



wwPDB X-ray Structure Validation Summary Report ⓘ

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PDB ID : 2QFI / pdb_00002qfi
Title : Structure of the zinc transporter YiiP
Authors : Lu, M.
Deposited on : 2007-06-27
Resolution : 3.80 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
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

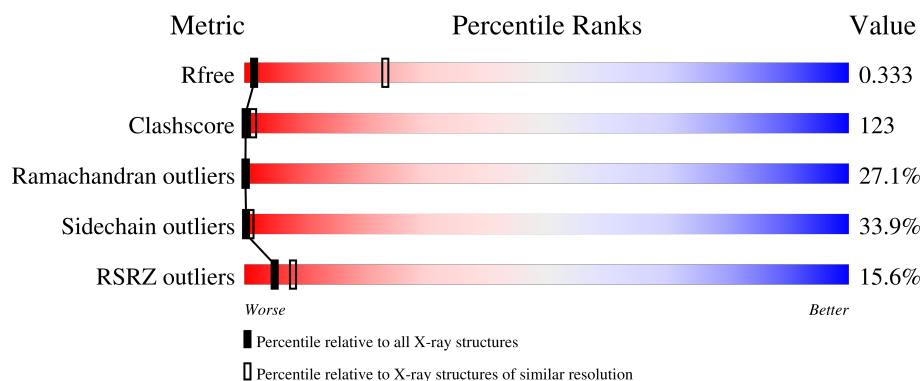
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.80 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	1065 (3.96-3.64)
Clashscore	190562	1012 (3.94-3.66)
Ramachandran outliers	187476	1048 (3.96-3.64)
Sidechain outliers	187428	1043 (3.96-3.64)
RSRZ outliers	180081	1064 (3.96-3.64)

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	300	
1	B	300	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4417 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 Ferrous-iron efflux pump fieF.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	286	Total	C	N	O	S	0	0	0
			2205	1419	378	397	11			
1	B	286	Total	C	N	O	S	0	0	0
			2205	1419	378	397	11			

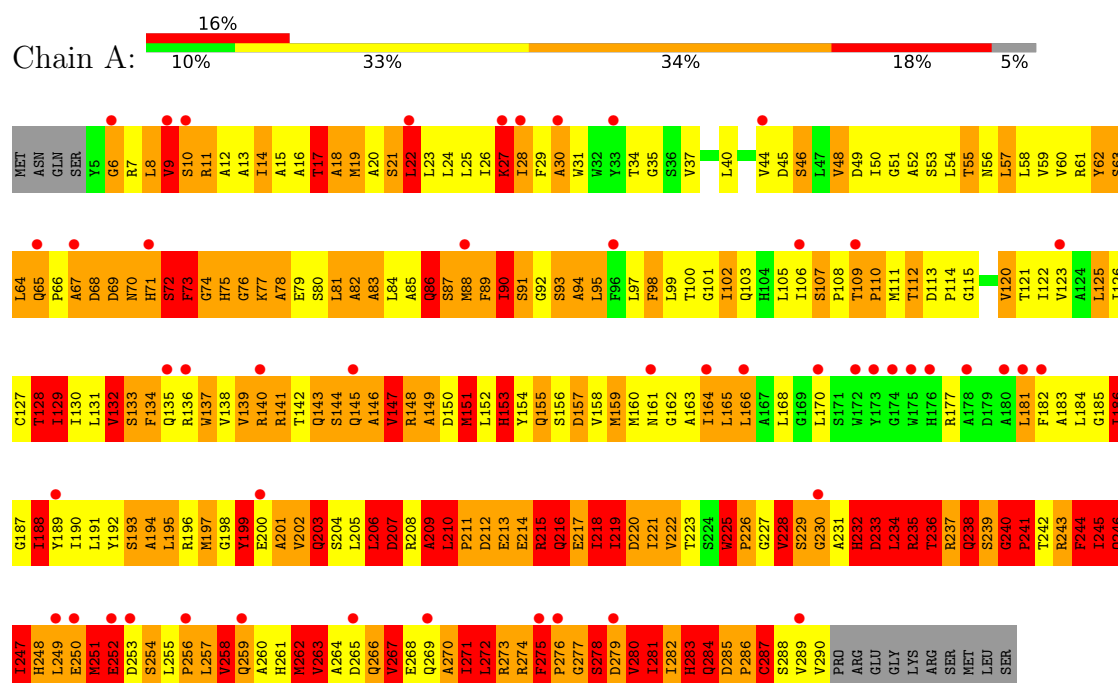
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	4	Total	Zn	0	0
			4	4		
2	B	3	Total	Zn	0	0
			3	3		

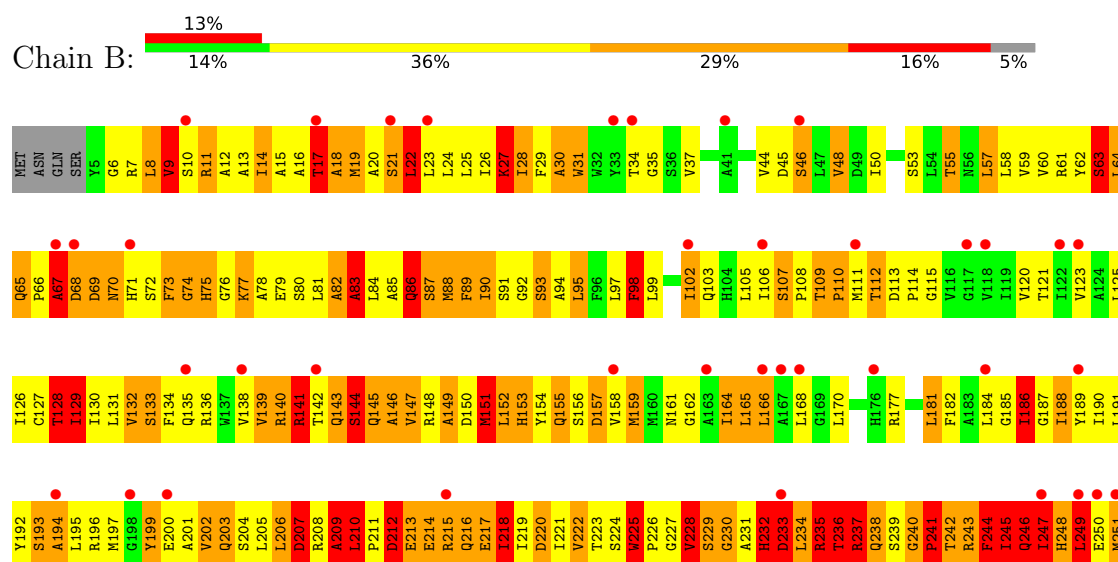
3 Residue-property plots

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: Ferrous-iron efflux pump fieF



• Molecule 1: Ferrous-iron efflux pump fieF



E252	D253	S254	L255	P256	L257	V258	Q259	A260	H261	N262	V263	A264	D265	Q266	V267	E268	Q269	A270	L271	L272	R273	R274	F275	P276	G277	S278	D279	V280	I281	I282	H283	Q284	D285	P286	C287	S288	V289	V290	PRO	ARG	GLU	GLY	LYS	ARG	SER	MET	LEU	SER
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4 Data and refinement statistics

Property	Value	Source
Space group	P 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	106.66Å 110.84Å 130.66Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	12.00 – 3.80 12.00 – 3.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (12.00-3.80) 94.1 (12.00-3.80)	Depositor EDS
R_{merge}	0.13	Depositor
R_{sym}	0.13	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 3.76Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.322 , 0.329 0.348 , 0.333	Depositor DCC
R_{free} test set	772 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	118.0	Xtriage
Anisotropy	0.553	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.12 , 90.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.40$, $\langle L^2 \rangle = 0.23$	Xtriage
Estimated twinning fraction	0.086 for k,h,-l	Xtriage
F_o, F_c correlation	0.88	EDS
Total number of atoms	4417	wwPDB-VP
Average B, all atoms (Å ²)	200.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.67% 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

5.1 Standard geometry

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

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	1.77	47/2252 (2.1%)	1.87	78/3069 (2.5%)
1	B	1.42	26/2252 (1.2%)	1.65	54/3069 (1.8%)
All	All	1.61	73/4504 (1.6%)	1.76	132/6138 (2.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	24
1	B	0	23
All	All	0	47

The worst 5 of 73 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	245	ILE	CA-CB	14.70	1.74	1.54
1	A	247	ILE	CA-CB	13.21	1.72	1.54
1	B	247	ILE	CA-CB	13.13	1.72	1.54
1	A	233	ASP	CA-C	12.09	1.66	1.52
1	A	238	GLN	N-CA	11.29	1.60	1.46

The worst 5 of 132 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	233	ASP	N-CA-C	15.77	133.95	107.93
1	B	233	ASP	N-CA-C	14.99	131.09	108.46
1	A	240	GLY	CA-C-N	13.85	137.16	119.84
1	A	240	GLY	C-N-CA	13.85	137.16	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	238	GLN	N-CA-C	13.22	129.68	110.24

There are no chirality outliers.

5 of 47 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	27	LYS	Peptide
1	A	6	GLY	Peptide
1	A	63	SER	Peptide
1	A	76	GLY	Peptide
1	A	97	LEU	Peptide

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	2205	0	2239	567	4
1	B	2205	0	2239	529	0
2	A	4	0	0	0	2
2	B	3	0	0	0	0
All	All	4417	0	4478	1092	4

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 123.

The worst 5 of 1092 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:232:HIS:CE1	1:B:245:ILE:HG21	1.36	1.61
1:B:245:ILE:CB	1:B:245:ILE:CA	1.74	1.56
1:B:232:HIS:CE1	1:B:245:ILE:CG2	1.96	1.49
1:B:232:HIS:NE2	1:B:245:ILE:CG2	1.79	1.41
1:A:67:ALA:HB1	1:A:72:SER:O	1.31	1.30

All (4) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:HIS:NE2	2:A:306:ZN:ZN[4_556]	1.49	0.71
1:A:68:ASP:N	2:A:303:ZN:ZN[4_556]	1.54	0.66
1:A:261:HIS:CE1	1:A:285:ASP:OD1[4_556]	1.56	0.64
1:A:261:HIS:ND1	1:A:285:ASP:OD1[4_556]	2.09	0.11

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	284/300 (95%)	133 (47%)	76 (27%)	75 (26%)	0	0
1	B	284/300 (95%)	129 (45%)	76 (27%)	79 (28%)	0	0
All	All	568/600 (95%)	262 (46%)	152 (27%)	154 (27%)	0	0

5 of 154 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	ALA
1	A	21	SER
1	A	55	THR
1	A	67	ALA
1	A	69	ASP

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	236/249 (95%)	156 (66%)	80 (34%)	0	1

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	236/249 (95%)	156 (66%)	80 (34%)	0	1
All	All	472/498 (95%)	312 (66%)	160 (34%)	0	1

5 of 160 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	165	LEU
1	B	246	GLN
1	B	186	ILE
1	B	220	ASP
1	B	271	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 27 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	284	GLN
1	B	135	GLN
1	B	266	GLN
1	B	70	ASN
1	B	145	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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 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](#)

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	286/300 (95%)	1.08	49 (17%) 4 7	34, 112, 307, 364	0
1	B	286/300 (95%)	0.91	40 (13%) 6 9	48, 212, 575, 683	0
All	All	572/600 (95%)	1.00	89 (15%) 5 8	34, 151, 522, 683	0

The worst 5 of 89 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	174	GLY	10.5
1	A	249	LEU	7.3
1	A	250	GLU	6.5
1	B	184	LEU	6.4
1	A	10	SER	6.1

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($\text{\AA}^2$)	Q<0.9
2	ZN	A	307	1/1	0.94	0.08	109,109,109,109	0
2	ZN	B	305	1/1	0.95	0.04	77,77,77,77	0
2	ZN	B	301	1/1	0.96	0.04	25,25,25,25	0
2	ZN	A	303	1/1	0.96	0.03	26,26,26,26	0
2	ZN	A	306	1/1	0.97	0.04	28,28,28,28	0
2	ZN	A	302	1/1	0.97	0.05	28,28,28,28	0
2	ZN	B	304	1/1	0.99	0.06	8,8,8,8	0

6.5 Other polymers [i](#)

There are no such residues in this entry.