wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2P4L
Title	:	Structure and sodium channel activity of an excitatory I1-superfamily conotoxin
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This is a wwPDB NMR 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/NMRValidationReportHelp
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:

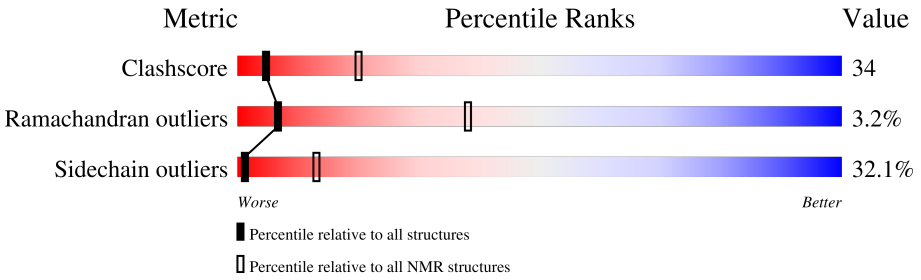
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment was not calculated.

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)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and 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%

Mol	Chain	Length	Quality of chain
1	A	46	33% 28% 11% 28%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
1	A	HYP	11	20	-

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 18 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	**Residue range (total)**	**Backbone RMSD (Å)**	**Medoid model**
1	A:4-A:10, A:12-A:28, A:30-A:38 (33)	0.79	18

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 2 clusters and 3 single-model clusters were found.

Cluster number	Models
1	1, 2, 6, 8, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19
2	4, 5, 12
Single-model clusters	3; 7; 20

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 652 atoms, of which 309 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called I-superfamily conotoxin r11a.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	46	652	212	309	54	69	8	0

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-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. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: I-superfamily conotoxin r11a

Chain A: 33% 28% 11% 28%

G1 P2 S3 K6 A7 D8 E9 K10 P11 C12 H15 A16 D17 C18 C19 N20 C21 C22 L23 S24 G25 I26 C27 A28 P29 S30 T31 N32 W33 I34 L35 S39 T40 S41 S42 F43 F44 K45 I46

4.2 Residue scores for the representative (medoid) model from the NMR ensemble

The representative model is number 18. Colouring as in section 4.1 above.

- Molecule 1: I-superfamily conotoxin r11a

Chain A: 30% 28% 13% 28%

G1 P2 S3 F4 C5 K6 A7 D8 E9 K10 P11 C12 E13 Y14 H15 A16 D17 C18 C19 N20 C21 C22 L23 S24 G25 I26 C27 A28 P29 S30 W33 I34 S39 T40 S41 S42 F43 F44 K45 I46

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *simulated annealing*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
X-PLOR	refinement	Xplor-nih 2.9.3
DYANA	structure solution	Cyana 1.0.6

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

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

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 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 each 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 averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	244	214	214	16±10
All	All	4880	4280	4280	310

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 34.

5 of 107 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:CYS:HB3	1:A:27:CYS:SG	0.80	2.16	17	13
1:A:22:CYS:CB	1:A:27:CYS:SG	0.77	2.72	19	14
1:A:25:GLY:O	1:A:26:ILE:HD12	0.77	1.78	3	1
1:A:22:CYS:SG	1:A:27:CYS:SG	0.75	2.85	9	1
1:A:18:CYS:SG	1:A:22:CYS:HB3	0.72	2.24	12	6

6.3 Torsion angles (i)

6.3.1 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 PDB entries followed by that with respect to all NMR entries. 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	33/46 (72%)	22±2 (66±5%)	10±1 (30±5%)	1±1 (3±2%)	7 38
All	All	660/920 (72%)	438 (66%)	201 (30%)	21 (3%)	7 38

5 of 8 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	20	ASN	6
1	A	33	TRP	5
1	A	38	CYS	4
1	A	37	GLY	2
1	A	26	ILE	1

6.3.2 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 PDB entries followed by that with respect to all NMR entries. 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	28/37 (76%)	19±1 (68±5%)	9±1 (32±5%)	1 13
All	All	560/740 (76%)	380 (68%)	180 (32%)	1 13

5 of 23 unique residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
1	A	26	ILE	19
1	A	33	TRP	19
1	A	6	LYS	17
1	A	10	LYS	17
1	A	15	HIS	15

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

3 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds 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 is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
1	HYP	A	2	1	6,8,9	0.73±0.05	0±0 (0±0%)
1	HYP	A	11	1	6,8,9	0.82±0.08	0±0 (0±0%)
1	HYP	A	29	1	6,8,9	0.75±0.05	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of 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 angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
1	HYP	A	2	1	5,10,12	1.44±0.13	1±0 (19±4%)
1	HYP	A	11	1	5,10,12	1.61±0.24	1±0 (19±4%)
1	HYP	A	29	1	5,10,12	1.33±0.24	1±0 (12±9%)

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
1	HYP	A	29	1	-	0±0,0,11,13	0±0,1,1,1
1	HYP	A	11	1	1±0,1,2,4	0±0,0,11,13	0±0,1,1,1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	HYP	A	2	1	-	0±0,0,11,13	0±0,1,1,1

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	11	HYP	CB-CG-CD	3.88	108.02	103.27	13	19
1	A	29	HYP	CB-CG-CD	3.70	107.80	103.27	7	12
1	A	2	HYP	CB-CG-CD	3.00	106.94	103.27	7	19

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	11	HYP	CG	20

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

No chemical shift data were provided