Full wwPDB NMR Structure Validation Report (i)

Feb 26, 2022 – 09:45 AM EST

PDB ID	:	2CQW
Title	:	Solution structure of RSGI RUH-041, a SMB-like domain from mouse cDNA
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Deposited on	:	2005-05-20

This is a Full wwPDB NMR Structure Validation 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:

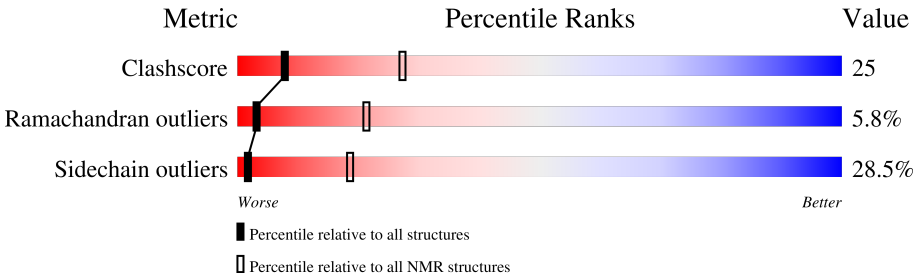
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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	84	14% 23% 6% 57%

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:20-A:55 (36)	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 2 clusters and 4 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1101 atoms, of which 525 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Sushi domain containing 2.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	84	1101	349	525	97	120	10	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q9DBX3
A	2	SER	-	cloning artifact	UNP Q9DBX3
A	3	SER	-	cloning artifact	UNP Q9DBX3
A	4	GLY	-	cloning artifact	UNP Q9DBX3
A	5	SER	-	cloning artifact	UNP Q9DBX3
A	6	SER	-	cloning artifact	UNP Q9DBX3
A	7	GLY	-	cloning artifact	UNP Q9DBX3
A	79	SER	-	cloning artifact	UNP Q9DBX3
A	80	GLY	-	cloning artifact	UNP Q9DBX3
A	81	PRO	-	cloning artifact	UNP Q9DBX3
A	82	SER	-	cloning artifact	UNP Q9DBX3
A	83	SER	-	cloning artifact	UNP Q9DBX3
A	84	GLY	-	cloning artifact	UNP Q9DBX3

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: Sushi domain containing 2

Chain A: 14% 23% 6% 57%

G1 S2 S3 G4 S5 S6 G7 I8 P9 G10 P11 G12 F13 T14 A15 G16 A17 Q18 G19 S20 C21 S22 L23 R24 C25 G26 A27 Q28 D29 C32 S33 C34 H35 P36 T37 C38 L41 G42 T43 C44 C45 F48 L49 D50 Y51 C52 L53 E54 I55 L56 P57 S58 S59 G60 S61 M62 M63

G64 G65 K66 D67 F68 V69 V70 Q71 H72 L73 K74 W75 T76 D77 P78 S79 G80 P81 S82 S83 G84

4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: Sushi domain containing 2

Chain A: 17% 20% 6% 57%

G1 S2 S3 G4 S5 S6 G7 I8 P9 G10 P11 G12 F13 T14 A15 G16 A17 Q18 G19 S20 C21 S22 L23 R24 C25 G26 A27 C32 S33 C34 H35 P36 T37 C38 S39 G42 T43 C44 C45 E46 D47 F48 L49 D50 Y51 C52 L53 L56 P57 S58 S59 G60 S61 M62 M63 G64 G65

K66 D67 F68 V69 V70 Q71 H72 L73 K74 W75 T76 D77 P78 S79 G80 P81 S82 S83 G84

4.2.2 Score per residue for model 2 (medoid)

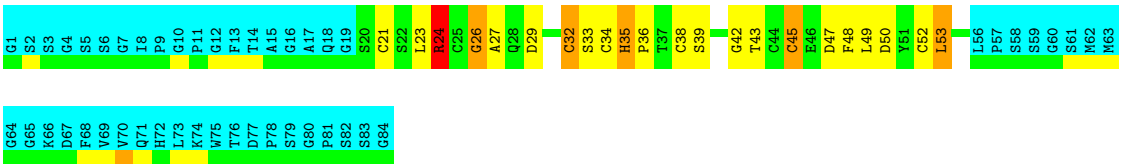
• Molecule 1: Sushi domain containing 2

Chain A: 14% 23% 6% 57%

4.2.3 Score per residue for model 3

- Molecule 1: Sushi domain containing 2

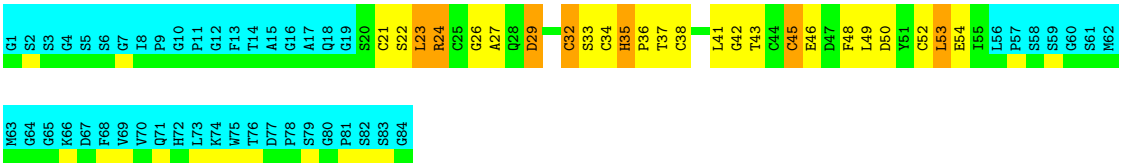
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: Sushi domain containing 2

Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: Sushi domain containing 2

Chain A:

4.2.6 Score per residue for model 6

- Molecule 1: Sushi domain containing 2

Chain A: 17% 19% 6% • 57%

G1 S2 S3 G4 S5 S6 G7 I8 P9 G10 P11 G12 F13 T14 A15 G16 A17 Q18 G19 S20 C21 S22 L23 R24 C25 G26 A27 C32 S33 C34 H35 P36 T37 C38 L41 G42 T43 C44 C45 F48 L49 D50 Y51 C52 L53 E54 I55 L56 P57 S58 S59 G60 S61 M62 M63 G64 G65

K66 D67 F68 V69 V70 Q71 H72 L73 K74 W75 T76 D77 P78 S79 G80 P81 S82 S83 G84

4.2.7 Score per residue for model 7

- Molecule 1: Sushi domain containing 2

Chain A: 19% 19% 5% 57%

G1 S2 S3 G4 S5 S6 G7 I8 P9 G10 P11 G12 F13 T14 A15 G16 A17 Q18 G19 S20 C21 S22 L23 R24 C25 G26 A27 Q28 D29 C34 H35 P36 T37 C38 L41 G42 C45 F48 L49 D50 Y51 C52 L53 E54 I55 L56 P57 S58 S59 G60 S61 M62 M63 G64 G65 K66

D67 F68 V69 V70 Q71 H72 L73 K74 W75 T76 D77 P78 S79 G80 P81 S82 S83 G84

4.2.8 Score per residue for model 8

- Molecule 1: Sushi domain containing 2

Chain A: 10% 24% 10% 57%

G1 S2 S3 G4 S5 S6 G7 I8 P9 G10 P11 G12 F13 T14 A15 G16 A17 Q18 G19 S20 C21 S22 L23 R24 C25 G26 A27 Q28 D29 G30 L31 C32 S33 C34 H35 P36 T37 C38 S39 G40 L41 G42 T43 C44 C45 E46 D47 F48 L49 D50 Y51 C52 L53 E54 I55 L56 P57 S58 S59 G60

S61 M62 M63 G64 G65 K66 D67 F68 V69 V70 Q71 H72 L73 K74 W75 T76 D77 P78 S79 G80 P81 S82 S83 G84

4.2.9 Score per residue for model 9

- Molecule 1: Sushi domain containing 2

Chain A: 13% 23% 6% • 57%

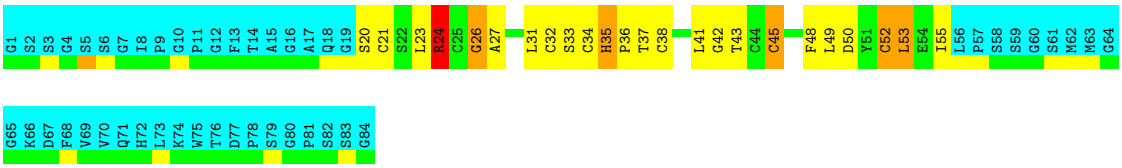
G1 S2 S3 G4 S5 S6 G7 I8 P9 G10 P11 G12 F13 T14 A15 G16 A17 Q18 G19 S20 C21 S22 L23 R24 C25 G26 A27 Q28 D29 C32 S33 C34 H35 P36 T37 C38 L41 G42 T43 C44 C45 E46 D47 F48 L49 D50 Y51 C52 L53 E54 I55 L56 P57 S58 S59 G60 S61 M62

M63 G64 G65 K66 D67 F68 V69 V70 Q71 H72 L73 K74 W75 T76 D77 P78 S79 G80 P81 S82 S83 G84

4.2.10 Score per residue for model 10

- Molecule 1: Sushi domain containing 2

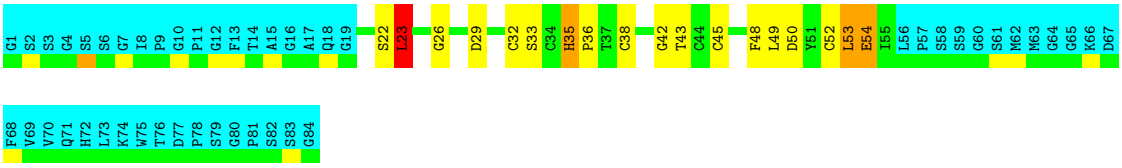
Chain A: 14% 21% 6% • 57%



4.2.11 Score per residue for model 11

- Molecule 1: Sushi domain containing 2

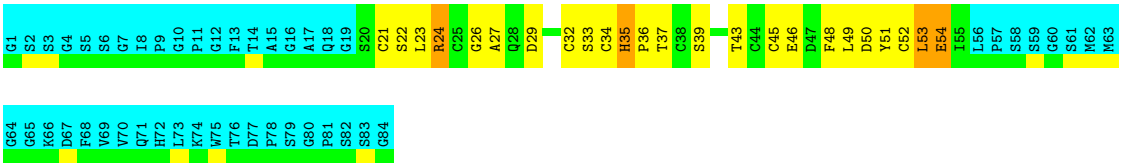
Chain A: 21% 17% • • 57%



4.2.12 Score per residue for model 12

- Molecule 1: Sushi domain containing 2

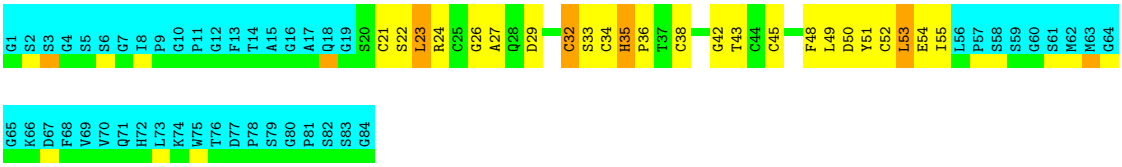
Chain A: 14% 24% 5% 57%



4.2.13 Score per residue for model 13

- Molecule 1: Sushi domain containing 2

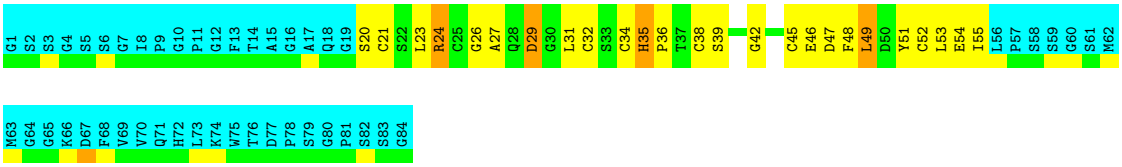
Chain A: 14% 24% 5% 57%



4.2.14 Score per residue for model 14

- Molecule 1: Sushi domain containing 2

Chain A: 13% 25% 5% 57%



4.2.15 Score per residue for model 15

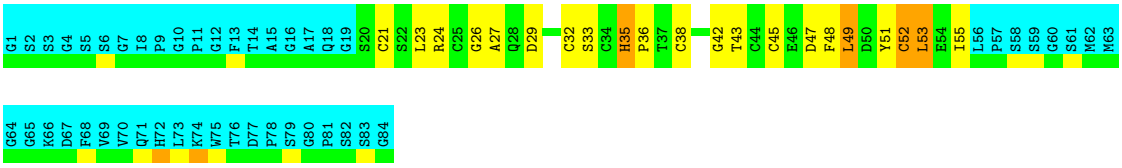
- Molecule 1: Sushi domain containing 2

Chain A: 13% 23% 7% 57%

4.2.16 Score per residue for model 16

- Molecule 1: Sushi domain containing 2

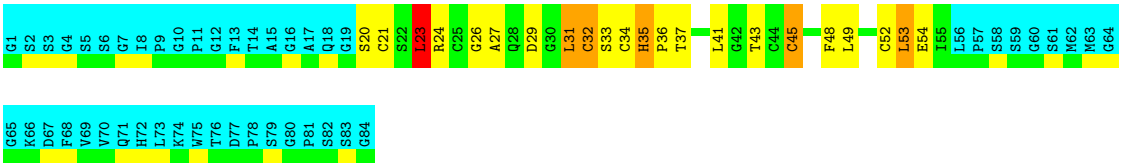
Chain A: 18% 20% 5% 57%



4.2.17 Score per residue for model 17

- Molecule 1: Sushi domain containing 2

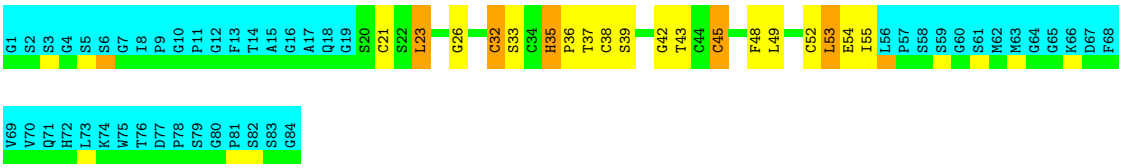
Chain A: 17% 19% 6% • 57%



4.2.18 Score per residue for model 18

- Molecule 1: Sushi domain containing 2

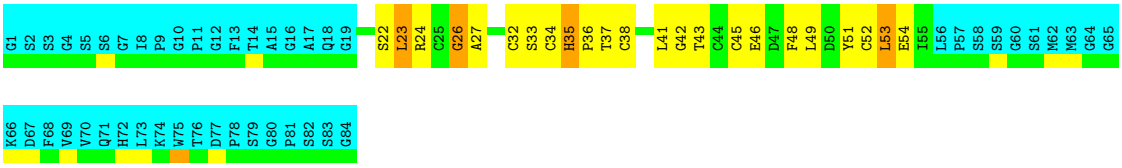
Chain A: 20% 17% 6% 57%



4.2.19 Score per residue for model 19

- Molecule 1: Sushi domain containing 2

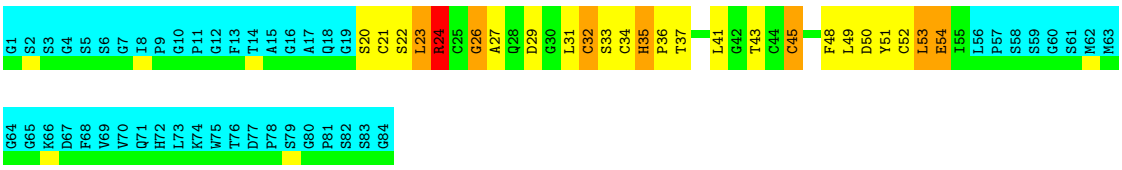
Chain A: 15% 23% 5% 57%



4.2.20 Score per residue for model 20

- Molecule 1: Sushi domain containing 2

Chain A: 13% 20% 8% • 57%



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	1.0.8
CYANA	refinement	1.0.8

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	257	226	226	12±2
All	All	5140	4520	4520	244

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 25.

All unique clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:CYS:SG	1:A:45:CYS:SG	1.04	2.56	14	18
1:A:23:LEU:O	1:A:23:LEU:HD22	0.86	1.70	6	2
1:A:23:LEU:HD22	1:A:23:LEU:C	0.73	2.04	20	2
1:A:37:THR:O	1:A:41:LEU:HD12	0.69	1.88	4	9
1:A:49:LEU:N	1:A:49:LEU:HD13	0.66	2.04	14	3
1:A:52:CYS:HB3	1:A:55:ILE:HD13	0.63	1.70	14	5
1:A:24:ARG:HD2	1:A:27:ALA:HB3	0.62	1.70	14	16
1:A:48:PHE:CZ	1:A:55:ILE:HD11	0.60	2.31	8	2
1:A:22:SER:O	1:A:51:TYR:CD1	0.59	2.55	6	1
1:A:48:PHE:CE1	1:A:55:ILE:HD11	0.57	2.34	8	1
1:A:23:LEU:HD13	1:A:23:LEU:N	0.56	2.16	13	3
1:A:23:LEU:C	1:A:23:LEU:HD12	0.55	2.22	3	1
1:A:38:CYS:SG	1:A:48:PHE:CE2	0.52	3.03	18	1
1:A:48:PHE:CD2	1:A:49:LEU:CD1	0.51	2.93	14	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:ARG:CB	1:A:34:CYS:SG	0.50	3.00	17	1
1:A:21:CYS:O	1:A:51:TYR:CB	0.50	2.60	8	7
1:A:23:LEU:HD13	1:A:24:ARG:N	0.50	2.22	6	1
1:A:49:LEU:O	1:A:53:LEU:CB	0.50	2.59	1	18
1:A:49:LEU:O	1:A:53:LEU:CG	0.50	2.60	18	14
1:A:23:LEU:CD1	1:A:23:LEU:C	0.50	2.80	17	1
1:A:23:LEU:C	1:A:23:LEU:CD2	0.49	2.78	20	1
1:A:29:ASP:CB	1:A:32:CYS:O	0.49	2.60	4	2
1:A:28:GLN:NE2	1:A:35:HIS:ND1	0.49	2.61	5	1
1:A:49:LEU:H	1:A:49:LEU:HD22	0.48	1.67	16	1
1:A:23:LEU:HD13	1:A:23:LEU:H	0.47	1.67	13	1
1:A:48:PHE:O	1:A:52:CYS:N	0.47	2.48	20	20
1:A:31:LEU:H	1:A:31:LEU:HD22	0.47	1.70	20	2
1:A:49:LEU:HD23	1:A:52:CYS:O	0.47	2.10	7	1
1:A:49:LEU:N	1:A:49:LEU:CD1	0.47	2.75	14	3
1:A:23:LEU:HD12	1:A:24:ARG:N	0.46	2.26	10	2
1:A:33:SER:N	1:A:43:THR:O	0.46	2.49	12	18
1:A:22:SER:HA	1:A:51:TYR:CD2	0.46	2.46	20	2
1:A:48:PHE:CD2	1:A:49:LEU:HD13	0.46	2.46	16	1
1:A:35:HIS:CG	1:A:36:PRO:HD2	0.46	2.46	18	19
1:A:23:LEU:C	1:A:23:LEU:HD13	0.46	2.32	6	2
1:A:38:CYS:O	1:A:42:GLY:N	0.45	2.50	3	16
1:A:32:CYS:SG	1:A:33:SER:N	0.45	2.90	8	10
1:A:27:ALA:O	1:A:34:CYS:N	0.45	2.49	10	11
1:A:22:SER:HB3	1:A:23:LEU:HD13	0.45	1.89	15	1
1:A:23:LEU:CD2	1:A:23:LEU:C	0.44	2.86	15	2
1:A:26:GLY:N	1:A:34:CYS:O	0.44	2.49	19	6
1:A:24:ARG:NE	1:A:27:ALA:CB	0.44	2.81	17	1
1:A:34:CYS:HA	1:A:48:PHE:CD1	0.44	2.47	17	1
1:A:22:SER:HA	1:A:51:TYR:CE2	0.44	2.47	20	1
1:A:22:SER:HA	1:A:51:TYR:CD1	0.43	2.49	12	1
1:A:23:LEU:C	1:A:23:LEU:HD22	0.41	2.36	15	1
1:A:22:SER:HA	1:A:51:TYR:CG	0.41	2.51	13	1
1:A:41:LEU:N	1:A:41:LEU:CD2	0.41	2.83	7	1
1:A:23:LEU:C	1:A:23:LEU:CD1	0.41	2.89	18	1
1:A:23:LEU:HD23	1:A:23:LEU:C	0.41	2.36	19	1
1:A:27:ALA:O	1:A:35:HIS:N	0.41	2.54	7	1
1:A:52:CYS:HB3	1:A:55:ILE:CD1	0.40	2.47	16	1
1:A:23:LEU:C	1:A:23:LEU:HD23	0.40	2.37	2	1
1:A:35:HIS:O	1:A:38:CYS:SG	0.40	2.80	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	36/84 (43%)	30±1 (82±3%)	4±2 (12±4%)	2±1 (6±2%)	3 21
All	All	720/1680 (43%)	591 (82%)	87 (12%)	42 (6%)	3 21

All 5 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	26	GLY	20
1	A	54	GLU	14
1	A	24	ARG	5
1	A	23	LEU	2
1	A	22	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	31/65 (48%)	22±2 (71±6%)	9±2 (29±6%)	2 18
All	All	620/1300 (48%)	443 (71%)	177 (29%)	2 18

All 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	35	HIS	20
1	A	53	LEU	20
1	A	23	LEU	18
1	A	32	CYS	15
1	A	50	ASP	15

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Mol	Chain	Res	Type	Models (Total)
1	A	45	CYS	13
1	A	29	ASP	13
1	A	24	ARG	12
1	A	39	SER	8
1	A	46	GLU	7
1	A	54	GLU	7
1	A	47	ASP	5
1	A	31	LEU	4
1	A	49	LEU	4
1	A	52	CYS	4
1	A	20	SER	4
1	A	22	SER	3
1	A	37	THR	3
1	A	41	LEU	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 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