wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2E5K
Title	:	Solution structure of SH3 domain in Suppressor of T-cell receptor signaling 1
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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:

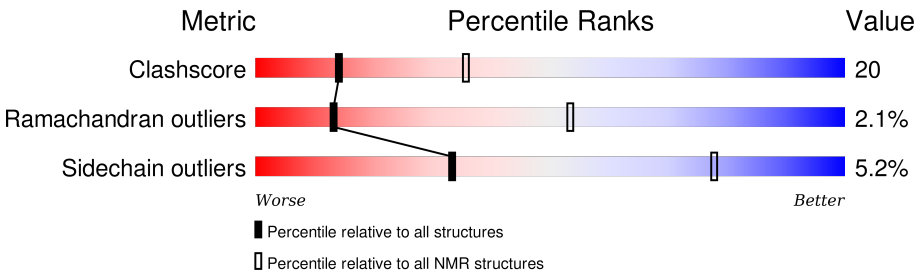
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 is 94%.

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	94	40% 23% • 35%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 2 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:257-A:317 (61)	0.13	2

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1362 atoms, of which 650 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Suppressor of T-cell receptor signaling 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	94	1362	443	650	113	152	4	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	241	GLY	-	CLONING ARTIFACT	UNP Q8TF42
A	242	SER	-	CLONING ARTIFACT	UNP Q8TF42
A	243	SER	-	CLONING ARTIFACT	UNP Q8TF42
A	244	GLY	-	CLONING ARTIFACT	UNP Q8TF42
A	245	SER	-	CLONING ARTIFACT	UNP Q8TF42
A	246	SER	-	CLONING ARTIFACT	UNP Q8TF42
A	247	GLY	-	CLONING ARTIFACT	UNP Q8TF42
A	329	SER	-	CLONING ARTIFACT	UNP Q8TF42
A	330	GLY	-	CLONING ARTIFACT	UNP Q8TF42
A	331	PRO	-	CLONING ARTIFACT	UNP Q8TF42
A	332	SER	-	CLONING ARTIFACT	UNP Q8TF42
A	333	SER	-	CLONING ARTIFACT	UNP Q8TF42
A	334	GLY	-	CLONING ARTIFACT	UNP Q8TF42

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: Suppressor of T-cell receptor signaling 1

Chain A: 40% 23% • 35%

G241 S242 S243 G244 S245 S246 G247 S248 R249 D250 I251 R252 F253 A254 N255 H256 L259 I262 Y263 D270 D271 E272 L275 F282 M283 S284 E287 Q288 T289 S290 T291 G294 W295 I296 Y297 L301 L308 L309 P310 Y313 I314 A317 D318 E319 C320 S321 T322 W323 I324

F325 H326 G327 S328 S329 G330 P331 S332 S333 G334

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

The representative model is number 2. Colouring as in section 4.1 above.

- Molecule 1: Suppressor of T-cell receptor signaling 1

Chain A: 39% 23% • 35%

G241 S242 S243 G244 S245 S246 G247 S248 R249 D250 I251 R252 F253 A254 N255 H256 L259 I262 Y263 P267 D271 E272 L275 M283 S284 E287 Q288 T289 S290 T291 S292 E293 G294 W295 I296 Y297 G298 T299 C305 L308 L309 P310 Y313 I314 D318 E319 C320 S321 T322

W323 I324 F325 H326 G327 S328 S329 G330 P331 S332 S333 G334

5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the least restraint violations, structures with the lowest energy, target function.*

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

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 10337
Number of chemical shift lists	1
Total number of shifts	974
Number of shifts mapped to atoms	974
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	94%

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	476	448	448	19±5
All	All	9520	8960	8960	377

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 20.

5 of 91 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:265:TYR:CB	1:A:275:LEU:HD12	0.92	1.95	18	4
1:A:259:LEU:HD13	1:A:314:ILE:HD13	0.90	1.39	14	20
1:A:265:TYR:HB2	1:A:275:LEU:HD12	0.82	1.50	3	4
1:A:280:PHE:O	1:A:281:ILE:HD13	0.72	1.84	3	3
1:A:289:THR:O	1:A:308:LEU:HD21	0.72	1.85	1	11

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	61/94 (65%)	55±1 (90±2%)	5±2 (8±3%)	1±1 (2±1%)	13 53
All	All	1220/1880 (65%)	1100 (90%)	94 (8%)	26 (2%)	13 53

5 of 6 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	294	GLY	14
1	A	317	ALA	8
1	A	292	SER	1
1	A	288	GLN	1
1	A	300	SER	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	55/81 (68%)	52±1 (95±2%)	3±1 (5±2%)	33 78
All	All	1100/1620 (68%)	1043 (95%)	57 (5%)	33 78

5 of 12 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	309	LEU	20
1	A	271	ASP	15
1	A	316	LYS	9
1	A	284	SER	4
1	A	269	ASN	2

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 94% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 10337

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	974
Number of shifts mapped to atoms	974
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	79	-0.02 ± 0.18	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	73	0.17 ± 0.17	None needed (< 0.5 ppm)
$^{13}C'$	78	0.01 ± 0.11	None needed (< 0.5 ppm)
^{15}N	72	0.09 ± 0.35	None needed (< 0.5 ppm)

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 94%, i.e. 665 atoms were assigned a chemical shift out of a possible 704. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	293/295 (99%)	117/117 (100%)	121/122 (99%)	55/56 (98%)
Sidechain	312/347 (90%)	192/203 (95%)	116/138 (84%)	4/6 (67%)

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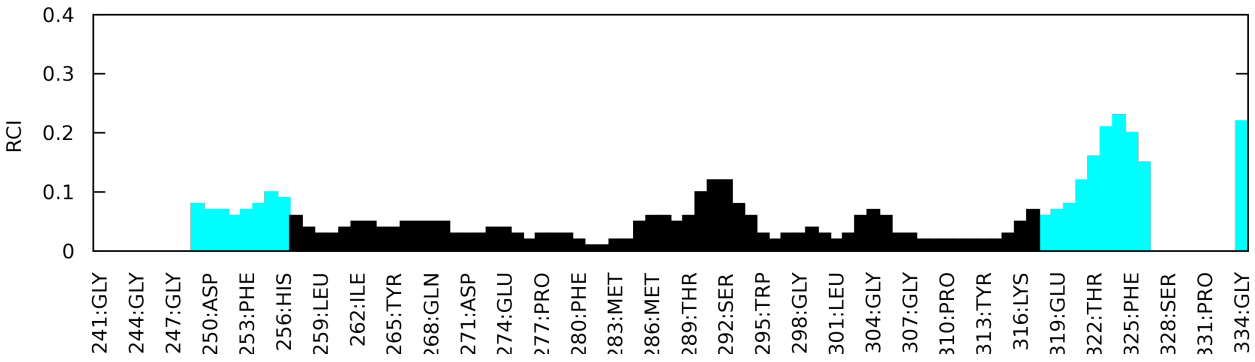
	Total	^{1}H	^{13}C	^{15}N
Aromatic	60/62 (97%)	30/32 (94%)	29/29 (100%)	1/1 (100%)
Overall	665/704 (94%)	339/352 (96%)	266/289 (92%)	60/63 (95%)

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	310	PRO	HG3	-0.12	3.56 – 0.26	-6.2

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: