



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 04:04 am GMT

PDB ID : 5AX3
Title : Crystal structure of ERK2 complexed with allosteric and ATP-competitive inhibitors.
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Deposited on : 2015-07-14
Resolution : 2.98 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

<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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : recalc28949

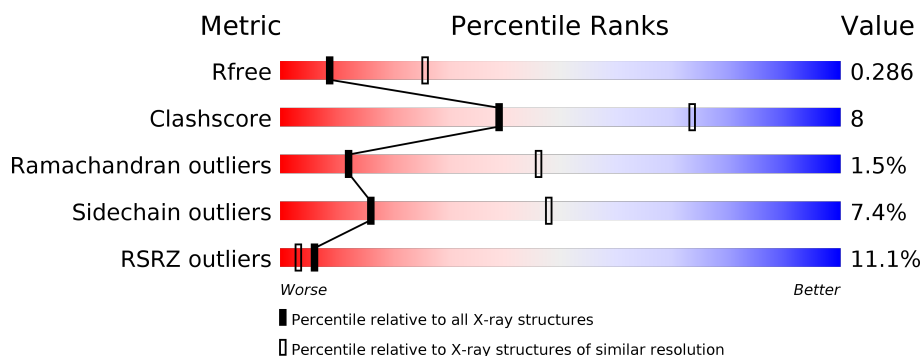
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.98 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}	100719	2168 (3.00-2.96)
Clashscore	112137	2535 (3.00-2.96)
Ramachandran outliers	110173	2451 (3.00-2.96)
Sidechain outliers	110143	2454 (3.00-2.96)
RSRZ outliers	101464	2192 (3.00-2.96)

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.

Mol	Chain	Length	Quality of chain
1	A	368	<div> <div>9%</div> <div> <div>67%</div> <div>20%</div> <div>•</div> <div>11%</div> </div> </div>
2	B	12	<div> <div>50%</div> <div> <div>67%</div> <div>17%</div> <div>8%</div> <div>8%</div> </div> </div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2831 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 Mitogen-activated protein kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	329	2705	1746	458	487	14	0	0	0

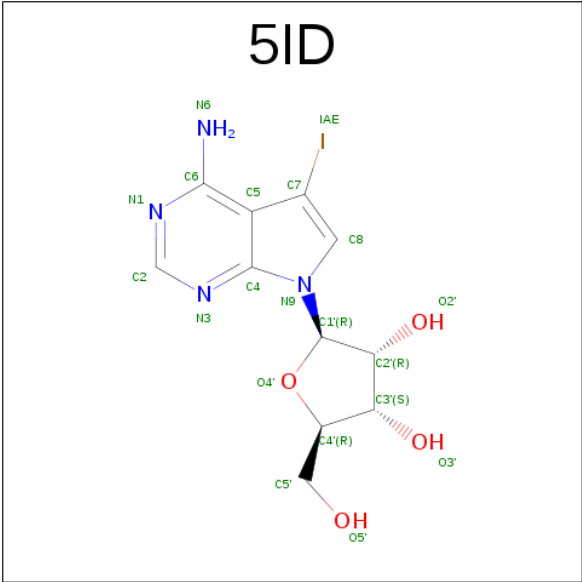
There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	GLY	-	expression tag	UNP P28482
A	-15	ASP	-	expression tag	UNP P28482
A	-14	LEU	-	expression tag	UNP P28482
A	-13	GLY	-	expression tag	UNP P28482
A	-12	SER	-	expression tag	UNP P28482
A	-11	ASP	-	expression tag	UNP P28482
A	-10	GLU	-	expression tag	UNP P28482
A	-9	LEU	-	expression tag	UNP P28482

- Molecule 2 is a protein called allosteric and ATP-competitive inhibitor.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	B	12	106	73	16	17	0	0	0

- Molecule 3 is (2R,3R,4S,5R)-2-(4-AMINO-5-iodo-7H-PYRROLO[2,3-D]PYRIMIDIN-7-YL)-5-(HYDROXYMETHYL)TETRAHYDROFURAN-3,4-DIOL (three-letter code: 5ID) (formula: C₁₁H₁₃IN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	I	N	O		
3	A	1	20	11	1	4	4	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	43.84Å 66.47Å 116.87Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.89 – 2.98 43.89 – 2.98	Depositor EDS
% Data completeness (in resolution range)	99.5 (43.89-2.98) 99.6 (43.89-2.98)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 3.01Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, R_{free}	0.236 , 0.285 0.244 , 0.286	Depositor DCC
R_{free} test set	614 reflections (4.60%)	DCC
Wilson B-factor (Å ²)	82.8	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 80.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	2831	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.11% 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

Bond lengths and bond angles in the following residue types are not validated in this section: 5ID

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	0.22	0/2767	0.38	0/3741
2	B	0.25	0/108	0.66	0/144
All	All	0.22	0/2875	0.40	0/3885

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

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	2705	0	2715	46	0
2	B	106	0	114	3	0
3	A	20	0	13	4	0
All	All	2831	0	2842	48	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 8.

All (48) 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:15:ARG:HD2	1:A:37:VAL:HG23	1.63	0.80
1:A:15:ARG:HD2	1:A:37:VAL:CG2	2.16	0.76
1:A:18:ASN:O	1:A:41:ARG:NH2	2.22	0.72
1:A:189:ILE:HD11	1:A:199:ILE:HB	1.74	0.69
1:A:238:SER:HB2	1:A:240:GLU:HG2	1.73	0.69
2:B:357:LEU:O	2:B:358:TRP:HB2	1.94	0.67
1:A:102:ASP:OD2	3:A:401:5ID:O3'	2.15	0.64
1:A:295:GLU:H	1:A:298:LEU:HD23	1.62	0.63
1:A:305:GLN:NE2	2:B:353:TYR:OH	2.32	0.63
1:A:233:ILE:HA	1:A:263:VAL:HG12	1.80	0.62
1:A:99:MET:H	3:A:401:5ID:H2	1.68	0.58
1:A:15:ARG:CD	1:A:37:VAL:CG2	2.83	0.55
1:A:99:MET:H	3:A:401:5ID:C2	2.21	0.54
1:A:186:ALA:HB3	1:A:189:ILE:HG13	1.90	0.53
1:A:15:ARG:CD	1:A:37:VAL:HG21	2.39	0.53
1:A:22:ILE:HD11	1:A:32:SER:HB3	1.90	0.53
1:A:149:ASN:HB3	1:A:153:ASP:HB2	1.92	0.52
1:A:164:VAL:HG11	1:A:321:PHE:HE1	1.75	0.51
1:A:131:ILE:HD13	1:A:159:PHE:HE1	1.76	0.50
1:A:230:ILE:HG12	1:A:234:LEU:HB2	1.94	0.50
1:A:185:ARG:O	1:A:202:TRP:NE1	2.44	0.49
1:A:120:PHE:HB2	1:A:211:MET:HE1	1.95	0.48
1:A:107:LEU:HD21	1:A:211:MET:HG2	1.95	0.48
2:B:359:ASN:OD1	2:B:359:ASN:N	2.47	0.48
1:A:47:ILE:HG12	1:A:49:PRO:HD3	1.95	0.48
1:A:225:ASP:O	1:A:229:HIS:N	2.39	0.47
1:A:22:ILE:HG21	3:A:401:5ID:H1'	1.97	0.47
1:A:19:LEU:HD13	1:A:33:ALA:HB2	1.97	0.46
1:A:16:TYR:HE2	1:A:81:ILE:HD11	1.80	0.46
1:A:123:GLN:NE2	1:A:152:CYS:O	2.46	0.45
1:A:213:SER:HB3	1:A:269:PHE:HE1	1.82	0.44
1:A:121:LEU:HD22	1:A:208:LEU:HD13	1.99	0.44
1:A:16:TYR:CZ	1:A:95:VAL:HG11	2.53	0.44
1:A:209:ALA:HB2	1:A:280:LEU:HD11	1.98	0.44
1:A:174:PHE:O	1:A:176:THR:N	2.45	0.43
1:A:263:VAL:HG13	1:A:268:LEU:HD21	2.01	0.43
1:A:125:LEU:HB3	1:A:298:LEU:HD21	2.01	0.43
1:A:67:LEU:HD21	1:A:344:PHE:HE2	1.84	0.42
1:A:213:SER:HB3	1:A:269:PHE:CE1	2.53	0.42
1:A:301:PRO:HA	1:A:304:GLU:HG3	2.02	0.42
1:A:101:THR:OG1	1:A:102:ASP:N	2.52	0.42
1:A:198:SER:O	1:A:291:ARG:NH1	2.53	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:138:HIS:NE2	1:A:157:CYS:O	2.44	0.42
1:A:71:HIS:CD2	1:A:127:GLY:HA2	2.55	0.41
1:A:163:ARG:HA	1:A:163:ARG:HD2	1.89	0.41
1:A:79:ASP:HA	1:A:344:PHE:CE1	2.56	0.41
1:A:298:LEU:HB3	1:A:307:TYR:CD1	2.57	0.40
1:A:212:LEU:HA	1:A:212:LEU:HD12	1.93	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	317/368 (86%)	287 (90%)	27 (8%)	3 (1%)	20	60
2	B	10/12 (83%)	4 (40%)	4 (40%)	2 (20%)	0	0
All	All	327/380 (86%)	291 (89%)	31 (10%)	5 (2%)	12	46

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	292	ILE
2	B	358	TRP
1	A	49	PRO
2	B	359	ASN
1	A	178	TYR

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	299/324 (92%)	277 (93%)	22 (7%)	16	48
2	B	11/11 (100%)	10 (91%)	1 (9%)	11	37
All	All	310/335 (92%)	287 (93%)	23 (7%)	16	48

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ARG
1	A	17	THR
1	A	52	HIS
1	A	71	HIS
1	A	106	LEU
1	A	112	LEU
1	A	131	ILE
1	A	158	ASP
1	A	163	ARG
1	A	174	PHE
1	A	181	THR
1	A	185	ARG
1	A	196	THR
1	A	222	HIS
1	A	226	GLN
1	A	230	ILE
1	A	234	LEU
1	A	261	ASN
1	A	266	ASN
1	A	294	VAL
1	A	311	ASP
1	A	345	GLN
2	B	358	TRP

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

Mol	Chain	Res	Type
1	A	305	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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

1 ligand 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$
3	5ID	A	401	-	20,22,22	1.19	1 (5%)	19,33,33	2.11	2 (10%)

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	5ID	A	401	-	-	0/2/22/22	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	401	5ID	C7-C5	4.02	1.46	1.42

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	A	401	5ID	N3-C2-N1	-7.84	122.03	128.86
3	A	401	5ID	C7-C8-N9	-2.96	105.01	108.20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	5ID	4	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	329/368 (89%)	0.52	32 (9%) 8 4	43, 79, 119, 146	0
2	B	12/12 (100%)	3.01	6 (50%) 0 0	109, 132, 139, 142	0
All	All	341/380 (89%)	0.61	38 (11%) 6 3	43, 80, 127, 146	0

All (38) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	351	LYS	6.1
1	A	194	GLY	5.7
2	B	354	ILE	5.2
1	A	1	GLY	5.1
2	B	350	VAL	5.1
2	B	357	LEU	4.7
1	A	27	TYR	4.4
1	A	175	LEU	4.0
1	A	235	GLY	4.0
2	B	353	TYR	3.8
1	A	191	LEU	3.8
1	A	325	LEU	3.8
1	A	348	TYR	3.4
1	A	327	ASP	3.1
1	A	258	PRO	3.1
1	A	321	PHE	3.0
1	A	174	PHE	2.9
1	A	250	ALA	2.9
1	A	248	LEU	2.7
1	A	223	TYR	2.7
1	A	220	GLY	2.6
1	A	301	PRO	2.6
1	A	239	GLN	2.6
1	A	320	LYS	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	4	MET	2.6
1	A	56	CYS	2.5
1	A	236	SER	2.5
1	A	221	LYS	2.4
1	A	241	ASP	2.4
1	A	232	GLY	2.4
2	B	355	LEU	2.4
1	A	190	MET	2.3
1	A	285	THR	2.2
1	A	222	HIS	2.2
1	A	261	ASN	2.1
1	A	55	TYR	2.0
1	A	178	TYR	2.0
1	A	234	LEU	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
3	5ID	A	401	20/20	0.92	0.17	-0.81	71,85,108,120	0

6.5 Other polymers [i](#)

There are no such residues in this entry.