy	0.349	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 46.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Outliers	1 of 57892 reflections (0.002%)	Xtriage
F_o,F_c correlation	0.94	EDS
Total number of atoms	13299	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.08% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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	0.66	0/1597	0.77	1/2156 (0.0%)
1	B	0.64	0/1604	0.73	0/2165
1	C	0.68	1/1588 (0.1%)	0.74	0/2144
1	D	0.70	0/1610	0.76	0/2173
All	All	0.67	1/6399 (0.0%)	0.75	1/8638 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	143	CYS	CB-SG	-5.77	1.72	1.81

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	65	ARG	NE-CZ-NH2	-5.41	117.60	120.30

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	1566	1579	1575	15	0
1	B	1576	1591	1587	10	0
1	C	1560	1573	1569	8	0
1	D	1576	1591	1589	12	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	143	0	0	0	0
2	B	177	0	0	2	0
2	C	195	0	0	3	0
2	D	172	0	0	2	0
All	All	6965	6334	6320	40	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.

All (40) 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:D:26:ARG:NH1	2:D:459:HOH:O	2.28	0.60
1:A:16:ASP:OD2	1:B:65:ARG:NH2	2.34	0.60
1:A:98:PHE:CZ	1:A:185:ILE:HD13	2.38	0.58
1:B:98:PHE:CE2	1:B:185:ILE:HD13	2.41	0.56
1:A:14:ILE:HG13	1:C:130:LEU:HD13	1.86	0.56
1:A:30:SER:HB2	1:B:14:ILE:HD12	1.89	0.54
1:B:127:ILE:CG2	1:B:176:THR:HG22	2.38	0.52
1:A:126:VAL:HG21	1:A:141:LEU:CD2	2.40	0.52
1:B:65:ARG:HD2	2:B:395:HOH:O	2.10	0.51
1:C:35:MET:HE2	2:C:428:HOH:O	2.11	0.51
1:D:173:TYR:CD2	1:D:173:TYR:N	2.79	0.50
1:D:112:ASP:OD2	1:D:202:ARG:NH1	2.45	0.50
1:D:73:PHE:O	1:D:76[A]:MET:HG2	2.12	0.49
1:A:197:ARG:NH1	1:A:212:SER:HA	2.27	0.49
1:D:183:ILE:HD11	1:D:185:ILE:HD12	1.95	0.48
1:A:211:GLU:O	1:A:212:SER:CB	2.62	0.47
1:D:126:VAL:HG21	1:D:141:LEU:CD2	2.44	0.47
1:A:110:MET:HG2	1:A:124:PHE:CE1	2.49	0.47
1:C:147:LYS:NZ	2:C:388:HOH:O	2.47	0.47
1:B:89:GLY:HA2	1:B:117:VAL:HB	1.96	0.46
1:D:133:GLU:OE2	1:D:136:ARG:NE	2.43	0.46
1:C:127:ILE:CG2	1:C:176:THR:HG22	2.46	0.46
1:A:98:PHE:CE2	1:A:185:ILE:HD13	2.50	0.46
1:D:127:ILE:CG2	1:D:176:THR:HG22	2.45	0.46
1:C:127:ILE:HG22	1:C:176:THR:HG22	1.98	0.46
1:C:173:TYR:CD2	1:C:173:TYR:N	2.85	0.45
1:B:98:PHE:CZ	1:B:185:ILE:HD13	2.52	0.44
1:B:127:ILE:HG22	1:B:176:THR:HG22	2.00	0.44
1:D:172:GLN:HB3	1:D:173:TYR:CE2	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:199:SER:HB2	1:D:209:TRP:CZ2	2.54	0.43
1:A:127:ILE:CG2	1:A:176:THR:HG22	2.48	0.42
1:D:39:GLU:HA	2:D:328:HOH:O	2.19	0.42
1:B:65:ARG:CD	2:B:395:HOH:O	2.66	0.41
1:A:30:SER:HB2	1:B:14:ILE:CD1	2.50	0.41
1:A:126:VAL:HG21	1:A:141:LEU:HD22	2.00	0.41
1:A:183:ILE:HD11	1:A:185:ILE:HD12	2.03	0.41
1:C:129:ALA:O	2:C:304:HOH:O	2.22	0.40
1:A:172:GLN:HG3	1:A:173:TYR:CE2	2.56	0.40
1:C:53:TRP:CE3	1:D:42:ARG:HD2	2.56	0.40
1:A:80:VAL:HB	1:A:125:ILE:HD11	2.04	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	201/217 (93%)	200 (100%)	1 (0%)	0	100	100
1	B	202/217 (93%)	201 (100%)	1 (0%)	0	100	100
1	C	200/217 (92%)	198 (99%)	2 (1%)	0	100	100
1	D	203/217 (94%)	202 (100%)	1 (0%)	0	100	100
All	All	806/868 (93%)	801 (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	Percentiles
1	A	174/186 (94%)	173 (99%)	1 (1%)	90 92
1	B	174/186 (94%)	173 (99%)	1 (1%)	90 92
1	C	173/186 (93%)	173 (100%)	0	100 100
1	D	175/186 (94%)	173 (99%)	2 (1%)	80 82
All	All	696/744 (94%)	692 (99%)	4 (1%)	90 92

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

Mol	Chain	Res	Type
1	A	90	ARG
1	B	90	ARG
1	D	56	LYS
1	D	172	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	172	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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, 95^{th} 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	202/217 (93%)	0.42	12 (5%) 26 30	14, 32, 61, 78	0
1	B	204/217 (94%)	0.30	6 (2%) 55 58	15, 33, 59, 81	0
1	C	202/217 (93%)	0.16	2 (0%) 84 86	16, 29, 57, 74	0
1	D	203/217 (93%)	0.28	9 (4%) 38 42	16, 29, 55, 76	0
All	All	811/868 (93%)	0.29	29 (3%) 46 50	14, 30, 59, 81	0

All (29) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	11	ALA	4.7
1	D	167	THR	4.0
1	B	10	ARG	3.8
1	A	167	THR	3.6
1	D	11	ALA	3.5
1	D	149	HIS	3.5
1	D	170	PRO	3.3
1	B	147	LYS	3.2
1	A	147	LYS	3.2
1	A	166	GLU	3.1
1	A	161	SER	3.0
1	A	168	CYS	2.8
1	D	148	THR	2.7
1	A	162	LEU	2.7
1	A	169	ASP	2.7
1	D	151	LEU	2.7
1	C	161	SER	2.6
1	B	11	ALA	2.6
1	A	148	THR	2.5
1	A	144	ALA	2.4
1	C	166	GLU	2.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	172	GLN	2.3
1	D	169	ASP	2.2
1	D	90	ARG	2.2
1	B	114	LYS	2.2
1	A	183	ILE	2.1
1	B	145	LYS	2.1
1	A	150	ALA	2.1
1	B	163	PRO	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 carbohydrates 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.