



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:53 AM UTC

PDB ID : 7XBQ / pdb_00007xbq
Title : Crystal structure of potato 14-3-3 protein St14f
Authors : Harada, K.; Kojima, C.; Yamashita, E.; Nakagawa, A.
Deposited on : 2022-03-21
Resolution : 2.45 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
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

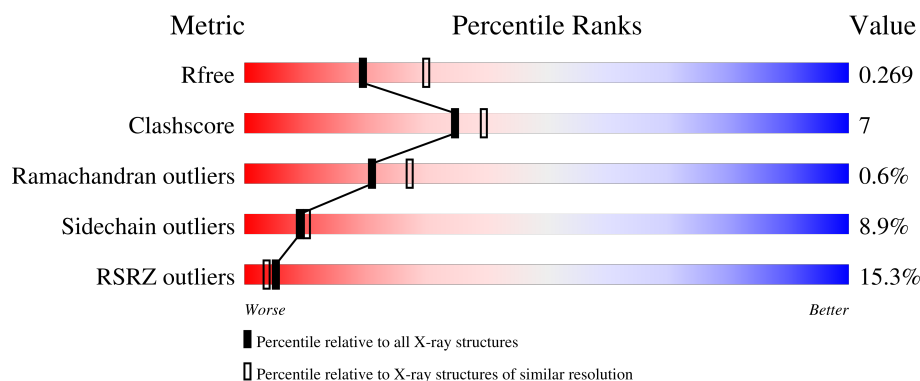
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1190 (2.46-2.46)
Clashscore	190562	1229 (2.46-2.46)
Ramachandran outliers	187476	1218 (2.46-2.46)
Sidechain outliers	187428	1218 (2.46-2.46)
RSRZ outliers	180081	1190 (2.46-2.46)

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	258	7% 65% 21% 5% 10%
1	B	258	5% 72% 16% • 9%
1	C	258	29% 73% 16% • 10%

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5347 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 Putative 14-3-3 protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	233	Total	C	N	O	S	0	0	0
			1823	1142	307	365	9			
1	B	235	Total	C	N	O	S	0	0	0
			1859	1164	316	370	9			
1	C	233	Total	C	N	O	S	0	0	0
			1665	1030	291	336	8			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P93785
A	-2	PRO	-	expression tag	UNP P93785
A	-1	GLY	-	expression tag	UNP P93785
A	0	HIS	-	expression tag	UNP P93785
B	-3	GLY	-	expression tag	UNP P93785
B	-2	PRO	-	expression tag	UNP P93785
B	-1	GLY	-	expression tag	UNP P93785
B	0	HIS	-	expression tag	UNP P93785
C	-3	GLY	-	expression tag	UNP P93785
C	-2	PRO	-	expression tag	UNP P93785
C	-1	GLY	-	expression tag	UNP P93785
C	0	HIS	-	expression tag	UNP P93785

L195	A196	K197	Q198	A199	F200	D201	E202	A203	T204	A205	E206	L207	D208	T209	L210	G211	E212	E213	S214	Y215	K216	D217	S218	T219	R222	Q223	L224	L225	R226	D227	N228	L229	T230	L231	W232	T233	SER	ASP	MET	GLN	ASP	ASP	GLY	ALA	ASP	GLU	ILE	LYS	GLU	THR	LYS	PRO	ASP	ASN	GLU	GLN
------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	230.20Å 105.28Å 60.99Å 90.00° 104.84° 90.00°	Depositor
Resolution (Å)	47.58 – 2.45 47.58 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.3 (47.58-2.45) 99.3 (47.58-2.45)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.72 (at 2.45Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.209 , 0.277 0.202 , 0.269	Depositor DCC
R_{free} test set	2573 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	1.097	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 77.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.016 for -h-2*k,l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5347	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% 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	1.31	5/1850 (0.3%)	1.77	21/2496 (0.8%)
1	B	1.28	2/1886 (0.1%)	1.66	12/2540 (0.5%)
1	C	1.32	2/1686 (0.1%)	1.76	10/2286 (0.4%)
All	All	1.30	9/5422 (0.2%)	1.73	43/7322 (0.6%)

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
1	B	0	1
All	All	0	2

The worst 5 of 9 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	158	ASP	CG-OD1	7.28	1.39	1.25
1	B	35	SER	C-O	-5.98	1.16	1.24
1	C	100	GLY	C-O	5.80	1.30	1.23
1	B	54	ILE	N-CA	5.62	1.53	1.46
1	A	130	HIS	CE1-NE2	5.50	1.38	1.32

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	3	ARG	CB-CA-C	6.98	124.31	110.42
1	B	54	ILE	N-CA-CB	6.82	119.82	110.54
1	A	20	GLU	CB-CG-CD	6.78	124.13	112.60
1	A	108	ASN	N-CA-CB	6.67	121.76	110.49
1	B	208	ASP	CA-CB-CG	6.49	119.09	112.60

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	3	ARG	Peptide
1	B	76	ASN	Peptide

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	1823	0	1773	32	0
1	B	1859	0	1828	24	0
1	C	1665	0	1479	23	0
All	All	5347	0	5080	78	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 7.

The worst 5 of 78 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:C:26:MET:HA	1:C:26:MET:HE2	1.25	1.10
1:A:22:MET:HE3	1:A:49:ALA:HA	1.41	1.02
1:A:19:TYR:HD1	1:A:22:MET:HE2	1.31	0.94
1:B:10:ALA:CB	1:B:26:MET:HE2	2.06	0.85
1:A:203:ALA:HB3	1:A:222:MET:HE3	1.60	0.83

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	231/258 (90%)	211 (91%)	18 (8%)	2 (1%)	14	17
1	B	233/258 (90%)	215 (92%)	17 (7%)	1 (0%)	30	37
1	C	231/258 (90%)	210 (91%)	20 (9%)	1 (0%)	30	37
All	All	695/774 (90%)	636 (92%)	55 (8%)	4 (1%)	21	27

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	187	ASN
1	A	115	ASN
1	A	209	THR
1	B	215	TYR

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	192/222 (86%)	171 (89%)	21 (11%)	6	5
1	B	198/222 (89%)	182 (92%)	16 (8%)	11	13
1	C	149/222 (67%)	138 (93%)	11 (7%)	13	16
All	All	539/666 (81%)	491 (91%)	48 (9%)	9	10

5 of 48 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	88	SER
1	B	226	ARG
1	B	107	SER
1	B	217	ASP
1	C	1	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 7 such

sidechains are listed below:

Mol	Chain	Res	Type
1	B	76	ASN
1	B	130	HIS
1	C	76	ASN
1	B	228	ASN
1	A	228	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	233/258 (90%)	0.43	17 (7%) 21 18	39, 60, 132, 173	0
1	B	235/258 (91%)	0.32	14 (5%) 27 24	44, 65, 117, 168	0
1	C	233/258 (90%)	1.43	76 (32%) 1 1	56, 103, 187, 226	0
All	All	701/774 (90%)	0.72	107 (15%) 5 4	39, 74, 169, 226	0

The worst 5 of 107 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	182	TYR	6.7
1	A	2	ALA	5.8
1	C	208	ASP	5.5
1	C	230	THR	5.3
1	C	155	ALA	5.2

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.