



# Full wwPDB X-ray Structure Validation Report

Mar 1, 2014 – 01:50 AM GMT

PDB ID : 3CPC  
Title : Crystal structure of the VEGFR2 kinase domain in complex with a pyridone inhibitor  
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Deposited on : 2008-03-31  
Resolution : 2.40 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

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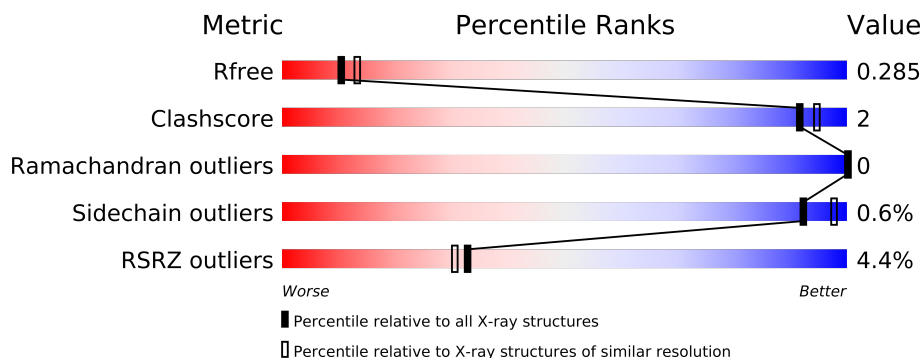
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
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 2.40 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))
$R_{free}$	66092	2207 (2.40-2.40)
Clashscore	79885	2789 (2.40-2.40)
Ramachandran outliers	78287	2736 (2.40-2.40)
Sidechain outliers	78261	2737 (2.40-2.40)
RSRZ outliers	66119	2210 (2.40-2.40)

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  $\geq 3$ , 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.

Mol	Chain	Length	Quality of chain
1	A	314	
1	B	314	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 4580 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.

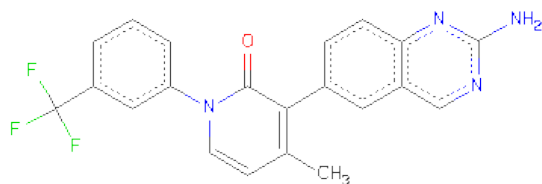
- Molecule 1 is a protein called Vascular endothelial growth factor receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	284	Total	C	N	O	S	0	0	0
			2302	1477	402	407	16			
1	B	262	Total	C	N	O	S	0	0	0
			2107	1359	360	372	16			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	817	ALA	CYS	engineered	UNP P35968
A	916	THR	VAL	engineered	UNP P35968
A	990	VAL	GLU	engineered	UNP P35968
A	1172	ARG	-	expression tag	UNP P35968
A	1173	HIS	-	expression tag	UNP P35968
A	1174	HIS	-	expression tag	UNP P35968
A	1175	HIS	-	expression tag	UNP P35968
A	1176	HIS	-	expression tag	UNP P35968
A	1177	HIS	-	expression tag	UNP P35968
A	1178	HIS	-	expression tag	UNP P35968

- Molecule 2 is 3-(2-AMINOQUINAZOLIN-6-YL)-4-METHYL-1-[3-(TRIFLUOROMETHYL)PHENYL]PYRIDIN-2(1H)-ONE (three-letter code: C52) (formula: C<sub>21</sub>H<sub>15</sub>F<sub>3</sub>N<sub>4</sub>O).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	F	N	O	0	0
			29	21	3	4	1		
2	B	1	Total	C	F	N	O	0	0
			29	21	3	4	1		

- Molecule 3 is water.

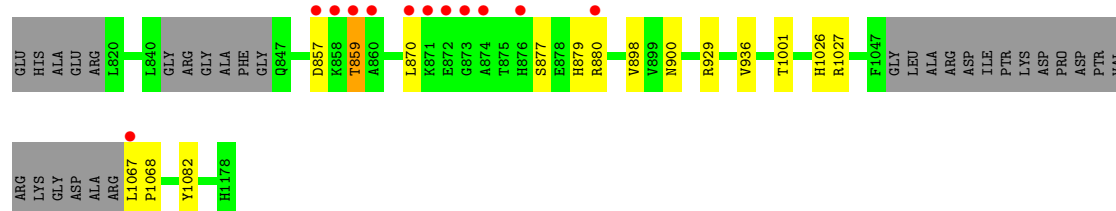
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	86	Total	O	0	0
			86	86		
3	B	27	Total	O	0	0
			27	27		

### 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.

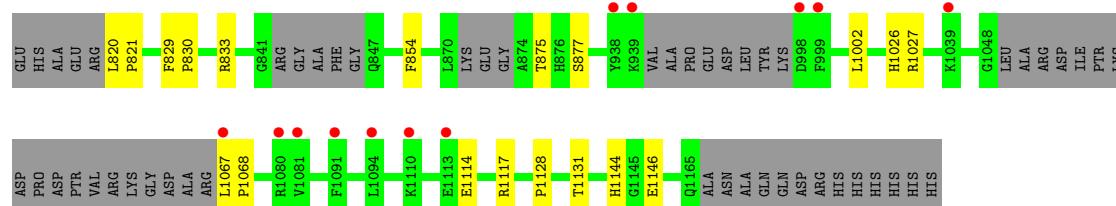
- Molecule 1: Vascular endothelial growth factor receptor 2

Chain A: 



- Molecule 1: Vascular endothelial growth factor receptor 2

Chain B: 



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.36Å 66.86Å 89.86Å 90.00° 93.35° 90.00°	Depositor
Resolution (Å)	30.00 – 2.40 28.61 – 2.40	Depositor EDS
% Data completeness (in resolution range)	93.7 (30.00-2.40) 93.6 (28.61-2.40)	Depositor EDS
$R_{merge}$	0.08	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.73 (at 2.42Å)	Xtriage
Refinement program	REFMAC 5	Depositor
R, $R_{free}$	0.218 , 0.272 0.236 , 0.285	Depositor DCC
$R_{free}$ test set	1422 reflections (6.28%)	DCC
Wilson B-factor (Å <sup>2</sup> )	34.9	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.36 , 35.2	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.51$ , $\langle L^2 \rangle = 0.35$	Xtriage
Outliers	0 of 24049 reflections	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	4580	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	35.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.63% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: C52

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	0.37	0/2362	0.50	0/3192
1	B	0.35	0/2157	0.48	0/2912
All	All	0.36	0/4519	0.49	0/6104

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

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	2302	0	2290	8	0
1	B	2107	0	2117	9	0
2	A	29	0	15	0	0
2	B	29	0	15	0	0
3	A	86	0	0	0	0
3	B	27	0	0	0	0
All	All	4580	0	4437	17	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 2.

All (17) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:875:THR:HG22	1:B:877:SER:H	1.69	0.58
1:B:1128:PRO:HG2	1:B:1131:THR:HB	1.87	0.55
1:A:870:LEU:HD11	1:A:879:HIS:HA	1.88	0.54
1:A:936:VAL:O	1:A:1001:THR:HA	2.08	0.54
1:B:1144:HIS:HD2	1:B:1146:GLU:H	1.55	0.53
1:A:1027:ARG:HG2	1:A:1082:TYR:CD2	2.44	0.53
1:B:1067:LEU:N	1:B:1068:PRO:HD2	2.26	0.50
1:A:877:SER:HA	1:A:880:ARG:HD2	1.95	0.48
1:A:857:ASP:HB3	1:A:859:THR:H	1.79	0.48
1:B:1114:GLU:HG2	1:B:1117:ARG:HH12	1.80	0.46
1:B:833:ARG:HG2	1:B:854:PHE:HD2	1.84	0.43
1:A:1067:LEU:HA	1:A:1068:PRO:HD3	1.89	0.42
1:B:1026:HIS:O	1:B:1027:ARG:HB2	2.19	0.41
1:A:898:VAL:O	1:A:900:ASN:ND2	2.51	0.41
1:A:1026:HIS:O	1:A:1027:ARG:HB2	2.21	0.41
1:B:820:LEU:HA	1:B:821:PRO:HD3	1.97	0.41
1:B:829:PHE:HA	1:B:830:PRO:HD3	1.95	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	278/314 (88%)	271 (98%)	7 (2%)	0	100	100
1	B	252/314 (80%)	246 (98%)	6 (2%)	0	100	100
All	All	530/628 (84%)	517 (98%)	13 (2%)	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	251/270 (93%)	249 (99%)	2 (1%)	89	96
1	B	231/270 (86%)	230 (100%)	1 (0%)	95	98
All	All	482/540 (89%)	479 (99%)	3 (1%)	92	98

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	859	THR
1	A	929	ARG
1	B	1002	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	933	ASN
1	A	1040	ASN
1	A	1162	ASN
1	A	1169	GLN
1	B	847	GLN
1	B	1040	ASN
1	B	1144	HIS
1	B	1162	ASN

### 5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

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	$\# Z  > 2$
2	C52	A	1	-	32,32,32	1.31	4 (12%)	46,48,48	1.47	6 (13%)
2	C52	B	2	-	32,32,32	1.24	4 (12%)	46,48,48	1.52	7 (15%)

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	C52	A	1	-	-	0/14/14/14	0/2/4/4
2	C52	B	2	-	-	0/14/14/14	0/2/4/4

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	C52	C11-N4	3.63	1.41	1.36
2	B	2	C52	C11-N4	2.99	1.40	1.36
2	A	1	C52	C9-C7	-2.82	1.41	1.49
2	B	2	C52	C9-C7	-2.74	1.41	1.49
2	A	1	C52	C10-N4	2.67	1.42	1.35
2	B	2	C52	C10-N4	2.45	1.42	1.35
2	B	2	C52	C15-N4	-2.42	1.41	1.44
2	A	1	C52	C15-N4	-2.25	1.41	1.44

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	C52	N2-C1-N1	-4.83	120.90	125.86
2	B	2	C52	N2-C1-N1	-4.81	120.92	125.86
2	A	1	C52	C4-N2-C1	3.93	120.80	115.89
2	B	2	C52	C4-N2-C1	3.74	120.56	115.89
2	A	1	C52	F3-C21-C17	-3.07	105.87	112.97
2	B	2	C52	C16-C15-N4	2.71	121.97	119.22
2	B	2	C52	C20-C15-C16	-2.55	119.31	121.55
2	A	1	C52	C20-C15-C16	-2.45	119.39	121.55
2	B	2	C52	N3-C1-N2	2.28	119.48	117.42
2	A	1	C52	C3-C4-N2	-2.12	119.95	123.83
2	B	2	C52	F3-C21-C17	-2.07	108.19	112.97
2	B	2	C52	C3-C4-N2	-2.05	120.06	123.83
2	A	1	C52	N3-C1-N2	2.00	119.22	117.42

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 ⓘ

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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	284/314 (90%)	-0.07	12 (4%) 35 32	17, 28, 49, 60	0
1	B	262/314 (83%)	0.30	12 (4%) 31 29	26, 41, 54, 59	0
All	All	546/628 (86%)	0.11	24 (4%) 33 30	17, 35, 54, 60	0

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	859	THR	5.0
1	A	1067	LEU	4.9
1	B	999	PHE	4.2
1	A	858	LYS	4.2
1	B	939	LYS	3.8
1	A	860	ALA	3.8
1	A	873	GLY	3.7
1	A	876	HIS	3.1
1	B	1110	LYS	2.9
1	B	1113	GLU	2.9
1	A	874	ALA	2.9
1	B	938	TYR	2.9
1	B	1067	LEU	2.7
1	A	871	LYS	2.7
1	A	880	ARG	2.7
1	B	1080	ARG	2.5
1	A	857	ASP	2.4
1	B	1081	VAL	2.4
1	B	1091	PHE	2.3
1	A	870	LEU	2.2
1	A	872	GLU	2.2
1	B	1039	LYS	2.1
1	B	1094	LEU	2.1
1	B	998	ASP	2.0

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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, 95<sup>th</sup> 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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
2	C52	A	1	29/29	0.12	-0.71	24,25,26,28	0
2	C52	B	2	29/29	0.11	-1.20	27,27,30,31	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.