



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 04:27 PM UTC

PDB ID : 2PUK / pdb_00002puk
Title : Crystal structure of the binary complex between ferredoxin: thioredoxin reductase and thioredoxin m
Authors : Dai, S.; Friemann, R.; Schurmann, P.; Eklund, H.
Deposited on : 2007-05-09
Resolution : 3.00 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 ⓘ 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
Mogul : 2022.3.0, CSD as543be (2022)
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

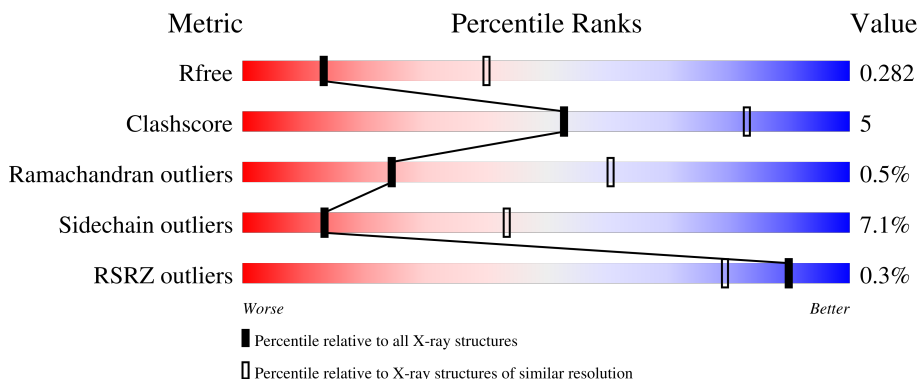
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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.



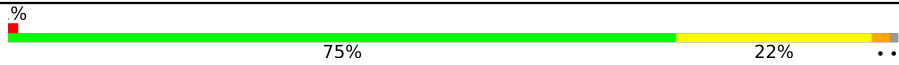
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	2672 (3.00-3.00)
Clashscore	190562	2977 (3.00-3.00)
Ramachandran outliers	187476	2877 (3.00-3.00)
Sidechain outliers	187428	2880 (3.00-3.00)
RSRZ outliers	180081	2671 (3.00-3.00)

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	109	86% 12% ..
1	E	109	83% 17% .
2	B	73	82% 16% .
2	F	73	82% 16% .
3	C	106	79% 19% .

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Mol	Chain	Length	Quality of chain
3	G	106	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into two segments: a green segment on the left labeled '75%' and a yellow segment on the right labeled '22%'. A small red square is at the far left end, and two small black dots are at the far right end. A '%' symbol is positioned above the bar on the left side.</p>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SF4	E	1000	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4578 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 Ferredoxin-thioredoxin reductase, catalytic chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	108	858	534	145	168	11	0	0	0
1	E	109	866	538	147	170	11	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	ASN	-	cloning artifact	UNP Q55389
E	7	ASN	-	cloning artifact	UNP Q55389

- Molecule 2 is a protein called Ferredoxin-thioredoxin reductase, variable chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	73	586	374	106	104	2	0	0	0
2	F	73	586	374	106	104	2	0	0	0

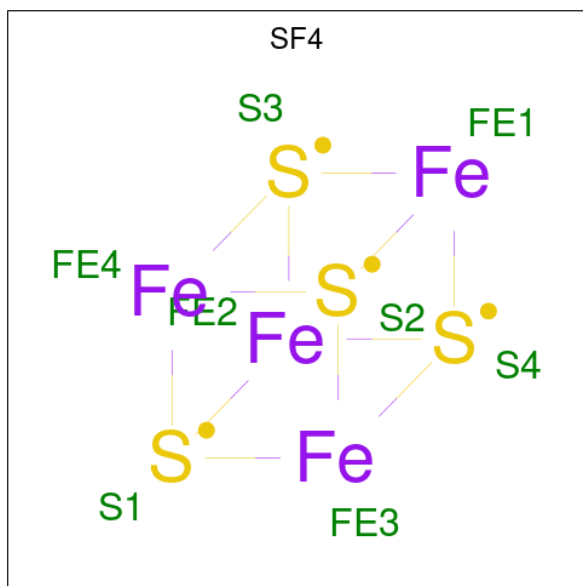
- Molecule 3 is a protein called Thioredoxin M-type, chloroplast (TRX-M).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	106	836	541	130	163	2	0	0	0
3	G	105	830	538	129	161	2	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	40	SER	CYS	engineered mutation	UNP P07591
G	40	SER	CYS	engineered mutation	UNP P07591

- Molecule 4 is IRON/SULFUR CLUSTER (CCD ID: SF4) (formula: Fe₄S₄).




Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
4	A	1	Total	Fe	S	0	0
			8	4	4		
4	E	1	Total	Fe	S	0	0
			8	4	4		

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.

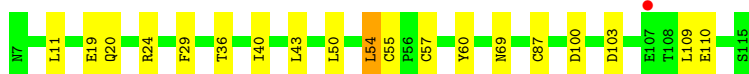
- Molecule 1: Ferredoxin-thioredoxin reductase, catalytic chain

Chain A:  86% 12% ..




- Molecule 1: Ferredoxin-thioredoxin reductase, catalytic chain

Chain E:  83% 17% .




- Molecule 2: Ferredoxin-thioredoxin reductase, variable chain

Chain B:  82% 16% .




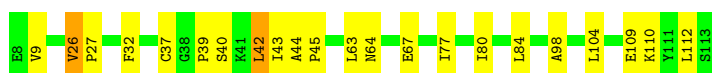
- Molecule 2: Ferredoxin-thioredoxin reductase, variable chain

Chain F:  82% 16% .




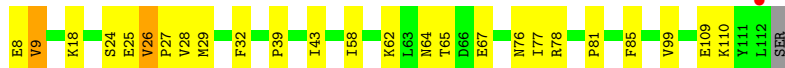
- Molecule 3: Thioredoxin M-type, chloroplast (TRX-M)

Chain C:  79% 19% .



- Molecule 3: Thioredoxin M-type, chloroplast (TRX-M)

Chain G:  %



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	53.95Å 42.22Å 145.34Å 90.00° 90.29° 90.00°	Depositor
Resolution (Å)	30.00 – 3.00 30.00 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.8 (30.00-3.00) 99.7 (30.00-3.00)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.93 (at 3.00Å)	Xtrriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.235 , 0.284 0.231 , 0.282	Depositor DCC
R_{free} test set	663 reflections (4.91%)	wwPDB-VP
Wilson B-factor (Å ²)	56.0	Xtrriage
Anisotropy	0.555	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 8.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	4578	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.20% 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](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SF4

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	0.44	0/876	0.84	0/1182
1	E	0.44	0/884	0.86	0/1193
2	B	0.45	0/600	0.70	0/813
2	F	0.54	0/600	0.78	0/813
3	C	0.49	0/856	0.84	0/1165
3	G	0.46	0/850	0.79	0/1157
All	All	0.47	0/4666	0.81	0/6323

There are no bond length outliers.

There are no bond angle outliers.

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	858	0	817	7	0
1	E	866	0	823	11	0
2	B	586	0	588	7	0
2	F	586	0	588	5	0
3	C	836	0	831	8	0
3	G	830	0	826	10	0
4	A	8	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	E	8	0	0	2	0
All	All	4578	0	4473	45	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 5.

The worst 5 of 45 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:E:69:ASN:HD21	2:F:39:LEU:HD22	1.55	0.72
3:C:39:PRO:HB3	3:C:98:ALA:HB2	1.79	0.64
2:F:6:ARG:HD2	2:F:34:GLU:HG3	1.84	0.60
1:A:62:ASP:OD2	2:B:45:ARG:HD2	2.04	0.57
1:E:29:PHE:CD1	1:E:36:THR:HG21	2.40	0.57

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	106/109 (97%)	101 (95%)	5 (5%)	0	100	100
1	E	107/109 (98%)	104 (97%)	3 (3%)	0	100	100
2	B	71/73 (97%)	66 (93%)	5 (7%)	0	100	100
2	F	71/73 (97%)	64 (90%)	7 (10%)	0	100	100
3	C	104/106 (98%)	97 (93%)	5 (5%)	2 (2%)	6	30
3	G	103/106 (97%)	96 (93%)	6 (6%)	1 (1%)	12	45
All	All	562/576 (98%)	528 (94%)	31 (6%)	3 (0%)	24	60

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	9	VAL
3	C	112	LEU
3	C	9	VAL

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	95/96 (99%)	90 (95%)	5 (5%)	20	54
1	E	96/96 (100%)	93 (97%)	3 (3%)	35	68
2	B	64/64 (100%)	59 (92%)	5 (8%)	11	39
2	F	64/64 (100%)	59 (92%)	5 (8%)	11	39
3	C	94/94 (100%)	86 (92%)	8 (8%)	10	36
3	G	93/94 (99%)	83 (89%)	10 (11%)	6	26
All	All	506/508 (100%)	470 (93%)	36 (7%)	13	43

5 of 36 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	G	25	GLU
3	G	110	LYS
3	G	26	VAL
3	G	65	THR
3	C	43	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	86	HIS
2	F	18	HIS
3	G	76	ASN
2	F	21	HIS
1	E	69	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](#)

2 ligands are modelled in this entry.

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
4	SF4	A	1000	1	0,12,12	-	-	-		
4	SF4	E	1000	1	0,12,12	-	-	-		

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	A	1000	1	-	-	0/6/5/5
4	SF4	E	1000	1	-	-	0/6/5/5

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.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	1000	SF4	2	0

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	108/109 (99%)	-0.16	0 100 100	32, 42, 75, 83	0
1	E	109/109 (100%)	0.13	1 (0%) 81 61	33, 49, 78, 83	0
2	B	73/73 (100%)	-0.12	0 100 100	35, 48, 60, 64	0
2	F	73/73 (100%)	0.23	0 100 100	44, 61, 76, 77	0
3	C	106/106 (100%)	-0.09	0 100 100	37, 49, 61, 65	0
3	G	105/106 (99%)	0.12	1 (0%) 79 59	45, 56, 70, 73	0
All	All	574/576 (99%)	0.01	2 (0%) 90 79	32, 51, 73, 83	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	G	112	LEU	2.4
1	E	107	GLU	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](#)

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, 95th 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(\AA^2)	Q<0.9
4	SF4	A	1000	8/8	0.98	0.04	31,32,32,33	0
4	SF4	E	1000	8/8	0.99	0.04	29,30,30,31	0

6.5 Other polymers [i](#)

There are no such residues in this entry.