

# Full wwPDB X-ray Structure Validation Report (i)

Jan 2, 2024 – 06:25 pm GMT

PDB ID : 4Y5I

Title : Crystal structure of C-terminal modified Tau peptide-hybrid 126B with 14-3-

3sigma

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Deposited on : 2015-02-11

Resolution : 1.40 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 (i) 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 (1)) were used in the production of this report:

Mol Probity : 4.02b-467

Mogul : 1.8.4, CSD as541be (2020)

Xtriage (Phenix) : 1.13 EDS : 2.36

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

 $Refmac \quad : \quad 5.8.0158$ 

CCP4 : 7.0.044 (Gargrove)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

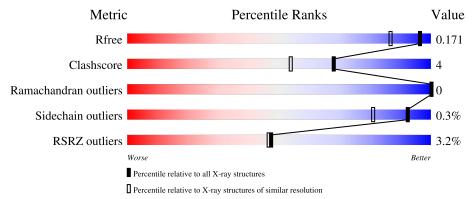
Validation Pipeline (wwPDB-VP) : 2.36

## 1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: X-RAY DIFFRACTION

The reported resolution of this entry is 1.40 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 $(\# \mathrm{Entries})$	$\begin{array}{c} {\rm Similar\ resolution} \\ (\#{\rm Entries,\ resolution\ range(\mathring{A})}) \end{array}$
$R_{free}$	130704	1714 (1.40-1.40)
Clashscore	141614	1812 (1.40-1.40)
Ramachandran outliers	138981	1763 (1.40-1.40)
Sidechain outliers	138945	1762 (1.40-1.40)
RSRZ outliers	127900	1674 (1.40-1.40)

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 <=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	236	3%	91%		6% •		
1	В	236	3%	92%		5% •		
2	F	9	22%					
2	G	9	22%	33%	11%	33%		



# 2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 4684 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 sigma.

Mol	Chain	Residues	${f Atoms}$					ZeroOcc	AltConf	Trace
1	A	227	Total 1934	C 1231	N 310	O 380	S 13	10	32	0
1	В	228	Total 1893	C 1194	N 314	O 374	S 11	0	20	0

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	GLY	-	expression tag	UNP P31947
A	-3	ALA	-	expression tag	UNP P31947
A	-2	MET	-	expression tag	UNP P31947
A	-1	GLY	-	expression tag	UNP P31947
A	0	SER	-	expression tag	UNP P31947
В	-4	GLY	-	expression tag	UNP P31947
В	-3	ALA	-	expression tag	UNP P31947
В	-2	MET	-	expression tag	UNP P31947
В	-1	GLY	-	expression tag	UNP P31947
В	0	SER	_	expression tag	UNP P31947

• Molecule 2 is a protein called Microtubule-associated protein tau.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	0	Total	С	N	О	Р	0	0	0
2	2 F	9	66	40	11	14	1			
2	С	6	Total	С	N	О	Р	0	0	0
2	2 G	U	46	27	6	12	1	U	U	U

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
F	1	ACE	-	acetylation	UNP P10636
F	9	PIP	-	expression tag	UNP P10636

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Chain	Residue	Modelled	Actual	Comment	Reference
G	1	ACE	-	acetylation	UNP P10636
G	9	PIP	-	expression tag	UNP P10636

 $\bullet$  Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

	Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
Ī	3	A	1	Total Cl 1 1	0	0
	3	В	1	Total Cl 1 1	0	0

#### • Molecule 4 is water.

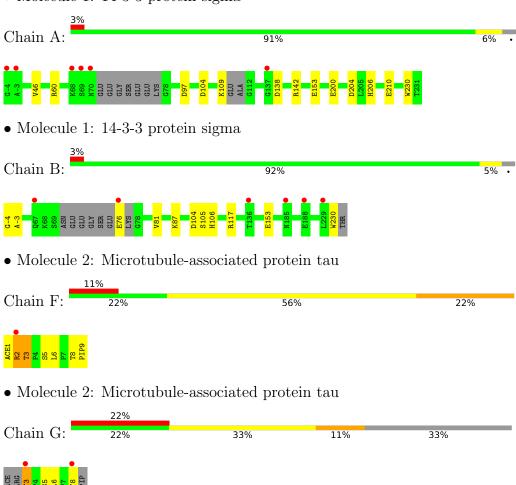
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	364	Total O 364 364	0	0
4	В	350	Total O 350 350	0	0
4	F	23	Total O 23 23	0	0
4	G	6	Total O 6 6	0	0



# 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 sigma





# 4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants	63.10Å 70.21Å 129.11Å	Donositor
a, b, c, $\alpha$ , $\beta$ , $\gamma$	90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.12 - 1.40	Depositor
rtesolution (A)	46.93 - 1.40	EDS
% Data completeness	100.0 (45.12-1.40)	Depositor
(in resolution range)	97.2 (46.93-1.40)	EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$< I/\sigma(I) > 1$	3.12 (at 1.40Å)	Xtriage
Refinement program	PHENIX	Depositor
D D.	0.147 , 0.172	Depositor
$R, R_{free}$	0.148 , 0.171	DCC
$R_{free}$ test set	5679  reflections  (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	15.7	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$ , $B_{sol}(Å^2)$	0.35, 42.5	EDS
L-test for twinning <sup>2</sup>	$ < L > = 0.47, < L^2> = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	4684	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 5.75% of the height of the origin peak. No significant pseudotranslation is detected.

<sup>&</sup>lt;sup>2</sup>Theoretical values of <|L|>,  $<L^2>$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



<sup>&</sup>lt;sup>1</sup>Intensities estimated from amplitudes.

# 5 Model quality (i)

### 5.1 Standard geometry (i)

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

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	Bo	nd lengths	Bond angles		
MIOI		RMSZ	# Z  > 5	RMSZ	# Z  > 5	
1	A	0.31	0/2055	0.47	0/2760	
1	В	0.28	0/1987	0.44	0/2669	
2	F	2.87	5/48 (10.4%)	1.14	0/65	
2	G	2.14	$2/36 \ (5.6\%)$	1.39	0/49	
All	All	0.47	7/4126 (0.2%)	0.49	0/5543	

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\operatorname{Observed}(\operatorname{\AA})$	Ideal(Å)
2	F	2	ARG	NE-CZ	11.07	1.47	1.33
2	F	2	ARG	CZ-NH2	8.50	1.44	1.33
2	G	6	LEU	C-N	7.39	1.48	1.34
2	G	3	THR	C-N	6.60	1.46	1.34
2	F	6	LEU	C-N	6.49	1.46	1.34
2	F	3	THR	C-N	5.75	1.45	1.34
2	F	2	ARG	C-N	5.65	1.47	1.34

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

#### 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	1934	0	2018	16	0
1	В	1893	0	1941	11	0
2	F	66	0	69	5	0
2	G	46	0	42	2	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	A	364	0	0	14	4
4	В	350	0	0	8	2
4	F	23	0	0	2	0
4	G	6	0	0	0	0
All	All	4684	0	4070	30	4

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 4.

All (30) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic	Clash
1 A 140 ADO MIIO	4 A 401 HOH O	distance (Å)	overlap (Å)
1:A:142:ARG:NH2	4:A:401:HOH:O	1.86	1.04
1:A:204:ASP:OD1	4:A:402:HOH:O	1.88	0.91
1:A:206:HIS:NE2	4:A:404:HOH:O	2.09	0.84
1:B:76:GLU:N	4:B:404:HOH:O	2.14	0.81
1:A:138:ASP:OD1	4:A:403:HOH:O	2.01	0.78
1:A:46[B]:VAL:HG23	2:F:9:PIP:H31	1.67	0.74
1:B:104:ASP:OD1	4:B:401:HOH:O	2.05	0.74
1:A:210:GLU:OE2	4:A:405:HOH:O	2.09	0.70
1:A:153[A]:GLU:HG3	4:A:631:HOH:O	1.93	0.69
2:F:1:ACE:O	4:F:101:HOH:O	2.12	0.68
1:A:104[A]:ASP:OD2	4:A:406:HOH:O	2.11	0.68
1:A:200[A]:GLU:HG3	4:A:426:HOH:O	1.96	0.66
1:B:153:GLU:OE1	4:B:402:HOH:O	2.14	0.65
1:B:-3:ALA:O	4:B:405:HOH:O	2.14	0.64
1:A:60:ARG:NH2	4:A:407:HOH:O	2.16	0.62
1:B:117[A]:ARG:NH1	4:B:408:HOH:O	2.29	0.58
1:A:97:ASP:OD2	4:A:408:HOH:O	2.18	0.54
1:A:109:LYS:HD2	4:A:448:HOH:O	2.09	0.52
1:B:-4:GLY:N	4:B:406:HOH:O	2.22	0.51
1:A:60:ARG:NE	4:A:407:HOH:O	2.37	0.51
1:B:81[A]:VAL:HG23	4:B:554:HOH:O	2.10	0.51
1:A:104[A]:ASP:CG	4:A:412:HOH:O	2.50	0.50
1:B:230:TRP:HZ2	2:G:3:THR:HG21	1.78	0.49
1:B:87:LYS:NZ	4:B:418:HOH:O	2.47	0.48

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Atom-1	Atom-2	$egin{aligned} &  ext{Interatomic} \ &  ext{distance} \ &  ext{(Å)} \end{aligned}$	Clash overlap (Å)
		( )	- , ,
2:F:8:THR:HB	2:F:9:PIP:H61	1.96	0.47
1:B:105:SER:HA	1:B:106:HIS:CG	2.50	0.47
2:F:2:ARG:NE	4:F:102:HOH:O	2.48	0.45
1:B:230:TRP:CZ2	2:G:3:THR:HG21	2.53	0.44
1:A:60:ARG:NH1	4:A:436:HOH:O	2.51	0.43
1:A:230:TRP:CZ2	2:F:3:THR:HG21	2.53	0.43

All (4) 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	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)	
4:A:410:HOH:O	4:A:591:HOH:O[4_455]	1.99	0.21	
4:A:410:HOH:O	4:A:697:HOH:O[4_455]	2.10	0.10	
4:A:630:HOH:O	4:B:608:HOH:O[1_455]	2.10	0.10	
4:A:672:HOH:O	4:B:406:HOH:O[4_455]	2.15	0.05	

### 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	Favoured Allowed		Percentiles	
1	A	253/236 (107%)	251 (99%)	2 (1%)	0	100	100
1	В	$245/236\ (104\%)$	241 (98%)	4 (2%)	0	100	100
2	F	5/9~(56%)	5 (100%)	0	0	100	100
2	G	3/9 (33%)	3 (100%)	0	0	100	100
All	All	506/490 (103%)	500 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.



#### 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	223/198~(113%)	223 (100%)	0	100	100	
1	В	213/198 (108%)	213 (100%)	0	100	100	
2	F	6/6 (100%)	6 (100%)	0	100	100	
2	G	5/6 (83%)	4 (80%)	1 (20%)	1	0	
All	All	447/408 (110%)	446 (100%)	1 (0%)	92	82	

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	G	8	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

#### 5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

2 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	Mol Type Chain Re		Ros	Res	Ros	Ros	Ros	Dog	Dog	Pag	Res Link	Bond lengths			Bond angles		
WIOI	туре	Chain	Lilik		Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2							
2	SEP	F	5	2	8,9,10	0.99	1 (12%)	8,12,14	0.61	0							



	Mol	Type	Chain	Res	Link	B	ond leng	$_{ m gths}$	Bond angles		
	WIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
Ī	2	SEP	G	5	2	8,9,10	1.10	1 (12%)	8,12,14	0.53	0

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	F	5	2	-	0/5/8/10	-
2	SEP	G	5	2	-	0/5/8/10	-

#### All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	Ideal(A)
2	G	5	SEP	CA-N	-2.40	1.40	1.48
2	F	5	SEP	CA-N	-2.22	1.41	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

### 5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

### 5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.



# 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,  $95^{th}$  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>	$\# \mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q < 0.9
1	A	227/236 (96%)	-0.22	6 (2%) 56 55	11, 17, 33, 59	0
1	В	228/236 (96%)	-0.42	6 (2%) 56 55	13, 19, 34, 77	0
2	F	6/9 (66%)	0.68	1 (16%) 1 1	16, 20, 22, 56	0
2	G	5/9~(55%)	1.98	2 (40%) 0 0	21, 34, 47, 53	0
All	All	466/490 (95%)	-0.28	15 (3%) 47 46	11, 18, 35, 77	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res Type		RSRZ	
2	G	3	THR	3.8	
1	A	-4	GLY	3.7	
2	F	2	ARG	3.5	
2	G	8	THR	3.4	
1	A	70	ASN	3.1	
1	В	185	ASN	2.9	
1	A	137	GLY	2.7	
1	В	229	LEU	2.6	
1	В	136	THR	2.6	
1	В	188	GLU	2.3	
1	A	68	LYS	2.2	
1	В	67	GLN	2.2	
1	A	69	SER	2.1	
1	A	-3	ALA	2.1	
1	В	76	GLU	2.0	

### 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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
2	SEP	G	5	10/11	0.98	0.08	18,19,21,24	0
2	SEP	F	5	10/11	0.99	0.06	13,15,16,17	0

### 6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

### 6.4 Ligands (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,  $95^{th}$  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	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q<0.9
3	CL	A	301	1/1	0.99	0.03	22,22,22,22	0
3	CL	В	301	1/1	1.00	0.04	21,21,21,21	0

### 6.5 Other polymers (i)

There are no such residues in this entry.

