



Full wwPDB NMR Structure Validation Report ⓘ

Apr 5, 2022 – 04:22 pm BST

PDB ID : 7ZEY
Title : RNA binding induces an allosteric switch in Cyp33 to repress MLL1 mediated transcription
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Deposited on : 2022-03-31

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:

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

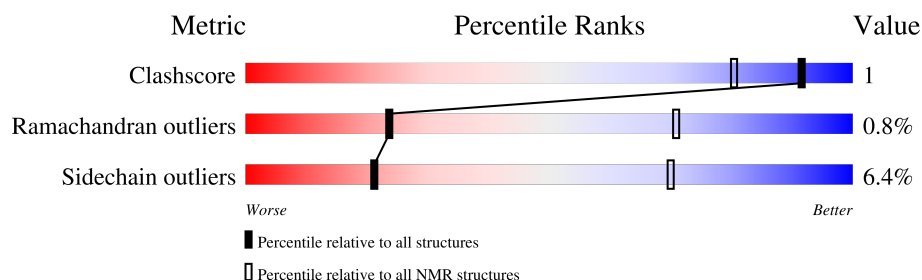
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 77%.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. A cyan segment indicates the fraction of residues that are not part of the well-defined cores, and a grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	117	
2	B	64	

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

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:3-A:88, A:92-A:107, B:1568-B:1627 (162)	0.36	1

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 5 clusters and 1 single-model cluster was found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2808 atoms, of which 1368 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Peptidyl-prolyl cis-trans isomerase E.

Mol	Chain	Residues	Atoms						Trace
1	A	117	Total	C	H	N	O	S	0
			1836	589	908	157	179	3	

There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	ALA	-	expression tag	UNP Q9UNP9
A	-2	GLY	-	expression tag	UNP Q9UNP9
A	-1	HIS	-	expression tag	UNP Q9UNP9

- Molecule 2 is a protein called MLL cleavage product N320.

Mol	Chain	Residues	Atoms						Trace
2	B	64	Total	C	H	N	O	S	0
			970	310	460	83	106	11	

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

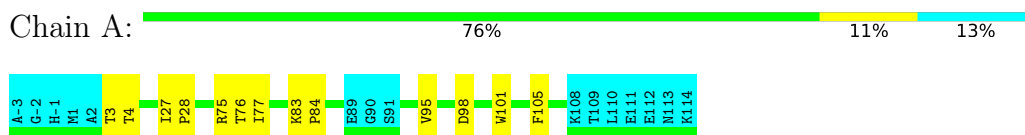
Mol	Chain	Residues	Atoms	
3	B	2	Total	Zn
			2	2

4 Residue-property plots

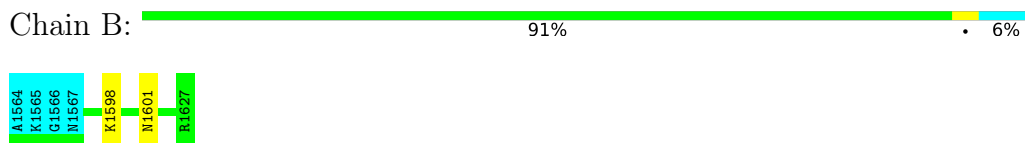
4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outliers are shown as green connectors. Residues which are classified as ill-defined in the NMR ensemble, are shown in cyan with an underline colour-coded according to the previous scheme. Residues which were present in the experimental sample, but not modelled in the final structure are shown in grey.

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E



- Molecule 2: MLL cleavage product N320

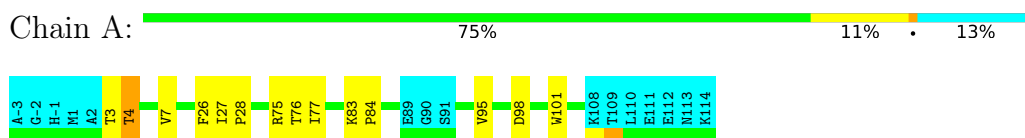


4.2 Scores per residue for each member of the ensemble

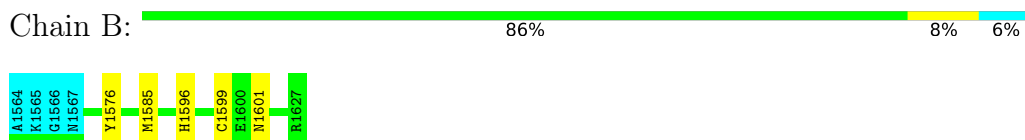
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

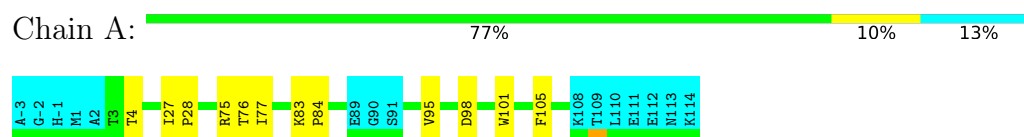


- Molecule 2: MLL cleavage product N320

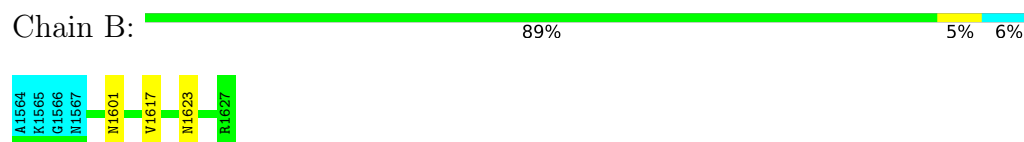


4.2.2 Score per residue for model 2

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

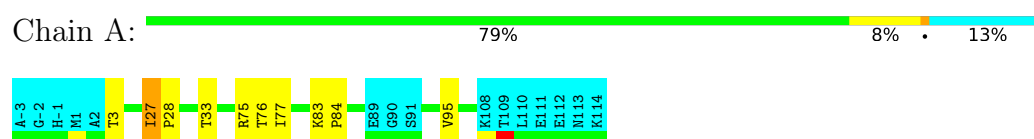


- Molecule 2: MLL cleavage product N320

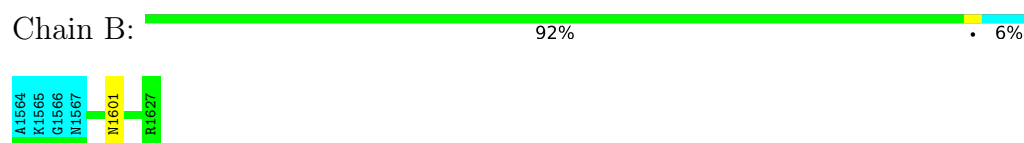


4.2.3 Score per residue for model 3

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

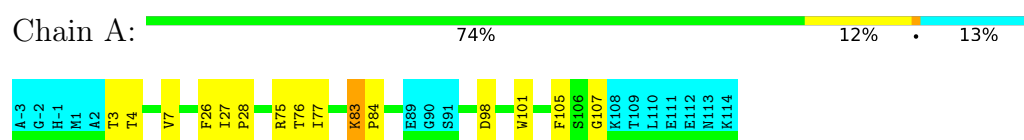


- Molecule 2: MLL cleavage product N320

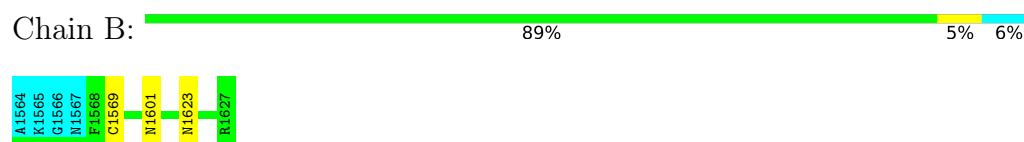


4.2.4 Score per residue for model 4

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E




- Molecule 2: MLL cleavage product N320




4.2.5 Score per residue for model 5

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  80% 7% 13%




- Molecule 2: MLL cleavage product N320

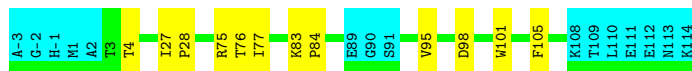
Chain B:  88% 6% 6%




4.2.6 Score per residue for model 6

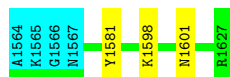
- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  77% 10% 13%




- Molecule 2: MLL cleavage product N320

Chain B:  89% 5% 6%




4.2.7 Score per residue for model 7

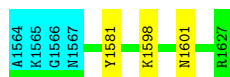
- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  77% 10% 13%




- Molecule 2: MLL cleavage product N320

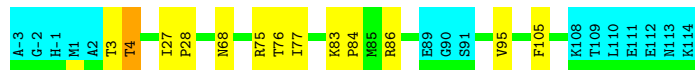
Chain B:  89% 5% 6%




4.2.8 Score per residue for model 8

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  76% 10% 13%



- Molecule 2: MLL cleavage product N320

Chain B:  88% 5% 6%




4.2.9 Score per residue for model 9

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  74% 13% 13%



- Molecule 2: MLL cleavage product N320

Chain B:  88% 6% 6%



4.2.10 Score per residue for model 10

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  76% 11% 13%




- Molecule 2: MLL cleavage product N320

Chain B:  86% 8% 6%




4.2.11 Score per residue for model 11

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  82% 5% 13%




- Molecule 2: MLL cleavage product N320

Chain B:  84% 9% 6%




4.2.12 Score per residue for model 12

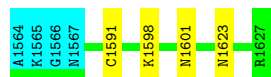
- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  79% 9% 13%




- Molecule 2: MLL cleavage product N320

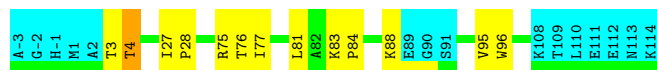
Chain B:  88% 6% 6%




4.2.13 Score per residue for model 13

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  76% 10% 13%



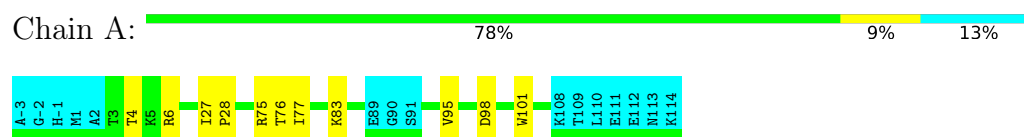
- Molecule 2: MLL cleavage product N320

Chain B:  86% 8% 6%

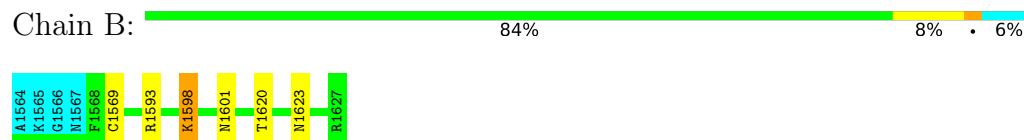


4.2.14 Score per residue for model 14

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

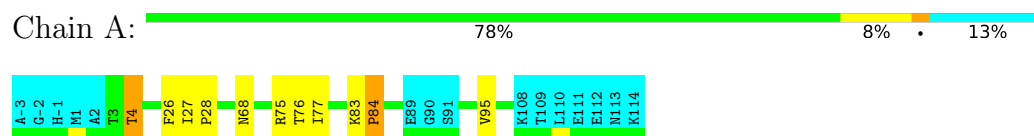


- Molecule 2: MLL cleavage product N320

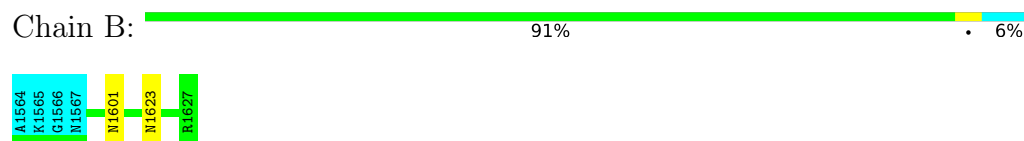


4.2.15 Score per residue for model 15

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

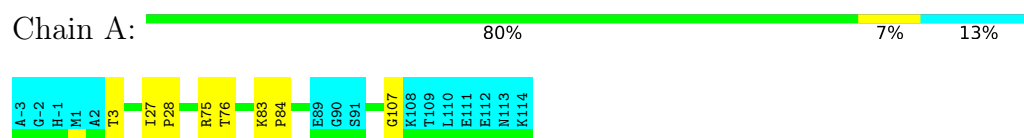


- Molecule 2: MLL cleavage product N320

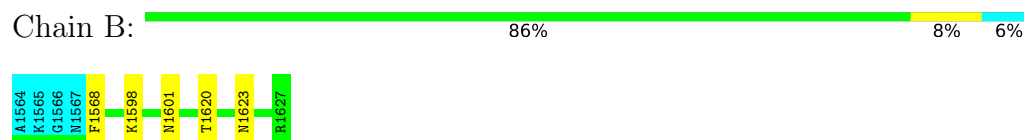


4.2.16 Score per residue for model 16

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E




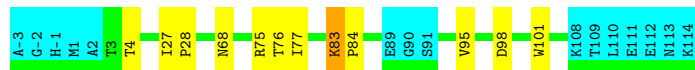
- Molecule 2: MLL cleavage product N320




4.2.17 Score per residue for model 17

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  77% 9% 13%



- Molecule 2: MLL cleavage product N320

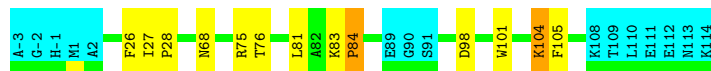
Chain B:  81% 12% 6%




4.2.18 Score per residue for model 18

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  76% 9% 13%




- Molecule 2: MLL cleavage product N320

Chain B:  88% 6% 6%




4.2.19 Score per residue for model 19

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E

Chain A:  77% 10% 13%



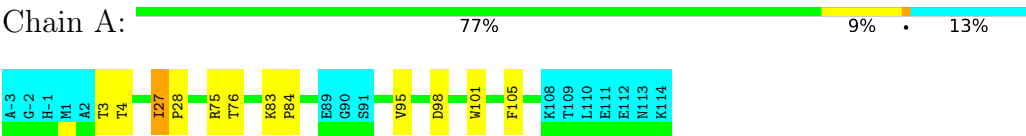
- Molecule 2: MLL cleavage product N320

Chain B:  84% 9% 6%

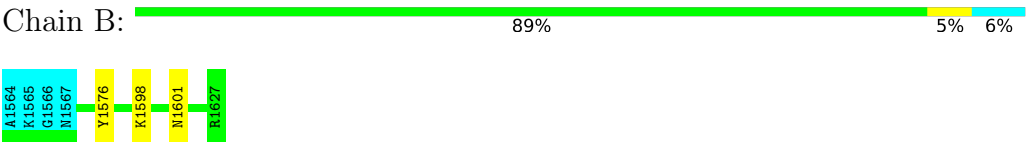


4.2.20 Score per residue for model 20

- Molecule 1: Peptidyl-prolyl cis-trans isomerase E



- Molecule 2: MLL cleavage product N320



5 Refinement protocol and experimental data overview

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

Of the 250 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
Amber	refinement	
CYANA	structure calculation	

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	2
Total number of shifts	1872
Number of shifts mapped to atoms	1872
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	77%

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:
ZN

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	818	801	801	3±1
2	B	484	433	433	1±1
All	All	26080	24680	24680	74

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 1.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:LYS:N	1:A:84:PRO:CD	0.52	2.72	16	14
1:A:27:ILE:N	1:A:28:PRO:CD	0.50	2.75	4	20
2:B:1585:MET:SD	2:B:1596:HIS:CD2	0.48	3.06	17	2
2:B:1584:LYS:HE3	2:B:1607:TYR:CE2	0.47	2.44	11	1
1:A:98:ASP:HA	1:A:101:TRP:CD1	0.46	2.45	7	8
1:A:88:LYS:HE2	1:A:96:TRP:CZ2	0.44	2.47	13	1
1:A:83:LYS:N	1:A:84:PRO:HD2	0.44	2.27	5	6
2:B:1598:LYS:HE2	2:B:1598:LYS:N	0.44	2.28	6	3
2:B:1598:LYS:CA	2:B:1598:LYS:HE2	0.44	2.43	16	1
1:A:81:LEU:H	1:A:81:LEU:HD22	0.44	1.73	13	3
1:A:98:ASP:O	1:A:101:TRP:CD1	0.42	2.72	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:PHE:C	1:A:28:PRO:HD2	0.42	2.35	1	4
2:B:1598:LYS:HE2	2:B:1598:LYS:HA	0.42	1.91	16	1
2:B:1596:HIS:HB2	2:B:1599:CYS:SG	0.41	2.56	1	1
1:A:104:LYS:HA	1:A:104:LYS:HE3	0.41	1.92	18	1
2:B:1598:LYS:N	2:B:1598:LYS:HE2	0.41	2.31	5	3
2:B:1598:LYS:HE2	2:B:1598:LYS:CA	0.40	2.46	7	1
1:A:81:LEU:HD22	1:A:81:LEU:H	0.40	1.77	9	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	102/117 (87%)	91±2 (89±2%)	10±2 (10±2%)	1±1 (1±1%)	18	66
2	B	59/64 (92%)	55±2 (94±3%)	4±2 (6±3%)	0±0 (0±1%)	50	82
All	All	3220/3620 (89%)	2922 (91%)	273 (8%)	25 (1%)	24	71

All 5 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	95	VAL	14
1	A	4	THR	4
1	A	107	GLY	3
2	B	1576	TYR	2
1	A	84	PRO	2

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	86/97 (89%)	80±1 (93±2%)	6±1 (7±2%)	20	68
2	B	58/60 (97%)	55±2 (94±3%)	3±2 (6±3%)	23	72
All	All	2880/3140 (92%)	2696 (94%)	184 (6%)	21	70

All 32 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	75	ARG	20
1	A	76	THR	20
2	B	1601	ASN	19
1	A	4	THR	14
1	A	77	ILE	14
1	A	3	THR	11
1	A	105	PHE	11
2	B	1623	ASN	10
1	A	68	ASN	8
2	B	1569	CYS	7
2	B	1620	THR	6
2	B	1581	TYR	6
1	A	86	ARG	4
2	B	1598	LYS	4
1	A	83	LYS	3
2	B	1610	LEU	3
1	A	7	VAL	2
2	B	1617	VAL	2
1	A	27	ILE	2
2	B	1591	CYS	2
1	A	104	LYS	2
1	A	6	ARG	2
2	B	1593	ARG	2
2	B	1568	PHE	2
1	A	33	THR	1
2	B	1622	VAL	1
2	B	1574	LYS	1
2	B	1584	LYS	1
2	B	1619	TYR	1
1	A	40	ASP	1
2	B	1595	VAL	1
2	B	1576	TYR	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 monosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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 77% for the well-defined parts and 76% for the entire structure.

7.1 Chemical shift list 1

File name: `working_cs.cif`

Chemical shift list name: `MLL_renumb.str`

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	629
Number of shifts mapped to atoms	629
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
$^{13}\text{C}_\alpha$	58	-0.53 ± 0.20	Should be applied
$^{13}\text{C}_\beta$	57	0.07 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	54	-0.42 ± 0.62	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 27%, i.e. 542 atoms were assigned a chemical shift out of a possible 1992. 7 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	210/798 (26%)	105/318 (33%)	54/324 (17%)	51/156 (33%)
Sidechain	285/1017 (28%)	180/596 (30%)	101/378 (27%)	4/43 (9%)

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	Total	¹ H	¹³ C	¹⁵ N
Aromatic	47/177 (27%)	29/94 (31%)	17/77 (22%)	1/6 (17%)
Overall	542/1992 (27%)	314/1008 (31%)	172/779 (22%)	56/205 (27%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 26%, i.e. 576 atoms were assigned a chemical shift out of a possible 2201. 7 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	224/893 (25%)	112/356 (31%)	58/362 (16%)	54/175 (31%)
Sidechain	305/1124 (27%)	193/659 (29%)	107/417 (26%)	5/48 (10%)
Aromatic	47/184 (26%)	29/98 (30%)	17/79 (22%)	1/7 (14%)
Overall	576/2201 (26%)	334/1113 (30%)	182/858 (21%)	60/230 (26%)

7.1.4 Statistically unusual chemical shifts ⓘ

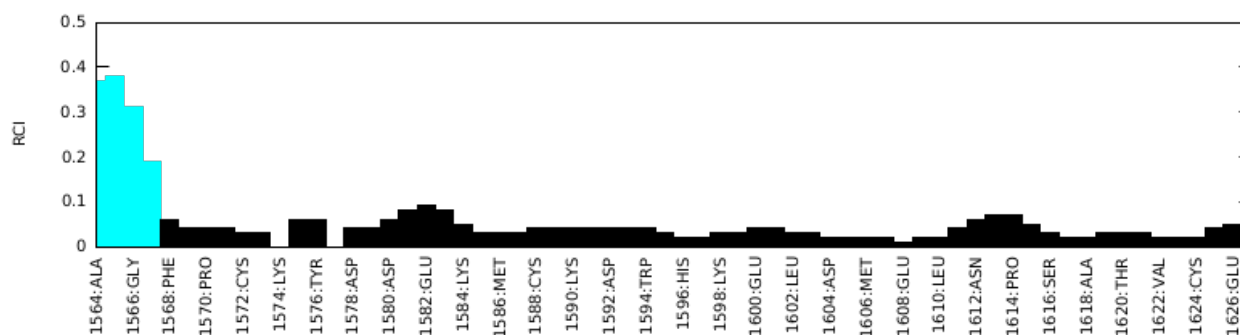
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
2	B	1594	TRP	NE1	114.59	139.19 – 119.59	-7.6
2	B	1587	GLN	HG3	0.79	3.75 – 0.85	-5.2

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 B:



7.2 Chemical shift list 2

File name: working_cs.cif

Chemical shift list name: *shift_set_1*

7.2.1 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	1243
Number of shifts mapped to atoms	1243
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

7.2.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	100	-0.37 ± 0.22	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	102	-0.01 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	106	0.44 ± 0.24	None needed (< 0.5 ppm)

7.2.3 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 50%, i.e. 987 atoms were assigned a chemical shift out of a possible 1992. 14 out of 22 assigned methyl groups (LEU and VAL) were assigned

stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	374/798 (47%)	187/318 (59%)	92/324 (28%)	95/156 (61%)
Sidechain	523/1017 (51%)	322/596 (54%)	197/378 (52%)	4/43 (9%)
Aromatic	90/177 (51%)	56/94 (60%)	32/77 (42%)	2/6 (33%)
Overall	987/1992 (50%)	565/1008 (56%)	321/779 (41%)	101/205 (49%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 50%, i.e. 1090 atoms were assigned a chemical shift out of a possible 2201. 14 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	412/893 (46%)	206/356 (58%)	100/362 (28%)	106/175 (61%)
Sidechain	584/1124 (52%)	361/659 (55%)	218/417 (52%)	5/48 (10%)
Aromatic	94/184 (51%)	58/98 (59%)	34/79 (43%)	2/7 (29%)
Overall	1090/2201 (50%)	625/1113 (56%)	352/858 (41%)	113/230 (49%)

7.2.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

7.2.5 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.

Random coil index (RCI) for chain A:

