



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:47 AM UTC

PDB ID : 8EEC / pdb_00008eec
Title : Crystal structure of HPK1 citron-homology domain
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Deposited on : 2022-09-06
Resolution : 2.50 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
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (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

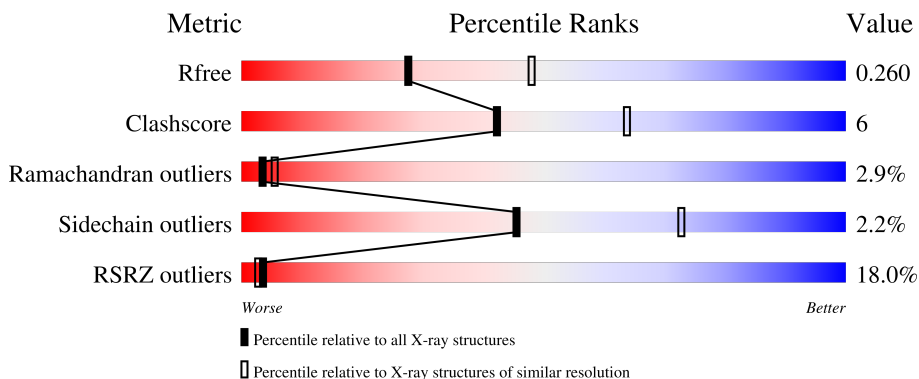
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	343	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 2553 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 Isoform 2 of Mitogen-activated protein kinase kinase kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	317	2429	1553	415	444	17	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	479	GLY	-	expression tag	UNP Q92918
A	480	SER	-	expression tag	UNP Q92918
A	593	ALA	ARG	conflict	UNP Q92918

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O P		
2	A	1	5	4 1	0	0

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		
2	A	1	Total	O	P	0	0
			5	4	1		

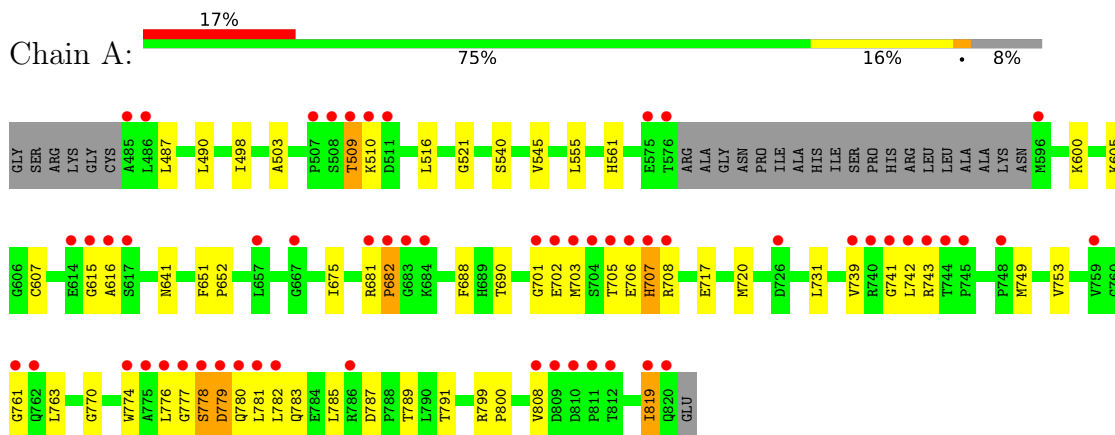
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	94	Total	O	0	0
			94	94		

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: Isoform 2 of Mitogen-activated protein kinase kinase kinase kinase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	81.67Å 81.67Å 140.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.61 – 2.50 44.61 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.61-2.50) 100.0 (44.61-2.50)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.65 (at 2.51Å)	Xtrriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.208 , 0.257 0.213 , 0.260	Depositor DCC
R_{free} test set	866 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtrriage
Anisotropy	0.298	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 56.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	2553	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.67% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4

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	0.38	1/2486 (0.0%)	0.73	2/3388 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	783	GLN	CD-OE1	5.23	1.33	1.23

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	770	GLY	N-CA-C	6.54	120.29	110.75
1	A	761	GLY	N-CA-C	-5.24	108.02	115.30

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	2429	0	2466	30	0
2	A	30	0	0	1	0
3	A	94	0	0	3	1
All	All	2553	0	2466	31	1

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 6.

All (31) 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:503:ALA:HB2	1:A:800:PRO:HD3	1.73	0.70
1:A:490:LEU:HD11	1:A:819:ILE:HG23	1.74	0.67
1:A:641:ASN:ND2	3:A:1003:HOH:O	2.22	0.64
2:A:905:PO4:O3	3:A:1001:HOH:O	2.16	0.60
1:A:509:THR:HG22	1:A:510:LYS:H	1.68	0.58
1:A:779:ASP:N	1:A:779:ASP:OD1	2.38	0.56
1:A:605:LYS:O	3:A:1002:HOH:O	2.17	0.54
1:A:774:TRP:CH2	1:A:781:LEU:HD13	2.48	0.49
1:A:717:GLU:HB2	1:A:720:MET:HB3	1.94	0.48
1:A:701:GLY:C	1:A:703:MET:H	2.22	0.48
1:A:615:GLY:HA3	1:A:616:ALA:HA	1.51	0.47
1:A:555:LEU:HD11	1:A:607:CYS:HB3	1.96	0.47
1:A:741:GLY:HA2	1:A:742:LEU:HA	1.64	0.47
1:A:749:MET:SD	1:A:753:VAL:HG21	2.55	0.47
1:A:799:ARG:HA	1:A:800:PRO:HA	1.66	0.47
1:A:701:GLY:O	1:A:703:MET:N	2.42	0.46
1:A:688:PHE:HB3	1:A:690:THR:HG23	1.98	0.46
1:A:742:LEU:HB3	1:A:743:ARG:H	1.49	0.46
1:A:521:GLY:HA2	1:A:540:SER:O	2.16	0.45
1:A:706:GLU:O	1:A:708:ARG:N	2.49	0.45
1:A:791:THR:OG1	1:A:808:VAL:HG22	2.16	0.45
1:A:498:ILE:HD13	1:A:516:LEU:HD23	2.00	0.44
1:A:787:ASP:OD2	1:A:789:THR:OG1	2.22	0.44
1:A:777:GLY:O	1:A:778:SER:HB3	2.18	0.43
1:A:731:LEU:O	1:A:739:VAL:HG22	2.19	0.42
1:A:707:HIS:HB2	1:A:708:ARG:H	1.68	0.41
1:A:681:ARG:HA	1:A:682:PRO:HD3	1.93	0.41
1:A:490:LEU:HG	1:A:819:ILE:HG12	2.02	0.41
1:A:763:LEU:HB3	1:A:774:TRP:HB2	2.02	0.41
1:A:651:PHE:HA	1:A:652:PRO:HD3	1.92	0.40
1:A:561:HIS:CD2	1:A:600:LYS:HD3	2.56	0.40

All (1) 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)
3:A:1028:HOH:O	3:A:1078:HOH:O[4_564]	2.05	0.15

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	313/343 (91%)	285 (91%)	19 (6%)	9 (3%)	3 5

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	778	SER
1	A	705	THR
1	A	707	HIS
1	A	702	GLU
1	A	776	LEU
1	A	682	PRO
1	A	779	ASP
1	A	782	LEU
1	A	780	GLN

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	273/292 (94%)	267 (98%)	6 (2%)	45 73

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	487	LEU
1	A	509	THR
1	A	545	VAL
1	A	675	ILE
1	A	785	LEU
1	A	819	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

6 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	PO4	A	905	-	4,4,4	0.92	0	6,6,6	0.47	0
2	PO4	A	903	-	4,4,4	0.92	0	6,6,6	0.50	0
2	PO4	A	906	-	4,4,4	0.95	0	6,6,6	0.43	0
2	PO4	A	901	-	4,4,4	0.96	0	6,6,6	0.45	0
2	PO4	A	902	-	4,4,4	0.97	0	6,6,6	0.51	0
2	PO4	A	904	-	4,4,4	0.94	0	6,6,6	0.47	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	905	PO4	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

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	317/343 (92%)	0.75	57 (17%) 3 3	27, 48, 118, 145	0

All (57) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	779	ASP	6.4
1	A	778	SER	6.0
1	A	776	LEU	6.0
1	A	616	ALA	5.7
1	A	742	LEU	4.9
1	A	707	HIS	4.8
1	A	777	GLY	4.8
1	A	744	THR	4.8
1	A	774	TRP	4.6
1	A	780	GLN	4.5
1	A	703	MET	4.2
1	A	781	LEU	4.1
1	A	596	MET	4.0
1	A	615	GLY	3.9
1	A	782	LEU	3.7
1	A	509	THR	3.6
1	A	708	ARG	3.6
1	A	809	ASP	3.6
1	A	775	ALA	3.5
1	A	705	THR	3.4
1	A	683	GLY	3.4
1	A	745	PRO	3.4
1	A	576	THR	3.3
1	A	701	GLY	3.3
1	A	811	PRO	3.3
1	A	485	ALA	3.3
1	A	739	VAL	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	575	GLU	3.1
1	A	617	SER	3.0
1	A	812	THR	3.0
1	A	808	VAL	2.9
1	A	706	GLU	2.9
1	A	486	LEU	2.9
1	A	510	LYS	2.8
1	A	702	GLU	2.8
1	A	820	GLN	2.8
1	A	684	LYS	2.8
1	A	511	ASP	2.8
1	A	704	SER	2.8
1	A	759	VAL	2.7
1	A	614	GLU	2.7
1	A	786	ARG	2.6
1	A	741	GLY	2.6
1	A	681	ARG	2.5
1	A	667	GLY	2.5
1	A	743	ARG	2.4
1	A	682	PRO	2.4
1	A	740	ARG	2.3
1	A	762	GLN	2.3
1	A	657	LEU	2.3
1	A	507	PRO	2.3
1	A	810	ASP	2.2
1	A	761	GLY	2.1
1	A	508	SER	2.1
1	A	819	ILE	2.1
1	A	726	ASP	2.1
1	A	748	PRO	2.1

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(Å ²)	Q<0.9
2	PO4	A	901	5/5	0.68	0.17	121,123,123,125	0
2	PO4	A	905	5/5	0.72	0.18	92,95,96,98	0
2	PO4	A	906	5/5	0.79	0.11	92,92,94,96	0
2	PO4	A	902	5/5	0.82	0.17	78,79,80,81	0
2	PO4	A	903	5/5	0.85	0.13	93,94,96,100	0
2	PO4	A	904	5/5	0.90	0.12	89,93,93,94	0

6.5 Other polymers [i](#)

There are no such residues in this entry.