



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:01 PM UTC

PDB ID : 2A0B / pdb_00002a0b
Title : HISTIDINE-CONTAINING PHOSPHOTRANSFER DOMAIN OF ARCB
FROM ESCHERICHIA COLI
Authors : Kato, M.; Mizuno, T.; Shimizu, T.; Hakoshima, T.
Deposited on : 1998-04-02
Resolution : 1.57 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 : 4-5-2 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

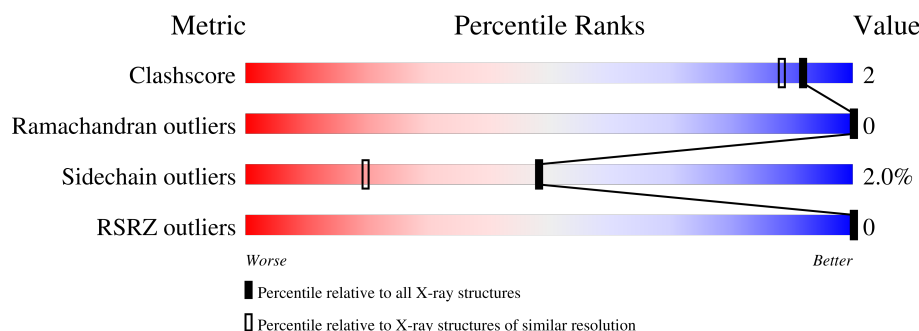
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.57 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))
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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	125	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1112 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 HPT DOMAIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	118	Total	C	N	O	S	0	7	0
			955	612	157	180	6			

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

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

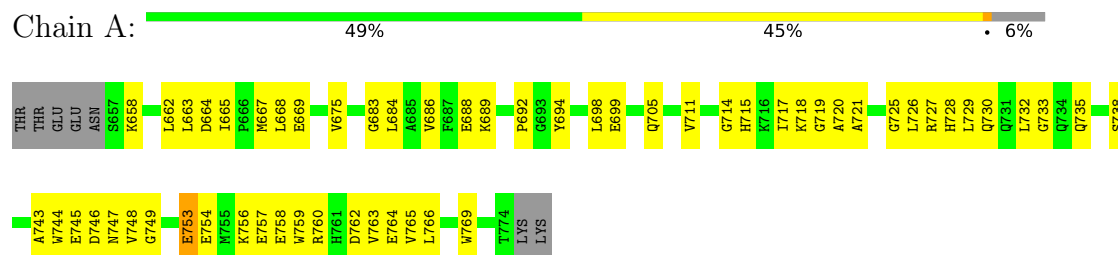
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	156	Total	O	0	0
			156	156		

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: HPT DOMAIN



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	30.46Å 34.92Å 110.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	6.00 – 1.57 6.00 – 1.57	Depositor EDS
% Data completeness (in resolution range)	95.0 (6.00-1.57) 93.2 (6.00-1.57)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.05	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.74 (at 1.57Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.190 , 0.245 0.179 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	23.1	Xtriage
Anisotropy	0.406	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.61 , 88.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	1112	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 14.05% 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: 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	1.66	13/1001 (1.3%)	2.70	94/1351 (7.0%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	726	LEU	N-CA	7.97	1.57	1.46
1	A	763	VAL	N-CA	6.52	1.54	1.46
1	A	758	GLU	CA-C	6.51	1.60	1.52
1	A	662	LEU	CA-C	6.20	1.60	1.52
1	A	663	LEU	N-CA	6.05	1.53	1.45
1	A	718	LYS	CA-C	5.86	1.60	1.52
1	A	714	GLY	CA-C	5.81	1.58	1.51
1	A	762	ASP	CA-C	5.79	1.60	1.52
1	A	732	LEU	C-N	5.58	1.41	1.33
1	A	759	TRP	N-CA	5.49	1.53	1.46
1	A	766	LEU	N-CA	5.24	1.52	1.46
1	A	759	TRP	NE1-CE2	5.04	1.43	1.37
1	A	719	GLY	N-CA	5.02	1.52	1.45

All (94) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	725	GLY	O-C-N	13.71	139.33	122.32
1	A	758	GLU	O-C-N	12.33	137.51	122.35
1	A	762	ASP	O-C-N	12.14	134.98	122.12
1	A	718	LYS	O-C-N	11.34	133.88	122.09
1	A	758	GLU	CA-C-O	-10.97	106.98	119.05
1	A	662	LEU	O-C-N	10.75	136.90	122.49
1	A	762	ASP	CA-C-O	-10.62	109.30	120.55
1	A	732	LEU	CA-C-O	10.38	131.55	120.55

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	758	GLU	CA-C-N	-9.44	105.96	120.31
1	A	758	GLU	C-N-CA	-9.44	105.96	120.31
1	A	764	GLU	O-C-N	-9.28	111.36	122.22
1	A	765	VAL	O-C-N	8.94	130.54	121.87
1	A	746	ASP	OD1-CG-OD2	8.74	143.89	122.90
1	A	662	LEU	CA-C-N	-8.38	108.73	122.81
1	A	662	LEU	C-N-CA	-8.38	108.73	122.81
1	A	760[A]	ARG	O-C-N	-8.32	113.30	122.12
1	A	760[B]	ARG	O-C-N	-8.32	113.30	122.12
1	A	725	GLY	CA-C-O	-8.30	108.65	119.44
1	A	726	LEU	CA-C-O	-8.24	112.89	122.37
1	A	733	GLY	CA-C-O	-8.24	111.24	120.30
1	A	717	ILE	O-C-N	-7.84	113.76	121.83
1	A	745	GLU	O-C-N	7.83	131.08	122.15
1	A	694	TYR	O-C-N	7.79	131.03	122.15
1	A	732	LEU	O-C-N	-7.56	114.11	122.12
1	A	683	GLY	O-C-N	7.52	129.41	122.19
1	A	662	LEU	CA-C-O	-7.39	111.02	119.14
1	A	718	LYS	CA-C-N	-7.34	111.94	119.94
1	A	718	LYS	C-N-CA	-7.34	111.94	119.94
1	A	727	ARG	CD-NE-CZ	7.30	134.62	124.40
1	A	769	TRP	O-C-N	7.23	130.39	122.15
1	A	669	GLU	O-C-N	7.21	130.37	122.15
1	A	725	GLY	CA-C-N	-7.10	111.50	122.16
1	A	725	GLY	C-N-CA	-7.10	111.50	122.16
1	A	717	ILE	CA-C-N	7.03	130.03	120.54
1	A	717	ILE	C-N-CA	7.03	130.03	120.54
1	A	759	TRP	O-C-N	7.01	130.90	122.27
1	A	726	LEU	O-C-N	6.92	130.69	122.46
1	A	721	ALA	N-CA-C	6.91	118.81	111.28
1	A	684	LEU	O-C-N	-6.76	114.95	122.12
1	A	698	LEU	O-C-N	6.71	128.98	122.07
1	A	686	VAL	O-C-N	6.65	128.68	121.83
1	A	765	VAL	CA-C-O	-6.57	114.12	120.95
1	A	759	TRP	CA-C-O	-6.53	112.47	119.97
1	A	746	ASP	CB-CG-OD2	-6.49	103.48	118.40
1	A	764	GLU	CA-C-N	6.36	129.18	120.46
1	A	764	GLU	C-N-CA	6.36	129.18	120.46
1	A	754	GLU	O-C-N	6.36	128.62	122.07
1	A	728	HIS	O-C-N	-6.20	114.65	122.27
1	A	658	LYS	CA-CB-CG	6.17	126.44	114.10
1	A	664	ASP	CA-C-N	6.09	124.08	120.24

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	664	ASP	C-N-CA	6.09	124.08	120.24
1	A	759	TRP	CG-CD2-CE3	-6.06	127.84	133.90
1	A	753	GLU	CA-C-N	6.02	128.26	120.44
1	A	753	GLU	C-N-CA	6.02	128.26	120.44
1	A	688	GLU	O-C-N	-5.98	115.23	122.22
1	A	749	GLY	CA-C-O	-5.95	113.75	120.30
1	A	694	TYR	CE1-CZ-CE2	5.86	132.02	120.30
1	A	745	GLU	CA-C-O	-5.83	114.24	120.42
1	A	694	TYR	CD1-CG-CD2	5.81	126.82	118.10
1	A	769	TRP	CA-C-O	-5.81	114.26	120.42
1	A	705	GLN	CB-CG-CD	5.79	122.44	112.60
1	A	748	VAL	O-C-N	-5.67	116.37	121.87
1	A	743	ALA	O-C-N	-5.66	114.02	122.39
1	A	744	TRP	N-CA-C	5.65	117.89	111.11
1	A	764	GLU	CA-C-O	5.64	126.48	120.10
1	A	747	ASN	OD1-CG-ND2	5.52	128.12	122.60
1	A	729	LEU	N-CA-CB	5.48	118.27	110.16
1	A	735	GLN	CA-C-N	5.46	127.94	120.46
1	A	735	GLN	C-N-CA	5.46	127.94	120.46
1	A	747	ASN	CA-C-O	-5.46	113.05	119.05
1	A	720	ALA	CA-C-O	5.38	126.47	120.82
1	A	711	VAL	CA-C-O	-5.37	115.16	120.85
1	A	733	GLY	O-C-N	5.33	128.09	122.28
1	A	747	ASN	CA-C-N	-5.32	113.17	120.46
1	A	747	ASN	C-N-CA	-5.32	113.17	120.46
1	A	665[A]	ILE	O-C-N	5.32	123.85	120.07
1	A	665[B]	ILE	O-C-N	5.32	123.85	120.07
1	A	738	SER	O-C-N	5.28	126.22	121.42
1	A	669	GLU	CA-C-O	-5.22	114.89	120.42
1	A	711	VAL	O-C-N	5.19	127.18	121.83
1	A	743	ALA	CA-C-O	5.18	125.91	119.12
1	A	667[A]	MET	O-C-N	-5.17	116.74	122.07
1	A	667[B]	MET	O-C-N	-5.17	116.74	122.07
1	A	715	HIS	CA-C-O	-5.13	115.11	120.55
1	A	728	HIS	ND1-CG-CD2	5.13	111.23	106.10
1	A	730	GLN	O-C-N	5.09	127.52	122.12
1	A	683	GLY	N-CA-C	-5.09	106.63	112.73
1	A	692	PRO	O-C-N	-5.07	116.70	122.18
1	A	668	LEU	CA-C-O	-5.05	115.19	120.55
1	A	727	ARG	CA-C-N	-5.05	112.63	120.31
1	A	727	ARG	C-N-CA	-5.05	112.63	120.31
1	A	762	ASP	CA-C-N	-5.01	113.30	120.42

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	762	ASP	C-N-CA	-5.01	113.30	120.42
1	A	735	GLN	O-C-N	-5.01	116.81	122.12

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	955	0	961	3	0
2	A	1	0	0	0	0
3	A	156	0	0	1	0
All	All	1112	0	961	3	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 2.

All (3) 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:699[A]:GLU:OE2	1:A:756:LYS:HD2	2.08	0.52
1:A:753:GLU:OE2	1:A:757:GLU:OE2	2.34	0.46
1:A:756:LYS:HE3	3:A:865:HOH:O	2.20	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	Percentiles	
1	A	123/125 (98%)	123 (100%)	0	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains ⓘ

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	105/106 (99%)	103 (98%)	2 (2%)	50	21

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	675	VAL
1	A	689	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	701	ASN
1	A	730	GLN
1	A	761	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 1 ligands modelled in this entry, 1 is 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	118/125 (94%)	-0.51	0 100 100	13, 24, 41, 48	7 (5%)

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 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(Å ²)	Q<0.9
2	ZN	A	800	1/1	1.00	0.03	24,24,24,24	0

6.5 Other polymers [i](#)

There are no such residues in this entry.