Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2N6J
Title	:	Solution structure of Zmp1, a zinc-dependent metalloprotease secreted by Clostridium difficile
Authors	:	Banci, L.; Cantini, F.; Scarselli, M.; Rubino, J.T.; Martinelli, M.
Deposited on	:	2015-08-24

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:

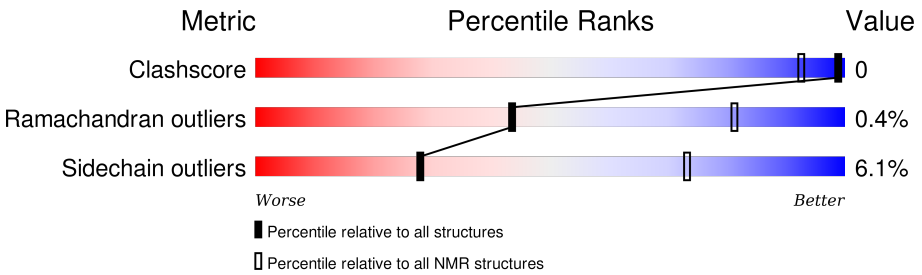
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	unknown
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	rb-20027457
Ideal 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 (i)

The following experimental techniques were used to determine the structure:
SOLUTION NMR

The overall completeness of chemical shifts assignment is 91%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	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	A	195	91% • 5%

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 13 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *fewest violations*.

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:28-A:100, A:109-A:220 (185)	0.55	13

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 6 single-model clusters were found.

Cluster number	Models
1	1, 7, 18, 30
2	5, 8, 14, 17
3	6, 13, 29
4	11, 34, 40
Single-model clusters	2; 23; 24; 36; 38; 28

3 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 3040 atoms, of which 1511 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Zinc metalloprotease Zmp1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	195	3036	969	1509	259	297	2	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	26	GLY	-	EXPRESSION TAG	UNP Q183R7

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	1	1	1

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		
			Total	H	O
3	A	1	3	2	1

4 Residue-property plots (i)

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: Zinc metalloprotease Zmp1

Chain A:

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: Zinc metalloprotease Zmp1

Chain A:

4.2.2 Score per residue for model 2

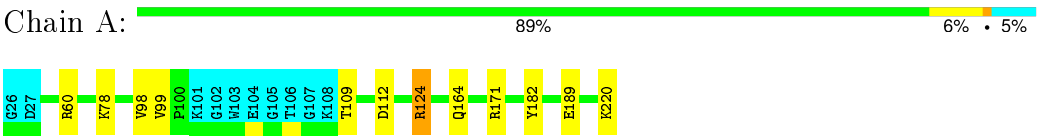
- Molecule 1: Zinc metalloprotease Zmp1

Chain A:

4.2.3 Score per residue for model 5

- Molecule 1: Zinc metalloprotease Zmp1

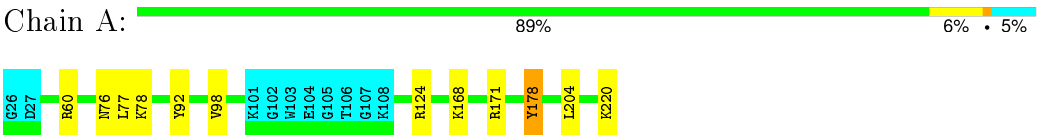
Chain A:



4.2.4 Score per residue for model 6

- Molecule 1: Zinc metalloprotease Zmp1

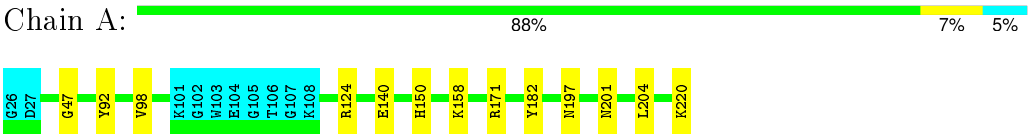
Chain A:



4.2.5 Score per residue for model 7

- Molecule 1: Zinc metalloprotease Zmp1

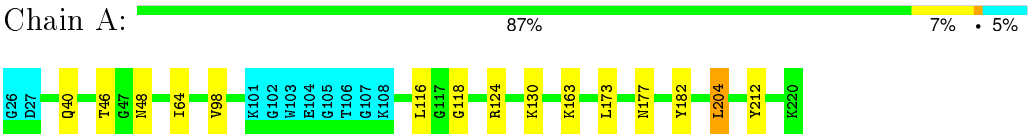
Chain A:



4.2.6 Score per residue for model 8

- Molecule 1: Zinc metalloprotease Zmp1

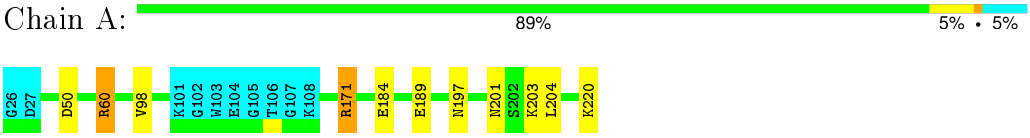
Chain A:



4.2.7 Score per residue for model 11

- Molecule 1: Zinc metalloprotease Zmp1

Chain A:



4.2.8 Score per residue for model 13 (medoid)

- Molecule 1: Zinc metalloprotease Zmp1

Chain A: 87% 8% 5%

G26 D27 K35 R60 L77 K78 K90 V98 K101 G102 W103 E104 G105 T106 G107 K108 R124 L139 H150 K163 K168 R171 Y178 L204 K220

4.2.9 Score per residue for model 14

- Molecule 1: Zinc metalloprotease Zmp1

Chain A: 89% 5% • 5%

G26 D27 R60 M63 K78 V98 K101 G102 W103 E104 G105 T106 G107 K108 L116 R124 K168 R171 S172 L173 Y182 F186 L204 K220

4.2.10 Score per residue for model 17

- Molecule 1: Zinc metalloprotease Zmp1

Chain A: 87% 8% 5%

G26 D27 Q32 R60 L77 K78 V98 K101 G102 W103 E104 G105 T106 G107 K108 R124 I137 N138 L139 E140 Q161 R171 Y193 Y194 Y195 L196 K203 L204 K220

4.2.11 Score per residue for model 18

- Molecule 1: Zinc metalloprotease Zmp1

Chain A: 84% 9% • 5%

G26 D27 N48 R60 K78 I79 K80 S83 Y94 V98 K101 G102 W103 E104 G105 T106 G107 K108 T109 R124 D149 H150 Q164 K168 R171 S172 L173 Y178 Y193 L196 K203 L204 K220

4.2.12 Score per residue for model 23

- Molecule 1: Zinc metalloprotease Zmp1

Chain A: 90% 5% • 5%

G26 D27 Q40 R60 E91 V98 K101 G102 W103 E104 G105 T106 G107 K108 R124 K163 Q164 K168 R171 K220

4.2.13 Score per residue for model 24

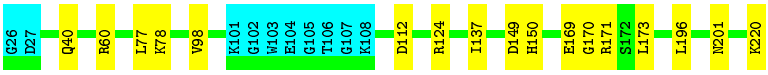
- Molecule 1: Zinc metalloprotease Zmp1

Chain A:

4.2.14 Score per residue for model 29

- Molecule 1: Zinc metalloprotease Zmp1

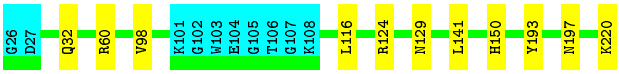
Chain A:



4.2.15 Score per residue for model 30

- Molecule 1: Zinc metalloprotease Zmp1

Chain A:



4.2.16 Score per residue for model 34

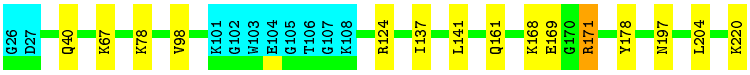
- Molecule 1: Zinc metalloprotease Zmp1

Chain A:

4.2.17 Score per residue for model 36

- Molecule 1: Zinc metalloprotease Zmp1

Chain A:



4.2.18 Score per residue for model 38

- Molecule 1: Zinc metalloprotease Zmp1

Chain A:

4.2.19 Score per residue for model 40

- Molecule 1: Zinc metalloprotease Zmp1

Chain A:

4.2.20 Score per residue for model 28

- Molecule 1: Zinc metalloprotease Zmp1

Chain A:

5 Refinement protocol and experimental data overview (i)

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

Of the 400 calculated structures, 20 were deposited, based on the following criterion: *target function.*

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

Software name	Classification	Version
CYANA	structure solution	2.1
CYANA	refinement	2.1
PSVS	structure solution	
PSVS	refinement	
AMBER	refinement	10
CARA	refinement	2

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)	2n6j_cs.str
Number of chemical shift lists	1
Total number of shifts	2373
Number of shifts mapped to atoms	2373
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

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

6 Model quality (i)

6.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ZN

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.71±0.00	0±0/1483 (0.0±0.0%)	0.99±0.02	3±1/2004 (0.1±0.1%)
All	All	0.71	0/29660 (0.0%)	0.99	53/40080 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.9±0.8
All	All	0	19

There are no bond-length outliers.

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})	Models	
								Worst	Total
1	A	60	ARG	NE-CZ-NH1	9.59	125.10	120.30	30	14
1	A	124	ARG	NE-CZ-NH1	9.44	125.02	120.30	28	16
1	A	171	ARG	NE-CZ-NH1	8.07	124.33	120.30	5	15
1	A	178	TYR	CB-CG-CD2	-6.51	117.10	121.00	18	5
1	A	60	ARG	NE-CZ-NH2	-5.95	117.32	120.30	28	1
1	A	171	ARG	NE-CZ-NH2	-5.21	117.69	120.30	18	1
1	A	193	TYR	CB-CG-CD2	-5.08	117.95	121.00	30	1

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	92	TYR	Sidechain	3
1	A	173	LEU	Peptide	2
1	A	119	SER	Peptide	2
1	A	60	ARG	Sidechain	2
1	A	171	ARG	Peptide,Sidechain	2
1	A	168	LYS	Peptide	1
1	A	182	TYR	Sidechain	1
1	A	193	TYR	Sidechain	1
1	A	124	ARG	Sidechain	1
1	A	178	TYR	Sidechain	1
1	A	212	TYR	Sidechain	1
1	A	137	ILE	Peptide	1
1	A	195	TYR	Sidechain	1

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	1455	1442	1441	0±0
All	All	29140	28880	28820	5

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 0.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:173:LEU:HD23	1:A:186:PHE:CD1	0.51	2.40	14	1
1:A:193:TYR:CG	1:A:204:LEU:HD23	0.45	2.46	18	1
1:A:110:TRP:HA	1:A:113:VAL:HG13	0.44	1.88	34	1
1:A:173:LEU:HD13	1:A:204:LEU:HD21	0.43	1.90	8	1
1:A:194:TYR:CZ	1:A:212:TYR:CD2	0.41	3.09	24	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	184/195 (94%)	174±3 (94±1%)	9±3 (5±2%)	1±1 (0±1%)	43	81
All	All	3680/3900 (94%)	3476 (94%)	189 (5%)	15 (0%)	43	81

All 10 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	130	LYS	2
1	A	64	ILE	2
1	A	127	PHE	2
1	A	170	GLY	2
1	A	28	SER	2
1	A	47	GLY	1
1	A	129	ASN	1
1	A	65	ASP	1
1	A	118	GLY	1
1	A	48	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	
1	A	157/163 (96%)	147±3 (94±2%)	10±3 (6±2%)	28	73
All	All	3140/3260 (96%)	2949 (94%)	191 (6%)	28	73

All 59 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	98	VAL	19
1	A	220	LYS	15
1	A	78	LYS	11
1	A	204	LEU	11
1	A	150	HIS	7
1	A	40	GLN	6
1	A	197	ASN	6
1	A	173	LEU	5
1	A	168	LYS	5
1	A	196	LEU	5
1	A	182	TYR	4
1	A	124	ARG	4
1	A	116	LEU	4
1	A	77	LEU	4
1	A	163	LYS	4
1	A	109	THR	3
1	A	112	ASP	3
1	A	203	LYS	3
1	A	60	ARG	3
1	A	161	GLN	3
1	A	140	GLU	3
1	A	169	GLU	3
1	A	171	ARG	3
1	A	63	ASN	3
1	A	178	TYR	3
1	A	149	ASP	3
1	A	201	ASN	3
1	A	164	GLN	3
1	A	137	ILE	2
1	A	138	ASN	2
1	A	36	ASP	2
1	A	67	LYS	2
1	A	90	LYS	2
1	A	83	SER	2
1	A	185	GLU	2
1	A	189	GLU	2
1	A	32	GLN	2
1	A	48	ASN	2
1	A	141	LEU	2
1	A	73	LYS	1
1	A	96	LYS	1
1	A	216	GLN	1
1	A	165	ILE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	94	TYR	1
1	A	139	LEU	1
1	A	35	LYS	1
1	A	135	ASP	1
1	A	46	THR	1
1	A	80	LYS	1
1	A	184	GLU	1
1	A	158	LYS	1
1	A	43	VAL	1
1	A	91	GLU	1
1	A	87	THR	1
1	A	99	VAL	1
1	A	50	ASP	1
1	A	177	ASN	1
1	A	213	SER	1
1	A	76	ASN	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)

Of 1 ligands modelled in this entry, 1 is 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 91% for the well-defined parts and 90% for the entire structure.

7.1 Chemical shift list 1

File name: 2n6j_cs.str

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	2373
Number of shifts mapped to atoms	2373
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	12

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	192	-0.66 ± 0.20	Should be applied
$^{13}C_{\beta}$	176	0.38 ± 0.16	None needed (< 0.5 ppm)
$^{13}C'$	154	-0.28 ± 0.22	None needed (< 0.5 ppm)
^{15}N	184	0.59 ± 0.29	Should be applied

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 91%, i.e. 2045 atoms were assigned a chemical shift out of a possible 2259. 29 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	869/915 (95%)	361/365 (99%)	331/370 (89%)	177/180 (98%)
Sidechain	1022/1148 (89%)	628/669 (94%)	367/427 (86%)	27/52 (52%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	154/196 (79%)	81/102 (79%)	64/85 (75%)	9/9 (100%)
Overall	2045/2259 (91%)	1070/1136 (94%)	762/882 (86%)	213/241 (88%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 90%, i.e. 2124 atoms were assigned a chemical shift out of a possible 2365. 29 out of 30 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

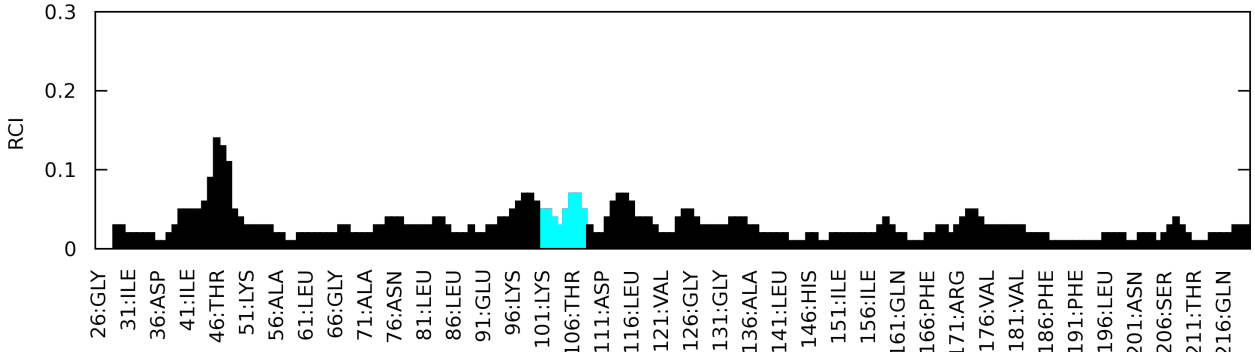
	Total	^{1}H	^{13}C	^{15}N
Backbone	905/965 (94%)	375/385 (97%)	346/390 (89%)	184/190 (97%)
Sidechain	1055/1192 (89%)	649/695 (93%)	379/443 (86%)	27/54 (50%)
Aromatic	164/208 (79%)	86/108 (80%)	68/90 (76%)	10/10 (100%)
Overall	2124/2365 (90%)	1110/1188 (93%)	793/923 (86%)	221/254 (87%)

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	124	ARG	NE	137.43	92.63 – 76.73	33.2
1	A	60	ARG	NE	135.95	92.63 – 76.73	32.2
1	A	100	PRO	HG3	-0.63	3.56 – 0.26	-7.7
1	A	95	LEU	HG	-0.56	3.16 – -0.14	-6.3
1	A	124	ARG	HD3	1.64	4.36 – 1.86	-5.9
1	A	194	TYR	HD2	5.18	8.44 – 5.44	-5.9
1	A	194	TYR	HD1	5.18	8.44 – 5.44	-5.9
1	A	100	PRO	HG2	0.12	3.48 – 0.38	-5.8
1	A	65	ASP	H	5.02	11.17 – 5.47	-5.8
1	A	170	GLY	HA2	1.88	5.87 – 2.07	-5.5
1	A	136	ALA	H	11.40	11.19 – 5.19	5.4
1	A	210	GLN	H	11.29	11.17 – 5.27	5.2

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 A: