

wwPDB X-ray Structure Validation Summary Report (i)

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PDB ID : 2GNG

Title: Protein kinase A fivefold mutant model of Rho-kinase

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Deposited on : 2006-04-10

Resolution : 1.87 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

https://www.wwpdb.org/validation/2017/XrayValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

MolProbity : 4.02b-467

Mogul: 1.8.5 (274361), CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.23.2

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)

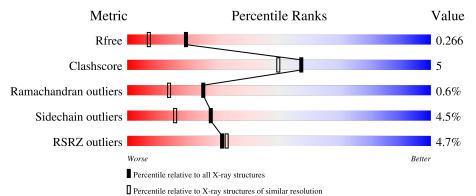
Validation Pipeline (wwPDB-VP) : 2.23.2

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 1.87 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	Similar resolution $(\# \text{Entries, resolution range}(\text{\AA}))$
R_{free}	130704	9470 (1.90-1.86)
Clashscore	141614	10282 (1.90-1.86)
Ramachandran outliers	138981	10152 (1.90-1.86)
Sidechain outliers	138945	10152 (1.90-1.86)
RSRZ outliers	127900	9303 (1.90-1.86)

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	350	85%	11% ••
2	I	20	90%	10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:



Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
1	SEP	A	10	_	-	X	X



2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3214 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 cAMP-dependent protein kinase, alpha-catalytic subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
1	A	341	Total 2821	C 1823	N 472	O 513	P 3	S 10	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	10	SEP	SER	modified residue	UNP P00517
A	49	ILE	LEU	engineered mutation	UNP P00517
A	123	MET	VAL	engineered mutation	UNP P00517
A	127	ASP	GLU	engineered mutation	UNP P00517
A	181	LYS	GLN	engineered mutation	UNP P00517
A	183	ALA	THR	engineered mutation	UNP P00517
A	197	TPO	THR	modified residue	UNP P00517
A	338	SEP	SER	modified residue	UNP P00517

• Molecule 2 is a protein called cAMP-dependent protein kinase inhibitor alpha.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	I	20	Total 157		N 32	O 31	0	0	0

• Molecule 3 is water.

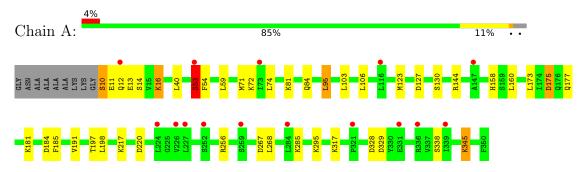
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	213	Total O 213 213	0	0
3	I	23	Total O 23 23	0	0



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: cAMP-dependent protein kinase, alpha-catalytic subunit



• Molecule 2: cAMP-dependent protein kinase inhibitor alpha

Chain I: 90% 10%





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	71.91Å 76.40Å 80.72Å	Depositor
a, b, c, α , β , γ	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	21.98 - 1.87	Depositor
resolution (A)	21.96 - 1.76	EDS
% Data completeness	79.1 (21.98-1.87)	Depositor
(in resolution range)	78.0 (21.96-1.76)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.05 (at 1.76Å)	Xtriage
Refinement program	REFMAC 5.1.24	Depositor
P.P.	0.195 , 0.258	Depositor
R, R_{free}	0.206 , 0.266	DCC
R_{free} test set	1800 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.489	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.35, 43.6	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	3214	wwPDB-VP
Average B, all atoms $(Å^2)$	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.55% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical 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.



¹Intensities estimated from amplitudes.

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: TPO, SEP

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		nd lengths	Bond angles		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.79	1/2861 (0.0%)	0.86	8/3851 (0.2%)	
2	I	0.70	0/159	1.08	1/212 (0.5%)	
All	All	0.78	1/3020 (0.0%)	0.88	9/4063 (0.2%)	

All (1) bond length outliers are listed below:

Mo	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
1	A	71	MET	SD-CE	-6.38	1.42	1.77

The worst 5 of 9 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
1	A	127	ASP	CB-CG-OD2	9.01	126.41	118.30
1	A	144	ARG	NE-CZ-NH2	-7.37	116.61	120.30
1	A	144	ARG	NE-CZ-NH1	6.95	123.77	120.30
1	A	191	VAL	CB-CA-C	-6.59	98.88	111.40
1	A	328	ASP	CB-CG-OD2	6.57	124.21	118.30

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	2821	0	2793	29	2
2	I	157	0	146	0	1
3	A	213	0	0	8	5
3	I	23	0	0	0	2
All	All	3214	0	2939	29	5

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.

The worst 5 of 29 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:A:10:SEP:HA	1:A:13:GLU:HB2	1.38	1.06
1:A:54:PHE:CE2	1:A:84:GLN:HG3	2.06	0.90
1:A:10:SEP:N	1:A:13:GLU:HG3	1.89	0.86
1:A:123:MET:HE1	1:A:175:ASP:HB3	1.59	0.85
1:A:11:GLU:HG2	1:A:12:GLN:NE2	1.94	0.81

All (5) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ (\rm \mathring{A}) \end{array}$	$\begin{array}{c} \text{Clash} \\ \text{overlap } (\text{\AA}) \end{array}$
2:I:16:THR:CB	3:A:527:HOH:O[2_655]	1.70	0.50
3:A:391:HOH:O	3:I:599:HOH:O[2_654]	1.72	0.48
1:A:53:SER:OG	3:A:595:HOH:O[4_555]	1.95	0.25
1:A:13:GLU:CB	3:A:610:HOH:O[3_644]	2.06	0.14
3:A:486:HOH:O	3:I:579:HOH:O[2_654]	2.16	0.04

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	Perce	entiles
1	A	$337/350 \ (96\%)$	323 (96%)	12 (4%)	2 (1%)	25	14
2	I	18/20 (90%)	17 (94%)	1 (6%)	0	100	100
All	All	355/370~(96%)	340 (96%)	13 (4%)	2 (1%)	25	14

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	53	SER
1	A	184	ASP

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	Analysed Rotameric Outliers		Percentiles		
1	A	298/301 (99%)	284 (95%)	14 (5%)	26 14		
2	I	15/15 (100%)	15 (100%)	0	100 100		
All	All	313/316 (99%)	299 (96%)	14 (4%)	27 16		

5 of 14 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	198	LEU
1	A	256	ARG
1	A	345	LYS
1	A	295	LYS
1	A	317	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	12	GLN
1	A	42	GLN
1	A	77	GLN
1	A	113	ASN

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Mol	Chain	Res	Type
1	A	158	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues 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	В	ond leng	$_{ m gths}$	В	ond ang	cles
WIOI	Type	Chain	ites	LIIIK	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	SEP	A	10	1	8,9,10	1.64	1 (12%)	8,12,14	1.66	1 (12%)
1	TPO	A	197	1	8,10,11	0.88	0	10,14,16	1.02	1 (10%)
1	SEP	A	338	1	8,9,10	1.33	1 (12%)	8,12,14	1.98	2 (25%)

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.

I	Mol	\mathbf{Type}	Chain	Res	Link	Chirals	Torsions	Rings
	1	SEP	A	10	1	-	4/5/8/10	-
	1	TPO	A	197	1	-	1/9/11/13	-
	1	SEP	A	338	1	-	2/5/8/10	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\text{\AA})$	Ideal(A)
1	A	10	SEP	P-O1P	3.54	1.62	1.50
1	A	338	SEP	P-O1P	2.85	1.59	1.50



All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^{o})$	$\operatorname{Ideal}({}^{o})$
1	A	338	SEP	OG-CB-CA	4.80	112.81	108.14
1	A	10	SEP	OG-CB-CA	3.88	111.92	108.14
1	A	338	SEP	OG-P-O1P	2.13	112.45	106.47
1	A	197	TPO	OG1-P-O1P	2.13	117.62	109.39

There are no chirality outliers.

5 of 7 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	10	SEP	CA-CB-OG-P
1	A	10	SEP	CB-OG-P-O1P
1	A	10	SEP	CB-OG-P-O2P
1	A	10	SEP	CB-OG-P-O3P
1	A	197	TPO	O-C-CA-CB

There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	10	SEP	5	0

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, 95^{th} 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 $>$	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	338/350~(96%)	0.24	15 (4%) 34 35	25, 36, 51, 60	6 (1%)
2	I	20/20 (100%)	0.09	2 (10%) 7 7	28, 31, 58, 62	0
All	All	358/370 (96%)	0.23	17 (4%) 31 33	25, 35, 51, 62	6 (1%)

The worst 5 of 17 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	12	GLN	5.7
2	I	24	ASP	3.4
1	A	339	ILE	3.2
1	A	331	GLU	3.0
2	I	23	HIS	2.7

6.2 Non-standard residues in protein, DNA, RNA chains (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. The B-factors column lists the minimum, median, 95^{th} 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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
1	SEP	A	10	10/11	0.70	0.53	55,56,60,60	10
1	SEP	A	338	10/11	0.95	0.15	47,48,49,50	0
1	TPO	A	197	11/12	0.98	0.07	25,28,30,31	0

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.

