



Full wwPDB NMR Structure Validation Report ⓘ

Jan 22, 2018 – 02:02 PM EST

PDB ID : 6F0Y
Title : Rtt109 peptide bound to Asf1
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Deposited on : 2017-11-21

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

<http://wwpdb.org/validation/2016/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 : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20030736
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

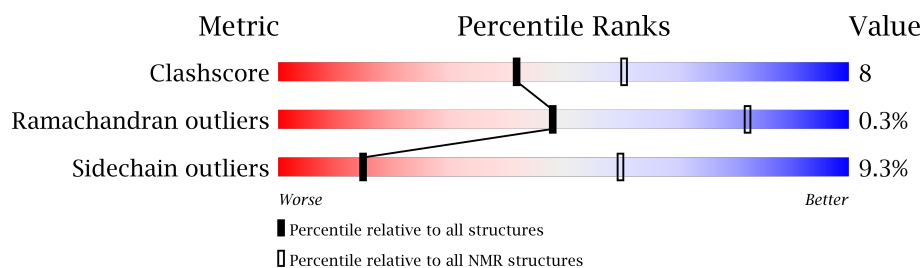
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 90%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	172	 63% 19% • 17%
2	B	15	 20% 20% 60%

2 Ensemble composition and analysis

This entry contains 10 models. Model 5 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *medoid*.

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:46, A:55-A:152, B:421-B:426 (149)	0.31	5

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, 6, 7, 8, 10
2	1, 3, 9

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2961 atoms, of which 1480 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Histone chaperone ASF1.

Mol	Chain	Residues	Atoms						Trace
1	A	172	Total	C	H	N	O	S	0
			2695	871	1331	221	269	3	

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP P32447
A	-1	ALA	-	expression tag	UNP P32447
A	0	MET	-	expression tag	UNP P32447
A	1	GLY	-	expression tag	UNP P32447

- Molecule 2 is a protein called histone acetyltransferase Rtt109 C-terminus.

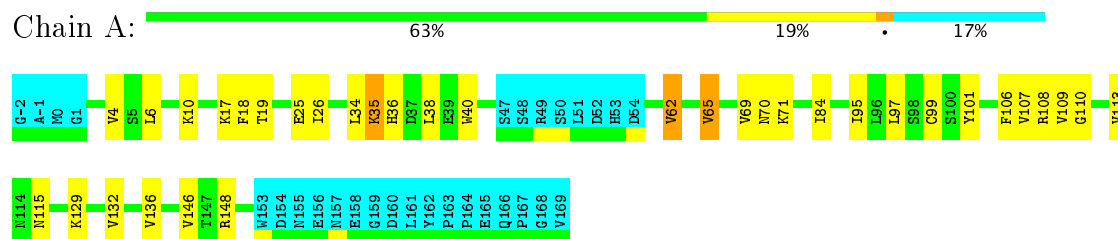
Mol	Chain	Residues	Atoms						Trace
2	B	15	Total	C	H	N	O	S	0
			266	77	149	22	17	1	

4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Histone chaperone ASF1



- Molecule 2: histone acetyltransferase Rtt109 C-terminus

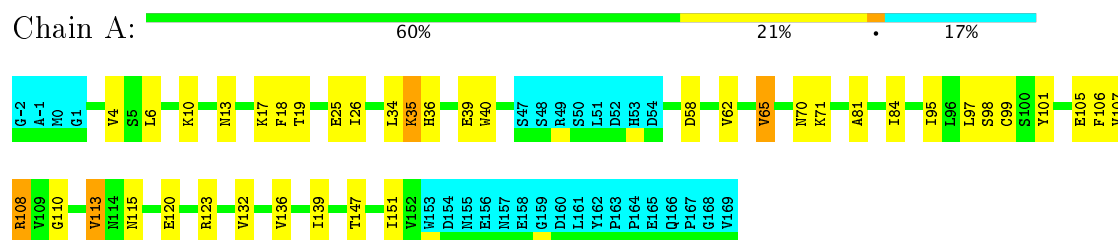


4.2 Scores per residue for each member of the ensemble

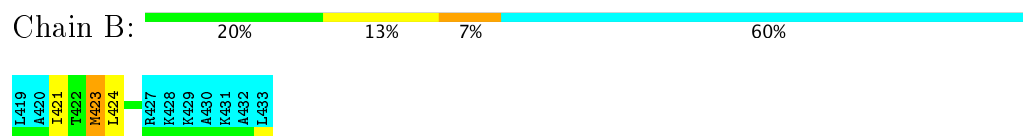
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Histone chaperone ASF1

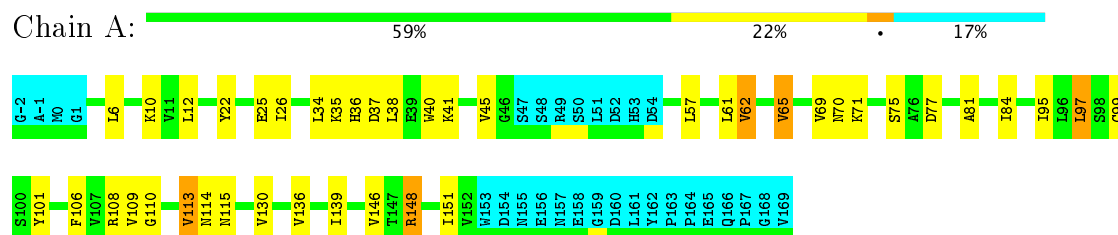


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

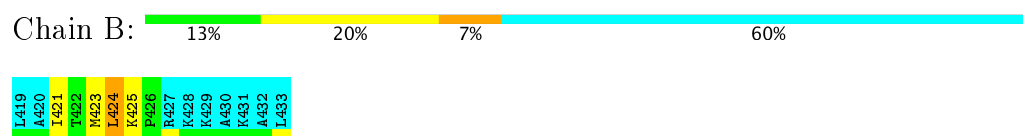


4.2.2 Score per residue for model 2

- Molecule 1: Histone chaperone ASF1

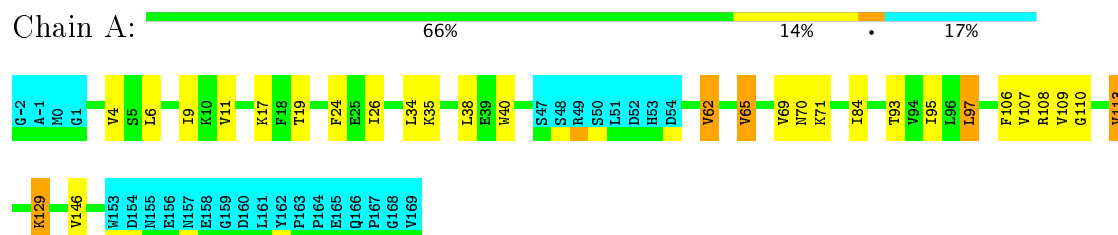


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

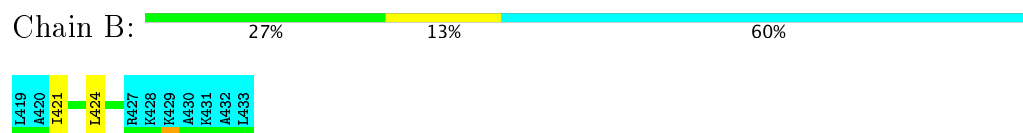


4.2.3 Score per residue for model 3

- Molecule 1: Histone chaperone ASF1

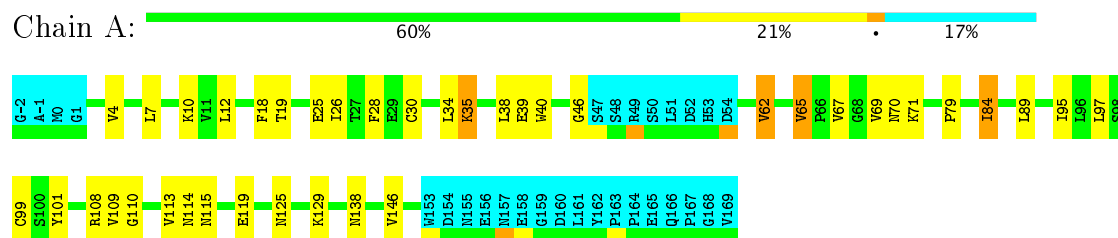


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

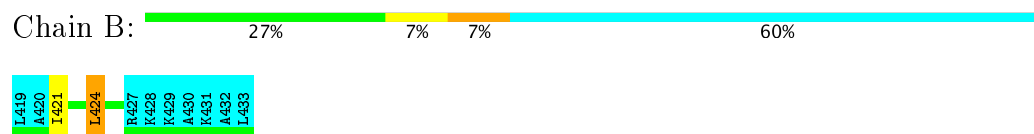


4.2.4 Score per residue for model 4

- Molecule 1: Histone chaperone ASF1

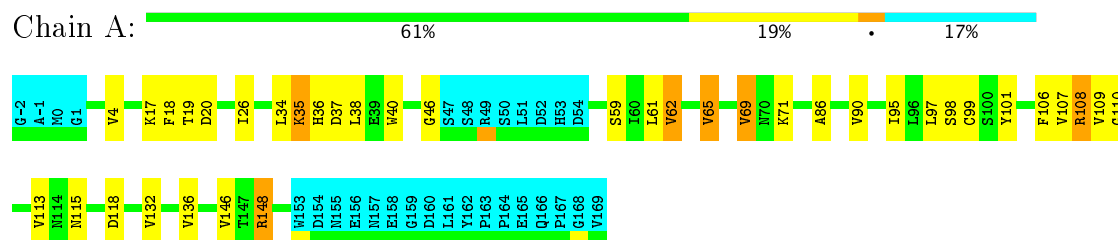


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

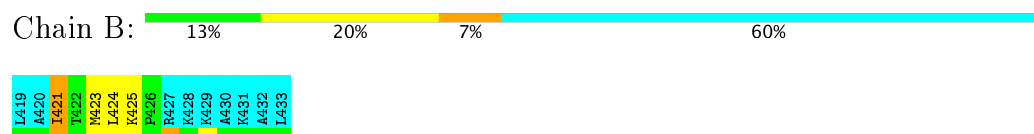


4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: Histone chaperone ASF1

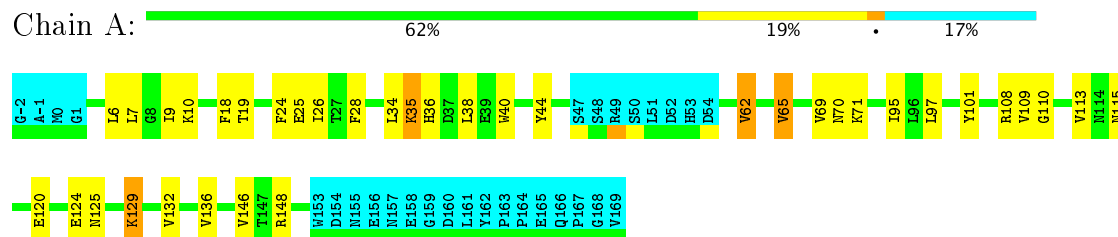


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

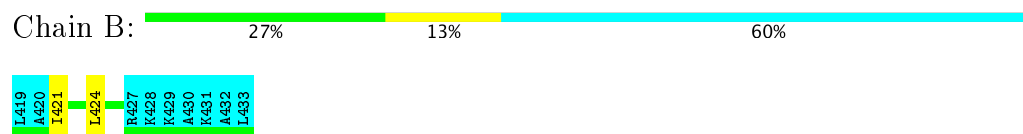


4.2.6 Score per residue for model 6

- Molecule 1: Histone chaperone ASF1

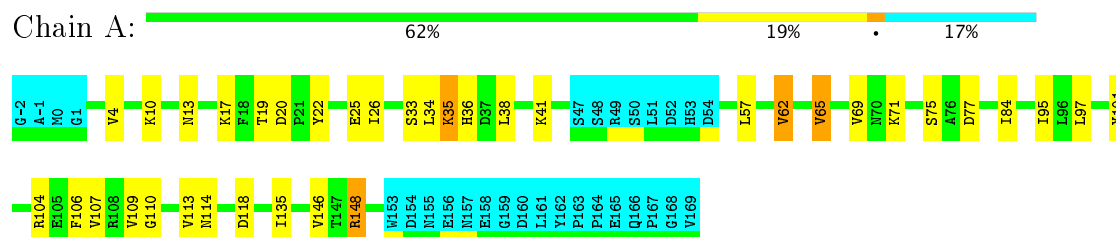


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

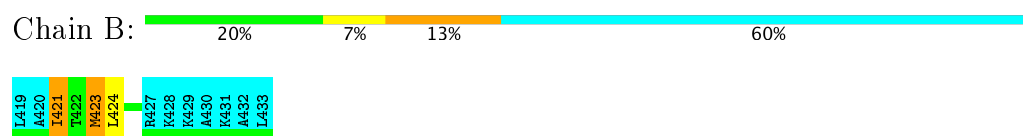


4.2.7 Score per residue for model 7

- Molecule 1: Histone chaperone ASF1

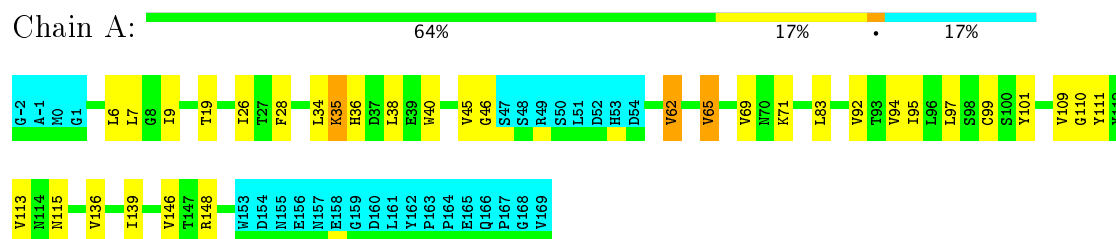


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

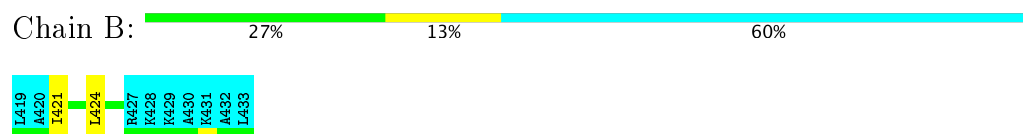


4.2.8 Score per residue for model 8

- Molecule 1: Histone chaperone ASF1

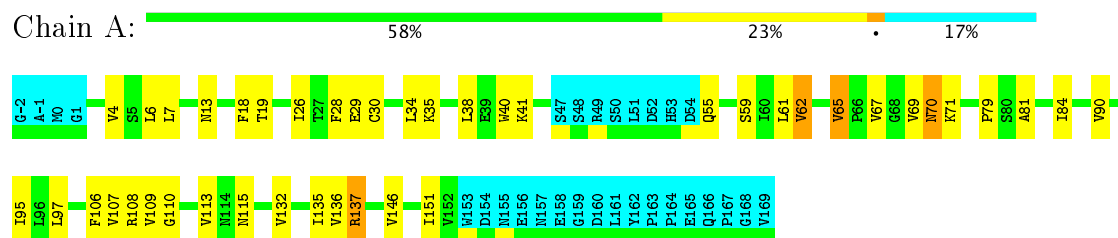


- Molecule 2: histone acetyltransferase Rtt109 C-terminus

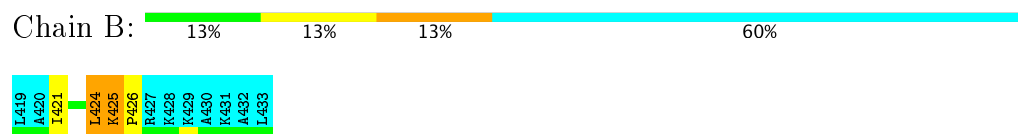


4.2.9 Score per residue for model 9

- Molecule 1: Histone chaperone ASF1

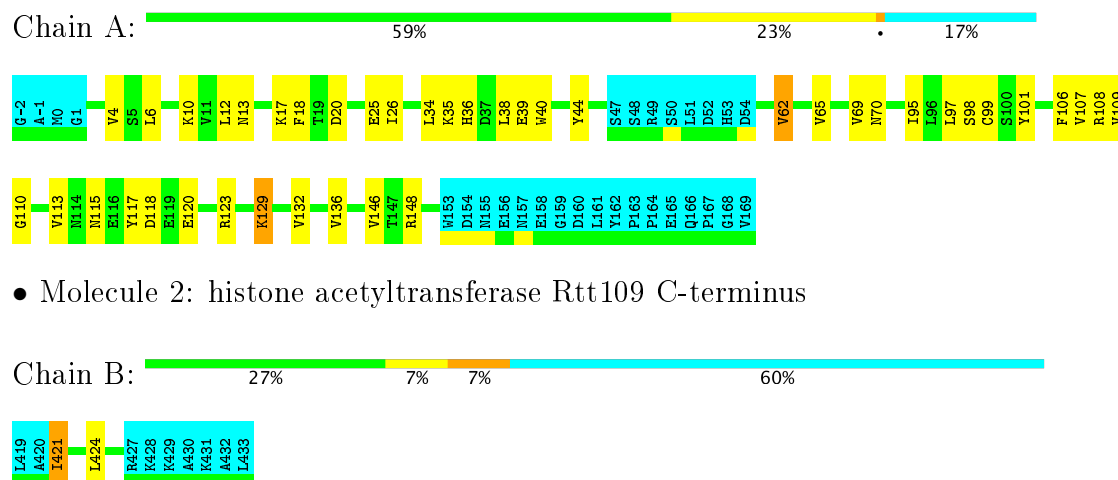


- Molecule 2: histone acetyltransferase Rtt109 C-terminus



4.2.10 Score per residue for model 10

- Molecule 1: Histone chaperone ASF1



- Molecule 2: histone acetyltransferase Rtt109 C-terminus

5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing, torsion angle dynamics, molecular dynamics*.

Of the 100 calculated structures, 10 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 calculation	1.21
ARIA	structure calculation	2.3
CNS	structure calculation	1.21
CNS	structure calculation	1.21

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)	6f0y_cs.cif
Number of chemical shift lists	2
Total number of shifts	2420
Number of shifts mapped to atoms	2420
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	90%

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)

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	1141	1142	1140	20±3
2	B	47	58	58	1±1
All	All	11880	12000	11980	200

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 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:109:VAL:HG13	1:A:146:VAL:HG22	0.79	1.54	6	9
1:A:34:LEU:HD23	1:A:65:VAL:HG22	0.66	1.66	4	9
1:A:113:VAL:HG12	1:A:139:ILE:HA	0.65	1.68	8	2
1:A:95:ILE:O	1:A:110:GLY:HA2	0.62	1.94	8	10
1:A:26:ILE:HD11	1:A:97:LEU:HD11	0.61	1.71	1	10
2:B:421:ILE:HB	2:B:423:MET:SD	0.57	2.38	7	1
1:A:115:ASN:HA	1:A:136:VAL:O	0.56	1.99	6	7
1:A:17:LYS:HG2	1:A:135:ILE:O	0.55	2.01	7	1
1:A:36:HIS:HB2	1:A:101:TYR:CZ	0.55	2.36	2	6
1:A:114:ASN:OD1	1:A:138:ASN:HB3	0.55	2.01	4	1
1:A:18:PHE:HB3	1:A:132:VAL:CG1	0.55	2.31	10	5
1:A:55:GLN:OE1	1:A:79:PRO:HB3	0.54	2.03	9	1
1:A:38:LEU:HB2	1:A:62:VAL:HG23	0.53	1.79	5	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:35:LYS:HD2	1:A:35:LYS:H	0.53	1.64	5	3
1:A:62:VAL:HG12	2:B:424:LEU:HD12	0.52	1.80	9	1
1:A:106:PHE:CD2	1:A:107:VAL:HG23	0.52	2.40	1	2
1:A:26:ILE:O	1:A:71:LYS:HA	0.52	2.04	8	9
1:A:34:LEU:HD12	1:A:101:TYR:CE1	0.52	2.40	8	3
1:A:71:LYS:O	2:B:423:MET:HA	0.52	2.05	1	1
1:A:22:TYR:O	1:A:75:SER:HA	0.52	2.04	7	2
1:A:106:PHE:O	1:A:148:ARG:HA	0.52	2.05	10	4
1:A:106:PHE:CD1	1:A:107:VAL:HG23	0.52	2.40	9	2
1:A:115:ASN:HB2	1:A:137:ARG:NH2	0.52	2.20	9	1
1:A:117:TYR:O	1:A:123:ARG:HD2	0.51	2.05	10	1
1:A:129:LYS:H	1:A:129:LYS:HD3	0.51	1.66	6	1
1:A:40:TRP:CE3	1:A:99:CYS:HB2	0.51	2.41	10	4
1:A:35:LYS:H	1:A:35:LYS:HD2	0.51	1.66	4	2
1:A:34:LEU:HD12	1:A:101:TYR:CE2	0.51	2.40	5	3
1:A:36:HIS:HB2	1:A:101:TYR:CE2	0.51	2.41	5	1
1:A:108:ARG:O	1:A:108:ARG:HD3	0.49	2.07	1	1
1:A:108:ARG:CD	1:A:147:THR:HB	0.49	2.37	1	1
1:A:6:LEU:HD13	1:A:40:TRP:CH2	0.48	2.44	1	7
1:A:129:LYS:N	1:A:129:LYS:HD2	0.48	2.23	3	2
1:A:61:LEU:O	2:B:426:PRO:HA	0.48	2.09	9	1
2:B:425:LYS:HG2	2:B:425:LYS:O	0.48	2.07	9	1
1:A:10:LYS:HB3	1:A:25:GLU:HB3	0.48	1.85	6	6
1:A:106:PHE:HB2	1:A:151:ILE:HD13	0.48	1.85	9	1
1:A:28:PHE:CZ	1:A:70:ASN:HB2	0.48	2.44	6	2
1:A:4:VAL:HG13	1:A:28:PHE:CD1	0.47	2.44	4	1
1:A:18:PHE:CZ	1:A:79:PRO:HG2	0.47	2.45	4	1
1:A:113:VAL:CG1	1:A:139:ILE:HG12	0.47	2.40	1	1
1:A:115:ASN:OD1	1:A:135:ILE:HG23	0.46	2.10	9	1
1:A:129:LYS:HD2	1:A:129:LYS:O	0.46	2.11	10	1
1:A:70:ASN:OD1	2:B:424:LEU:HD23	0.46	2.09	2	2
1:A:41:LYS:HG2	1:A:59:SER:CB	0.46	2.40	9	1
1:A:94:VAL:HA	1:A:111:TYR:O	0.46	2.10	8	1
1:A:30:CYS:SG	1:A:67:VAL:HA	0.46	2.51	9	2
1:A:81:ALA:HB1	1:A:130:VAL:HG11	0.45	1.88	2	1
1:A:90:VAL:HA	1:A:115:ASN:CG	0.45	2.32	9	1
1:A:57:LEU:HB3	1:A:77:ASP:O	0.45	2.11	2	2
1:A:97:LEU:O	1:A:108:ARG:HA	0.45	2.11	5	5
2:B:425:LYS:HD3	2:B:425:LYS:H	0.45	1.71	9	1
1:A:39:GLU:O	1:A:99:CYS:HA	0.45	2.12	1	3
1:A:98:SER:HA	1:A:107:VAL:O	0.45	2.11	1	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:9:ILE:CG2	1:A:24:PHE:HB3	0.44	2.42	6	1
1:A:36:HIS:HB2	1:A:101:TYR:OH	0.44	2.13	7	1
1:A:86:ALA:O	1:A:90:VAL:HG23	0.44	2.13	5	1
1:A:26:ILE:HD11	1:A:97:LEU:HD21	0.44	1.90	4	2
1:A:40:TRP:CZ3	1:A:99:CYS:HB2	0.44	2.47	5	2
1:A:9:ILE:HD11	1:A:109:VAL:HG21	0.43	1.90	3	1
1:A:89:LEU:O	1:A:115:ASN:HB3	0.43	2.13	4	1
1:A:7:LEU:HD13	1:A:28:PHE:HA	0.43	1.90	8	3
1:A:37:ASP:HB2	1:A:61:LEU:HD21	0.43	1.89	5	1
1:A:120:GLU:O	1:A:124:GLU:HG2	0.43	2.13	6	1
1:A:10:LYS:O	1:A:12:LEU:HD22	0.43	2.14	10	3
1:A:11:VAL:HG12	1:A:24:PHE:CE1	0.43	2.49	3	1
1:A:18:PHE:CZ	1:A:84:ILE:HD11	0.43	2.48	4	1
1:A:37:ASP:HB3	1:A:61:LEU:HD21	0.43	1.88	2	1
1:A:108:ARG:HD2	1:A:147:THR:HB	0.43	1.91	1	1
1:A:106:PHE:HB3	1:A:151:ILE:HD13	0.42	1.92	2	2
1:A:69:VAL:CG1	2:B:421:ILE:HG23	0.42	2.45	5	1
1:A:7:LEU:HD11	1:A:29:GLU:HB2	0.42	1.92	9	1
1:A:92:VAL:HA	1:A:113:VAL:O	0.41	2.15	8	1
1:A:98:SER:HB2	1:A:105:GLU:CD	0.41	2.36	1	1
1:A:33:SER:O	1:A:35:LYS:HE3	0.41	2.15	7	1
1:A:129:LYS:CD	1:A:129:LYS:N	0.41	2.83	6	1
1:A:81:ALA:HB2	1:A:132:VAL:HG21	0.41	1.93	9	2
1:A:93:THR:OG1	1:A:113:VAL:HG23	0.41	2.15	3	1
1:A:120:GLU:HA	1:A:123:ARG:HD3	0.41	1.92	10	1
1:A:9:ILE:HD11	1:A:97:LEU:HD22	0.40	1.92	8	1
1:A:118:ASP:HB2	1:A:136:VAL:CG2	0.40	2.47	5	1
1:A:120:GLU:HG3	1:A:123:ARG:NH2	0.40	2.31	1	1
1:A:129:LYS:N	1:A:129:LYS:HD3	0.40	2.32	6	1
1:A:34:LEU:HD22	1:A:34:LEU:N	0.40	2.31	10	1
1:A:109:VAL:HG13	1:A:146:VAL:CG2	0.40	2.44	7	1
1:A:26:ILE:HD11	1:A:97:LEU:CD1	0.40	2.46	7	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	143/172 (83%)	137±1 (96±1%)	6±1 (4±1%)	0±0 (0±0%)	100	100
2	B	6/15 (40%)	4±1 (70±18%)	1±1 (23±15%)	0±0 (7±8%)	3	18
All	All	1490/1870 (80%)	1414 (95%)	72 (5%)	4 (0%)	48	82

All 2 unique Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Models (Total)
2	B	421	ILE	3
2	B	425	LYS	1

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	131/155 (85%)	121±2 (92±1%)	10±2 (8±1%)	19	65
2	B	6/12 (50%)	4±1 (62±11%)	2±1 (38±11%)	1	6
All	All	1370/1670 (82%)	1243 (91%)	127 (9%)	15	60

All 28 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	35	LYS	10
1	A	62	VAL	10
1	A	65	VAL	10
2	B	424	LEU	10
1	A	113	VAL	9
1	A	69	VAL	9
2	B	421	ILE	8
1	A	19	THR	8
1	A	84	ILE	6
1	A	148	ARG	5
1	A	13	ASN	4
1	A	70	ASN	4
1	A	17	LYS	4
1	A	108	ARG	4

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Mol	Chain	Res	Type	Models (Total)
2	B	423	MET	4
1	A	129	LYS	3
1	A	20	ASP	3
1	A	97	LEU	2
1	A	41	LYS	2
1	A	118	ASP	2
1	A	125	ASN	2
1	A	114	ASN	2
1	A	58	ASP	1
1	A	59	SER	1
2	B	425	LYS	1
1	A	119	GLU	1
1	A	83	LEU	1
1	A	137	ARG	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

The completeness of assignment taking into account all chemical shift lists is 90% for the well-defined parts and 88% for the entire structure.

7.1 Chemical shift list 1

File name: 6f0y_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	128
Number of shifts mapped to atoms	128
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 2%, i.e. 41 atoms were assigned a chemical shift out of a possible 1858. 0 out of 35 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	11/723 (2%)	11/287 (4%)	0/298 (0%)	0/138 (0%)
Sidechain	30/996 (3%)	30/580 (5%)	0/380 (0%)	0/36 (0%)
Aromatic	0/139 (0%)	0/73 (0%)	0/61 (0%)	0/5 (0%)
Overall	41/1858 (2%)	41/940 (4%)	0/739 (0%)	0/179 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 4%, i.e. 100 atoms were assigned a chemical shift out of a possible 2309. 0 out of 40 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	27/907 (3%)	27/360 (8%)	0/374 (0%)	0/173 (0%)
Sidechain	73/1235 (6%)	73/722 (10%)	0/465 (0%)	0/48 (0%)
Aromatic	0/167 (0%)	0/87 (0%)	0/72 (0%)	0/8 (0%)
Overall	100/2309 (4%)	100/1169 (9%)	0/911 (0%)	0/229 (0%)

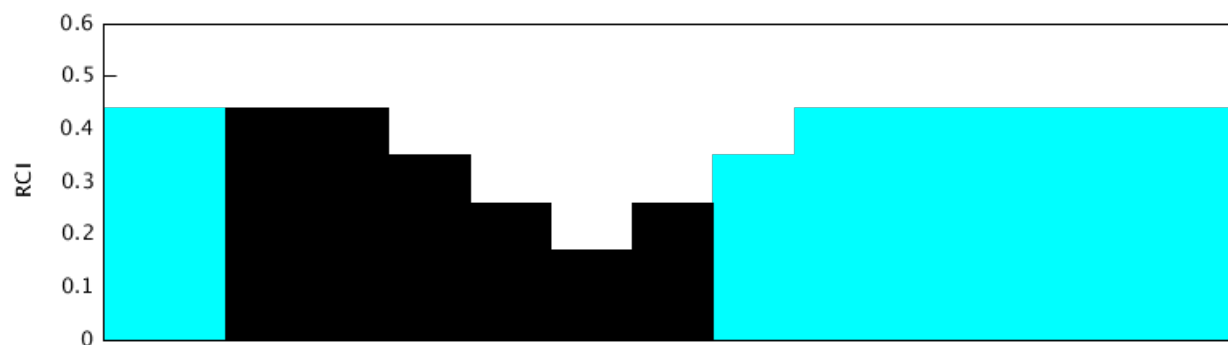
7.1.4 Statistically unusual chemical shifts [i](#)

There are no statistically unusual chemical shifts.

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.

Random coil index (RCI) for chain B:



7.2 Chemical shift list 2

File name: 6f0y_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1_2*

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	2292
Number of shifts mapped to atoms	2292

Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.2.2 Chemical shift referencing ⓘ

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	168	0.07 ± 0.11	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	158	0.00 ± 0.10	None needed (< 0.5 ppm)
$^{13}\text{C}'$	149	0.20 ± 0.11	None needed (< 0.5 ppm)
^{15}N	154	-0.43 ± 0.26	None needed (< 0.5 ppm)

7.2.3 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 90%, i.e. 1666 atoms were assigned a chemical shift out of a possible 1858. 0 out of 35 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	674/723 (93%)	282/287 (98%)	263/298 (88%)	129/138 (93%)
Sidechain	869/996 (87%)	544/580 (94%)	309/380 (81%)	16/36 (44%)
Aromatic	123/139 (88%)	67/73 (92%)	55/61 (90%)	1/5 (20%)
Overall	1666/1858 (90%)	893/940 (95%)	627/739 (85%)	146/179 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 88%, i.e. 2024 atoms were assigned a chemical shift out of a possible 2309. 0 out of 40 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	824/907 (91%)	353/360 (98%)	317/374 (85%)	154/173 (89%)
Sidechain	1053/1235 (85%)	677/722 (94%)	356/465 (77%)	20/48 (42%)
Aromatic	147/167 (88%)	79/87 (91%)	66/72 (92%)	2/8 (25%)
Overall	2024/2309 (88%)	1109/1169 (95%)	739/911 (81%)	176/229 (77%)

7.2.4 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 con-

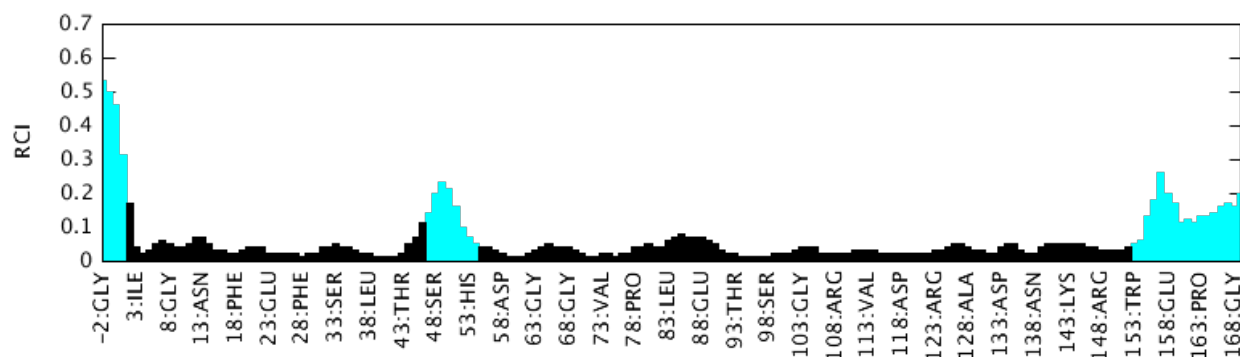
taining paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	3	ILE	HB	-0.03	3.24 – 0.34	-6.3
1	A	70	ASN	HB3	0.92	4.41 – 1.11	-5.6
1	A	40	TRP	HE1	7.22	12.85 – 7.35	-5.2
1	A	99	CYS	HB3	0.48	5.25 – 0.55	-5.2

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

The images below report *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:



Random coil index (RCI) for chain B:

