Full wwPDB X-ray Structure Validation Report (i)

Jan 30, 2024 – 09:35 PM EST

PDB ID	:	1ISB
Title	:	STRUCTURE-FUNCTION IN E. COLI IRON SUPEROXIDE DISMUTASE: COMPARISONS WITH THE MANGANESE ENZYME FROM T. THERMOPHILUS
Authors	:	Lah, M.S.; Dixon, M.; Pattridge, K.A.; Stallings, W.C.; Fee, J.A.; Ludwig, M.L.
Deposited on	:	1994-07-12
Resolution	:	1.85 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:

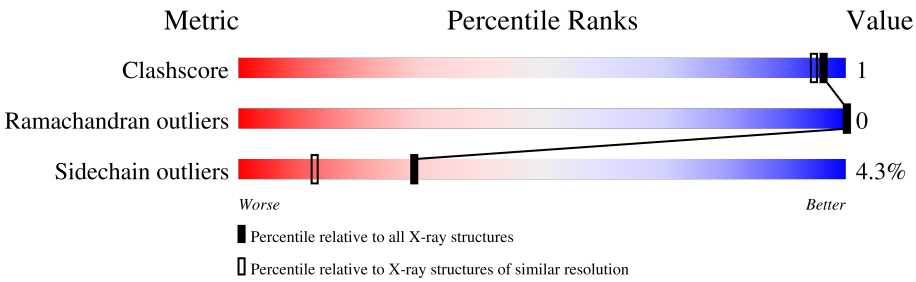
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.85 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))
Clashscore	141614	2625 (1.86-1.86)
Ramachandran outliers	138981	2592 (1.86-1.86)
Sidechain outliers	138945	2592 (1.86-1.86)

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	192	92% 7% •
1	B	192	89% 11% •

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3289 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 IRON(III) SUPEROXIDE DISMUTASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	192	1503	971	249	282	1	0	0	0
1	B	192	1503	971	249	282	1	0	0	0

- Molecule 2 is FE (III) ION (three-letter code: FE) (formula: Fe).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Fe		
2	A	1	1	1	0	0
2	B	1	1	1	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	144	144	144	0	0
3	B	137	137	137	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.

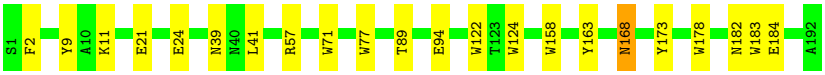
Note EDS was not executed.

• Molecule 1: IRON(III) SUPEROXIDE DISMUTASE

Chain A:

• Molecule 1: IRON(III) SUPEROXIDE DISMUTASE

Chain B:



4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	81.62Å 75.28Å 71.61Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.00 – 1.85	Depositor
% Data completeness (in resolution range)	(Not available) (40.00-1.85)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	PROLSQ	Depositor
R, R_{free}	0.184 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	3289	wwPDB-VP
Average B, all atoms ($Å^2$)	12.0	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: FE

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	0.76	0/1551	1.36	27/2119 (1.3%)
1	B	0.78	0/1551	1.41	27/2119 (1.3%)
All	All	0.77	0/3102	1.38	54/4238 (1.3%)

There are no bond length outliers.

All (54) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	178	TRP	CD1-CG-CD2	8.37	112.99	106.30
1	A	71	TRP	CD1-CG-CD2	8.23	112.89	106.30
1	B	77	TRP	CD1-CG-CD2	8.18	112.84	106.30
1	B	183	TRP	CD1-CG-CD2	8.03	112.72	106.30
1	B	71	TRP	CD1-CG-CD2	7.99	112.69	106.30
1	B	124	TRP	CD1-CG-CD2	7.98	112.69	106.30
1	A	178	TRP	CD1-CG-CD2	7.66	112.43	106.30
1	B	178	TRP	CE2-CD2-CG	-7.64	101.19	107.30
1	B	77	TRP	CE2-CD2-CG	-7.64	101.19	107.30
1	B	183	TRP	CE2-CD2-CG	-7.50	101.30	107.30
1	A	124	TRP	CD1-CG-CD2	7.47	112.28	106.30
1	A	77	TRP	CE2-CD2-CG	-7.40	101.38	107.30
1	A	124	TRP	CE2-CD2-CG	-7.33	101.44	107.30
1	B	158	TRP	CD1-CG-CD2	7.28	112.12	106.30
1	A	183	TRP	CD1-CG-CD2	7.25	112.10	106.30
1	A	178	TRP	CE2-CD2-CG	-7.21	101.53	107.30
1	B	122	TRP	CD1-CG-CD2	7.11	111.99	106.30
1	B	71	TRP	CE2-CD2-CG	-7.08	101.64	107.30
1	B	124	TRP	CE2-CD2-CG	-6.99	101.70	107.30
1	B	158	TRP	CE2-CD2-CG	-6.99	101.71	107.30
1	A	122	TRP	CD1-CG-CD2	6.94	111.85	106.30
1	A	71	TRP	CE2-CD2-CG	-6.93	101.75	107.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	57	ARG	NE-CZ-NH2	-6.80	116.90	120.30
1	B	122	TRP	CE2-CD2-CG	-6.80	101.86	107.30
1	A	77	TRP	CD1-CG-CD2	6.79	111.74	106.30
1	A	122	TRP	CE2-CD2-CG	-6.75	101.90	107.30
1	A	183	TRP	CE2-CD2-CG	-6.72	101.92	107.30
1	B	178	TRP	CG-CD2-CE3	6.56	139.80	133.90
1	A	158	TRP	CD1-CG-CD2	6.30	111.34	106.30
1	A	71	TRP	CG-CD1-NE1	-6.20	103.90	110.10
1	A	158	TRP	CE2-CD2-CG	-6.07	102.45	107.30
1	B	77	TRP	CG-CD2-CE3	6.05	139.35	133.90
1	B	173	TYR	CB-CG-CD2	-6.05	117.37	121.00
1	A	23	ILE	CG1-CB-CG2	-5.98	98.25	111.40
1	B	178	TRP	CG-CD1-NE1	-5.79	104.31	110.10
1	A	57	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	B	77	TRP	CB-CG-CD1	-5.63	119.68	127.00
1	B	183	TRP	CG-CD2-CE3	5.61	138.95	133.90
1	B	178	TRP	CB-CG-CD1	-5.40	119.98	127.00
1	A	178	TRP	CB-CG-CD1	-5.35	120.04	127.00
1	A	71	TRP	CB-CG-CD1	-5.35	120.05	127.00
1	A	77	TRP	CB-CG-CD1	-5.31	120.10	127.00
1	B	77	TRP	CG-CD1-NE1	-5.29	104.81	110.10
1	B	71	TRP	CG-CD1-NE1	-5.25	104.86	110.10
1	A	183	TRP	CG-CD1-NE1	-5.22	104.88	110.10
1	A	71	TRP	CG-CD2-CE3	5.20	138.58	133.90
1	A	178	TRP	CG-CD2-CE3	5.20	138.58	133.90
1	A	173	TYR	CB-CG-CD2	-5.15	117.91	121.00
1	B	158	TRP	CG-CD1-NE1	-5.12	104.98	110.10
1	B	183	TRP	CB-CG-CD1	-5.11	120.36	127.00
1	A	166	TYR	CB-CG-CD1	-5.08	117.95	121.00
1	A	77	TRP	CG-CD2-CE3	5.07	138.46	133.90
1	B	183	TRP	CG-CD1-NE1	-5.02	105.08	110.10
1	A	178	TRP	CG-CD1-NE1	-5.00	105.10	110.10

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	1503	0	1423	2	0
1	B	1503	0	1423	4	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	144	0	0	0	0
3	B	137	0	0	0	0
All	All	3289	0	2846	6	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 1.

All (6) 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:2:PHE:H	1:B:39:ASN:HD21	1.36	0.73
1:A:168:ASN:HD22	1:A:168:ASN:H	1.51	0.59
1:B:168:ASN:HD22	1:B:168:ASN:H	1.53	0.54
1:A:168:ASN:H	1:A:168:ASN:ND2	2.14	0.45
1:B:21:GLU:HA	1:B:24:GLU:HG2	2.01	0.41
1:B:2:PHE:H	1:B:39:ASN:ND2	2.12	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	190/192 (99%)	182 (96%)	8 (4%)	0	100	100
1	B	190/192 (99%)	187 (98%)	3 (2%)	0	100	100
All	All	380/384 (99%)	369 (97%)	11 (3%)	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	151/151 (100%)	147 (97%)	4 (3%)	46 30
1	B	151/151 (100%)	142 (94%)	9 (6%)	19 5
All	All	302/302 (100%)	289 (96%)	13 (4%)	29 12

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3	GLU
1	A	163	TYR
1	A	168	ASN
1	A	182	ASN
1	B	9	TYR
1	B	11	LYS
1	B	41	LEU
1	B	89	THR
1	B	94	GLU
1	B	163	TYR
1	B	168	ASN
1	B	182	ASN
1	B	184	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	37	ASN
1	A	66	ASN
1	A	140	ASN
1	A	168	ASN
1	A	182	ASN
1	A	189	ASN
1	B	39	ASN
1	B	66	ASN
1	B	140	ASN

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Mol	Chain	Res	Type
1	B	168	ASN
1	B	182	ASN
1	B	189	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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.