



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:50 AM UTC

PDB ID : 1FMK / pdb_00001fmk
Title : CRYSTAL STRUCTURE OF HUMAN TYROSINE-PROTEIN KINASE C-SRC
Authors : Xu, W.; Harrison, S.C.; Eck, M.J.
Deposited on : 1997-01-24
Resolution : 1.50 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 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
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

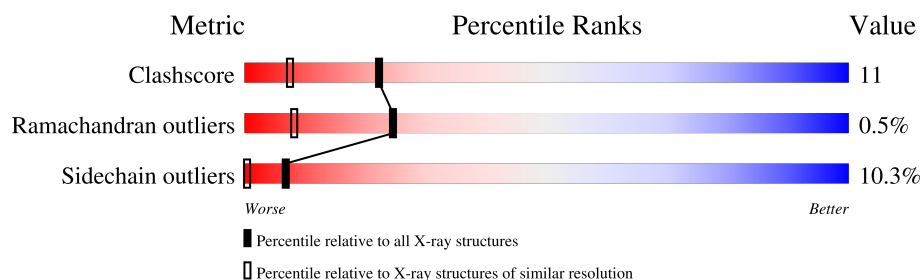
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.50 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	190562	4235 (1.50-1.50)
Ramachandran outliers	187476	4153 (1.50-1.50)
Sidechain outliers	187428	4150 (1.50-1.50)

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 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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	452	 72% 19% 6%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 4006 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 TYROSINE-PROTEIN KINASE SRC.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	P	S			
1	A	438	3516	2235	597	663	1	20	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	527	PTR	TYR	modified residue	UNP P12931

- Molecule 2 is water.

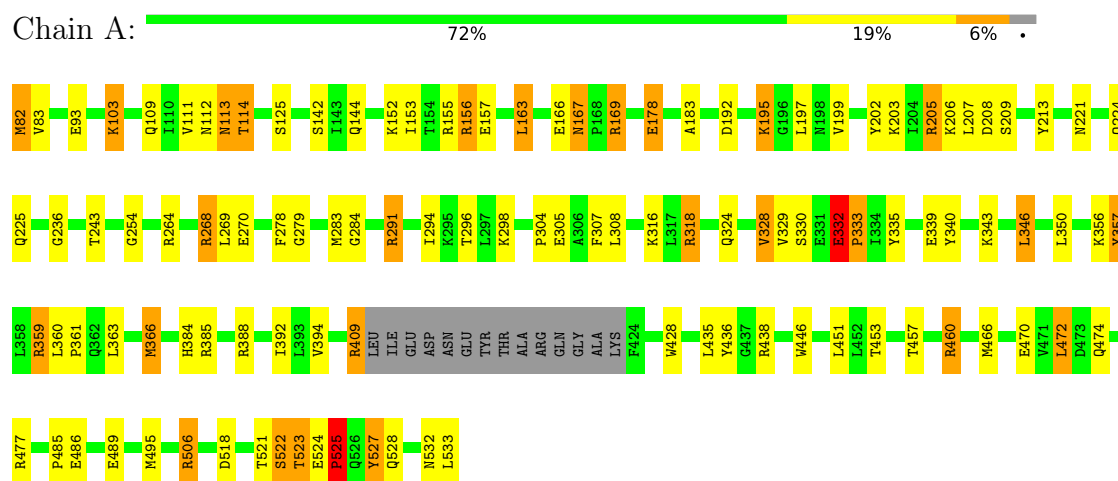
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	490	Total	O	0	0
			490	490		

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. 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: TYROSINE-PROTEIN KINASE SRC



4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	51.76Å 87.38Å 101.30Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 1.50	Depositor
% Data completeness (in resolution range)	(Not available) (20.00-1.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	0.05	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.210 , 0.264	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4006	wwPDB-VP
Average B, all atoms (Å ²)	29.0	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: 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	0.70	1/3581 (0.0%)	0.88	4/4849 (0.1%)

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	9

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	366	MET	SD-CE	-5.28	1.66	1.79

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	332	GLU	CA-C-N	7.05	128.65	119.84
1	A	332	GLU	C-N-CA	7.05	128.65	119.84
1	A	522	SER	N-CA-C	5.19	121.86	110.80
1	A	82	MET	CB-CA-C	-5.11	100.40	110.10

There are no chirality outliers.

All (9) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	156	ARG	Sidechain
1	A	169	ARG	Sidechain

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Mol	Chain	Res	Type	Group
1	A	205	ARG	Sidechain
1	A	268	ARG	Sidechain
1	A	291	ARG	Sidechain
1	A	332	GLU	Peptide
1	A	359	ARG	Sidechain
1	A	409	ARG	Sidechain
1	A	506	ARG	Sidechain

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	3516	0	3457	74	1
2	A	490	0	0	15	1
All	All	4006	0	3457	74	1

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 11.

All (74) 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:155:ARG:HD2	1:A:524:GLU:CB	1.91	0.99
1:A:155:ARG:HD2	1:A:524:GLU:HB3	0.98	0.98
1:A:155:ARG:CD	1:A:524:GLU:HB3	1.94	0.98
1:A:236:GLY:HA2	1:A:532:ASN:HB2	1.46	0.96
1:A:207:LEU:HD21	1:A:213:TYR:CE2	2.06	0.90
1:A:523:THR:HG23	2:A:1235:HOH:O	1.76	0.86
1:A:207:LEU:HD21	1:A:213:TYR:HE2	1.40	0.83
1:A:457:THR:O	1:A:460:ARG:HG3	1.79	0.82
1:A:318:ARG:HD3	2:A:1365:HOH:O	1.79	0.80
1:A:474:GLN:HE22	1:A:477:ARG:HH11	1.32	0.78
1:A:357:TYR:HD2	2:A:1417:HOH:O	1.68	0.74
1:A:144:GLN:H	1:A:144:GLN:NE2	1.86	0.73
1:A:203:LYS:HG2	2:A:1321:HOH:O	1.88	0.72
1:A:142:SER:HB2	1:A:144:GLN:NE2	2.06	0.70

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:474:GLN:NE2	1:A:477:ARG:HH11	1.90	0.70
1:A:485:PRO:O	1:A:486:GLU:HB2	1.89	0.70
1:A:113:ASN:HD22	1:A:113:ASN:H	1.40	0.69
1:A:142:SER:HB2	1:A:144:GLN:HE22	1.56	0.69
1:A:167:ASN:HB2	2:A:1328:HOH:O	1.92	0.68
1:A:264:ARG:NH2	1:A:333:PRO:HD2	2.09	0.68
1:A:359:ARG:HB3	1:A:361:PRO:HD2	1.76	0.67
1:A:279:GLY:HA3	1:A:296:THR:O	1.94	0.66
1:A:221:ASN:HB2	2:A:1474:HOH:O	1.97	0.63
1:A:269:LEU:HD23	1:A:294:ILE:HD13	1.79	0.63
1:A:254:GLY:H	1:A:324:GLN:HE22	1.44	0.63
1:A:114:THR:HG22	2:A:1293:HOH:O	2.02	0.59
1:A:269:LEU:HD21	1:A:294:ILE:HG21	1.84	0.59
1:A:278:PHE:HZ	2:A:1458:HOH:O	1.86	0.57
1:A:278:PHE:O	1:A:298:LYS:HG3	2.05	0.56
1:A:524:GLU:HA	1:A:524:GLU:OE1	2.06	0.55
1:A:270:GLU:HG2	1:A:284:GLY:HA2	1.89	0.55
1:A:254:GLY:H	1:A:324:GLN:NE2	2.05	0.54
1:A:329:VAL:HB	1:A:335:TYR:HB2	1.89	0.54
1:A:474:GLN:HE22	1:A:477:ARG:NH1	2.03	0.53
1:A:167:ASN:C	1:A:167:ASN:HD22	2.16	0.53
1:A:225:GLN:HG2	2:A:1462:HOH:O	2.08	0.53
1:A:269:LEU:CD2	1:A:294:ILE:HD13	2.39	0.52
1:A:524:GLU:N	1:A:525:PRO:HD3	2.24	0.52
1:A:453:THR:HG22	1:A:495:MET:SD	2.48	0.52
1:A:264:ARG:CZ	1:A:333:PRO:HD2	2.40	0.51
1:A:183:ALA:HB1	2:A:1321:HOH:O	2.11	0.50
1:A:163:LEU:HD12	1:A:197:LEU:HG	1.95	0.49
1:A:283:MET:HG3	1:A:340:TYR:CE1	2.48	0.49
1:A:142:SER:CB	1:A:144:GLN:NE2	2.78	0.47
1:A:466:MET:HA	1:A:470:GLU:OE1	2.15	0.47
1:A:388:ARG:HB3	1:A:428:TRP:CD1	2.50	0.47
1:A:346:LEU:HB2	1:A:392:ILE:HB	1.97	0.46
1:A:192:ASP:OD2	1:A:195:LYS:HD2	2.16	0.46
1:A:207:LEU:HD12	2:A:1324:HOH:O	2.15	0.46
1:A:384:HIS:O	1:A:385:ARG:HB2	2.17	0.45
1:A:156:ARG:HD2	2:A:1152:HOH:O	2.16	0.45
1:A:308:LEU:HD21	1:A:330:SER:OG	2.17	0.45
1:A:112:ASN:ND2	2:A:1041:HOH:O	2.49	0.45
1:A:307:PHE:CE2	1:A:328:VAL:HG21	2.53	0.44
1:A:103:LYS:H	1:A:103:LYS:HG3	1.68	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:83:VAL:HG11	1:A:109:GLN:HB3	2.00	0.43
1:A:83:VAL:HG22	1:A:111:VAL:HG22	2.00	0.43
1:A:363:LEU:HD23	1:A:366:MET:CE	2.49	0.42
1:A:524:GLU:HG2	2:A:1152:HOH:O	2.18	0.42
1:A:518:ASP:HA	1:A:522:SER:H	1.83	0.42
1:A:360:LEU:HB3	1:A:361:PRO:HD3	2.02	0.42
1:A:178:GLU:HG3	1:A:527:PTR:O3P	2.20	0.42
1:A:460:ARG:HH11	1:A:460:ARG:HD2	1.75	0.42
1:A:474:GLN:NE2	1:A:477:ARG:NH1	2.64	0.41
1:A:343:LYS:HB2	1:A:394:VAL:O	2.20	0.41
1:A:153:ILE:HD11	1:A:157:GLU:C	2.46	0.41
1:A:82:MET:HE3	1:A:83:VAL:O	2.20	0.41
1:A:163:LEU:HD13	1:A:199:VAL:HG23	2.03	0.41
1:A:304:PRO:HG3	1:A:332:GLU:HG3	2.02	0.41
1:A:202:TYR:CD1	1:A:528:GLN:HB2	2.55	0.41
1:A:318:ARG:NE	2:A:1301:HOH:O	2.48	0.41
1:A:435:LEU:HD23	1:A:472:LEU:HD11	2.03	0.41
1:A:446:TRP:CD1	1:A:446:TRP:C	2.99	0.41
1:A:436:TYR:HB2	1:A:438:ARG:HG3	2.03	0.40

All (1) 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:82:MET:N	2:A:1256:HOH:O[3_545]	2.19	0.01

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	433/452 (96%)	412 (95%)	19 (4%)	2 (0%)	24 8

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	525	PRO
1	A	333	PRO

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	379/391 (97%)	340 (90%)	39 (10%)	7 0

All (39) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	93	GLU
1	A	103	LYS
1	A	113	ASN
1	A	114	THR
1	A	125	SER
1	A	152	LYS
1	A	163	LEU
1	A	166	GLU
1	A	167	ASN
1	A	169	ARG
1	A	178	GLU
1	A	195	LYS
1	A	205	ARG
1	A	206	LYS
1	A	208	ASP
1	A	209	SER
1	A	224	GLN
1	A	243	THR
1	A	268	ARG
1	A	291	ARG
1	A	305	GLU
1	A	316	LYS
1	A	318	ARG

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Mol	Chain	Res	Type
1	A	328	VAL
1	A	339	GLU
1	A	346	LEU
1	A	350	LEU
1	A	356	LYS
1	A	357	TYR
1	A	409	ARG
1	A	451	LEU
1	A	460	ARG
1	A	472	LEU
1	A	489	GLU
1	A	506	ARG
1	A	521	THR
1	A	523	THR
1	A	525	PRO
1	A	533	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	109	GLN
1	A	113	ASN
1	A	128	GLN
1	A	144	GLN
1	A	164	ASN
1	A	167	ASN
1	A	198	ASN
1	A	251	GLN
1	A	324	GLN
1	A	397	ASN
1	A	474	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	527	1	15,16,17	1.09	1 (6%)	17,22,24	1.21	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	527	1	-	0/10/11/13	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	527	PTR	P-OH	2.28	1.64	1.59

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	527	PTR	CD2-CE2-CZ	-2.59	116.77	119.73

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	527	PTR	1	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry

There are no ligands in this entry.

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.