wwPDB NMR Structure Validation Summary Report (i)

Mar 6, 2022 – 10:49 PM EST

PDB ID	:	2KLS
Title	:	Apo-form of the second Ca2+ binding domain of NCX1.4
Authors	:	Hilge, M.; Aelen, J.; Foarce, A.; Perrakis, A.; Vuister, G.W.
Deposited on	:	2009-07-08

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

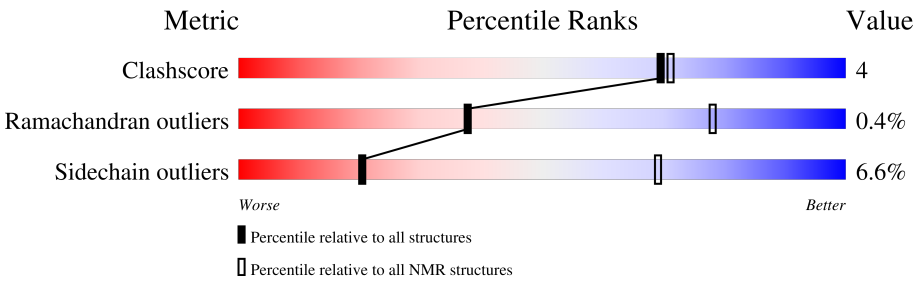
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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	164	

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:502-A:576, A:585-A:597, A:634-A:647 (102)	0.26	1

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 3 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2465 atoms, of which 1215 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Sodium/calcium exchanger 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	157	2465	784	1215	201	261	4	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: Sodium/calcium exchanger 1

Chain A: 57% 5% • 34% •

MET SER HIS HIS HIS HIS HIS H501 S515 M521 E522 V523 T528 I536 V568 K569 T570 D577 D578 E579 E580 Y581 E582 K583 N584 L589 E598 M599 S600 E601 K602 K603 G604 G605 F606 T607 I608 T609 E610 E611 Y612 D613 D614 K615 Q616 P617 L618 T619 S620 K621 E622 E623

E624 E625 R626 R627 I628 A629 E630 M631 G632 R633 L636 E648 S649 Y650 E651 F652 K653 S654 T655 V656 D657

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

The representative model is number 1. Colouring as in section 4.1 above.

- Molecule 1: Sodium/calcium exchanger 1

Chain A: 54% 8% • 34% •

MET SER HIS HIS HIS HIS HIS H501 A502 E508 M521 E522 V523 T528 N534 R547 Q563 K569 T570 I571 D577 D578 E579 E580 Y581 E582 K583 N584 L589 E598 M599 S600 E601 K602 K603 G604 G605 F606 T607 I608 T609 E610 E611 Y612 D613 D614 K615 Q616 P617 L618

T619 S620 K621 E622 E623 E624 E625 R626 R627 I628 A629 E630 M631 G632 R633 L636 E648 S649 Y650 E651 F652 K653 S654 T655 V656 D657

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *torsion angle dynamics*.

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
CYANA	structure solution	2.1
X-PLOR	refinement	

No chemical shift data was provided.

6 Model quality (i)

6.1 Standard geometry (i)

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

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	Planarity
1	A	0.0±0.0	0.2±0.4
All	All	0	5

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	547	ARG	Sidechain	2
1	A	527	ARG	Sidechain	2
1	A	595	ARG	Sidechain	1

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	789	799	799	6±2
All	All	15780	15980	15980	118

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.

5 of 35 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:505:PHE:CE1	1:A:527:ARG:HA	0.61	2.31	20	1
1:A:505:PHE:CD2	1:A:528:THR:HG23	0.54	2.36	20	4
1:A:502:ALA:O	1:A:528:THR:HB	0.53	2.03	7	5
1:A:515:SER:O	1:A:518:ILE:HG22	0.52	2.05	4	5
1:A:527:ARG:CZ	1:A:562:PHE:HD1	0.50	2.19	6	1

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	102/164 (62%)	96±1 (94±1%)	5±2 (5±1%)	0±1 (0±1%)	38	78
All	All	2040/3280 (62%)	1926 (94%)	105 (5%)	9 (0%)	38	78

All 4 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	567	ILE	3
1	A	544	GLY	3
1	A	502	ALA	2
1	A	550	GLY	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	88/146 (60%)	82±1 (93±1%)	6±1 (7±1%)	20	69
All	All	1760/2920 (60%)	1643 (93%)	117 (7%)	20	69

5 of 21 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	521	MET	20
1	A	589	LEU	20
1	A	636	LEU	19
1	A	554	GLU	10
1	A	569	LYS	8

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

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