



wwPDB X-ray Structure Validation Summary Report ⓘ

Apr 25, 2026 – 10:31 AM EDT

PDB ID : 2RF9 / pdb_00002rf9
Title : Crystal structure of the complex between the EGFR kinase domain and a Mig6 peptide
Authors : Zhang, X.; Pickin, K.A.; Bose, R.; Jura, N.; Cole, P.A.; Kuriyan, J.
Deposited on : 2007-09-28
Resolution : 3.50 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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Xtrriage (Phenix) : 2.0
EDS : 3.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

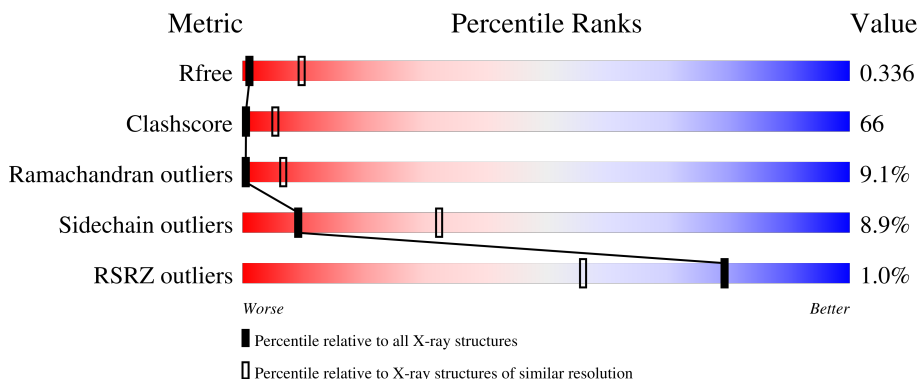
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.50 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))
R_{free}	180053	1085 (3.54-3.46)
Clashscore	190562	1140 (3.54-3.46)
Ramachandran outliers	187476	1113 (3.54-3.46)
Sidechain outliers	187428	1114 (3.54-3.46)
RSRZ outliers	180081	1084 (3.54-3.46)

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 $\leq 5\%$. 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	330	
1	B	330	
2	C	65	
2	D	65	

2 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 4435 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 Epidermal growth factor receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	280	2068	1336	345	372	15	0	0	0
1	B	269	2010	1298	334	363	15	0	0	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	669	GLY	-	expression tag	UNP P00533
A	670	ALA	-	expression tag	UNP P00533
A	671	MET	-	expression tag	UNP P00533
B	669	GLY	-	expression tag	UNP P00533
B	670	ALA	-	expression tag	UNP P00533
B	671	MET	-	expression tag	UNP P00533

- Molecule 2 is a protein called ERBB receptor feedback inhibitor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	27	183	119	27	36	1	0	0	0
2	D	26	174	113	26	34	1	0	0	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	310	GLY	-	expression tag	UNP Q9UJM3
C	311	PRO	-	expression tag	UNP Q9UJM3
C	312	LEU	-	expression tag	UNP Q9UJM3
C	313	GLY	-	expression tag	UNP Q9UJM3
C	314	SER	-	expression tag	UNP Q9UJM3
D	310	GLY	-	expression tag	UNP Q9UJM3

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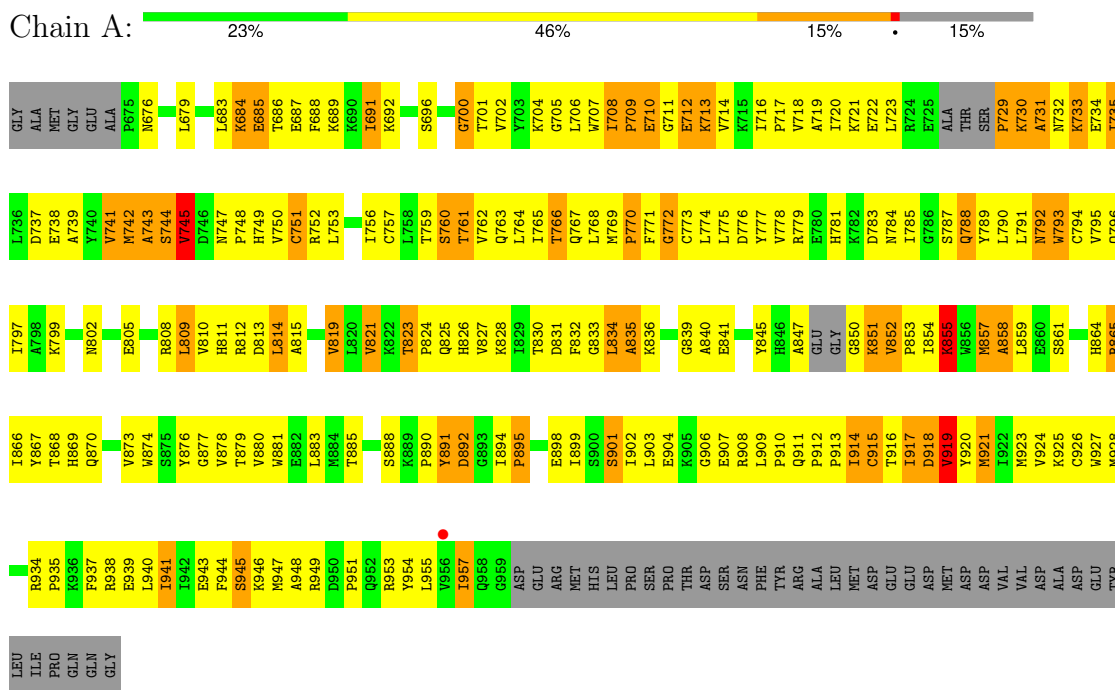
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Chain	Residue	Modelled	Actual	Comment	Reference
D	311	PRO	-	expression tag	UNP Q9UJM3
D	312	LEU	-	expression tag	UNP Q9UJM3
D	313	GLY	-	expression tag	UNP Q9UJM3
D	314	SER	-	expression tag	UNP Q9UJM3

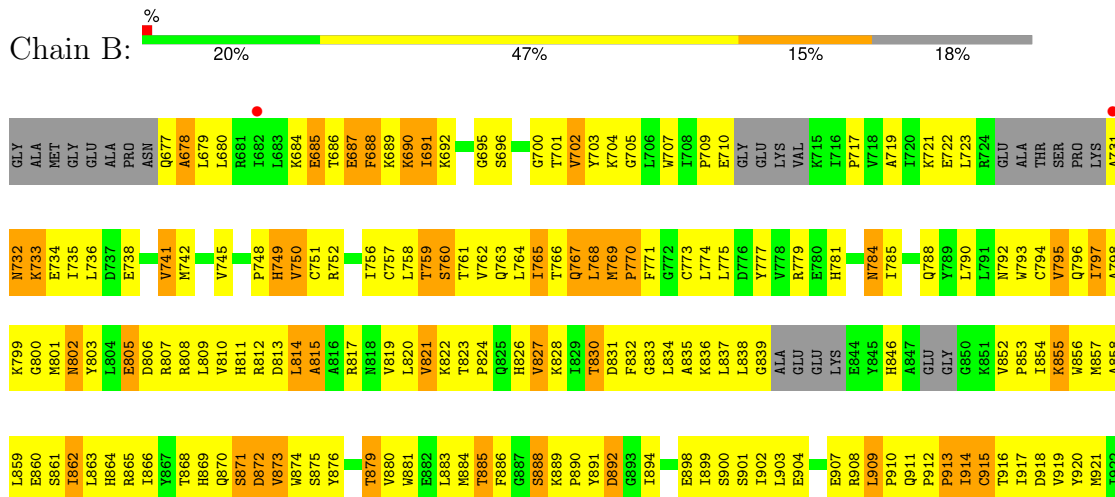
3 Residue-property plots

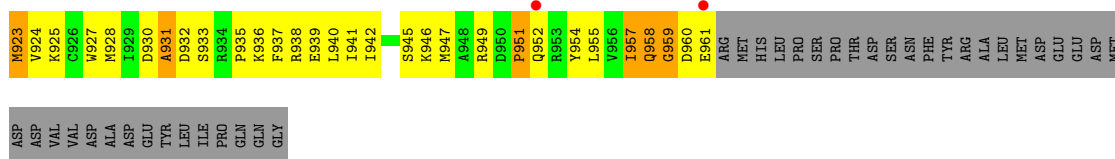
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Epidermal growth factor receptor

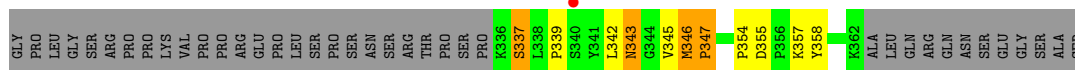
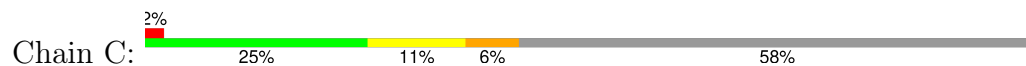


- Molecule 1: Epidermal growth factor receptor

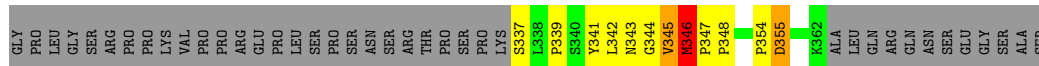




- Molecule 2: ERBB receptor feedback inhibitor 1



- Molecule 2: ERBB receptor feedback inhibitor 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	188.76Å 42.65Å 99.73Å 90.00° 109.12° 90.00°	Depositor
Resolution (Å)	47.11 – 3.50 47.11 – 3.50	Depositor EDS
% Data completeness (in resolution range)	84.5 (47.11-3.50) 84.5 (47.11-3.50)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.19 (at 3.48Å)	Xtrriage
Refinement program	CNS	Depositor
R, R_{free}	0.272 , 0.329 0.275 , 0.336	Depositor DCC
R_{free} test set	495 reflections (5.45%)	wwPDB-VP
Wilson B-factor (Å ²)	70.1	Xtrriage
Anisotropy	0.699	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 115.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	4435	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.45% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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	0.62	0/2114	1.18	19/2887 (0.7%)
1	B	0.60	0/2054	1.18	22/2800 (0.8%)
2	C	0.86	0/190	1.35	4/264 (1.5%)
2	D	0.73	0/181	1.39	6/251 (2.4%)
All	All	0.63	0/4539	1.20	51/6202 (0.8%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

The worst 5 of 51 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	731	ALA	N-CA-C	-9.85	101.46	113.19
1	B	760	SER	N-CA-C	-9.82	100.98	113.16
1	B	822	LYS	N-CA-C	-9.57	100.81	111.14
1	A	700	GLY	N-CA-C	9.16	120.65	111.95
1	A	760	SER	N-CA-C	-8.74	103.14	112.93

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	891	TYR	Sidechain

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	2068	0	1961	271	0
1	B	2010	0	1902	271	0
2	C	183	0	152	22	0
2	D	174	0	138	28	0
All	All	4435	0	4153	570	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 66.

The worst 5 of 570 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)
2:D:341:TYR:CE2	2:D:347:PRO:HD2	1.80	1.17
1:A:880:VAL:HB	1:A:923:MET:HE3	1.34	1.09
2:D:341:TYR:HE2	2:D:347:PRO:HD2	0.95	1.09
2:D:339:PRO:CB	2:D:341:TYR:HE1	1.71	1.03
1:A:907:GLU:O	1:A:908:ARG:HD3	1.57	1.03

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	274/330 (83%)	188 (69%)	57 (21%)	29 (11%)	0 5
1	B	259/330 (78%)	183 (71%)	54 (21%)	22 (8%)	0 7

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
2	C	25/65 (38%)	21 (84%)	3 (12%)	1 (4%)	2 19
2	D	24/65 (37%)	15 (62%)	8 (33%)	1 (4%)	2 19
All	All	582/790 (74%)	407 (70%)	122 (21%)	53 (9%)	0 7

5 of 53 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	713	LYS
1	A	730	LYS
1	A	751	CYS
1	A	788	GLN
1	A	835	ALA

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	203/288 (70%)	183 (90%)	20 (10%)	7 29
1	B	200/288 (69%)	182 (91%)	18 (9%)	9 32
2	C	18/58 (31%)	18 (100%)	0	100 100
2	D	16/58 (28%)	15 (94%)	1 (6%)	16 42
All	All	437/692 (63%)	398 (91%)	39 (9%)	9 32

5 of 39 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	784	ASN
1	B	909	LEU
1	B	795	VAL
1	B	862	ILE
1	B	957	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 13 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	784	ASN
1	B	788	GLN
1	B	911	GLN
1	B	811	HIS
1	B	825	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](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides 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, 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	280/330 (84%)	0.15	1 (0%) 88 72	24, 62, 106, 126	0
1	B	269/330 (81%)	0.23	4 (1%) 72 47	41, 71, 102, 111	0
2	C	27/65 (41%)	0.65	1 (3%) 45 25	71, 84, 98, 100	0
2	D	26/65 (40%)	0.42	0 100 100	68, 83, 92, 102	0
All	All	602/790 (76%)	0.22	6 (0%) 79 56	24, 70, 102, 126	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	961	GLU	2.9
1	B	952	GLN	2.8
1	B	731	ALA	2.4
2	C	340	SER	2.3
1	A	956	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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.