Full wwPDB X-ray Structure Validation Report ⓘ

May 22, 2020 – 04:04 am BST

PDB ID	:	2IVU
Title	:	Crystal structure of phosphorylated RET tyrosine kinase domain complexed with the inhibitor ZD6474
Authors	:	Knowles, P.P.; Murray-Rust, J.; McDonald, N.Q.
Deposited on	:	2006-06-16
Resolution	:	2.50 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 ⓘ symbol.

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

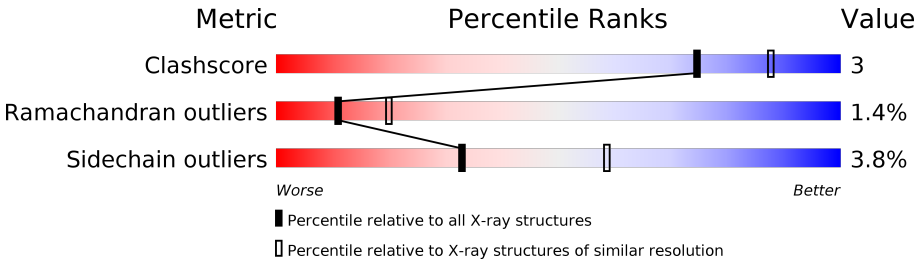
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 2.50 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	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)

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 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%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	314	83% 8% • 8%

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
2	FMT	A	3014	-	-	X	-

2 Entry composition

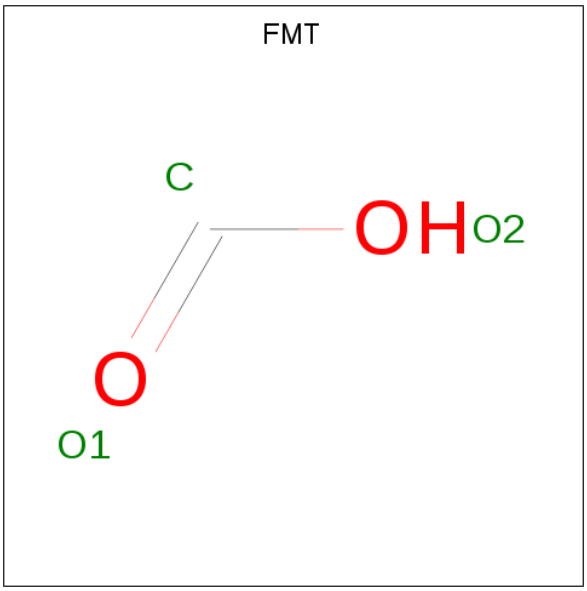
There are 4 unique types of molecules in this entry. The entry contains 2296 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RECEPTOR RET PRECURSOR.

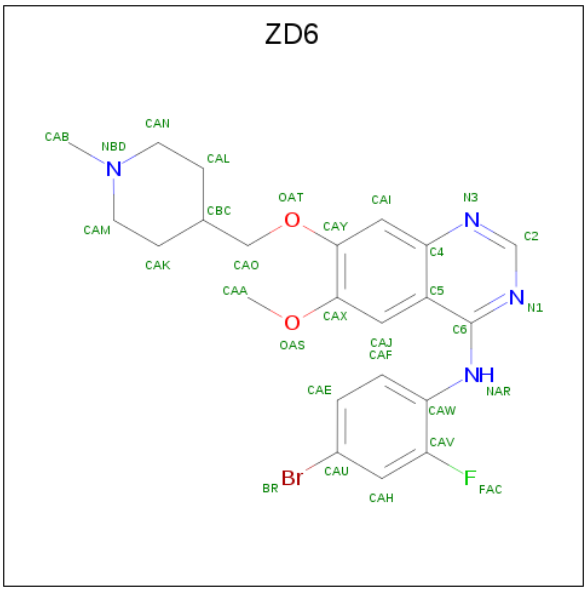
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	289	2189	1420	369	385	1	14	0	0	0

- Molecule 2 is FORMIC ACID (three-letter code: FMT) (formula: CH_2O_2).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
2	A	1	3	1	2		0	0
2	A	1	Total	C	O		0	0
			3	1	2			

- Molecule 3 is Vandetanib (three-letter code: ZD6) (formula: $C_{22}H_{24}BrFN_4O_2$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	Br	C	F	N	O	0	0
			30	1	22	1	4	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	71	Total	O	0	0
			71	71		

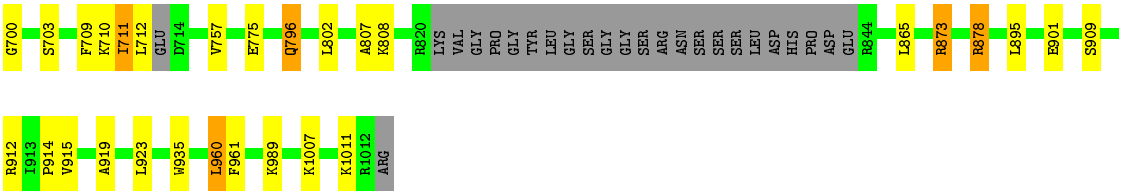
3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA 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. 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. 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: PROTO-ONCOGENE TYROSINE-PROTEIN KINASE RECEPTOR RET PRECURSOR

Chain A:



4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	71.41Å 71.42Å 78.83Å 90.00° 101.23° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50	Depositor
% Data completeness (in resolution range)	99.5 (50.00-2.50)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.190 , 0.248	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2296	wwPDB-VP
Average B, all atoms (Å^2)	37.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: FMT, ZD6, PTR

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	0.72	0/2219	0.76	2/3002 (0.1%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	960	LEU	CA-CB-CG	-5.43	102.80	115.30
1	A	873	ARG	NE-CZ-NH2	-5.18	117.71	120.30

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	2189	0	2132	14	0
2	A	6	0	2	2	0
3	A	30	0	24	2	0
4	A	71	0	0	1	0
All	All	2296	0	2158	14	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 3.

All (14) 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:775:GLU:OE2	4:A:2029:HOH:O	2.13	0.66
1:A:807:ALA:H	3:A:3015:ZD6:H3	1.45	0.64
1:A:873:ARG:HD3	1:A:895:LEU:O	2.00	0.61
1:A:808:LYS:O	3:A:3015:ZD6:HAK2	2.08	0.54
1:A:923:LEU:HD22	1:A:961:PHE:CE1	2.44	0.52
1:A:700:GLY:N	1:A:703:SER:HG	2.07	0.52
1:A:878:ARG:NH2	1:A:914:PRO:HG2	2.28	0.49
1:A:912:ARG:H	2:A:3014:FMT:C	2.28	0.46
1:A:1007:LYS:O	1:A:1011:LYS:HG3	2.14	0.46
1:A:919:ALA:HA	1:A:935:TRP:CD2	2.51	0.46
1:A:709:PHE:C	1:A:711:ILE:H	2.19	0.46
1:A:912:ARG:HB2	2:A:3014:FMT:H	1.98	0.45
1:A:757:VAL:HA	1:A:802:LEU:O	2.20	0.41
1:A:935:TRP:C	1:A:935:TRP:CD1	2.95	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	282/314 (90%)	273 (97%)	5 (2%)	4 (1%)	11 20

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	710	LYS
1	A	796	GLN
1	A	901	GLU
1	A	711	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	213/271 (79%)	205 (96%)	8 (4%)	33 58

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	712	LEU
1	A	796	GLN
1	A	865	LEU
1	A	878	ARG
1	A	909	SER
1	A	915	VAL
1	A	960	LEU
1	A	989	LYS

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	931	GLN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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	PTR	A	905	1	15,16,17	2.07	2 (13%)	19,22,24	0.99	1 (5%)

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	PTR	A	905	1	-	2/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	905	PTR	OH-CZ	-7.01	1.24	1.40
1	A	905	PTR	P-OH	2.86	1.63	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	905	PTR	P-OH-CZ	2.45	131.61	123.75

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	905	PTR	CE2-CZ-OH-P
1	A	905	PTR	CE1-CZ-OH-P

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no carbohydrates in this entry.

5.6 Ligand geometry (i)

3 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	FMT	A	3014	-	0,2,2	0.00	-	0,1,1	0.00	-
2	FMT	A	3013	-	0,2,2	0.00	-	0,1,1	0.00	-
3	ZD6	A	3015	-	33,33,33	1.35	4 (12%)	46,46,46	2.46	19 (41%)

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	ZD6	A	3015	-	-	1/11/21/21	0/4/4/4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	3015	ZD6	C6-NAR	5.08	1.43	1.36
3	A	3015	ZD6	C6-C5	-2.19	1.42	1.44
3	A	3015	ZD6	CAJ-CAX	2.13	1.40	1.36
3	A	3015	ZD6	C5-C4	-2.07	1.39	1.42

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	3015	ZD6	C2-N1-C6	5.85	121.61	116.59
3	A	3015	ZD6	CAN-NBD-CAM	5.24	116.84	109.52
3	A	3015	ZD6	FAC-CAV-CAW	5.03	123.82	117.50
3	A	3015	ZD6	N3-C2-N1	-4.81	121.16	128.68
3	A	3015	ZD6	CAB-NBD-CAM	-4.20	104.39	110.66
3	A	3015	ZD6	BR-CAU-CAE	4.02	125.14	119.30
3	A	3015	ZD6	C2-N3-C4	3.99	120.90	115.40
3	A	3015	ZD6	BR-CAU-CAH	-3.82	113.96	119.27

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	3015	ZD6	C6-C5-C4	3.32	117.97	115.88
3	A	3015	ZD6	C5-C6-N1	-3.16	118.75	121.35
3	A	3015	ZD6	CAB-NBD-CAN	-3.15	105.95	110.66
3	A	3015	ZD6	C5-C4-N3	-3.05	119.58	122.83
3	A	3015	ZD6	CAV-CAH-CAU	2.99	119.77	117.40
3	A	3015	ZD6	CAW-NAR-C6	-2.85	121.40	129.29
3	A	3015	ZD6	CAF-CAW-CAV	2.59	119.78	117.17
3	A	3015	ZD6	CAJ-C5-C6	-2.58	122.56	124.88
3	A	3015	ZD6	CAH-CAV-CAW	-2.48	121.14	123.50
3	A	3015	ZD6	CAI-C4-N3	2.21	120.49	117.97
3	A	3015	ZD6	OAT-CAO-CBC	-2.02	102.94	108.21

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	3015	ZD6	OAT-CAO-CBC-CAL

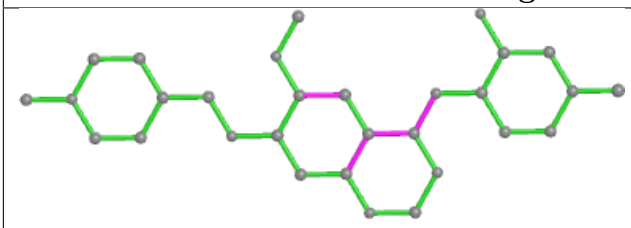
There are no ring outliers.

2 monomers are involved in 4 short contacts:

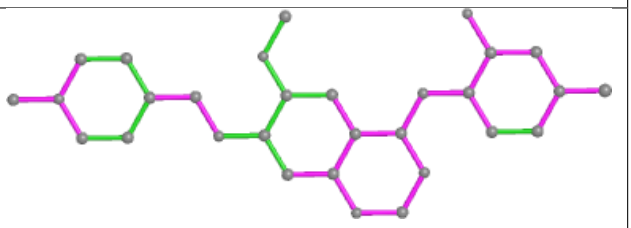
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	3014	FMT	2	0
3	A	3015	ZD6	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

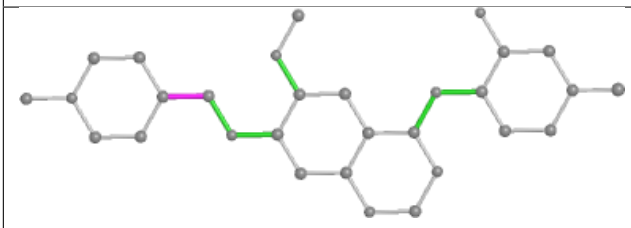
Ligand ZD6 A 3015



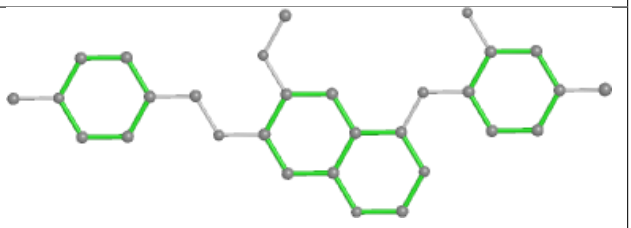
Bond lengths



Bond angles



Torsions



Rings

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 is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.