Full wwPDB NMR Structure Validation Report (i)

Feb 27, 2022 – 11:39 PM EST

PDB ID	:	2EAO
Title	:	Solution structure of the C-terminal SAM-domain of mouse ephrin type-B receptor 1 precursor (EC 2.7.1.112)
Authors	:	Goroncy, A.K.; Sato, M.; Koshiba, S.; Inoue, M.; Kigawa, T.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)
Deposited on	:	2007-01-31

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:

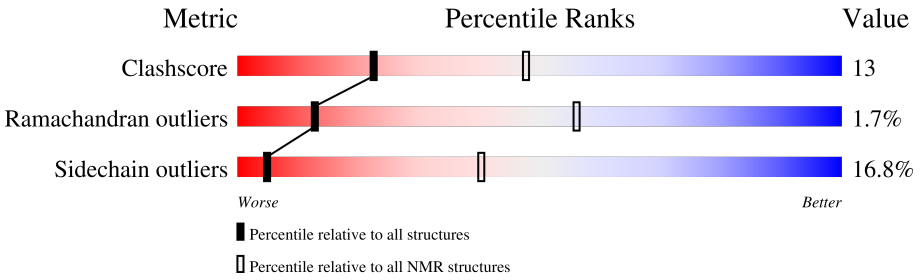
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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	99	37% 17% • 41%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:25-A:82 (58)	0.10	1

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1481 atoms, of which 741 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ephrin type-B receptor 1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	99	1481	461	741	127	148	4	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP P54762
A	2	SER	-	cloning artifact	UNP P54762
A	3	SER	-	cloning artifact	UNP P54762
A	4	GLY	-	cloning artifact	UNP P54762
A	5	SER	-	cloning artifact	UNP P54762
A	6	SER	-	cloning artifact	UNP P54762
A	7	GLY	-	cloning artifact	UNP P54762
A	94	SER	-	cloning artifact	UNP P54762
A	95	GLY	-	cloning artifact	UNP P54762
A	96	PRO	-	cloning artifact	UNP P54762
A	97	SER	-	cloning artifact	UNP P54762
A	98	SER	-	cloning artifact	UNP P54762
A	99	GLY	-	cloning artifact	UNP P54762

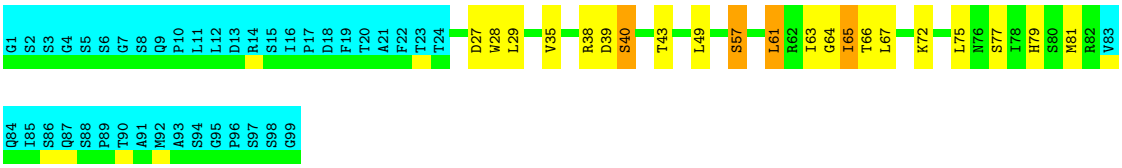
4 Residue-property plots (i)

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: Ephrin type-B receptor 1

Chain A: 37% 17% • 41%



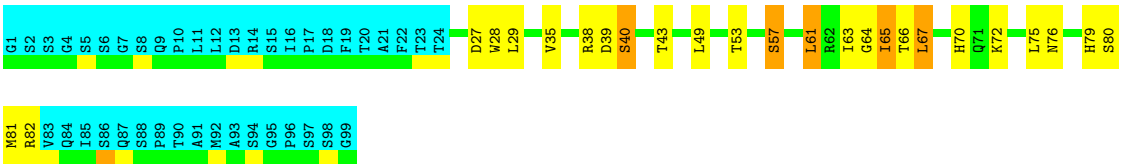
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

• Molecule 1: Ephrin type-B receptor 1

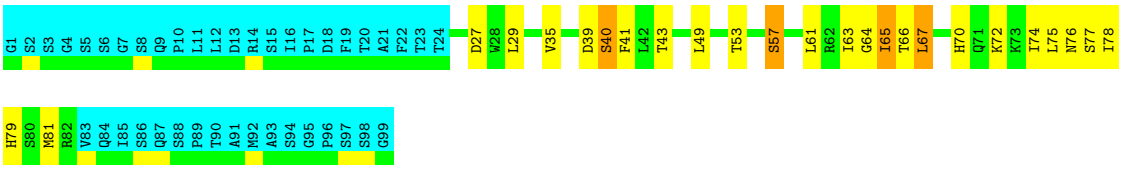
Chain A: 33% 20% 5% 41%



4.2.2 Score per residue for model 2

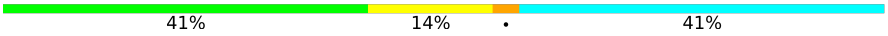
• Molecule 1: Ephrin type-B receptor 1

Chain A: 33% 21% • 41%



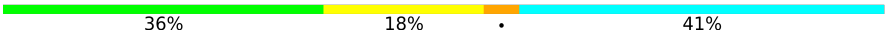
4.2.3 Score per residue for model 3

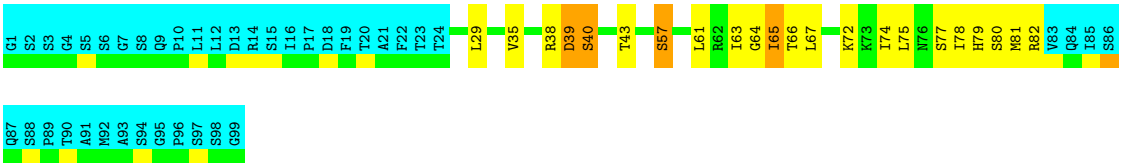
- Molecule 1: Ephrin type-B receptor 1

Chain A: 

4.2.4 Score per residue for model 4

- Molecule 1: Ephrin type-B receptor 1

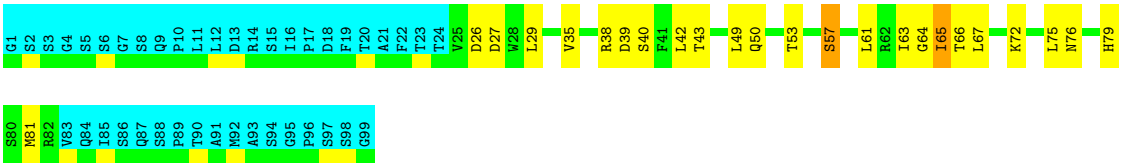
Chain A: 



4.2.5 Score per residue for model 5

- Molecule 1: Ephrin type-B receptor 1

Chain A:



4.2.6 Score per residue for model 6

- Molecule 1: Ephrin type-B receptor 1

Chain A: 31% 21% 6% 41%

G1 S2 S3 G4 S5 S6 G7 S8 Q9 P10 L11 L12 D13 R14 S15 I16 P17 D18 F19 T20 A21 F22 T23 T24 V25 D26 D27 W28 L29 V35 R38 D39 S40 F41 L42 T43 F46 L49 Q50 T56 S57 E58 L61 R62 I63 G64 I65 T66 K72 K73 I74 L75 N76

S77 I78 H79 S80 M81 R82 V83 Q84 I85 S86 Q87 S88 P89 T90 A91 M92 A93 S94 G95 P96 S97 S98 G99

4.2.7 Score per residue for model 7

- Molecule 1: Ephrin type-B receptor 1

Chain A: 34% 20% • 41%

G1 S2 S3 G4 S5 S6 G7 S8 Q9 P10 L11 L12 D13 R14 S15 I16 P17 D18 F19 T20 A21 F22 T23 T24 D27 W28 L29 V35 R38 D39 S40 F41 L42 T43 L49 Q50 L51 V52 T53 S57 L61 R62 I63 G64 I65 T66 L67 L75 N76 S77 I78 H79 S80

M81 R82 V83 Q84 I85 S86 Q87 S88 P89 T90 A91 M92 A93 S94 G95 P96 S97 S98 G99

4.2.8 Score per residue for model 8

- Molecule 1: Ephrin type-B receptor 1

Chain A: 33% 22% • 41%

G1 S2 S3 G4 S5 S6 G7 S8 Q9 P10 L11 L12 D13 R14 S15 I16 P17 D18 F19 T20 A21 F22 T23 T24 V25 D26 D27 W28 L29 V35 R38 D39 S40 F41 L42 T43 L49 T56 S57 E58 D59 L60 L61 R62 I63 G64 I65 T66 L67 K72 L75 N76 S77 I78

H79 V83 Q84 I85 S86 Q87 S88 P89 T90 A91 M92 A93 S94 G95 P96 S97 S98 G99

4.2.9 Score per residue for model 9

- Molecule 1: Ephrin type-B receptor 1

Chain A: 38% 16% • 41%

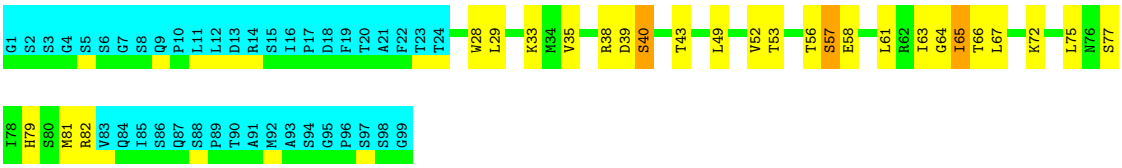
G1 S2 S3 G4 S5 S6 G7 S8 Q9 P10 L11 L12 D13 R14 S15 I16 P17 D18 F19 T20 A21 F22 T23 T24 V25 D26 D27 W28 L29 V35 D39 S40 F41 L42 T43 V52 L61 R62 I63 G64 I65 T66 L67 H70 Q71 K72 N76 S77 I78 H79 V83 Q84 I85

S86 Q87 S88 P89 T90 A91 M92 A93 S94 G95 P96 S97 S98 G99

4.2.10 Score per residue for model 10

- Molecule 1: Ephrin type-B receptor 1

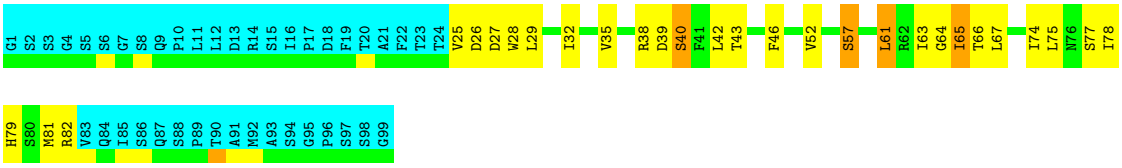
Chain A: 32% 23% • 41%



4.2.11 Score per residue for model 11

- Molecule 1: Ephrin type-B receptor 1

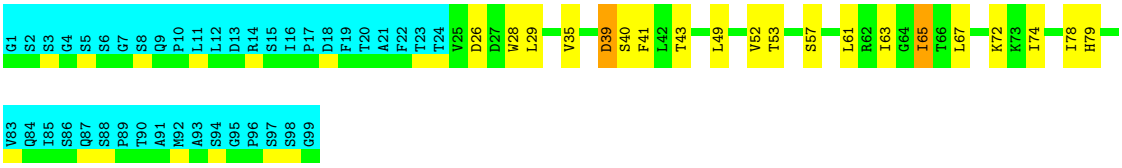
Chain A: 30% 24% • 41%



4.2.12 Score per residue for model 12

- Molecule 1: Ephrin type-B receptor 1

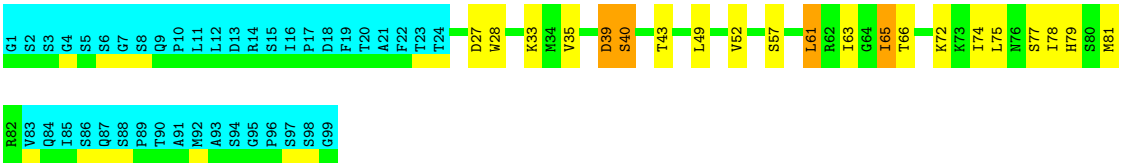
Chain A: 38% 18% • 41%



4.2.13 Score per residue for model 13

- Molecule 1: Ephrin type-B receptor 1

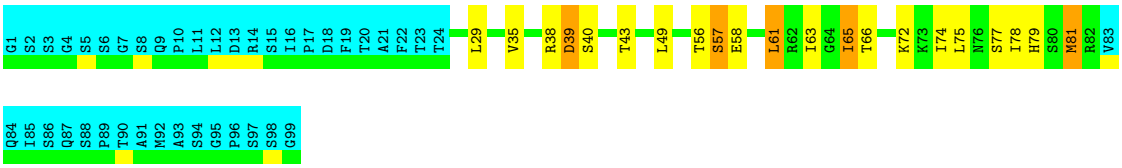
Chain A: 37% 17% • 41%



4.2.14 Score per residue for model 14

- Molecule 1: Ephrin type-B receptor 1

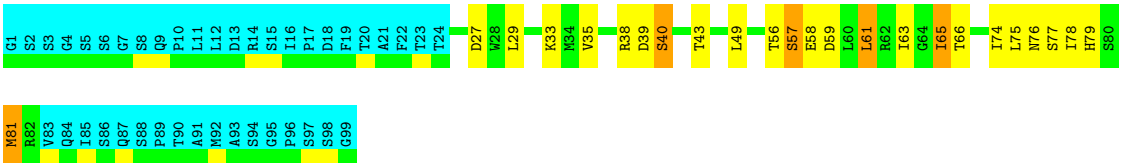
Chain A: 37% 16% 5% 41%



4.2.15 Score per residue for model 15

- Molecule 1: Ephrin type-B receptor 1

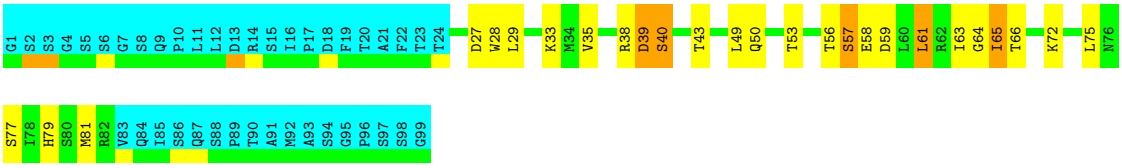
Chain A: 34% 19% 5% 41%



4.2.16 Score per residue for model 16

- Molecule 1: Ephrin type-B receptor 1

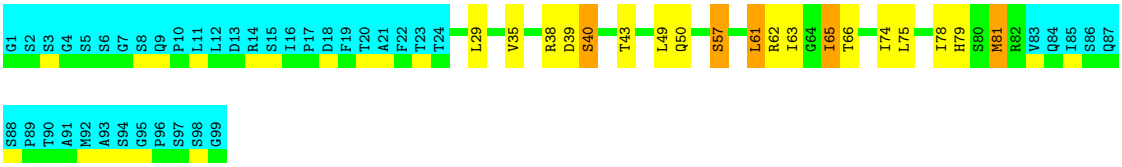
Chain A: 32% 21% 5% 41%



4.2.17 Score per residue for model 17

- Molecule 1: Ephrin type-B receptor 1

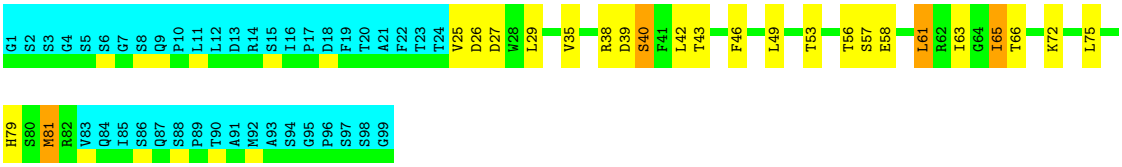
Chain A: 39% 14% 5% 41%



4.2.18 Score per residue for model 18

- Molecule 1: Ephrin type-B receptor 1

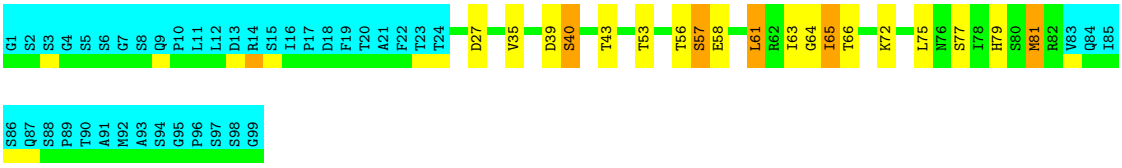
Chain A: 34% 20% • 41%



4.2.19 Score per residue for model 19

- Molecule 1: Ephrin type-B receptor 1

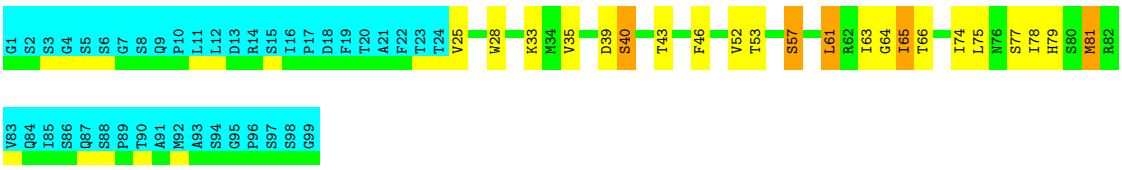
Chain A: 39% 14% 5% 41%



4.2.20 Score per residue for model 20

- Molecule 1: Ephrin type-B receptor 1

Chain A: 36% 17% 5% 41%



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: *structures with the least restraint violations*.

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

Software name	Classification	Version
CYANA	refinement	2.2.2
CYANA	structure solution	2.2.2

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	460	475	475	12±2
All	All	9200	9500	9500	236

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 13.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:LEU:HD23	1:A:66:THR:HG22	0.84	1.47	19	13
1:A:63:ILE:HD11	1:A:65:ILE:HD12	0.77	1.54	20	20
1:A:63:ILE:HD11	1:A:65:ILE:CD1	0.60	2.26	13	20
1:A:49:LEU:O	1:A:53:THR:HG23	0.59	1.96	18	4
1:A:57:SER:N	1:A:75:LEU:HD21	0.59	2.12	4	5
1:A:57:SER:HB3	1:A:75:LEU:HD11	0.57	1.76	20	13
1:A:40:SER:HB3	1:A:63:ILE:HD12	0.57	1.76	13	17
1:A:57:SER:CA	1:A:75:LEU:HD21	0.56	2.31	14	15
1:A:39:ASP:O	1:A:43:THR:HG22	0.56	2.00	2	20
1:A:64:GLY:O	1:A:66:THR:HG23	0.56	2.01	2	12
1:A:57:SER:HA	1:A:75:LEU:HD21	0.54	1.78	7	12
1:A:28:TRP:CZ3	1:A:52:VAL:HG11	0.53	2.37	13	8
1:A:61:LEU:CD2	1:A:66:THR:HG22	0.52	2.32	15	4
1:A:28:TRP:CB	1:A:49:LEU:HD21	0.51	2.35	13	5

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:53:THR:HG22	1:A:81:MET:HB3	0.51	1.81	19	6
1:A:49:LEU:HD12	1:A:81:MET:CE	0.51	2.36	7	8
1:A:67:LEU:HD22	1:A:70:HIS:CE1	0.50	2.41	1	3
1:A:26:ASP:OD2	1:A:42:LEU:HD11	0.50	2.06	5	2
1:A:74:ILE:HG22	1:A:78:ILE:CD1	0.48	2.38	2	10
1:A:74:ILE:HG22	1:A:78:ILE:HD11	0.48	1.84	12	2
1:A:29:LEU:HD11	1:A:41:PHE:CD2	0.47	2.44	2	4
1:A:25:VAL:HG21	1:A:46:PHE:O	0.47	2.10	11	4
1:A:57:SER:CB	1:A:75:LEU:HD11	0.46	2.40	4	1
1:A:29:LEU:HD12	1:A:38:ARG:HA	0.46	1.88	5	13
1:A:38:ARG:O	1:A:42:LEU:HD12	0.46	2.11	11	2
1:A:26:ASP:OD1	1:A:42:LEU:HD11	0.45	2.12	8	1
1:A:28:TRP:HB2	1:A:49:LEU:HD21	0.45	1.88	16	1
1:A:56:THR:HG23	1:A:58:GLU:H	0.44	1.71	16	8
1:A:29:LEU:HD23	1:A:32:ILE:HD11	0.41	1.91	11	1
1:A:61:LEU:HD23	1:A:66:THR:CG2	0.41	2.33	16	1
1:A:56:THR:HG22	1:A:59:ASP:OD2	0.40	2.16	15	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	58/99 (59%)	55±1 (95±1%)	2±1 (4±1%)	1±0 (2±0%)	13	56
All	All	1160/1980 (59%)	1098 (95%)	42 (4%)	20 (2%)	13	56

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	65	ILE	20

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	52/85 (61%)	43±1 (83±2%)	9±1 (17±2%)	5 40
All	All	1040/1700 (61%)	865 (83%)	175 (17%)	5 40

All 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	35	VAL	20
1	A	61	LEU	20
1	A	40	SER	19
1	A	57	SER	16
1	A	72	LYS	15
1	A	77	SER	14
1	A	27	ASP	12
1	A	67	LEU	11
1	A	81	MET	11
1	A	39	ASP	8
1	A	76	ASN	5
1	A	82	ARG	5
1	A	50	GLN	5
1	A	33	LYS	5
1	A	26	ASP	3
1	A	80	SER	2
1	A	59	ASP	2
1	A	62	ARG	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