Full wwPDB NMR Structure Validation Report (i)

Feb 26, 2022 – 09:26 AM EST

PDB ID	:	2CR6
Title	:	Solution structure of the Ig domain (2998-3100) of human obscurin
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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:

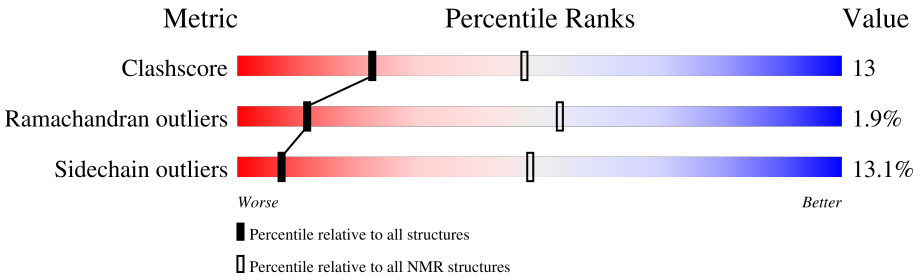
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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	115	52% 23% • 22%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 16 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:14-A:103 (90)	0.10	16

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 6 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1723 atoms, of which 845 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called KIAA1556 protein.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	115	1723	543	845	159	175	1	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q9HCL6
A	2	SER	-	cloning artifact	UNP Q9HCL6
A	3	SER	-	cloning artifact	UNP Q9HCL6
A	4	GLY	-	cloning artifact	UNP Q9HCL6
A	5	SER	-	cloning artifact	UNP Q9HCL6
A	6	SER	-	cloning artifact	UNP Q9HCL6
A	7	GLY	-	cloning artifact	UNP Q9HCL6
A	110	SER	-	cloning artifact	UNP Q9HCL6
A	111	GLY	-	cloning artifact	UNP Q9HCL6
A	112	PRO	-	cloning artifact	UNP Q9HCL6
A	113	SER	-	cloning artifact	UNP Q9HCL6
A	114	SER	-	cloning artifact	UNP Q9HCL6
A	115	GLY	-	cloning artifact	UNP Q9HCL6

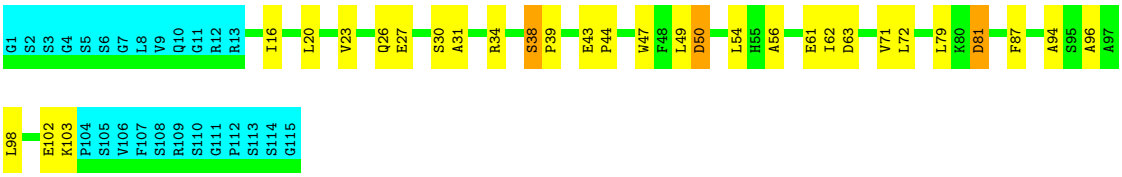
4 Residue-property plots (i)

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: KIAA1556 protein

Chain A:



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

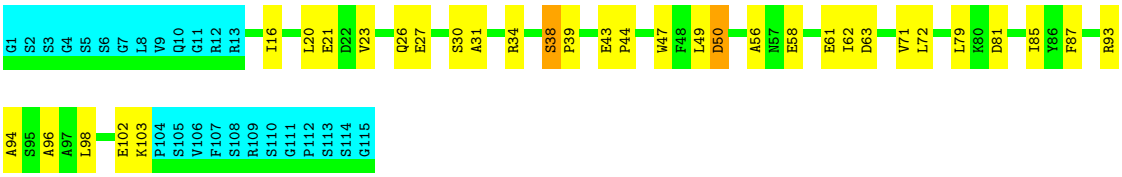
• Molecule 1: KIAA1556 protein

Chain A:

4.2.2 Score per residue for model 2

• Molecule 1: KIAA1556 protein

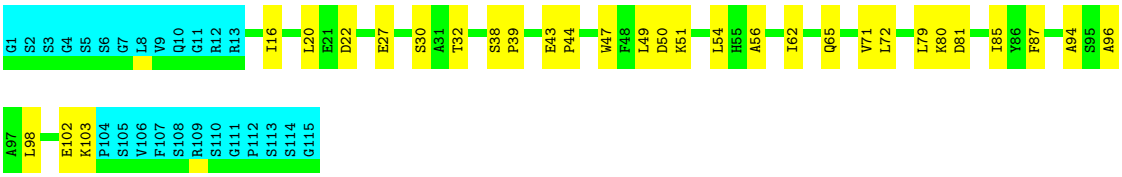
Chain A:



4.2.3 Score per residue for model 3

- Molecule 1: KIAA1556 protein

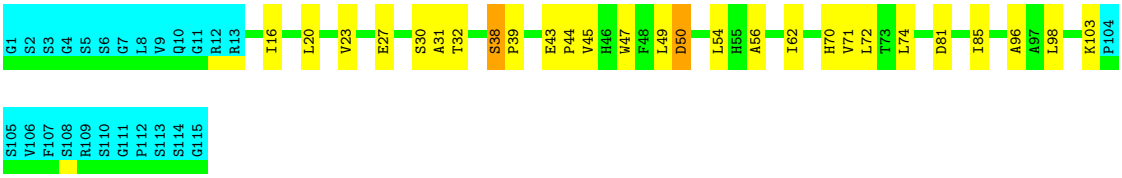
Chain A:



4.2.4 Score per residue for model 4

- Molecule 1: KIAA1556 protein

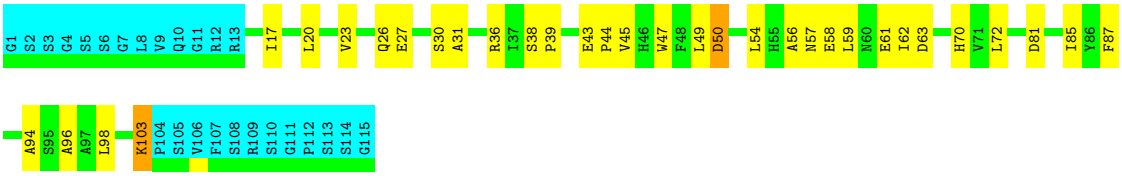
Chain A:



4.2.5 Score per residue for model 5

- Molecule 1: KIAA1556 protein

Chain A:



4.2.6 Score per residue for model 6

- Molecule 1: KIAA1556 protein

Chain A: 53% 23% • 22%

G1 S2 S3 G4 S5 S6 G7 L8 V9 Q10 G11 R12 R13 D19 L20 E21 D22 Q26 E27 S30 A31 T32 F33 R34 S38 P39 E43 P44 V45 H46 W47 F48 L49 D50 A56 I62 H70 V71 L72 L79 K80 D81 A94 S95 A96 A97 L98 E102 K103

P104 S105 V106 F107 S108 R109 S110 G111 P112 S113 S114 G115

4.2.7 Score per residue for model 7

- Molecule 1: KIAA1556 protein

Chain A: 50% 25% • 22%

G1 S2 S3 G4 S5 S6 G7 L8 V9 Q10 G11 R12 R13 L20 Q26 E27 S30 R34 S38 P39 E43 P44 V45 H46 W47 F48 L49 D50 L54 H55 A56 L59 N60 E61 I62 D63 H70 V71 L72 Q76 L77 A78 L79 K80 D81 T84 F87

A94 S95 A96 A97 L98 R99 V100 T101 E102 K103 P104 S105 V106 F107 S108 R109 S110 G111 P112 S113 S114 G115

4.2.8 Score per residue for model 8

- Molecule 1: KIAA1556 protein

Chain A: 50% 26% • 22%

G1 S2 S3 G4 S5 S6 G7 L8 V9 Q10 G11 R12 R13 I16 L20 E21 D22 V23 Q26 E27 S30 A31 R34 S38 P39 E43 P44 W47 F48 L49 D50 L54 H55 A56 E61 I62 V71 L72 T73 L74 L79 K80 D81 I85 Y86 F87

A94 S95 A96 A97 L98 E102 K103 P104 S105 V106 F107 S108 R109 S110 G111 P112 S113 S114 G115

4.2.9 Score per residue for model 9

- Molecule 1: KIAA1556 protein

Chain A: 49% 27% • 22%

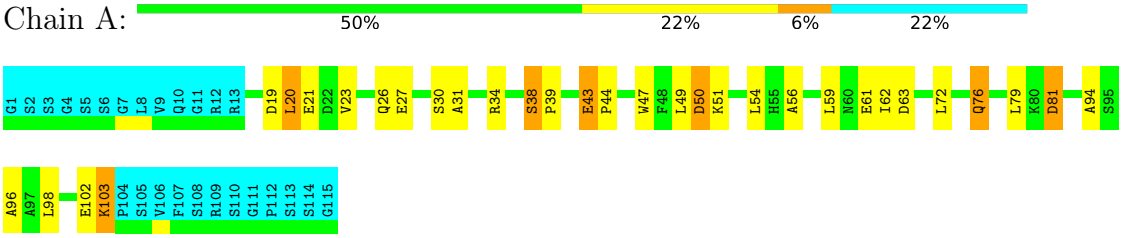
G1 S2 S3 G4 S5 S6 G7 L8 V9 Q10 G11 R12 R13 I16 L20 V23 E27 S30 A31 T32 S38 P39 E43 P44 W47 F48 L49 D50 L54 H55 A56 E61 I62 D63 V71 L72 T73 L74 L77 A78 L79 K80 D81 S82 F87 A94

S95 A96 A97 L98 R99 V100 T101 E102 K103 P104 S105 V106 F107 S108 R109 S110 G111 P112 S113 S114 G115

4.2.10 Score per residue for model 10

- Molecule 1: KIAA1556 protein

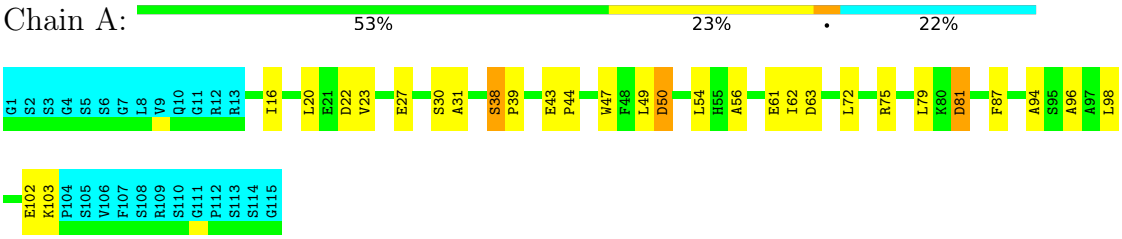
Chain A:



4.2.11 Score per residue for model 11

- Molecule 1: KIAA1556 protein

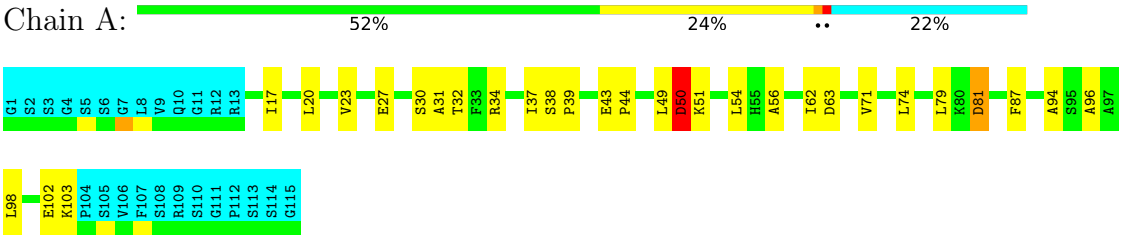
Chain A:



4.2.12 Score per residue for model 12

- Molecule 1: KIAA1556 protein

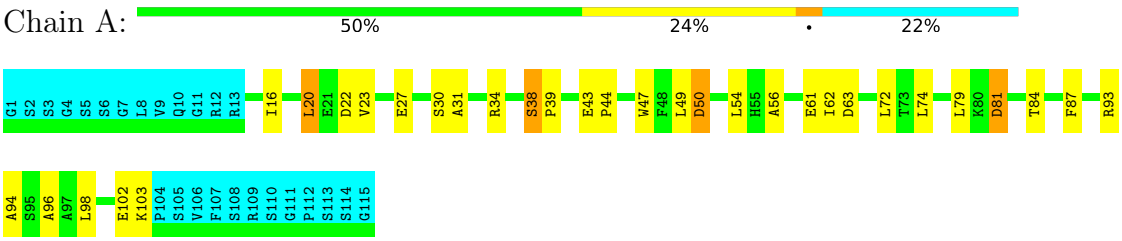
Chain A:



4.2.13 Score per residue for model 13

- Molecule 1: KIAA1556 protein

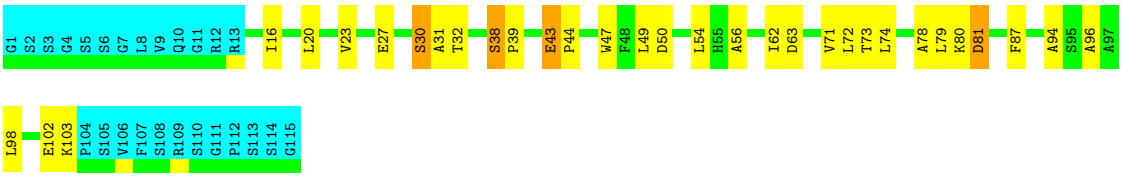
Chain A:



4.2.14 Score per residue for model 14

- Molecule 1: KIAA1556 protein

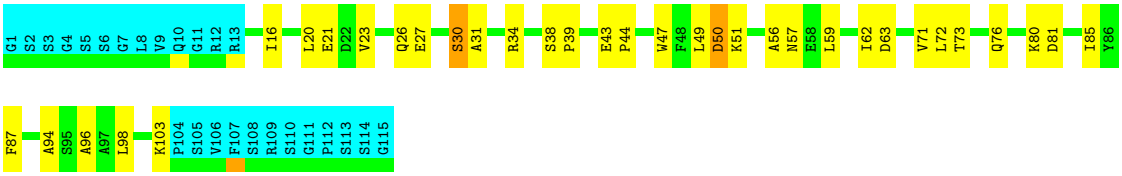
Chain A: 50% 24% • 22%



4.2.15 Score per residue for model 15

- Molecule 1: KIAA1556 protein

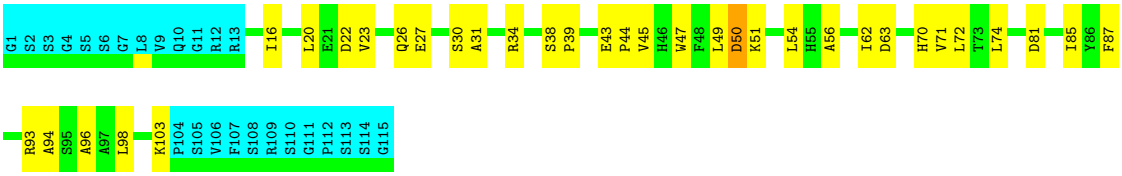
Chain A: 49% 28% • 22%



4.2.16 Score per residue for model 16 (medoid)

- Molecule 1: KIAA1556 protein

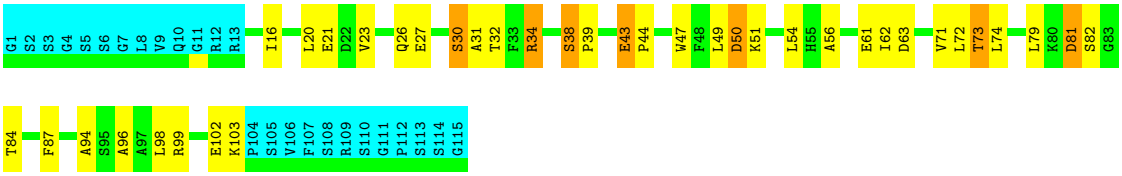
Chain A: 49% 29% • 22%



4.2.17 Score per residue for model 17

- Molecule 1: KIAA1556 protein

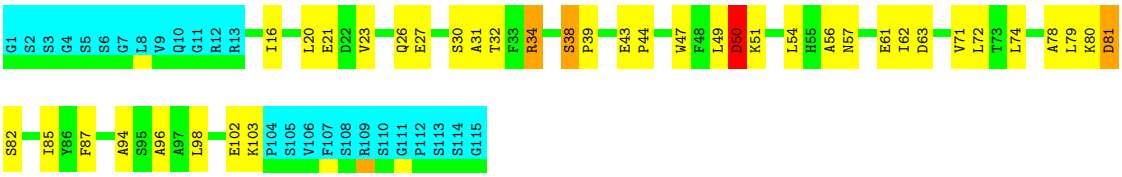
Chain A: 45% 27% 6% 22%



4.2.18 Score per residue for model 18

- Molecule 1: KIAA1556 protein

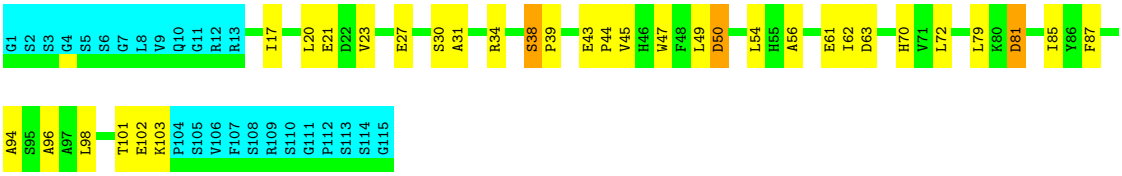
Chain A: 44% 30% 22%



4.2.19 Score per residue for model 19

- Molecule 1: KIAA1556 protein

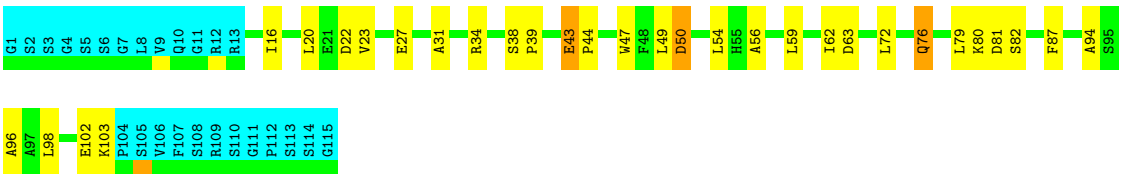
Chain A: 50% 26% 22%



4.2.20 Score per residue for model 20

- Molecule 1: KIAA1556 protein

Chain A: 51% 24% 22%



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *Trsion angle dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function,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.

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	711	683	683	18±1
All	All	14220	13660	13660	353

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:23:VAL:HG11	1:A:31:ALA:HB1	0.78	1.56	17	17
1:A:56:ALA:HB2	1:A:62:ILE:HD12	0.73	1.61	19	20
1:A:20:LEU:HB2	1:A:96:ALA:HB2	0.68	1.65	6	20
1:A:47:TRP:CE3	1:A:72:LEU:HD22	0.67	2.25	5	18
1:A:79:LEU:HD21	1:A:102:GLU:N	0.65	2.07	13	5
1:A:81:ASP:OD2	1:A:100:VAL:HG21	0.65	1.92	9	2
1:A:79:LEU:HD21	1:A:102:GLU:HA	0.63	1.70	10	12
1:A:20:LEU:HD23	1:A:34:ARG:O	0.62	1.95	10	11
1:A:49:LEU:CD2	1:A:98:LEU:HD23	0.62	2.25	8	20
1:A:49:LEU:HB2	1:A:54:LEU:HD11	0.60	1.73	20	12
1:A:79:LEU:HD11	1:A:102:GLU:HB3	0.60	1.73	13	2
1:A:17:ILE:HD11	1:A:38:SER:HB2	0.60	1.74	12	2
1:A:20:LEU:CB	1:A:96:ALA:HB2	0.59	2.26	13	20
1:A:30:SER:HB3	1:A:73:THR:HG22	0.59	1.75	14	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:81:ASP:OD2	1:A:98:LEU:HD21	0.56	2.01	20	3
1:A:49:LEU:HD21	1:A:98:LEU:HD23	0.55	1.79	11	20
1:A:34:ARG:CG	1:A:71:VAL:HG22	0.53	2.34	1	4
1:A:49:LEU:HD11	1:A:81:ASP:O	0.53	2.03	13	15
1:A:54:LEU:HD22	1:A:74:LEU:HD21	0.51	1.83	1	10
1:A:79:LEU:HD21	1:A:102:GLU:CA	0.51	2.36	11	11
1:A:34:ARG:HG3	1:A:71:VAL:HG22	0.50	1.83	17	6
1:A:87:PHE:HB3	1:A:94:ALA:HB3	0.50	1.83	19	17
1:A:32:THR:HG23	1:A:71:VAL:CG1	0.50	2.37	14	9
1:A:77:LEU:HD22	1:A:81:ASP:CG	0.49	2.27	7	2
1:A:81:ASP:OD1	1:A:98:LEU:HD21	0.49	2.06	9	2
1:A:57:ASN:ND2	1:A:59:LEU:H	0.49	2.05	5	1
1:A:59:LEU:HD22	1:A:76:GLN:HG3	0.48	1.86	10	2
1:A:84:THR:HG23	1:A:96:ALA:O	0.48	2.09	13	3
1:A:19:ASP:OD1	1:A:94:ALA:HB1	0.47	2.08	10	2
1:A:38:SER:HA	1:A:39:PRO:C	0.47	2.29	12	20
1:A:56:ALA:CB	1:A:62:ILE:HD12	0.46	2.37	19	2
1:A:85:ILE:HD11	1:A:98:LEU:HD22	0.46	1.87	5	9
1:A:49:LEU:O	1:A:49:LEU:HD13	0.46	2.11	20	12
1:A:45:VAL:HG11	1:A:70:HIS:CE1	0.46	2.46	1	3
1:A:79:LEU:HD11	1:A:102:GLU:CG	0.44	2.43	20	1
1:A:17:ILE:HD12	1:A:36:ARG:HG2	0.44	1.88	5	1
1:A:79:LEU:HD21	1:A:101:THR:C	0.44	2.33	19	1
1:A:32:THR:HG23	1:A:71:VAL:HG13	0.43	1.88	12	2
1:A:45:VAL:HG11	1:A:70:HIS:NE2	0.43	2.28	4	4
1:A:43:GLU:HA	1:A:44:PRO:C	0.43	2.34	12	20
1:A:62:ILE:CG1	1:A:72:LEU:HD12	0.42	2.45	13	1
1:A:65:GLN:NE2	1:A:71:VAL:HG21	0.42	2.30	3	1
1:A:59:LEU:HD22	1:A:76:GLN:CD	0.41	2.35	15	1
1:A:49:LEU:HD13	1:A:50:ASP:HB2	0.40	1.93	12	2
1:A:59:LEU:HD22	1:A:76:GLN:HB2	0.40	1.93	20	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	90/115 (78%)	70±2 (77±2%)	19±2 (21±2%)	2±1 (2±1%)	11 53
All	All	1800/2300 (78%)	1392 (77%)	374 (21%)	34 (2%)	11 53

All 3 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	50	ASP	19
1	A	16	ILE	13
1	A	20	LEU	2

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	76/95 (80%)	66±2 (87±3%)	10±2 (13±3%)	7 48
All	All	1520/1900 (80%)	1321 (87%)	199 (13%)	7 48

All 25 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	27	GLU	20
1	A	30	SER	19
1	A	103	LYS	19
1	A	50	ASP	18
1	A	63	ASP	16
1	A	81	ASP	16
1	A	38	SER	14
1	A	61	GLU	12
1	A	26	GLN	11
1	A	80	LYS	9
1	A	21	GLU	7
1	A	51	LYS	7
1	A	22	ASP	6
1	A	82	SER	4
1	A	43	GLU	4

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Mol	Chain	Res	Type	Models (Total)
1	A	93	ARG	3
1	A	76	GLN	3
1	A	58	GLU	2
1	A	57	ASN	2
1	A	34	ARG	2
1	A	75	ARG	1
1	A	37	ILE	1
1	A	20	LEU	1
1	A	73	THR	1
1	A	99	ARG	1

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