



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 08:02 AM UTC

PDB ID : 2MSV / pdb_00002msv
BMRB ID : 25135
Title : Solution structure of the MLKL N-terminal domain
Authors : Su, L.; Rizo, J.; Quade, B.; Wang, H.; Sun, L.; Wang, X.
Deposited on : 2014-08-07

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
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

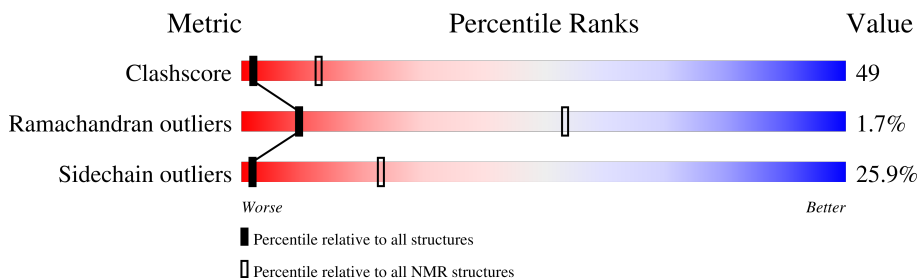
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 91%.

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	166	

2 Ensemble composition and analysis

This entry contains 20 models. Model 18 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:2-A:47, A:55-A:145 (137)	0.38	18

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 2 single-model clusters were found.

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

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2548 atoms, of which 1291 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Mixed lineage kinase domain-like protein.

Mol	Chain	Residues	Atoms					Trace	
			Total	C	H	N	O		S
1	A	154	2548	780	1291	236	232	9	0

There are 13 discrepancies between the modelled and reference sequences:

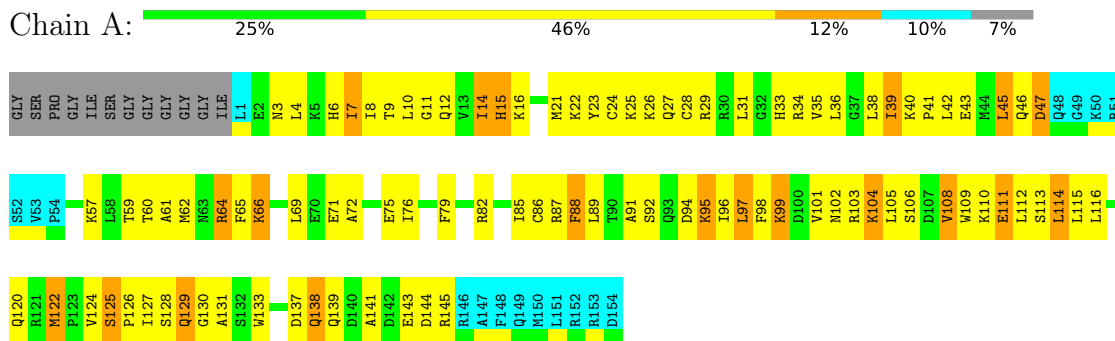
Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	GLY	-	expression tag	UNP Q8NB16
A	-10	SER	-	expression tag	UNP Q8NB16
A	-9	PRO	-	expression tag	UNP Q8NB16
A	-8	GLY	-	expression tag	UNP Q8NB16
A	-7	ILE	-	expression tag	UNP Q8NB16
A	-6	SER	-	expression tag	UNP Q8NB16
A	-5	GLY	-	expression tag	UNP Q8NB16
A	-4	GLY	-	expression tag	UNP Q8NB16
A	-3	GLY	-	expression tag	UNP Q8NB16
A	-2	GLY	-	expression tag	UNP Q8NB16
A	-1	GLY	-	expression tag	UNP Q8NB16
A	0	ILE	-	expression tag	UNP Q8NB16
A	1	LEU	MET	engineered mutation	UNP Q8NB16

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: Mixed lineage kinase domain-like protein

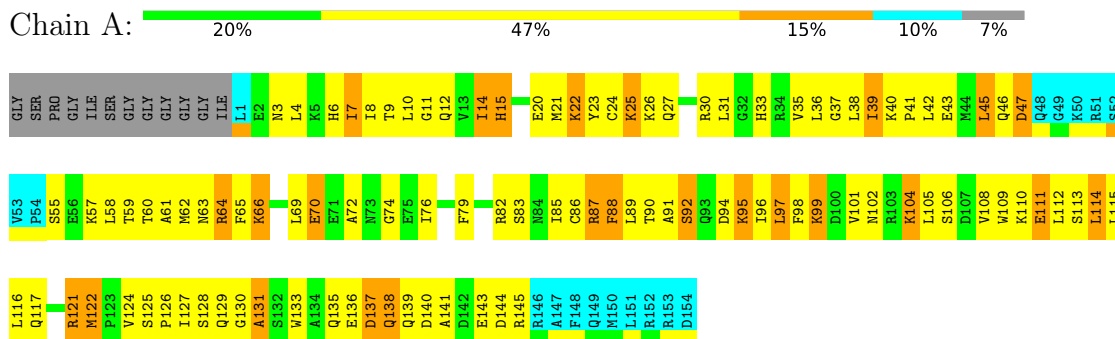


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

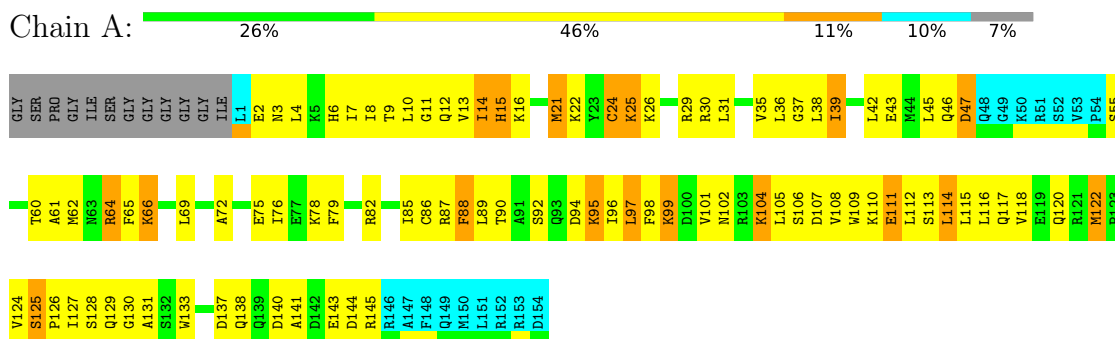
4.2.1 Score per residue for model 1

- Molecule 1: Mixed lineage kinase domain-like protein



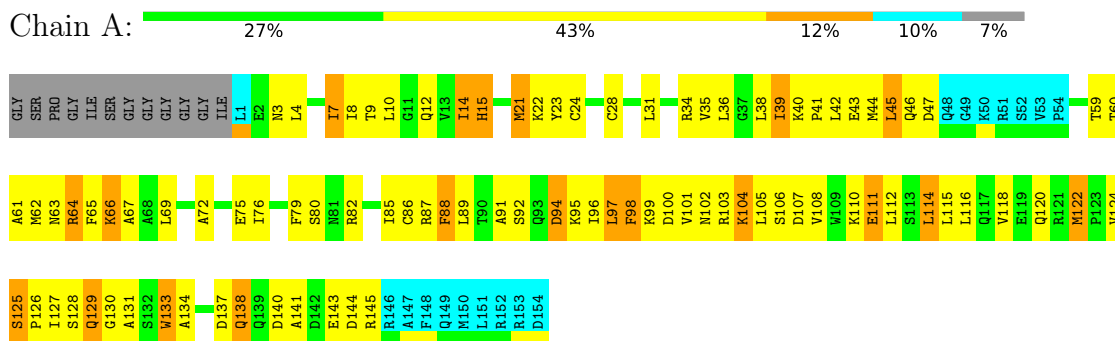
4.2.2 Score per residue for model 2

- Molecule 1: Mixed lineage kinase domain-like protein



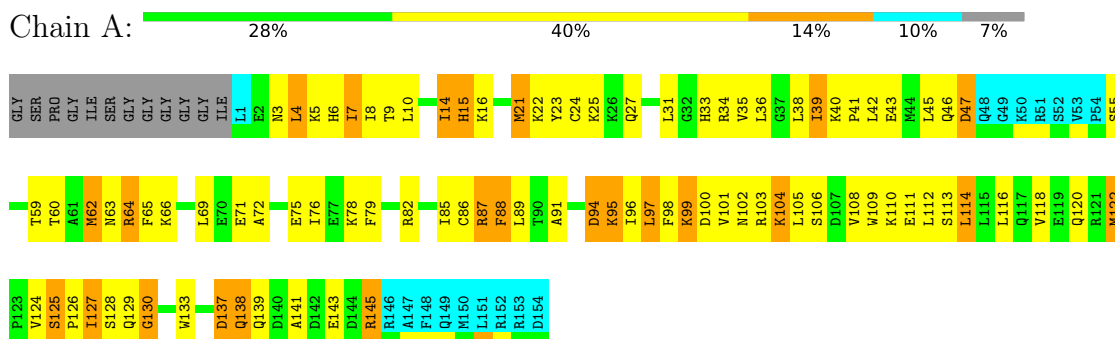
4.2.3 Score per residue for model 3

- Molecule 1: Mixed lineage kinase domain-like protein



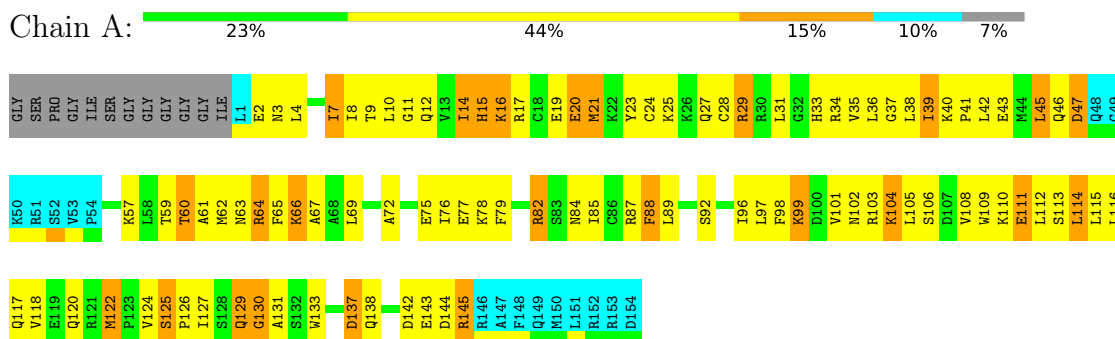
4.2.4 Score per residue for model 4

- Molecule 1: Mixed lineage kinase domain-like protein



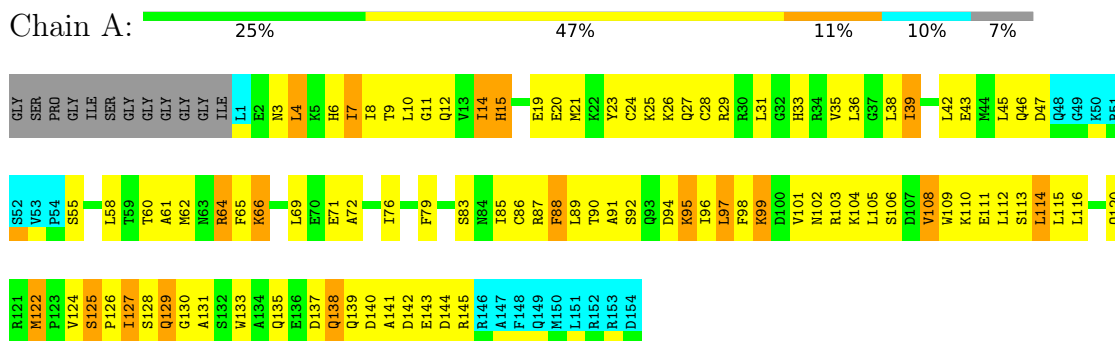
4.2.8 Score per residue for model 8

- Molecule 1: Mixed lineage kinase domain-like protein



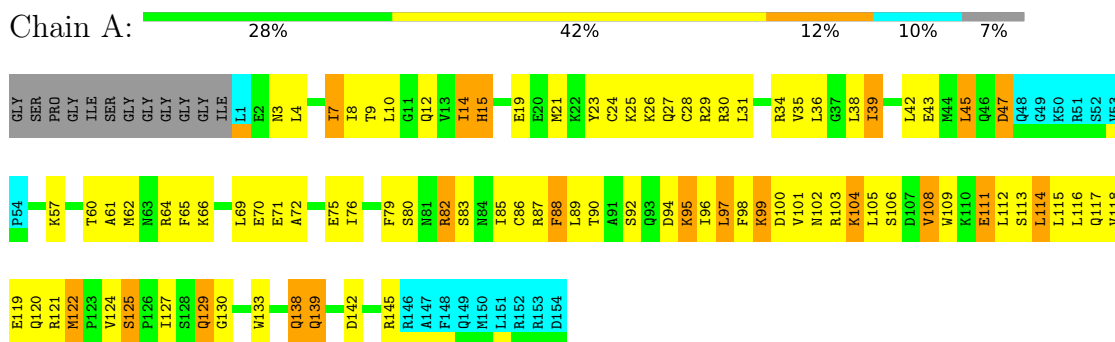
4.2.9 Score per residue for model 9

- Molecule 1: Mixed lineage kinase domain-like protein



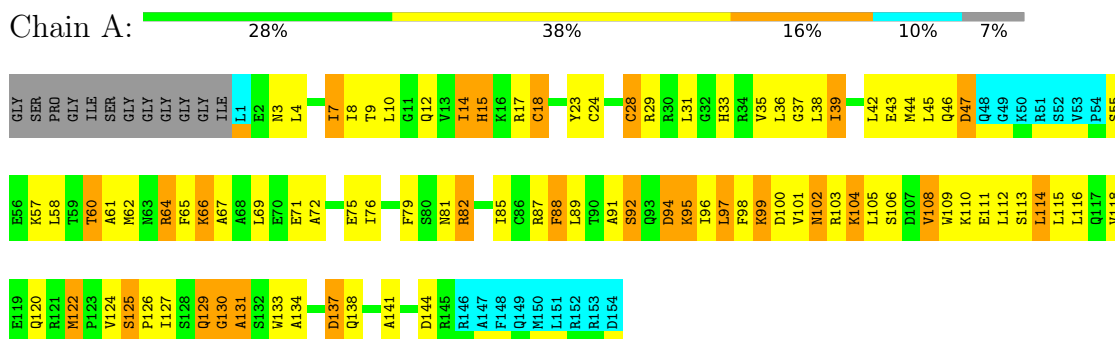
4.2.10 Score per residue for model 10

- Molecule 1: Mixed lineage kinase domain-like protein



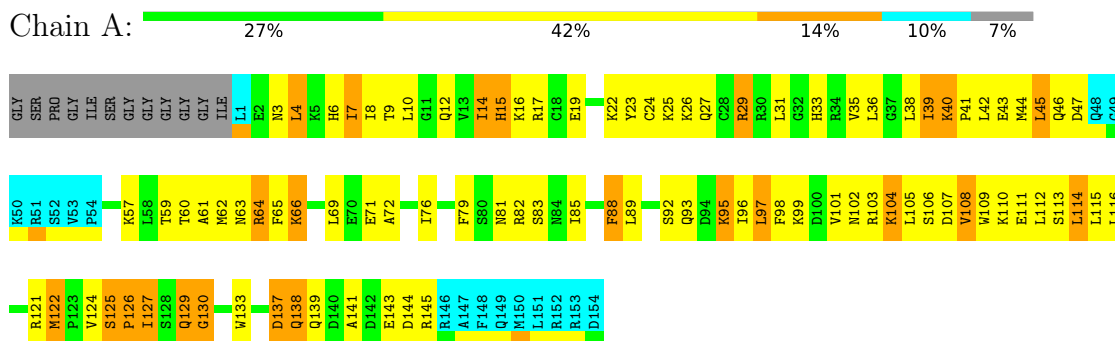
4.2.11 Score per residue for model 11

- Molecule 1: Mixed lineage kinase domain-like protein



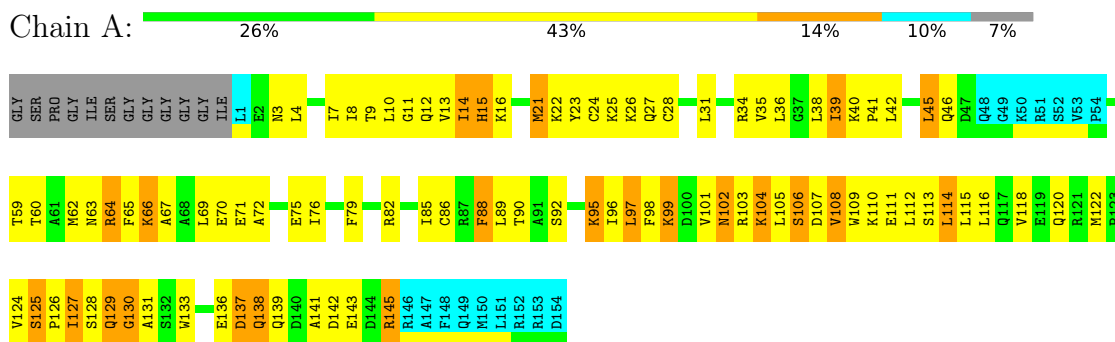
4.2.12 Score per residue for model 12

- Molecule 1: Mixed lineage kinase domain-like protein



4.2.13 Score per residue for model 13

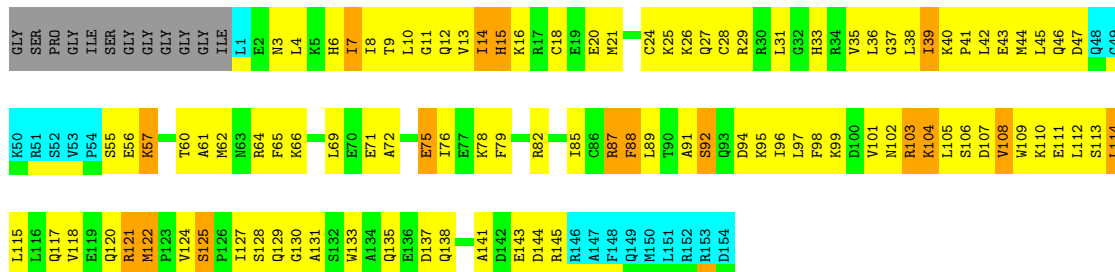
- Molecule 1: Mixed lineage kinase domain-like protein



4.2.14 Score per residue for model 14

- Molecule 1: Mixed lineage kinase domain-like protein

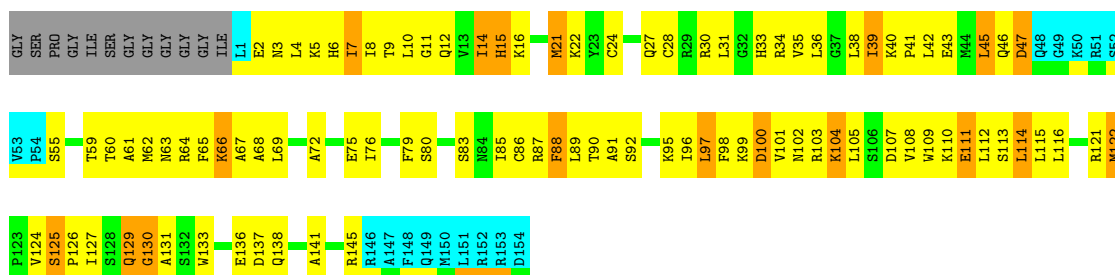
Chain A: 22% 51% 10% 10% 7%



4.2.15 Score per residue for model 15

- Molecule 1: Mixed lineage kinase domain-like protein

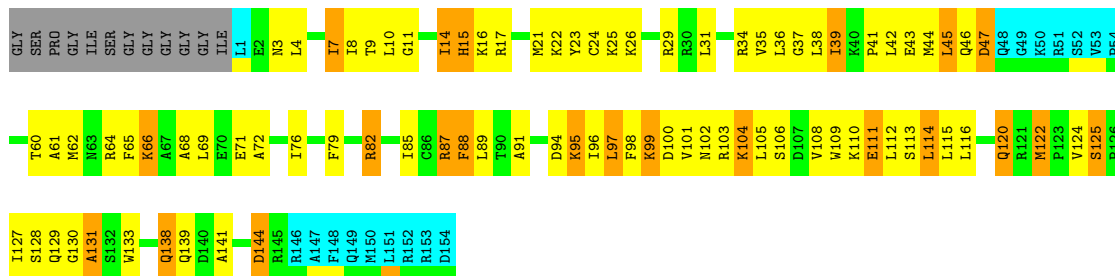
Chain A: 25% 47% 11% 10% 7%



4.2.16 Score per residue for model 16

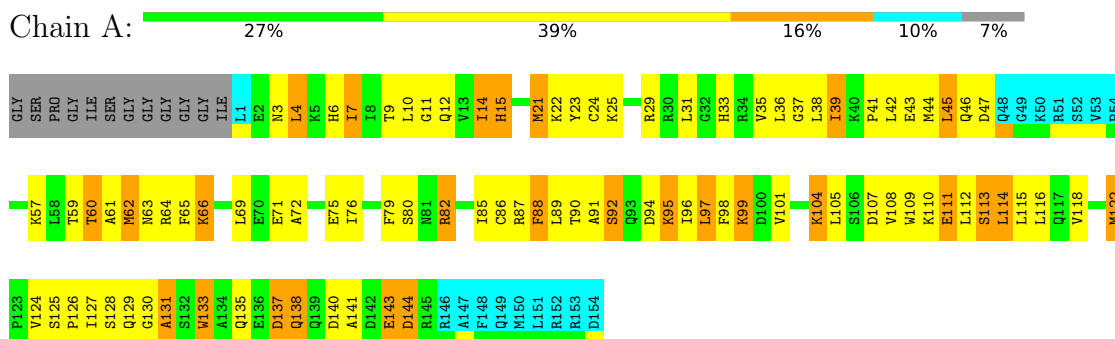
- Molecule 1: Mixed lineage kinase domain-like protein

Chain A: 31% 39% 13% 10% 7%



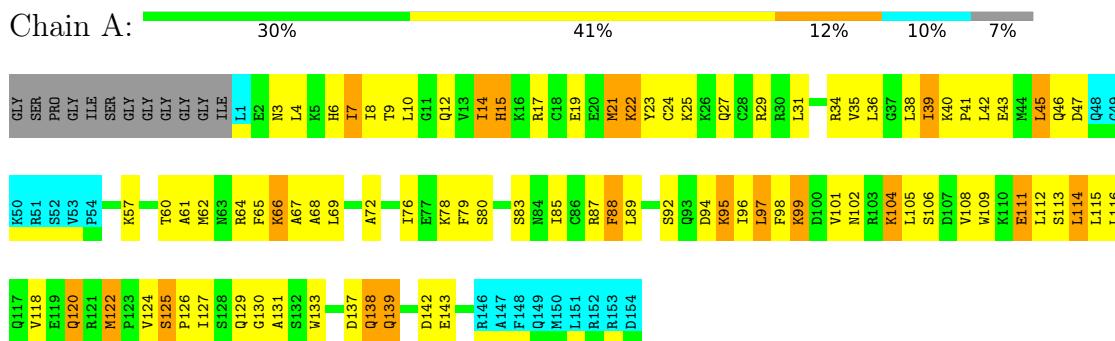
4.2.17 Score per residue for model 17

- Molecule 1: Mixed lineage kinase domain-like protein



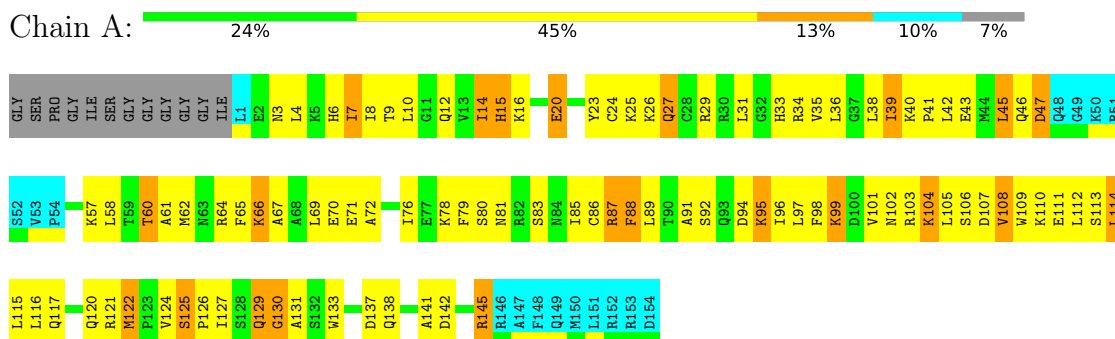
4.2.18 Score per residue for model 18 (medoid)

- Molecule 1: Mixed lineage kinase domain-like protein



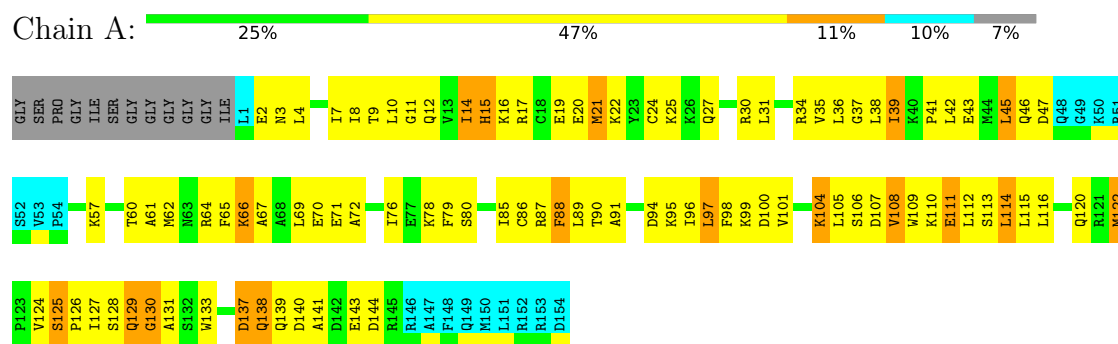
4.2.19 Score per residue for model 19

- Molecule 1: Mixed lineage kinase domain-like protein



4.2.20 Score per residue for model 20

- Molecule 1: Mixed lineage kinase domain-like protein



5 Refinement protocol and experimental data overview

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

Of the 5000 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
CNS	structure solution	
CNS	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	1994
Number of shifts mapped to atoms	1994
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

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	1113	1137	1134	111±9
All	All	22260	22740	22680	2217

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 49.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:LEU:HD21	1:A:72:ALA:HB1	1.08	1.25	6	20
1:A:72:ALA:HB2	1:A:101:VAL:HG11	1.04	1.27	9	20
1:A:7:ILE:HG23	1:A:69:LEU:HD11	0.95	1.36	13	15
1:A:38:LEU:HD23	1:A:129:GLN:HG3	0.93	1.39	13	9
1:A:114:LEU:HD13	1:A:115:LEU:N	0.90	1.82	12	16
1:A:7:ILE:HG21	1:A:65:PHE:CE2	0.87	2.05	15	20
1:A:137:ASP:OD1	1:A:138:GLN:N	0.86	2.08	3	1
1:A:31:LEU:HD21	1:A:72:ALA:CB	0.83	2.04	5	20
1:A:38:LEU:HD23	1:A:129:GLN:CG	0.83	2.03	13	4
1:A:122:MET:HE3	1:A:124:VAL:HG21	0.83	1.50	13	16
1:A:7:ILE:HG21	1:A:65:PHE:CD2	0.81	2.09	13	20
1:A:65:PHE:HA	1:A:108:VAL:HG11	0.81	1.50	18	20
1:A:3:ASN:O	1:A:7:ILE:HD12	0.80	1.75	8	20
1:A:71:GLU:CG	1:A:101:VAL:HG22	0.79	2.07	11	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:116:LEU:CB	1:A:122:MET:HE2	0.78	2.08	13	3
1:A:23:TYR:CD1	1:A:85:ILE:HG21	0.78	2.12	19	2
1:A:127:ILE:HG22	1:A:129:GLN:HG2	0.76	1.57	20	7
1:A:38:LEU:CD1	1:A:105:LEU:HD21	0.75	2.10	3	20
1:A:104:LYS:O	1:A:108:VAL:HG23	0.75	1.81	7	20
1:A:35:VAL:HG22	1:A:105:LEU:HD11	0.74	1.56	11	20
1:A:31:LEU:HD13	1:A:98:PHE:CD2	0.74	2.18	16	8
1:A:31:LEU:HD23	1:A:76:ILE:HD11	0.73	1.59	6	20
1:A:65:PHE:CD2	1:A:112:LEU:CD2	0.73	2.71	16	20
1:A:64:ARG:HG3	1:A:108:VAL:HG13	0.73	1.58	15	3
1:A:114:LEU:O	1:A:118:VAL:HG23	0.73	1.84	14	10
1:A:31:LEU:HD13	1:A:98:PHE:CE2	0.73	2.18	16	3
1:A:111:GLU:HA	1:A:114:LEU:HD12	0.73	1.61	15	16
1:A:4:LEU:HD13	1:A:46:GLN:HB3	0.72	1.61	14	14
1:A:45:LEU:HD22	1:A:46:GLN:N	0.72	1.99	13	1
1:A:72:ALA:CB	1:A:101:VAL:HG11	0.72	2.13	9	17
1:A:45:LEU:HD23	1:A:120:GLN:CD	0.72	2.09	14	11
1:A:39:ILE:HA	1:A:42:LEU:HD12	0.71	1.61	1	20
1:A:21:MET:HE3	1:A:28:CYS:SG	0.71	2.24	13	7
1:A:116:LEU:HD13	1:A:122:MET:HE2	0.71	1.62	16	16
1:A:79:PHE:CD2	1:A:97:LEU:HD13	0.71	2.21	5	5
1:A:15:HIS:CG	1:A:36:LEU:HD11	0.71	2.21	16	19
1:A:88:PHE:CE2	1:A:97:LEU:HG	0.71	2.20	17	15
1:A:65:PHE:CA	1:A:108:VAL:HG11	0.70	2.15	15	20
1:A:7:ILE:HD11	1:A:62:MET:O	0.70	1.86	16	20
1:A:61:ALA:HB2	1:A:115:LEU:HD12	0.70	1.62	10	15
1:A:40:LYS:O	1:A:44:MET:HE3	0.70	1.85	12	1
1:A:38:LEU:HD23	1:A:129:GLN:CD	0.69	2.12	7	8
1:A:87:ARG:O	1:A:91:ALA:HB3	0.69	1.88	5	12
1:A:88:PHE:CE2	1:A:89:LEU:HD23	0.68	2.24	18	20
1:A:86:CYS:O	1:A:90:THR:HG22	0.67	1.89	15	10
1:A:4:LEU:HD22	1:A:46:GLN:HG2	0.67	1.65	17	7
1:A:8:ILE:HD11	1:A:46:GLN:HG2	0.67	1.67	4	17
1:A:110:LYS:HD3	1:A:127:ILE:HD11	0.67	1.64	6	1
1:A:31:LEU:CD2	1:A:72:ALA:HB1	0.67	2.12	5	18
1:A:24:CYS:SG	1:A:97:LEU:HD21	0.67	2.30	11	13
1:A:88:PHE:CZ	1:A:97:LEU:HG	0.67	2.24	18	15
1:A:31:LEU:O	1:A:35:VAL:HG23	0.67	1.90	14	19
1:A:114:LEU:HD22	1:A:114:LEU:O	0.66	1.90	15	16
1:A:4:LEU:CD2	1:A:42:LEU:HD13	0.66	2.20	3	6
1:A:114:LEU:C	1:A:114:LEU:HD22	0.66	2.16	12	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:LEU:HD22	1:A:98:PHE:CD2	0.66	2.26	13	4
1:A:31:LEU:HD22	1:A:98:PHE:CG	0.66	2.26	13	8
1:A:4:LEU:HG	1:A:62:MET:HE3	0.65	1.67	18	14
1:A:96:ILE:HG23	1:A:141:ALA:HB2	0.65	1.68	4	9
1:A:4:LEU:HD21	1:A:42:LEU:HD22	0.65	1.68	11	2
1:A:127:ILE:HG22	1:A:129:GLN:CG	0.65	2.22	8	6
1:A:101:VAL:O	1:A:105:LEU:N	0.65	2.30	11	20
1:A:114:LEU:HD22	1:A:114:LEU:C	0.64	2.17	15	6
1:A:45:LEU:HD23	1:A:120:GLN:NE2	0.64	2.06	6	6
1:A:116:LEU:HB2	1:A:122:MET:HE2	0.64	1.66	13	1
1:A:105:LEU:HD23	1:A:105:LEU:O	0.64	1.93	7	18
1:A:23:TYR:CD2	1:A:85:ILE:HG21	0.64	2.28	17	5
1:A:111:GLU:HA	1:A:114:LEU:HD23	0.63	1.68	14	3
1:A:45:LEU:HD21	1:A:122:MET:HG2	0.63	1.70	14	16
1:A:24:CYS:SG	1:A:97:LEU:HD22	0.63	2.34	18	3
1:A:95:LYS:O	1:A:141:ALA:HB1	0.63	1.94	6	7
1:A:127:ILE:HG22	1:A:129:GLN:H	0.62	1.53	11	1
1:A:38:LEU:HD23	1:A:129:GLN:HE21	0.62	1.54	9	3
1:A:45:LEU:HD23	1:A:120:GLN:HG2	0.62	1.71	16	2
1:A:127:ILE:HD12	1:A:131:ALA:HB2	0.62	1.70	7	15
1:A:72:ALA:HB2	1:A:101:VAL:CG1	0.62	2.17	9	9
1:A:45:LEU:HD13	1:A:45:LEU:H	0.62	1.55	13	1
1:A:3:ASN:C	1:A:7:ILE:HD12	0.62	2.20	9	20
1:A:45:LEU:HD21	1:A:122:MET:CG	0.62	2.23	1	19
1:A:38:LEU:HD12	1:A:105:LEU:HD21	0.62	1.71	2	10
1:A:71:GLU:HG3	1:A:101:VAL:HG22	0.62	1.71	16	9
1:A:31:LEU:HD23	1:A:76:ILE:CD1	0.61	2.24	5	8
1:A:88:PHE:CE2	1:A:97:LEU:HD22	0.61	2.29	16	5
1:A:79:PHE:CD2	1:A:97:LEU:HD23	0.61	2.30	2	2
1:A:38:LEU:HD11	1:A:105:LEU:HD21	0.61	1.69	3	6
1:A:3:ASN:HB2	1:A:62:MET:HE2	0.61	1.72	14	17
1:A:127:ILE:CD1	1:A:131:ALA:HB2	0.61	2.25	19	13
1:A:109:TRP:CH2	1:A:122:MET:HE1	0.61	2.31	13	1
1:A:130:GLY:O	1:A:133:TRP:NE1	0.60	2.35	13	20
1:A:21:MET:HE1	1:A:79:PHE:C	0.60	2.21	15	10
1:A:71:GLU:HG2	1:A:101:VAL:HG22	0.60	1.74	11	7
1:A:41:PRO:HA	1:A:44:MET:HE3	0.59	1.74	17	3
1:A:127:ILE:HG21	1:A:131:ALA:HB2	0.59	1.71	13	1
1:A:7:ILE:HG23	1:A:69:LEU:CD1	0.59	2.21	13	4
1:A:79:PHE:HB3	1:A:85:ILE:HD11	0.59	1.75	18	20
1:A:105:LEU:C	1:A:105:LEU:HD23	0.59	2.23	17	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:LEU:O	1:A:46:GLN:N	0.59	2.36	13	4
1:A:45:LEU:HG	1:A:122:MET:CB	0.59	2.28	13	1
1:A:24:CYS:SG	1:A:85:ILE:HD12	0.59	2.37	13	5
1:A:13:VAL:HG22	1:A:16:LYS:HE2	0.59	1.75	13	3
1:A:14:ILE:HD11	1:A:69:LEU:O	0.58	1.99	14	19
1:A:110:LYS:HG2	1:A:127:ILE:HD11	0.58	1.75	4	6
1:A:88:PHE:CE2	1:A:89:LEU:CD2	0.58	2.87	11	20
1:A:105:LEU:HD23	1:A:105:LEU:C	0.58	2.23	7	9
1:A:96:ILE:HG21	1:A:137:ASP:HB3	0.57	1.75	20	10
1:A:25:LYS:O	1:A:29:ARG:N	0.57	2.33	19	10
1:A:96:ILE:HB	1:A:99:LYS:CB	0.57	2.29	15	20
1:A:88:PHE:CE2	1:A:97:LEU:CD2	0.57	2.87	20	5
1:A:96:ILE:HB	1:A:99:LYS:HB3	0.57	1.75	4	12
1:A:127:ILE:HD12	1:A:131:ALA:CB	0.57	2.29	18	10
1:A:35:VAL:CG2	1:A:105:LEU:HD11	0.57	2.29	11	6
1:A:116:LEU:HB3	1:A:122:MET:HE2	0.57	1.75	13	1
1:A:122:MET:HE3	1:A:124:VAL:CG2	0.57	2.29	11	15
1:A:113:SER:HB2	1:A:124:VAL:HG11	0.57	1.77	6	4
1:A:42:LEU:HD21	1:A:109:TRP:CH2	0.57	2.34	13	1
1:A:113:SER:OG	1:A:124:VAL:HG11	0.56	1.99	13	1
1:A:21:MET:HE2	1:A:76:ILE:O	0.56	2.01	2	7
1:A:125:SER:O	1:A:127:ILE:N	0.56	2.38	5	20
1:A:21:MET:HE1	1:A:79:PHE:CB	0.56	2.30	13	6
1:A:45:LEU:HG	1:A:122:MET:HB2	0.56	1.78	13	1
1:A:21:MET:HE1	1:A:79:PHE:O	0.55	2.01	15	3
1:A:130:GLY:O	1:A:133:TRP:CD1	0.55	2.60	12	19
1:A:27:GLN:CD	1:A:97:LEU:HD12	0.55	2.27	10	1
1:A:12:GLN:HE21	1:A:39:ILE:HD11	0.55	1.61	12	17
1:A:114:LEU:C	1:A:114:LEU:HD12	0.55	2.26	4	4
1:A:88:PHE:CD1	1:A:88:PHE:C	0.55	2.84	10	18
1:A:114:LEU:HD13	1:A:114:LEU:C	0.55	2.26	6	16
1:A:109:TRP:HH2	1:A:122:MET:HE1	0.54	1.62	13	1
1:A:4:LEU:HD23	1:A:42:LEU:HD13	0.54	1.77	3	5
1:A:79:PHE:O	1:A:85:ILE:HD11	0.54	2.03	19	2
1:A:109:TRP:CD1	1:A:127:ILE:HA	0.54	2.38	11	1
1:A:14:ILE:HD12	1:A:69:LEU:CD2	0.54	2.32	11	2
1:A:96:ILE:HD11	1:A:138:GLN:CB	0.54	2.32	8	17
1:A:110:LYS:O	1:A:114:LEU:HB3	0.54	2.03	17	16
1:A:96:ILE:HD11	1:A:138:GLN:HB3	0.53	1.79	15	7
1:A:31:LEU:CD2	1:A:76:ILE:HD11	0.53	2.32	5	16
1:A:4:LEU:HD13	1:A:46:GLN:CB	0.53	2.33	14	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:45:LEU:HD21	1:A:122:MET:SD	0.53	2.43	13	1
1:A:8:ILE:HA	1:A:39:ILE:HD12	0.53	1.80	13	12
1:A:40:LYS:HB2	1:A:41:PRO:HD3	0.53	1.81	18	7
1:A:24:CYS:CB	1:A:97:LEU:HD23	0.53	2.32	16	4
1:A:45:LEU:HD23	1:A:120:GLN:OE1	0.53	2.03	9	4
1:A:64:ARG:HB3	1:A:108:VAL:HG13	0.53	1.80	7	17
1:A:21:MET:HE1	1:A:79:PHE:HB3	0.53	1.80	8	2
1:A:8:ILE:HG22	1:A:12:GLN:NE2	0.52	2.18	6	1
1:A:79:PHE:CG	1:A:97:LEU:HD23	0.52	2.40	12	2
1:A:98:PHE:O	1:A:98:PHE:CD2	0.52	2.63	8	7
1:A:14:ILE:HD12	1:A:69:LEU:HD22	0.52	1.79	11	1
1:A:27:GLN:OE1	1:A:141:ALA:HB2	0.52	2.05	13	3
1:A:7:ILE:CG2	1:A:65:PHE:CE2	0.52	2.92	16	14
1:A:109:TRP:CD1	1:A:127:ILE:HD13	0.52	2.40	11	1
1:A:27:GLN:OE1	1:A:97:LEU:HD12	0.52	2.04	10	1
1:A:8:ILE:HD13	1:A:46:GLN:NE2	0.52	2.20	2	7
1:A:14:ILE:HD13	1:A:69:LEU:HD23	0.52	1.82	14	5
1:A:38:LEU:HD22	1:A:109:TRP:CG	0.52	2.40	11	1
1:A:45:LEU:H	1:A:45:LEU:CD1	0.52	2.17	13	1
1:A:38:LEU:CD2	1:A:129:GLN:HG3	0.51	2.35	3	7
1:A:98:PHE:CG	1:A:98:PHE:O	0.51	2.62	3	2
1:A:57:LYS:O	1:A:115:LEU:HD13	0.51	2.04	14	3
1:A:31:LEU:HD12	1:A:35:VAL:HG23	0.51	1.82	12	5
1:A:111:GLU:HA	1:A:114:LEU:CD2	0.51	2.36	14	4
1:A:38:LEU:HD21	1:A:133:TRP:HZ2	0.51	1.65	13	1
1:A:14:ILE:O	1:A:18:CYS:HB2	0.51	2.05	6	2
1:A:110:LYS:HE3	1:A:127:ILE:HD11	0.51	1.83	7	1
1:A:40:LYS:CB	1:A:41:PRO:HD3	0.51	2.36	13	5
1:A:79:PHE:CE2	1:A:97:LEU:HD23	0.50	2.41	2	1
1:A:12:GLN:NE2	1:A:39:ILE:HD11	0.50	2.21	12	13
1:A:37:GLY:C	1:A:129:GLN:HG2	0.50	2.32	17	7
1:A:38:LEU:HD11	1:A:133:TRP:CH2	0.50	2.42	16	3
1:A:27:GLN:O	1:A:98:PHE:CE1	0.49	2.65	15	9
1:A:38:LEU:CD1	1:A:105:LEU:CD2	0.49	2.90	18	13
1:A:106:SER:OG	1:A:133:TRP:CZ3	0.49	2.65	10	4
1:A:98:PHE:CE2	1:A:102:ASN:HB3	0.49	2.42	13	4
1:A:65:PHE:N	1:A:108:VAL:HG11	0.49	2.23	7	11
1:A:96:ILE:HG21	1:A:137:ASP:HB2	0.49	1.83	3	1
1:A:127:ILE:HG13	1:A:131:ALA:HB2	0.49	1.85	11	1
1:A:98:PHE:CE2	1:A:102:ASN:ND2	0.49	2.81	12	1
1:A:62:MET:CG	1:A:112:LEU:HD11	0.48	2.38	15	18

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:ILE:O	1:A:11:GLY:N	0.48	2.46	7	12
1:A:111:GLU:CA	1:A:114:LEU:HD12	0.48	2.38	6	15
1:A:42:LEU:O	1:A:46:GLN:HG3	0.48	2.08	13	1
1:A:98:PHE:CE1	1:A:137:ASP:OD2	0.48	2.66	20	6
1:A:31:LEU:HD22	1:A:98:PHE:CB	0.48	2.38	15	3
1:A:7:ILE:HG13	1:A:66:LYS:HA	0.48	1.84	15	13
1:A:102:ASN:OD1	1:A:103:ARG:N	0.48	2.47	6	8
1:A:7:ILE:HG13	1:A:66:LYS:CA	0.48	2.39	15	17
1:A:43:GLU:O	1:A:47:ASP:CB	0.48	2.62	3	19
1:A:109:TRP:CE2	1:A:113:SER:HB3	0.48	2.44	2	16
1:A:36:LEU:O	1:A:40:LYS:N	0.48	2.47	13	6
1:A:122:MET:CE	1:A:124:VAL:HG21	0.48	2.38	18	2
1:A:8:ILE:HG23	1:A:39:ILE:HG13	0.47	1.86	6	1
1:A:4:LEU:HD21	1:A:42:LEU:HD13	0.47	1.85	19	1
1:A:13:VAL:HG22	1:A:16:LYS:CE	0.47	2.40	2	1
1:A:4:LEU:HD13	1:A:46:GLN:HB2	0.47	1.85	13	1
1:A:94:ASP:O	1:A:95:LYS:HB2	0.47	2.09	9	2
1:A:21:MET:HE2	1:A:28:CYS:SG	0.47	2.50	14	2
1:A:66:LYS:HE2	1:A:67:ALA:HB2	0.47	1.87	20	8
1:A:45:LEU:HD21	1:A:122:MET:CB	0.47	2.39	6	9
1:A:102:ASN:O	1:A:106:SER:CB	0.47	2.63	12	7
1:A:100:ASP:O	1:A:104:LYS:HB3	0.47	2.10	4	5
1:A:134:ALA:O	1:A:137:ASP:OD1	0.47	2.33	3	1
1:A:61:ALA:HA	1:A:64:ARG:NE	0.47	2.25	16	1
1:A:108:VAL:O	1:A:112:LEU:N	0.47	2.48	16	12
1:A:23:TYR:CE1	1:A:82:ARG:CB	0.46	2.98	6	6
1:A:88:PHE:CD1	1:A:88:PHE:O	0.46	2.69	5	4
1:A:34:ARG:CD	1:A:133:TRP:CD1	0.46	2.98	19	4
1:A:88:PHE:O	1:A:92:SER:N	0.46	2.47	18	15
1:A:98:PHE:O	1:A:98:PHE:CG	0.46	2.68	8	6
1:A:35:VAL:HG22	1:A:105:LEU:CD1	0.46	2.36	11	1
1:A:31:LEU:O	1:A:31:LEU:HD12	0.46	2.11	13	2
1:A:27:GLN:NE2	1:A:97:LEU:HD12	0.46	2.26	18	1
1:A:9:THR:CG2	1:A:10:LEU:N	0.46	2.78	3	20
1:A:23:TYR:CE2	1:A:82:ARG:CB	0.46	2.98	11	1
1:A:18:CYS:HB3	1:A:76:ILE:HD13	0.46	1.88	14	1
1:A:140:ASP:O	1:A:144:ASP:HB2	0.46	2.11	7	2
1:A:31:LEU:HB2	1:A:98:PHE:CD2	0.46	2.46	3	1
1:A:14:ILE:CD1	1:A:72:ALA:HB3	0.46	2.41	6	1
1:A:79:PHE:CD2	1:A:97:LEU:CD1	0.46	2.99	20	3
1:A:122:MET:HG3	1:A:122:MET:O	0.46	2.11	19	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:31:LEU:HD23	1:A:76:ILE:CG1	0.46	2.40	5	1
1:A:110:LYS:CG	1:A:127:ILE:HD11	0.46	2.41	11	2
1:A:38:LEU:HD21	1:A:133:TRP:CZ2	0.46	2.45	13	1
1:A:64:ARG:O	1:A:68:ALA:HB2	0.46	2.11	18	2
1:A:61:ALA:O	1:A:64:ARG:HG2	0.46	2.11	18	1
1:A:4:LEU:CG	1:A:62:MET:HE1	0.45	2.41	4	1
1:A:109:TRP:CD1	1:A:127:ILE:HG23	0.45	2.46	9	1
1:A:140:ASP:O	1:A:144:ASP:CB	0.45	2.64	1	5
1:A:31:LEU:HD21	1:A:72:ALA:CA	0.45	2.42	5	2
1:A:98:PHE:CZ	1:A:137:ASP:OD1	0.45	2.70	12	8
1:A:106:SER:HB2	1:A:133:TRP:CZ3	0.45	2.46	3	6
1:A:31:LEU:HB2	1:A:98:PHE:CE2	0.45	2.46	12	2
1:A:114:LEU:C	1:A:114:LEU:CD2	0.45	2.87	3	14
1:A:61:ALA:CB	1:A:112:LEU:HD13	0.45	2.42	15	9
1:A:117:GLN:HB3	1:A:124:VAL:HG23	0.45	1.89	8	1
1:A:8:ILE:HD11	1:A:46:GLN:CD	0.45	2.36	13	1
1:A:28:CYS:SG	1:A:29:ARG:N	0.45	2.89	11	1
1:A:27:GLN:HE22	1:A:141:ALA:HB2	0.45	1.70	12	1
1:A:117:GLN:NE2	1:A:124:VAL:HB	0.45	2.27	8	2
1:A:116:LEU:CD2	1:A:120:GLN:NE2	0.45	2.80	7	3
1:A:88:PHE:CE2	1:A:89:LEU:HD21	0.45	2.47	20	1
1:A:138:GLN:HG3	1:A:139:GLN:N	0.45	2.26	1	10
1:A:98:PHE:CZ	1:A:137:ASP:OD2	0.45	2.70	5	5
1:A:35:VAL:HA	1:A:38:LEU:HD12	0.45	1.88	11	1
1:A:127:ILE:CG2	1:A:129:GLN:OE1	0.45	2.65	18	1
1:A:94:ASP:O	1:A:95:LYS:CB	0.45	2.65	20	8
1:A:98:PHE:CD2	1:A:98:PHE:O	0.45	2.69	12	4
1:A:68:ALA:CB	1:A:108:VAL:HG21	0.45	2.41	16	1
1:A:110:LYS:HE2	1:A:127:ILE:HD11	0.44	1.87	14	1
1:A:117:GLN:O	1:A:121:ARG:HA	0.44	2.12	1	5
1:A:65:PHE:CD2	1:A:112:LEU:HD23	0.44	2.47	13	12
1:A:106:SER:HB3	1:A:133:TRP:CZ3	0.44	2.46	11	4
1:A:98:PHE:CE1	1:A:137:ASP:OD1	0.44	2.71	8	5
1:A:57:LYS:C	1:A:115:LEU:HD13	0.44	2.38	14	5
1:A:71:GLU:HG2	1:A:104:LYS:NZ	0.44	2.27	19	1
1:A:23:TYR:CZ	1:A:82:ARG:CB	0.44	3.00	16	1
1:A:79:PHE:CE2	1:A:97:LEU:HA	0.44	2.47	19	1
1:A:40:LYS:CB	1:A:41:PRO:CD	0.44	2.95	15	5
1:A:96:ILE:O	1:A:97:LEU:C	0.44	2.60	5	2
1:A:71:GLU:CB	1:A:101:VAL:HG22	0.44	2.43	7	1
1:A:21:MET:HG3	1:A:76:ILE:HG23	0.44	1.88	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:56:GLU:O	1:A:59:THR:HG22	0.44	2.12	7	1
1:A:98:PHE:CE2	1:A:137:ASP:OD1	0.44	2.71	1	1
1:A:96:ILE:HG12	1:A:141:ALA:CB	0.44	2.43	6	7
1:A:87:ARG:O	1:A:91:ALA:CB	0.44	2.66	9	3
1:A:116:LEU:CD1	1:A:122:MET:HE2	0.44	2.42	11	2
1:A:124:VAL:HG12	1:A:125:SER:N	0.44	2.28	4	12
1:A:38:LEU:HD22	1:A:109:TRP:CB	0.44	2.43	11	1
1:A:36:LEU:HD23	1:A:39:ILE:HD13	0.44	1.90	16	1
1:A:59:THR:O	1:A:63:ASN:N	0.44	2.50	4	10
1:A:98:PHE:CD2	1:A:102:ASN:OD1	0.44	2.71	1	2
1:A:102:ASN:OD1	1:A:134:ALA:HB2	0.44	2.12	11	1
1:A:75:GLU:O	1:A:79:PHE:CD2	0.43	2.71	4	7
1:A:16:LYS:O	1:A:20:GLU:CG	0.43	2.66	8	3
1:A:98:PHE:CZ	1:A:137:ASP:CG	0.43	2.96	9	2
1:A:4:LEU:O	1:A:8:ILE:HG13	0.43	2.13	10	11
1:A:109:TRP:CZ2	1:A:113:SER:HB2	0.43	2.48	17	4
1:A:101:VAL:C	1:A:103:ARG:N	0.43	2.76	9	5
1:A:30:ARG:O	1:A:34:ARG:HG2	0.43	2.13	15	1
1:A:57:LYS:O	1:A:60:THR:HG22	0.43	2.14	17	5
1:A:109:TRP:CE2	1:A:113:SER:CB	0.43	3.01	8	3
1:A:96:ILE:HB	1:A:99:LYS:HB2	0.43	1.90	14	2
1:A:117:GLN:HG3	1:A:124:VAL:HG23	0.43	1.90	19	2
1:A:23:TYR:HD2	1:A:85:ILE:HG21	0.43	1.67	17	4
1:A:122:MET:SD	1:A:124:VAL:HG22	0.43	2.53	12	1
1:A:23:TYR:CE1	1:A:82:ARG:HB3	0.43	2.49	4	7
1:A:64:ARG:O	1:A:68:ALA:CB	0.43	2.67	15	2
1:A:25:LYS:O	1:A:26:LYS:C	0.43	2.61	19	5
1:A:27:GLN:CG	1:A:140:ASP:CB	0.43	2.97	7	1
1:A:114:LEU:HD13	1:A:115:LEU:H	0.43	1.70	13	1
1:A:38:LEU:CD2	1:A:129:GLN:OE1	0.42	2.67	18	1
1:A:105:LEU:C	1:A:105:LEU:CD2	0.42	2.93	17	3
1:A:88:PHE:CZ	1:A:97:LEU:N	0.42	2.87	15	1
1:A:37:GLY:O	1:A:41:PRO:CD	0.42	2.67	7	2
1:A:98:PHE:CE1	1:A:137:ASP:CG	0.42	2.97	14	2
1:A:122:MET:HE3	1:A:124:VAL:HG22	0.42	1.92	17	1
1:A:98:PHE:CE2	1:A:137:ASP:OD2	0.42	2.72	1	4
1:A:102:ASN:OD1	1:A:102:ASN:C	0.42	2.62	10	2
1:A:38:LEU:HD11	1:A:105:LEU:CD2	0.42	2.44	5	4
1:A:127:ILE:CD1	1:A:131:ALA:CB	0.42	2.98	5	2
1:A:95:LYS:O	1:A:96:ILE:CG1	0.42	2.67	20	2
1:A:8:ILE:HG23	1:A:39:ILE:HD12	0.42	1.90	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:122:MET:CE	1:A:124:VAL:CG2	0.42	2.98	20	4
1:A:31:LEU:HB2	1:A:98:PHE:CZ	0.42	2.49	5	1
1:A:35:VAL:O	1:A:39:ILE:HG23	0.42	2.14	6	2
1:A:45:LEU:HD11	1:A:122:MET:SD	0.42	2.55	14	1
1:A:122:MET:O	1:A:122:MET:HG3	0.42	2.14	3	1
1:A:134:ALA:HA	1:A:137:ASP:OD2	0.42	2.14	3	1
1:A:70:GLU:O	1:A:74:GLY:N	0.42	2.50	1	1
1:A:23:TYR:O	1:A:24:CYS:C	0.42	2.63	8	3
1:A:27:GLN:NE2	1:A:97:LEU:CD1	0.42	2.83	14	3
1:A:100:ASP:O	1:A:104:LYS:HG3	0.42	2.15	10	1
1:A:109:TRP:CE2	1:A:113:SER:HB2	0.42	2.50	18	1
1:A:95:LYS:C	1:A:96:ILE:CG1	0.41	2.93	6	8
1:A:27:GLN:O	1:A:98:PHE:CZ	0.41	2.73	7	1
1:A:31:LEU:O	1:A:35:VAL:CG2	0.41	2.68	9	2
1:A:38:LEU:HD23	1:A:129:GLN:OE1	0.41	2.15	18	1
1:A:127:ILE:HG23	1:A:129:GLN:OE1	0.41	2.15	18	1
1:A:23:TYR:CZ	1:A:82:ARG:HB2	0.41	2.50	12	1
1:A:140:ASP:O	1:A:144:ASP:N	0.41	2.54	3	3
1:A:8:ILE:HD11	1:A:46:GLN:CG	0.41	2.41	4	2
1:A:134:ALA:O	1:A:138:GLN:HG3	0.41	2.15	5	1
1:A:24:CYS:SG	1:A:97:LEU:HD11	0.41	2.55	6	1
1:A:38:LEU:HA	1:A:129:GLN:NE2	0.41	2.30	18	1
1:A:127:ILE:O	1:A:129:GLN:N	0.41	2.52	10	1
1:A:116:LEU:HD22	1:A:120:GLN:HG3	0.41	1.93	11	1
1:A:38:LEU:HD23	1:A:129:GLN:NE2	0.41	2.29	7	2
1:A:88:PHE:CZ	1:A:89:LEU:HD23	0.41	2.51	10	1
1:A:69:LEU:O	1:A:72:ALA:N	0.41	2.53	9	1
1:A:125:SER:CB	1:A:126:PRO:CD	0.41	2.99	9	1
1:A:104:LYS:HG2	1:A:105:LEU:N	0.41	2.29	16	2
1:A:122:MET:CE	1:A:124:VAL:HG22	0.41	2.45	17	1
1:A:101:VAL:O	1:A:102:ASN:C	0.41	2.64	3	1
1:A:127:ILE:CG2	1:A:129:GLN:HG2	0.41	2.45	3	1
1:A:129:GLN:N	1:A:129:GLN:OE1	0.41	2.53	13	1
1:A:125:SER:CB	1:A:126:PRO:HD2	0.41	2.46	3	3
1:A:46:GLN:CD	1:A:47:ASP:N	0.41	2.78	4	2
1:A:34:ARG:HD3	1:A:133:TRP:CD1	0.41	2.50	8	1
1:A:37:GLY:O	1:A:41:PRO:HD3	0.41	2.16	20	2
1:A:96:ILE:CD1	1:A:138:GLN:HB3	0.41	2.46	19	3
1:A:14:ILE:CD1	1:A:69:LEU:HD23	0.41	2.45	11	1
1:A:102:ASN:ND2	1:A:133:TRP:CB	0.41	2.83	12	1
1:A:34:ARG:NE	1:A:133:TRP:CD1	0.41	2.89	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:VAL:HA	1:A:16:LYS:CD	0.41	2.46	6	1
1:A:96:ILE:CD1	1:A:138:GLN:CB	0.41	2.98	8	2
1:A:11:GLY:O	1:A:36:LEU:CD2	0.41	2.69	9	2
1:A:79:PHE:CE1	1:A:88:PHE:CD2	0.41	3.09	19	1
1:A:101:VAL:HA	1:A:104:LYS:HD2	0.41	1.93	1	1
1:A:111:GLU:O	1:A:115:LEU:HG	0.41	2.16	15	1
1:A:14:ILE:CD1	1:A:69:LEU:CD2	0.40	2.98	11	1
1:A:88:PHE:CD2	1:A:89:LEU:HD23	0.40	2.51	11	1
1:A:22:LYS:O	1:A:23:TYR:CD1	0.40	2.75	18	2
1:A:20:GLU:O	1:A:21:MET:C	0.40	2.64	8	1
1:A:34:ARG:HG2	1:A:133:TRP:CD1	0.40	2.51	20	2
1:A:37:GLY:C	1:A:129:GLN:CG	0.40	2.94	11	1
1:A:8:ILE:CD1	1:A:46:GLN:NE2	0.40	2.84	15	2
1:A:66:LYS:HA	1:A:69:LEU:HD12	0.40	1.92	16	1
1:A:34:ARG:HD3	1:A:133:TRP:CG	0.40	2.51	5	1
1:A:114:LEU:CD1	1:A:115:LEU:HG	0.40	2.46	8	1
1:A:127:ILE:HD13	1:A:131:ALA:HB2	0.40	1.93	5	1
1:A:109:TRP:CD1	1:A:129:GLN:OE1	0.40	2.75	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	137/166 (83%)	120±2 (88±1%)	15±2 (11±2%)	2±1 (2±1%)	9	53
All	All	2740/3320 (83%)	2398 (88%)	295 (11%)	47 (2%)	9	53

All 7 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	126	PRO	14
1	A	97	LEU	12
1	A	130	GLY	9
1	A	131	ALA	6

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Mol	Chain	Res	Type	Models (Total)
1	A	127	ILE	4
1	A	24	CYS	1
1	A	47	ASP	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	124/144 (86%)	92±3 (74±2%)	32±3 (26±2%)	2	23
All	All	2480/2880 (86%)	1838 (74%)	642 (26%)	2	23

All 83 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	14	ILE	20
1	A	15	HIS	20
1	A	39	ILE	20
1	A	60	THR	20
1	A	66	LYS	20
1	A	88	PHE	20
1	A	114	LEU	20
1	A	104	LYS	19
1	A	122	MET	19
1	A	7	ILE	17
1	A	125	SER	17
1	A	95	LYS	16
1	A	138	GLN	16
1	A	6	HIS	13
1	A	45	LEU	13
1	A	99	LYS	13
1	A	22	LYS	12
1	A	33	HIS	12
1	A	47	ASP	12
1	A	128	SER	12
1	A	21	MET	11
1	A	64	ARG	11

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Mol	Chain	Res	Type	Models (Total)
1	A	129	GLN	11
1	A	55	SER	10
1	A	87	ARG	10
1	A	111	GLU	10
1	A	137	ASP	10
1	A	107	ASP	10
1	A	108	VAL	10
1	A	94	ASP	9
1	A	145	ARG	9
1	A	78	LYS	9
1	A	82	ARG	9
1	A	80	SER	9
1	A	92	SER	8
1	A	20	GLU	7
1	A	83	SER	7
1	A	16	LYS	7
1	A	19	GLU	7
1	A	25	LYS	6
1	A	26	LYS	6
1	A	17	ARG	6
1	A	142	ASP	6
1	A	70	GLU	5
1	A	121	ARG	5
1	A	135	GLN	5
1	A	75	GLU	5
1	A	102	ASN	5
1	A	71	GLU	5
1	A	97	LEU	5
1	A	144	ASP	5
1	A	103	ARG	5
1	A	30	ARG	4
1	A	57	LYS	4
1	A	2	GLU	4
1	A	34	ARG	4
1	A	4	LEU	4
1	A	81	ASN	4
1	A	29	ARG	4
1	A	120	GLN	4
1	A	136	GLU	3
1	A	86	CYS	3
1	A	100	ASP	3
1	A	139	GLN	3

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Mol	Chain	Res	Type	Models (Total)
1	A	133	TRP	2
1	A	62	MET	2
1	A	18	CYS	2
1	A	27	GLN	2
1	A	143	GLU	2
1	A	98	PHE	1
1	A	5	LYS	1
1	A	43	GLU	1
1	A	132	SER	1
1	A	124	VAL	1
1	A	77	GLU	1
1	A	84	ASN	1
1	A	119	GLU	1
1	A	28	CYS	1
1	A	40	LYS	1
1	A	93	GLN	1
1	A	106	SER	1
1	A	56	GLU	1
1	A	113	SER	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](#)

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

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 91% for the well-defined parts and 90% 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 [i](#)

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	1994
Number of shifts mapped to atoms	1994
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	153	-0.47 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	147	0.12 ± 0.07	None needed (< 0.5 ppm)
$^{13}\text{C}'$	145	-0.39 ± 0.08	None needed (< 0.5 ppm)
^{15}N	149	0.18 ± 0.26	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments [i](#)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 91%, i.e. 1774 atoms were assigned a chemical shift out of a possible 1959. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	673/684 (98%)	274/276 (99%)	266/274 (97%)	133/134 (99%)
Sidechain	1021/1178 (87%)	694/756 (92%)	311/363 (86%)	16/59 (27%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	80/97 (82%)	40/48 (83%)	38/41 (93%)	2/8 (25%)
Overall	1774/1959 (91%)	1008/1080 (93%)	615/678 (91%)	151/201 (75%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 1994 atoms were assigned a chemical shift out of a possible 2227. 0 out of 25 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	755/768 (98%)	308/310 (99%)	298/308 (97%)	149/150 (99%)
Sidechain	1153/1352 (85%)	783/867 (90%)	352/411 (86%)	18/74 (24%)
Aromatic	86/107 (80%)	44/53 (83%)	40/46 (87%)	2/8 (25%)
Overall	1994/2227 (90%)	1135/1230 (92%)	690/765 (90%)	169/232 (73%)

7.1.4 Statistically unusual chemical shifts [i](#)

The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	34	ARG	HD3	0.27	1.81 – 4.39	-11.0
1	A	113	SER	HB3	2.48	2.49 – 5.20	-5.0

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:

