



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 12:34 AM GMT

PDB ID : 2AWU  
Title : Synapse associated protein 97 PDZ2 domain variant C378G  
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Deposited on : 2005-09-02  
Resolution : 2.44 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

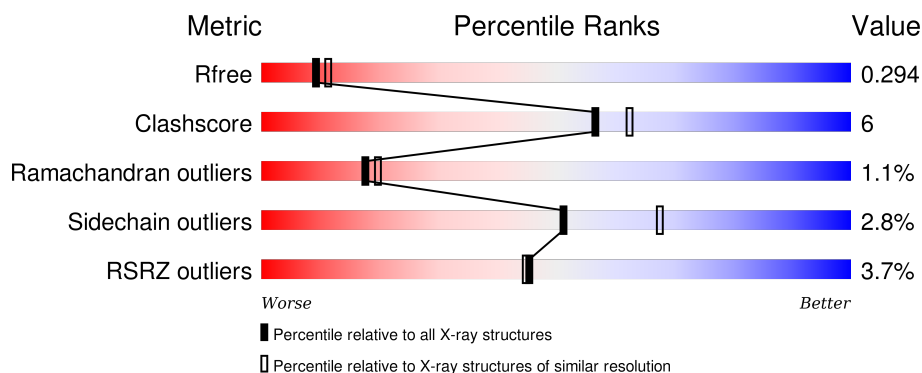
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.44 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))
$R_{free}$	91344	1003 (2.46-2.42)
Clashscore	102246	1071 (2.46-2.42)
Ramachandran outliers	100387	1065 (2.46-2.42)
Sidechain outliers	100360	1065 (2.46-2.42)
RSRZ outliers	91569	1005 (2.46-2.42)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	105	<div> <div>3%</div> <div>72%</div> <div>17%</div> <div>10%</div> </div>
1	B	105	<div> <div>3%</div> <div>76%</div> <div>9%</div> <div>14%</div> </div>
2	C	3	<div> <div>33%</div> <div>100%</div> </div>

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1455 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 Synapse-associated protein 97.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	95	Total	C	N	O	S	0	0	0
			698	446	116	134	2			
1	B	90	Total	C	N	O		0	0	0
			657	420	110	127				

There are 28 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	314	MET	-	CLONING ARTIFACT	UNP Q62696
A	315	GLU	ARG	SEE REMARK 999	UNP Q62696
A	317	ILE	ASN	SEE REMARK 999	UNP Q62696
A	318	MET	HIS	SEE REMARK 999	UNP Q62696
A	378	GLY	CYS	ENGINEERED	UNP Q62696
A	402	VAL	ALA	SEE REMARK 999	UNP Q62696
A	411	SER	-	CLONING ARTIFACT	UNP Q62696
A	412	ARG	-	CLONING ARTIFACT	UNP Q62696
A	413	HIS	-	CLONING ARTIFACT	UNP Q62696
A	414	HIS	-	CLONING ARTIFACT	UNP Q62696
A	415	HIS	-	CLONING ARTIFACT	UNP Q62696
A	416	HIS	-	CLONING ARTIFACT	UNP Q62696
A	417	HIS	-	CLONING ARTIFACT	UNP Q62696
A	418	HIS	-	CLONING ARTIFACT	UNP Q62696
B	314	MET	-	CLONING ARTIFACT	UNP Q62696
B	315	GLU	ARG	SEE REMARK 999	UNP Q62696
B	317	ILE	ASN	SEE REMARK 999	UNP Q62696
B	318	MET	HIS	SEE REMARK 999	UNP Q62696
B	378	GLY	CYS	ENGINEERED	UNP Q62696
B	402	VAL	ALA	SEE REMARK 999	UNP Q62696
B	411	SER	-	CLONING ARTIFACT	UNP Q62696
B	412	ARG	-	CLONING ARTIFACT	UNP Q62696
B	413	HIS	-	CLONING ARTIFACT	UNP Q62696
B	414	HIS	-	CLONING ARTIFACT	UNP Q62696
B	415	HIS	-	CLONING ARTIFACT	UNP Q62696

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Chain	Residue	Modelled	Actual	Comment	Reference
B	416	HIS	-	CLONING ARTIFACT	UNP Q62696
B	417	HIS	-	CLONING ARTIFACT	UNP Q62696
B	418	HIS	-	CLONING ARTIFACT	UNP Q62696

- Molecule 2 is a protein called AHH.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
2	C	3	Total	C	N	O	0	0	0
			26	15	7	4			

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	38	Total	O	0	0
			38	38		
3	B	35	Total	O	0	0
			35	35		
3	C	1	Total	O	0	0
			1	1		

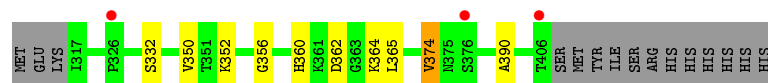
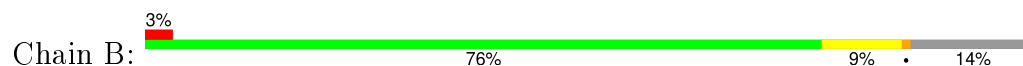
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Synapse-associated protein 97



#### • Molecule 1: Synapse-associated protein 97



#### • Molecule 2: AHH



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	32.22Å 52.14Å 52.64Å 90.00° 102.74° 90.00°	Depositor
Resolution (Å)	19.65 – 2.44 19.65 – 2.44	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.65-2.44) 97.2 (19.65-2.44)	Depositor EDS
$R_{merge}$	0.03	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	11.86 (at 2.44Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, $R_{free}$	0.180 , 0.295 0.180 , 0.294	Depositor DCC
$R_{free}$ test set	311 reflections (5.26%)	DCC
Wilson B-factor (Å <sup>2</sup> )	20.8	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 30.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 6220 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	1455	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 9.31% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

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

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

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	0.73	0/708	0.74	0/955
1	B	0.70	0/666	0.74	0/900
2	C	0.69	0/27	0.50	0/34
All	All	0.72	0/1401	0.73	0/1889

There are no bond length outliers.

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	698	0	711	11	0
1	B	657	0	670	6	0
2	C	26	0	18	0	0
3	A	38	0	0	2	0
3	B	35	0	0	1	0
3	C	1	0	0	0	0
All	All	1455	0	1399	17	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 6.

The worst 5 of 17 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:408:MET:O	1:A:409:TYR:HB2	1.72	0.85
1:B:350:VAL:HG21	1:B:365:LEU:HD11	1.75	0.69
1:A:408:MET:O	1:A:409:TYR:CB	2.48	0.62
1:B:356:GLY:H	1:B:360:HIS:HD2	1.48	0.62
1:A:368:GLY:HA2	1:A:410:ILE:CB	2.42	0.49

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	93/105 (89%)	86 (92%)	5 (5%)	2 (2%)	8	5
1	B	88/105 (84%)	82 (93%)	6 (7%)	0	100	100
2	C	1/3 (33%)	1 (100%)	0	0	100	100
All	All	182/213 (85%)	169 (93%)	11 (6%)	2 (1%)	17	20

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	409	TYR
1	A	407	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	73/86 (85%)	71 (97%)	2 (3%)	52	69
1	B	68/86 (79%)	66 (97%)	2 (3%)	50	66
2	C	2/2 (100%)	2 (100%)	0	100	100
All	All	143/174 (82%)	139 (97%)	4 (3%)	51	67

All (4) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	395	SER
1	A	409	TYR
1	B	362	ASP
1	B	374	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	360	HIS
1	B	360	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.6 Ligand geometry ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	95/105 (90%)	-0.25	3 (3%) 51 49	6, 14, 29, 55	0
1	B	90/105 (85%)	-0.21	3 (3%) 50 48	8, 15, 24, 34	0
2	C	3/3 (100%)	1.38	1 (33%) 0 0	32, 32, 37, 39	0
All	All	188/213 (88%)	-0.20	7 (3%) 45 45	6, 15, 29, 55	0

The worst 5 of 7 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	409	TYR	4.3
1	A	410	ILE	3.4
1	B	406	THR	3.2
1	B	326	PRO	2.8
1	B	376	SER	2.7

### 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 carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

## 6.5 Other polymers ⓘ

There are no such residues in this entry.