Full wwPDB NMR Structure Validation Report (i)

Apr 26, 2016 – 03:59 PM BST

PDB ID	:	1L1M
Title	:	SOLUTION STRUCTURE OF A DIMER OF LAC REPRESSOR DNA-BINDING DOMAIN COMPLEXED TO ITS NATURAL OPERATOR O1
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Deposited on	:	2002-02-19

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 (i) symbol.

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

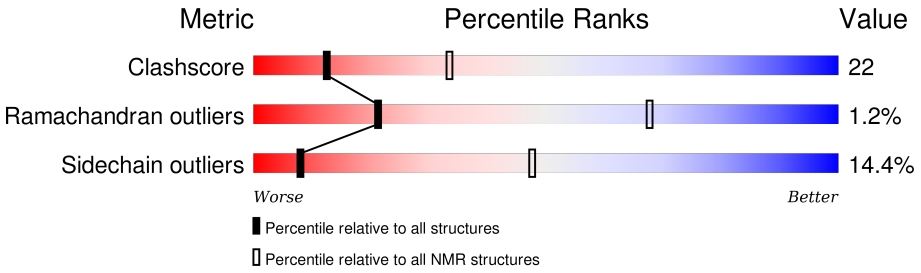
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20027457

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 67%.

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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 <=5%

Mol	Chain	Length	Quality of chain
1	C	23	57% 43%
2	D	23	57% 43%
3	A	62	60% 31% 10%
3	B	62	52% 24% 6% 18%

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:58, B:4-B:25, B:29-B:57 (107)	0.39	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 3 clusters. No single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3382 atoms, of which 1491 are hydrogens and 0 are deuteriums.

- Molecule 1 is a DNA chain called 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
1	C	23	737	228	262	90	135	22	0

- Molecule 2 is a DNA chain called 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	P	
2	D	23	725	224	263	79	137	22	0

- Molecule 3 is a protein called Lactose operon repressor.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
3	A	62	960	296	483	85	93	3	0
3	B	62	Total	C	H	N	O	S	0
			960	296	483	85	93	3	

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	CYS	VAL	ENGINEERED	UNP P03023
B	52	CYS	VAL	ENGINEERED	UNP P03023

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: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

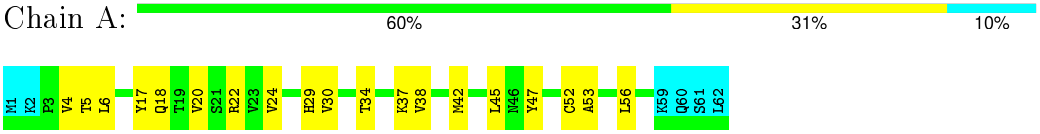
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

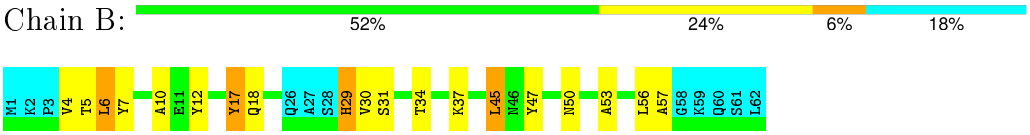
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



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: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

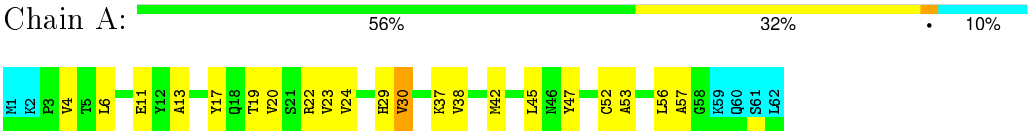
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

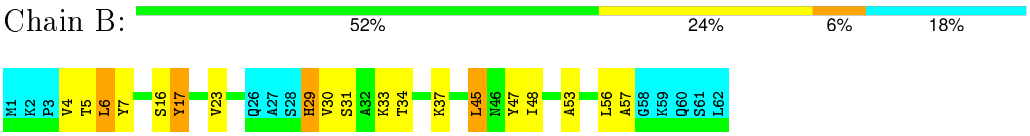
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.2 Score per residue for model 2

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

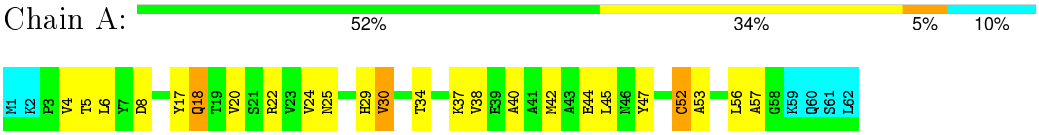
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

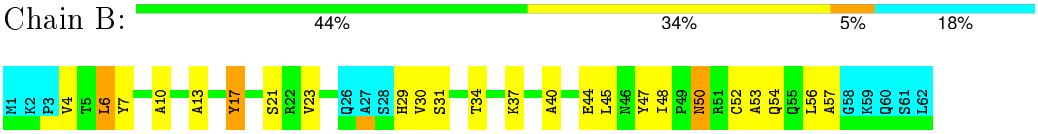
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



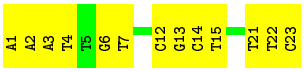
4.2.3 Score per residue for model 3

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

Chain C:

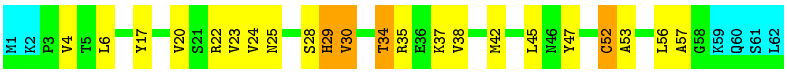
• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:



• Molecule 3: Lactose operon repressor

Chain A:



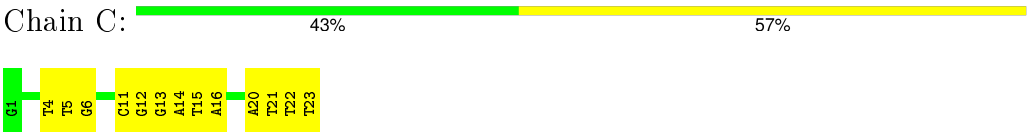
• Molecule 3: Lactose operon repressor

Chain B:

4.2.4 Score per residue for model 4

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

Chain C:

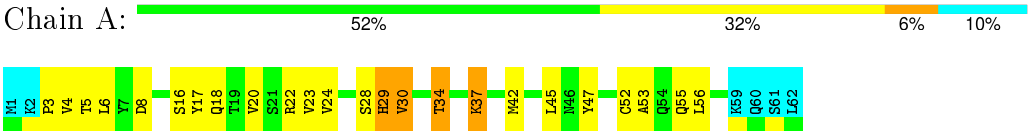


• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

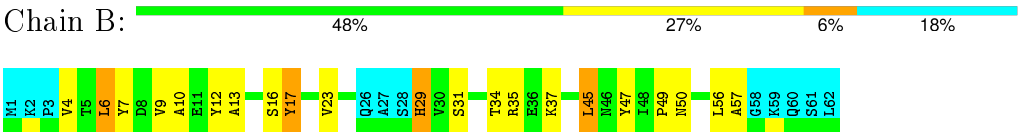
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



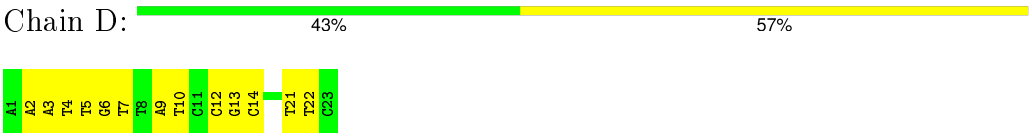
4.2.5 Score per residue for model 5

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

Chain C:

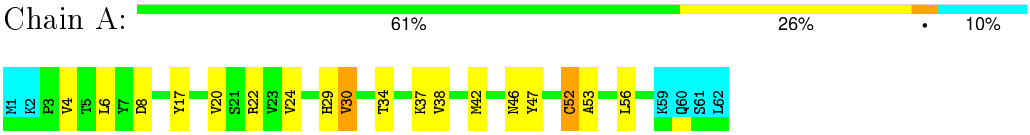
• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:



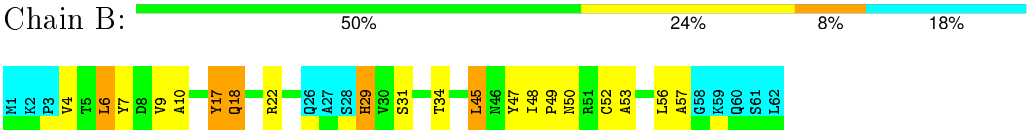
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

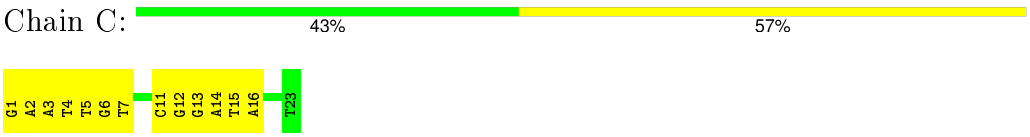
Chain B:



4.2.6 Score per residue for model 6

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

Chain C:

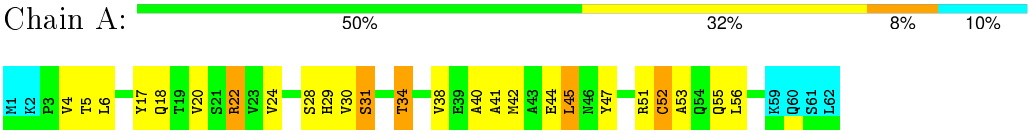


• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

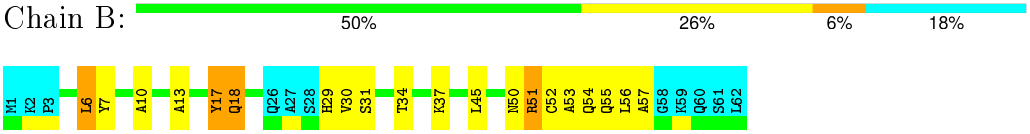
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.7 Score per residue for model 7

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*C
P*AP*AP*TP*TP*T)-3'

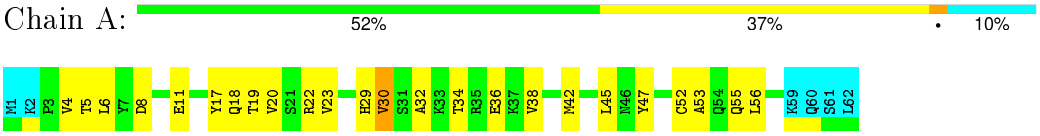
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*C
P*AP*AP*TP*TP*C)-3'

Chain D:

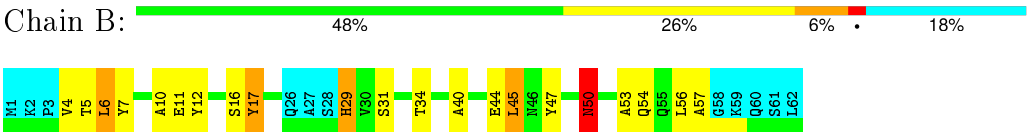
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.8 Score per residue for model 8

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*C
P*AP*AP*TP*TP*T)-3'

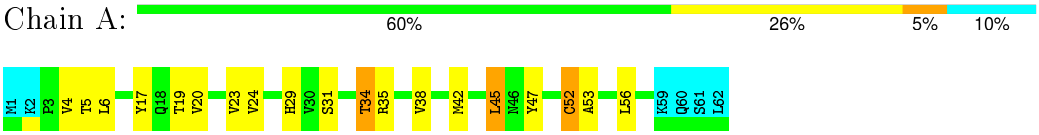
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*C
P*AP*AP*TP*TP*C)-3'

Chain D:

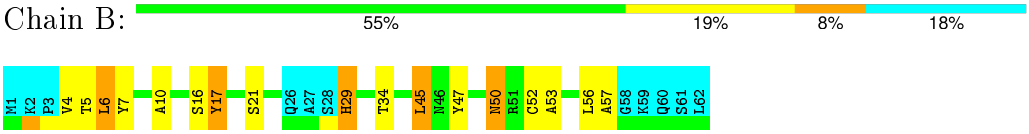
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.9 Score per residue for model 9

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

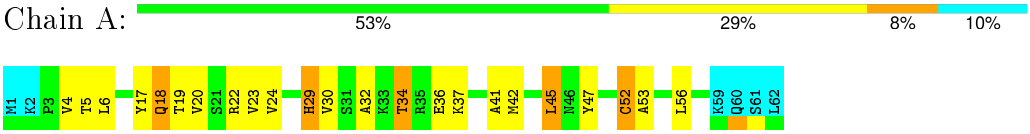
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

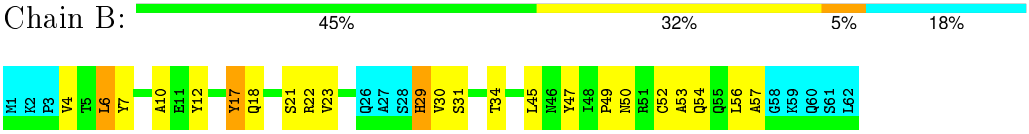
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.10 Score per residue for model 10

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

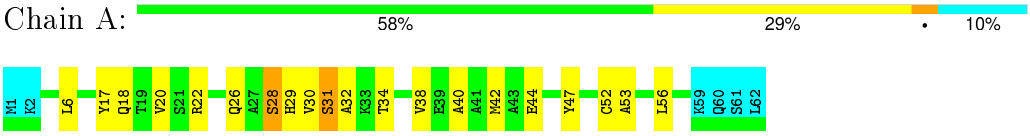
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

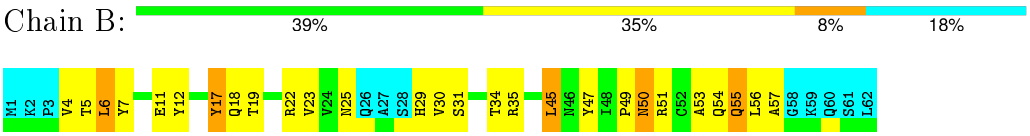
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.11 Score per residue for model 11

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

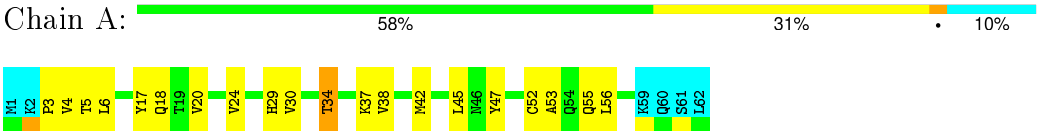
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

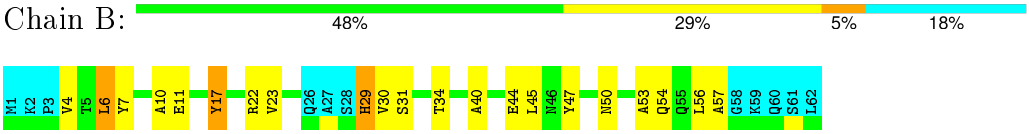
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

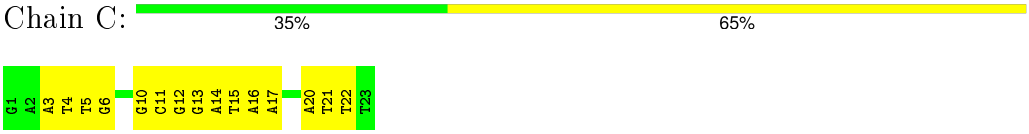
Chain B:



4.2.12 Score per residue for model 12

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

Chain C:

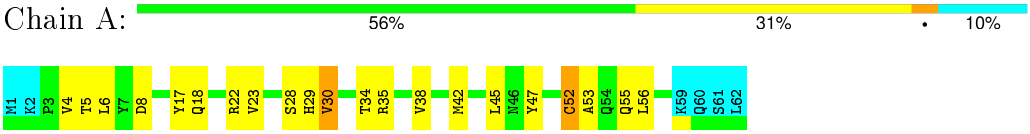


• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

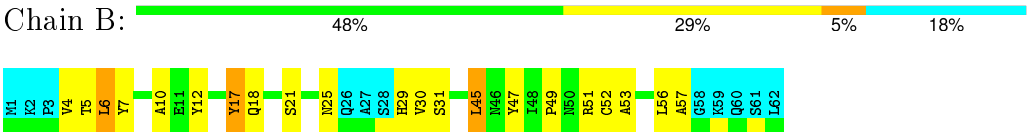
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

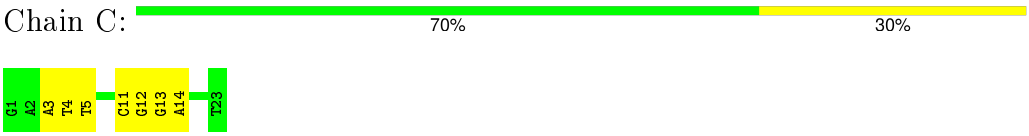
Chain B:



4.2.13 Score per residue for model 13

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

Chain C:

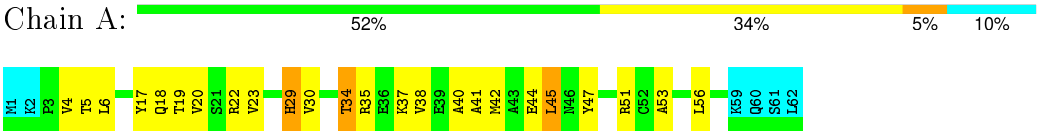


• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

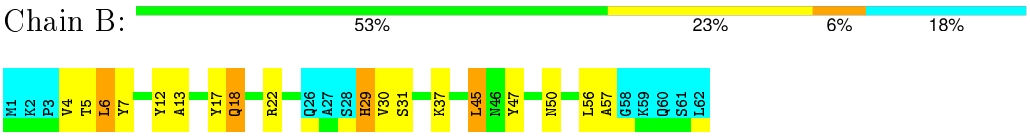
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.14 Score per residue for model 14

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

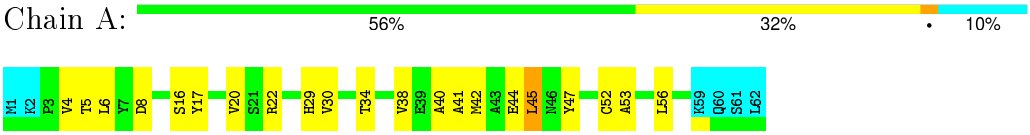
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

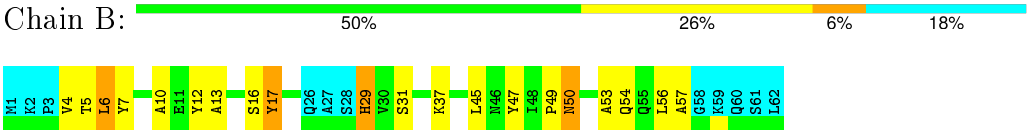
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.15 Score per residue for model 15

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

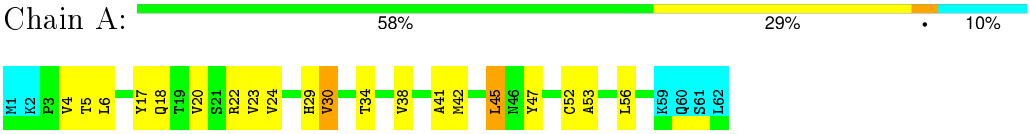
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

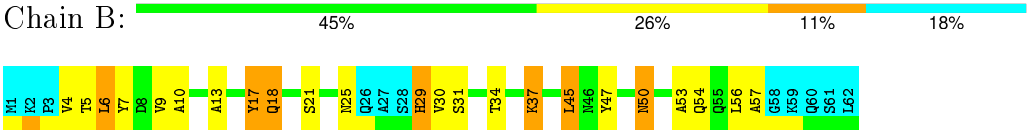
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.16 Score per residue for model 16

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

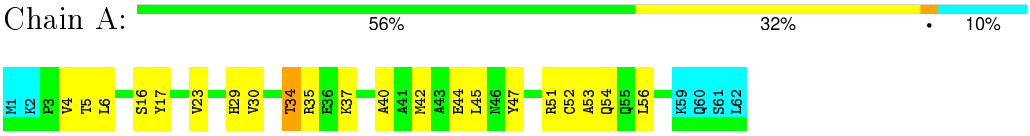
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

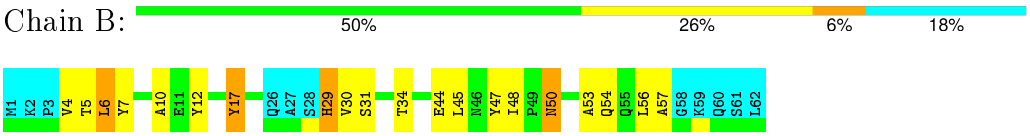
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.17 Score per residue for model 17

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

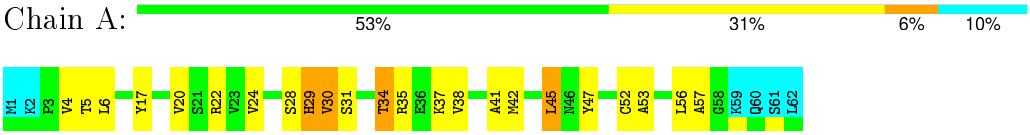
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

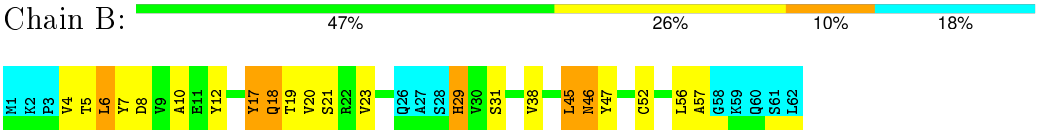
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.18 Score per residue for model 18

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

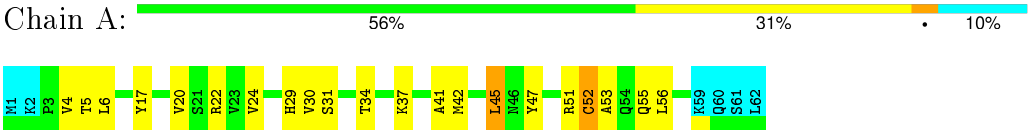
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

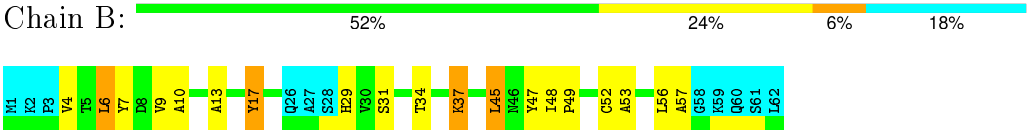
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



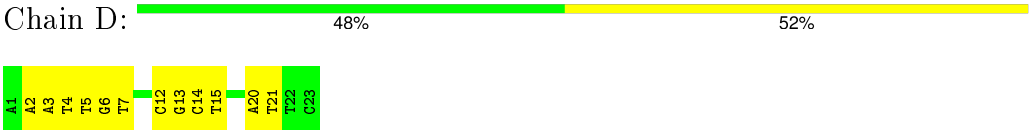
4.2.19 Score per residue for model 19

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

Chain C:

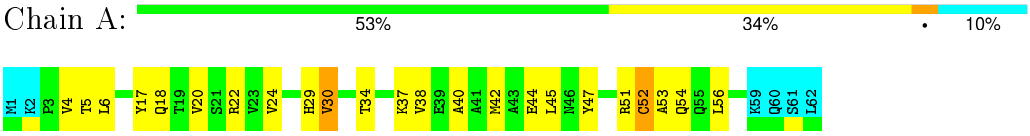
• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:



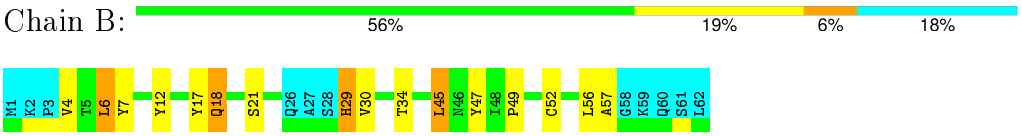
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



4.2.20 Score per residue for model 20

• Molecule 1: 5'-D(*GP*AP*AP*TP*TP*GP*TP*GP*AP*GP*CP*GP*GP*AP*TP*AP*AP*CP*AP*AP*TP*TP*T)-3'

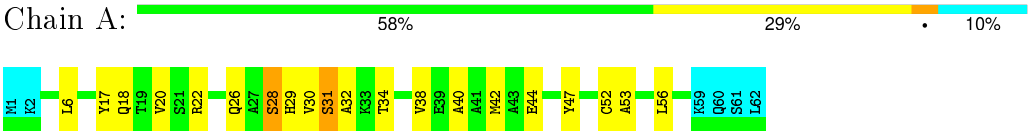
Chain C:

• Molecule 2: 5'-D(*AP*AP*AP*TP*TP*GP*TP*TP*AP*TP*CP*CP*GP*CP*TP*CP*AP*CP*AP*AP*TP*TP*C)-3'

Chain D:

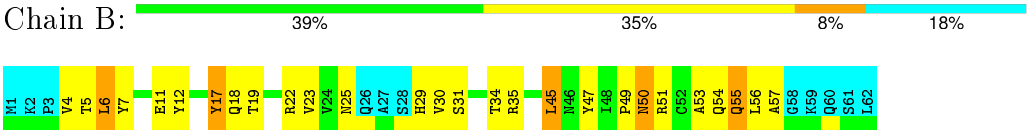
• Molecule 3: Lactose operon repressor

Chain A:



• Molecule 3: Lactose operon repressor

Chain B:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *SIMULATED ANNEALING FOLLOWED BY RESTRAINED MDR.*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *STRUCTURES WITH THE LOWEST ENERGY.*

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CNS	structure solution	1.1
CNS	refinement	1.1

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)	BMRB entry 5345
Number of chemical shift lists	4
Total number of shifts	3248
Number of shifts mapped to atoms	3248
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	67%

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

6 Model quality

6.1 Standard geometry

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

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	C	475	262	262	30±4
2	D	462	263	263	21±3
3	A	427	422	421	19±3
3	B	396	394	393	24±2
All	All	35200	26820	26780	1363

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 22.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:13:DG:C2	3:B:56:LEU:HD21	0.92	1.99	1	20
3:A:4:VAL:HB	3:A:47:TYR:HA	0.88	1.46	7	16
2:D:12:DC:H2"	2:D:13:DG:N7	0.83	1.89	14	20
3:A:6:LEU:HG	3:A:17:TYR:HB2	0.83	1.51	3	20
2:D:5:DT:C7	3:B:29:HIS:HB3	0.79	2.07	12	7
3:A:22:ARG:HG3	3:A:30:VAL:HG22	0.79	1.55	18	4
1:C:12:DG:C2	3:A:56:LEU:HD21	0.74	2.18	8	20
3:B:4:VAL:HB	3:B:47:TYR:HA	0.74	1.59	5	18
1:C:5:DT:C7	3:A:29:HIS:HB3	0.73	2.13	16	16
1:C:14:DA:OP2	3:B:6:LEU:HB3	0.73	1.82	13	20
1:C:3:DA:C8	1:C:4:DT:H72	0.72	2.19	12	16

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:4:DT:H72	3:B:29:HIS:CG	0.72	2.20	5	13
2:D:3:DA:C8	2:D:4:DT:H72	0.70	2.20	14	5
3:A:42:MET:HB2	3:A:47:TYR:HB3	0.70	1.63	1	20
1:C:13:DG:H21	3:B:57:ALA:HB1	0.70	1.45	5	20
3:A:23:VAL:HG22	3:A:30:VAL:HG11	0.69	1.62	15	3
1:C:13:DG:C2'	3:B:7:TYR:HE1	0.69	2.00	12	20
2:D:12:DC:H2"	2:D:13:DG:C8	0.68	2.23	16	20
2:D:16:DC:N4	3:A:18:GLN:HE22	0.68	1.86	7	1
1:C:4:DT:H72	3:A:29:HIS:CG	0.67	2.25	3	4
3:A:22:ARG:HB3	3:A:30:VAL:HG22	0.67	1.64	1	7
1:C:14:DA:P	3:B:6:LEU:HB3	0.67	2.29	2	20
2:D:6:DG:C2'	2:D:7:DT:H71	0.66	2.20	5	11
3:B:6:LEU:HD23	3:B:17:TYR:CE1	0.66	2.25	19	1
1:C:13:DG:H2'	3:B:7:TYR:HE1	0.66	1.51	19	8
1:C:4:DT:C6	1:C:5:DT:H72	0.66	2.25	16	1
1:C:13:DG:H2'	3:B:7:TYR:CE1	0.65	2.27	13	20
1:C:15:DT:OP2	3:B:21:SER:HB2	0.65	1.91	8	1
2:D:13:DG:C4	3:B:56:LEU:HD11	0.64	2.28	3	16
2:D:6:DG:H2"	2:D:7:DT:H71	0.62	1.72	5	5
3:A:34:THR:HA	3:A:37:LYS:HG2	0.61	1.71	17	9
1:C:13:DG:C2'	3:B:7:TYR:CE1	0.60	2.84	17	19
3:A:52:CYS:HB3	3:B:52:CYS:HA	0.60	1.72	3	10
1:C:12:DG:H1'	1:C:13:DG:O5'	0.60	1.97	18	19
3:A:18:GLN:O	3:A:22:ARG:HG2	0.60	1.97	2	2
2:D:14:DC:C5'	3:A:53:ALA:HB3	0.60	2.27	7	20
2:D:13:DG:C5	2:D:14:DC:C4	0.59	2.90	19	20
2:D:5:DT:H71	3:B:29:HIS:HB3	0.59	1.74	15	5
3:B:4:VAL:HG21	3:B:45:LEU:O	0.59	1.98	15	12
2:D:13:DG:N2	3:B:56:LEU:HD21	0.59	2.11	2	15
1:C:4:DT:H73	3:A:29:HIS:CG	0.58	2.33	7	16
3:B:4:VAL:HB	3:B:48:ILE:H	0.58	1.57	16	3
3:A:4:VAL:HG11	3:A:45:LEU:HG	0.58	1.74	17	7
3:B:50:ASN:O	3:B:54:GLN:HB2	0.58	1.98	11	6
2:D:4:DT:C7	3:B:29:HIS:HB3	0.58	2.29	10	2
1:C:15:DT:OP2	3:B:21:SER:HB3	0.57	1.99	15	3
3:B:23:VAL:HG13	3:B:35:ARG:HG3	0.57	1.77	4	1
1:C:13:DG:H1'	1:C:14:DA:H5'	0.57	1.76	19	10
1:C:14:DA:OP1	3:B:6:LEU:HB3	0.56	2.01	9	17
3:B:10:ALA:HB2	3:B:17:TYR:HA	0.55	1.76	8	12
1:C:5:DT:H72	3:A:22:ARG:CZ	0.55	2.32	5	1
3:B:22:ARG:HD2	3:B:29:HIS:HB2	0.55	1.79	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:4:DT:H73	3:B:29:HIS:CG	0.55	2.37	12	5
3:B:23:VAL:HG22	3:B:30:VAL:HG11	0.54	1.80	10	4
2:D:6:DG:C8	2:D:7:DT:H72	0.54	2.37	4	9
2:D:13:DG:C4	2:D:14:DC:C5	0.53	2.96	3	18
2:D:1:DA:H8	2:D:1:DA:HO5'	0.53	1.47	3	3
1:C:12:DG:N3	3:A:56:LEU:HD21	0.53	2.19	18	12
1:C:12:DG:H1'	1:C:13:DG:C5'	0.53	2.34	18	20
1:C:13:DG:OP1	3:B:5:THR:HG21	0.53	2.03	17	6
3:B:12:TYR:HB3	3:B:45:LEU:HD21	0.53	1.79	17	3
1:C:12:DG:C4	1:C:13:DG:C8	0.52	2.97	16	16
2:D:14:DC:OP2	3:A:6:LEU:HB3	0.52	2.04	3	16
3:B:9:VAL:HA	3:B:45:LEU:HD23	0.52	1.80	3	5
3:B:10:ALA:CB	3:B:17:TYR:HA	0.52	2.34	2	10
3:B:13:ALA:HB1	3:B:37:LYS:HG2	0.52	1.80	14	5
1:C:20:DA:C8	1:C:21:DT:H72	0.52	2.40	14	8
1:C:13:DG:H2"	3:B:7:TYR:HE1	0.52	1.65	5	8
1:C:14:DA:C8	3:B:17:TYR:HE2	0.52	2.22	13	2
1:C:2:DA:C6	1:C:3:DA:C6	0.52	2.98	9	4
3:B:40:ALA:O	3:B:44:GLU:HG2	0.52	2.05	7	3
2:D:15:DT:C2	2:D:16:DC:C5	0.51	2.98	12	5
3:B:6:LEU:HD23	3:B:17:TYR:OH	0.51	2.05	13	1
3:B:12:TYR:CB	3:B:45:LEU:HD21	0.51	2.35	17	10
1:C:6:DG:C2'	1:C:7:DT:H71	0.51	2.36	9	5
3:B:18:GLN:O	3:B:22:ARG:HG2	0.51	2.05	13	4
3:B:4:VAL:HG13	3:B:8:ASP:HB2	0.51	1.82	17	1
2:D:4:DT:C6	3:B:29:HIS:HB3	0.51	2.41	4	2
2:D:21:DT:C6	2:D:22:DT:H72	0.51	2.41	9	3
1:C:14:DA:H1'	1:C:15:DT:O5'	0.51	2.05	15	3
1:C:12:DG:O4'	3:A:56:LEU:HD11	0.51	2.06	3	13
1:C:13:DG:O4'	3:B:53:ALA:HB1	0.51	2.06	8	16
3:A:41:ALA:O	3:A:45:LEU:HD22	0.51	2.06	13	7
1:C:1:DG:H8	1:C:1:DG:HO5'	0.51	1.49	9	1
1:C:14:DA:C2	1:C:15:DT:C2	0.50	2.99	15	2
1:C:11:DC:C5	1:C:12:DG:O6	0.50	2.64	2	19
3:A:4:VAL:HG13	3:A:8:ASP:HB2	0.50	1.83	4	2
2:D:6:DG:C4	2:D:7:DT:C5	0.50	2.99	19	1
1:C:5:DT:H1'	1:C:6:DG:O5'	0.50	2.06	15	1
1:C:4:DT:OP2	3:A:29:HIS:HA	0.50	2.06	9	10
2:D:2:DA:C6	2:D:3:DA:C6	0.50	3.00	14	6
1:C:15:DT:C2	1:C:16:DA:N7	0.50	2.79	17	6
3:B:7:TYR:O	3:B:11:GLU:HG3	0.50	2.07	11	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:3:DA:H2'	2:D:4:DT:H71	0.50	1.83	2	1
2:D:4:DT:OP2	3:B:29:HIS:HA	0.50	2.07	10	3
1:C:12:DG:H2"	1:C:13:DG:OP2	0.49	2.05	13	19
2:D:4:DT:H73	3:B:29:HIS:CD2	0.49	2.42	4	1
3:A:34:THR:O	3:A:38:VAL:HG23	0.49	2.07	8	8
3:A:23:VAL:HG13	3:A:35:ARG:HG3	0.49	1.85	12	5
3:B:33:LYS:O	3:B:37:LYS:HG3	0.49	2.07	1	1
3:B:13:ALA:HB1	3:B:37:LYS:HG3	0.49	1.83	15	2
1:C:11:DC:H2"	1:C:12:DG:C8	0.49	2.43	8	5
1:C:7:DT:H71	3:A:18:GLN:HB2	0.48	1.85	6	2
1:C:12:DG:C4	1:C:13:DG:N7	0.48	2.81	4	16
3:A:22:ARG:HD3	3:A:29:HIS:HB2	0.48	1.85	1	2
2:D:13:DG:N3	3:B:56:LEU:HD11	0.48	2.23	19	7
1:C:12:DG:C6	1:C:13:DG:C6	0.48	3.01	17	14
2:D:20:DA:C8	2:D:21:DT:H72	0.48	2.43	7	7
1:C:10:DG:C4	1:C:11:DC:C5	0.48	3.00	10	8
3:A:20:VAL:O	3:A:24:VAL:HG23	0.48	2.08	18	13
1:C:12:DG:H1'	1:C:13:DG:C8	0.48	2.43	13	12
3:A:6:LEU:CG	3:A:17:TYR:HB2	0.48	2.34	3	3
3:A:18:GLN:O	3:A:22:ARG:HG3	0.48	2.08	7	3
2:D:3:DA:C5	2:D:4:DT:C4	0.48	3.02	15	7
2:D:5:DT:C7	3:B:29:HIS:HB2	0.47	2.39	4	4
1:C:15:DT:C4	1:C:16:DA:N6	0.47	2.82	18	6
2:D:5:DT:H2"	2:D:6:DG:OP2	0.47	2.08	2	13
3:A:40:ALA:O	3:A:44:GLU:HG2	0.47	2.10	13	8
3:A:4:VAL:HG21	3:A:45:LEU:O	0.47	2.08	8	3
3:B:6:LEU:HB2	3:B:47:TYR:CZ	0.47	2.45	13	1
3:B:5:THR:OG1	3:B:7:TYR:HB2	0.47	2.10	7	3
1:C:6:DG:H2"	1:C:7:DT:H71	0.47	1.85	9	1
1:C:15:DT:H71	3:B:21:SER:OG	0.47	2.10	19	1
2:D:5:DT:C4	2:D:6:DG:C6	0.47	3.03	7	1
1:C:16:DA:N6	3:B:18:GLN:OE1	0.47	2.47	15	4
3:A:20:VAL:HA	3:A:38:VAL:HG11	0.47	1.87	10	10
1:C:14:DA:C8	3:B:17:TYR:OH	0.47	2.66	10	4
1:C:13:DG:H21	3:B:57:ALA:CB	0.47	2.23	13	10
3:B:5:THR:HA	3:B:50:ASN:OD1	0.46	2.11	13	3
2:D:14:DC:H5'	3:A:53:ALA:CB	0.46	2.41	16	20
3:B:50:ASN:HB2	3:B:54:GLN:HG3	0.46	1.86	10	2
2:D:2:DA:C4	2:D:3:DA:N7	0.46	2.84	5	1
2:D:22:DT:C4	2:D:23:DC:N4	0.46	2.83	3	1
3:A:22:ARG:HG3	3:A:28:SER:O	0.46	2.11	10	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
2:D:20:DA:C2'	2:D:21:DT:H71	0.46	2.41	10	6
2:D:13:DG:N9	2:D:14:DC:C5	0.46	2.84	8	15
3:A:34:THR:HA	3:A:37:LYS:HE2	0.46	1.87	4	1
1:C:5:DT:H73	3:A:29:HIS:HB3	0.46	1.88	2	3
1:C:12:DG:C5	1:C:13:DG:N7	0.46	2.84	16	1
3:B:52:CYS:O	3:B:56:LEU:HB2	0.46	2.11	2	2
3:A:18:GLN:O	3:A:22:ARG:HB2	0.45	2.11	15	3
2:D:19:DA:C4	2:D:20:DA:N7	0.45	2.84	10	2
2:D:3:DA:C2'	2:D:4:DT:H71	0.45	2.42	6	5
1:C:13:DG:H5"	3:B:50:ASN:HD22	0.45	1.71	5	1
2:D:6:DG:C2'	2:D:7:DT:H72	0.45	2.42	10	6
1:C:16:DA:H2"	1:C:17:DA:OP2	0.45	2.11	10	5
3:A:34:THR:O	3:A:37:LYS:HG2	0.45	2.12	13	1
2:D:5:DT:H73	3:B:29:HIS:HB3	0.45	1.88	6	2
2:D:14:DC:H5'	3:A:53:ALA:HB3	0.45	1.88	13	6
3:A:45:LEU:HD22	3:A:45:LEU:H	0.45	1.71	17	4
1:C:21:DT:C2'	1:C:22:DT:H71	0.45	2.42	11	3
1:C:12:DG:H1'	1:C:13:DG:H5'	0.45	1.89	1	17
3:A:32:ALA:O	3:A:36:GLU:HG3	0.45	2.11	9	2
2:D:4:DT:H73	3:B:29:HIS:CB	0.45	2.42	14	1
3:A:19:THR:O	3:A:23:VAL:HG23	0.44	2.12	8	5
2:D:12:DC:C2'	2:D:13:DG:N7	0.44	2.77	8	5
2:D:4:DT:H72	3:B:29:HIS:CD2	0.44	2.46	5	5
3:B:12:TYR:CE2	3:B:44:GLU:HG3	0.44	2.46	16	1
3:A:19:THR:HA	3:A:22:ARG:HE	0.44	1.71	9	1
1:C:20:DA:C2'	1:C:21:DT:H71	0.44	2.42	2	2
1:C:14:DA:N7	3:B:17:TYR:OH	0.44	2.47	7	2
2:D:9:DA:H2"	2:D:10:DT:OP2	0.44	2.12	8	7
1:C:5:DT:H2"	1:C:6:DG:OP2	0.44	2.12	10	7
1:C:21:DT:C6	1:C:22:DT:H72	0.44	2.47	3	4
3:B:18:GLN:HA	3:B:21:SER:HB3	0.44	1.89	9	2
1:C:10:DG:C4	1:C:11:DC:C4	0.44	3.06	14	2
1:C:4:DT:C3'	3:A:31:SER:HB3	0.44	2.43	18	1
2:D:15:DT:OP1	3:A:54:GLN:HG3	0.44	2.13	19	1
2:D:13:DG:H2"	3:A:6:LEU:HD22	0.44	1.90	4	6
1:C:2:DA:C4	1:C:3:DA:N7	0.44	2.86	10	3
1:C:4:DT:H3'	3:A:31:SER:HB3	0.44	1.89	18	1
1:C:14:DA:C8	3:B:17:TYR:CE2	0.43	3.05	13	1
3:A:13:ALA:HB1	3:A:37:LYS:HG2	0.43	1.90	1	1
2:D:2:DA:C4	2:D:3:DA:C5	0.43	3.06	14	2
2:D:5:DT:C7	3:B:29:HIS:CB	0.43	2.96	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:12:DG:C1'	1:C:13:DG:H5'	0.43	2.43	1	8
3:B:51:ARG:HD3	3:B:51:ARG:H	0.43	1.74	6	1
3:B:30:VAL:HB	3:B:35:ARG:NH2	0.43	2.28	10	2
3:B:6:LEU:CD2	3:B:17:TYR:HD2	0.43	2.27	11	7
2:D:7:DT:H72	3:B:18:GLN:HB2	0.43	1.90	19	1
1:C:2:DA:C4	1:C:3:DA:C5	0.43	3.07	10	3
1:C:11:DC:C4	1:C:12:DG:O6	0.43	2.72	16	1
3:B:7:TYR:O	3:B:11:GLU:HG2	0.43	2.14	7	1
3:A:45:LEU:H	3:A:45:LEU:HD22	0.43	1.74	13	1
2:D:13:DG:H1'	2:D:14:DC:H5'	0.43	1.90	17	5
2:D:15:DT:H5'	3:A:57:ALA:HB3	0.43	1.89	17	4
2:D:3:DA:C8	2:D:4:DT:C7	0.43	3.02	15	2
1:C:7:DT:C7	3:A:16:SER:HB2	0.43	2.43	16	2
3:B:5:THR:HG22	3:B:50:ASN:HD21	0.43	1.74	14	1
3:A:24:VAL:HG21	3:A:47:TYR:HE2	0.43	1.74	11	2
2:D:4:DT:H72	3:B:29:HIS:ND1	0.43	2.28	2	1
2:D:1:DA:O5'	2:D:1:DA:C8	0.42	2.72	2	2
2:D:13:DG:C8	2:D:14:DC:C5	0.42	3.07	19	2
1:C:1:DG:C8	1:C:1:DG:O5'	0.42	2.71	5	1
1:C:19:DA:C6	1:C:20:DA:N6	0.42	2.87	2	1
2:D:13:DG:C4	2:D:14:DC:C4	0.42	3.07	13	4
1:C:3:DA:C5	1:C:4:DT:C4	0.42	3.08	8	3
3:B:51:ARG:O	3:B:55:GLN:HB2	0.42	2.14	10	2
1:C:1:DG:C6	1:C:2:DA:C6	0.42	3.08	15	2
2:D:14:DC:C5'	3:A:53:ALA:CB	0.42	2.98	2	1
1:C:4:DT:H72	3:A:29:HIS:CD2	0.42	2.49	3	1
1:C:11:DC:N4	2:D:12:DC:N4	0.42	2.68	15	2
3:A:31:SER:O	3:A:35:ARG:HB2	0.42	2.15	17	1
3:A:29:HIS:CD2	3:A:29:HIS:N	0.42	2.87	13	1
3:B:45:LEU:O	3:B:46:ASN:HB3	0.42	2.15	17	1
3:B:19:THR:O	3:B:23:VAL:HG23	0.42	2.14	17	1
1:C:4:DT:OP2	3:A:29:HIS:CA	0.42	2.68	2	3
2:D:1:DA:C8	2:D:1:DA:O5'	0.42	2.72	14	2
3:A:51:ARG:O	3:A:55:GLN:HG3	0.42	2.15	6	1
1:C:3:DA:C4	1:C:4:DT:C5	0.41	3.08	5	4
1:C:2:DA:H2"	1:C:3:DA:OP2	0.41	2.15	17	3
2:D:5:DT:H1'	2:D:6:DG:C8	0.41	2.49	1	1
3:A:52:CYS:CB	3:B:52:CYS:HA	0.41	2.45	19	3
3:B:19:THR:HA	3:B:22:ARG:HE	0.41	1.75	10	2
1:C:13:DG:H4'	3:B:50:ASN:HD22	0.41	1.75	4	1
3:B:6:LEU:HD23	3:B:17:TYR:HD2	0.41	1.75	8	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:C:9:DA:H2"	1:C:10:DG:OP2	0.41	2.15	16	1
2:D:3:DA:H2'	2:D:4:DT:H72	0.41	1.91	11	1
2:D:8:DT:C4	2:D:9:DA:N6	0.41	2.88	2	3
2:D:21:DT:C2'	2:D:22:DT:H71	0.41	2.46	3	2
2:D:9:DA:C2	2:D:10:DT:C2	0.41	3.09	15	1
3:B:6:LEU:HB2	3:B:47:TYR:OH	0.41	2.15	19	2
1:C:5:DT:C2	1:C:6:DG:C8	0.41	3.08	15	1
3:A:56:LEU:HD23	3:B:56:LEU:HD23	0.41	1.92	10	2
2:D:4:DT:H72	3:B:29:HIS:HB3	0.41	1.93	10	2
3:B:20:VAL:HG13	3:B:38:VAL:CG1	0.41	2.45	17	1
2:D:5:DT:C4	2:D:6:DG:O6	0.41	2.73	9	1
1:C:6:DG:H2"	1:C:7:DT:OP2	0.41	2.14	6	1
3:B:13:ALA:O	3:B:37:LYS:HD3	0.41	2.16	13	1
3:B:49:PRO:HB3	3:B:54:GLN:OE1	0.41	2.16	14	1
3:A:42:MET:HB2	3:A:47:TYR:CB	0.41	2.46	17	1
1:C:14:DA:H5"	3:B:54:GLN:HG2	0.41	1.93	9	1
3:A:22:ARG:HD2	3:A:28:SER:O	0.40	2.15	4	1
1:C:7:DT:O4	3:A:18:GLN:HG3	0.40	2.17	9	1
2:D:16:DC:H41	3:A:18:GLN:CD	0.40	2.19	2	1
2:D:16:DC:N4	3:A:18:GLN:OE1	0.40	2.54	12	1
1:C:22:DT:C6	1:C:23:DT:H72	0.40	2.51	4	1
1:C:4:DT:H73	3:A:29:HIS:CB	0.40	2.46	9	1
1:C:14:DA:H2"	1:C:15:DT:OP2	0.40	2.16	2	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	
3	A	56/62 (90%)	51±1 (92±2%)	4±1 (8±2%)	0±1 (0±1%)	43	81
3	B	51/62 (82%)	45±1 (88±2%)	5±1 (10±2%)	1±1 (2±1%)	13	53
All	All	2140/2480 (86%)	1919 (90%)	195 (9%)	26 (1%)	21	68

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)
3	B	49	PRO	9
3	B	50	ASN	9
3	A	31	SER	3
3	A	32	ALA	2
3	B	30	VAL	1
3	B	25	ASN	1
3	B	46	ASN	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
3	A	45/51 (88%)	39±1 (87±3%)	6±1 (13±3%)	10 51
3	B	42/51 (82%)	35±1 (84±3%)	7±1 (16±3%)	7 44
All	All	1740/2040 (85%)	1490 (86%)	250 (14%)	8 47

All 35 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)
3	B	6	LEU	20
3	B	45	LEU	18
3	B	31	SER	18
3	A	52	CYS	18
3	B	17	TYR	18
3	B	34	THR	16
3	A	45	LEU	16
3	A	30	VAL	15
3	A	5	THR	15
3	B	29	HIS	14
3	A	34	THR	13
3	B	18	GLN	9
3	B	30	VAL	8
3	A	28	SER	5
3	A	29	HIS	5
3	B	16	SER	5
3	A	8	ASP	4
3	A	31	SER	4

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Mol	Chain	Res	Type	Models (Total)
3	A	51	ARG	4
3	A	18	GLN	3
3	B	37	LYS	2
3	A	26	GLN	2
3	A	25	ASN	2
3	B	11	GLU	2
3	A	11	GLU	2
3	B	51	ARG	2
3	B	55	GLN	2
3	B	25	ASN	1
3	A	22	ARG	1
3	A	46	ASN	1
3	A	54	GLN	1
3	B	50	ASN	1
3	A	55	GLN	1
3	A	37	LYS	1
3	A	16	SER	1

6.3.3 RNA

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates

There are no carbohydrates in this entry.

6.6 Ligand geometry

There are no ligands in this entry.

6.7 Other polymers

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

The completeness of assignment taking into account all chemical shift lists is 67% for the well-defined parts and 67% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 5345

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	1446
Number of shifts mapped to atoms	1446
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	6

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	120	-0.57 ± 0.14	Should be applied
$^{13}C_{\beta}$	112	-0.04 ± 0.18	None needed (< 0.5 ppm)
$^{13}C'$	114	-0.54 ± 0.16	Should be applied
^{15}N	116	0.37 ± 0.46	None needed (< 0.5 ppm)

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 52%, i.e. 1132 atoms were assigned a chemical shift out of a possible 2169. 20 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	529/529 (100%)	211/211 (100%)	214/214 (100%)	104/104 (100%)
Sidechain	563/662 (85%)	353/383 (92%)	191/244 (78%)	19/35 (54%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	40/80 (50%)	36/40 (90%)	4/36 (11%)	0/4 (0%)
Overall	1132/2169 (52%)	600/1164 (52%)	409/808 (51%)	123/197 (62%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 53%, i.e. 1276 atoms were assigned a chemical shift out of a possible 2388. 22 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	586/612 (96%)	236/244 (97%)	234/248 (94%)	116/120 (97%)
Sidechain	650/798 (81%)	410/466 (88%)	218/290 (75%)	22/42 (52%)
Aromatic	40/80 (50%)	36/40 (90%)	4/36 (11%)	0/4 (0%)
Overall	1276/2388 (53%)	682/1280 (53%)	456/888 (51%)	138/220 (63%)

7.1.4 Statistically unusual chemical shifts (i)

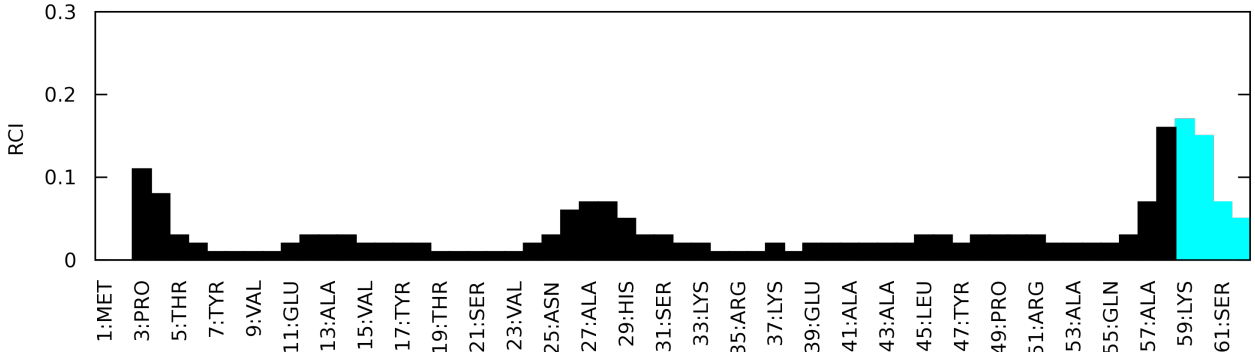
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	12	TYR	CD1	31.06	139.11 – 126.41	-80.1
2	B	12	TYR	CD1	31.06	139.11 – 126.41	-80.1
2	B	12	TYR	CD2	31.06	140.11 – 125.31	-68.7
1	A	12	TYR	CD2	31.06	140.11 – 125.31	-68.7
1	A	42	MET	HB3	0.00	3.70 – 0.30	-5.9
2	B	42	MET	HB3	0.00	3.70 – 0.30	-5.9

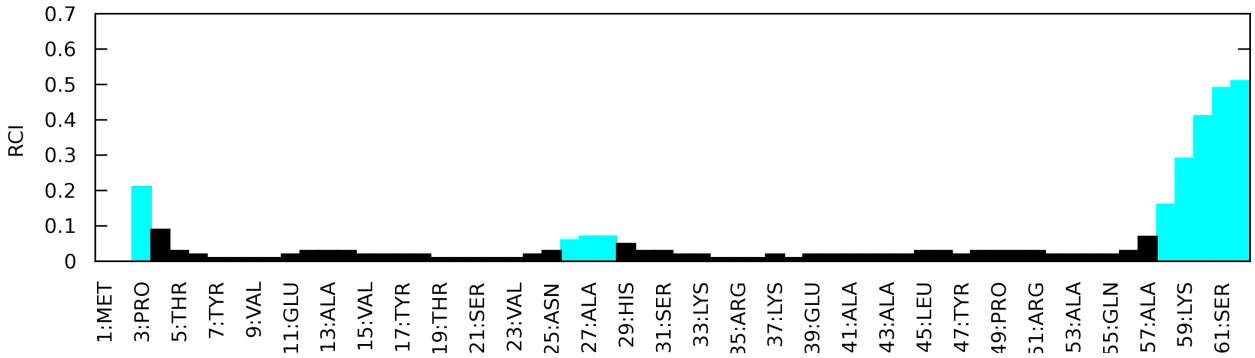
7.1.5 Random Coil Index (RCI) plots (i)

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:



7.2 Chemical shift list 2

File name: BMRB entry 5345

Chemical shift list name: *assigned_chem_shift_list_2*

7.2.1 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	1444
Number of shifts mapped to atoms	1444
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	8

7.2.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	120	-0.73 ± 0.14	Should be applied
$^{13}C_{\beta}$	108	0.08 ± 0.23	None needed (< 0.5 ppm)
$^{13}C'$	112	-0.47 ± 0.08	None needed (< 0.5 ppm)
^{15}N	116	0.37 ± 0.45	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 52%, i.e. 1124 atoms were assigned a chemical shift out of a possible 2169. 22 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	528/529 (100%)	211/211 (100%)	213/214 (100%)	104/104 (100%)
Sidechain	560/662 (85%)	353/383 (92%)	188/244 (77%)	19/35 (54%)
Aromatic	36/80 (45%)	36/40 (90%)	0/36 (0%)	0/4 (0%)
Overall	1124/2169 (52%)	600/1164 (52%)	401/808 (50%)	123/197 (62%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 53%, i.e. 1268 atoms were assigned a chemical shift out of a possible 2388. 24 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	584/612 (95%)	236/244 (97%)	232/248 (94%)	116/120 (97%)
Sidechain	648/798 (81%)	410/466 (88%)	216/290 (74%)	22/42 (52%)
Aromatic	36/80 (45%)	36/40 (90%)	0/36 (0%)	0/4 (0%)
Overall	1268/2388 (53%)	682/1280 (53%)	448/888 (50%)	138/220 (63%)

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 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	39	GLU	CD	0.00	192.68 – 172.48	-90.4
2	B	39	GLU	CD	0.00	192.68 – 172.48	-90.4
1	A	22	ARG	HE	1.15	10.48 – 4.28	-10.0
2	B	22	ARG	HE	1.15	10.48 – 4.28	-10.0
1	A	62	LEU	HB2	3.74	3.32 – -0.08	6.2
2	B	62	LEU	HB2	3.74	3.32 – -0.08	6.2
1	A	62	LEU	HB3	3.74	3.34 – -0.26	6.1

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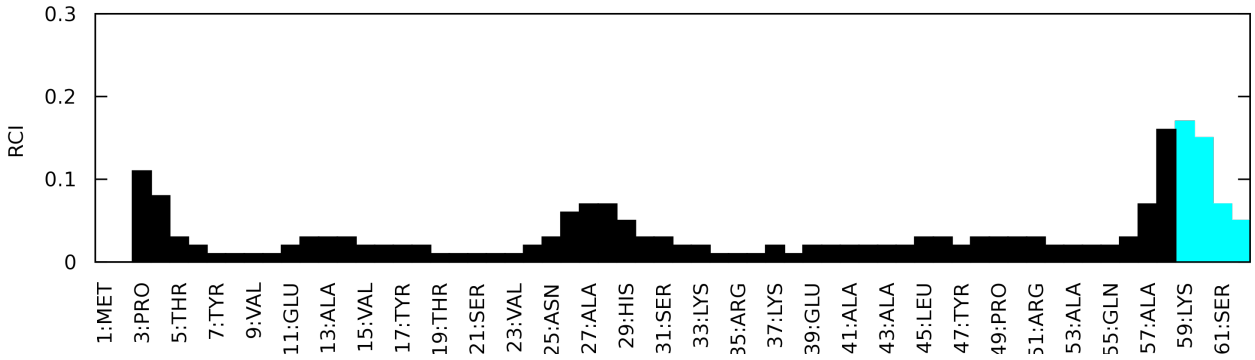
Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
2	B	62	LEU	HB3	3.74	3.34 – -0.26	6.1

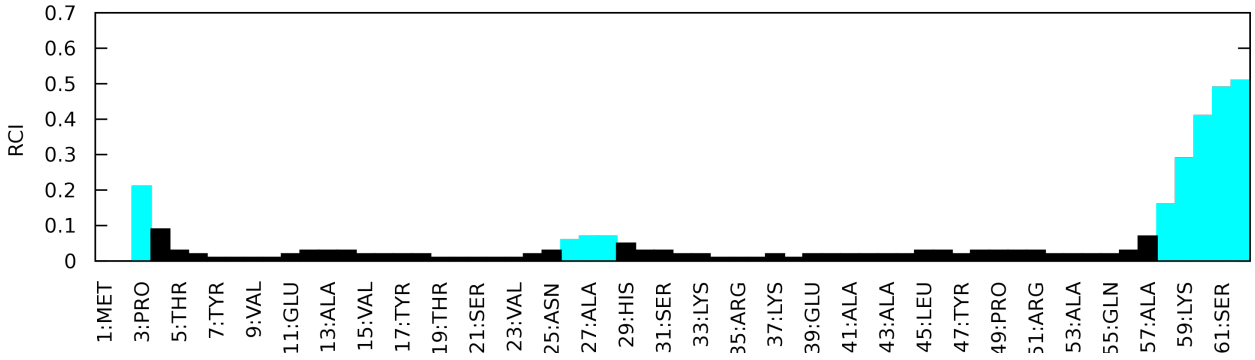
7.2.5 Random Coil Index (RCI) plots

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:



7.3 Chemical shift list 3

File name: BMRB entry 5345

Chemical shift list name: *assigned_ chem_ shift_ list_ 3*

7.3.1 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	172
Number of shifts mapped to atoms	172
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

7.3.2 Chemical shift referencing

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

7.3.3 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 7%, i.e. 154 atoms were assigned a chemical shift out of a possible 2169. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	0/529 (0%)	0/211 (0%)	0/214 (0%)	0/104 (0%)
Sidechain	0/662 (0%)	0/383 (0%)	0/244 (0%)	0/35 (0%)
Aromatic	0/80 (0%)	0/40 (0%)	0/36 (0%)	0/4 (0%)
Overall	154/2169 (7%)	154/1164 (13%)	0/808 (0%)	0/197 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 6%, i.e. 154 atoms were assigned a chemical shift out of a possible 2388. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	0/612 (0%)	0/244 (0%)	0/248 (0%)	0/120 (0%)
Sidechain	0/798 (0%)	0/466 (0%)	0/290 (0%)	0/42 (0%)
Aromatic	0/80 (0%)	0/40 (0%)	0/36 (0%)	0/4 (0%)
Overall	154/2388 (6%)	154/1280 (12%)	0/888 (0%)	0/220 (0%)

7.3.4 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
3	C	15	DT	H3	4.79	17.70 – 9.10	-10.0

7.3.5 Random Coil Index (RCI) plots

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_3). RCI is only applicable to proteins.

7.4 Chemical shift list 4

File name: BMRB entry 5345

Chemical shift list name: *assigned_chem_shift_list_4*

7.4.1 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	186
Number of shifts mapped to atoms	186
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

7.4.2 Chemical shift referencing

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

7.4.3 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 7%, i.e. 162 atoms were assigned a chemical shift out of a possible 2169. 0 out of 22 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	0/529 (0%)	0/211 (0%)	0/214 (0%)	0/104 (0%)
Sidechain	0/662 (0%)	0/383 (0%)	0/244 (0%)	0/35 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/80 (0%)	0/40 (0%)	0/36 (0%)	0/4 (0%)
Overall	162/2169 (7%)	162/1164 (14%)	0/808 (0%)	0/197 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 7%, i.e. 162 atoms were assigned a chemical shift out of a possible 2388. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	0/612 (0%)	0/244 (0%)	0/248 (0%)	0/120 (0%)
Sidechain	0/798 (0%)	0/466 (0%)	0/290 (0%)	0/42 (0%)
Aromatic	0/80 (0%)	0/40 (0%)	0/36 (0%)	0/4 (0%)
Overall	162/2388 (7%)	162/1280 (13%)	0/888 (0%)	0/220 (0%)

7.4.4 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.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
3	D	2	DA	H3'	6.04	5.65 – 4.25	7.8

7.4.5 Random Coil Index (RCI) plots (i)

No *random coil index* (RCI) plot could be generated from the current chemical shift list (assigned_chem_shift_list_4). RCI is only applicable to proteins.