



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:43 PM UTC

PDB ID : 2H7O / pdb_00002h7o
Title : Crystal structure of the Rho-GTPase binding domain of YpkA
Authors : Prehna, G.; Ivanov, M.; Bliska, J.B.; Stebbins, C.E.
Deposited on : 2006-06-02
Resolution : 2.00 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 ⓘ 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

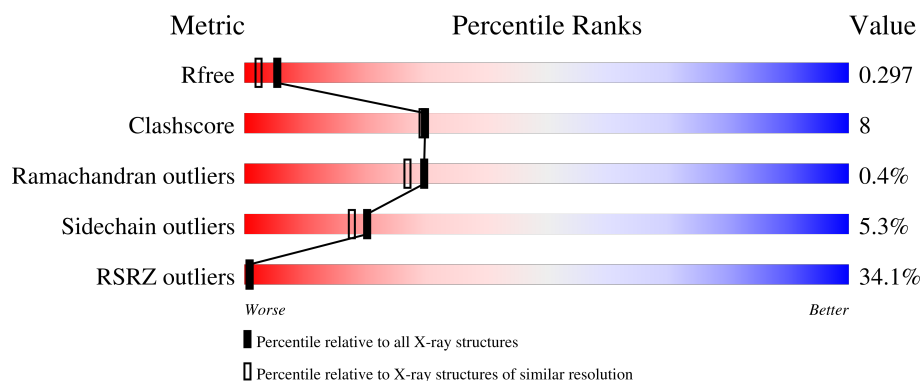
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	303	30% 73% 14% 11%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2445 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 Protein kinase ypkA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	270	Total	C	N	O	S	0	0	0
			2169	1356	389	417	7			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	430	GLY	-	cloning artifact	UNP Q05608
A	431	PRO	-	cloning artifact	UNP Q05608
A	432	VAL	-	cloning artifact	UNP Q05608
A	433	ASP	-	cloning artifact	UNP Q05608

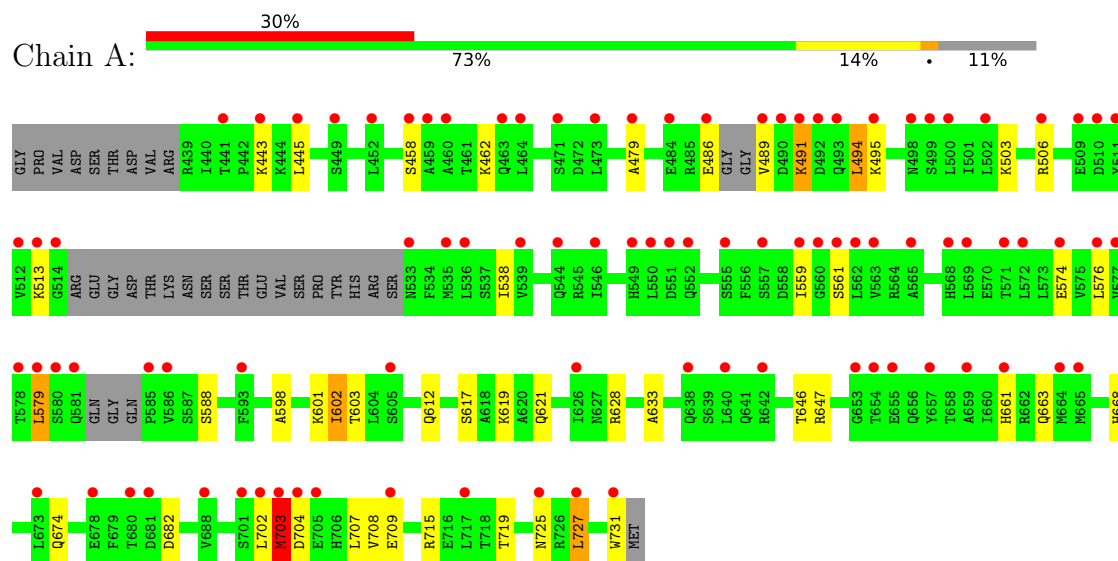
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	276	Total	O	0	0
			276	276		

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: Protein kinase ypkA



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	60.01Å 60.01Å 402.02Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	33.88 – 2.00 33.88 – 2.00	Depositor EDS
% Data completeness (in resolution range)	98.5 (33.88-2.00) 98.5 (33.88-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.71 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.208 , 0.237 0.272 , 0.297	Depositor DCC
R_{free} test set	1485 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	39.5	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	2445	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.79% 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](#)

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	1.28	5/2194 (0.2%)	1.13	2/2953 (0.1%)

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	1

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	725	ASN	CB-CG	6.49	1.68	1.52
1	A	559	ILE	N-CA	-5.66	1.40	1.46
1	A	588	SER	C-O	-5.24	1.18	1.24
1	A	633	ALA	CA-CB	-5.06	1.45	1.53
1	A	443	LYS	CD-CE	5.02	1.67	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	538	ILE	CB-CA-C	-6.06	106.56	111.71
1	A	479	ALA	N-CA-C	5.20	116.64	111.07

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	703	MET	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	2169	0	2212	37	0
2	A	276	0	0	18	2
All	All	2445	0	2212	37	2

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 8.

All (37) 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:702:LEU:O	1:A:704:ASP:N	2.09	0.85
1:A:628:ARG:HD2	2:A:801:HOH:O	1.81	0.78
1:A:598:ALA:O	1:A:602:ILE:HG23	1.88	0.74
1:A:682:ASP:OD2	2:A:996:HOH:O	2.06	0.74
1:A:612:GLN:NE2	2:A:992:HOH:O	2.08	0.73
1:A:709:GLU:HG3	2:A:896:HOH:O	1.92	0.69
1:A:619:LYS:NZ	2:A:915:HOH:O	2.31	0.62
1:A:601:LYS:NZ	2:A:1004:HOH:O	2.26	0.62
1:A:495:LYS:HG3	2:A:899:HOH:O	1.99	0.62
1:A:491:LYS:HD2	2:A:899:HOH:O	1.99	0.61
1:A:646:THR:OG1	1:A:668:HIS:NE2	2.25	0.61
1:A:621:GLN:CG	2:A:871:HOH:O	2.49	0.60
1:A:503:LYS:NZ	2:A:998:HOH:O	2.36	0.58
1:A:719:THR:HG22	2:A:999:HOH:O	2.06	0.56
1:A:647:ARG:HA	1:A:668:HIS:CE1	2.42	0.53
1:A:702:LEU:HB2	1:A:708:VAL:CG2	2.38	0.53
1:A:621:GLN:HG3	2:A:871:HOH:O	2.09	0.52
1:A:702:LEU:HB2	1:A:708:VAL:HG23	1.92	0.51
1:A:661:HIS:HB3	2:A:827:HOH:O	2.13	0.49
1:A:445:LEU:HD22	1:A:489:VAL:HG11	1.95	0.48
1:A:617:SER:O	1:A:621:GLN:HG3	2.16	0.46
1:A:715:ARG:O	1:A:719:THR:HG23	2.15	0.46
1:A:727:LEU:HD22	1:A:731:TRP:CD1	2.51	0.46
1:A:709:GLU:CG	2:A:896:HOH:O	2.58	0.46
1:A:663:GLN:HG2	2:A:815:HOH:O	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:495:LYS:CG	2:A:899:HOH:O	2.60	0.45
1:A:663:GLN:CG	2:A:815:HOH:O	2.65	0.45
1:A:674:GLN:HE21	1:A:674:GLN:HA	1.82	0.44
1:A:702:LEU:HD13	1:A:707:LEU:HD23	2.00	0.44
1:A:576:LEU:HD12	1:A:579:LEU:HD22	2.00	0.44
1:A:602:ILE:HG13	1:A:603:THR:N	2.29	0.43
1:A:674:GLN:NE2	2:A:890:HOH:O	2.51	0.43
1:A:489:VAL:HG11	1:A:494:LEU:HD13	1.99	0.43
1:A:702:LEU:HD13	1:A:707:LEU:CD2	2.50	0.42
1:A:703:MET:SD	1:A:703:MET:N	2.93	0.41
1:A:727:LEU:HD22	1:A:731:TRP:HD1	1.86	0.41
1:A:674:GLN:HA	1:A:674:GLN:NE2	2.36	0.41

All (2) 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)
2:A:991:HOH:O	2:A:997:HOH:O[12_564]	1.93	0.27
2:A:753:HOH:O	2:A:1002:HOH:O[8_665]	2.13	0.07

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	262/303 (86%)	261 (100%)	0	1 (0%)	30 27

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	703	MET

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	245/273 (90%)	232 (95%)	13 (5%)	20	18

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	458	SER
1	A	462	LYS
1	A	486	GLU
1	A	491	LYS
1	A	494	LEU
1	A	506	ARG
1	A	513	LYS
1	A	561	SER
1	A	574	GLU
1	A	579	LEU
1	A	602	ILE
1	A	703	MET
1	A	727	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	595	ASN
1	A	606	GLN
1	A	674	GLN
1	A	706	HIS
1	A	725	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](#)

There are no ligands in this entry.

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

6.1 Protein, DNA and RNA chains

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	270/303 (89%)	1.74	92 (34%) 1 1	32, 45, 59, 76	0

All (92) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	703	MET	5.7
1	A	492	ASP	5.3
1	A	678	GLU	5.3
1	A	514	GLY	5.3
1	A	581	GLN	5.3
1	A	512	VAL	5.0
1	A	502	LEU	4.7
1	A	551	ASP	4.2
1	A	489	VAL	4.2
1	A	561	SER	4.2
1	A	510	ASP	4.2
1	A	495	LYS	4.1
1	A	506	ARG	4.1
1	A	513	LYS	4.1
1	A	511	TYR	3.9
1	A	642	ARG	3.9
1	A	509	GLU	3.8
1	A	705	GLU	3.7
1	A	578	THR	3.6
1	A	565	ALA	3.6
1	A	579	LEU	3.5
1	A	546	ILE	3.5
1	A	458	SER	3.5
1	A	484	GLU	3.3
1	A	709	GLU	3.3
1	A	701	SER	3.3
1	A	680	THR	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	552	GLN	3.3
1	A	490	ASP	3.3
1	A	704	ASP	3.3
1	A	731	TRP	3.2
1	A	585	PRO	3.2
1	A	445	LEU	3.0
1	A	560	GLY	3.0
1	A	486	GLU	3.0
1	A	479	ALA	2.9
1	A	580	SER	2.9
1	A	562	LEU	2.9
1	A	563	VAL	2.9
1	A	459	ALA	2.8
1	A	654	THR	2.7
1	A	577	VAL	2.7
1	A	574	GLU	2.7
1	A	491	LYS	2.7
1	A	533	ASN	2.7
1	A	471	SER	2.7
1	A	702	LEU	2.6
1	A	464	LEU	2.6
1	A	569	LEU	2.6
1	A	605	SER	2.6
1	A	638	GLN	2.5
1	A	626	ILE	2.5
1	A	688	VAL	2.5
1	A	550	LEU	2.5
1	A	539	VAL	2.4
1	A	665	MET	2.4
1	A	452	LEU	2.4
1	A	657	TYR	2.4
1	A	500	LEU	2.3
1	A	555	SER	2.3
1	A	568	HIS	2.3
1	A	473	LEU	2.3
1	A	717	LEU	2.3
1	A	571	THR	2.3
1	A	664	MET	2.3
1	A	498	ASN	2.3
1	A	659	ALA	2.3
1	A	661	HIS	2.2
1	A	463	GLN	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	499	SER	2.2
1	A	653	GLY	2.2
1	A	673	LEU	2.2
1	A	572	LEU	2.2
1	A	544	GLN	2.2
1	A	725	ASN	2.2
1	A	681	ASP	2.2
1	A	460	ALA	2.2
1	A	593	PHE	2.1
1	A	655	GLU	2.1
1	A	535	MET	2.1
1	A	493	GLN	2.1
1	A	549	HIS	2.1
1	A	449	SER	2.1
1	A	557	SER	2.1
1	A	586	VAL	2.1
1	A	441	THR	2.1
1	A	443	LYS	2.1
1	A	640	LEU	2.0
1	A	559	ILE	2.0
1	A	536	LEU	2.0
1	A	576	LEU	2.0
1	A	727	LEU	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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.