wwPDB NMR Structure Validation Summary Report (i)

Apr 26, 2016 – 02:12 PM BST

PDB ID	:	1D4B
Title	:	CIDE-N DOMAIN OF HUMAN CIDE-B
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Deposited on	:	1999-10-02

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
http://wwpdb.org/validation/2016/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:

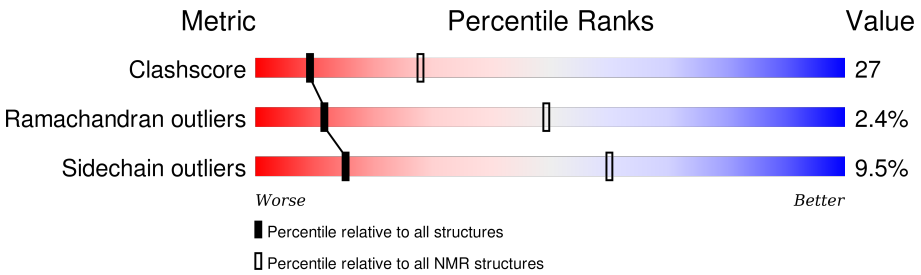
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

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 is 81%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	122	37% 19% • 40%

2 Ensemble composition and analysis (i)

This entry contains 15 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations,lowest energy.*

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:35-A:107 (73)	0.39	13

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. No single-model clusters were found.

Cluster number	Models
1	1, 3, 6, 7, 8, 9, 12, 13, 15
2	2, 5, 10, 11
3	4, 14

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1918 atoms, of which 952 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called HUMAN CELL DEATH-INDUCING EFFECTOR B.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	122	1918	603	952	176	183	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 and DNA 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: HUMAN CELL DEATH-INDUCING EFFECTOR B

Chain A: 37% 19% • 40%

M1 E2 Y3 L4 S5 A6 L7 N8 P9 S10 D11 L12 L13 R14 S15 V16 S17 N18 I19 S20 S21 E22 F23 G24 R25 R26 V27 W28 T29 S30 A31 P32 P33 P34 Q35 R36 R39 V40 C41 D42 H43 K44 R45 T46 I47 R48 R56 L60 A61 K62 A63 L64 E65 T66 L67 L68 L69

L73 T74 L75 V76 L77 F89 L93 T97 C98 L99 M100 V101 L102 Q106 S107 W108 S109 P110 T111 R112 S113 G114 V115 L116 H117 H118 H119 H120 H121 H122

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

The representative model is number 13. Colouring as in section 4.1 above.

- Molecule 1: HUMAN CELL DEATH-INDUCING EFFECTOR B

Chain A: 34% 19% 7% 40%

M1 E2 Y3 L4 S5 A6 L7 N8 P9 S10 D11 L12 L13 R14 S15 V16 S17 N18 I19 S20 S21 E22 F23 G24 R25 R26 V27 W28 T29 S30 A31 P32 P33 P34 Q35 R36 R39 V40 C41 D42 H43 K44 R45 R48 A54 T55 R56 Q57 E58 L59 L60 A61 K62 A63 L64 E65 T66

L67 L68 L69 L73 T74 L75 V76 L77 F89 L93 T97 C98 L99 M100 V101 L102 Q103 S104 G105 Q106 S107 W108 S109 P110 T111 R112 S113 G114 V115 L116 H117 H118 H119 H120 H121 H122

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DISTANCE GEOMETRY SIMULATED ANNEALING TORSION ANGLE DYNAMICS RELAXATION DATA*.

Of the 30 calculated structures, 15 were deposited, based on the following criterion: *STRUCTURES WITH THE LEAST RESTRAINT VIOLATIONS,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	3.18
DYANA	structure solution	1.5

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	BMRB entry 4574
Number of chemical shift lists	1
Total number of shifts	1238
Number of shifts mapped to atoms	1238
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	81%

No validations of the models with respect to experimental NMR restraints is performed at this time.

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	5.0±0.0
All	All	0	75

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	56	ARG	Sidechain	15
1	A	39	ARG	Sidechain	15
1	A	45	ARG	Sidechain	15
1	A	48	ARG	Sidechain	15
1	A	36	ARG	Sidechain	15

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	570	581	581	31±6
All	All	8550	8715	8715	459

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 27.

5 of 136 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:77:LEU:HD13	1:A:93:LEU:HD21	1.15	1.18	6	14
1:A:63:ALA:HB2	1:A:99:LEU:HD11	0.96	1.33	1	11
1:A:63:ALA:HB1	1:A:99:LEU:HD21	0.89	1.42	7	7
1:A:82:THR:HG21	1:A:92:LEU:HD21	0.88	1.46	4	2
1:A:77:LEU:CD1	1:A:93:LEU:HD21	0.85	2.02	9	10

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	73/122 (60%)	61±2 (83±2%)	10±1 (14±2%)	2±1 (2±1%)	12	49
All	All	1095/1830 (60%)	912 (83%)	157 (14%)	26 (2%)	12	49

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	43	HIS	15
1	A	89	PHE	6
1	A	104	SER	4
1	A	79	GLU	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	64/109 (59%)	58±2 (91±3%)	6±2 (9±3%)	15	60
All	All	960/1635 (59%)	869 (91%)	91 (9%)	15	60

5 of 18 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	77	LEU	13
1	A	102	LEU	11
1	A	97	THR	11
1	A	62	LYS	9
1	A	60	LEU	7

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 carbohydrates 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)

The completeness of assignment taking into account all chemical shift lists is 81% for the well-defined parts and 71% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 4574

Chemical shift list name: *assigned_ chem_ shift_ list_ 1*

7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1238
Number of shifts mapped to atoms	1238
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	110	0.47 ± 0.13	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	102	0.40 ± 0.22	None needed (< 0.5 ppm)
$^{13}C'$	112	2.48 ± 0.14	Should be applied
^{15}N	107	0.76 ± 0.50	None needed (imprecise)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 81%, i.e. 722 atoms were assigned a chemical shift out of a possible 896. 17 out of 19 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	363/363 (100%)	145/145 (100%)	146/146 (100%)	72/72 (100%)
Sidechain	344/499 (69%)	235/287 (82%)	109/188 (58%)	0/24 (0%)

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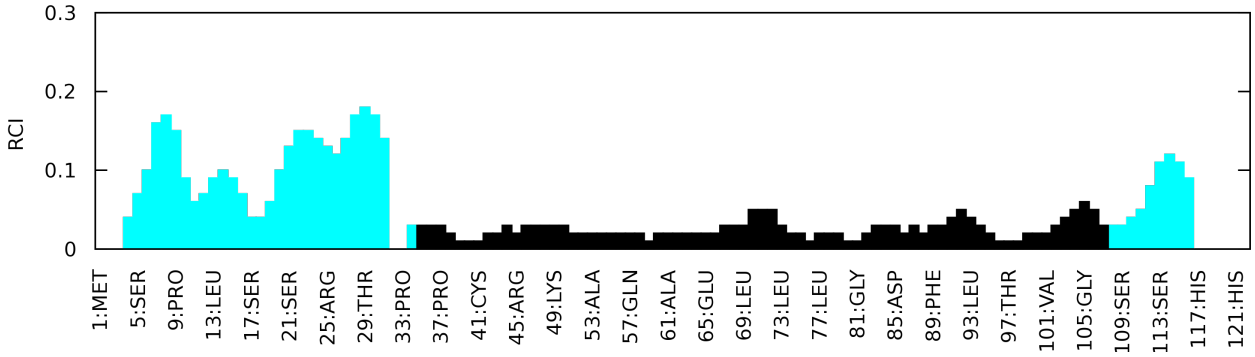
	Total	^{1}H	^{13}C	^{15}N
Aromatic	15/34 (44%)	15/19 (79%)	0/14 (0%)	0/1 (0%)
Overall	722/896 (81%)	395/451 (88%)	255/348 (73%)	72/97 (74%)

7.1.4 Statistically unusual chemical shifts (i)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	78	GLU	HB2	0.76	3.08 – 0.98	-6.0
1	A	78	GLU	HB3	0.76	3.10 – 0.90	-5.6
1	A	44	LYS	HD2	0.43	2.76 – 0.46	-5.1
1	A	44	LYS	HD3	0.43	2.75 – 0.45	-5.1

7.1.5 Random Coil Index (RCI) plots (i)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A: