



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 10:27 AM UTC

PDB ID : 5YQG / pdb_00005yqg
Title : The structure of 14-3-3 and pNumb peptide
Authors : Chen, X.; Liu, Z.; Wen, W.
Deposited on : 2017-11-06
Resolution : 2.10 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
Mogul	:	2022.3.0, CSD as543be (2022)
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

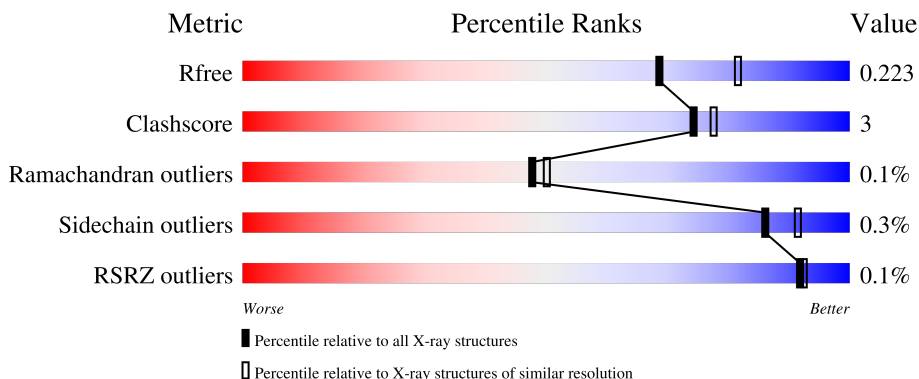
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

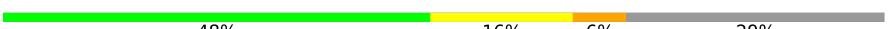
The reported resolution of this entry is 2.10 Å.

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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	252	 83% 6% 11%
1	B	252	 86% 8% 6%
1	C	252	 87% 7% 6%
1	D	252	 86% 10% 4%
2	E	31	 48% 16% 6% 29%

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Mol	Chain	Length	Quality of chain
2	F	31	 A horizontal bar chart showing the quality of chain F. The bar is divided into three segments: a green segment representing 52%, a yellow segment representing 6%, and a grey segment representing 39%. A small black dot is located at the end of the yellow segment.

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 7835 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 14-3-3 protein eta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	225	Total	C	N	O	S	0	0	0
			1691	1080	286	315	10			
1	B	236	Total	C	N	O	S	0	1	0
			1828	1162	303	353	10			
1	C	237	Total	C	N	O	S	0	1	0
			1843	1169	307	357	10			
1	D	227	Total	C	N	O	S	0	0	0
			1713	1090	289	325	9			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	expression tag	UNP P68510
A	-4	PRO	-	expression tag	UNP P68510
A	-3	GLY	-	expression tag	UNP P68510
A	-2	SER	-	expression tag	UNP P68510
A	-1	GLU	-	expression tag	UNP P68510
A	0	PHE	-	expression tag	UNP P68510
B	-5	GLY	-	expression tag	UNP P68510
B	-4	PRO	-	expression tag	UNP P68510
B	-3	GLY	-	expression tag	UNP P68510
B	-2	SER	-	expression tag	UNP P68510
B	-1	GLU	-	expression tag	UNP P68510
B	0	PHE	-	expression tag	UNP P68510
C	-5	GLY	-	expression tag	UNP P68510
C	-4	PRO	-	expression tag	UNP P68510
C	-3	GLY	-	expression tag	UNP P68510
C	-2	SER	-	expression tag	UNP P68510
C	-1	GLU	-	expression tag	UNP P68510
C	0	PHE	-	expression tag	UNP P68510
D	-5	GLY	-	expression tag	UNP P68510
D	-4	PRO	-	expression tag	UNP P68510
D	-3	GLY	-	expression tag	UNP P68510

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-2	SER	-	expression tag	UNP P68510
D	-1	GLU	-	expression tag	UNP P68510
D	0	PHE	-	expression tag	UNP P68510

- Molecule 2 is a protein called Peptide from Protein numb homolog.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
2	E	22	Total 143	C 86	N 23	O 31	P 2	S 1	0	0	0
2	F	19	Total 133	C 82	N 20	O 28	P 2	S 1	0	0	0

- Molecule 3 is water.

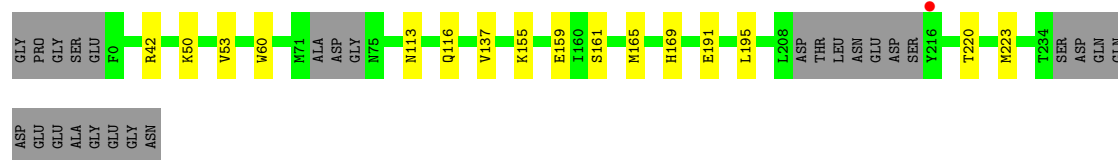
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	97	Total 97	O 97	0	0
3	B	131	Total 131	O 131	0	0
3	C	122	Total 122	O 122	0	0
3	D	114	Total 114	O 114	0	0
3	E	9	Total 9	O 9	0	0
3	F	11	Total 11	O 11	0	0

3 Residue-property plots [i](#)

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: 14-3-3 protein eta

Chain A: 



- Molecule 1: 14-3-3 protein eta

Chain B: 



- Molecule 1: 14-3-3 protein eta

Chain C: 



- Molecule 1: 14-3-3 protein eta

Chain D: 



- Molecule 2: Peptide from Protein numb homolog

Chain E: 



● Molecule 2: Peptide from Protein numb homolog

Chain F:

52%

6%

•

39%

LEU	ALA	ARG	Q263	G264	S265	F266	R267	GLY	PHE	PRO	ALA	LEU	S273	S284	L285	R286	ILE	ASN	GLU	LEU
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4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	59.26Å 74.63Å 134.14Å 90.00° 90.07° 90.00°	Depositor
Resolution (Å)	49.88 – 2.10 49.88 – 2.10	Depositor EDS
% Data completeness (in resolution range)	97.1 (49.88-2.10) 97.1 (49.88-2.10)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.59 (at 2.10Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.184 , 0.224 0.184 , 0.223	Depositor DCC
R_{free} test set	3329 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å ²)	23.6	Xtriage
Anisotropy	0.077	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.457 for h,-k,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	7835	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 24.43 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.8422e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

Bond lengths and bond angles in the following residue types are not validated in this section: SEP

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	0.36	0/1716	0.47	0/2318
1	B	0.31	0/1856	0.46	0/2509
1	C	0.35	1/1873 (0.1%)	0.48	0/2531
1	D	0.37	0/1737	0.53	2/2347 (0.1%)
2	E	1.08	0/120	1.64	5/157 (3.2%)
2	F	0.21	0/112	0.42	0/146
All	All	0.37	1/7414 (0.0%)	0.52	7/10008 (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
2	E	0	1
2	F	0	1
All	All	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	27	MET	C-O	-5.07	1.18	1.24

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	274	GLN	N-CA-C	-8.92	99.10	113.19
1	D	71	MET	N-CA-C	-7.72	98.45	109.96
1	D	71	MET	CB-CA-C	7.09	120.38	110.16
2	E	275	LYS	N-CA-C	-6.88	102.89	112.45

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	273	SER	N-CA-C	-6.09	99.71	109.39

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	E	284	SEP	Mainchain
2	F	284	SEP	Mainchain

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	1691	0	1563	11	0
1	B	1828	0	1724	14	0
1	C	1843	0	1745	10	0
1	D	1713	0	1587	8	0
2	E	143	0	93	2	0
2	F	133	0	94	1	0
3	A	97	0	0	2	0
3	B	131	0	0	1	0
3	C	122	0	0	1	0
3	D	114	0	0	1	0
3	E	9	0	0	0	0
3	F	11	0	0	0	0
All	All	7835	0	6806	44	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 3.

The worst 5 of 44 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:113:ASN:H	1:B:116:GLN:HE21	1.18	0.85
1:D:113:ASN:H	1:D:116:GLN:HE21	1.24	0.85

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:113:ASN:H	1:B:116:GLN:NE2	1.87	0.71
1:D:113:ASN:H	1:D:116:GLN:NE2	1.93	0.66
1:C:168:THR:OG1	1:C:211:LEU:HD11	2.02	0.60

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	219/252 (87%)	213 (97%)	6 (3%)	0	100	100
1	B	235/252 (93%)	232 (99%)	3 (1%)	0	100	100
1	C	236/252 (94%)	233 (99%)	3 (1%)	0	100	100
1	D	221/252 (88%)	218 (99%)	3 (1%)	0	100	100
2	E	15/31 (48%)	12 (80%)	2 (13%)	1 (7%)	1	0
2	F	13/31 (42%)	12 (92%)	1 (8%)	0	100	100
All	All	939/1070 (88%)	920 (98%)	18 (2%)	1 (0%)	48	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	E	277	SER

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	151/217 (70%)	150 (99%)	1 (1%)	76	83
1	B	173/217 (80%)	173 (100%)	0	100	100
1	C	179/217 (82%)	179 (100%)	0	100	100
1	D	156/217 (72%)	155 (99%)	1 (1%)	78	86
2	E	6/25 (24%)	6 (100%)	0	100	100
2	F	6/25 (24%)	6 (100%)	0	100	100
All	All	671/918 (73%)	669 (100%)	2 (0%)	86	91

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	53	VAL
1	D	39	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	229	ASN
1	D	98	ASN
1	D	116	GLN
1	A	229	ASN
1	B	34	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 non-standard protein/DNA/RNA residues 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	SEP	E	284	2	8,9,10	1.45	1 (12%)	7,12,14	1.40	1 (14%)
2	SEP	E	265	2	8,9,10	1.52	1 (12%)	7,12,14	0.89	0
2	SEP	F	265	2	8,9,10	1.55	1 (12%)	7,12,14	0.81	0
2	SEP	F	284	2	8,9,10	1.44	1 (12%)	7,12,14	1.43	1 (14%)

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	SEP	E	284	2	-	0/6/8/10	-
2	SEP	E	265	2	-	0/6/8/10	-
2	SEP	F	265	2	-	1/6/8/10	-
2	SEP	F	284	2	-	0/6/8/10	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	F	265	SEP	P-O1P	3.50	1.61	1.50
2	E	265	SEP	P-O1P	3.47	1.61	1.50
2	F	284	SEP	P-O1P	3.16	1.60	1.50
2	E	284	SEP	P-O1P	2.91	1.59	1.50

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	284	SEP	OG-CB-CA	3.33	111.38	108.14
2	F	284	SEP	OG-CB-CA	2.97	111.03	108.14

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	F	265	SEP	C-CA-CB-OG

There are no ring outliers.

No monomer is involved in short contacts.

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	225/252 (89%)	-1.21	1 (0%) 88 90	16, 33, 59, 90	0
1	B	236/252 (93%)	-1.34	0 100 100	15, 29, 53, 74	1 (0%)
1	C	237/252 (94%)	-1.37	0 100 100	15, 30, 56, 69	1 (0%)
1	D	227/252 (90%)	-1.21	0 100 100	16, 33, 63, 86	0
2	E	20/31 (64%)	-0.68	0 100 100	34, 66, 88, 94	0
2	F	17/31 (54%)	-0.56	0 100 100	36, 64, 101, 103	0
All	All	962/1070 (89%)	-1.26	1 (0%) 92 92	15, 32, 64, 103	2 (0%)

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	216	TYR	2.9

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

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. 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	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SEP	E	265	10/11	1.00	0.03	16,20,29,30	0
2	SEP	E	284	10/11	1.00	0.02	22,26,29,30	0
2	SEP	F	265	10/11	1.00	0.02	19,22,28,32	0
2	SEP	F	284	10/11	1.00	0.02	26,30,34,34	0

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.