

Full wwPDB X-ray Structure Validation Report (i)

Oct 11, 2021 – 06:43 AM EDT

PDB ID : 2PUK

Title : Crystal structure of the binary complex between ferredoxin: thioredoxin re-

ductase and thioredoxin m

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Deposited on : 2007-05-09

Resolution : 3.00 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 following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.23.2

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Refmac : 5.8.0158

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

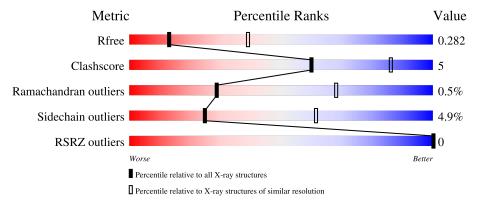
Validation Pipeline (wwPDB-VP) : 2.23.2

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 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	Similar resolution
Metric	$(\# ext{Entries})$	$(\# ext{Entries}, ext{ resolution range}(ext{Å}))$
R_{free}	130704	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (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 <=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	88%	10%	
1	Е	109	82%	7%	
2	В	73	82%	.8%	
2	F	73	88%	11%	<u>.</u>
3	С	106	84% 1	.4%	•



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Mol	Chain	Length	Quality of chain		
3	G	106	78%	19%	•••

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 (i)

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	${f Atoms}$					ZeroOcc	AltConf	Trace
1	Λ	108	Total	С	N	О	S	0	0	0
1	1 A	100	858	534	145	168	11	0	0	U
1	E	109	Total	al C N O S 0	0	0				
1	15	109	866	538	147	170	11	0	U	0

There are 2 discrepancies between the modelled and reference sequences:

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

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	73	Total	С	N	О	S	0	0	0
		13	586	374	106	104	2	0	0	. 0
9	E	73	Total	С	N	О	S	0	0	0
2	Г	13	586	374	106	104	2	0	0	U

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

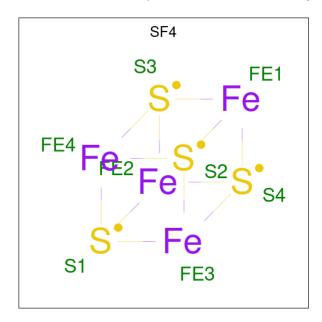
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	106	Total	С	N	О	S	0	0	0
3		100	836	541	130	163	2	0	0	
9	С	105	Total	С	N	О	S	0	0	0
3	3 G	G 105	830	538	129	161	2	0	0	U

There are 2 discrepancies between the modelled and reference sequences:

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



 \bullet Molecule 4 is IRON/SULFUR CLUSTER (three-letter code: SF4) (formula: Fe_4S_4).



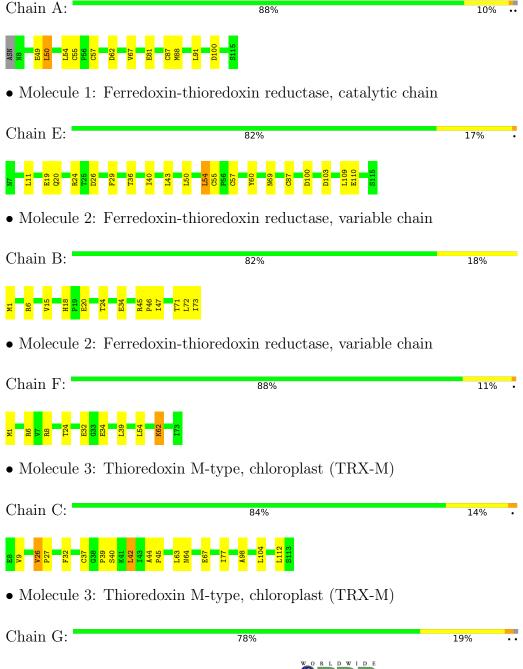
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Fe S 8 4 4	0	0
4	Е	1	Total Fe S 8 4 4	0	0



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: Ferredoxin-thioredoxin reductase, catalytic chain









4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	53.95Å 42.22Å 145.34Å	Donogitor
a, b, c, α , β , γ	90.00° 90.29° 90.00°	Depositor
Resolution (Å)	30.00 - 3.00	Depositor
resolution (A)	27.54 - 3.00	EDS
% Data completeness	99.8 (30.00-3.00)	Depositor
(in resolution range)	99.8 (27.54-3.00)	EDS
R_{merge}	0.10	Depositor
R_{sym}	0.10	Depositor
$< I/\sigma(I) > 1$	2.93 (at 3.00Å)	Xtriage
Refinement program	REFMAC	Depositor
Ρ. Р.	0.235 , 0.284	Depositor
R, R_{free}	0.231 , 0.282	DCC
R_{free} test set	663 reflections (4.92%)	wwPDB-VP
Wilson B-factor (Å ²)	56.0	Xtriage
Anisotropy	0.555	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.30 , 12.7	EDS
L-test for twinning ²	$< L >=0.50, < L^2>=0.33$	Xtriage
Estimated twinning fraction	0.032 for h,-k,-l	Xtriage
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

Xtriage'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.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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	Bo	nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z >5	
1	A	0.36	0/876	0.51	0/1182	
1	Е	0.40	0/884	0.55	0/1193	
2	В	0.36	0/600	0.50	0/813	
2	F	0.48	1/600~(0.2%)	0.52	0/813	
3	С	0.38	0/856	0.49	0/1165	
3	G	0.35	0/850	0.48	0/1157	
All	All	0.39	$1/4666 \ (0.0\%)$	0.51	0/6323	

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$Ideal(\AA)$
2	F	62	LYS	CD-CE	5.89	1.66	1.51

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	Е	866	0	823	11	0
2	В	586	0	588	6	0
2	F	586	0	588	4	0



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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	С	836	0	831	8	0
3	G	830	0	826	9	0
4	A	8	0	0	0	0
4	Е	8	0	0	2	0
All	All	4578	0	4473	42	0

The all-atom clash score is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clash score for this structure is 5.

All (42) 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
2:F:54:LEU:HD11	2:F:62:LYS:HB3	1.86	0.56
1:E:19:GLU:HG2	1:E:103:ASP:HA	1.88	0.55
2:B:6:ARG:HH11	2:B:34:GLU:HG3	1.74	0.52
1:A:57:CYS:HB2	1:A:87:CYS:SG	2.49	0.52
2:F:8:ARG:HG3	2:F:32:GLU:HG2	1.91	0.51
1:A:49:GLU:HG3	1:A:50:LEU:HD13	1.95	0.48
3:G:32:PHE:CE2	3:G:77:ILE:HG13	2.49	0.48
2:B:6:ARG:HB3	2:B:73:ILE:HD12	1.94	0.47
3:G:39:PRO:HB2	3:G:81:PRO:HD3	1.96	0.47
3:C:32:PHE:CE2	3:C:77:ILE:HG13	2.50	0.47
3:G:76:ASN:HD21	3:G:78:ARG:NH1	2.12	0.47
1:A:81:GLU:O	2:B:15:VAL:HA	2.14	0.47
1:A:88:MET:HG2	1:A:91:LEU:HD21	1.96	0.47
1:A:55:CYS:SG	1:A:87:CYS:SG	3.13	0.47
3:G:64:ASN:HB3	3:G:67:GLU:HG2	1.97	0.47
3:G:9:VAL:HG11	3:G:62:LYS:HG3	1.96	0.46
3:G:26:VAL:HG22	3:G:27:PRO:HD2	1.98	0.46
3:C:26:VAL:HG22	3:C:27:PRO:HD2	1.98	0.46
3:C:37:CYS:O	3:C:40:SER:HB2	2.15	0.46
3:G:32:PHE:CD2	3:G:77:ILE:HG13	2.51	0.46
1:E:57:CYS:HB2	1:E:87:CYS:SG	2.56	0.45
1:E:87:CYS:SG	4:E:1000:SF4:S1	3.14	0.44
1:E:54:LEU:HD22	1:E:60:TYR:CZ	2.53	0.44
3:C:32:PHE:CD2	3:C:63:LEU:HD22	2.54	0.42



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Atom-1	Atom-2	Interatomic	Clash
Atom-1	Atom-2	${ m distance}({ m \AA})$	overlap (Å)
1:E:20:GLN:NE2	1:E:24:ARG:HH11	2.17	0.42
3:G:27:PRO:HB2	3:G:58:ILE:HG22	2.00	0.42
1:A:50:LEU:HB3	1:A:67:VAL:HG21	2.01	0.42
2:B:18:HIS:HE1	2:B:20:GLU:HG2	1.84	0.42
1:E:11:LEU:HD11	1:E:109:LEU:HD22	2.03	0.41
1:E:50:LEU:HD23	1:E:54:LEU:HD12	2.02	0.41
2:B:45:ARG:HA	2:B:46:PRO:HD3	1.89	0.41
3:C:42:LEU:HD12	3:C:42:LEU:HA	1.89	0.41
3:C:44:ALA:HB3	3:C:45:PRO:HD3	2.03	0.41
3:C:64:ASN:HB3	3:C:67:GLU:HB2	2.03	0.41
1:E:55:CYS:HB2	4:E:1000:SF4:S2	2.62	0.40
3:G:29:MET:HG3	3:G:85:PHE:CE2	2.57	0.40
1:E:40:ILE:HA	1:E:43:LEU:HD12	2.03	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	Perce	entiles
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	В	71/73 (97%)	66 (93%)	5 (7%)	0	100	100
2	F	71/73 (97%)	64 (90%)	7 (10%)	0	100	100
3	С	104/106 (98%)	97 (93%)	5 (5%)	2 (2%)	8	36
3	G	103/106 (97%)	96 (93%)	6 (6%)	1 (1%)	15	53
All	All	562/576 (98%)	528 (94%)	31 (6%)	3 (0%)	29	68

All (3) Ramachandran outliers are listed below:



Mol	Chain	Res	Type
3	G	9	VAL
3	С	112	LEU
3	С	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	P	erce	ntiles
1	A	95/96 (99%)	92 (97%)	3 (3%)		39	74
1	E	96/96 (100%)	92 (96%)	4 (4%)		30	66
2	В	64/64 (100%)	59 (92%)	5 (8%)		12	42
2	F	64/64 (100%)	62 (97%)	2 (3%)		40	75
3	С	94/94 (100%)	91 (97%)	3 (3%)		39	74
3	G	93/94 (99%)	85 (91%)	8 (9%)		10	37
All	All	$506/508 \; (100\%)$	481 (95%)	25 (5%)		25	61

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LEU
1	A	54	LEU
1	A	100	ASP
2	В	1	MET
2	В	24	THR
2	В	47	ILE
2	В	71	THR
2	В	72	LEU
3	С	26	VAL
3	С	42	LEU
3	С	104	LEU
1	Е	26	ASP
1	Е	54	LEU
1	Е	100	ASP
1	Е	110	GLU
2	F	1	MET



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Mol	Chain	Res	Type
2	F	24	THR
3	G	8	GLU
3	G	18	LYS
3	G	26	VAL
3	G	33	TRP
3	G	43	ILE
3	G	99	VAL
3	G	106	ASP
3	G	109	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
2	В	29	GLN
1	Е	20	GLN
1	Е	69	ASN
2	F	18	HIS
2	F	21	HIS
3	G	76	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)

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	Trino	Chain	Res	Link	В	ond leng	gths	В	ond angles
MIOI	Type	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	$\mid \text{RMSZ} \mid \# Z > 2 \mid$
4	SF4	Ε	1000	1	0,12,12	-	-	-	
4	SF4	A	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.

\mathbf{Mol}	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	SF4	Е	1000	1	-	-	0/6/5/5
4	SF4	A	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	Ε	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, 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 $>$	$\#\mathrm{RSRZ}{>}2$		Z>2	$OWAB(Å^2)$	Q<0.9
1	A	108/109 (99%)	-0.37	0	100	100	32, 42, 75, 83	0
1	E	109/109 (100%)	-0.26	0	100	100	33, 49, 78, 83	0
2	В	73/73 (100%)	-0.33	0	100	100	35, 48, 60, 64	0
2	F	73/73 (100%)	-0.10	0	100	100	44, 61, 76, 77	0
3	C	106/106 (100%)	-0.37	0	100	100	37, 49, 61, 65	0
3	G	105/106~(99%)	-0.31	0	100	100	45, 56, 70, 73	0
All	All	574/576 (99%)	-0.30	0	100	100	32, 51, 73, 83	0

There are no RSRZ outliers to report.

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 monosaccharides 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, 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	${f B-factors}({f A}^2)$	Q < 0.9
4	SF4	A	1000	8/8	0.99	0.12	31,32,32,33	0
4	SF4	Е	1000	8/8	0.99	0.12	29,30,30,31	0



6.5 Other polymers (i)

There are no such residues in this entry.

