wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2DIX
Title	:	Solution structure of the DSRM domain of Protein activator of the interferon-induced protein kinase
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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
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:

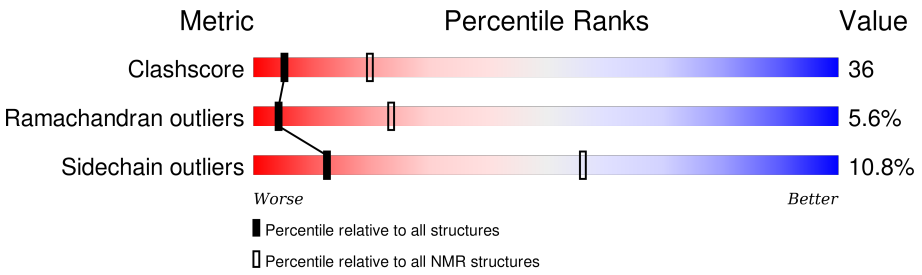
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 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	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	84	39% 35% 7% 19%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 9 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *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:8-A:75 (68)	0.11	9

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 4 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1240 atoms, of which 622 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Interferon-inducible double stranded RNA-dependent protein kinase activator A.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	84	1240	382	622	111	122	3	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	CLONING ARTIFACT	UNP O75569
A	2	SER	-	CLONING ARTIFACT	UNP O75569
A	3	SER	-	CLONING ARTIFACT	UNP O75569
A	4	GLY	-	CLONING ARTIFACT	UNP O75569
A	5	SER	-	CLONING ARTIFACT	UNP O75569
A	6	SER	-	CLONING ARTIFACT	UNP O75569
A	7	GLY	-	CLONING ARTIFACT	UNP O75569
A	79	SER	-	CLONING ARTIFACT	UNP O75569
A	80	GLY	-	CLONING ARTIFACT	UNP O75569
A	81	PRO	-	CLONING ARTIFACT	UNP O75569
A	82	SER	-	CLONING ARTIFACT	UNP O75569
A	83	SER	-	CLONING ARTIFACT	UNP O75569
A	84	GLY	-	CLONING ARTIFACT	UNP O75569

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: Interferon-inducible double stranded RNA-dependent protein kinase activator A

Chain A: 39% 35% 7% 19%

G1 S2 S3 G4 S5 S6 G7 K8 T9 P10 I11 Q12 V13 L14 H15 E16 Y17 G18 M19 K20 T21 K22 N23 I24 P25 V34 Q35 I36 H37 V38 R44 V45 G48 T57 S58 K59 K60 L61 A62 K63 H64 R65 A66 A67 A70 I71 N72 I73 L74 K75 A76 N77 A78 S79 G80

P81 S82 S83 G84

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

The representative model is number 9. Colouring as in section 4.1 above.

• Molecule 1: Interferon-inducible double stranded RNA-dependent protein kinase activator A

Chain A: 32% 39% 8% • 19%

G1 S2 S3 G4 S5 S6 G7 K8 T9 P10 I11 Q12 V13 L14 H15 E16 Y17 G18 M19 K20 T21 K22 N23 I24 P25 V26 Y27 V34 Q35 I36 H37 V38 P39 T40 R44 V45 C52 T53 G56 T57 S58 K59 K60 L61 A62 K63 H64 R65 A66 A67 A70 I71 N72 I73 L74

K75 A76 N77 A78 S79 G80 P81 S82 S83 G84

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: *target function, structures with the lowest energy, structures with the least restraint violations.*

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

Software name	Classification	Version
CYANA	structure solution	2.0.17
CYANA	refinement	2.0.17

No chemical shift data was provided. 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.

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	531	549	549	39±3
All	All	10620	10980	10980	786

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 36.

5 of 108 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:57:THR:O	1:A:62:ALA:HB2	0.85	1.72	12	20
1:A:61:LEU:HD12	1:A:61:LEU:O	0.78	1.79	11	8
1:A:61:LEU:O	1:A:61:LEU:HD12	0.78	1.77	8	11
1:A:61:LEU:C	1:A:61:LEU:HD12	0.73	2.04	8	9
1:A:61:LEU:HD12	1:A:61:LEU:C	0.72	2.05	10	9

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	68/84 (81%)	49±2 (72±3%)	15±2 (23±3%)	4±1 (6±1%)	4 23
All	All	1360/1680 (81%)	977 (72%)	307 (23%)	76 (6%)	4 23

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	59	LYS	20
1	A	71	ILE	19
1	A	22	LYS	14
1	A	48	GLY	11
1	A	18	GLY	5

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	59/68 (87%)	53±1 (89±2%)	6±1 (11±2%)	12 56
All	All	1180/1360 (87%)	1052 (89%)	128 (11%)	12 56

5 of 17 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	14	LEU	20
1	A	36	ILE	20
1	A	57	THR	20
1	A	9	THR	18
1	A	61	LEU	17

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)

No chemical shift data were provided