



Full wwPDB X-ray Structure Validation Report i

Feb 27, 2014 – 03:03 AM GMT

PDB ID : 1PME
Title : STRUCTURE OF PENTA MUTANT HUMAN ERK2 MAP KINASE COM-
PLEXED WITH A SPECIFIC INHIBITOR OF HUMAN P38 MAP KINASE
Authors : Xie, X.
Deposited on : 1998-06-08
Resolution : 2.00 Å(reported)

This is a full wwPDB validation 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/ValidationPDFNotes.html>

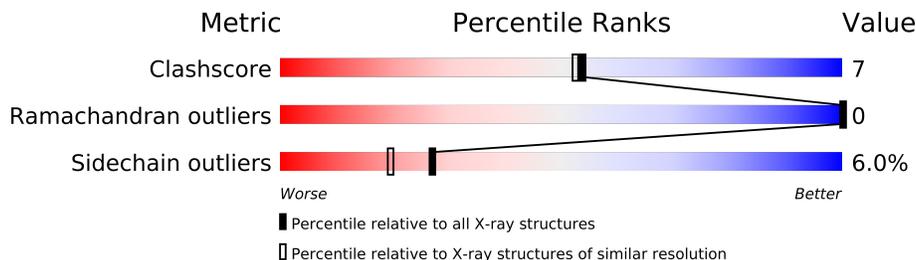
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 21963
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

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))
Clashscore	79885	6188 (2.00-2.00)
Ramachandran outliers	78287	6102 (2.00-2.00)
Sidechain outliers	78261	6100 (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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	380	

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2973 atoms, of which 0 are hydrogen and 0 are deuterium.

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.

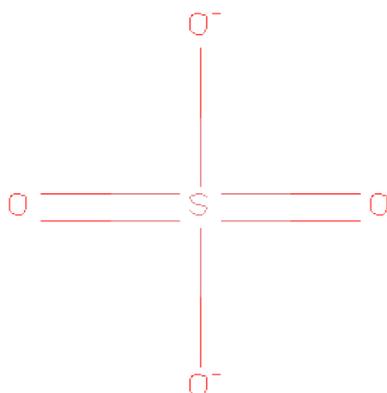
- Molecule 1 is a protein called ERK2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	334	2730	1758	471	487	14	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

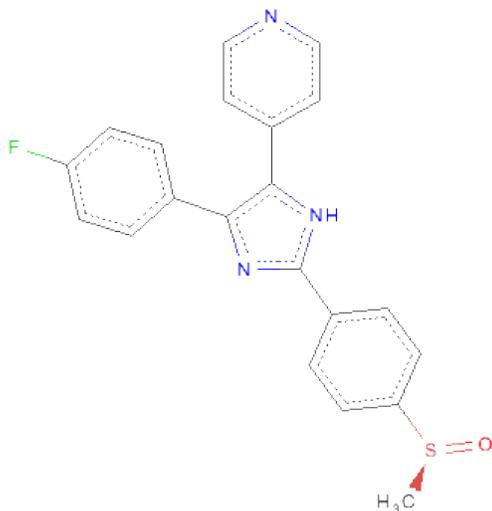
Chain	Residue	Modelled	Actual	Comment	Reference
A	103	LEU	ILE	ENGINEERED	UNP P28482
A	105	THR	GLN	ENGINEERED	UNP P28482
A	106	HIS	ASP	ENGINEERED	UNP P28482
A	109	GLY	GLU	ENGINEERED	UNP P28482
A	110	ALA	THR	ENGINEERED	UNP P28482
A	161	CME	CYS	MODIFIED	UNP P28482

- Molecule 2 is SULFATE ION (three-letter code: SO₄) (formula: O₄S).



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

- Molecule 3 is 4-[5-(4-FLUORO-PHENYL)-2-(4-METHANESULFINYL-PHENYL)-3H-IMIDAZOL-4-YL]-PYRIDINE (three-letter code: SB2) (formula: C₂₁H₁₆FN₃OS).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	
3	A	1	Total	C	F	N	O	S	0	0
			27	21	1	3	1	1		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	211	Total	O	0	0
			211	211		

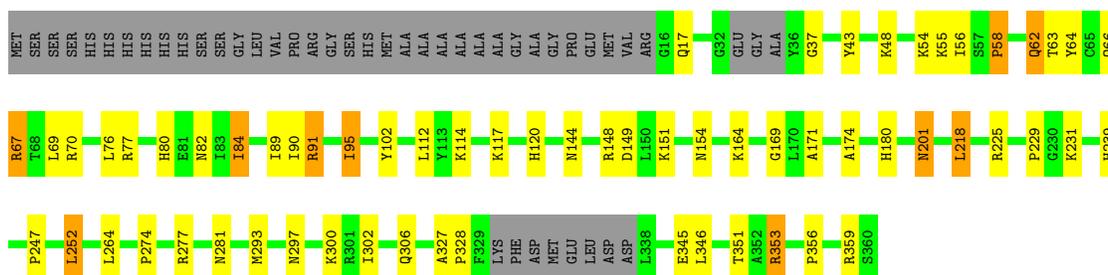
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

Note EDS was not executed.

- Molecule 1: ERK2

Chain A:



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	48.64Å 69.68Å 60.28Å 90.00° 109.25° 90.00°	Depositor
Resolution (Å)	6.00 – 2.00	Depositor
% Data completeness (in resolution range)	95.3 (6.00-2.00)	Depositor
R_{merge}	0.03	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.8	Depositor
R, R_{free}	0.212 , 0.273	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2973	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

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: SB2, CME, SO4

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	0.34	0/2786	0.65	0/3774

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2730	0	2742	38	0
2	A	5	0	0	0	0
3	A	27	0	16	1	0
4	A	211	0	0	4	0
All	All	2973	0	2758	38	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 7.

All (38) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:70:ARG:HD3	1:A:171:ALA:O	1.91	0.71
1:A:114:LYS:HA	1:A:117:LYS:HE2	1.80	0.62
1:A:95:ILE:HD11	1:A:345:GLU:HA	1.83	0.59
1:A:80:HIS:CD2	1:A:82:ASN:H	2.21	0.58
1:A:218:LEU:HD12	1:A:293:MET:CE	2.34	0.56
1:A:356:PRO:HA	1:A:359:ARG:HB3	1.88	0.56
1:A:239:HIS:HE1	4:A:2122:HOH:O	1.88	0.55
1:A:37:GLY:HA3	1:A:55:LYS:O	2.08	0.54
1:A:231:LYS:NZ	4:A:2122:HOH:O	2.40	0.54
1:A:56:ILE:HG22	1:A:58:PRO:HD3	1.90	0.54
1:A:80:HIS:HD2	1:A:82:ASN:H	1.56	0.53
1:A:180:HIS:HE1	4:A:2006:HOH:O	1.92	0.52
1:A:63:THR:O	1:A:66:GLN:HG2	2.10	0.52
1:A:144:ASN:ND2	1:A:174:ALA:HB3	2.25	0.52
1:A:247:PRO:HB2	1:A:252:LEU:HD13	1.93	0.50
1:A:225:ARG:NH2	1:A:229:PRO:HG3	2.26	0.50
1:A:148:ARG:HG2	1:A:148:ARG:HH11	1.79	0.48
1:A:91:ARG:HD3	1:A:351:THR:OG1	2.13	0.47
1:A:151:LYS:HE3	3:A:1001:SB2:C1	2.44	0.47
1:A:90:ILE:HB	1:A:102:TYR:HB2	1.98	0.46
1:A:43:TYR:OH	1:A:48:LYS:HD2	2.16	0.46
1:A:149:ASP:O	1:A:154:ASN:ND2	2.49	0.45
1:A:64:TYR:N	1:A:64:TYR:CD1	2.84	0.45
1:A:54:LYS:HE3	1:A:56:ILE:HD11	1.99	0.45
1:A:302:ILE:HG12	1:A:306:GLN:HB2	2.00	0.44
1:A:89:ILE:HD13	1:A:351:THR:HG22	1.99	0.43
1:A:297:ASN:HD22	1:A:300:LYS:HE3	1.83	0.43
1:A:302:ILE:CG1	1:A:306:GLN:HB2	2.48	0.43
1:A:239:HIS:CE1	4:A:2122:HOH:O	2.66	0.42
1:A:67:ARG:HG3	1:A:169:GLY:O	2.20	0.42
1:A:180:HIS:CE1	1:A:201:ASN:HB2	2.55	0.42
1:A:274:PRO:HB2	1:A:277:ARG:HB2	2.01	0.42
1:A:64:TYR:N	1:A:64:TYR:HD1	2.18	0.42
1:A:84:ILE:HD12	1:A:164:LYS:HB3	2.03	0.41
1:A:327:ALA:HA	1:A:328:PRO:HD2	1.87	0.41
1:A:201:ASN:N	1:A:201:ASN:HD22	2.18	0.41
1:A:76:LEU:HD23	1:A:353:ARG:CZ	2.51	0.41
1:A:62:GLN:HE21	1:A:62:GLN:HB3	1.70	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	327/380 (86%)	315 (96%)	12 (4%)	0	100 100

There are no Ramachandran outliers to report.

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	300/333 (90%)	282 (94%)	18 (6%)	27 20

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	58	PRO
1	A	62	GLN
1	A	67	ARG
1	A	69	LEU
1	A	77	ARG
1	A	84	ILE
1	A	91	ARG
1	A	95	ILE
1	A	112	LEU
1	A	120	HIS
1	A	201	ASN
1	A	218	LEU
1	A	252	LEU
1	A	264	LEU
1	A	281	ASN

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Mol	Chain	Res	Type
1	A	346	LEU
1	A	353	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	17	GLN
1	A	62	GLN
1	A	80	HIS
1	A	123	ASN
1	A	144	ASN
1	A	180	HIS
1	A	201	ASN
1	A	253	ASN
1	A	262	ASN

5.3.3 RNA ⓘ

There are no RNA chains in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is 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	$\# Z > 2$
1	CME	A	161	1	9,9,10	6.17	3 (33%)	7,9,11	2.71	3 (42%)

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
1	CME	A	161	1	-	0/6/8/10	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	161	CME	O-C	18.10	1.23	1.11
1	A	161	CME	CA-C	2.67	1.53	1.48
1	A	161	CME	CB-CA	2.55	1.57	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	161	CME	CB-SG-SD	5.12	114.08	103.87
1	A	161	CME	C-CA-N	3.71	117.53	113.83
1	A	161	CME	CB-CA-N	2.28	114.14	110.27

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

2 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
3	SB2	A	1001	-	29,30,30	1.75	4 (13%)	42,42,42	2.42	5 (11%)
2	SO4	A	3001	-	4,4,4	2.93	3 (75%)	6,6,6	0.29	0

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
3	SB2	A	1001	-	-	0/16/16/16	0/4/4/4
2	SO4	A	3001	-	-	0/0/0/0	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	1001	SB2	CC5-NC1	7.89	1.44	1.36
2	A	3001	SO4	O1-S	3.95	1.59	1.47
2	A	3001	SO4	O3-S	2.96	1.57	1.47
3	A	1001	SB2	CC4-NC3	2.56	1.44	1.37
2	A	3001	SO4	O2-S	2.55	1.55	1.47
3	A	1001	SB2	CA6-CC2	2.48	1.50	1.47
3	A	1001	SB2	FD3-CD3	-2.08	1.31	1.36

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	1001	SB2	C1-S1-CA3	10.58	128.46	98.41
3	A	1001	SB2	O2-S1-C1	9.61	119.72	105.55
3	A	1001	SB2	CA5-CA4-CA3	2.85	121.89	119.44
3	A	1001	SB2	CA6-CC2-NC1	2.65	125.98	121.22
3	A	1001	SB2	CA4-CA3-CA2	-2.08	118.06	120.87

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 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.