



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 06:50 PM UTC

PDB ID : 9BPN / pdb_00009bpn
Title : Crystal structure of the allosteric MKP5 mutant Y435W
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Deposited on : 2024-05-07
Resolution : 2.40 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

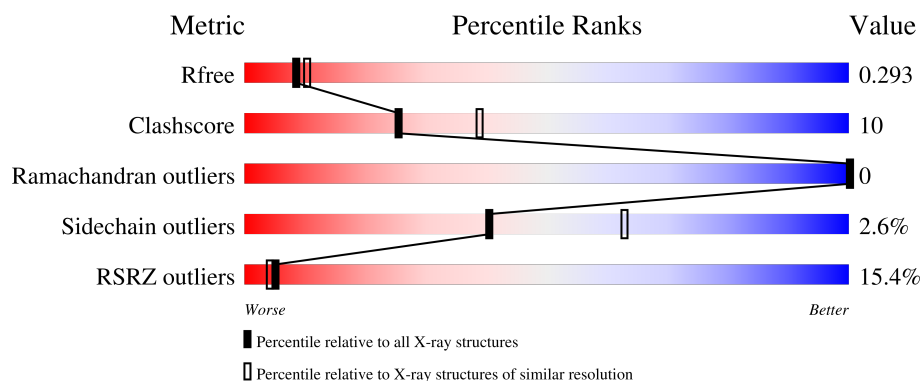
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	148	26% 69% 26% • •
1	B	148	5% 87% 11% •

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4412 atoms, of which 2120 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 Dual specificity protein phosphatase 10.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	144	Total	C	H	N	O	S	0	0	0
			2051	688	973	181	202	7			
1	B	148	Total	C	H	N	O	S	0	0	0
			2326	759	1147	198	214	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	319	MET	-	initiating methionine	UNP Q9Y6W6
A	435	TRP	TYR	engineered mutation	UNP Q9Y6W6
B	319	MET	-	initiating methionine	UNP Q9Y6W6
B	435	TRP	TYR	engineered mutation	UNP Q9Y6W6

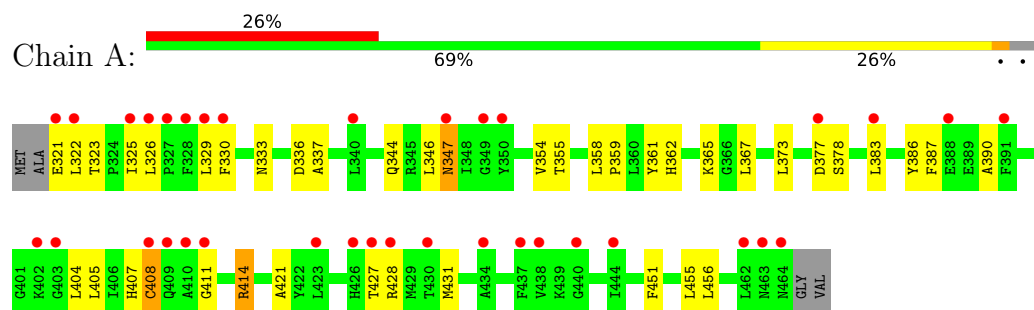
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	12	Total	O	0	0
			12	12		
2	B	23	Total	O	0	0
			23	23		

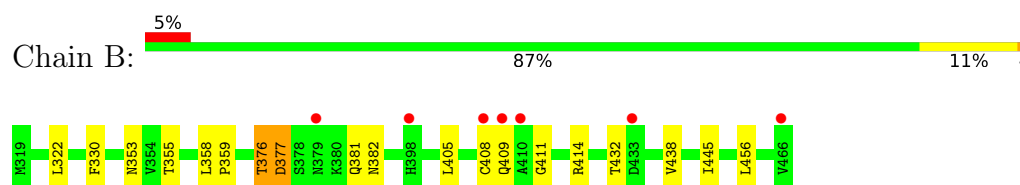
3 Residue-property plots [i](#)

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: Dual specificity protein phosphatase 10



- Molecule 1: Dual specificity protein phosphatase 10



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	97.86Å 44.74Å 87.33Å 90.00° 109.04° 90.00°	Depositor
Resolution (Å)	28.00 – 2.40 28.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	99.9 (28.00-2.40) 99.8 (28.00-2.40)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.66 (at 2.39Å)	Xtriage
Refinement program	PHENIX (1.18_3845: ???)	Depositor
R, R_{free}	0.226 , 0.288 0.235 , 0.293	Depositor DCC
R_{free} test set	699 reflections (4.90%)	wwPDB-VP
Wilson B-factor (Å ²)	43.0	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 45.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	4412	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.35% 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

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	0.63	1/1101 (0.1%)	0.79	1/1501 (0.1%)
1	B	0.77	0/1206	0.85	0/1633
All	All	0.71	1/2307 (0.0%)	0.83	1/3134 (0.0%)

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 (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	347	ASN	N-CA	-5.91	1.37	1.46

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	408	CYS	N-CA-C	-5.17	99.80	110.80

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	414	ARG	Sidechain

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	1078	973	986	31	0
1	B	1179	1147	1149	12	0
2	A	12	0	0	0	0
2	B	23	0	0	0	0
All	All	2292	2120	2135	42	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 10.

All (42) 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:431:MET:HE1	1:A:456:LEU:HD23	1.50	0.91
1:A:431:MET:HE2	1:A:455:LEU:HB3	1.70	0.73
1:A:431:MET:CE	1:A:456:LEU:HD23	2.21	0.71
1:A:322:LEU:O	1:A:322:LEU:HD23	1.91	0.69
1:A:323:THR:HG22	1:A:325:ILE:HD13	1.75	0.69
1:A:355:THR:HG22	1:A:414:ARG:HH11	1.60	0.67
1:A:322:LEU:HD12	1:A:405:LEU:HD13	1.77	0.66
1:A:431:MET:HE2	1:A:455:LEU:CB	2.28	0.63
1:A:390:ALA:O	1:A:394:ILE:HG13	1.99	0.63
1:A:337:ALA:HB2	1:A:407:HIS:CD2	2.34	0.62
1:A:355:THR:HG21	1:A:358:LEU:HD12	1.79	0.62
1:B:408:CYS:SG	1:B:411:GLY:N	2.73	0.62
1:A:321:GLU:HA	1:A:321:GLU:OE1	2.00	0.62
1:B:438:VAL:HG12	1:B:445:ILE:HD13	1.83	0.60
1:A:322:LEU:HD21	1:A:330:PHE:CB	2.33	0.58
1:B:322:LEU:HD11	1:B:405:LEU:HD13	1.89	0.55
1:B:377:ASP:OD2	1:B:414:ARG:NH1	2.45	0.50
1:B:355:THR:HG21	1:B:358:LEU:HD12	1.94	0.50
1:B:376:THR:HG22	1:B:381:GLN:OE1	2.11	0.50
1:B:408:CYS:SG	1:B:409:GLN:N	2.84	0.50
1:A:322:LEU:HD11	1:A:330:PHE:CB	2.41	0.50
1:A:333:ASN:OD1	1:A:336:ASP:CG	2.55	0.49
1:A:359:PRO:HG2	1:A:361:TYR:CE1	2.48	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:355:THR:HG22	1:A:414:ARG:NH1	2.27	0.49
1:B:330:PHE:CD2	1:B:330:PHE:N	2.81	0.48
1:A:383:LEU:HG	1:A:451:PHE:CE2	2.49	0.48
1:A:387:PHE:CE2	1:A:421:ALA:CB	2.98	0.47
1:A:329:LEU:HD23	1:A:330:PHE:N	2.30	0.46
1:A:325:ILE:O	1:A:326:LEU:HD23	2.15	0.46
1:A:408:CYS:SG	1:A:411:GLY:N	2.84	0.45
1:B:456:LEU:HD23	1:B:456:LEU:HA	1.89	0.45
1:A:373:LEU:HD22	1:A:386:TYR:HB3	2.00	0.44
1:A:346:LEU:O	1:A:347:ASN:CB	2.64	0.44
1:A:365:LYS:HB3	1:A:367:LEU:HG	2.00	0.44
1:A:354:VAL:HG22	1:A:373:LEU:HD12	2.00	0.43
1:A:427:THR:HG22	1:A:428:ARG:N	2.34	0.43
1:A:361:TYR:O	1:A:362:HIS:HB2	2.19	0.43
1:A:322:LEU:HD23	1:A:322:LEU:C	2.44	0.42
1:A:394:ILE:HA	1:A:404:LEU:HD13	2.02	0.41
1:B:382:ASN:OD1	1:B:382:ASN:C	2.64	0.41
1:B:353:ASN:OD1	1:B:353:ASN:C	2.63	0.40
1:A:359:PRO:HB3	1:B:359:PRO:HD3	2.03	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

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	142/148 (96%)	131 (92%)	11 (8%)	0	100	100
1	B	146/148 (99%)	138 (94%)	8 (6%)	0	100	100
All	All	288/296 (97%)	269 (93%)	19 (7%)	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	104/130 (80%)	101 (97%)	3 (3%)	37	60
1	B	124/130 (95%)	121 (98%)	3 (2%)	43	65
All	All	228/260 (88%)	222 (97%)	6 (3%)	40	63

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

Mol	Chain	Res	Type
1	A	344	GLN
1	A	377	ASP
1	A	378	SER
1	B	376	THR
1	B	377	ASP
1	B	432	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	338	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

There are no ligands in this entry.

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

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	144/148 (97%)	1.44	38 (26%) 1 1	42, 67, 95, 141	0
1	B	148/148 (100%)	0.38	7 (4%) 36 32	31, 45, 58, 82	0
All	All	292/296 (98%)	0.90	45 (15%) 5 4	31, 53, 91, 141	0

All (45) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	428	ARG	4.2
1	A	399	GLN	4.2
1	A	322	LEU	4.1
1	A	328	PHE	4.1
1	A	462	LEU	3.6
1	A	410	ALA	3.6
1	A	321	GLU	3.4
1	A	398	HIS	3.3
1	A	326	LEU	3.3
1	A	463	ASN	3.2
1	A	423	LEU	3.2
1	B	410	ALA	3.2
1	A	427	THR	3.0
1	A	349	GLY	2.8
1	B	466	VAL	2.8
1	A	388	GLU	2.8
1	A	444	ILE	2.7
1	A	403	GLY	2.7
1	B	409	GLN	2.7
1	B	398	HIS	2.7
1	A	438	VAL	2.6
1	A	426	HIS	2.6
1	A	430	THR	2.5
1	A	340	LEU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	350	TYR	2.5
1	A	347	ASN	2.4
1	A	437	PHE	2.4
1	B	408	CYS	2.3
1	A	411	GLY	2.3
1	A	329	LEU	2.3
1	A	408	CYS	2.3
1	A	464	ASN	2.3
1	A	402	LYS	2.3
1	A	409	GLN	2.3
1	A	440	GLY	2.3
1	A	400	CYS	2.3
1	B	379	ASN	2.2
1	A	377	ASP	2.2
1	B	433	ASP	2.1
1	A	327	PRO	2.1
1	A	391	PHE	2.1
1	A	330	PHE	2.1
1	A	383	LEU	2.0
1	A	434	ALA	2.0
1	A	325	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 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.