wwPDB X-ray Structure Validation Summary Report (i)

Oct 29, 2024 – 06:48 AM EDT

PDB ID	:	3P2A
Title	:	Crystal Structure of Thioredoxin 2 from Yersinia pestis
Authors	:	Kim, Y.; Zhou, M.; Grimshaw, S.; Anderson, W.F.; Joachimiak, A.; Center for Structural Genomics of Infectious Diseases (CSGID)
Deposited on	:	2010-10-01
Resolution	:	2.19 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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:

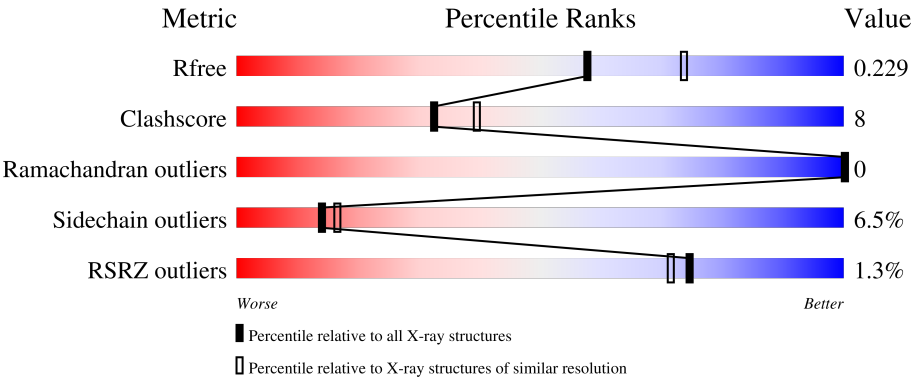
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

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 2.19 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}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

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% 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	148	2% 84% 13%
1	B	148	% 81% 13%
1	C	148	% 71% 22% 5%
1	D	148	% 78% 16%

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4818 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 Putative thioredoxin-like protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	145	Total	C	N	O	S	Se	0	0	0
			1127	706	199	210	6	6			
1	B	144	Total	C	N	O	S	Se	0	0	0
			1120	701	198	209	6	6			
1	C	141	Total	C	N	O	S	Se	0	0	0
			1099	690	194	203	6	6			
1	D	142	Total	C	N	O	S	Se	0	1	0
			1112	697	197	206	6	6			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	SER	-	expression tag	UNP Q7CK81
A	-1	ASN	-	expression tag	UNP Q7CK81
A	0	ALA	-	expression tag	UNP Q7CK81
B	-2	SER	-	expression tag	UNP Q7CK81
B	-1	ASN	-	expression tag	UNP Q7CK81
B	0	ALA	-	expression tag	UNP Q7CK81
C	-2	SER	-	expression tag	UNP Q7CK81
C	-1	ASN	-	expression tag	UNP Q7CK81
C	0	ALA	-	expression tag	UNP Q7CK81
D	-2	SER	-	expression tag	UNP Q7CK81
D	-1	ASN	-	expression tag	UNP Q7CK81
D	0	ALA	-	expression tag	UNP Q7CK81

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

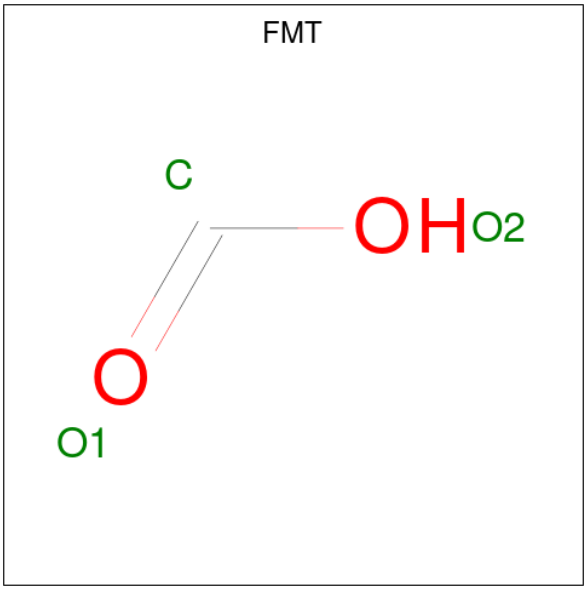
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		
2	B	1	Total	Zn	0	0
			1	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	C	1	Total Zn 1 1	0	0
2	D	1	Total Zn 1 1	0	0

- Molecule 3 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 3 1 2	0	0

- Molecule 4 is water.

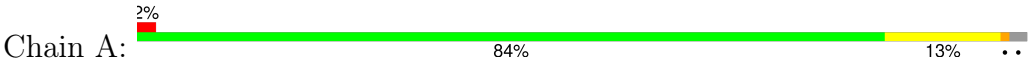
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	112	Total O 112 112	0	0
4	B	100	Total O 100 100	0	0
4	C	59	Total O 59 59	0	0
4	D	82	Total O 82 82	0	0

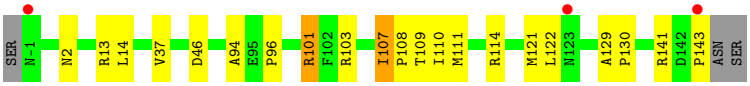
3 Residue-property plots (i)

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 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: Putative thioredoxin-like protein

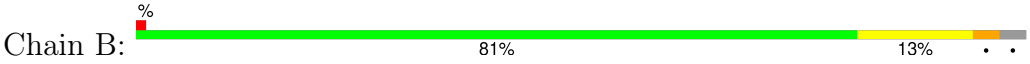
Chain A:

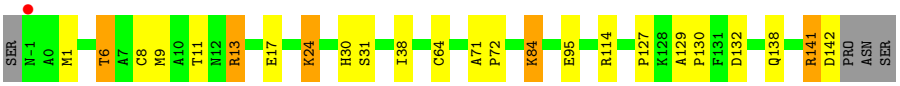




• Molecule 1: Putative thioredoxin-like protein

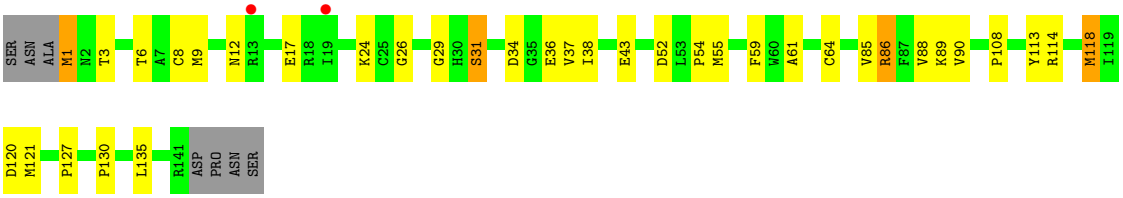
Chain B:





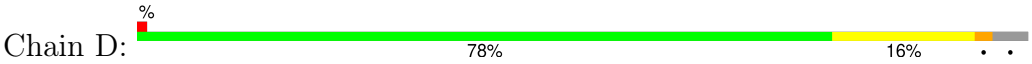
• Molecule 1: Putative thioredoxin-like protein

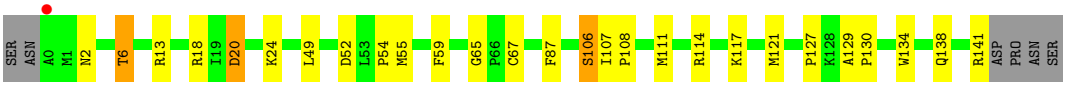
Chain C:



• Molecule 1: Putative thioredoxin-like protein

Chain D:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	53.97Å 75.58Å 81.51Å 90.00° 90.85° 90.00°	Depositor
Resolution (Å)	34.28 – 2.19 34.28 – 2.19	Depositor EDS
% Data completeness (in resolution range)	98.9 (34.28-2.19) 98.9 (34.28-2.19)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.13	Depositor
$< I/\sigma(I) >$ [1]	2.61 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.184 , 0.234 0.179 , 0.229	Depositor DCC
R_{free} test set	1692 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å^2)	30.3	Xtriage
Anisotropy	0.437	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 42.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.098 for h,-k,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4818	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 5.63% 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, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, FMT

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	0.67	0/1145	0.77	1/1543 (0.1%)
1	B	0.65	0/1137	0.76	0/1531
1	C	0.62	0/1117	0.76	0/1505
1	D	0.62	0/1129	0.75	0/1520
All	All	0.64	0/4528	0.76	1/6099 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	101	ARG	NE-CZ-NH2	-5.71	117.45	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	1127	0	1106	12	0
1	B	1120	0	1099	16	0
1	C	1099	0	1084	25	0
1	D	1112	0	1094	17	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	A	3	0	1	0	0
4	A	112	0	0	0	0
4	B	100	0	0	7	0
4	C	59	0	0	1	0
4	D	82	0	0	3	0
All	All	4818	0	4384	69	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 8.

The worst 5 of 69 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:C:37:VAL:HG11	1:C:89:LYS:HD2	1.42	1.00
1:C:34:ASP:HB3	1:C:36:GLU:HB2	1.46	0.95
1:C:12:ASN:HD21	1:C:26:GLY:H	1.16	0.92
1:C:118:MSE:SE	1:C:121:MSE:HE2	2.21	0.91
1:B:84:LYS:HE2	4:B:296:HOH:O	1.84	0.78

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	143/148 (97%)	142 (99%)	1 (1%)	0	100	100
1	B	142/148 (96%)	137 (96%)	5 (4%)	0	100	100
1	C	139/148 (94%)	131 (94%)	8 (6%)	0	100	100
1	D	141/148 (95%)	130 (92%)	11 (8%)	0	100	100

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	565/592 (95%)	540 (96%)	25 (4%)	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	121/118 (102%)	117 (97%)	4 (3%)	33 44
1	B	120/118 (102%)	108 (90%)	12 (10%)	6 6
1	C	118/118 (100%)	109 (92%)	9 (8%)	11 12
1	D	119/118 (101%)	113 (95%)	6 (5%)	20 26
All	All	478/472 (101%)	447 (94%)	31 (6%)	14 16

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	141	ARG
1	D	24	LYS
1	C	6	THR
1	D	117	LYS
1	C	118	MSE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-1	ASN
1	B	39	ASN
1	C	12	ASN
1	D	30	HIS
1	D	50	GLN

5.3.3 RNA

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains

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

5.5 Carbohydrates

There are no oligosaccharides in this entry.

5.6 Ligand geometry

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	FMT	A	152	-	2,2,2	0.70	0	1,1,1	0.05	0

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

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, 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	139/148 (93%)	-0.47	3 (2%)	62	58	19, 27, 62, 83	0
1	B	138/148 (93%)	-0.44	1 (0%)	84	82	19, 30, 56, 88	0
1	C	135/148 (91%)	-0.01	2 (1%)	71	68	18, 41, 80, 104	2 (1%)
1	D	136/148 (91%)	-0.39	1 (0%)	84	82	17, 33, 63, 87	1 (0%)
All	All	548/592 (92%)	-0.33	7 (1%)	74	71	17, 32, 68, 104	3 (0%)

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	143	PRO	4.5
1	C	19	ILE	3.2
1	A	123	ASN	2.9
1	A	-1	ASN	2.6
1	B	-1	ASN	2.6

6.2 Non-standard residues in protein, DNA, RNA chains

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	FMT	A	152	3/3	0.82	0.17	61,61,63,64	0
2	ZN	C	151	1/1	0.99	0.02	49,49,49,49	0
2	ZN	A	151	1/1	1.00	0.02	28,28,28,28	0
2	ZN	D	151	1/1	1.00	0.02	31,31,31,31	0
2	ZN	B	151	1/1	1.00	0.01	35,35,35,35	0

6.5 Other polymers (i)

There are no such residues in this entry.