Full wwPDB NMR Structure Validation Report (i)

Mar 6, 2022 – 07:50 AM EST

PDB ID	:	2K9K
Title	:	Molecular characterization of the tonb2 protein from vibrio anguillarum
Authors	:	Lopez, C.S.; Peacock, R.S.; Crosa, J.H.; Vogel, H.J.
Deposited on	:	2008-10-15

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:

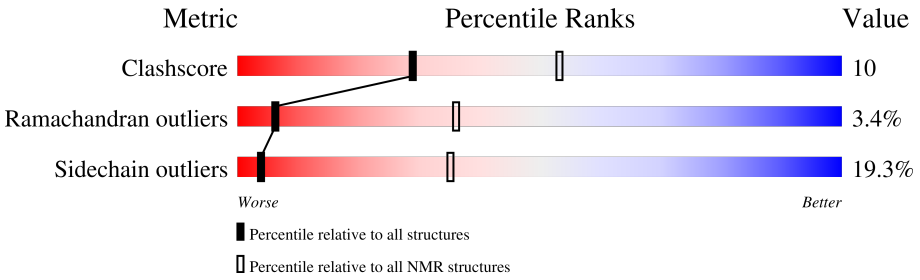
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)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

1 Overall quality at a glance

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	106	47% 24% • • 25%

2 Ensemble composition and analysis

This entry contains 20 models. Model 20 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:119-A:183, A:191-A:204 (79)	0.28	20

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 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1674 atoms, of which 837 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called TonB2.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	106	1674	536	837	143	155	3	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	101	ASP	-	insertion	UNP Q5SDB0
A	102	HIS	-	insertion	UNP Q5SDB0
A	103	PRO	-	insertion	UNP Q5SDB0
A	104	PHE	-	insertion	UNP Q5SDB0
A	105	THR	-	insertion	UNP Q5SDB0

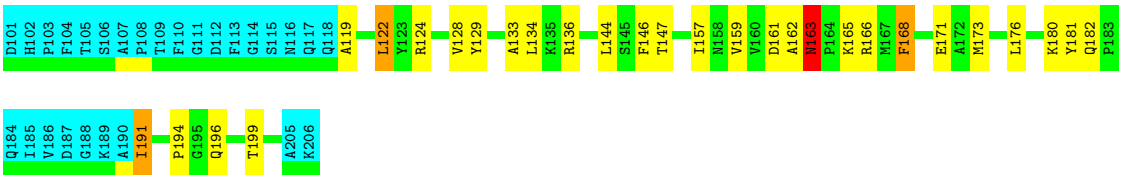
4 Residue-property plots

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: TonB2

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

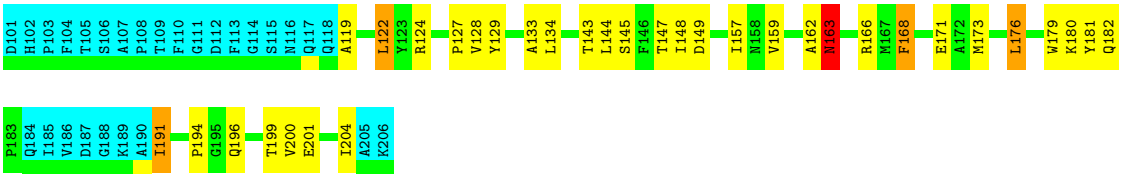
• Molecule 1: TonB2

Chain A:

4.2.2 Score per residue for model 2

• Molecule 1: TonB2

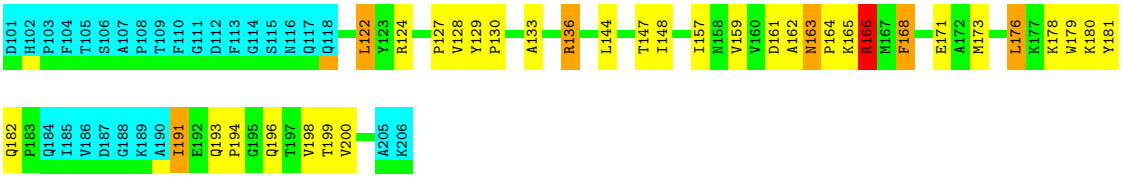
Chain A:



4.2.3 Score per residue for model 3

• Molecule 1: TonB2

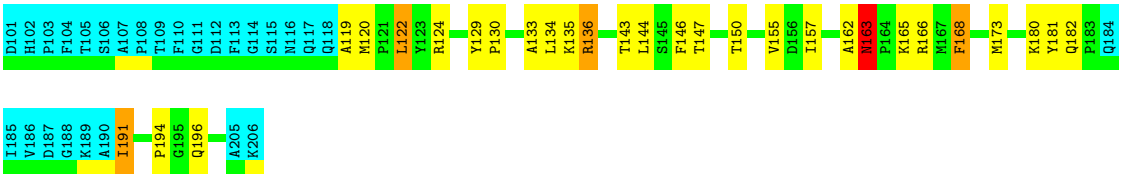
Chain A: 42% 26% 6% 25%



4.2.4 Score per residue for model 4

• Molecule 1: TonB2

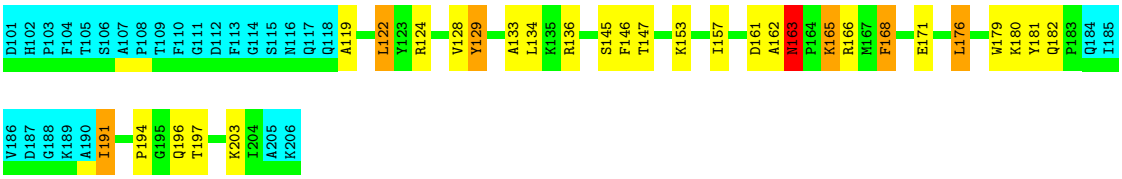
Chain A: 47% 23% 25%



4.2.5 Score per residue for model 5

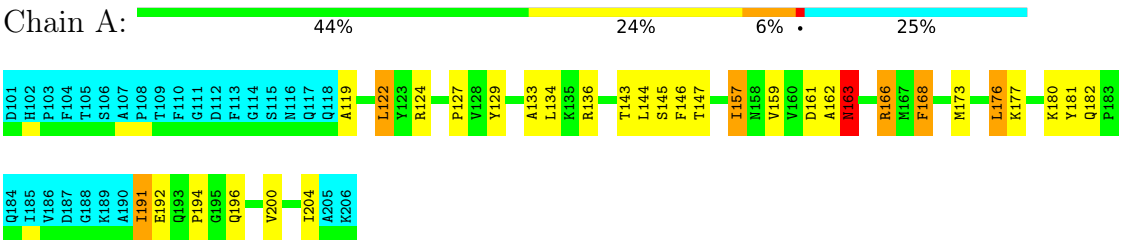
• Molecule 1: TonB2

Chain A: 46% 22% 6% 25%



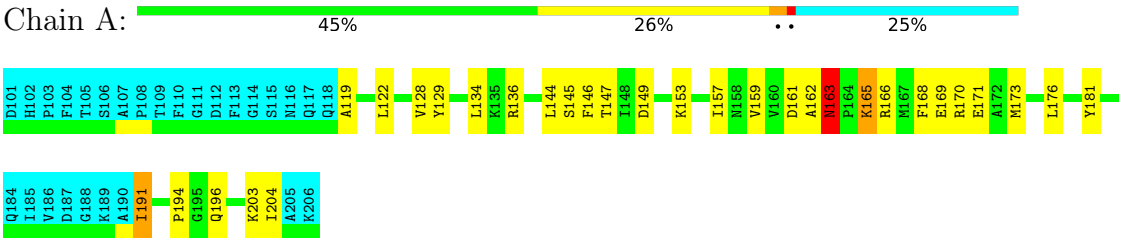
4.2.6 Score per residue for model 6

• Molecule 1: TonB2



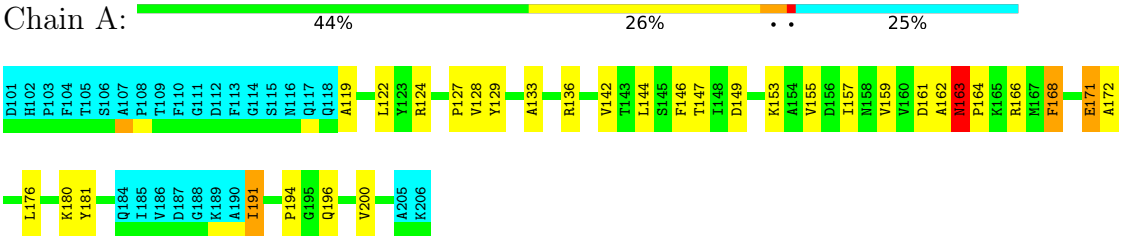
4.2.7 Score per residue for model 7

• Molecule 1: TonB2



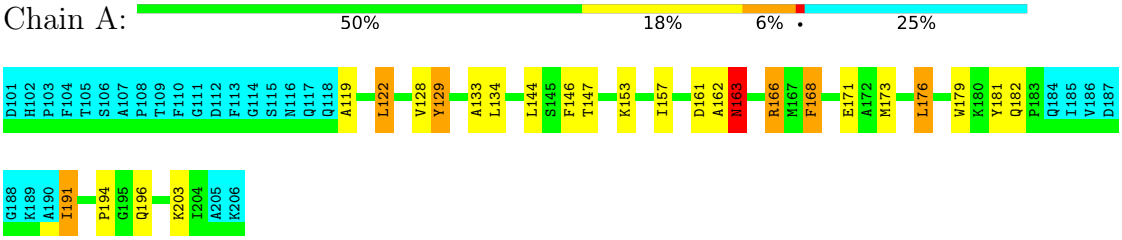
4.2.8 Score per residue for model 8

• Molecule 1: TonB2



4.2.9 Score per residue for model 9

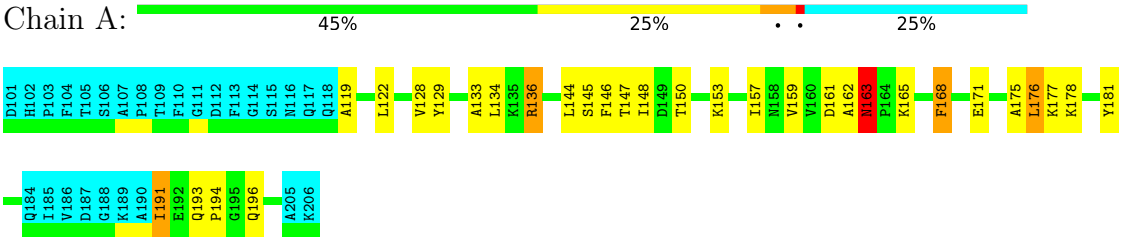
• Molecule 1: TonB2



4.2.10 Score per residue for model 10

• Molecule 1: TonB2

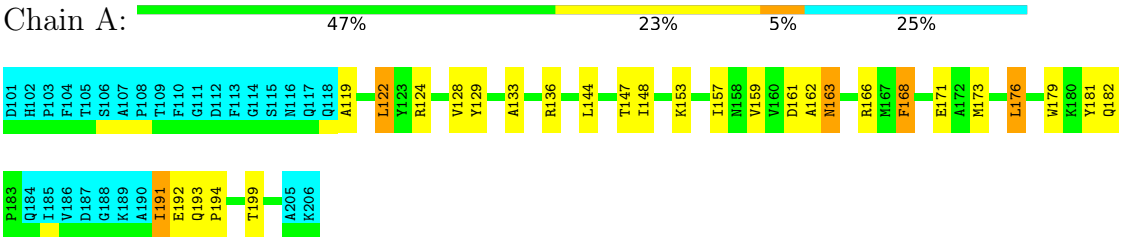
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: TonB2

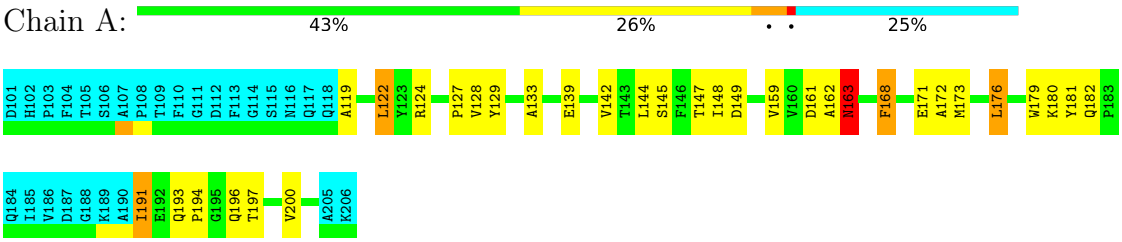
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: TonB2

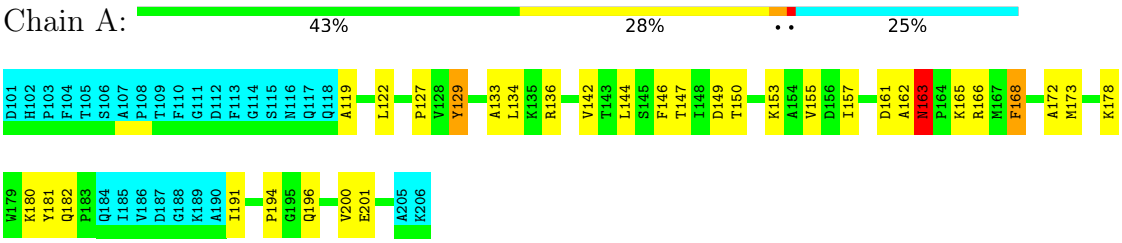
Chain A:



4.2.13 Score per residue for model 13

• Molecule 1: TonB2

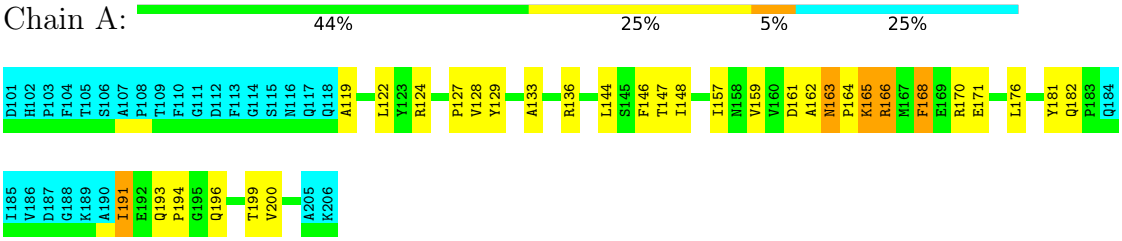
Chain A:



4.2.14 Score per residue for model 14

• Molecule 1: TonB2

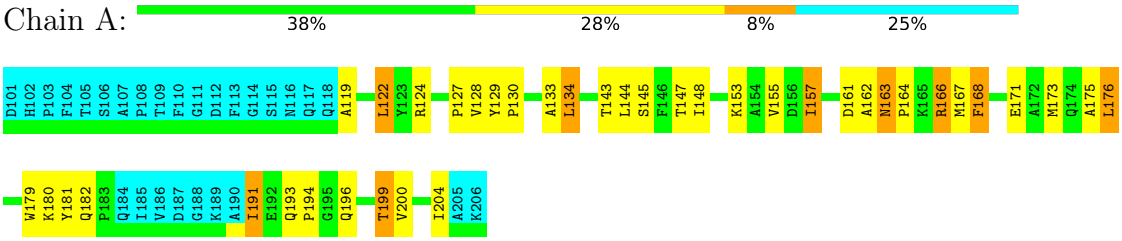
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: TonB2

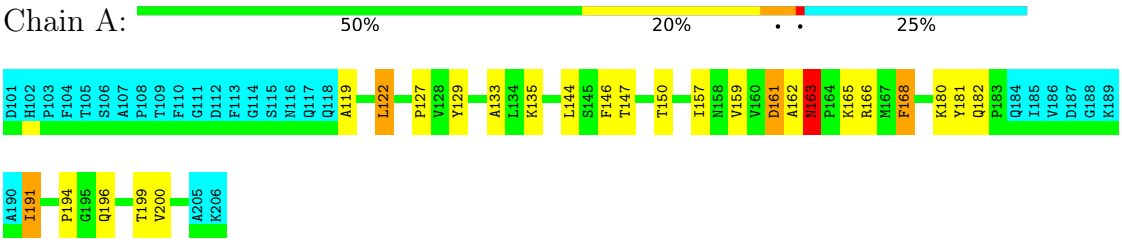
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: TonB2

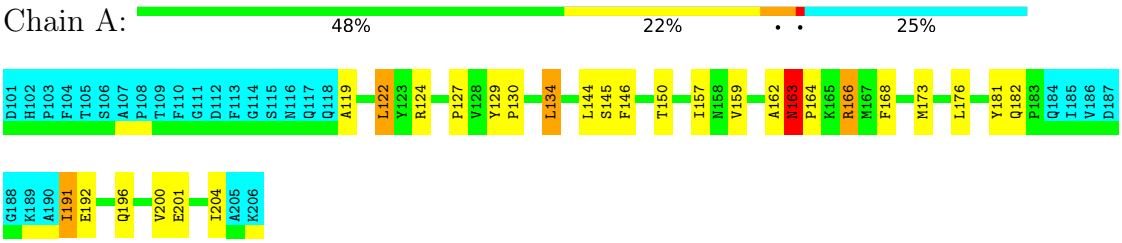
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: TonB2

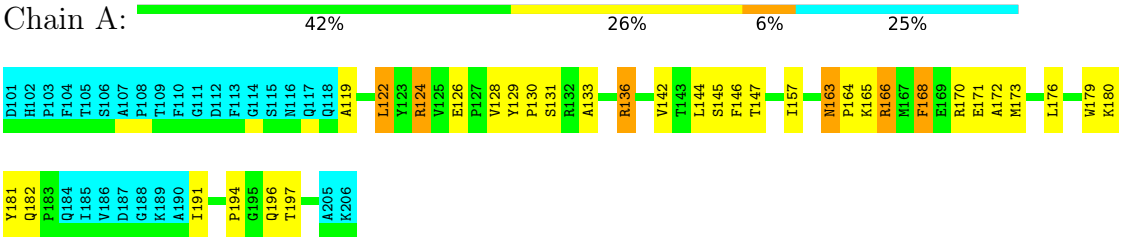
Chain A:



4.2.18 Score per residue for model 18

• Molecule 1: TonB2

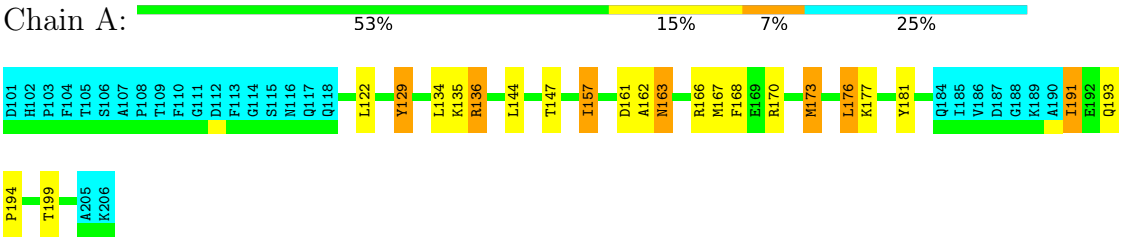
Chain A:



4.2.19 Score per residue for model 19

• Molecule 1: TonB2

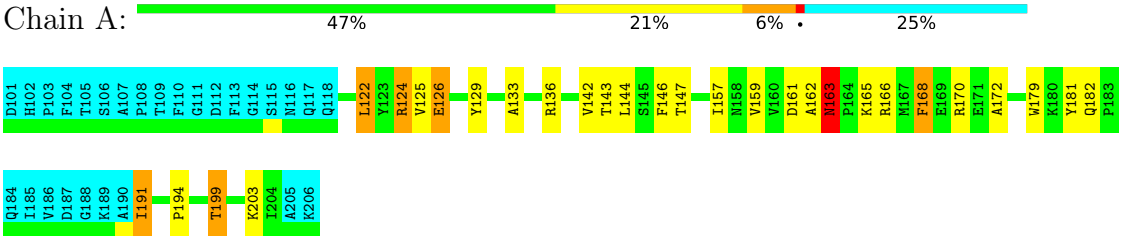
Chain A:



4.2.20 Score per residue for model 20 (medoid)

• Molecule 1: TonB2

Chain A:



5 Refinement protocol and experimental data overview

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	structure solution	102.0
CYANA	refinement	102.0

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

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	635	653	653	13±3
All	All	12700	13060	13060	266

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 10.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:157:ILE:HD11	1:A:176:LEU:HD12	0.69	1.64	9	4
1:A:147:THR:HG22	1:A:194:PRO:O	0.68	1.89	16	19
1:A:142:VAL:HG11	1:A:172:ALA:CB	0.67	2.19	13	4
1:A:133:ALA:HB1	1:A:168:PHE:CE1	0.66	2.25	1	14
1:A:146:PHE:HB3	1:A:157:ILE:HD13	0.65	1.68	9	13
1:A:128:VAL:HG13	1:A:171:GLU:HB3	0.64	1.70	18	10
1:A:144:LEU:HG	1:A:159:VAL:HG22	0.62	1.71	16	11
1:A:142:VAL:HG11	1:A:172:ALA:HB3	0.62	1.72	18	2
1:A:119:ALA:HB2	1:A:196:GLN:OE1	0.61	1.95	2	3
1:A:122:LEU:HD21	1:A:182:GLN:HB2	0.61	1.73	6	14
1:A:146:PHE:CE1	1:A:176:LEU:HD11	0.60	2.32	10	2
1:A:176:LEU:HD22	1:A:179:TRP:CZ3	0.60	2.32	9	7
1:A:142:VAL:HG12	1:A:144:LEU:HD13	0.59	1.73	18	2
1:A:119:ALA:HB2	1:A:196:GLN:CD	0.59	2.17	5	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:128:VAL:HG13	1:A:171:GLU:HB2	0.58	1.73	1	3
1:A:144:LEU:HD12	1:A:159:VAL:HG13	0.57	1.76	17	4
1:A:130:PRO:CG	1:A:133:ALA:HB3	0.56	2.29	15	3
1:A:133:ALA:HB1	1:A:168:PHE:CE2	0.56	2.35	3	3
1:A:148:ILE:HD12	1:A:193:GLN:NE2	0.56	2.16	1	4
1:A:119:ALA:HB2	1:A:196:GLN:CG	0.56	2.31	10	3
1:A:129:TYR:CE1	1:A:134:LEU:HD23	0.56	2.36	13	1
1:A:134:LEU:O	1:A:204:ILE:HG23	0.55	2.00	1	3
1:A:163:ASN:HD21	1:A:166:ARG:N	0.55	1.99	15	1
1:A:162:ALA:O	1:A:163:ASN:O	0.55	2.25	9	9
1:A:127:PRO:HG3	1:A:200:VAL:HG11	0.54	1.79	14	9
1:A:143:THR:OG1	1:A:199:THR:HG23	0.53	2.03	15	3
1:A:134:LEU:O	1:A:204:ILE:HD12	0.52	2.04	6	1
1:A:163:ASN:OD1	1:A:163:ASN:C	0.52	2.47	11	2
1:A:142:VAL:HG11	1:A:172:ALA:HB1	0.52	1.82	12	1
1:A:144:LEU:HD21	1:A:173:MET:HA	0.51	1.82	3	14
1:A:145:SER:OG	1:A:197:THR:HG22	0.51	2.05	5	3
1:A:142:VAL:HG12	1:A:144:LEU:CD1	0.51	2.36	18	1
1:A:191:ILE:HG22	1:A:192:GLU:H	0.50	1.66	6	2
1:A:119:ALA:HB1	1:A:148:ILE:HD11	0.50	1.84	12	4
1:A:134:LEU:HA	1:A:204:ILE:HD12	0.50	1.83	17	2
1:A:119:ALA:CB	1:A:148:ILE:HD11	0.50	2.37	1	1
1:A:125:VAL:O	1:A:126:GLU:CG	0.50	2.59	20	1
1:A:142:VAL:HG11	1:A:172:ALA:HB2	0.49	1.84	20	2
1:A:162:ALA:O	1:A:163:ASN:CG	0.49	2.51	14	4
1:A:122:LEU:HD21	1:A:182:GLN:CB	0.49	2.38	11	3
1:A:162:ALA:C	1:A:163:ASN:CG	0.49	2.71	13	13
1:A:129:TYR:HB3	1:A:134:LEU:HD12	0.48	1.83	9	3
1:A:163:ASN:ND2	1:A:167:MET:H	0.48	2.07	19	1
1:A:146:PHE:CB	1:A:157:ILE:HD13	0.47	2.39	5	2
1:A:153:LYS:HG2	1:A:155:VAL:HG13	0.47	1.86	8	4
1:A:148:ILE:HD12	1:A:193:GLN:HE21	0.47	1.70	15	1
1:A:128:VAL:HG12	1:A:175:ALA:HB2	0.46	1.88	10	2
1:A:133:ALA:HB2	1:A:167:MET:O	0.46	2.11	15	1
1:A:147:THR:OG1	1:A:155:VAL:HG23	0.46	2.10	4	1
1:A:165:LYS:O	1:A:166:ARG:O	0.46	2.34	3	2
1:A:163:ASN:HB2	1:A:164:PRO:HD2	0.46	1.87	14	3
1:A:125:VAL:O	1:A:126:GLU:O	0.46	2.32	20	1
1:A:150:THR:O	1:A:191:ILE:HG21	0.45	2.11	16	1
1:A:133:ALA:HB1	1:A:168:PHE:HE1	0.45	1.70	16	1
1:A:119:ALA:HB2	1:A:196:GLN:HE21	0.45	1.71	15	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:130:PRO:HG2	1:A:133:ALA:HB3	0.45	1.89	18	1
1:A:127:PRO:HG3	1:A:200:VAL:HG21	0.44	1.89	3	2
1:A:144:LEU:CD1	1:A:159:VAL:HG22	0.44	2.43	7	1
1:A:134:LEU:O	1:A:134:LEU:HD23	0.44	2.11	10	1
1:A:162:ALA:O	1:A:163:ASN:OD1	0.44	2.35	15	1
1:A:165:LYS:O	1:A:166:ARG:C	0.44	2.56	1	1
1:A:133:ALA:HB1	1:A:168:PHE:CD1	0.44	2.48	15	1
1:A:162:ALA:HB3	1:A:169:GLU:HG3	0.43	1.90	7	1
1:A:163:ASN:ND2	1:A:168:PHE:H	0.43	2.11	8	1
1:A:163:ASN:CB	1:A:164:PRO:HD2	0.43	2.43	8	2
1:A:130:PRO:O	1:A:134:LEU:HD12	0.43	2.13	4	1
1:A:134:LEU:HD13	1:A:134:LEU:C	0.42	2.35	13	1
1:A:130:PRO:O	1:A:134:LEU:HD23	0.42	2.14	17	1
1:A:134:LEU:HD13	1:A:134:LEU:O	0.42	2.15	13	1
1:A:144:LEU:HD12	1:A:159:VAL:HG23	0.42	1.91	8	1
1:A:144:LEU:CG	1:A:159:VAL:HG22	0.42	2.44	2	2
1:A:146:PHE:CZ	1:A:176:LEU:HD11	0.42	2.50	10	1
1:A:128:VAL:HG13	1:A:128:VAL:O	0.42	2.14	11	2
1:A:191:ILE:O	1:A:192:GLU:CG	0.41	2.68	6	1
1:A:144:LEU:CD1	1:A:159:VAL:HG13	0.41	2.45	17	1
1:A:157:ILE:HD12	1:A:176:LEU:HB3	0.41	1.91	19	1
1:A:124:ARG:HB2	1:A:179:TRP:CD1	0.40	2.51	20	1
1:A:124:ARG:CB	1:A:179:TRP:CD1	0.40	3.04	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	79/106 (75%)	63±1 (79±2%)	14±1 (17±1%)	3±1 (3±1%)	6	36
All	All	1580/2120 (75%)	1256 (79%)	270 (17%)	54 (3%)	6	36

All 9 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	166	ARG	18
1	A	163	ASN	17
1	A	157	ILE	7
1	A	136	ARG	6
1	A	165	LYS	2
1	A	164	PRO	1
1	A	161	ASP	1
1	A	192	GLU	1
1	A	126	GLU	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	69/90 (77%)	56±1 (81±2%)	13±1 (19±2%)	4	35
All	All	1380/1800 (77%)	1113 (81%)	267 (19%)	4	35

All 36 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	129	TYR	20
1	A	168	PHE	20
1	A	181	TYR	20
1	A	191	ILE	20
1	A	122	LEU	19
1	A	163	ASN	16
1	A	176	LEU	15
1	A	161	ASP	15
1	A	136	ARG	14
1	A	124	ARG	13
1	A	180	LYS	11
1	A	165	LYS	10
1	A	199	THR	9
1	A	145	SER	6
1	A	149	ASP	5
1	A	166	ARG	5
1	A	153	LYS	5

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Mol	Chain	Res	Type	Models (Total)
1	A	170	ARG	5
1	A	135	LYS	4
1	A	150	THR	4
1	A	203	LYS	4
1	A	143	THR	3
1	A	201	GLU	3
1	A	178	LYS	3
1	A	177	LYS	3
1	A	193	GLN	3
1	A	196	GLN	2
1	A	134	LEU	2
1	A	156	ASP	1
1	A	120	MET	1
1	A	171	GLU	1
1	A	139	GLU	1
1	A	182	GLN	1
1	A	126	GLU	1
1	A	131	SER	1
1	A	173	MET	1

6.3.3 RNA

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates

There are no monosaccharides in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

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

No chemical shift data were provided