Full wwPDB X-ray Structure Validation Report (i)

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PDB ID	:	6OTS
Title	:	Rat ERK2 E320K
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Deposited on	:	2019-05-03
Resolution	:	2.10 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 (i) 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 (1)) were used in the production of this report:

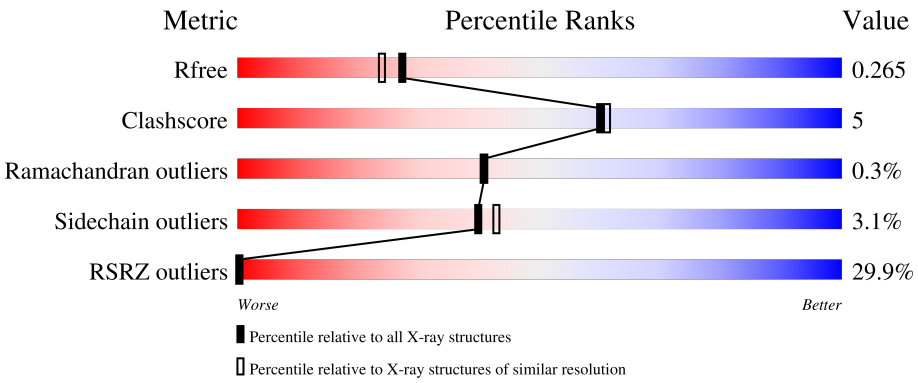
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

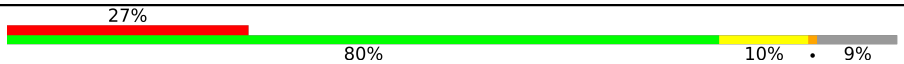
The reported resolution of this entry is 2.10 Å.

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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (2.10-2.10)

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 <=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	358	

2 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 5367 atoms, of which 2629 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	H	N	O	S			
1	A	324	5262	1694	2629	448	476	15	0	2	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	320	LYS	GLU	engineered mutation	UNP P63086

- Molecule 2 is water.

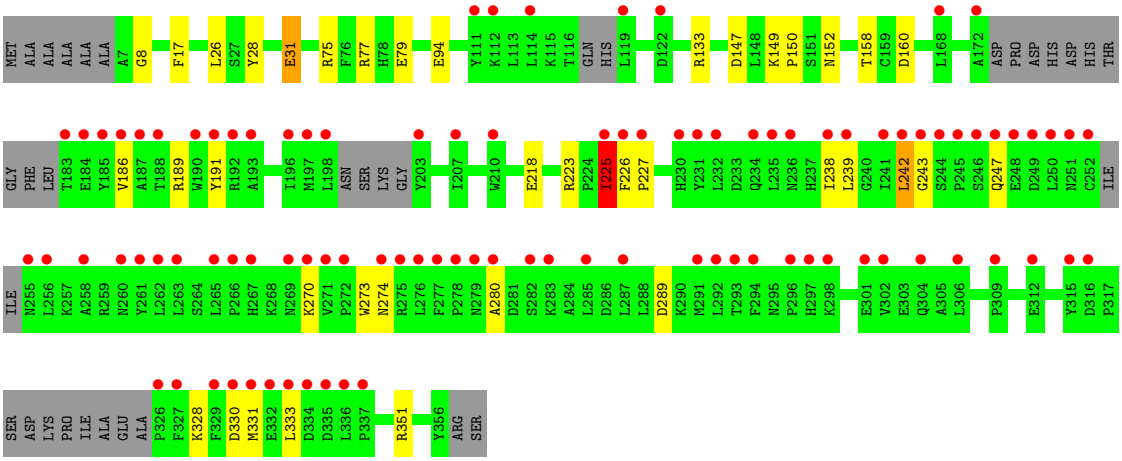
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
2	A	105	105	105	0	0

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: Mitogen-activated protein kinase 1

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	182.31Å 41.95Å 50.34Å 90.00° 105.86° 90.00°	Depositor
Resolution (Å)	43.84 – 2.10 43.84 – 2.10	Depositor EDS
% Data completeness (in resolution range)	78.4 (43.84-2.10) 78.4 (43.84-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.23 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.11.1_2575: ???)	Depositor
R, R_{free}	0.231 , 0.264 0.231 , 0.265	Depositor DCC
R_{free} test set	967 reflections (5.68%)	wwPDB-VP
Wilson B-factor (Å^2)	24.0	Xtriage
Anisotropy	0.261	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 79.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	0.029 for -h-2*l,-k,l	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	5367	wwPDB-VP
Average B, all atoms (Å^2)	82.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.15% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

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	0.25	0/2695	0.45	0/3646

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 (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	2633	2629	2622	24	2
2	A	105	0	0	6	0
All	All	2738	2629	2622	24	2

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 5.

All (24) 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:160:ASP:OD1	2:A:401:HOH:O	2.01	0.77
1:A:242:LEU:O	1:A:242:LEU:HD22	1.87	0.74
1:A:79:GLU:OE2	1:A:133:ARG:NH1	2.35	0.59
1:A:77:ARG:NH1	2:A:405:HOH:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:LEU:C	1:A:242:LEU:HD13	2.29	0.53
1:A:351:ARG:NH1	2:A:408:HOH:O	2.43	0.50
1:A:242:LEU:HA	1:A:270:LYS:HG3	1.94	0.50
1:A:158:THR:O	2:A:401:HOH:O	2.20	0.49
1:A:147:ASP:O	1:A:152:ASN:ND2	2.46	0.48
1:A:28:TYR:OH	1:A:31:GLU:OE1	2.32	0.48
1:A:239:LEU:O	1:A:243:GLY:HA2	2.14	0.47
1:A:273:TRP:NE1	1:A:289:ASP:OD1	2.44	0.46
1:A:226:PHE:CE1	1:A:238:ILE:HA	2.51	0.46
1:A:225:ILE:O	1:A:226:PHE:CD1	2.69	0.46
1:A:328:LYS:N	2:A:417:HOH:O	2.49	0.45
1:A:189:ARG:NH1	2:A:420:HOH:O	2.50	0.44
1:A:191:TYR:OH	1:A:218:GLU:OE1	2.26	0.43
1:A:226:PHE:N	1:A:227:PRO:HD3	2.34	0.42
1:A:223:ARG:NH1	1:A:225:ILE:HG22	2.34	0.42
1:A:242:LEU:H	1:A:242:LEU:HD12	1.86	0.41
1:A:238:ILE:HG22	1:A:242:LEU:HD11	2.02	0.41
1:A:330:ASP:O	1:A:331:MET:HB2	2.20	0.41
1:A:149:LYS:HB2	1:A:150:PRO:HD2	2.02	0.41

All (2) 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:A:274:ASN:ND2	1:A:280:ALA:O[2_556]	2.09	0.11
1:A:8:GLY:O	1:A:77:ARG:HH22[4_445]	1.59	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	314/358 (88%)	285 (91%)	28 (9%)	1 (0%)	41 41

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	225	ILE

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	288/318 (91%)	279 (97%)	9 (3%)	40 43

All (9) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	17	PHE
1	A	31	GLU
1	A	75	ARG
1	A	94	GLU
1	A	186	VAL
1	A	225	ILE
1	A	242	LEU
1	A	247	GLN
1	A	333	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

There are no ligands in this entry.

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 (i)

6.1 Protein, DNA and RNA chains (i)

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	324/358 (90%)	1.63	97 (29%) 0 0	7, 71, 155, 180	0

All (97) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	256	LEU	11.4
1	A	239	LEU	9.4
1	A	262	LEU	9.0
1	A	247	GLN	8.7
1	A	329	PHE	8.5
1	A	251	ASN	8.0
1	A	242	LEU	7.3
1	A	241	ILE	7.1
1	A	245	PRO	7.1
1	A	238	ILE	7.1
1	A	250	LEU	7.0
1	A	261	TYR	6.9
1	A	326	PRO	6.8
1	A	270	LYS	6.8
1	A	263	LEU	6.7
1	A	265	LEU	6.7
1	A	252	CYS	6.4
1	A	187	ALA	5.6
1	A	231	TYR	5.6
1	A	276	LEU	5.6
1	A	298	LYS	5.5
1	A	188	THR	5.0
1	A	272	PRO	4.9
1	A	315	TYR	4.8
1	A	243	GLY	4.8
1	A	258	ALA	4.8
1	A	225	ILE	4.8

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Mol	Chain	Res	Type	RSRZ
1	A	260	ASN	4.7
1	A	267	HIS	4.5
1	A	255	ASN	4.3
1	A	294	PHE	4.3
1	A	198	LEU	4.3
1	A	271	VAL	4.3
1	A	287	LEU	4.1
1	A	334	ASP	4.1
1	A	269	ASN	4.0
1	A	316	ASP	3.9
1	A	330	ASP	3.8
1	A	277	PHE	3.8
1	A	185	TYR	3.8
1	A	119	LEU	3.8
1	A	236	ASN	3.7
1	A	336	LEU	3.7
1	A	197	MET	3.7
1	A	335	ASP	3.7
1	A	244	SER	3.6
1	A	279	ASN	3.5
1	A	248	GLU	3.5
1	A	249	ASP	3.4
1	A	293	THR	3.4
1	A	278	PRO	3.4
1	A	327	PHE	3.4
1	A	234	GLN	3.3
1	A	168	LEU	3.2
1	A	196	ILE	3.2
1	A	331	MET	3.2
1	A	191	TYR	3.2
1	A	232	LEU	3.2
1	A	301	GLU	3.1
1	A	193	ALA	3.0
1	A	190	TRP	3.0
1	A	235	LEU	3.0
1	A	309	PRO	3.0
1	A	226	PHE	2.9
1	A	306	LEU	2.9
1	A	337	PRO	2.8
1	A	184	GLU	2.8
1	A	203	TYR	2.8
1	A	207	ILE	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	275	ARG	2.6
1	A	112	LYS	2.6
1	A	230	HIS	2.6
1	A	297	HIS	2.6
1	A	296	PRO	2.6
1	A	186	VAL	2.6
1	A	304	GLN	2.6
1	A	291	MET	2.5
1	A	282	SER	2.5
1	A	292	LEU	2.5
1	A	285	LEU	2.5
1	A	266	PRO	2.4
1	A	210	TRP	2.4
1	A	111	TYR	2.4
1	A	274	ASN	2.3
1	A	312	GLU	2.3
1	A	246	SER	2.3
1	A	114	LEU	2.3
1	A	227	PRO	2.3
1	A	280	ALA	2.2
1	A	302	VAL	2.2
1	A	192	ARG	2.2
1	A	333	LEU	2.2
1	A	122	ASP	2.2
1	A	283	LYS	2.2
1	A	332	GLU	2.1
1	A	172	ALA	2.1
1	A	183	THR	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 monosaccharides 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.