



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 26, 2026 – 07:37 AM UTC

PDB ID : 1MRV / pdb_00001mrv
Title : crystal structure of an inactive Akt2 kinase domain
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Deposited on : 2002-09-18
Resolution : 2.80 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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

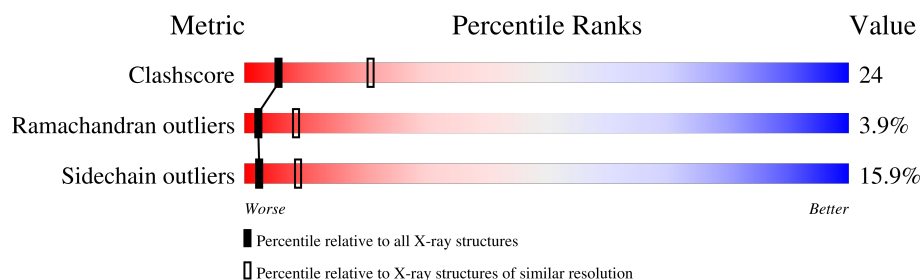
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)

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 $\leq 5\%$

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	339	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2150 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 RAC-beta serine/threonine kinase.

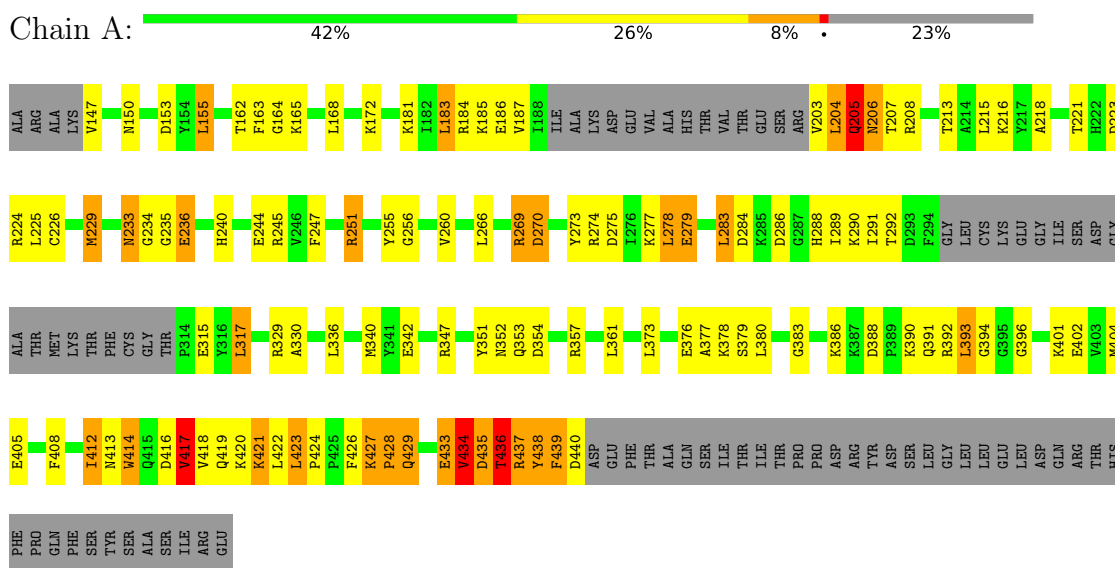
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	261	Total	C	N	O	S	0	0	0
			2076	1348	352	365	11			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	74	Total	O	0	0
			74	74		

Note EDS was not executed.

- Molecule 1: RAC-beta serine/threonine kinase



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	150.44Å 150.44Å 40.18Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	100.00 – 2.80	Depositor
% Data completeness (in resolution range)	94.4 (100.00-2.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.247 , 0.295	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2150	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

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	0.58	1/2126 (0.0%)	1.01	8/2871 (0.3%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	417	VAL	CA-CB	5.15	1.60	1.54

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	206	ASN	N-CA-C	7.59	122.57	113.16
1	A	164	GLY	N-CA-C	7.23	121.23	110.97
1	A	414	TRP	N-CA-C	5.91	117.72	111.28
1	A	394	GLY	N-CA-C	-5.30	108.77	115.08
1	A	439	PHE	N-CA-C	-5.22	106.17	112.54
1	A	427	LYS	CA-C-N	5.22	126.36	119.84
1	A	427	LYS	C-N-CA	5.22	126.36	119.84
1	A	234	GLY	N-CA-C	-5.09	104.21	112.31

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	2076	0	2004	96	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	74	0	0	5	0
All	All	2150	0	2004	96	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 24.

All (96) 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:205:GLN:HG2	1:A:206:ASN:H	1.19	1.02
1:A:413:ASN:HD22	1:A:416:ASP:CB	1.94	0.81
1:A:279:GLU:CD	1:A:279:GLU:H	1.90	0.77
1:A:256:GLY:O	1:A:260:VAL:HG23	1.86	0.76
1:A:205:GLN:HG2	1:A:206:ASN:N	1.99	0.74
1:A:213:THR:HG21	1:A:292:THR:HG22	1.69	0.74
1:A:205:GLN:CG	1:A:206:ASN:H	2.01	0.73
1:A:153:ASP:OD1	1:A:172:LYS:HD2	1.90	0.72
1:A:186:GLU:HA	2:A:66:HOH:O	1.90	0.71
1:A:422:LEU:HD12	1:A:422:LEU:H	1.56	0.71
1:A:203:VAL:O	1:A:204:LEU:HB2	1.88	0.71
1:A:163:PHE:O	1:A:183:LEU:HD12	1.90	0.70
1:A:422:LEU:HD12	1:A:422:LEU:N	2.09	0.68
1:A:357:ARG:O	1:A:361:LEU:HG	1.93	0.68
1:A:401:LYS:O	1:A:405:GLU:HG2	1.94	0.67
1:A:184:ARG:HB3	1:A:187:VAL:CB	2.25	0.66
1:A:233:ASN:OD1	1:A:433:GLU:HA	1.96	0.65
1:A:203:VAL:HA	1:A:205:GLN:HE22	1.62	0.65
1:A:373:LEU:O	1:A:378:LYS:HE3	1.99	0.62
1:A:436:THR:O	1:A:436:THR:HG23	2.00	0.62
1:A:244:GLU:O	1:A:245:ARG:HB3	2.00	0.62
1:A:315:GLU:CG	1:A:317:LEU:HD13	2.29	0.61
1:A:373:LEU:HD23	1:A:378:LYS:HG2	1.81	0.61
1:A:416:ASP:HA	1:A:421:LYS:HE3	1.83	0.61
1:A:236:GLU:H	1:A:236:GLU:CD	2.08	0.60
1:A:419:GLN:HB2	1:A:421:LYS:HG3	1.85	0.59
1:A:185:LYS:HG2	1:A:225:LEU:HD13	1.83	0.58
1:A:417:VAL:HA	1:A:422:LEU:HD13	1.87	0.56
1:A:185:LYS:HE2	1:A:225:LEU:CD1	2.35	0.56
1:A:203:VAL:HA	1:A:205:GLN:NE2	2.20	0.56
1:A:435:ASP:O	1:A:437:ARG:N	2.39	0.56
1:A:277:LYS:HD2	1:A:279:GLU:HG2	1.88	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:251:ARG:NH1	1:A:255:TYR:OH	2.38	0.55
1:A:373:LEU:HD23	1:A:378:LYS:CG	2.36	0.55
1:A:207:THR:HG21	1:A:266:LEU:HD23	1.88	0.55
1:A:279:GLU:CD	1:A:279:GLU:N	2.64	0.55
1:A:388:ASP:OD2	1:A:391:GLN:HG2	2.07	0.55
1:A:273:TYR:O	1:A:274:ARG:HB2	2.07	0.54
1:A:428:PRO:O	1:A:429:GLN:CB	2.55	0.54
1:A:275:ASP:CB	2:A:65:HOH:O	2.56	0.53
1:A:286:ASP:O	1:A:424:PRO:HG2	2.07	0.53
1:A:380:LEU:HD22	1:A:408:PHE:CD2	2.43	0.53
1:A:421:LYS:HB2	1:A:421:LYS:HZ2	1.73	0.52
1:A:315:GLU:HG2	1:A:317:LEU:HD13	1.91	0.52
1:A:284:ASP:OD1	1:A:288:HIS:N	2.44	0.51
1:A:404:MET:HG2	1:A:414:TRP:CE2	2.47	0.50
1:A:155:LEU:HB2	1:A:168:LEU:O	2.11	0.50
1:A:373:LEU:HG	1:A:377:ALA:HB3	1.93	0.50
1:A:422:LEU:H	1:A:422:LEU:CD1	2.24	0.50
1:A:435:ASP:C	1:A:437:ARG:H	2.19	0.49
1:A:336:LEU:O	1:A:340:MET:HG2	2.12	0.49
1:A:413:ASN:HB3	1:A:416:ASP:CB	2.43	0.49
1:A:329:ARG:NH2	1:A:396:GLY:O	2.46	0.49
1:A:221:THR:OG1	1:A:224:ARG:HB2	2.12	0.48
1:A:215:LEU:HD12	1:A:229:MET:HG3	1.96	0.48
1:A:315:GLU:HG3	1:A:317:LEU:HD13	1.95	0.48
1:A:383:GLY:HA2	1:A:386:LYS:NZ	2.29	0.47
1:A:244:GLU:O	1:A:245:ARG:CB	2.62	0.47
1:A:347:ARG:HD2	1:A:351:TYR:CE2	2.49	0.47
1:A:186:GLU:O	1:A:187:VAL:C	2.58	0.47
1:A:207:THR:HG21	1:A:266:LEU:CD2	2.45	0.47
1:A:434:VAL:O	1:A:436:THR:N	2.48	0.47
1:A:437:ARG:HG2	1:A:438:TYR:N	2.29	0.47
1:A:396:GLY:HA3	1:A:402:GLU:OE1	2.15	0.46
1:A:352:ASN:O	1:A:353:GLN:CG	2.64	0.46
1:A:329:ARG:NH1	2:A:72:HOH:O	2.48	0.46
1:A:423:LEU:HD22	1:A:424:PRO:HD2	1.98	0.46
1:A:419:GLN:O	1:A:420:LYS:HB2	2.17	0.45
1:A:236:GLU:OE1	1:A:236:GLU:N	2.39	0.45
1:A:347:ARG:HD2	1:A:351:TYR:CZ	2.52	0.45
1:A:277:LYS:HD2	1:A:279:GLU:CG	2.47	0.45
1:A:383:GLY:HA2	1:A:386:LYS:HZ2	1.82	0.44
1:A:439:PHE:O	1:A:440:ASP:CB	2.65	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:283:LEU:HD12	1:A:283:LEU:HA	1.85	0.44
1:A:437:ARG:O	1:A:439:PHE:N	2.50	0.44
1:A:390:LYS:HE2	1:A:390:LYS:HB2	1.86	0.44
1:A:269:ARG:O	1:A:270:ASP:HB2	2.18	0.44
1:A:422:LEU:N	1:A:422:LEU:CD1	2.80	0.44
1:A:235:GLY:H	1:A:240:HIS:HE1	1.65	0.43
1:A:235:GLY:H	1:A:240:HIS:CE1	2.37	0.43
1:A:236:GLU:CD	1:A:236:GLU:N	2.75	0.43
1:A:278:LEU:HD12	1:A:342:GLU:OE1	2.19	0.43
1:A:215:LEU:HD21	1:A:218:ALA:HB2	2.01	0.42
1:A:185:LYS:HD2	1:A:223:ASP:HA	2.00	0.42
1:A:290:LYS:HD2	2:A:6:HOH:O	2.18	0.42
1:A:213:THR:HG23	1:A:291:ILE:O	2.18	0.42
1:A:251:ARG:NH1	1:A:426:PHE:HB3	2.35	0.41
1:A:412:ILE:HG21	1:A:414:TRP:CE2	2.54	0.41
1:A:433:GLU:H	1:A:433:GLU:HG2	1.65	0.41
1:A:181:LYS:O	1:A:226:CYS:HA	2.20	0.41
1:A:284:ASP:O	1:A:428:PRO:HG2	2.21	0.41
1:A:393:LEU:HD23	1:A:393:LEU:HA	1.86	0.41
1:A:247:PHE:HB3	1:A:251:ARG:HG2	2.03	0.41
1:A:330:ALA:HB3	2:A:49:HOH:O	2.20	0.40
1:A:433:GLU:O	1:A:434:VAL:HG23	2.22	0.40
1:A:233:ASN:HD22	1:A:233:ASN:HA	1.64	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	255/339 (75%)	223 (88%)	22 (9%)	10 (4%)	2 8

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	205	GLN
1	A	354	ASP
1	A	429	GLN
1	A	434	VAL
1	A	436	THR
1	A	437	ARG
1	A	438	TYR
1	A	204	LEU
1	A	392	ARG
1	A	435	ASP

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	208/298 (70%)	175 (84%)	33 (16%)	2 9

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	147	VAL
1	A	150	ASN
1	A	155	LEU
1	A	162	THR
1	A	165	LYS
1	A	183	LEU
1	A	205	GLN
1	A	208	ARG
1	A	216	LYS
1	A	229	MET
1	A	233	ASN
1	A	236	GLU
1	A	251	ARG
1	A	269	ARG
1	A	270	ASP
1	A	278	LEU
1	A	279	GLU

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Mol	Chain	Res	Type
1	A	283	LEU
1	A	289	ILE
1	A	317	LEU
1	A	376	GLU
1	A	379	SER
1	A	393	LEU
1	A	412	ILE
1	A	417	VAL
1	A	418	VAL
1	A	421	LYS
1	A	423	LEU
1	A	427	LYS
1	A	428	PRO
1	A	433	GLU
1	A	434	VAL
1	A	436	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	205	GLN
1	A	220	GLN
1	A	233	ASN
1	A	240	HIS
1	A	288	HIS
1	A	325	ASN
1	A	413	ASN
1	A	415	GLN

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 ⓘ

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

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.