



Full wwPDB NMR Structure Validation Report ⓘ

Mar 5, 2026 – 05:55 AM UTC

PDB ID : 2L98 / pdb_00002l98
BMRB ID : 17440
Title : Structure of trans-Resveratrol in complex with the cardiac regulatory protein Troponin C
Authors : Sykes, B.D.; Pineda-Sanabria, S.E.; Robertson, I.M.
Deposited on : 2011-02-02

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)
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

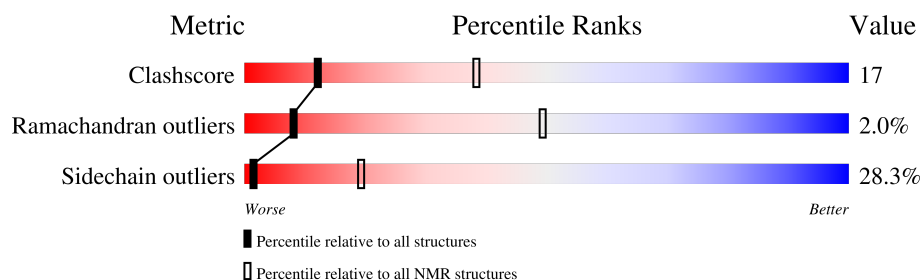
1 Overall quality at a glance

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	A	72	38% 44% 8% 10%

2 Ensemble composition and analysis

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:94-A:158 (65)	0.86	2

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 1 single-model cluster was found.

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

3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 1159 atoms, of which 557 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	A	72	Total	C	H	N	O	S	0
			1128	360	545	88	130	5	

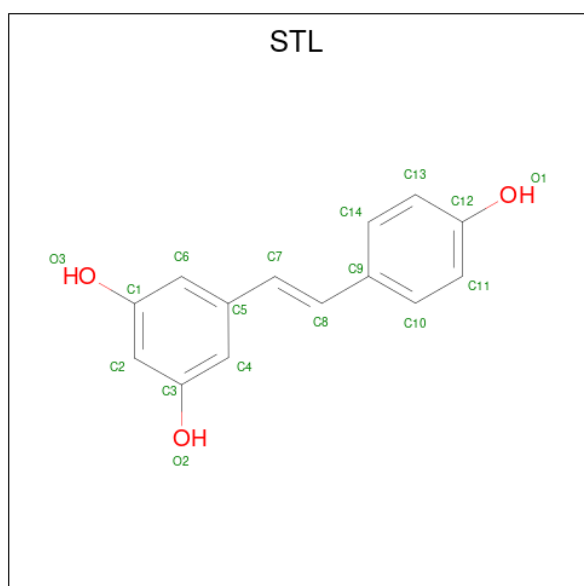
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	90	MET	-	initiating methionine	UNP P63316

- Molecule 2 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
2	A	2	Total	Ca
			2	2

- Molecule 3 is RESVERATROL (CCD ID: STL) (formula: C₁₄H₁₂O₃).



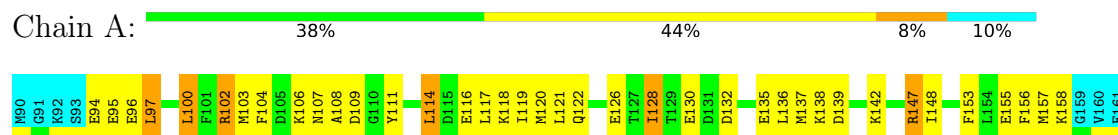
Mol	Chain	Residues	Atoms			
3	A	1	Total	C	H	O
			29	14	12	3

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

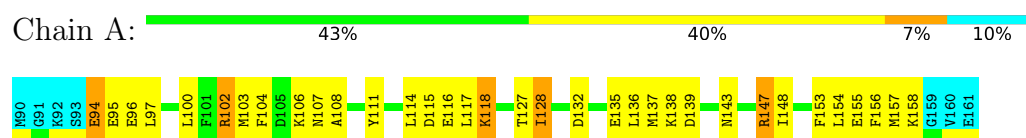


4.2 Scores per residue for each member of the ensemble

Colouring as in section [4.1](#) above.

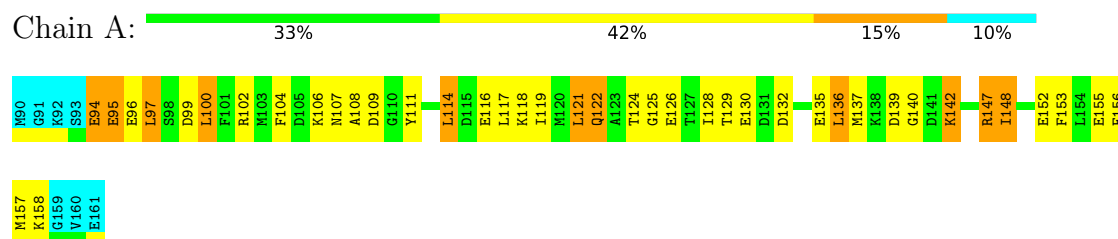
4.2.1 Score per residue for model 1

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



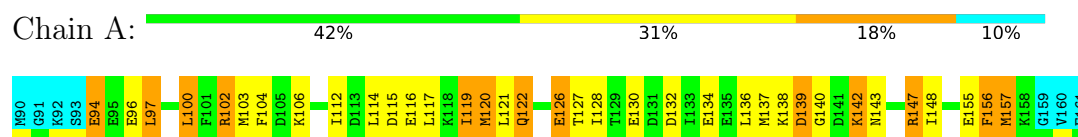
4.2.2 Score per residue for model 2 (medoid)

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



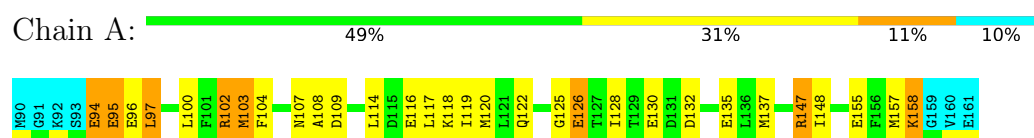
4.2.3 Score per residue for model 3

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



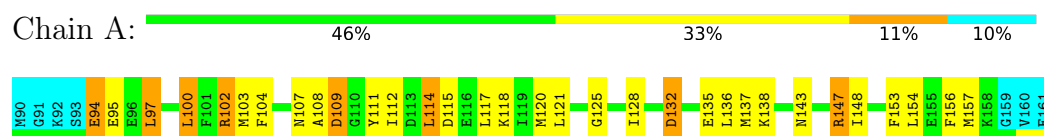
4.2.4 Score per residue for model 4

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



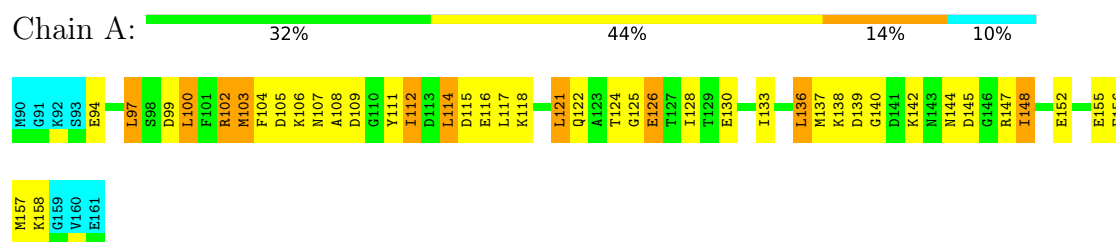
4.2.5 Score per residue for model 5

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



4.2.6 Score per residue for model 6

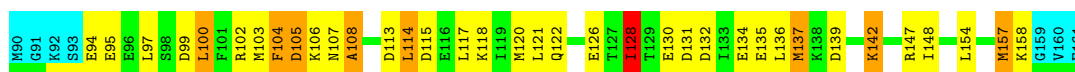
- Molecule 1: Troponin C, slow skeletal and cardiac muscles



4.2.7 Score per residue for model 7

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

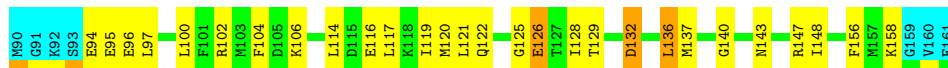




4.2.8 Score per residue for model 8

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

Chain A: 51% 35% 10%



4.2.9 Score per residue for model 9

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

Chain A: 46% 35% 10% 10%



4.2.10 Score per residue for model 10

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

Chain A: 47% 33% 10% 10%



4.2.11 Score per residue for model 11

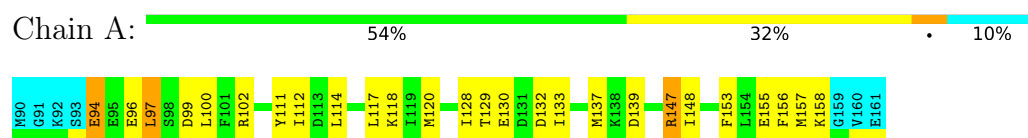
- Molecule 1: Troponin C, slow skeletal and cardiac muscles

Chain A: 43% 33% 14% 10%



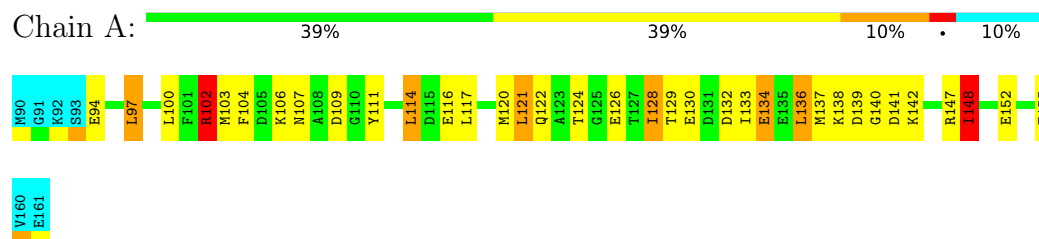
4.2.12 Score per residue for model 12

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



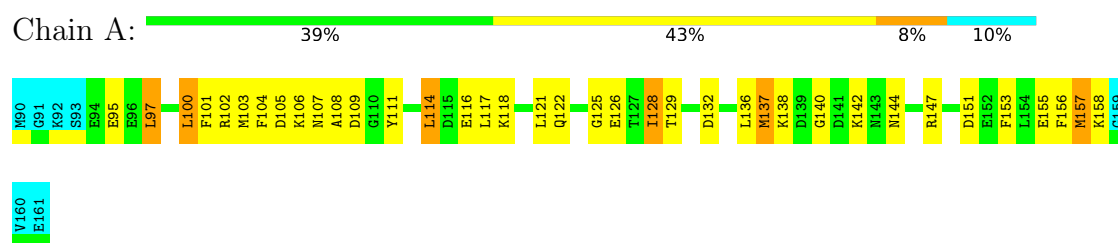
4.2.13 Score per residue for model 13

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



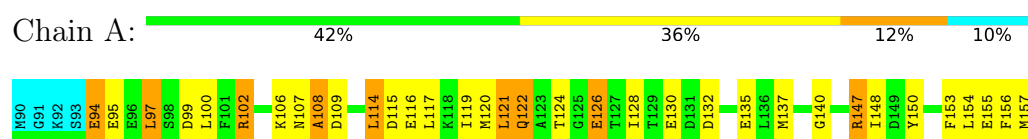
4.2.14 Score per residue for model 14

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



4.2.15 Score per residue for model 15

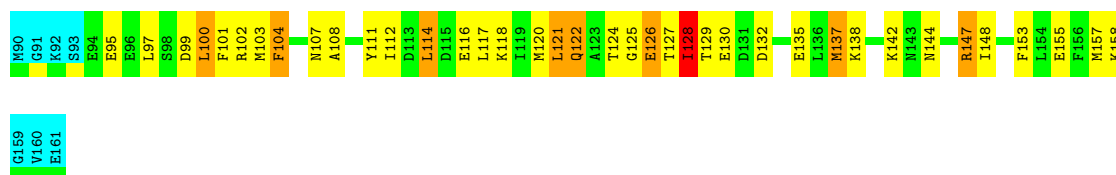
- Molecule 1: Troponin C, slow skeletal and cardiac muscles



4.2.16 Score per residue for model 16

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





4.2.17 Score per residue for model 17

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

Chain A:



4.2.18 Score per residue for model 18

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

Chain A:



4.2.19 Score per residue for model 19

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

Chain A:



4.2.20 Score per residue for model 20

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

Chain A:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *water refinement*.

Of the 100 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	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	9
Number of shifts mapped to atoms	9
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	0%

6 Model quality

6.1 Standard geometry

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

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	A	1.54±0.01	0±0/541 (0.0± 0.0%)	1.44±0.02	1±1/724 (0.1± 0.1%)
All	All	1.54	0/10820 (0.0%)	1.44	19/14480 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	2.0±0.0
All	All	0	40

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	A	128	ILE	N-CA-CB	-6.97	104.31	112.32	10	8
1	A	148	ILE	N-CA-CB	-5.83	104.36	110.72	6	5
1	A	104	PHE	CA-CB-CG	-5.45	108.35	113.80	17	1
1	A	112	ILE	N-CA-CB	-5.39	104.92	110.95	5	2
1	A	156	PHE	CA-CB-CG	-5.04	108.75	113.80	3	3

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	102	ARG	Sidechain	20

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	147	ARG	Sidechain	20

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	535	495	495	18±3
3	A	17	12	9	1±1
All	All	11080	10140	10080	364

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 17.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:137:MET:SD	1:A:148:ILE:HD11	0.86	2.09	12	8
1:A:114:LEU:HA	1:A:117:LEU:HD12	0.85	1.47	4	19
1:A:117:LEU:HD11	1:A:137:MET:SD	0.81	2.15	19	3
1:A:104:PHE:HA	1:A:120:MET:HE3	0.79	1.54	17	1
1:A:128:ILE:HD12	1:A:132:ASP:HB3	0.76	1.56	11	7
1:A:117:LEU:HD11	1:A:148:ILE:HD11	0.75	1.56	16	5
1:A:117:LEU:HD21	1:A:148:ILE:HD12	0.71	1.61	17	7
1:A:97:LEU:HD11	1:A:157:MET:HG3	0.71	1.60	17	2
1:A:97:LEU:HD11	1:A:157:MET:SD	0.71	2.25	7	2
1:A:117:LEU:HD22	3:A:162:STL:O1	0.71	1.86	8	4
1:A:97:LEU:HD12	1:A:154:LEU:HD23	0.68	1.65	5	1
1:A:121:LEU:HD13	1:A:124:THR:HB	0.67	1.65	16	2
1:A:97:LEU:HD21	1:A:157:MET:SD	0.67	2.29	18	2
1:A:128:ILE:HD13	1:A:132:ASP:HB2	0.67	1.67	1	1
1:A:128:ILE:HD12	1:A:132:ASP:CB	0.65	2.20	18	4
1:A:94:GLU:HA	1:A:97:LEU:HB2	0.64	1.71	15	14
1:A:117:LEU:CD1	1:A:137:MET:SD	0.63	2.87	1	5
1:A:137:MET:HE1	1:A:148:ILE:HG13	0.63	1.71	12	4
1:A:117:LEU:HD23	1:A:120:MET:SD	0.62	2.35	16	2
1:A:97:LEU:HD11	1:A:157:MET:CB	0.61	2.25	5	3
1:A:100:LEU:HD23	1:A:153:PHE:CZ	0.61	2.31	17	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:97:LEU:HD11	1:A:157:MET:CG	0.60	2.25	17	2
1:A:104:PHE:HB3	1:A:120:MET:HE2	0.60	1.71	16	2
1:A:117:LEU:HD11	1:A:148:ILE:CD1	0.60	2.25	16	4
1:A:112:ILE:HD13	1:A:120:MET:HE1	0.60	1.72	12	2
1:A:122:GLN:HA	1:A:126:GLU:HB2	0.60	1.74	4	5
1:A:95:GLU:HG2	1:A:96:GLU:N	0.60	2.09	9	4
1:A:117:LEU:HA	1:A:120:MET:SD	0.60	2.37	12	2
1:A:139:ASP:HB3	1:A:156:PHE:CD1	0.58	2.33	12	5
1:A:104:PHE:HB3	1:A:120:MET:HE3	0.58	1.75	3	3
1:A:107:ASN:HB2	1:A:116:GLU:CD	0.57	2.24	1	12
1:A:112:ILE:HD13	1:A:120:MET:CE	0.57	2.29	12	1
1:A:100:LEU:HD22	1:A:157:MET:HE2	0.57	1.76	5	2
1:A:137:MET:HE1	1:A:148:ILE:CG1	0.57	2.30	12	4
1:A:137:MET:HE2	1:A:148:ILE:CG1	0.57	2.29	8	5
1:A:121:LEU:HD13	1:A:124:THR:CG2	0.56	2.30	2	2
1:A:136:LEU:HB3	3:A:162:STL:H11	0.56	1.77	8	2
1:A:114:LEU:HG	1:A:137:MET:HE3	0.56	1.76	6	1
1:A:115:ASP:O	1:A:119:ILE:HD12	0.55	2.01	3	3
1:A:97:LEU:HD11	1:A:157:MET:HB2	0.55	1.78	15	1
1:A:106:LYS:HE3	1:A:119:ILE:HD13	0.55	1.79	8	1
1:A:128:ILE:HD12	1:A:132:ASP:HB2	0.55	1.79	4	1
1:A:118:LYS:HA	1:A:133:ILE:HD11	0.54	1.78	12	1
1:A:107:ASN:O	1:A:108:ALA:HB3	0.54	2.01	18	13
1:A:97:LEU:HD22	1:A:157:MET:SD	0.54	2.43	13	1
1:A:129:THR:HG22	1:A:132:ASP:OD2	0.54	2.02	2	3
1:A:97:LEU:HD12	1:A:154:LEU:HD13	0.53	1.80	15	1
1:A:97:LEU:CD2	1:A:157:MET:SD	0.53	2.96	18	1
1:A:100:LEU:HD23	1:A:153:PHE:HZ	0.53	1.61	17	3
1:A:140:GLY:HA2	1:A:156:PHE:HB2	0.53	1.79	15	6
1:A:112:ILE:HG21	3:A:162:STL:O1	0.53	2.02	6	1
1:A:104:PHE:HA	1:A:120:MET:CE	0.53	2.33	17	1
1:A:128:ILE:HD11	1:A:133:ILE:HD13	0.53	1.80	13	1
1:A:104:PHE:CA	1:A:120:MET:HE3	0.53	2.32	17	1
1:A:97:LEU:HD13	1:A:153:PHE:CE1	0.52	2.40	15	1
1:A:136:LEU:HD11	3:A:162:STL:H10	0.52	1.80	9	1
1:A:122:GLN:HG3	1:A:126:GLU:HB3	0.52	1.81	19	1
1:A:128:ILE:HB	1:A:132:ASP:CB	0.52	2.35	11	5
1:A:153:PHE:CE2	1:A:157:MET:HE2	0.52	2.39	19	1
1:A:136:LEU:HD23	1:A:156:PHE:HZ	0.51	1.64	3	2
1:A:137:MET:SD	1:A:148:ILE:CD1	0.51	2.95	3	1
1:A:126:GLU:O	1:A:127:THR:C	0.51	2.53	3	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:117:LEU:HD21	1:A:148:ILE:CD1	0.51	2.36	9	4
1:A:103:MET:HE3	1:A:103:MET:HA	0.51	1.83	5	1
1:A:114:LEU:HG	1:A:137:MET:HE2	0.51	1.81	18	1
1:A:97:LEU:HD21	1:A:157:MET:CG	0.51	2.36	9	1
1:A:130:GLU:HG2	1:A:131:ASP:N	0.51	2.21	17	1
1:A:139:ASP:HA	1:A:142:LYS:CE	0.50	2.37	2	1
1:A:133:ILE:O	1:A:136:LEU:HD23	0.50	2.07	6	1
1:A:97:LEU:HD13	1:A:157:MET:SD	0.50	2.47	13	1
1:A:114:LEU:HD21	1:A:137:MET:HG2	0.50	1.84	20	3
1:A:122:GLN:HA	1:A:126:GLU:CB	0.50	2.37	14	3
1:A:104:PHE:CG	1:A:120:MET:HG2	0.50	2.42	7	2
1:A:117:LEU:CD1	1:A:137:MET:HG2	0.50	2.37	16	1
1:A:114:LEU:HA	1:A:117:LEU:CD1	0.49	2.35	14	3
1:A:97:LEU:CD1	1:A:157:MET:HG3	0.49	2.37	18	1
1:A:136:LEU:HD23	1:A:136:LEU:N	0.49	2.22	2	1
1:A:137:MET:HE2	1:A:148:ILE:HG13	0.49	1.82	7	3
1:A:136:LEU:HD22	3:A:162:STL:H10	0.49	1.84	8	1
1:A:104:PHE:HB3	1:A:120:MET:HG3	0.49	1.83	8	1
1:A:114:LEU:HG	1:A:137:MET:SD	0.49	2.47	5	1
1:A:153:PHE:CZ	1:A:157:MET:HE2	0.49	2.42	2	1
1:A:111:TYR:CD1	1:A:111:TYR:N	0.48	2.81	10	11
1:A:111:TYR:N	1:A:111:TYR:CD1	0.48	2.82	6	2
1:A:97:LEU:HD11	1:A:157:MET:HG2	0.48	1.86	14	1
1:A:128:ILE:HG12	1:A:132:ASP:CB	0.48	2.38	16	2
1:A:137:MET:HG2	1:A:148:ILE:HD11	0.48	1.85	8	1
1:A:104:PHE:CB	1:A:120:MET:HE2	0.48	2.37	16	1
1:A:107:ASN:O	1:A:108:ALA:C	0.48	2.55	7	1
1:A:139:ASP:HB3	1:A:156:PHE:CD2	0.48	2.43	19	1
1:A:100:LEU:HD22	1:A:153:PHE:HZ	0.48	1.69	16	1
1:A:97:LEU:CD2	1:A:157:MET:HG3	0.47	2.39	20	1
1:A:97:LEU:HD22	1:A:157:MET:HG3	0.47	1.85	16	1
1:A:117:LEU:CD1	1:A:137:MET:CG	0.47	2.92	6	1
1:A:153:PHE:CE1	3:A:162:STL:H13	0.47	2.44	1	1
1:A:97:LEU:HD12	1:A:154:LEU:CD2	0.47	2.38	5	1
1:A:104:PHE:CD2	1:A:120:MET:SD	0.47	3.08	19	2
1:A:139:ASP:HA	1:A:142:LYS:HE2	0.47	1.87	3	1
1:A:104:PHE:HB3	1:A:120:MET:CE	0.47	2.38	16	2
1:A:95:GLU:CG	1:A:96:GLU:N	0.46	2.78	9	1
1:A:140:GLY:HA2	1:A:156:PHE:CG	0.46	2.45	8	1
1:A:104:PHE:CG	1:A:120:MET:HG3	0.46	2.45	9	1
1:A:122:GLN:HA	1:A:126:GLU:HB3	0.46	1.87	11	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:134:GLU:HB3	1:A:138:LYS:HE3	0.46	1.87	13	1
1:A:97:LEU:HD13	1:A:157:MET:HG3	0.46	1.88	18	1
1:A:100:LEU:O	1:A:104:PHE:HB2	0.46	2.11	19	8
1:A:121:LEU:HB3	1:A:126:GLU:HG2	0.45	1.88	15	1
1:A:101:PHE:CE2	1:A:112:ILE:HD12	0.45	2.46	16	1
1:A:115:ASP:C	1:A:119:ILE:HD12	0.45	2.35	18	1
1:A:117:LEU:CD1	1:A:137:MET:HG3	0.45	2.41	6	1
1:A:128:ILE:CD1	1:A:132:ASP:HB3	0.45	2.37	11	1
1:A:117:LEU:CD2	3:A:162:STL:H11	0.45	2.42	6	1
1:A:117:LEU:HD11	1:A:148:ILE:HD12	0.45	1.88	11	1
1:A:97:LEU:HD13	1:A:153:PHE:HE2	0.45	1.71	12	1
1:A:121:LEU:C	1:A:126:GLU:HB2	0.45	2.37	19	1
1:A:104:PHE:C	1:A:120:MET:HE3	0.44	2.36	7	1
1:A:128:ILE:HB	1:A:132:ASP:HB2	0.44	1.90	12	1
1:A:136:LEU:HD23	1:A:156:PHE:CZ	0.44	2.47	19	1
1:A:116:GLU:HA	1:A:119:ILE:HD12	0.44	1.89	10	2
1:A:104:PHE:HA	1:A:120:MET:HG2	0.44	1.89	4	1
1:A:139:ASP:HA	1:A:142:LYS:HD2	0.44	1.88	7	1
1:A:101:PHE:C	1:A:101:PHE:CD1	0.44	2.96	14	1
1:A:127:THR:HG23	1:A:127:THR:O	0.43	2.13	16	2
1:A:115:ASP:O	1:A:119:ILE:HG12	0.43	2.13	15	1
1:A:118:LYS:HG2	1:A:119:ILE:N	0.43	2.28	19	1
1:A:104:PHE:O	1:A:120:MET:HE3	0.43	2.13	13	1
1:A:102:ARG:HG2	1:A:103:MET:N	0.43	2.28	13	1
1:A:128:ILE:HG13	1:A:132:ASP:CB	0.43	2.44	3	1
1:A:135:GLU:HA	1:A:138:LYS:HD3	0.43	1.90	18	1
1:A:112:ILE:HD13	3:A:162:STL:O1	0.42	2.14	6	1
1:A:141:ASP:HB2	1:A:148:ILE:HG13	0.42	1.89	13	1
1:A:102:ARG:NH1	1:A:103:MET:HB2	0.42	2.30	4	1
1:A:99:ASP:O	1:A:103:MET:HB2	0.42	2.13	6	1
1:A:135:GLU:HA	1:A:138:LYS:HD2	0.42	1.91	1	1
1:A:122:GLN:N	1:A:126:GLU:HG2	0.42	2.29	3	1
1:A:104:PHE:HD2	1:A:120:MET:HE2	0.42	1.74	13	1
1:A:121:LEU:HD13	1:A:124:THR:HG22	0.42	1.91	2	1
1:A:140:GLY:O	1:A:152:GLU:HB3	0.42	2.15	6	3
1:A:121:LEU:HB3	1:A:126:GLU:HB2	0.42	1.91	20	1
1:A:106:LYS:CD	1:A:116:GLU:HA	0.42	2.45	8	1
1:A:100:LEU:HD22	1:A:157:MET:CE	0.42	2.44	17	1
1:A:114:LEU:HG	1:A:137:MET:CE	0.41	2.44	6	1
1:A:104:PHE:CD2	1:A:120:MET:HG2	0.41	2.50	11	1
1:A:136:LEU:HD13	1:A:156:PHE:HZ	0.41	1.74	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:117:LEU:HD13	1:A:137:MET:HG2	0.41	1.91	16	1
1:A:100:LEU:HG	1:A:104:PHE:CE2	0.41	2.49	8	1
1:A:128:ILE:N	1:A:128:ILE:HD13	0.41	2.30	20	1
1:A:139:ASP:HA	1:A:142:LYS:HE3	0.41	1.92	2	1
1:A:100:LEU:CD2	1:A:157:MET:HE2	0.41	2.46	15	1
1:A:104:PHE:CD2	1:A:120:MET:HE2	0.41	2.51	13	1
1:A:104:PHE:CE1	1:A:120:MET:HA	0.41	2.49	16	1
1:A:137:MET:HE2	1:A:148:ILE:CD1	0.41	2.45	7	1
1:A:155:GLU:HA	1:A:158:LYS:HE3	0.41	1.93	20	1
1:A:97:LEU:HD13	1:A:153:PHE:CE2	0.41	2.51	5	1
1:A:104:PHE:O	1:A:105:ASP:C	0.41	2.63	7	1
1:A:128:ILE:HB	1:A:132:ASP:CG	0.41	2.41	1	1
1:A:156:PHE:CD2	1:A:156:PHE:C	0.41	2.99	3	1
1:A:128:ILE:HD13	1:A:132:ASP:CB	0.41	2.42	1	1
1:A:118:LYS:HB3	1:A:133:ILE:CG2	0.41	2.45	18	1
1:A:134:GLU:HB3	1:A:138:LYS:NZ	0.41	2.31	3	1
1:A:121:LEU:HD13	1:A:124:THR:OG1	0.41	2.16	13	1
1:A:118:LYS:HB3	1:A:133:ILE:HG13	0.40	1.93	6	1
1:A:111:TYR:HB3	1:A:147:ARG:HB3	0.40	1.93	11	1
1:A:107:ASN:O	1:A:108:ALA:CB	0.40	2.69	18	1
1:A:100:LEU:HD13	1:A:157:MET:HE1	0.40	1.93	19	1
1:A:114:LEU:HD23	1:A:117:LEU:HD12	0.40	1.92	19	1
1:A:115:ASP:HA	1:A:118:LYS:HE2	0.40	1.92	7	1
1:A:107:ASN:CB	1:A:116:GLU:CD	0.40	2.94	15	1
1:A:106:LYS:HG3	1:A:116:GLU:HG2	0.40	1.93	3	1
1:A:157:MET:O	1:A:157:MET:SD	0.40	2.79	10	1
1:A:136:LEU:N	1:A:136:LEU:HD23	0.40	2.31	11	1
1:A:106:LYS:CG	1:A:116:GLU:HG2	0.40	2.46	3	1
1:A:115:ASP:HA	1:A:118:LYS:CE	0.40	2.47	1	1
1:A:117:LEU:HD13	1:A:137:MET:SD	0.40	2.54	1	1
1:A:155:GLU:HA	1:A:158:LYS:HD2	0.40	1.94	4	1
1:A:146:GLY:C	1:A:147:ARG:HD3	0.40	2.41	19	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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	65/72 (90%)	58±2 (90±3%)	5±1 (8±2%)	1±1 (2±1%)	8	49
All	All	1300/1440 (90%)	1169 (90%)	105 (8%)	26 (2%)	8	49

All 4 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	109	ASP	10
1	A	125	GLY	9
1	A	105	ASP	5
1	A	108	ALA	2

6.3.2 Protein sidechains ⓘ

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	59/64 (92%)	42±3 (72±5%)	17±3 (28±5%)	1	19
All	All	1180/1280 (92%)	846 (72%)	334 (28%)	1	19

All 44 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	158	LYS	16
1	A	100	LEU	16
1	A	121	LEU	16
1	A	97	LEU	15
1	A	155	GLU	14
1	A	130	GLU	14
1	A	94	GLU	13
1	A	95	GLU	13
1	A	106	LYS	13
1	A	136	LEU	13
1	A	135	GLU	12
1	A	103	MET	11
1	A	147	ARG	11
1	A	114	LEU	11

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Mol	Chain	Res	Type	Models (Total)
1	A	118	LYS	10
1	A	126	GLU	9
1	A	102	ARG	8
1	A	128	ILE	8
1	A	99	ASP	8
1	A	137	MET	8
1	A	142	LYS	8
1	A	96	GLU	7
1	A	122	GLN	7
1	A	157	MET	7
1	A	138	LYS	7
1	A	143	ASN	5
1	A	154	LEU	5
1	A	119	ILE	5
1	A	129	THR	5
1	A	139	ASP	4
1	A	132	ASP	4
1	A	144	ASN	4
1	A	109	ASP	3
1	A	115	ASP	3
1	A	104	PHE	3
1	A	113	ASP	3
1	A	152	GLU	2
1	A	120	MET	2
1	A	145	ASP	2
1	A	131	ASP	2
1	A	134	GLU	2
1	A	151	ASP	2
1	A	148	ILE	2
1	A	150	TYR	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 [i](#)

There are no oligosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are 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
3	STL	A	162	-	18,18,18	1.55±0.01	3±0 (16±2%)

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
3	STL	A	162	-	24,24,24	0.92±0.02	1±0 (4±0%)

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
3	STL	A	162	-	-	0±0,5,5,5	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
3	A	162	STL	C5-C7	3.04	1.38	1.47	9	20
3	A	162	STL	C9-C8	3.03	1.39	1.47	9	20
3	A	162	STL	C11-C10	2.25	1.42	1.38	7	17
3	A	162	STL	C6-C1	2.08	1.42	1.39	4	2

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
3	A	162	STL	C14-C9-C10	2.46	121.30	117.65	9	20

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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

The completeness of assignment taking into account all chemical shift lists is 0% for the well-defined parts and 0% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	9
Number of shifts mapped to atoms	9
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

7.1.3 Completeness of resonance assignments

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 880. 0 out of 7 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/329 (0%)	0/134 (0%)	0/130 (0%)	0/65 (0%)
Sidechain	0/493 (0%)	0/312 (0%)	0/166 (0%)	0/15 (0%)
Aromatic	0/58 (0%)	0/28 (0%)	0/30 (0%)	0/0 (—%)
Overall	0/880 (0%)	0/474 (0%)	0/326 (0%)	0/80 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 0%, i.e. 0 atoms were assigned a chemical shift out of a possible 960. 0 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	0/366 (0%)	0/150 (0%)	0/144 (0%)	0/72 (0%)
Sidechain	0/536 (0%)	0/340 (0%)	0/180 (0%)	0/16 (0%)
Aromatic	0/58 (0%)	0/28 (0%)	0/30 (0%)	0/0 (—%)
Overall	0/960 (0%)	0/518 (0%)	0/354 (0%)	0/88 (0%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

7.1.5 Random Coil Index (RCI) plots ⓘ

No *random coil index*(RCI) plot could be generated from the current chemical shift list. RCI is only applicable to proteins