WORLDWIDE PDB

PROTEIN DATA BANK

Full wwPDB X-ray Structure Validation Report ⓘ

Nov 11, 2014 – 11:06 AM EST

PDB ID   :   4WUN
Title   :   Structure of FGFR1 in complex with AZD4547 (N-{3-[2-(3,5-DIMETHOXY
              PHENYL)ETHYL]-1H-PYRAZOL-5-YL}-4-[(3R,5S)-3,5-DIMETHYLPIPER
              AZIN-1-YL]BENZAMIDE)at 1.65 angstrom
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Deposited on : 2014-11-02
Resolution : 1.65 Å(reported)

1 Overall quality at a glance ⓘ

The reported resolution of this entry is 1.65 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	Percentile Ranks	Value
Rfree		0.254
Clashscore		2
Ramachandran outliers		0
Sidechain outliers		0.5%
RSRZ outliers		4.5%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution
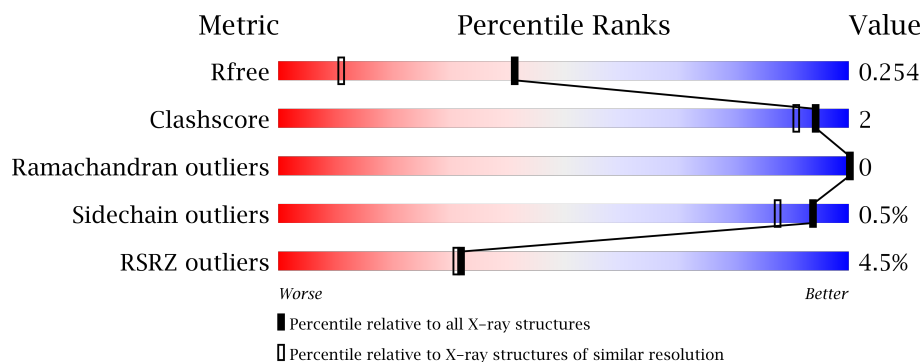
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	66092	1404 (1.68-1.64)
Clashscore	79885	1001 (1.66-1.66)
Ramachandran outliers	78287	1581 (1.68-1.64)
Sidechain outliers	78261	1580 (1.68-1.64)
RSRZ outliers	66119	1404 (1.68-1.64)

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. 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	311	
1	B	311	

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 4532 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 Fibroblast growth factor receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	282	Total	C	N	O	S	0	7	0
			2195	1398	377	399	21			
1	B	268	Total	C	N	O	S	0	2	0
			2062	1316	351	378	17			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	455	GLY	-	expression tag	UNP P11362
A	456	ALA	-	expression tag	UNP P11362
A	457	MET	-	expression tag	UNP P11362
A	458	SER	-	expression tag	UNP P11362
A	488	ALA	CYS	conflict	UNP P11362
A	584	SER	CYS	conflict	UNP P11362
B	455	GLY	-	expression tag	UNP P11362
B	456	ALA	-	expression tag	UNP P11362
B	457	MET	-	expression tag	UNP P11362
B	458	SER	-	expression tag	UNP P11362
B	488	ALA	CYS	conflict	UNP P11362
B	584	SER	CYS	conflict	UNP P11362

- Molecule 2 is N-{3-[2-(3,5-dimethoxyphenyl)ethyl]-1H-pyrazol-5-yl}-4-[(3R,5S)-3,5-dimethyl piperazin-1-yl]benzamide (three-letter code: 66T) (formula: $C_{26}H_{33}N_5O_3$).
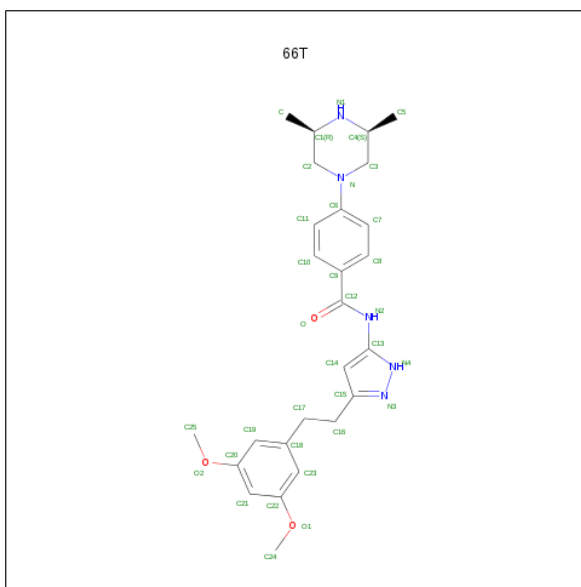
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total 34	C 26	N 5	O 3	0	0
2	B	1	Total 34	C 26	N 5	O 3	0	0

• Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	117	Total 117	O 117	0	0
3	B	90	Total 90	O 90	0	0

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.
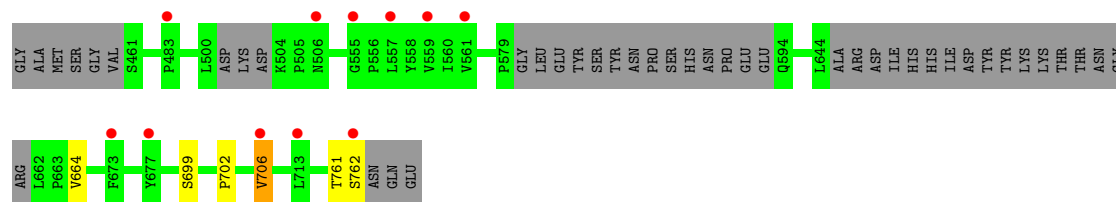
• Molecule 1: Fibroblast growth factor receptor 1

Chain A:
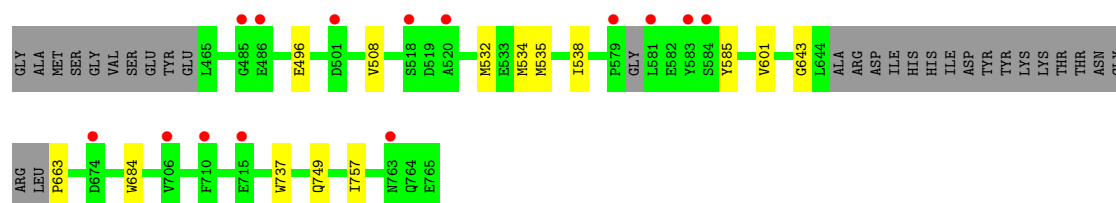
• Molecule 1: Fibroblast growth factor receptor 1

Chain B:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	65.49Å 50.52Å 201.28Å 90.00° 91.23° 90.00°	Depositor
Resolution (Å)	20.00 – 1.65 20.00 – 1.65	Depositor EDS
% Data completeness (in resolution range)	99.7 (20.00-1.65) 99.7 (20.00-1.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	6.36 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.8.0071	Depositor
R, R_{free}	0.225 , 0.247 0.233 , 0.254	Depositor DCC
R_{free} test set	4002 reflections (5.32%)	DCC
Wilson B-factor (Å^2)	24.1	Xtriage
Anisotropy	0.439	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 37.9	EDS
Estimated twinning fraction	0.017 for h,-k,-l	Xtriage
L-test for twinning	$< |L| > = 0.48, < L^2 > = 0.32$	Xtriage
Outliers	2 of 79232 reflections (0.003%)	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	4532	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.62% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]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: 66T

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	0.45	0/2254	0.66	0/3056
1	B	0.53	0/2104	0.73	0/2856
All	All	0.49	0/4358	0.69	0/5912

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	2195	0	2147	10	0
1	B	2062	0	2011	3	0
2	A	34	0	0	0	0
2	B	34	0	0	0	0
3	A	117	0	0	2	0
3	B	90	0	0	0	0
All	All	4532	0	4158	13	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 (13) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:B:664:VAL:HG21	1:B:706:VAL:HG13	1.70	0.73
1:A:496:GLU:HB3	1:A:508:VAL:CG2	2.25	0.67
1:A:749:GLN:HG2	3:A:928:HOH:O	2.01	0.60
1:A:663:PRO:N	3:A:970:HOH:O	2.38	0.56
1:A:532:MET:HA	1:A:535[A]:MET:HE2	1.91	0.52
1:A:534[B]:MET:C	1:A:534[B]:MET:SD	2.94	0.46
1:A:496:GLU:HB3	1:A:508:VAL:HG21	1.97	0.43
1:B:761:THR:O	1:B:762:SER:C	2.57	0.42
1:A:534[B]:MET:SD	1:A:643:GLY:HA2	2.61	0.41
1:A:684:TRP:CE3	1:A:737:TRP:HA	2.56	0.41
1:B:699:SER:O	1:B:702:PRO:HD3	2.21	0.41
1:A:601:VAL:HG11	1:A:757:ILE:HG22	2.02	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	283/311 (91%)	279 (99%)	4 (1%)	0	100	100
1	B	262/311 (84%)	257 (98%)	5 (2%)	0	100	100
All	All	545/622 (88%)	536 (98%)	9 (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	231/271 (85%)	230 (100%)	1 (0%)	95	91
1	B	215/271 (79%)	214 (100%)	1 (0%)	94	87
All	All	446/542 (82%)	444 (100%)	2 (0%)	94	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	585	TYR
1	B	706	VAL

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

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	66T	A	801	-	37,37,37	1.17	3 (8%)	50,51,51	1.00	3 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#|Z| > 2$	Counts	RMSZ	$\#|Z| > 2$
2	66T	B	801	-	37,37,37	1.12	2 (5%)	50,51,51	1.05	4 (8%)

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	66T	A	801	-	-	1/19/33/33	0/4/4/4
2	66T	B	801	-	-	1/19/33/33	0/4/4/4

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	801	66T	N4-N3	-4.77	1.29	1.37
2	A	801	66T	N4-N3	-4.54	1.29	1.37
2	A	801	66T	C14-C15	-3.24	1.34	1.39
2	B	801	66T	C14-C15	-2.83	1.35	1.39
2	A	801	66T	C3-N	2.42	1.52	1.46

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	801	66T	C16-C15-N3	-4.37	118.12	123.96
2	A	801	66T	C16-C15-N3	-3.40	119.41	123.96
2	A	801	66T	C2-N-C6	3.32	124.72	116.20
2	A	801	66T	C14-C13-N4	2.34	108.86	105.90
2	B	801	66T	C11-C6-N	-2.18	118.43	121.37
2	B	801	66T	C14-C13-N4	2.15	108.61	105.90
2	B	801	66T	C16-C17-C18	-2.14	105.99	113.28

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	801	66T	C17-C16-C15-N3
2	A	801	66T	C17-C16-C15-N3

There are no ring outliers.

5.7 Other polymers (i)

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, 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	282/311 (90%)	0.31	14 (4%)	28	25	19, 31, 51, 66	0
1	B	268/311 (86%)	0.31	11 (4%)	35	35	16, 31, 51, 62	0
All	All	550/622 (88%)	0.31	25 (4%)	32	31	16, 31, 51, 66	0

All (25) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	485	GLY	6.2
1	A	583	TYR	4.3
1	B	673	PHE	3.6
1	B	762	SER	3.1
1	A	579	PRO	2.8
1	B	706	VAL	2.8
1	B	555	GLY	2.7
1	B	559	VAL	2.7
1	A	710	PHE	2.7
1	A	706	VAL	2.6
1	A	674	ASP	2.5
1	A	518	SER	2.4
1	A	584	SER	2.3
1	A	715	GLU	2.3
1	B	483	PRO	2.3
1	B	506	ASN	2.2
1	B	713	LEU	2.2
1	A	520	ALA	2.1
1	A	763	ASN	2.1
1	B	677	TYR	2.1
1	A	486	GLU	2.1
1	A	581	LEU	2.1
1	A	501	ASP	2.0
1	B	561	VAL	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	557	LEU	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, 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	RSR	LLDF	B-factors(Å^2)	Q<0.9
2	66T	B	801	34/34	0.13	0.43	23,28,41,43	0
2	66T	A	801	34/34	0.11	-0.10	23,26,33,35	0

6.5   Other polymers ⓘ

There are no such residues in this entry.