



Full wwPDB NMR Structure Validation Report ⓘ

Apr 28, 2019 – 09:34 AM EDT

PDB ID : 5LXK
Title : NMR structure of the C-terminal domain of the Bacteriophage T5 decoration protein pb10.
Authors : Vernhes, E.; Gilquin, B.; Cuniasse, P.; Boulanger, P.; Zinn-Justin, S.
Deposited on : 2016-09-22

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

Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20171227.v01 (using entries in the PDB archive December 27th 2017)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20031633
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20031633

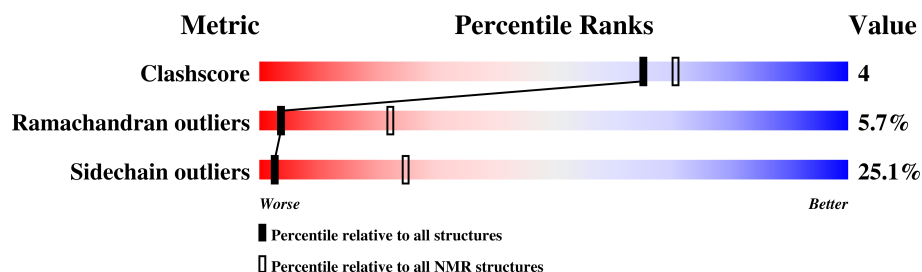
1 Overall quality at a glance

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	136327	12091
Ramachandran outliers	132723	10835
Sidechain outliers	132532	10811

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	101	

2 Ensemble composition and analysis

This entry contains 20 models. Model 7 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:79-A:156 (78)	0.29	7

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. No single-model clusters were found.

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

3 Entry composition

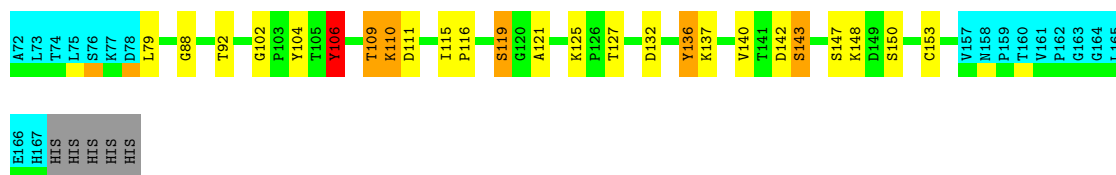
There is only 1 type of molecule in this entry. The entry contains 1334 atoms, of which 659 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Decoration protein.

Mol	Chain	Residues	Atoms						Trace
1	A	96	Total	C	H	N	O	S	0
			1334	417	659	107	149	2	

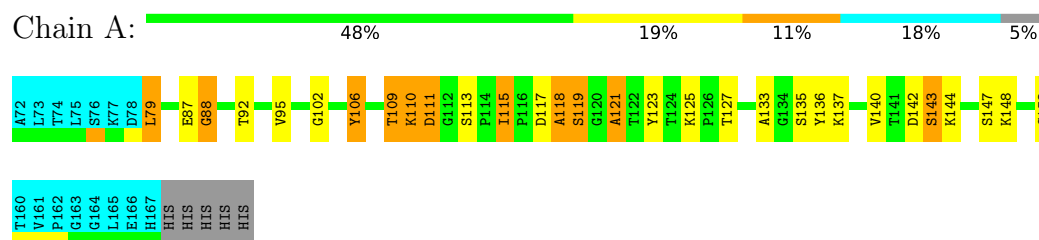
There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	72	ALA	-	expression tag	UNP Q6QGD6
A	165	LEU	-	expression tag	UNP Q6QGD6
A	166	GLU	-	expression tag	UNP Q6QGD6
A	167	HIS	-	expression tag	UNP Q6QGD6
A	168	HIS	-	expression tag	UNP Q6QGD6
A	169	HIS	-	expression tag	UNP Q6QGD6
A	170	HIS	-	expression tag	UNP Q6QGD6
A	171	HIS	-	expression tag	UNP Q6QGD6
A	172	HIS	-	expression tag	UNP Q6QGD6



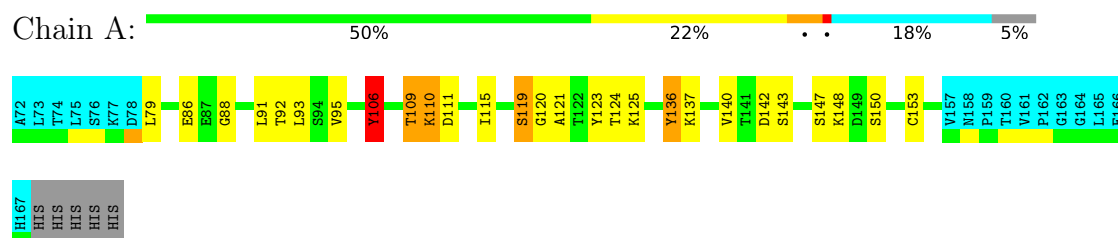
4.2.3 Score per residue for model 3

- Molecule 1: Decoration protein



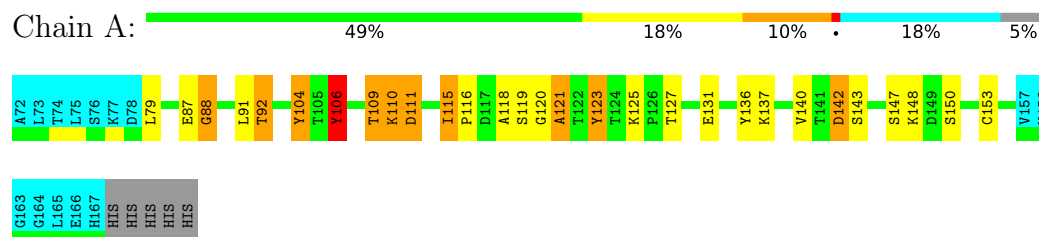
4.2.4 Score per residue for model 4

- Molecule 1: Decoration protein



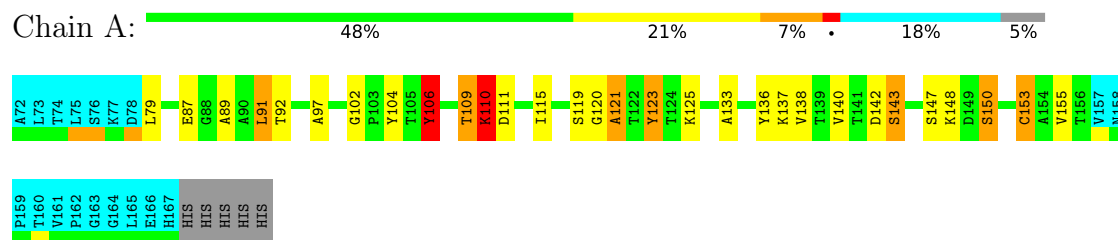
4.2.5 Score per residue for model 5

- Molecule 1: Decoration protein



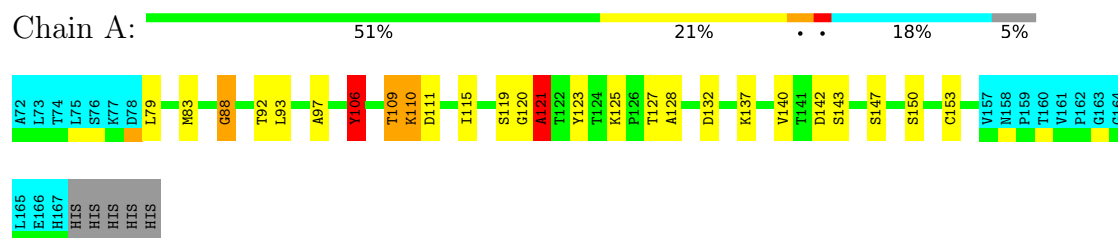
4.2.6 Score per residue for model 6

- Molecule 1: Decoration protein



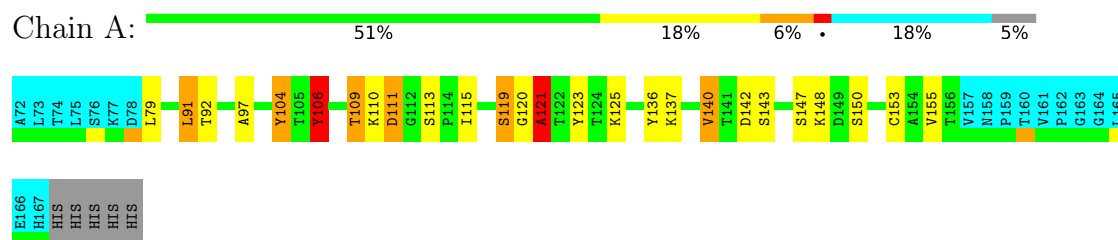
4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Decoration protein



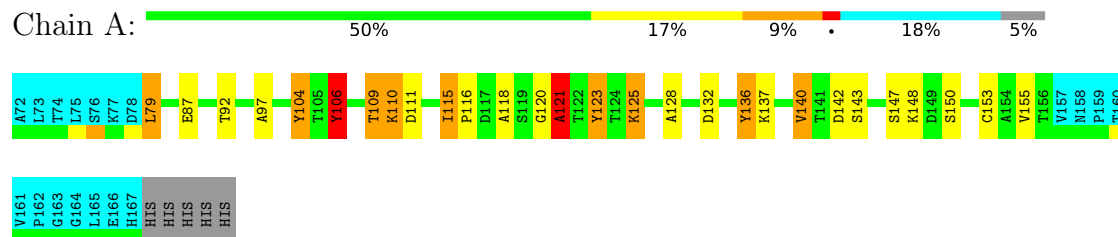
4.2.8 Score per residue for model 8

- Molecule 1: Decoration protein



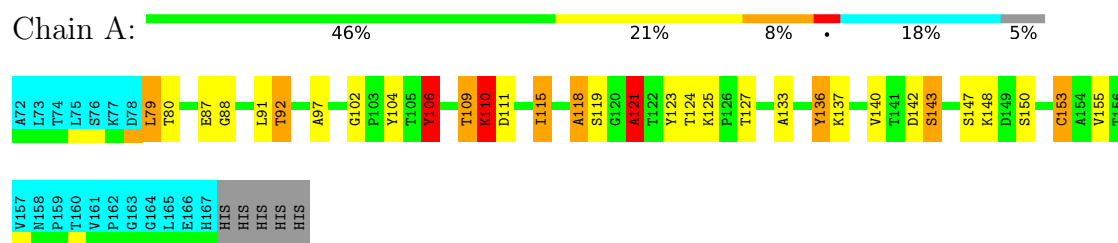
4.2.9 Score per residue for model 9

- Molecule 1: Decoration protein



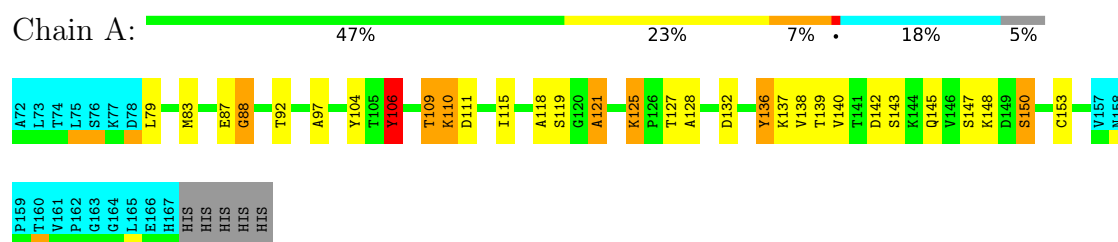
4.2.10 Score per residue for model 10

- Molecule 1: Decoration protein



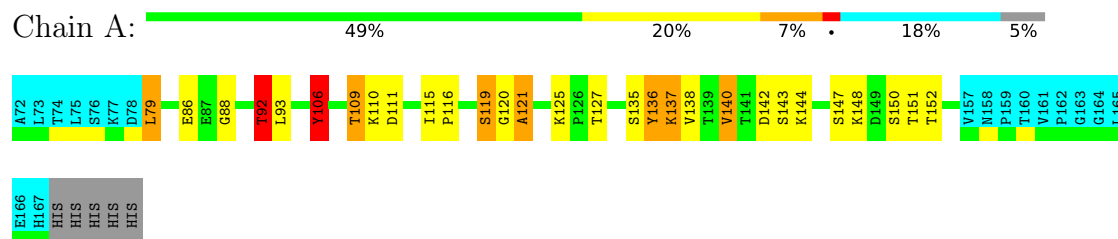
4.2.11 Score per residue for model 11

- Molecule 1: Decoration protein



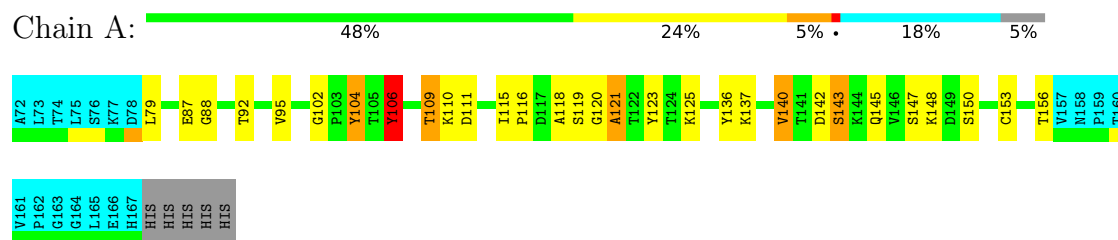
4.2.12 Score per residue for model 12

- Molecule 1: Decoration protein



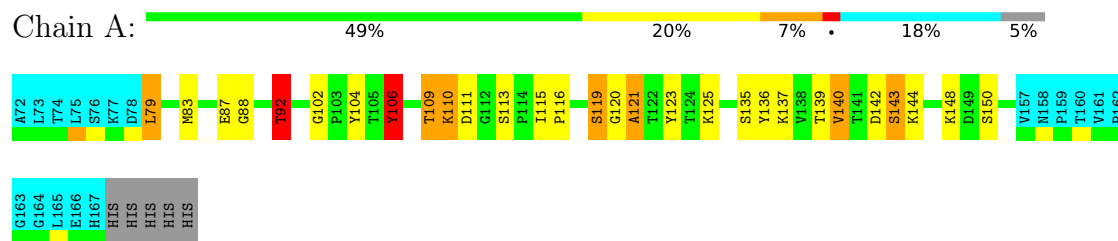
4.2.13 Score per residue for model 13

- Molecule 1: Decoration protein



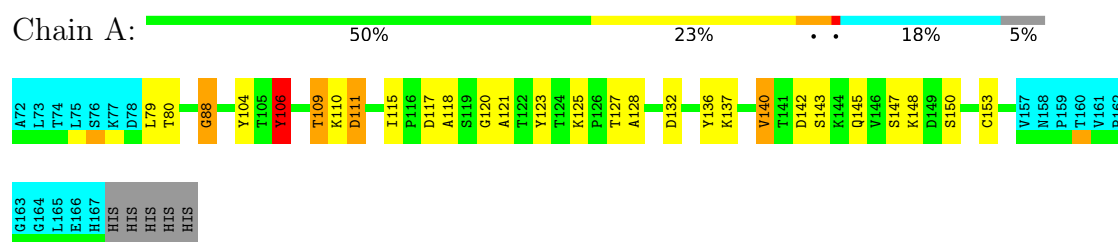
4.2.14 Score per residue for model 14

- Molecule 1: Decoration protein



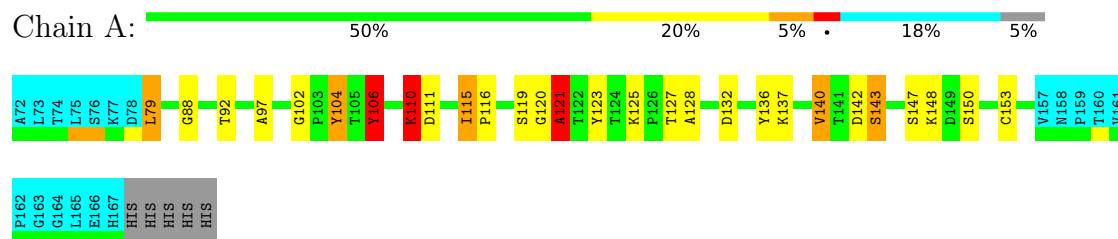
4.2.15 Score per residue for model 15

- Molecule 1: Decoration protein



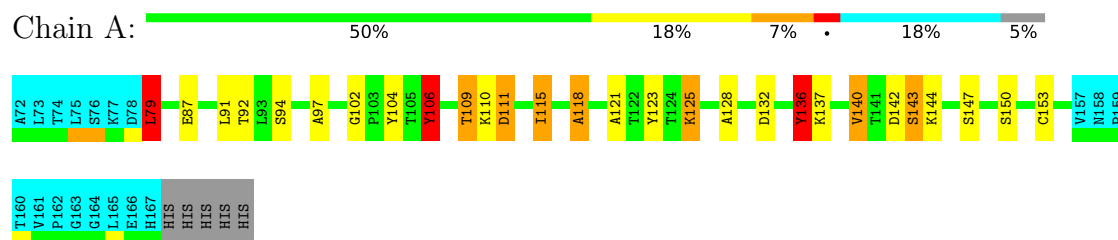
4.2.16 Score per residue for model 16

- Molecule 1: Decoration protein



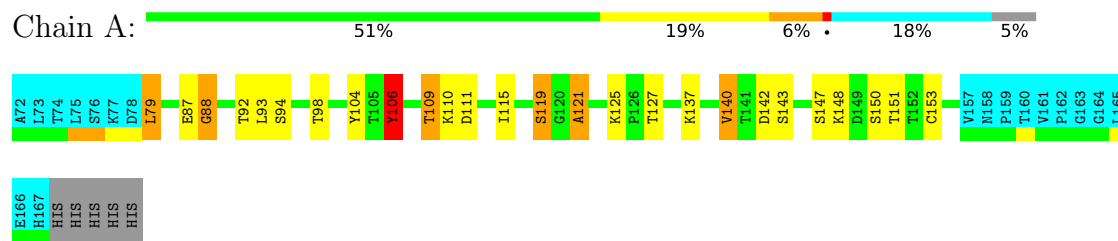
4.2.17 Score per residue for model 17

- Molecule 1: Decoration protein



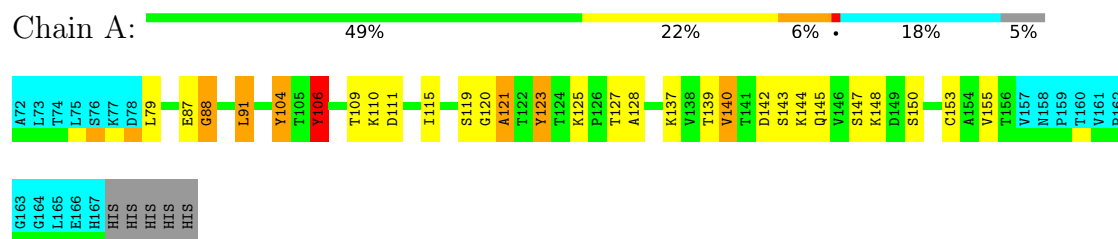
4.2.18 Score per residue for model 18

- Molecule 1: Decoration protein



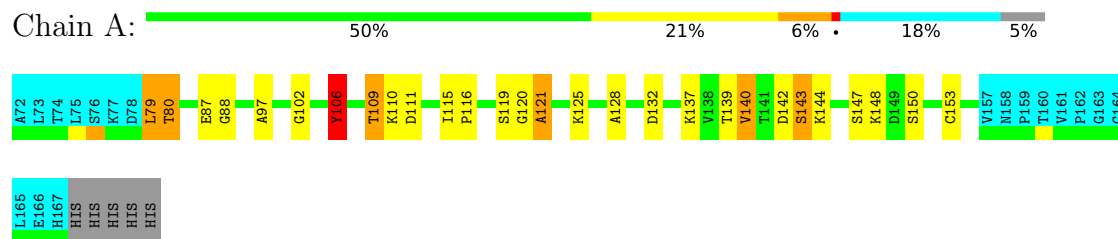
4.2.19 Score per residue for model 19

- Molecule 1: Decoration protein



4.2.20 Score per residue for model 20

- Molecule 1: Decoration protein



5 Refinement protocol and experimental data overview

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

Of the 200 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
INCA	structure calculation	
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)	5lxx_cs.cif
Number of chemical shift lists	1
Total number of shifts	1054
Number of shifts mapped to atoms	1054
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%

No validations of the models with respect to experimental NMR restraints is performed at this time.

6 Model quality i

6.1 Standard geometry i

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	0.97±0.02	0±0/556 (0.0±0.0%)	1.75±0.04	10±2/764 (1.4±0.3%)
All	All	0.97	0/11120 (0.0%)	1.75	208/15280 (1.4%)

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	1.0±0.0	2.8±0.9
All	All	20	56

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	106	TYR	CB-CG-CD2	-10.19	114.89	121.00	11	10
1	A	111	ASP	N-CA-CB	9.30	127.35	110.60	5	20
1	A	119	SER	N-CA-CB	-8.40	97.91	110.50	20	7
1	A	106	TYR	CB-CG-CD1	8.08	125.85	121.00	11	16
1	A	121	ALA	N-CA-CB	7.60	120.74	110.10	12	16
1	A	79	LEU	CB-CG-CD1	7.58	123.89	111.00	17	2
1	A	109	THR	N-CA-CB	7.51	124.58	110.30	17	17
1	A	150	SER	C-N-CA	7.36	140.10	121.70	20	19
1	A	111	ASP	O-C-N	7.15	135.35	123.20	14	20
1	A	125	LYS	N-CA-CB	7.09	123.37	110.60	11	4
1	A	118	ALA	N-CA-CB	6.73	119.52	110.10	17	1
1	A	104	TYR	CB-CG-CD1	6.72	125.03	121.00	13	5
1	A	150	SER	CB-CA-C	6.57	122.58	110.10	19	4
1	A	91	LEU	N-CA-CB	-6.32	97.77	110.40	8	1
1	A	142	ASP	C-N-CA	6.29	137.43	121.70	1	20

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	104	TYR	CB-CG-CD2	6.29	124.77	121.00	17	6
1	A	97	ALA	N-CA-C	6.15	127.60	111.00	11	3
1	A	92	THR	CA-CB-CG2	6.01	120.81	112.40	12	3
1	A	150	SER	N-CA-CB	5.94	119.41	110.50	8	1
1	A	111	ASP	C-N-CA	5.92	134.73	122.30	14	7
1	A	136	TYR	CB-CG-CD1	-5.76	117.54	121.00	17	1
1	A	135	SER	N-CA-CB	5.72	119.08	110.50	3	3
1	A	136	TYR	CB-CG-CD2	5.62	124.37	121.00	17	1
1	A	142	ASP	N-CA-CB	5.49	120.48	110.60	3	4
1	A	104	TYR	N-CA-C	5.35	125.45	111.00	5	1
1	A	110	LYS	CA-CB-CG	5.31	125.08	113.40	16	1
1	A	80	THR	CA-CB-CG2	5.23	119.72	112.40	20	1
1	A	150	SER	O-C-N	5.22	131.05	122.70	16	1
1	A	79	LEU	O-C-N	-5.20	114.39	122.70	16	2
1	A	144	LYS	C-N-CA	5.15	134.58	121.70	12	3
1	A	118	ALA	C-N-CA	5.13	134.52	121.70	13	1
1	A	140	VAL	CG1-CB-CG2	-5.12	102.71	110.90	20	1
1	A	79	LEU	CB-CG-CD2	5.10	119.67	111.00	20	1
1	A	87	GLU	N-CA-CB	5.07	119.73	110.60	6	1
1	A	97	ALA	C-N-CA	5.07	134.37	121.70	20	2
1	A	111	ASP	CA-C-O	-5.06	109.47	120.10	3	1
1	A	123	TYR	CB-CG-CD2	-5.01	118.00	121.00	13	1

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
1	A	111	ASP	CA	20

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	106	TYR	Sidechain	20
1	A	110	LYS	Peptide	13
1	A	123	TYR	Sidechain	11
1	A	136	TYR	Sidechain	9
1	A	104	TYR	Sidechain	3

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	546	528	528	5±2
All	All	10920	10560	10560	96

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 4.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:91:LEU:HD21	1:A:136:TYR:CZ	0.68	2.23	8	1
1:A:110:LYS:HG2	1:A:115:ILE:HG22	0.67	1.66	17	1
1:A:91:LEU:HD21	1:A:128:ALA:HB2	0.65	1.68	19	1
1:A:128:ALA:HB1	1:A:132:ASP:CB	0.57	2.27	15	8
1:A:110:LYS:HZ1	1:A:132:ASP:HA	0.57	1.60	9	2
1:A:79:LEU:O	1:A:92:THR:HG22	0.56	2.01	12	3
1:A:138:VAL:HG13	1:A:150:SER:HB2	0.56	1.77	1	1
1:A:93:LEU:HD11	1:A:136:TYR:CD2	0.53	2.38	12	1
1:A:93:LEU:HD21	1:A:136:TYR:CD2	0.53	2.38	4	1
1:A:138:VAL:HG13	1:A:150:SER:OG	0.53	2.04	11	1
1:A:93:LEU:HD11	1:A:136:TYR:CD1	0.51	2.40	1	1
1:A:115:ILE:HD11	1:A:118:ALA:HB2	0.50	1.81	10	2
1:A:102:GLY:H	1:A:143:SER:HB3	0.50	1.66	16	9
1:A:97:ALA:HB3	1:A:121:ALA:HB2	0.49	1.85	10	5
1:A:88:GLY:HA2	1:A:127:THR:HG23	0.48	1.84	11	9
1:A:110:LYS:HD3	1:A:136:TYR:CE2	0.47	2.44	6	1
1:A:79:LEU:HD22	1:A:94:SER:H	0.47	1.69	18	1
1:A:110:LYS:HD2	1:A:136:TYR:CZ	0.47	2.44	11	5
1:A:138:VAL:HG13	1:A:140:VAL:HG22	0.47	1.87	12	1
1:A:91:LEU:HD21	1:A:128:ALA:CB	0.46	2.38	19	1
1:A:91:LEU:HD12	1:A:153:CYS:SG	0.46	2.49	6	1
1:A:91:LEU:HD23	1:A:136:TYR:CZ	0.46	2.46	4	2
1:A:91:LEU:HD23	1:A:136:TYR:CE1	0.46	2.45	17	1
1:A:104:TYR:HB3	1:A:140:VAL:HG12	0.45	1.89	15	9
1:A:106:TYR:HB3	1:A:140:VAL:HG13	0.45	1.88	17	1
1:A:115:ILE:HB	1:A:116:PRO:CD	0.45	2.42	16	1
1:A:79:LEU:HD13	1:A:153:CYS:SG	0.45	2.52	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:115:ILE:HB	1:A:116:PRO:HD2	0.44	1.89	5	2
1:A:106:TYR:CD1	1:A:106:TYR:N	0.44	2.85	16	4
1:A:106:TYR:CD2	1:A:106:TYR:N	0.44	2.86	14	1
1:A:91:LEU:O	1:A:124:THR:HG23	0.43	2.12	4	2
1:A:110:LYS:CB	1:A:136:TYR:HA	0.43	2.43	2	3
1:A:106:TYR:N	1:A:106:TYR:CD1	0.43	2.87	10	3
1:A:137:LYS:HE2	1:A:152:THR:HG22	0.43	1.90	12	1
1:A:79:LEU:HB3	1:A:93:LEU:HA	0.43	1.91	18	1
1:A:91:LEU:HG	1:A:136:TYR:CE2	0.42	2.49	6	1
1:A:106:TYR:N	1:A:106:TYR:CD2	0.42	2.86	12	1
1:A:79:LEU:HG	1:A:94:SER:H	0.41	1.75	17	1
1:A:79:LEU:HD12	1:A:79:LEU:H	0.41	1.75	3	1
1:A:110:LYS:NZ	1:A:136:TYR:CZ	0.41	2.86	10	1
1:A:115:ILE:CD1	1:A:118:ALA:HB2	0.40	2.46	3	1
1:A:104:TYR:CE2	1:A:142:ASP:CG	0.40	2.95	5	1
1:A:80:THR:HB	1:A:153:CYS:SG	0.40	2.56	10	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	78/101 (77%)	63±1 (81±2%)	10±2 (13±2%)	4±1 (6±1%)	4	22
All	All	1560/2020 (77%)	1268 (81%)	203 (13%)	89 (6%)	4	22

All 8 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	121	ALA	20
1	A	143	SER	20
1	A	120	GLY	14
1	A	88	GLY	14
1	A	119	SER	7
1	A	118	ALA	7

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Mol	Chain	Res	Type	Models (Total)
1	A	116	PRO	5
1	A	117	ASP	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	59/79 (75%)	44±1 (75±2%)	15±1 (25±2%)	2	25
All	All	1180/1580 (75%)	884 (75%)	296 (25%)	2	25

All 34 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	137	LYS	20
1	A	106	TYR	20
1	A	140	VAL	20
1	A	115	ILE	20
1	A	109	THR	19
1	A	125	LYS	19
1	A	79	LEU	19
1	A	147	SER	19
1	A	148	LYS	18
1	A	92	THR	17
1	A	153	CYS	17
1	A	87	GLU	11
1	A	119	SER	10
1	A	110	LYS	10
1	A	123	TYR	6
1	A	139	THR	5
1	A	155	VAL	5
1	A	111	ASP	5
1	A	145	GLN	4
1	A	144	LYS	4
1	A	83	MET	4
1	A	113	SER	3
1	A	127	THR	3

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Mol	Chain	Res	Type	Models (Total)
1	A	95	VAL	3
1	A	131	GLU	2
1	A	91	LEU	2
1	A	80	THR	2
1	A	151	THR	2
1	A	86	GLU	2
1	A	98	THR	1
1	A	150	SER	1
1	A	156	THR	1
1	A	93	LEU	1
1	A	138	VAL	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 carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation [i](#)

The completeness of assignment taking into account all chemical shift lists is 91% for the well-defined parts and 91% for the entire structure.

7.1 Chemical shift list 1

File name: 5lxk_cs.cif

Chemical shift list name: *c72_depchim_renum.bmrB*

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	1054
Number of shifts mapped to atoms	1054
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

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
$^{13}\text{C}_\alpha$	96	0.21 ± 0.25	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	87	0.06 ± 0.19	None needed (< 0.5 ppm)
$^{13}\text{C}'$	94	0.49 ± 0.17	None needed (< 0.5 ppm)
^{15}N	88	-1.24 ± 0.49	Should be applied

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. 717 atoms were assigned a chemical shift out of a possible 787. 1 out of 9 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	379/382 (99%)	150/152 (99%)	155/156 (99%)	74/74 (100%)
Sidechain	294/361 (81%)	176/207 (85%)	117/148 (79%)	1/6 (17%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	44/44 (100%)	22/22 (100%)	21/21 (100%)	1/1 (100%)
Overall	717/787 (91%)	348/381 (91%)	293/325 (90%)	76/81 (94%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 91%, i.e. 893 atoms were assigned a chemical shift out of a possible 984. 1 out of 14 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	460/468 (98%)	182/186 (98%)	190/192 (99%)	88/90 (98%)
Sidechain	389/465 (84%)	234/267 (88%)	153/190 (81%)	2/8 (25%)
Aromatic	44/51 (86%)	22/26 (85%)	21/23 (91%)	1/2 (50%)
Overall	893/984 (91%)	438/479 (91%)	364/405 (90%)	91/100 (91%)

7.1.4 Statistically unusual chemical shifts ⓘ

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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	123	TYR	HB3	0.59	4.75 – 0.95	-5.9

7.1.5 Random Coil Index (RCI) plots ⓘ

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.

Random coil index (RCI) for chain A:

