



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 17, 2024 – 11:06 AM EST

PDB ID : 3SKX
Title : Crystal structure of the ATP binding domain of Archaeoglobus fulgidus COPB
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Deposited on : 2011-06-23
Resolution : 1.59 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 ⓘ 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

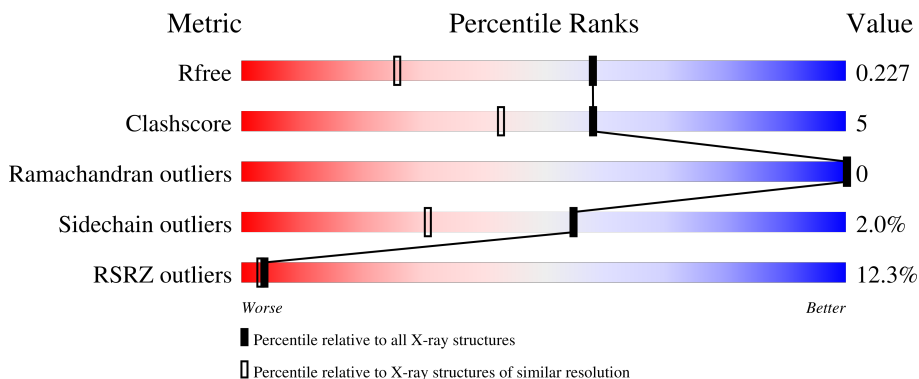
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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	280	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2333 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 Copper-exporting P-type ATPase B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	261	2064	1299	354	405	6	0	13	0

There are 15 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	371	MET	-	initiating methionine	UNP O30085
A	637	PHE	-	expression tag	UNP O30085
A	638	HIS	-	expression tag	UNP O30085
A	639	GLY	-	expression tag	UNP O30085
A	640	LEU	-	expression tag	UNP O30085
A	641	SER	-	expression tag	UNP O30085
A	642	ALA	-	expression tag	UNP O30085
A	643	TRP	-	expression tag	UNP O30085
A	644	SER	-	expression tag	UNP O30085
A	645	HIS	-	expression tag	UNP O30085
A	646	PRO	-	expression tag	UNP O30085
A	647	GLN	-	expression tag	UNP O30085
A	648	PHE	-	expression tag	UNP O30085
A	649	GLU	-	expression tag	UNP O30085
A	650	LYS	-	expression tag	UNP O30085

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: C₂H₃O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C O 4 2 2	0	0
2	A	1	Total C O 4 2 2	0	0

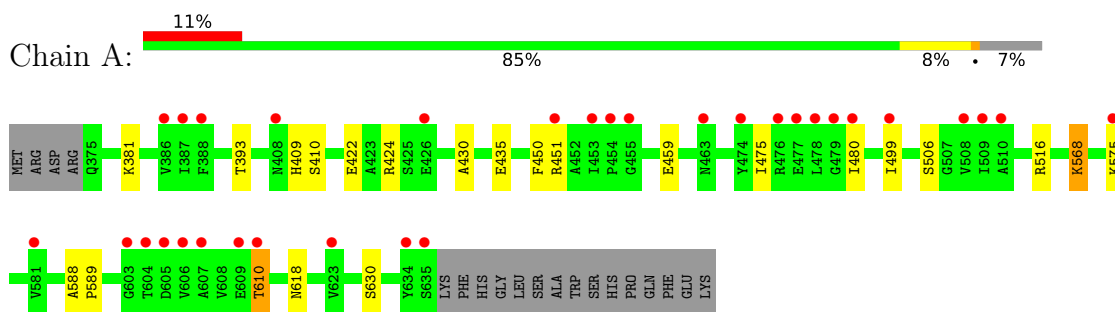
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	258	Total O 261 261	0	3

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: Copper-exporting P-type ATPase B



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α , β , γ	36.05Å 62.68Å 106.06Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	106.06 – 1.59 23.45 – 1.59	Depositor EDS
% Data completeness (in resolution range)	95.3 (106.06-1.59) 95.4 (23.45-1.59)	Depositor EDS
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 1.59Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.201 , 0.233 0.200 , 0.227	Depositor DCC
R_{free} test set	1602 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	25.5	Xtrriage
Anisotropy	0.448	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 50.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2333	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.46% 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: ACT

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	0.49	0/2110	0.61	0/2844

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	2064	0	2073	19	0
2	A	8	0	6	1	0
3	A	261	0	0	5	0
All	All	2333	0	2079	20	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.

All (20) 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:A:435:GLU:OE2	3:A:246:HOH:O	2.09	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:568[B]:LYS:HA	1:A:568[B]:LYS:HE3	1.81	0.63
1:A:516[B]:ARG:NH2	1:A:618:ASN:O	2.27	0.63
1:A:568[B]:LYS:HE3	1:A:568[B]:LYS:CA	2.35	0.54
1:A:516[B]:ARG:NH1	3:A:236:HOH:O	2.39	0.54
2:A:651:ACT:H1	3:A:90:HOH:O	2.07	0.54
1:A:610:THR:HG23	3:A:241:HOH:O	2.08	0.53
1:A:435:GLU:HG3	3:A:249:HOH:O	2.09	0.52
1:A:588:ALA:HB3	1:A:589:PRO:HD3	1.94	0.48
1:A:451:ARG:NH2	1:A:459:GLU:OE2	2.47	0.47
1:A:568[B]:LYS:HA	1:A:568[B]:LYS:CE	2.42	0.47
1:A:499:ILE:HD12	1:A:499:ILE:N	2.30	0.47
1:A:409:HIS:ND1	1:A:506[A]:SER:OG	2.49	0.46
1:A:475:ILE:HG23	1:A:480:ILE:HB	1.98	0.45
1:A:424:ARG:HD2	1:A:450:PHE:CE2	2.52	0.44
1:A:422:GLU:HB3	1:A:430:ALA:HB1	2.01	0.43
1:A:516[A]:ARG:NH2	1:A:618:ASN:ND2	2.67	0.43
1:A:381:LYS:HE3	1:A:630:SER:O	2.20	0.41
1:A:568[A]:LYS:HE3	1:A:568[A]:LYS:HB2	1.80	0.41

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	272/280 (97%)	265 (97%)	7 (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	213/225 (95%)	208 (98%)	5 (2%)	50 25

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	410	SER
1	A	568[A]	LYS
1	A	568[B]	LYS
1	A	575	LYS
1	A	610	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	491	GLN
1	A	574	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 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	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	ACT	A	1	-	3,3,3	0.81	0	3,3,3	1.36	0
2	ACT	A	651	-	3,3,3	0.70	0	3,3,3	1.55	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.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	651	ACT	1	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	261/280 (93%)	0.70	32 (12%) 4 3	14, 28, 54, 78	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	635	SER	7.2
1	A	604	THR	6.7
1	A	610	THR	6.5
1	A	479	GLY	6.2
1	A	463	ASN	5.5
1	A	454	PRO	4.9
1	A	634	TYR	4.5
1	A	408	ASN	4.2
1	A	387	ILE	4.2
1	A	480	ILE	4.0
1	A	606	VAL	3.9
1	A	607	ALA	3.7
1	A	603	GLY	3.6
1	A	476	ARG	3.6
1	A	388	PHE	3.6
1	A	474	TYR	3.5
1	A	477	GLU	3.3
1	A	581	VAL	3.2
1	A	605	ASP	3.1
1	A	478	LEU	3.0
1	A	386	VAL	3.0
1	A	453	ILE	2.7
1	A	609	GLU	2.4
1	A	451	ARG	2.4
1	A	455	GLY	2.3
1	A	508	VAL	2.3
1	A	623	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	509	ILE	2.2
1	A	510	ALA	2.2
1	A	575	LYS	2.1
1	A	426[A]	GLU	2.0
1	A	499	ILE	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 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, 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(Å ²)	Q<0.9
2	ACT	A	1	4/4	0.70	0.23	39,39,40,40	4
2	ACT	A	651	4/4	0.77	0.15	44,44,44,44	4

6.5 Other polymers [i](#)

There are no such residues in this entry.