



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:25 AM UTC

PDB ID : 3EUU / pdb_00003euu
Title : Crystal structure of the FGFR2 D2 domain
Authors : Sakon, J.; Guo, F.; Dakshinamurthy, R.; Kathir, K.M.; Thallapuranam, S.K.K.
Deposited on : 2008-10-10
Resolution : 2.34 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 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
Xtriage (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

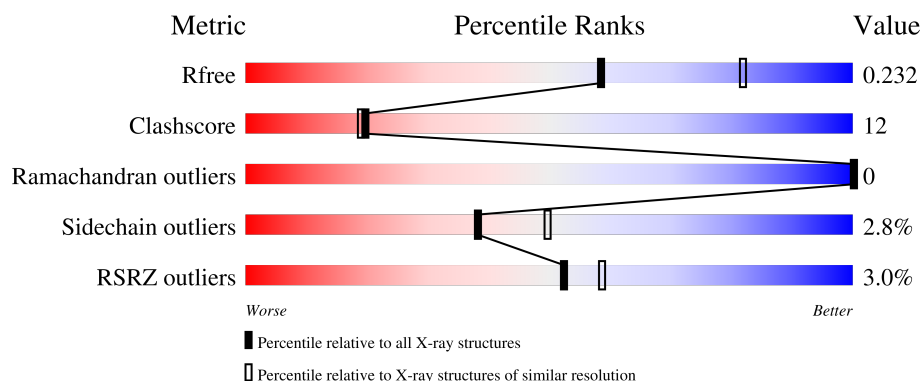
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.34 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	3031 (2.36-2.32)
Clashscore	190562	3127 (2.36-2.32)
Ramachandran outliers	187476	3095 (2.36-2.32)
Sidechain outliers	187428	3095 (2.36-2.32)
RSRZ outliers	180081	3033 (2.36-2.32)

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	100	
1	B	100	

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1729 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 Fibroblast growth factor receptor 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	100	Total	C	N	O	S	0	0	0
			814	513	151	144	6			
1	B	100	Total	C	N	O	S	0	0	0
			814	513	151	144	6			

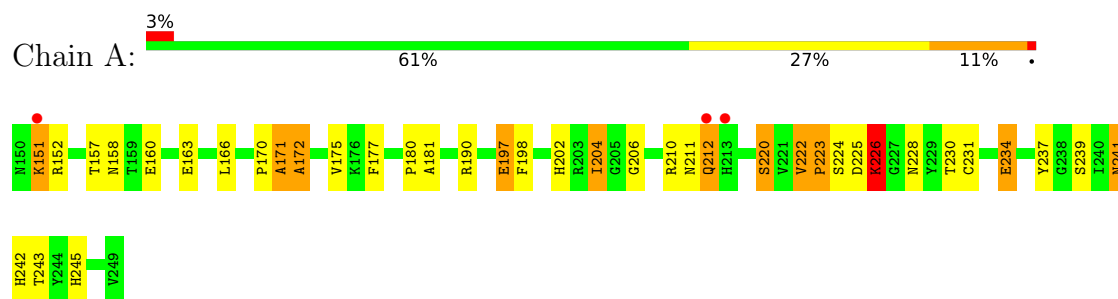
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	54	Total	O	0	0
			54	54		
2	B	47	Total	O	0	0
			47	47		

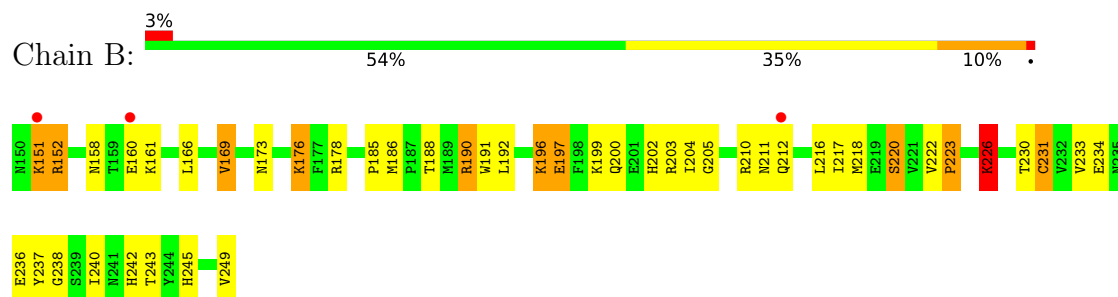
3 Residue-property plots

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: Fibroblast growth factor receptor 2



- Molecule 1: Fibroblast growth factor receptor 2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	106.10Å 42.46Å 79.62Å 90.00° 124.99° 90.00°	Depositor
Resolution (Å)	22.18 – 2.34 22.18 – 2.35	Depositor EDS
% Data completeness (in resolution range)	89.4 (22.18-2.34) 90.0 (22.18-2.35)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.85 (at 2.36Å)	Xtriage
Refinement program	REFMAC 5.3.0032	Depositor
R, R_{free}	0.184 , 0.228 0.186 , 0.232	Depositor DCC
R_{free} test set	533 reflections (4.77%)	wwPDB-VP
Wilson B-factor (Å ²)	27.3	Xtriage
Anisotropy	0.124	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 56.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	1729	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 12.85% 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 ⓘ

5.1 Standard geometry ⓘ

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	2.11	28/837 (3.3%)	1.41	8/1132 (0.7%)
1	B	2.15	32/837 (3.8%)	1.30	6/1132 (0.5%)
All	All	2.13	60/1674 (3.6%)	1.36	14/2264 (0.6%)

All (60) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	220	SER	CA-C	-10.17	1.42	1.53
1	A	172	ALA	N-CA	-9.38	1.28	1.46
1	A	242	HIS	CA-C	8.17	1.62	1.52
1	A	177	PHE	CA-C	7.92	1.62	1.52
1	A	202	HIS	C-O	-7.80	1.13	1.24
1	B	240	ILE	CA-CB	-7.64	1.43	1.55
1	B	160	GLU	CA-C	-7.05	1.43	1.52
1	A	220	SER	N-CA	7.04	1.56	1.46
1	A	223	PRO	C-O	-6.91	1.15	1.24
1	A	210	ARG	CA-C	6.90	1.61	1.53
1	B	190	ARG	CB-CG	-6.74	1.32	1.52
1	A	222	VAL	N-CA	-6.73	1.40	1.46
1	A	152	ARG	CB-CG	-6.71	1.32	1.52
1	A	228	ASN	CA-C	6.57	1.60	1.52
1	B	152	ARG	CB-CG	-6.46	1.33	1.52
1	B	192	LEU	CA-C	6.46	1.60	1.52
1	B	205	GLY	C-O	6.42	1.31	1.23
1	B	176	LYS	N-CA	-6.42	1.39	1.46
1	B	217	ILE	CA-CB	6.42	1.62	1.54
1	B	212	GLN	CG-CD	6.37	1.68	1.52
1	B	242	HIS	CA-C	6.31	1.60	1.52
1	B	169	VAL	CA-CB	6.28	1.62	1.54
1	A	224	SER	CA-C	6.23	1.61	1.52
1	A	230	THR	CA-C	-6.21	1.45	1.52
1	A	243	THR	N-CA	-6.07	1.38	1.46
1	A	226	LYS	CD-CE	6.04	1.70	1.52

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	220	SER	CA-C	-5.96	1.47	1.53
1	B	196	LYS	N-CA	5.93	1.52	1.45
1	A	151	LYS	CA-C	5.82	1.60	1.52
1	B	238	GLY	C-O	5.80	1.31	1.23
1	B	243	THR	CA-C	5.78	1.59	1.52
1	A	231	CYS	C-O	5.71	1.30	1.24
1	B	151	LYS	CA-C	5.69	1.60	1.52
1	B	173	ASN	C-O	5.69	1.31	1.23
1	B	233	VAL	CA-C	5.65	1.59	1.52
1	B	210	ARG	CA-C	5.63	1.60	1.53
1	B	216	LEU	CA-C	5.62	1.59	1.52
1	A	190	ARG	CB-CG	-5.62	1.35	1.52
1	A	160	GLU	CA-C	-5.58	1.45	1.52
1	A	206	GLY	N-CA	5.52	1.55	1.45
1	B	188	THR	C-O	5.49	1.30	1.23
1	B	222	VAL	N-CA	-5.41	1.42	1.46
1	B	231	CYS	CA-C	5.41	1.59	1.52
1	B	176	LYS	C-O	-5.39	1.18	1.24
1	A	175	VAL	CB-CG2	-5.38	1.34	1.52
1	B	173	ASN	CA-C	5.38	1.60	1.53
1	A	151	LYS	N-CA	-5.38	1.38	1.45
1	B	204	ILE	CA-C	-5.29	1.46	1.52
1	A	180	PRO	N-CA	5.21	1.54	1.47
1	A	212	GLN	CG-CD	5.17	1.65	1.52
1	B	211	ASN	N-CA	5.16	1.52	1.46
1	A	204	ILE	CA-C	-5.15	1.46	1.52
1	B	197	GLU	CD-OE2	5.15	1.35	1.25
1	B	186	MET	N-CA	5.12	1.52	1.45
1	A	198	PHE	N-CA	-5.07	1.40	1.46
1	A	197	GLU	CG-CD	5.06	1.64	1.52
1	B	230	THR	CA-C	-5.06	1.46	1.52
1	B	231	CYS	C-O	5.02	1.30	1.24
1	A	181	ALA	C-O	-5.01	1.17	1.23
1	B	243	THR	N-CA	-5.00	1.40	1.46

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	171	ALA	CA-C-N	9.27	138.38	121.70
1	A	171	ALA	C-N-CA	9.27	138.38	121.70
1	A	171	ALA	N-CA-C	-8.85	98.74	110.24
1	B	238	GLY	N-CA-C	8.15	120.66	110.96

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	234	GLU	N-CA-C	7.46	121.28	109.50
1	A	234	GLU	N-CA-C	6.97	120.04	109.23
1	A	171	ALA	O-C-N	-6.54	114.44	122.82
1	A	172	ALA	N-CA-C	-6.11	93.89	111.00
1	A	211	ASN	N-CA-C	6.09	118.70	111.33
1	B	211	ASN	N-CA-C	5.82	118.38	111.33
1	B	226	LYS	N-CA-CB	5.56	118.21	110.04
1	B	151	LYS	CB-CA-C	5.25	118.40	109.53
1	A	152	ARG	CG-CD-NE	-5.23	100.49	112.00
1	B	160	GLU	CA-CB-CG	-5.08	103.94	114.10

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	814	0	794	15	2
1	B	814	0	794	22	0
2	A	54	0	0	6	1
2	B	47	0	0	13	0
All	All	1729	0	1588	37	2

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 12.

All (37) 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:B:237:TYR:CD1	2:B:34:HOH:O	1.87	1.26
1:B:196:LYS:HD2	2:B:94:HOH:O	1.50	1.12
1:A:197:GLU:HG3	2:A:44:HOH:O	1.68	0.93
1:B:223:PRO:O	1:B:226:LYS:HD2	1.70	0.92
1:A:223:PRO:O	1:A:226:LYS:HD2	1.77	0.84
1:B:190:ARG:HD3	2:B:56:HOH:O	1.80	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:249:VAL:C	2:B:101:HOH:O	2.29	0.75
1:A:151:LYS:HE3	1:A:237:TYR:OH	1.93	0.69
1:B:197:GLU:HG3	2:B:42:HOH:O	1.95	0.66
1:B:151:LYS:HE3	1:B:237:TYR:OH	1.97	0.65
1:B:158:ASN:ND2	1:B:161:LYS:HD2	2.13	0.64
1:A:226:LYS:HG3	2:A:68:HOH:O	2.00	0.61
1:B:237:TYR:CE1	2:B:34:HOH:O	2.34	0.56
1:A:151:LYS:CE	1:A:237:TYR:OH	2.55	0.53
1:B:152:ARG:N	2:B:34:HOH:O	2.42	0.53
1:A:163:GLU:HG3	2:A:51:HOH:O	2.09	0.51
1:B:151:LYS:CE	1:B:237:TYR:OH	2.58	0.51
1:B:200:GLN:HG2	2:B:60:HOH:O	2.11	0.50
1:B:220:SER:HB3	2:B:70:HOH:O	2.12	0.49
1:B:176:LYS:HE3	2:B:30:HOH:O	2.11	0.49
1:A:166:LEU:HD23	1:A:245:HIS:HB3	1.95	0.48
1:A:158:ASN:C	1:A:158:ASN:HD22	2.23	0.47
1:A:234:GLU:HG2	1:A:239:SER:OG	2.15	0.47
1:B:203:ARG:HD2	1:B:218:MET:HE3	1.97	0.47
1:B:178:ARG:HD3	2:B:24:HOH:O	2.15	0.46
1:A:172:ALA:HB1	2:A:71:HOH:O	2.16	0.45
1:A:212:GLN:H	1:A:212:GLN:CD	2.24	0.45
1:B:199:LYS:HE2	1:B:202:HIS:HE1	1.83	0.44
1:B:185:PRO:HG2	2:B:11:HOH:O	2.17	0.44
1:A:220:SER:HB3	2:A:71:HOH:O	2.17	0.43
1:A:170:PRO:O	1:A:171:ALA:C	2.61	0.42
1:B:166:LEU:HD23	1:B:245:HIS:HB3	2.02	0.41
1:B:236:GLU:OE1	2:B:86:HOH:O	2.21	0.41
1:B:226:LYS:HE3	1:B:226:LYS:HB3	1.85	0.41
1:B:191:TRP:CH2	1:B:231:CYS:HB3	2.55	0.41
1:A:222:VAL:O	1:A:225:ASP:HB2	2.21	0.41
1:A:241:ASN:ND2	2:A:1:HOH:O	2.54	0.40

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:THR:O	1:A:157:THR:O[2_454]	1.68	0.52
1:A:204:ILE:CG1	2:A:92:HOH:O[4_454]	2.15	0.05

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	98/100 (98%)	94 (96%)	4 (4%)	0	100	100
1	B	98/100 (98%)	95 (97%)	3 (3%)	0	100	100
All	All	196/200 (98%)	189 (96%)	7 (4%)	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	88/88 (100%)	86 (98%)	2 (2%)	44	56
1	B	88/88 (100%)	85 (97%)	3 (3%)	32	42
All	All	176/176 (100%)	171 (97%)	5 (3%)	38	50

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	226	LYS
1	A	241	ASN
1	B	169	VAL
1	B	223	PRO
1	B	226	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	158	ASN
1	A	241	ASN
1	B	241	ASN

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	100/100 (100%)	-0.14	3 (3%) 52 59	16, 29, 56, 66	0
1	B	100/100 (100%)	-0.19	3 (3%) 52 59	16, 30, 57, 66	0
All	All	200/200 (100%)	-0.17	6 (3%) 52 59	16, 30, 57, 66	0

All (6) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	151	LYS	2.2
1	B	212	GLN	2.2
1	B	160	GLU	2.1
1	A	212	GLN	2.1
1	A	213	HIS	2.1
1	B	151	LYS	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.