Full wwPDB X-ray Structure Validation Report (i)

Oct 31, 2021 – 06:32 AM EDT

PDB ID	:	2AWW
Title	:	Synapse associated protein 97 PDZ2 domain variant C378G with C-terminal GluR-A peptide
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Deposited on	:	2005-09-02
Resolution	:	2.21 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 following versions of software and data (see references (1)) were used in the production of this report:

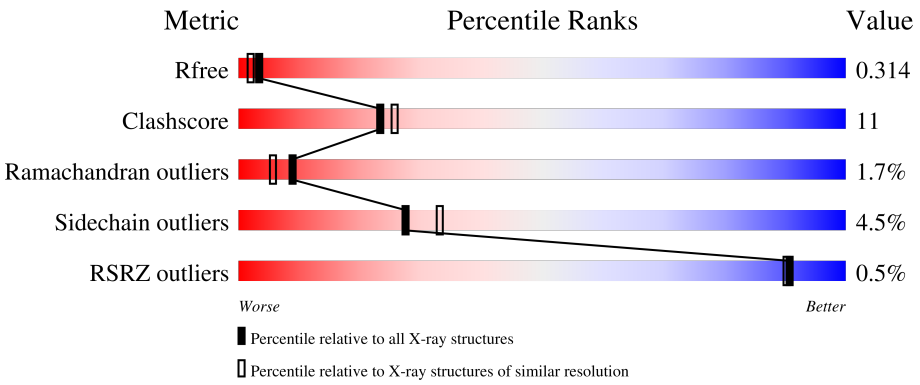
MolProbity	:	4.02b-467
Xtriage (Phenix)	:	1.13
EDS	:	2.23.2
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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 2.21 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}	130704	5912 (2.24-2.20)
Clashscore	141614	6646 (2.24-2.20)
Ramachandran outliers	138981	6543 (2.24-2.20)
Sidechain outliers	138945	6544 (2.24-2.20)
RSRZ outliers	127900	5797 (2.24-2.20)

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	105	57% 28% • 13%
1	B	105	% 71% 15% 13%
2	C	18	6% 11% 6% 78%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 1348 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
			Total	C	N	O	S			
1	A	91	660	421	111	127	1	0	0	0
1	B	91	636	407	108	120	1	0	0	0

There are 32 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	352	SER	LYS	conflict	UNP Q62696
A	354	VAL	ILE	conflict	UNP Q62696
A	378	GLY	CYS	engineered mutation	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	352	SER	LYS	conflict	UNP Q62696
B	354	VAL	ILE	conflict	UNP Q62696
B	378	GLY	CYS	engineered mutation	UNP Q62696
B	402	VAL	ALA	SEE REMARK 999	UNP Q62696
B	411	SER	-	cloning artifact	UNP Q62696

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Chain	Residue	Modelled	Actual	Comment	Reference
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
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 18-residue C-terminal peptide from glutamate receptor, ionotropic, AMPA1.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	C	4	25	15	4	6	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	19	19	19	0	0
			Total	O		
3	B	8	8	8	0	0

3 Residue-property plots (i)

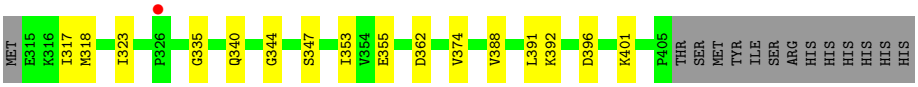
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Synapse associated protein 97

Chain A:

• Molecule 1: Synapse associated protein 97

Chain B:



• Molecule 2: 18-residue C-terminal peptide from glutamate receptor, ionotropic, AMPA1

Chain C:

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	34.35Å 54.31Å 54.64Å 90.00° 84.03° 90.00°	Depositor
Resolution (Å)	34.10 – 2.21 34.16 – 2.21	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.10-2.21) 99.7 (34.16-2.21)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.97 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.242 , 0.326 0.236 , 0.314	Depositor DCC
R_{free} test set	509 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	40.4	Xtriage
Anisotropy	0.062	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 48.4	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	1348	wwPDB-VP
Average B, all atoms (Å^2)	49.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.92% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] 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.

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	0.89	0/669	0.89	1/903 (0.1%)
1	B	0.64	0/644	0.77	0/870
2	C	0.68	0/24	0.86	0/30
All	All	0.77	0/1337	0.83	1/1803 (0.1%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	322	LEU	CA-CB-CG	5.56	128.08	115.30

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	660	0	669	23	0
1	B	636	0	631	7	0
2	C	25	0	25	6	0
3	A	19	0	0	0	0
3	B	8	0	0	0	0
All	All	1348	0	1325	30	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 11.

All (30) 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:329:LEU:HD21	1:A:398:VAL:HG21	1.69	0.74
1:A:391:LEU:HB3	2:C:18:LEU:HD22	1.71	0.71
1:A:331:PHE:O	2:C:18:LEU:HD12	1.96	0.66
1:B:388:VAL:O	1:B:392:LYS:HG2	1.99	0.63
1:A:317:ILE:HD12	1:A:372:LEU:HD11	1.81	0.62
1:B:335:GLY:HA3	1:B:347:SER:O	2.02	0.59
1:A:384:HIS:NE2	2:C:16:THR:OG1	2.35	0.56
1:A:324:LYS:NZ	1:A:394:THR:OG1	2.21	0.56
1:A:383:THR:HG22	1:A:385:GLU:H	1.71	0.54
1:B:374:VAL:O	1:B:374:VAL:HG13	2.07	0.54
1:A:375:ASN:ND2	1:A:394:THR:HG22	2.22	0.54
1:A:380:GLU:O	1:A:381:GLU:HB2	2.07	0.54
1:A:388:VAL:O	1:A:392:LYS:HG3	2.08	0.54
1:A:383:THR:HG22	1:A:385:GLU:OE1	2.08	0.53
1:A:391:LEU:CB	2:C:18:LEU:HD22	2.37	0.52
1:A:317:ILE:HD12	1:A:372:LEU:CD1	2.40	0.51
1:A:374:VAL:HG13	1:A:374:VAL:O	2.11	0.51
1:A:356:GLY:N	1:A:360:HIS:ND1	2.47	0.48
1:A:333:ILE:O	2:C:15:ALA:HA	2.14	0.47
1:B:340:GLN:OE1	1:B:344:GLY:N	2.43	0.46
1:B:323:ILE:HA	1:B:396:ASP:O	2.17	0.44
1:A:383:THR:CG2	1:A:385:GLU:OE1	2.65	0.44
1:B:318:MET:O	1:B:401:LYS:HA	2.19	0.43
1:A:362:ASP:OD2	1:A:364:LYS:HD2	2.19	0.43
1:A:332:SER:HA	2:C:16:THR:O	2.18	0.43
1:B:374:VAL:HG21	1:B:391:LEU:HD23	2.02	0.42
1:A:320:ILE:HG22	1:A:322:LEU:HG	2.01	0.41
1:A:375:ASN:HD21	1:A:394:THR:HG22	1.85	0.40
1:A:383:THR:HB	1:A:386:GLU:HG3	2.04	0.40
1:A:357:GLY:O	1:A:358:ALA:C	2.60	0.40

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	89/105 (85%)	79 (89%)	7 (8%)	3 (3%)	3	1
1	B	89/105 (85%)	83 (93%)	6 (7%)	0	100	100
2	C	2/18 (11%)	2 (100%)	0	0	100	100
All	All	180/228 (79%)	164 (91%)	13 (7%)	3 (2%)	9	6

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	395	SER
1	A	340	GLN
1	A	381	GLU

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	68/86 (79%)	67 (98%)	1 (2%)	65	76
1	B	63/86 (73%)	59 (94%)	4 (6%)	18	19
2	C	2/14 (14%)	1 (50%)	1 (50%)	0	0
All	All	133/186 (72%)	127 (96%)	6 (4%)	27	33

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	376	SER
1	B	317	ILE
1	B	353	ILE
1	B	355	GLU
1	B	362	ASP
2	C	18	LEU

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)

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

5.5 Carbohydrates (i)

There are no monosaccharides 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	91/105 (86%)	-0.17	0 100 100	29, 43, 53, 63	0
1	B	91/105 (86%)	-0.05	1 (1%) 80 79	42, 55, 70, 80	0
2	C	4/18 (22%)	0.13	0 100 100	63, 64, 65, 66	0
All	All	186/228 (81%)	-0.11	1 (0%) 91 90	29, 49, 69, 80	0

All (1) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	326	PRO	2.2

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 monosaccharides 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.