



Full wwPDB NMR Structure Validation Report ⓘ

Mar 6, 2026 – 04:17 PM UTC

PDB ID : 2KRD / pdb_00002krd
Title : Solution Structure of the Regulatory Domain of Human Cardiac Troponin C
in Complex with the Switch Region of cardiac Troponin I and W7
Authors : Oleszczuk, M.; Robertson, I.M.; Li, M.X.; Sykes, B.D.
Deposited on : 2009-12-16

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 ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

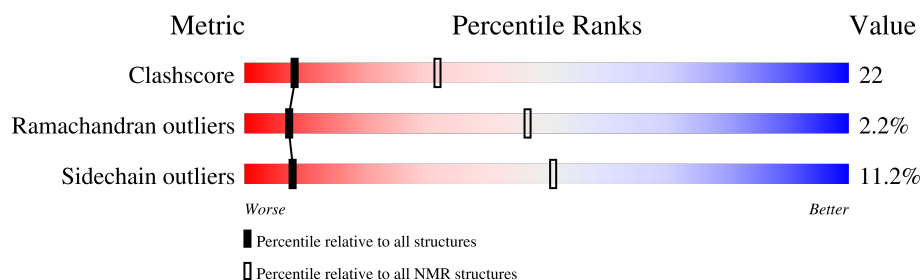
1 Overall quality at a glance

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	C	89	
2	I	17	

2 Ensemble composition and analysis

This entry contains 20 models. Model 10 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	C:2-C:86, I:147-I:157 (96)	1.28	10

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 1 single-model cluster was found.

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

3 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 1670 atoms, of which 825 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Troponin C, slow skeletal and cardiac muscles.

Mol	Chain	Residues	Atoms						Trace
1	C	89	Total	C	H	N	O	S	0
			1364	432	666	107	150	9	

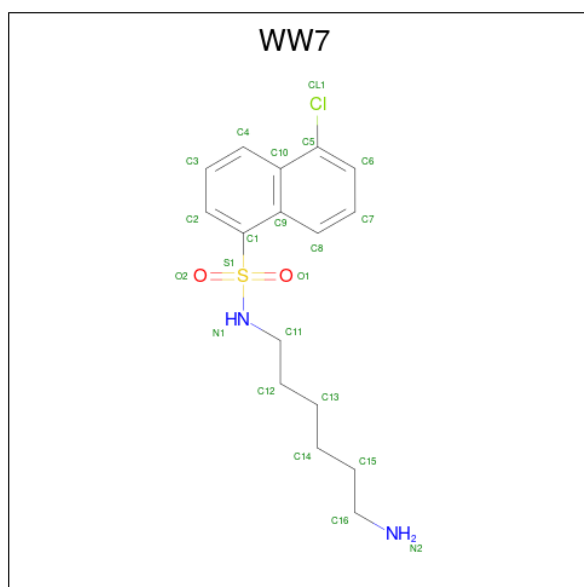
- Molecule 2 is a protein called Troponin I, cardiac muscle.

Mol	Chain	Residues	Atoms						Trace
2	I	17	Total	C	H	N	O	S	0
			261	75	137	25	22	2	

- Molecule 3 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
3	C	1	Total	Ca
			1	1

- Molecule 4 is N-(6-AMINOHEXYL)-5-CHLORO-1-NAPHTHALENESULFONAMIDE (CCD ID: WW7) (formula: C₁₆H₂₁ClN₂O₂S).



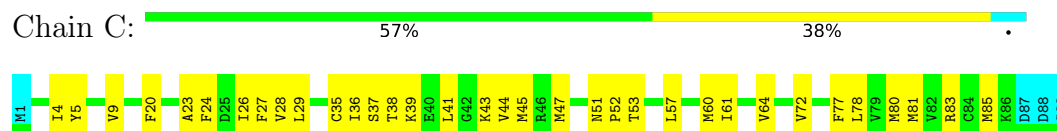
Mol	Chain	Residues	Atoms						
4	I	1	Total	C	Cl	H	N	O	S
			44	16	1	22	2	2	1

4 Residue-property plots [i](#)

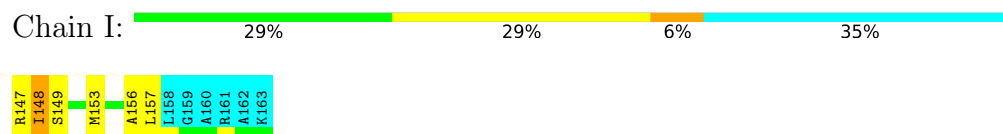
4.1 Average score per residue in the NMR ensemble

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: Troponin C, slow skeletal and cardiac muscles



- Molecule 2: Troponin I, cardiac muscle

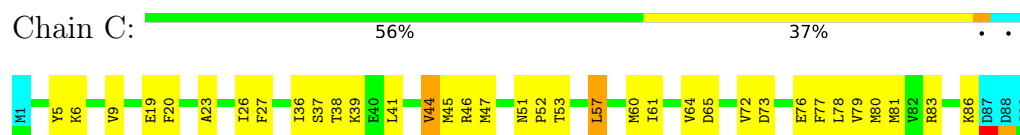


4.2 Scores per residue for each member of the ensemble

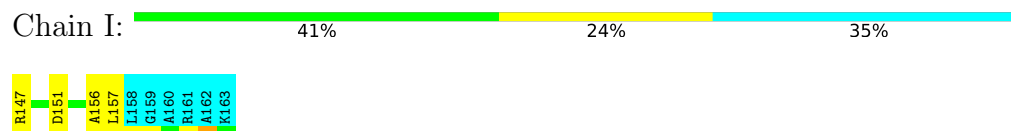
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

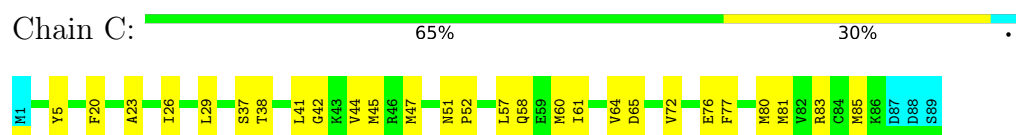


- Molecule 2: Troponin I, cardiac muscle

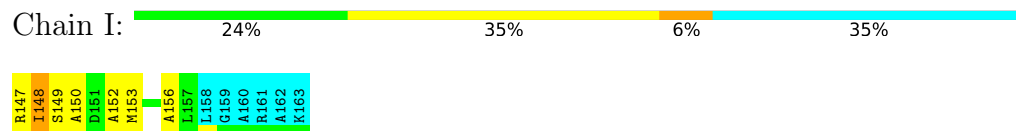


4.2.2 Score per residue for model 2

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

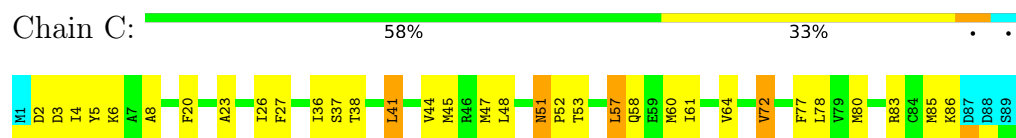


- Molecule 2: Troponin I, cardiac muscle

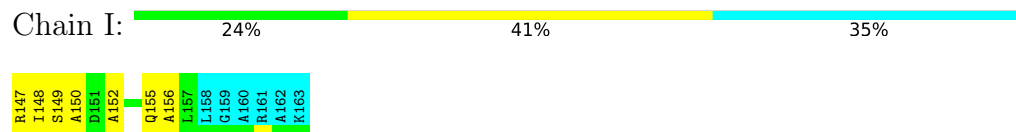


4.2.3 Score per residue for model 3

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

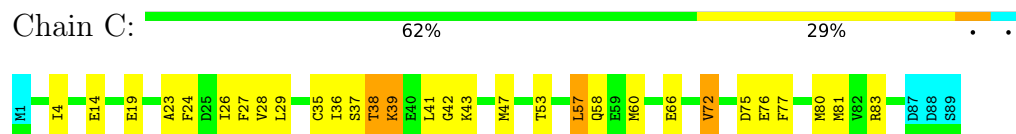


- Molecule 2: Troponin I, cardiac muscle

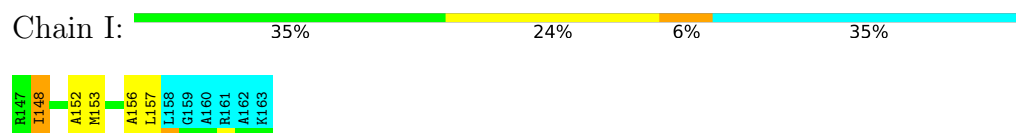


4.2.4 Score per residue for model 4

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

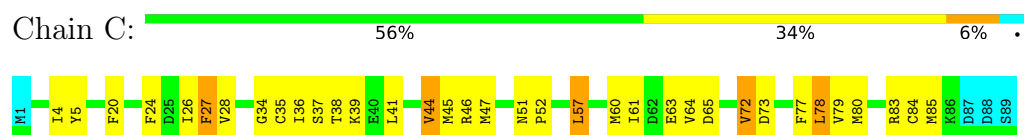


- Molecule 2: Troponin I, cardiac muscle

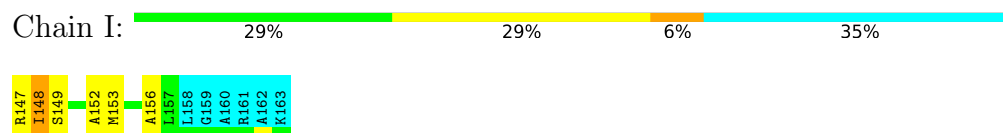


4.2.5 Score per residue for model 5

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

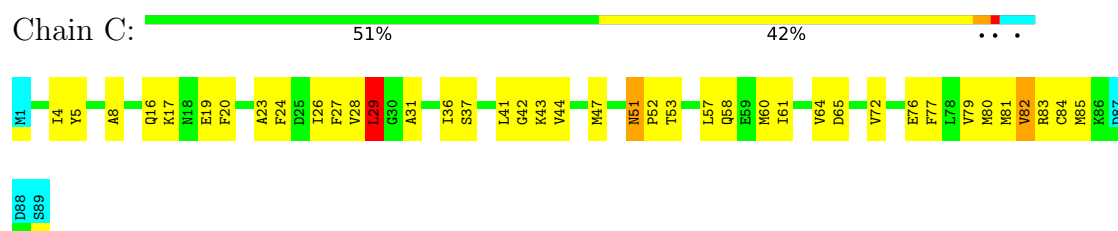


- Molecule 2: Troponin I, cardiac muscle

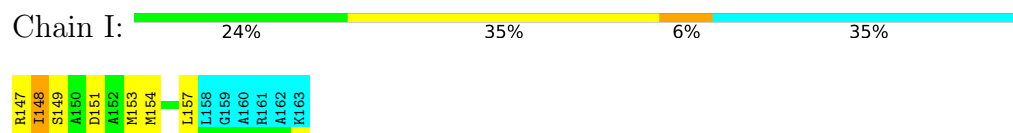


4.2.6 Score per residue for model 6

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

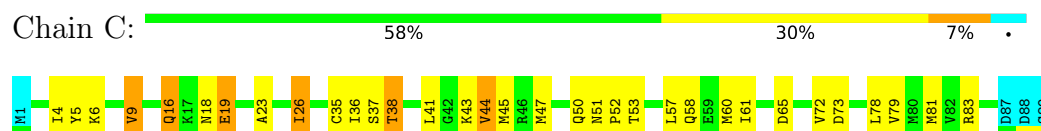


- Molecule 2: Troponin I, cardiac muscle

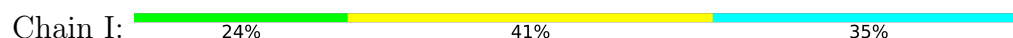


4.2.7 Score per residue for model 7

- Molecule 1: Troponin C, slow skeletal and cardiac muscles



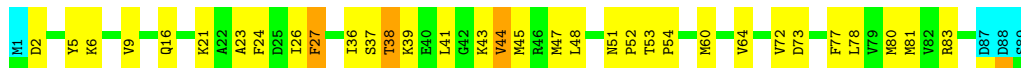
- Molecule 2: Troponin I, cardiac muscle





4.2.8 Score per residue for model 8

- Molecule 1: Troponin C, slow skeletal and cardiac muscles



- Molecule 2: Troponin I, cardiac muscle

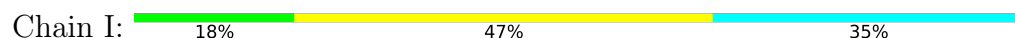


4.2.9 Score per residue for model 9

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

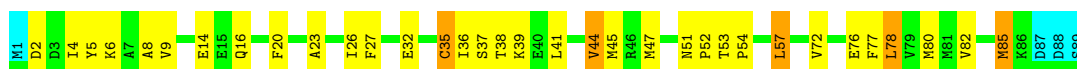


- Molecule 2: Troponin I, cardiac muscle

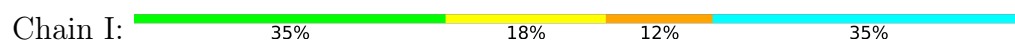


4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Troponin C, slow skeletal and cardiac muscles



- Molecule 2: Troponin I, cardiac muscle



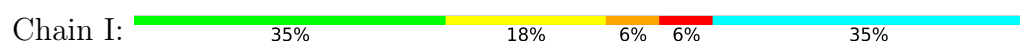


4.2.11 Score per residue for model 11

- Molecule 1: Troponin C, slow skeletal and cardiac muscles



- Molecule 2: Troponin I, cardiac muscle

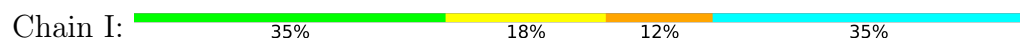


4.2.12 Score per residue for model 12

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

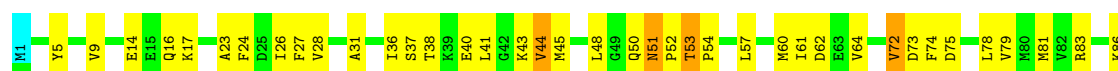


- Molecule 2: Troponin I, cardiac muscle

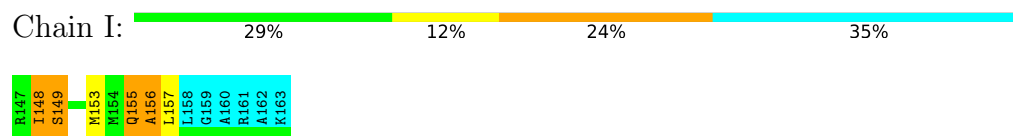


4.2.13 Score per residue for model 13

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

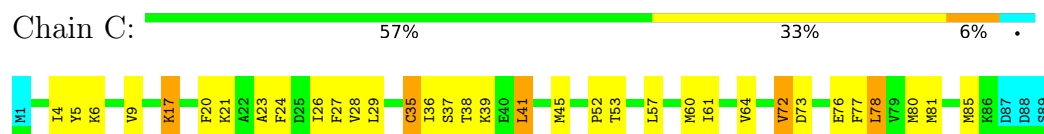


- Molecule 2: Troponin I, cardiac muscle

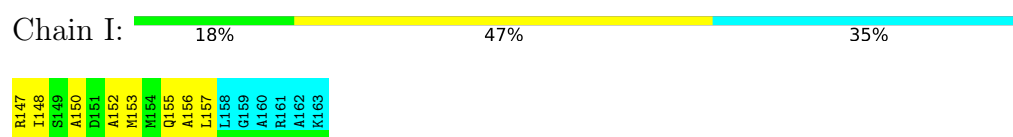


4.2.14 Score per residue for model 14

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

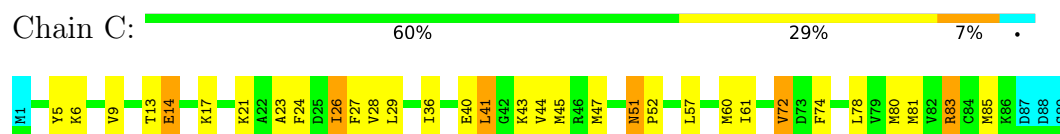


- Molecule 2: Troponin I, cardiac muscle

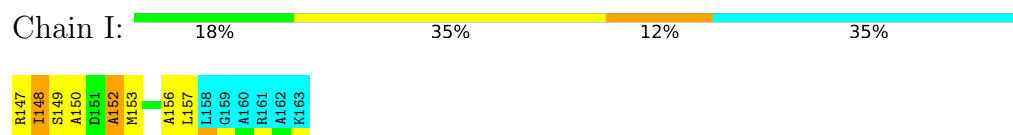


4.2.15 Score per residue for model 15

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

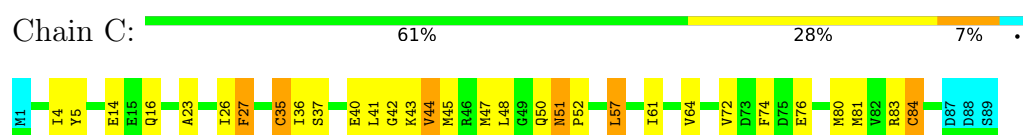


- Molecule 2: Troponin I, cardiac muscle

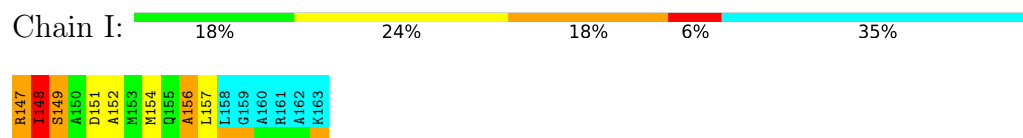


4.2.16 Score per residue for model 16

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

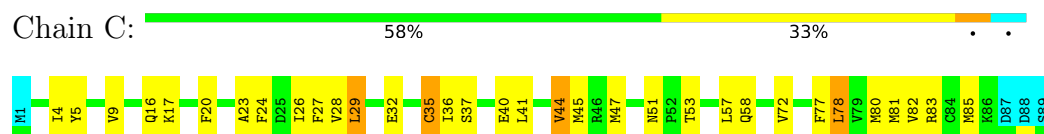


- Molecule 2: Troponin I, cardiac muscle

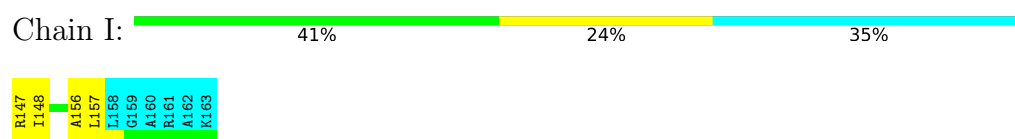


4.2.17 Score per residue for model 17

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

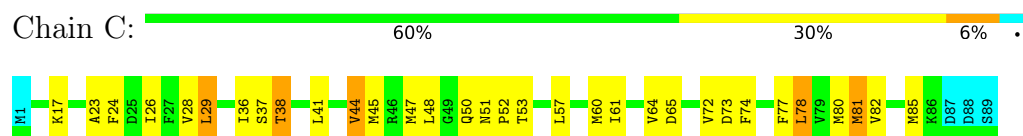


- Molecule 2: Troponin I, cardiac muscle

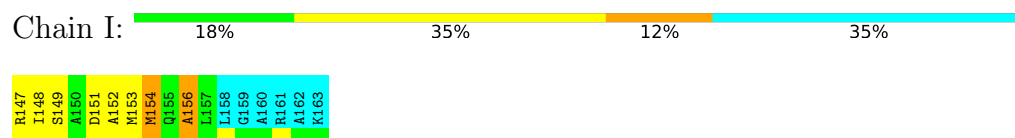


4.2.18 Score per residue for model 18

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

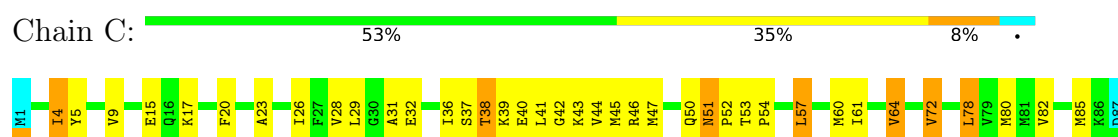


- Molecule 2: Troponin I, cardiac muscle



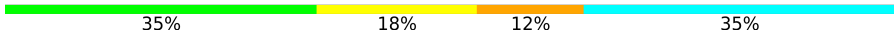
4.2.19 Score per residue for model 19

- Molecule 1: Troponin C, slow skeletal and cardiac muscles



D88
S89

- Molecule 2: Troponin I, cardiac muscle

Chain I: 

R147
I148
S149
M153
A156
L157
L158
G159
A160
R161
A162
K163

4.2.20 Score per residue for model 20

- Molecule 1: Troponin C, slow skeletal and cardiac muscles

Chain C: 

M1
I4
Y5
K17
F20
A23
F24
D25
I26
F27
V28
L29
G35
I36
S37
T38
K39
E40
L41
G42
K43
V44
M47
T53
L57
I61
V64
D65
E66
V72
L78
V79
M80
M81
V82
R83
C84
M85
R86
D87
D88
S89

- Molecule 2: Troponin I, cardiac muscle

Chain I: 

R147
I148
S149
A150
M153
M154
Q155
A156
L157
L158
G159
A160
R161
A162
K163

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing*.

Of the 300 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
X-PLOR NIH	structure solution	
X-PLOR NIH	refinement	

No chemical shift data was provided.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: CA, WW7

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	C	0.79±0.03	0±0/675 (0.0± 0.0%)	1.05±0.02	1±1/906 (0.1± 0.1%)
2	I	0.85±0.04	0±0/81 (0.0± 0.0%)	1.01±0.06	0±0/108 (0.0± 0.0%)
All	All	0.80	0/15120 (0.0%)	1.04	15/20280 (0.1%)

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	C	27	PHE	CA-CB-CG	-5.98	107.82	113.80	10	7
1	C	24	PHE	CA-CB-CG	-5.82	107.98	113.80	12	5
1	C	74	PHE	CA-CB-CG	-5.57	108.23	113.80	15	3

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	C	667	642	641	28±5
2	I	81	87	84	9±3
4	I	22	22	21	4±2
All	All	15420	15020	14921	657

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 22.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:I:148:ILE:HG21	4:I:91:WW7:H161	0.92	1.39	4	1
1:C:47:MET:SD	2:I:156:ALA:HB1	0.92	2.04	5	6
1:C:27:PHE:CZ	2:I:153:MET:HE1	0.89	2.03	6	1
1:C:45:MET:HE2	1:C:60:MET:SD	0.88	2.09	9	1
1:C:23:ALA:O	1:C:26:ILE:HG22	0.84	1.71	8	19
1:C:47:MET:SD	2:I:156:ALA:HB2	0.83	2.13	11	4
1:C:36:ILE:HB	1:C:72:VAL:HG23	0.78	1.54	7	17
1:C:27:PHE:CD1	1:C:44:VAL:HG21	0.77	2.13	15	1
1:C:45:MET:HE3	1:C:52:PRO:HG3	0.77	1.56	9	3
1:C:47:MET:SD	2:I:156:ALA:CB	0.76	2.73	11	7
1:C:64:VAL:HG12	1:C:80:MET:SD	0.76	2.20	8	1
1:C:79:VAL:O	1:C:82:VAL:HG22	0.75	1.81	9	1
1:C:6:LYS:O	1:C:9:VAL:HG12	0.75	1.82	1	6
1:C:60:MET:SD	4:I:91:WW7:H3	0.74	2.23	19	11
1:C:64:VAL:HB	1:C:80:MET:SD	0.73	2.21	5	2
1:C:37:SER:O	1:C:38:THR:HG22	0.73	1.83	2	13
2:I:148:ILE:HG23	2:I:149:SER:H	0.72	1.43	15	2
2:I:148:ILE:HG23	2:I:149:SER:N	0.71	2.01	11	3
1:C:60:MET:HE3	4:I:91:WW7:H3	0.70	1.62	6	1
1:C:44:VAL:O	1:C:47:MET:SD	0.70	2.49	12	1
1:C:26:ILE:HG21	1:C:47:MET:SD	0.69	2.27	6	1
2:I:153:MET:SD	4:I:91:WW7:H8	0.69	2.27	13	2
1:C:26:ILE:HD13	1:C:47:MET:SD	0.69	2.27	6	2
1:C:41:LEU:HD12	1:C:57:LEU:HD12	0.69	1.63	15	1
1:C:47:MET:HE1	2:I:153:MET:SD	0.69	2.27	18	4
1:C:85:MET:HE2	2:I:147:ARG:HB2	0.69	1.64	9	2
1:C:64:VAL:O	1:C:80:MET:SD	0.69	2.51	5	2
2:I:150:ALA:HB3	4:I:91:WW7:H141	0.68	1.63	9	1
2:I:153:MET:HE3	4:I:91:WW7:H8	0.68	1.65	2	1
1:C:80:MET:SD	1:C:80:MET:C	0.68	2.77	10	5
1:C:44:VAL:HA	1:C:47:MET:HE2	0.68	1.64	9	4
1:C:35:CYS:SG	1:C:36:ILE:N	0.68	2.67	4	5
1:C:85:MET:SD	2:I:147:ARG:N	0.67	2.68	20	1
1:C:85:MET:HE2	2:I:147:ARG:HG2	0.66	1.68	6	2
1:C:81:MET:SD	2:I:148:ILE:HD12	0.65	2.30	14	2
1:C:45:MET:SD	1:C:57:LEU:HD11	0.65	2.32	15	1
2:I:153:MET:HE2	4:I:91:WW7:O2	0.64	1.91	19	1
1:C:41:LEU:HD13	1:C:57:LEU:HD12	0.64	1.69	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:61:ILE:HG23	1:C:72:VAL:HG13	0.63	1.69	16	3
1:C:85:MET:HE2	2:I:147:ARG:N	0.63	2.09	14	1
1:C:45:MET:SD	1:C:52:PRO:CG	0.62	2.87	14	4
1:C:78:LEU:O	1:C:82:VAL:HG23	0.62	1.94	10	4
1:C:51:ASN:N	1:C:52:PRO:HD3	0.62	2.09	5	5
1:C:20:PHE:CE1	1:C:78:LEU:HD22	0.62	2.29	17	6
1:C:64:VAL:HG13	1:C:81:MET:SD	0.62	2.34	16	1
2:I:148:ILE:HG22	4:I:91:WW7:H131	0.62	1.71	18	1
1:C:41:LEU:HD22	1:C:61:ILE:HG13	0.61	1.71	9	7
1:C:23:ALA:HB2	2:I:157:LEU:HD21	0.61	1.73	6	1
1:C:64:VAL:O	1:C:80:MET:HE2	0.61	1.96	20	1
1:C:41:LEU:HG	1:C:57:LEU:HD12	0.60	1.73	7	4
1:C:60:MET:CE	4:I:91:WW7:H3	0.60	2.25	6	2
1:C:47:MET:SD	2:I:156:ALA:HA	0.60	2.36	20	2
1:C:27:PHE:CD2	1:C:36:ILE:HD11	0.60	2.32	9	4
1:C:81:MET:O	1:C:85:MET:SD	0.60	2.59	20	1
1:C:80:MET:HE1	1:C:81:MET:HE2	0.60	1.73	15	1
1:C:23:ALA:HB2	2:I:156:ALA:CB	0.59	2.26	13	1
1:C:47:MET:HE1	2:I:153:MET:CE	0.59	2.27	6	2
2:I:154:MET:SD	2:I:154:MET:N	0.59	2.76	18	1
1:C:24:PHE:O	1:C:28:VAL:HG22	0.59	1.97	5	6
1:C:77:PHE:CE1	1:C:81:MET:SD	0.59	2.96	17	2
1:C:77:PHE:CZ	2:I:153:MET:SD	0.59	2.96	14	1
1:C:26:ILE:O	1:C:29:LEU:HD11	0.58	1.98	17	2
1:C:27:PHE:CD1	1:C:36:ILE:HD13	0.58	2.33	15	1
1:C:45:MET:SD	1:C:52:PRO:HG3	0.58	2.39	10	4
1:C:61:ILE:HG23	1:C:72:VAL:HG23	0.58	1.75	13	2
1:C:47:MET:HE1	2:I:153:MET:HE1	0.58	1.76	19	1
1:C:28:VAL:HB	1:C:31:ALA:HB3	0.57	1.75	6	2
1:C:36:ILE:HB	1:C:72:VAL:HG12	0.57	1.75	13	1
1:C:65:ASP:HA	1:C:80:MET:SD	0.57	2.39	6	2
1:C:78:LEU:HD13	1:C:78:LEU:O	0.57	1.99	9	2
1:C:81:MET:SD	2:I:147:ARG:HB3	0.57	2.39	17	3
1:C:84:CYS:SG	1:C:85:MET:N	0.57	2.78	5	1
1:C:47:MET:SD	2:I:152:ALA:O	0.56	2.64	4	1
1:C:4:ILE:HD11	1:C:5:TYR:CE2	0.56	2.35	19	1
1:C:85:MET:HE2	2:I:147:ARG:HA	0.56	1.77	3	1
1:C:64:VAL:O	1:C:64:VAL:HG12	0.56	1.99	20	1
1:C:51:ASN:N	1:C:52:PRO:CD	0.56	2.67	15	10
1:C:9:VAL:HG12	1:C:17:LYS:HE2	0.56	1.78	13	1
1:C:61:ILE:O	1:C:65:ASP:N	0.56	2.37	7	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:20:PHE:CE1	1:C:77:PHE:CE2	0.55	2.94	2	1
1:C:57:LEU:HD13	1:C:60:MET:SD	0.55	2.41	7	1
1:C:31:ALA:HB2	1:C:40:GLU:CG	0.55	2.32	13	1
1:C:77:PHE:CZ	4:I:91:WW7:H7	0.55	2.36	17	1
1:C:38:THR:CB	1:C:61:ILE:HD12	0.55	2.31	18	4
2:I:154:MET:O	2:I:156:ALA:N	0.55	2.40	20	1
1:C:5:TYR:CD1	1:C:83:ARG:HD3	0.55	2.37	2	1
1:C:47:MET:HE1	2:I:153:MET:HE3	0.55	1.78	6	1
1:C:75:ASP:O	1:C:79:VAL:HG22	0.55	2.02	12	1
1:C:45:MET:SD	1:C:52:PRO:HG2	0.54	2.41	5	3
1:C:79:VAL:O	1:C:82:VAL:HG12	0.54	2.02	6	1
2:I:149:SER:O	2:I:150:ALA:HB3	0.54	2.02	10	1
1:C:85:MET:SD	2:I:147:ARG:HB3	0.54	2.42	2	1
4:I:91:WW7:O1	4:I:91:WW7:H8	0.54	2.02	18	9
2:I:147:ARG:O	2:I:148:ILE:HG22	0.54	2.02	19	3
1:C:41:LEU:O	1:C:44:VAL:N	0.54	2.38	18	11
1:C:77:PHE:HA	1:C:80:MET:HE2	0.54	1.80	17	1
2:I:153:MET:SD	4:I:91:WW7:C8	0.53	2.96	12	2
1:C:20:PHE:CZ	1:C:78:LEU:HA	0.53	2.39	17	2
1:C:38:THR:HG21	1:C:58:GLN:OE1	0.53	2.04	11	2
1:C:53:THR:HG22	1:C:54:PRO:HD2	0.53	1.78	12	5
1:C:77:PHE:CE1	4:I:91:WW7:H7	0.53	2.37	4	7
1:C:26:ILE:O	1:C:29:LEU:CD1	0.53	2.57	20	1
2:I:147:ARG:C	2:I:149:SER:H	0.53	2.11	16	2
1:C:64:VAL:O	1:C:80:MET:HE3	0.53	2.04	12	1
1:C:81:MET:HE2	2:I:148:ILE:CG1	0.53	2.34	16	2
1:C:38:THR:HA	1:C:41:LEU:CB	0.52	2.34	18	5
1:C:45:MET:SD	1:C:48:LEU:HD12	0.52	2.43	3	2
1:C:47:MET:SD	2:I:156:ALA:N	0.52	2.82	4	1
1:C:81:MET:SD	2:I:148:ILE:HB	0.52	2.45	15	2
1:C:47:MET:CG	2:I:156:ALA:HB1	0.52	2.35	17	1
1:C:81:MET:SD	2:I:148:ILE:HG12	0.52	2.45	12	2
2:I:147:ARG:O	2:I:148:ILE:C	0.52	2.52	15	5
1:C:45:MET:SD	1:C:50:GLN:HB2	0.52	2.45	13	3
2:I:148:ILE:HG23	4:I:91:WW7:H121	0.52	1.81	19	1
1:C:5:TYR:CE1	1:C:83:ARG:HG2	0.51	2.40	6	6
2:I:155:GLN:O	2:I:157:LEU:N	0.51	2.43	20	5
1:C:76:GLU:O	1:C:80:MET:HB3	0.51	2.05	12	6
2:I:147:ARG:O	2:I:149:SER:N	0.51	2.43	6	4
1:C:5:TYR:CZ	1:C:83:ARG:HD3	0.51	2.41	15	1
1:C:26:ILE:HD12	2:I:157:LEU:HD12	0.51	1.81	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:44:VAL:CG1	1:C:45:MET:N	0.51	2.74	10	6
1:C:47:MET:SD	1:C:48:LEU:HG	0.51	2.46	12	1
1:C:47:MET:HE3	2:I:156:ALA:CB	0.51	2.35	15	1
1:C:60:MET:HB3	4:I:91:WW7:H4	0.51	1.81	4	1
1:C:27:PHE:CE1	1:C:44:VAL:HG23	0.51	2.41	16	2
1:C:57:LEU:HD13	1:C:60:MET:HE2	0.51	1.81	14	1
1:C:47:MET:SD	2:I:156:ALA:CA	0.50	2.98	3	3
2:I:153:MET:HE2	4:I:91:WW7:H8	0.50	1.82	9	1
1:C:5:TYR:O	1:C:9:VAL:HG23	0.50	2.06	12	1
1:C:5:TYR:CE1	1:C:83:ARG:HD2	0.50	2.42	1	1
1:C:41:LEU:HD12	1:C:44:VAL:HG21	0.50	1.82	9	1
1:C:85:MET:HG2	2:I:147:ARG:HB3	0.50	1.82	19	1
4:I:91:WW7:H8	4:I:91:WW7:O1	0.50	2.07	12	1
1:C:61:ILE:HA	1:C:64:VAL:HG12	0.50	1.83	1	1
1:C:64:VAL:CG1	1:C:80:MET:SD	0.50	2.98	8	1
1:C:15:GLU:H	1:C:15:GLU:CD	0.50	2.15	19	3
1:C:82:VAL:HA	1:C:85:MET:SD	0.50	2.47	10	1
1:C:9:VAL:HG21	1:C:78:LEU:HD21	0.50	1.83	8	1
1:C:45:MET:SD	1:C:57:LEU:HD21	0.50	2.46	15	2
2:I:149:SER:O	2:I:150:ALA:CB	0.50	2.60	10	1
2:I:148:ILE:CG2	2:I:149:SER:N	0.49	2.72	11	1
1:C:41:LEU:HD12	1:C:61:ILE:HG13	0.49	1.85	14	1
1:C:81:MET:SD	2:I:148:ILE:CD1	0.49	3.01	14	1
1:C:45:MET:HE3	1:C:50:GLN:HB2	0.49	1.82	18	1
1:C:4:ILE:HG13	1:C:5:TYR:N	0.49	2.21	6	10
1:C:27:PHE:CE2	1:C:36:ILE:HD11	0.49	2.42	9	1
1:C:9:VAL:HG22	1:C:78:LEU:CD1	0.49	2.37	12	1
1:C:9:VAL:HG22	1:C:78:LEU:HD12	0.49	1.82	17	2
1:C:37:SER:C	1:C:39:LYS:H	0.49	2.15	8	4
2:I:149:SER:OG	4:I:91:WW7:H151	0.49	2.07	6	1
1:C:50:GLN:C	1:C:52:PRO:HD3	0.49	2.33	19	3
1:C:5:TYR:CZ	1:C:83:ARG:HG2	0.49	2.43	7	1
1:C:2:ASP:HB2	1:C:5:TYR:CE2	0.49	2.42	11	1
1:C:4:ILE:HD11	1:C:5:TYR:CZ	0.49	2.43	12	1
1:C:24:PHE:HA	1:C:27:PHE:CD2	0.49	2.41	20	2
1:C:45:MET:HE3	1:C:50:GLN:CB	0.49	2.37	18	1
2:I:153:MET:HE3	4:I:91:WW7:C8	0.48	2.34	2	1
1:C:5:TYR:OH	1:C:83:ARG:NE	0.48	2.43	9	1
1:C:20:PHE:CD1	1:C:78:LEU:HD22	0.48	2.43	14	3
1:C:64:VAL:HG11	1:C:81:MET:HE1	0.48	1.85	13	1
2:I:154:MET:C	2:I:156:ALA:N	0.48	2.71	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:I:148:ILE:O	2:I:150:ALA:N	0.48	2.41	3	4
1:C:81:MET:HE2	2:I:148:ILE:CD1	0.48	2.38	4	1
1:C:57:LEU:HD13	1:C:57:LEU:O	0.48	2.07	11	3
1:C:45:MET:HE2	1:C:52:PRO:HG2	0.48	1.86	3	1
1:C:45:MET:SD	1:C:52:PRO:HD2	0.48	2.49	5	1
1:C:41:LEU:HD12	1:C:44:VAL:CG2	0.48	2.38	9	2
2:I:148:ILE:CG2	4:I:91:WW7:H161	0.48	2.38	18	2
1:C:38:THR:HB	1:C:61:ILE:HD12	0.48	1.86	2	4
1:C:5:TYR:CD1	1:C:83:ARG:HD2	0.48	2.43	8	1
1:C:79:VAL:O	1:C:82:VAL:CG2	0.48	2.60	9	1
1:C:24:PHE:HA	1:C:27:PHE:CE2	0.48	2.43	12	1
1:C:37:SER:O	1:C:41:LEU:N	0.48	2.45	3	5
1:C:38:THR:HA	1:C:41:LEU:HB3	0.48	1.85	11	4
1:C:81:MET:CG	1:C:85:MET:HE3	0.48	2.39	2	1
1:C:28:VAL:O	1:C:29:LEU:C	0.48	2.56	6	1
2:I:148:ILE:CG2	4:I:91:WW7:HN1	0.48	2.22	16	2
1:C:28:VAL:HG23	1:C:28:VAL:O	0.48	2.08	12	2
1:C:24:PHE:O	1:C:28:VAL:HG13	0.48	2.08	13	1
1:C:81:MET:HE2	2:I:148:ILE:HD11	0.47	1.85	4	1
1:C:17:LYS:O	1:C:20:PHE:CB	0.47	2.62	6	2
1:C:84:CYS:SG	2:I:148:ILE:O	0.47	2.71	5	1
2:I:148:ILE:HG23	4:I:91:WW7:H132	0.47	1.86	5	1
1:C:17:LYS:O	1:C:20:PHE:HB3	0.47	2.09	17	2
1:C:16:GLN:O	1:C:20:PHE:HB2	0.47	2.09	10	1
2:I:148:ILE:HG21	4:I:91:WW7:HN1	0.47	1.67	16	1
1:C:85:MET:HG2	2:I:147:ARG:CB	0.47	2.39	19	1
2:I:153:MET:C	2:I:155:GLN:N	0.47	2.72	20	1
1:C:57:LEU:CD1	1:C:60:MET:HE2	0.47	2.38	15	2
1:C:38:THR:OG1	1:C:58:GLN:N	0.47	2.48	12	2
1:C:14:GLU:H	1:C:14:GLU:CD	0.47	2.18	4	2
1:C:64:VAL:HG12	1:C:80:MET:HE3	0.47	1.86	2	1
2:I:148:ILE:HG23	2:I:148:ILE:O	0.47	2.10	20	2
1:C:26:ILE:CG2	1:C:47:MET:SD	0.47	3.01	6	1
1:C:37:SER:O	1:C:39:LYS:N	0.47	2.46	19	4
2:I:148:ILE:HD11	4:I:91:WW7:H161	0.47	1.86	8	1
1:C:80:MET:SD	1:C:80:MET:O	0.47	2.72	20	2
1:C:5:TYR:O	1:C:8:ALA:HB3	0.47	2.09	6	2
1:C:28:VAL:HG23	1:C:29:LEU:N	0.47	2.24	4	1
1:C:41:LEU:CD1	1:C:44:VAL:HG21	0.46	2.39	9	2
1:C:27:PHE:CG	1:C:36:ILE:HG12	0.46	2.45	4	1
1:C:41:LEU:C	1:C:43:LYS:N	0.46	2.74	20	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:I:148:ILE:HG12	2:I:149:SER:H	0.46	1.69	5	1
1:C:85:MET:SD	2:I:147:ARG:CB	0.46	3.04	2	1
1:C:81:MET:HE2	2:I:148:ILE:HB	0.46	1.86	6	1
2:I:153:MET:O	2:I:156:ALA:HB3	0.46	2.11	7	2
1:C:31:ALA:HB2	1:C:40:GLU:HG2	0.46	1.86	13	1
1:C:84:CYS:SG	2:I:148:ILE:HA	0.46	2.50	16	1
1:C:5:TYR:CE1	1:C:83:ARG:HA	0.46	2.45	3	1
1:C:44:VAL:O	1:C:47:MET:HG3	0.46	2.10	8	1
1:C:45:MET:HE2	1:C:48:LEU:HD12	0.46	1.86	13	1
1:C:45:MET:SD	1:C:52:PRO:CD	0.46	3.03	8	1
1:C:37:SER:O	1:C:40:GLU:N	0.46	2.49	12	1
1:C:41:LEU:HD23	1:C:57:LEU:HD12	0.46	1.87	4	2
2:I:155:GLN:C	2:I:157:LEU:N	0.46	2.73	20	4
2:I:154:MET:C	2:I:156:ALA:H	0.46	2.19	20	1
1:C:20:PHE:CE2	2:I:147:ARG:HD3	0.46	2.45	1	1
1:C:27:PHE:CE1	2:I:153:MET:HE1	0.46	2.46	6	1
1:C:77:PHE:CD1	4:I:91:WW7:H7	0.46	2.45	11	2
1:C:41:LEU:HD13	1:C:41:LEU:O	0.46	2.11	15	1
1:C:76:GLU:O	1:C:80:MET:N	0.45	2.49	14	3
1:C:60:MET:CB	4:I:91:WW7:H3	0.45	2.41	6	1
1:C:35:CYS:SG	1:C:73:ASP:HA	0.45	2.51	7	1
1:C:8:ALA:CB	1:C:82:VAL:HG11	0.45	2.41	10	1
2:I:157:LEU:CD1	2:I:157:LEU:N	0.45	2.80	6	1
1:C:14:GLU:CD	1:C:14:GLU:H	0.45	2.19	15	1
2:I:148:ILE:HG23	4:I:91:WW7:H161	0.45	1.87	20	1
1:C:14:GLU:CD	1:C:14:GLU:N	0.45	2.73	4	1
1:C:23:ALA:HB1	1:C:27:PHE:CE2	0.45	2.46	13	1
1:C:27:PHE:O	1:C:40:GLU:HG3	0.45	2.12	12	1
1:C:74:PHE:CZ	1:C:78:LEU:HD23	0.45	2.47	11	1
1:C:27:PHE:HZ	2:I:153:MET:SD	0.45	2.34	12	1
2:I:148:ILE:O	4:I:91:WW7:H132	0.45	2.12	17	2
2:I:147:ARG:O	2:I:150:ALA:N	0.45	2.50	15	1
1:C:41:LEU:O	1:C:43:LYS:N	0.44	2.51	16	4
1:C:64:VAL:HG11	4:I:91:WW7:CL1	0.44	2.49	1	1
2:I:152:ALA:O	2:I:156:ALA:N	0.44	2.50	5	3
1:C:27:PHE:CZ	2:I:153:MET:SD	0.44	3.10	12	1
1:C:80:MET:CG	1:C:81:MET:N	0.44	2.80	17	1
1:C:9:VAL:O	1:C:17:LYS:NZ	0.44	2.50	19	1
1:C:64:VAL:HG12	1:C:80:MET:HE1	0.44	1.88	18	1
1:C:26:ILE:HG23	1:C:44:VAL:HG22	0.44	1.88	15	1
1:C:44:VAL:HG13	1:C:48:LEU:HD12	0.44	1.89	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:81:MET:HE2	2:I:148:ILE:HG13	0.44	1.89	16	1
1:C:73:ASP:O	1:C:77:PHE:N	0.44	2.44	5	1
2:I:148:ILE:HG23	4:I:91:WW7:C13	0.44	2.43	17	1
1:C:60:MET:O	1:C:64:VAL:HG23	0.44	2.13	8	2
1:C:73:ASP:O	1:C:77:PHE:CB	0.44	2.66	8	1
1:C:37:SER:O	1:C:38:THR:CG2	0.43	2.65	13	2
1:C:23:ALA:CB	2:I:153:MET:SD	0.43	3.06	7	1
1:C:45:MET:SD	1:C:57:LEU:CD1	0.43	3.04	15	1
1:C:21:LYS:O	1:C:25:ASP:N	0.43	2.46	11	1
1:C:64:VAL:HG12	1:C:64:VAL:O	0.43	2.13	13	3
1:C:78:LEU:CD1	1:C:78:LEU:C	0.43	2.91	12	1
1:C:20:PHE:CD1	1:C:77:PHE:CE2	0.43	3.06	3	1
2:I:148:ILE:HD12	4:I:91:WW7:O1	0.43	2.13	12	1
1:C:73:ASP:CG	1:C:74:PHE:N	0.43	2.76	18	2
1:C:60:MET:HE3	4:I:91:WW7:C3	0.43	2.41	6	1
1:C:26:ILE:CG2	1:C:27:PHE:N	0.43	2.81	5	1
2:I:152:ALA:CB	4:I:91:WW7:H111	0.43	2.44	2	1
1:C:41:LEU:HD23	1:C:57:LEU:O	0.43	2.14	13	1
1:C:27:PHE:HB3	1:C:36:ILE:CD1	0.43	2.44	20	1
2:I:148:ILE:O	2:I:148:ILE:HG23	0.43	2.14	7	1
2:I:155:GLN:C	2:I:157:LEU:H	0.43	2.22	14	2
1:C:27:PHE:CE1	1:C:44:VAL:HG21	0.43	2.48	15	1
1:C:44:VAL:O	1:C:47:MET:HB3	0.43	2.14	15	1
1:C:81:MET:HE3	4:I:91:WW7:C7	0.43	2.44	15	1
2:I:148:ILE:HG21	4:I:91:WW7:H131	0.42	1.91	12	1
1:C:47:MET:HE1	2:I:153:MET:HE2	0.42	1.92	4	1
1:C:34:GLY:C	1:C:35:CYS:SG	0.42	3.01	5	1
1:C:64:VAL:HG22	2:I:148:ILE:HD12	0.42	1.91	6	1
1:C:45:MET:HE3	1:C:60:MET:SD	0.42	2.54	19	1
1:C:76:GLU:O	1:C:80:MET:CB	0.42	2.68	16	2
4:I:91:WW7:H112	4:I:91:WW7:H2	0.42	1.90	12	1
1:C:23:ALA:CB	2:I:153:MET:HG3	0.42	2.44	14	1
1:C:23:ALA:HB3	2:I:153:MET:HG3	0.42	1.92	14	1
1:C:41:LEU:CD2	1:C:57:LEU:HD12	0.42	2.44	4	1
1:C:19:GLU:CG	2:I:157:LEU:HD23	0.42	2.45	6	1
1:C:44:VAL:CA	1:C:47:MET:HE2	0.42	2.42	6	2
1:C:8:ALA:HB1	1:C:82:VAL:HG11	0.42	1.91	10	1
1:C:47:MET:HG2	2:I:156:ALA:HB1	0.42	1.91	17	1
1:C:21:LYS:HG3	1:C:74:PHE:CZ	0.42	2.50	11	1
2:I:152:ALA:HB3	4:I:91:WW7:O2	0.42	2.15	14	1
1:C:36:ILE:HG21	1:C:41:LEU:HD13	0.42	1.92	5	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:64:VAL:O	1:C:64:VAL:CG1	0.42	2.68	20	1
2:I:157:LEU:N	2:I:157:LEU:HD12	0.42	2.30	6	1
2:I:148:ILE:CG2	2:I:149:SER:H	0.42	2.22	15	2
1:C:81:MET:HE1	4:I:91:WW7:C6	0.42	2.45	7	1
1:C:65:ASP:OD1	1:C:80:MET:SD	0.42	2.78	9	1
1:C:27:PHE:CZ	2:I:153:MET:HE2	0.42	2.50	12	1
1:C:35:CYS:SG	1:C:73:ASP:HB3	0.42	2.55	14	1
1:C:82:VAL:O	1:C:85:MET:HB2	0.42	2.15	19	1
1:C:21:LYS:O	1:C:24:PHE:N	0.41	2.53	8	1
1:C:40:GLU:O	1:C:43:LYS:HB2	0.41	2.14	15	1
1:C:66:GLU:HB2	1:C:83:ARG:NH2	0.41	2.31	4	1
1:C:81:MET:HE2	2:I:148:ILE:HG12	0.41	1.92	4	1
1:C:48:LEU:HD21	2:I:152:ALA:HB1	0.41	1.91	18	1
1:C:17:LYS:O	1:C:20:PHE:HB2	0.41	2.15	19	1
1:C:57:LEU:N	1:C:57:LEU:CD2	0.41	2.84	2	2
2:I:152:ALA:O	2:I:155:GLN:HG2	0.41	2.15	3	1
1:C:21:LYS:O	1:C:24:PHE:HB3	0.41	2.15	15	1
1:C:23:ALA:CB	2:I:153:MET:HB3	0.41	2.46	4	1
2:I:148:ILE:HB	4:I:91:WW7:H131	0.41	1.93	4	1
1:C:8:ALA:HB3	1:C:82:VAL:HG21	0.41	1.93	9	1
1:C:78:LEU:HD13	1:C:78:LEU:C	0.41	2.39	9	1
2:I:149:SER:HB2	4:I:91:WW7:H151	0.41	1.92	9	1
1:C:27:PHE:CZ	1:C:44:VAL:HG23	0.41	2.51	8	2
1:C:16:GLN:O	1:C:19:GLU:HG3	0.41	2.15	7	1
1:C:50:GLN:C	1:C:52:PRO:CD	0.41	2.94	9	1
1:C:41:LEU:HD13	1:C:57:LEU:CD1	0.41	2.45	14	1
4:I:91:WW7:O1	4:I:91:WW7:H121	0.41	2.16	1	1
1:C:45:MET:SD	1:C:57:LEU:CD2	0.41	3.08	5	1
1:C:77:PHE:CE2	4:I:91:WW7:H7	0.41	2.50	17	2
1:C:27:PHE:CZ	2:I:153:MET:HE3	0.41	2.51	9	1
1:C:21:LYS:CG	1:C:74:PHE:CZ	0.41	3.04	11	1
1:C:75:ASP:O	1:C:79:VAL:N	0.41	2.53	13	1
1:C:38:THR:HA	1:C:41:LEU:HB2	0.41	1.93	18	1
1:C:42:GLY:HA2	1:C:57:LEU:HD21	0.41	1.93	19	1
2:I:147:ARG:O	2:I:148:ILE:CG2	0.41	2.67	19	1
1:C:45:MET:SD	1:C:60:MET:HE1	0.40	2.56	1	1
1:C:27:PHE:CG	1:C:36:ILE:CD1	0.40	3.04	6	1
2:I:157:LEU:N	2:I:157:LEU:CD2	0.40	2.83	10	1
1:C:17:LYS:HA	1:C:20:PHE:HB2	0.40	1.93	14	1
1:C:80:MET:O	1:C:83:ARG:HG2	0.40	2.16	2	1
1:C:60:MET:HB3	4:I:91:WW7:H3	0.40	1.92	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:I:151:ASP:C	2:I:153:MET:N	0.40	2.79	6	1
1:C:76:GLU:OE2	1:C:80:MET:SD	0.40	2.80	2	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	C	85/89 (96%)	79±1 (93±2%)	5±2 (6±2%)	0±1 (1±1%)	26	74
2	I	10/17 (59%)	7±1 (68±12%)	2±1 (16±14%)	2±1 (16±12%)	0	4
All	All	1900/2120 (90%)	1722 (91%)	137 (7%)	41 (2%)	7	47

All 12 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	I	148	ILE	12
2	I	156	ALA	8
1	C	42	GLY	5
2	I	149	SER	4
2	I	150	ALA	3
2	I	151	ASP	2
2	I	152	ALA	2
1	C	29	LEU	1
1	C	30	GLY	1
1	C	38	THR	1
1	C	64	VAL	1
2	I	155	GLN	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	C	74/78 (95%)	66±3 (89±4%)	8±3 (11±4%)	8	51
2	I	8/11 (73%)	7±1 (87±13%)	1±1 (13±13%)	6	46
All	All	1640/1780 (92%)	1456 (89%)	184 (11%)	8	51

All 51 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	C	78	LEU	14
1	C	57	LEU	12
1	C	53	THR	11
1	C	72	VAL	10
1	C	44	VAL	9
1	C	51	ASN	8
1	C	29	LEU	7
1	C	38	THR	6
1	C	16	GLN	6
2	I	149	SER	5
1	C	35	CYS	5
1	C	19	GLU	4
1	C	46	ARG	4
1	C	79	VAL	4
1	C	41	LEU	4
1	C	58	GLN	4
2	I	154	MET	4
1	C	81	MET	4
1	C	2	ASP	3
1	C	4	ILE	3
1	C	39	LYS	3
2	I	148	ILE	3
1	C	82	VAL	3
1	C	84	CYS	3
1	C	32	GLU	3
1	C	85	MET	3
1	C	14	GLU	3
1	C	17	LYS	3
1	C	40	GLU	3
2	I	153	MET	2
1	C	26	ILE	2
2	I	147	ARG	2
1	C	43	LYS	2
2	I	151	ASP	2

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Mol	Chain	Res	Type	Models (Total)
1	C	21	LYS	2
1	C	56	GLU	2
2	I	155	GLN	2
1	C	73	ASP	1
1	C	6	LYS	1
1	C	75	ASP	1
1	C	63	GLU	1
1	C	9	VAL	1
1	C	18	ASN	1
1	C	47	MET	1
2	I	157	LEU	1
1	C	71	THR	1
1	C	62	ASP	1
1	C	13	THR	1
1	C	83	ARG	1
1	C	80	MET	1
1	C	66	GLU	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 oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	WW7	I	91	-	23,23,23	4.34±0.06	12±0 (52±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	WW7	I	91	-	31,31,31	1.07±0.04	2±1 (7±3%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	WW7	I	91	-	-	0±0,15,15,15	0±0,2,2,2

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
4	I	91	WW7	S1-N1	10.39	1.77	1.61	9	20
4	I	91	WW7	C2-C1	8.69	1.49	1.37	14	20
4	I	91	WW7	C10-C9	7.47	1.57	1.43	13	20
4	I	91	WW7	C7-C6	6.75	1.50	1.38	15	20
4	I	91	WW7	C7-C8	6.44	1.50	1.36	14	20
4	I	91	WW7	C3-C2	6.05	1.49	1.38	7	20
4	I	91	WW7	C3-C4	5.78	1.48	1.36	8	20
4	I	91	WW7	C6-C5	5.74	1.49	1.36	13	20
4	I	91	WW7	C5-C10	4.88	1.50	1.41	12	20
4	I	91	WW7	C1-C9	4.56	1.51	1.43	16	20
4	I	91	WW7	C4-C10	3.53	1.49	1.42	7	20
4	I	91	WW7	C8-C9	3.29	1.48	1.42	16	20
4	I	91	WW7	O2-S1	2.19	1.46	1.43	16	1

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst

occurrence in the ensemble.

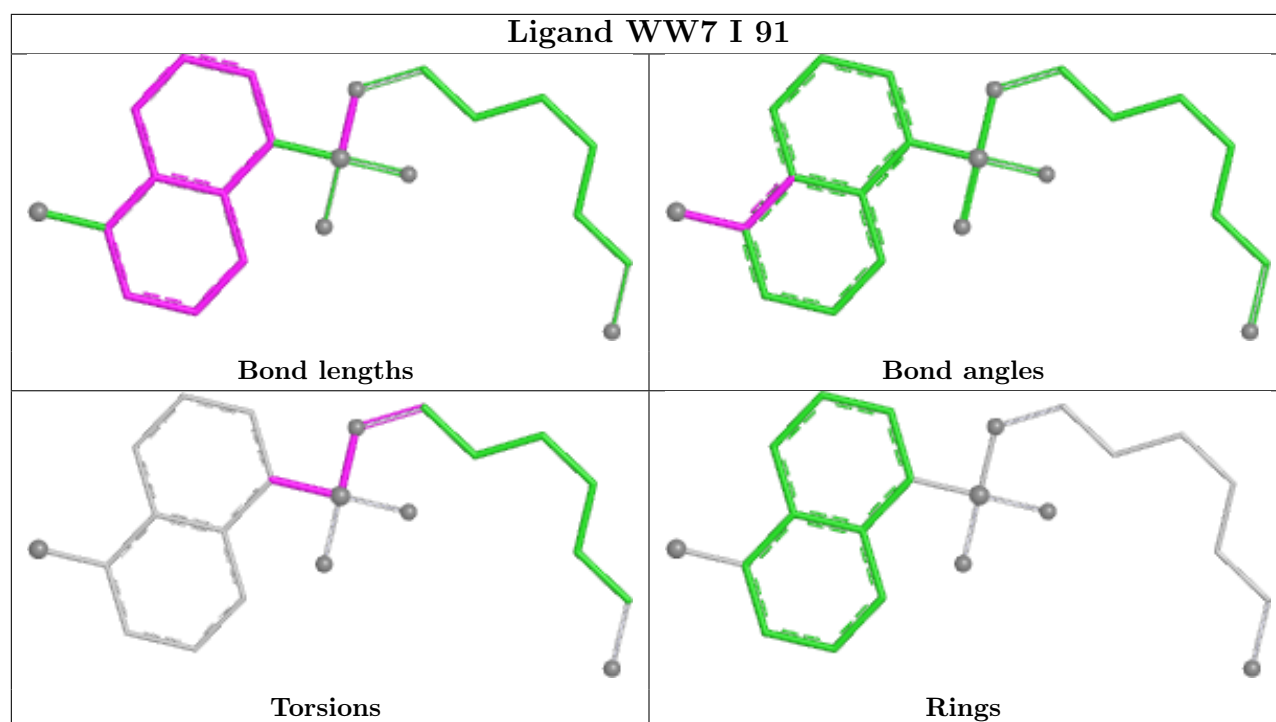
Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
4	I	91	WW7	O2-S1-O1	2.45	116.54	119.52	16	14
4	I	91	WW7	C10-C5-CL1	2.44	123.39	119.25	6	20
4	I	91	WW7	C5-C10-C9	2.43	119.39	117.62	14	6
4	I	91	WW7	C4-C10-C5	2.19	121.27	125.07	14	4
4	I	91	WW7	C12-C11-N1	2.16	115.54	111.03	5	1
4	I	91	WW7	O1-S1-C1	2.01	111.60	108.09	16	1

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

No chemical shift data were provided