wwPDB NMR Structure Validation Summary Report (i)

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PDB ID	:	2DHG
Title	:	Solution structure of the C-terminal RNA recognition motif in tRNA selenocysteine associated protein
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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 (i)) were used in the production of this report:

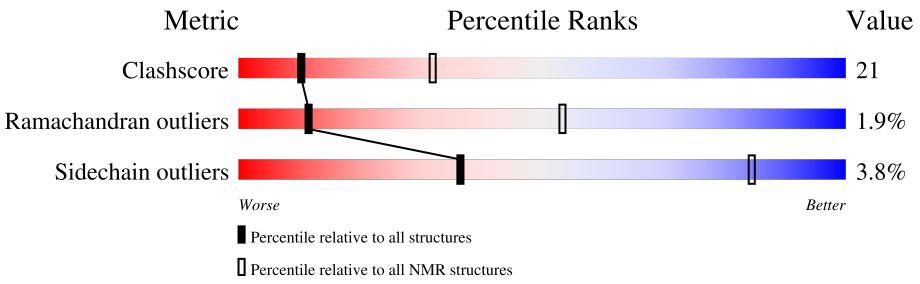
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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	104	52% 22% • 25%

2 Ensemble composition and analysis (i)

This entry contains 20 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: *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:96-A:173 (78)	0.13	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 4 clusters and 2 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1529 atoms, of which 763 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called tRNA selenocysteine associated protein (SECP43).

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	104	1529	484	763	127	152	3	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	87	GLY	-	cloning artifact	UNP Q9NX07
A	88	SER	-	cloning artifact	UNP Q9NX07
A	89	SER	-	cloning artifact	UNP Q9NX07
A	90	GLY	-	cloning artifact	UNP Q9NX07
A	91	SER	-	cloning artifact	UNP Q9NX07
A	92	SER	-	cloning artifact	UNP Q9NX07
A	93	GLY	-	cloning artifact	UNP Q9NX07
A	185	SER	-	cloning artifact	UNP Q9NX07
A	186	GLY	-	cloning artifact	UNP Q9NX07
A	187	PRO	-	cloning artifact	UNP Q9NX07
A	188	SER	-	cloning artifact	UNP Q9NX07
A	189	SER	-	cloning artifact	UNP Q9NX07
A	190	GLY	-	cloning artifact	UNP Q9NX07

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: tRNA selenocysteine associated protein (SECP43)

Chain A: 52% 22% • 25%

G87 S88 S89 G90 S91 S92 G93 P94 E95 L98 V107 E114 F115 F116 V117 K118 V119 Y120 V129 L130 D131 Y139 V142 Q150 A153 L154 T155 E156 C157 Q158 G159 A160 L163 V168 R169 L170 I174 P175 K176 A177 S178 R179 V180 K181 P182 V183 E184 S185 G186

P187 S188 S189 G190

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: tRNA selenocysteine associated protein (SECP43)

Chain A: 52% 23% 25%

G87 S88 S89 G90 S91 S92 G93 P94 E95 Y96 S97 L98 D102 V107 D108 M111 E114 F115 F116 V117 K118 V119 Y120 V129 G138 Y139 E147 A153 L154 T155 E156 C157 Q158 G159 A160 V168 R169 L170 I174 P175 K176 A177 S178 R179 V180 K181 P182 V183 E184 S185

G186 P187 S188 S189 G190

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: *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
CYANA	refinement	2.0

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.

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	596	595	595	25±5
All	All	11920	11900	11900	507

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 21.

5 of 125 unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:129:VAL:HG21	1:A:139:TYR:CE1	0.88	2.02	15	12
1:A:129:VAL:HG21	1:A:139:TYR:CZ	0.87	2.05	15	20
1:A:129:VAL:HG22	1:A:139:TYR:O	0.86	1.70	14	19
1:A:160:ALA:HB3	1:A:168:VAL:CG2	0.78	2.09	6	15
1:A:107:VAL:HG13	1:A:111:MET:HE2	0.77	1.57	18	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	78/104 (75%)	67±2 (86±3%)	10±2 (12±3%)	2±1 (2±1%)	11 53
All	All	1560/2080 (75%)	1336 (86%)	194 (12%)	30 (2%)	11 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	117	VAL	17
1	A	164	GLY	7
1	A	136	SER	3
1	A	112	LEU	1
1	A	162	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	65/85 (76%)	62±1 (96±2%)	2±1 (4±2%)	36 84
All	All	1300/1700 (76%)	1250 (96%)	50 (4%)	36 84

5 of 19 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	108	ASP	10
1	A	109	ASP	6
1	A	143	LYS	4
1	A	132	GLN	4
1	A	106	ASP	3

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