



wwPDB X-ray Structure Validation Summary Report

Feb 28, 2014 – 11:32 PM GMT

PDB ID : 3RCD
Title : HER2 Kinase Domain Complexed with TAK-285
Authors : Aertgeerts, K.; Skene, R.; Sogabe, S.
Deposited on : 2011-03-30
Resolution : 3.21 Å(reported)

This is a wwPDB validation summary report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

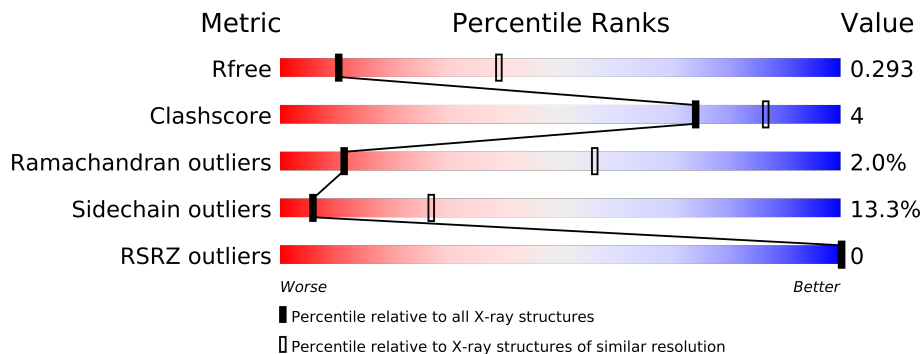
The following versions of software and data (see [references](#)) were used in the production of this report:

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 3.21 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	1205 (3.30-3.14)
Clashscore	79885	1072 (3.28-3.16)
Ramachandran outliers	78287	1052 (3.28-3.16)
Sidechain outliers	78261	1051 (3.28-3.16)
RSRZ outliers	66119	1206 (3.30-3.14)

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	338	
1	B	338	
1	C	338	
1	D	338	

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8970 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 Receptor tyrosine-protein kinase erbB-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	281	Total	C	N	O	S	0	0	0
			2254	1444	391	403	16			
1	B	271	Total	C	N	O	S	0	0	0
			2176	1398	381	381	16			
1	C	281	Total	C	N	O	S	0	0	0
			2254	1444	391	403	16			
1	D	271	Total	C	N	O	S	0	0	0
			2176	1398	381	381	16			

There are 88 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	702	MET	-	EXPRESSION TAG	UNP P04626
A	703	SER	-	EXPRESSION TAG	UNP P04626
A	704	GLY	-	EXPRESSION TAG	UNP P04626
A	705	ALA	-	EXPRESSION TAG	UNP P04626
A	706	ALA	-	EXPRESSION TAG	UNP P04626
A	707	PRO	-	EXPRESSION TAG	UNP P04626
A	708	ASN	-	EXPRESSION TAG	UNP P04626
A	709	GLN	-	EXPRESSION TAG	UNP P04626
A	710	ALA	-	EXPRESSION TAG	UNP P04626
A	711	LEU	-	EXPRESSION TAG	UNP P04626
A	712	LEU	-	EXPRESSION TAG	UNP P04626
A	1029	GLY	-	EXPRESSION TAG	UNP P04626
A	1030	ALA	-	EXPRESSION TAG	UNP P04626
A	1031	ALA	-	EXPRESSION TAG	UNP P04626
A	1032	ALA	-	EXPRESSION TAG	UNP P04626
A	1033	SER	-	EXPRESSION TAG	UNP P04626
A	1034	HIS	-	EXPRESSION TAG	UNP P04626
A	1035	HIS	-	EXPRESSION TAG	UNP P04626
A	1036	HIS	-	EXPRESSION TAG	UNP P04626
A	1037	HIS	-	EXPRESSION TAG	UNP P04626
A	1038	HIS	-	EXPRESSION TAG	UNP P04626

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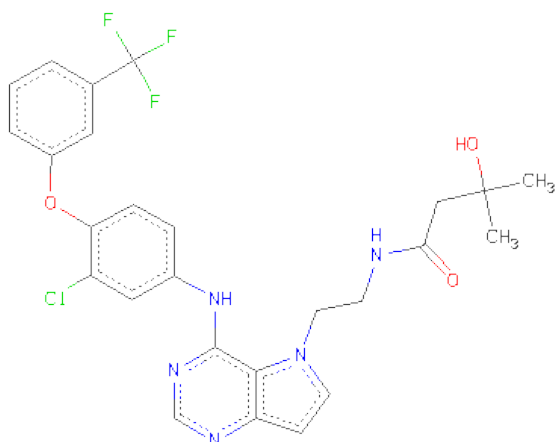
Chain	Residue	Modelled	Actual	Comment	Reference
A	1039	HIS	-	EXPRESSION TAG	UNP P04626
B	702	MET	-	EXPRESSION TAG	UNP P04626
B	703	SER	-	EXPRESSION TAG	UNP P04626
B	704	GLY	-	EXPRESSION TAG	UNP P04626
B	705	ALA	-	EXPRESSION TAG	UNP P04626
B	706	ALA	-	EXPRESSION TAG	UNP P04626
B	707	PRO	-	EXPRESSION TAG	UNP P04626
B	708	ASN	-	EXPRESSION TAG	UNP P04626
B	709	GLN	-	EXPRESSION TAG	UNP P04626
B	710	ALA	-	EXPRESSION TAG	UNP P04626
B	711	LEU	-	EXPRESSION TAG	UNP P04626
B	712	LEU	-	EXPRESSION TAG	UNP P04626
B	1029	GLY	-	EXPRESSION TAG	UNP P04626
B	1030	ALA	-	EXPRESSION TAG	UNP P04626
B	1031	ALA	-	EXPRESSION TAG	UNP P04626
B	1032	ALA	-	EXPRESSION TAG	UNP P04626
B	1033	SER	-	EXPRESSION TAG	UNP P04626
B	1034	HIS	-	EXPRESSION TAG	UNP P04626
B	1035	HIS	-	EXPRESSION TAG	UNP P04626
B	1036	HIS	-	EXPRESSION TAG	UNP P04626
B	1037	HIS	-	EXPRESSION TAG	UNP P04626
B	1038	HIS	-	EXPRESSION TAG	UNP P04626
B	1039	HIS	-	EXPRESSION TAG	UNP P04626
C	702	MET	-	EXPRESSION TAG	UNP P04626
C	703	SER	-	EXPRESSION TAG	UNP P04626
C	704	GLY	-	EXPRESSION TAG	UNP P04626
C	705	ALA	-	EXPRESSION TAG	UNP P04626
C	706	ALA	-	EXPRESSION TAG	UNP P04626
C	707	PRO	-	EXPRESSION TAG	UNP P04626
C	708	ASN	-	EXPRESSION TAG	UNP P04626
C	709	GLN	-	EXPRESSION TAG	UNP P04626
C	710	ALA	-	EXPRESSION TAG	UNP P04626
C	711	LEU	-	EXPRESSION TAG	UNP P04626
C	712	LEU	-	EXPRESSION TAG	UNP P04626
C	1029	GLY	-	EXPRESSION TAG	UNP P04626
C	1030	ALA	-	EXPRESSION TAG	UNP P04626
C	1031	ALA	-	EXPRESSION TAG	UNP P04626
C	1032	ALA	-	EXPRESSION TAG	UNP P04626
C	1033	SER	-	EXPRESSION TAG	UNP P04626
C	1034	HIS	-	EXPRESSION TAG	UNP P04626
C	1035	HIS	-	EXPRESSION TAG	UNP P04626
C	1036	HIS	-	EXPRESSION TAG	UNP P04626

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Chain	Residue	Modelled	Actual	Comment	Reference
C	1037	HIS	-	EXPRESSION TAG	UNP P04626
C	1038	HIS	-	EXPRESSION TAG	UNP P04626
C	1039	HIS	-	EXPRESSION TAG	UNP P04626
D	702	MET	-	EXPRESSION TAG	UNP P04626
D	703	SER	-	EXPRESSION TAG	UNP P04626
D	704	GLY	-	EXPRESSION TAG	UNP P04626
D	705	ALA	-	EXPRESSION TAG	UNP P04626
D	706	ALA	-	EXPRESSION TAG	UNP P04626
D	707	PRO	-	EXPRESSION TAG	UNP P04626
D	708	ASN	-	EXPRESSION TAG	UNP P04626
D	709	GLN	-	EXPRESSION TAG	UNP P04626
D	710	ALA	-	EXPRESSION TAG	UNP P04626
D	711	LEU	-	EXPRESSION TAG	UNP P04626
D	712	LEU	-	EXPRESSION TAG	UNP P04626
D	1029	GLY	-	EXPRESSION TAG	UNP P04626
D	1030	ALA	-	EXPRESSION TAG	UNP P04626
D	1031	ALA	-	EXPRESSION TAG	UNP P04626
D	1032	ALA	-	EXPRESSION TAG	UNP P04626
D	1033	SER	-	EXPRESSION TAG	UNP P04626
D	1034	HIS	-	EXPRESSION TAG	UNP P04626
D	1035	HIS	-	EXPRESSION TAG	UNP P04626
D	1036	HIS	-	EXPRESSION TAG	UNP P04626
D	1037	HIS	-	EXPRESSION TAG	UNP P04626
D	1038	HIS	-	EXPRESSION TAG	UNP P04626
D	1039	HIS	-	EXPRESSION TAG	UNP P04626

- Molecule 2 is N-{2-[4-({3-CHLORO-4-[3-(TRIFLUOROMETHYL)PHENOXY]PHENYL} AMINO)-5H-PYRROLO[3,2-D]PYRIMIDIN-5-YL]ETHYL}-3-HYDROXY-3-METHYLBUTANAMIDE (three-letter code: 03P) (formula: C₂₆H₂₅ClF₃N₅O₃).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	Cl	F	N	O	0	0
			38	26	1	3	5	3		
2	C	1	Total	C	Cl	F	N	O	0	0
			38	26	1	3	5	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	10	Total	O	0	0
			10	10		
3	B	9	Total	O	0	0
			9	9		
3	C	5	Total	O	0	0
			5	5		
3	D	10	Total	O	0	0
			10	10		

Age Group	Percentage
18-24	45%
25-34	35%
35-44	15%
45-54	5%
55-64	2%
65-74	1%
75-84	1%
85+	1%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	50.54Å 64.94Å 92.36Å 90.42° 89.72° 90.35°	Depositor
Resolution (Å)	40.00 – 3.21 46.18 – 3.21	Depositor EDS
% Data completeness (in resolution range)	76.0 (40.00-3.21) 75.9 (46.18-3.21)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 3.19Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.224 , 0.294 0.220 , 0.293	Depositor DCC
R_{free} test set	749 reflections (5.43%)	DCC
Wilson B-factor (Å ²)	52.2	Xtriage
Anisotropy	0.519	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 24.2	EDS
Estimated twinning fraction	0.058 for h,-k,-l 0.348 for -h,k,-l 0.056 for -h,-k,l	Xtriage
L-test for twinning	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 14545 reflections	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	8970	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities 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: 03P

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	0/2297	0.71	4/3104 (0.1%)
1	B	0.41	0/2220	0.58	0/3000
1	C	0.44	0/2297	0.74	6/3104 (0.2%)
1	D	0.41	0/2220	0.58	0/3000
All	All	0.43	0/9034	0.66	10/12208 (0.1%)

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	756	ARG	NE-CZ-NH1	-11.85	114.38	120.30
1	C	756	ARG	NE-CZ-NH2	10.29	125.44	120.30
1	A	756	ARG	NE-CZ-NH1	9.81	125.20	120.30
1	C	1006	ARG	NE-CZ-NH1	-7.88	116.36	120.30
1	A	756	ARG	NE-CZ-NH2	-7.71	116.45	120.30

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	2254	0	0	15	0
1	B	2176	0	0	4	0
1	C	2254	0	0	13	0
1	D	2176	0	0	5	0
2	A	38	0	0	0	0
2	C	38	0	0	0	0
3	A	10	0	0	1	0
3	B	9	0	0	0	0
3	C	5	0	0	0	0
3	D	10	0	0	0	0
All	All	8970	0	0	37	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 4.

The worst 5 of 37 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:A:940:ARG:NH1	3:A:2:HOH:O	2.14	0.80
1:C:809:HIS:O	1:C:813:ASN:ND2	2.35	0.59
1:C:751:ALA:N	1:C:798:THR:O	2.36	0.58
1:A:809:HIS:O	1:A:813:ASN:ND2	2.37	0.56
1:A:751:ALA:N	1:A:798:THR:O	2.39	0.56

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	271/338 (80%)	245 (90%)	19 (7%)	7 (3%)	8	47
1	B	263/338 (78%)	236 (90%)	24 (9%)	3 (1%)	21	72
1	C	271/338 (80%)	244 (90%)	19 (7%)	8 (3%)	7	42
1	D	263/338 (78%)	235 (89%)	25 (10%)	3 (1%)	21	72
All	All	1068/1352 (79%)	960 (90%)	87 (8%)	21 (2%)	11	56

5 of 21 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1018	VAL
1	B	864	PHE
1	C	1018	VAL
1	D	864	PHE
1	A	863	ASP

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	250/293 (85%)	210 (84%)	40 (16%)	3	16
1	B	241/293 (82%)	215 (89%)	26 (11%)	9	37
1	C	250/293 (85%)	211 (84%)	39 (16%)	4	17
1	D	241/293 (82%)	215 (89%)	26 (11%)	9	37
All	All	982/1172 (84%)	851 (87%)	131 (13%)	6	27

5 of 131 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	896	ARG
1	C	764	ASN
1	D	863	ASP
1	B	953	MET
1	C	711	LEU

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	03P	A	9001	-	41,41,41	1.05	4 (9%)	59,60,60	1.46	7 (11%)
2	03P	C	9001	-	41,41,41	0.99	3 (7%)	59,60,60	1.48	9 (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	03P	A	9001	-	-	0/25/25/25	0/2/4/4
2	03P	C	9001	-	-	0/25/25/25	0/2/4/4

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	9001	03P	C1-C3	-2.99	1.38	1.44
2	C	9001	03P	C1-C3	-2.67	1.38	1.44
2	A	9001	03P	C8-N3	2.22	1.38	1.33
2	C	9001	03P	C3-C2	-2.18	1.38	1.44
2	C	9001	03P	C1-N4	2.15	1.40	1.36

The worst 5 of 16 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	9001	03P	C9-C8-N3	-4.64	110.55	115.68
2	A	9001	03P	N4-C1-N1	4.48	123.49	118.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	9001	03P	C-N-C2	-4.18	112.14	115.37
2	A	9001	03P	C13-C12-CL	3.99	124.67	119.45
2	C	9001	03P	C13-C12-CL	3.98	124.65	119.45

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, 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	281/338 (83%)	-0.31	0 100 100	28, 42, 77, 97	3 (1%)
1	B	271/338 (80%)	-0.19	0 100 100	35, 56, 86, 107	5 (1%)
1	C	281/338 (83%)	-0.29	0 100 100	28, 43, 81, 99	5 (1%)
1	D	271/338 (80%)	-0.17	0 100 100	36, 55, 84, 108	5 (1%)
All	All	1104/1352 (81%)	-0.24	0 100 100	28, 49, 84, 108	18 (1%)

There are no RSRZ outliers to report.

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	03P	A	9001	38/38	0.19	-0.05	31,34,42,43	0
2	03P	C	9001	38/38	0.18	-0.37	45,46,47,48	0

6.5 Other polymers ⓘ

There are no such residues in this entry.