



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 05:15 AM GMT

PDB ID : 2PZY
Title : Structure of MK2 Complexed with Compound 76
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Deposited on : 2007-05-18
Resolution : 2.90 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

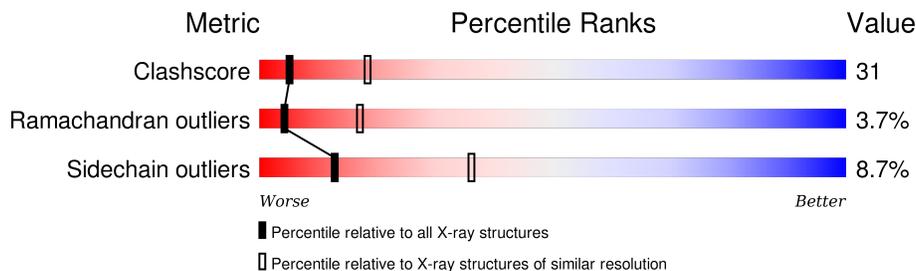
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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	102246	1668 (2.90-2.90)
Ramachandran outliers	100387	1630 (2.90-2.90)
Sidechain outliers	100360	1632 (2.90-2.90)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	324	
1	B	324	
1	C	324	
1	D	324	

2 Entry composition [i](#)

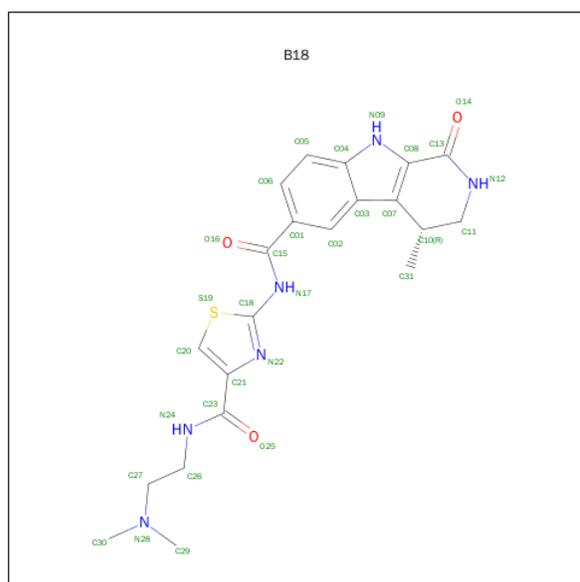
There are 3 unique types of molecules in this entry. The entry contains 9585 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 MAP kinase-activated protein kinase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	291	Total 2356	C 1509	N 405	O 425	S 17	0	0	0
1	B	283	Total 2300	C 1471	N 395	O 417	S 17	0	0	0
1	C	307	Total 2492	C 1590	N 428	O 456	S 18	0	0	0
1	D	288	Total 2340	C 1502	N 401	O 419	S 18	0	0	0

- Molecule 2 is (4R)-N-[4-({[2-(DIMETHYLAMINO)ETHYL]AMINO}CARBONYL)-1,3-THIAZOL-2-YL]-4-METHYL-1-OXO-2,3,4,9-TETRAHYDRO-1H-BETA-CARBOLINE-6-CARBOXAMIDE (three-letter code: B18) (formula: C₂₁H₂₄N₆O₃S).



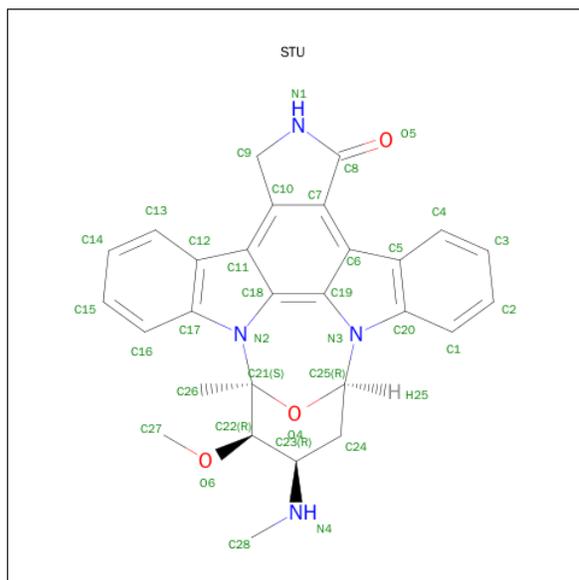
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	A	1	Total 31	C 21	N 6	O 3	S 1	0	0

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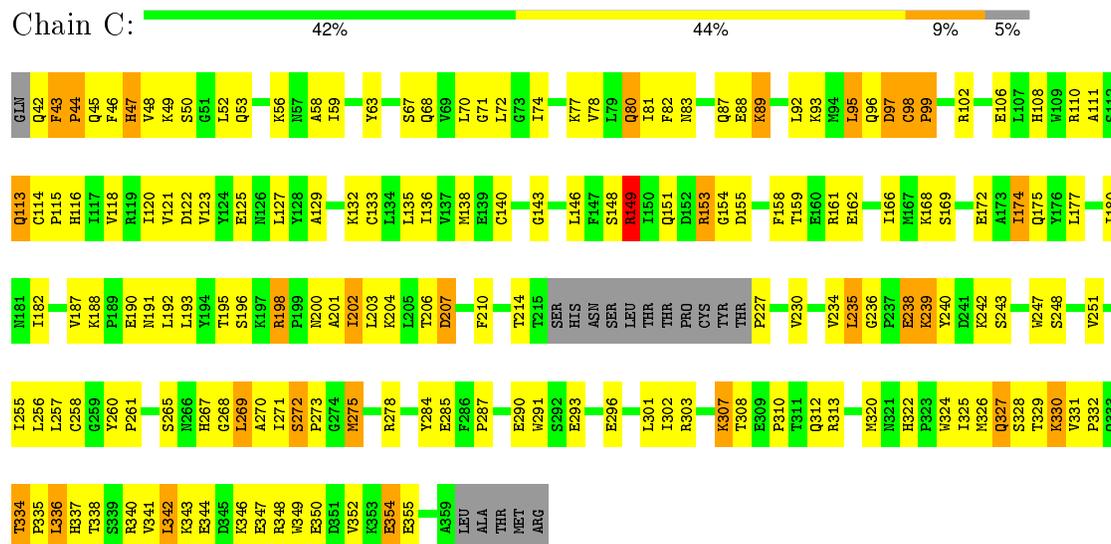
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
2	B	1	31	21	6	3	1	0	0

- Molecule 3 is STAUROSPORINE (three-letter code: STU) (formula: $C_{28}H_{26}N_4O_3$).

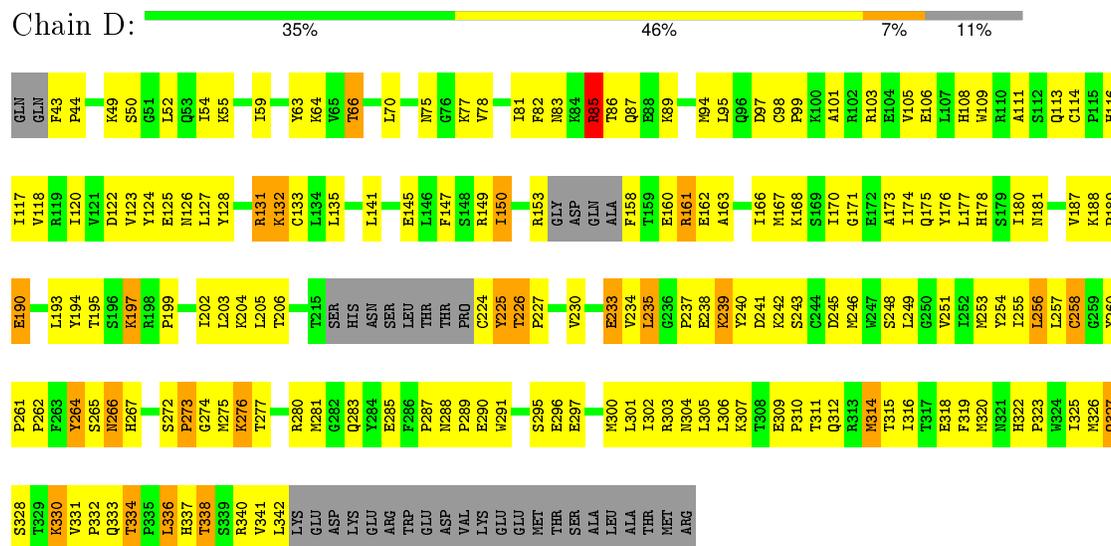


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
3	C	1	35	28	4	3	0	0	

- Molecule 1: MAP kinase-activated protein kinase 2



- Molecule 1: MAP kinase-activated protein kinase 2



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section will therefore be incomplete.

Property	Value	Source
Space group	P 63	Depositor
Cell constants a, b, c, α , β , γ	159.61Å 159.61Å 134.50Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	34.32 – 2.90	Depositor
% Data completeness (in resolution range)	(Not available) (34.32-2.90)	Depositor
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.251 , 0.313	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	9585	wwPDB-VP
Average B, all atoms (Å ²)	72.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: STU, B18

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	0.45	0/2409	0.60	0/3252
1	B	0.42	0/2350	0.63	0/3168
1	C	0.42	0/2548	0.61	0/3439
1	D	0.38	0/2394	0.57	0/3233
All	All	0.42	0/9701	0.60	0/13092

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
1	B	0	1
All	All	0	2

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	229	TYR	Sidechain
1	B	185	ARG	Peptide

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	2356	0	2375	141	0
1	B	2300	0	2328	129	0
1	C	2492	0	2501	167	1
1	D	2340	0	2368	187	1
2	A	31	0	24	0	0
2	B	31	0	24	0	0
3	C	35	0	26	8	0
All	All	9585	0	9646	590	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 31.

The worst 5 of 590 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:D:197:LYS:H	1:D:197:LYS:HD3	1.15	1.11
1:B:56:LYS:HG3	1:C:53:GLN:HG2	1.13	1.10
1:C:239:LYS:HG3	1:C:240:TYR:H	1.09	1.06
1:B:332:PRO:HB2	1:B:334:THR:HG22	1.38	1.06
1:C:149:ARG:HH11	1:C:149:ARG:HG2	0.91	1.05

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)
1:C:313:ARG:NH2	1:D:233:GLU:OE1[2_545]	2.19	0.01

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	285/324 (88%)	248 (87%)	31 (11%)	6 (2%)	9	32
1	B	277/324 (86%)	238 (86%)	32 (12%)	7 (2%)	7	27
1	C	303/324 (94%)	244 (80%)	45 (15%)	14 (5%)	3	11
1	D	282/324 (87%)	228 (81%)	39 (14%)	15 (5%)	2	8
All	All	1147/1296 (88%)	958 (84%)	147 (13%)	42 (4%)	4	17

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	238	GLU
1	A	239	LYS
1	A	330	LYS
1	A	345	ASP
1	B	239	LYS

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	261/293 (89%)	243 (93%)	18 (7%)	19	48
1	B	256/293 (87%)	231 (90%)	25 (10%)	10	30
1	C	276/293 (94%)	249 (90%)	27 (10%)	10	30
1	D	261/293 (89%)	239 (92%)	22 (8%)	14	37
All	All	1054/1172 (90%)	962 (91%)	92 (9%)	13	36

5 of 92 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	334	THR
1	C	149	ARG
1	D	276	LYS

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Mol	Chain	Res	Type
1	B	343	LYS
1	C	80	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	53	GLN
1	C	87	GLN
1	D	175	GLN
1	C	80	GLN
1	C	96	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 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	B18	A	1	-	28,34,34	2.46	8 (28%)	34,49,49	1.30	5 (14%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	B18	B	2	-	28,34,34	2.47	9 (32%)	34,49,49	1.23	5 (14%)
3	STU	C	3	-	27,42,42	1.91	4 (14%)	23,68,68	1.35	2 (8%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	B18	A	1	-	-	0/12/31/31	0/4/4/4
2	B18	B	2	-	-	0/12/31/31	0/4/4/4
3	STU	C	3	-	-	0/4/42/42	0/0/8/8

The worst 5 of 21 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	B18	C08-C13	-4.92	1.37	1.47
2	B	2	B18	C08-C13	-4.21	1.39	1.47
2	B	2	B18	C21-C23	-4.12	1.41	1.50
2	A	1	B18	C21-C23	-4.04	1.41	1.50
2	A	1	B18	C13-N12	2.11	1.36	1.34

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	B18	O14-C13-C08	-3.47	119.25	124.93
2	A	1	B18	C02-C03-C04	-3.42	118.99	120.34
2	B	2	B18	O14-C13-C08	-3.29	119.54	124.93
2	B	2	B18	C02-C03-C04	-2.88	119.20	120.34
3	C	3	STU	C24-C23-N4	-2.83	105.75	112.16

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	3	STU	8	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

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

6.3 Carbohydrates

EDS was not executed - this section will therefore be empty.

6.4 Ligands

EDS was not executed - this section will therefore be empty.

6.5 Other polymers

EDS was not executed - this section will therefore be empty.