Full wwPDB NMR Structure Validation Report (i)

Apr 20, 2024 – 09:35 AM EDT

PDB ID	:	2JT5
BMRB ID	:	15395
Title	:	solution structure of matrix metalloproteinase 3 (MMP-3) in the presence of n-hydroxy-2-[n-(2-hydroxyethyl)biphenyl-4-sulfonamide] hydroxamic acid (MLC88)
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Deposited on	:	2007-07-20

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/NMRValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

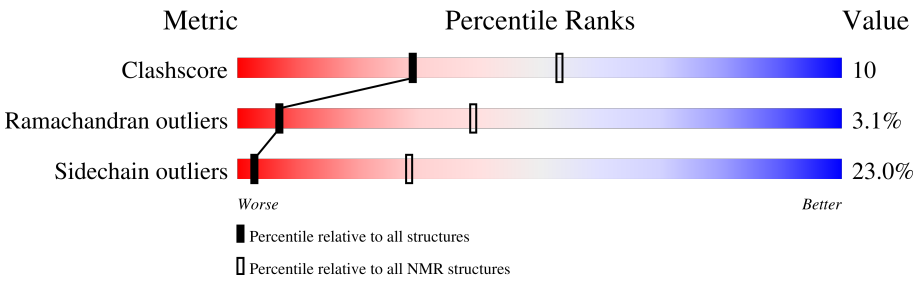
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 14%.

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



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

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

Mol	Chain	Length	Quality of chain
1	A	161	61% 33% 6%

2 Ensemble composition and analysis (i)

This entry contains 1 models. Identification of well-defined residues and clustering analysis are not possible.

3 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2536 atoms, of which 1230 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Stromelysin-1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	161	2491	818	1213	213	245	2	0

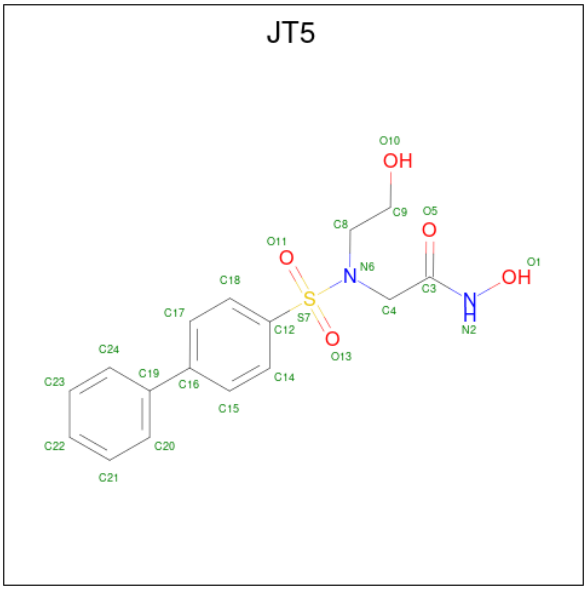
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
			Total	Zn
2	A	2	2	2

- Molecule 3 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
			Total	Ca
3	A	2	2	2

- Molecule 4 is N 2 -(biphenyl-4-ylsulfonyl)-N-hydroxy-N 2 -(2-hydroxyethyl)glycinamide (three-letter code: JT5) (formula: $C_{16}H_{18}N_2O_5S$).



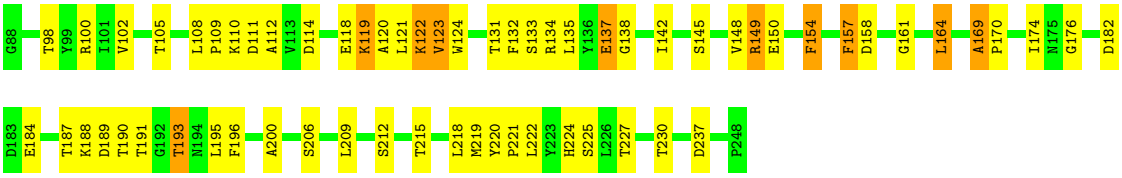
Mol	Chain	Residues	Atoms					
			Total	C	H	N	O	S
4	A	1	41	16	17	2	5	1

4 Residue-property plots (i)

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

- Molecule 1: Stromelysin-1

Chain A: 61% 33% 6%



5 Refinement protocol and experimental data overview (i)

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

Of the 100 calculated structures, 1 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
X-PLOR NIH	refinement	
AutoDock	refinement	3.0

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	300
Number of shifts mapped to atoms	298
Number of unparsed shifts	0
Number of shifts with mapping errors	2
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	14%

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: CA, ZN, JT5

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	1278	1213	1207	25
4	A	24	17	17	2
All	All	1306	1230	1224	26

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 10.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:149:ARG:HA	1:A:157:PHE:HB3	0.78	1.55
1:A:120:ALA:HB1	1:A:200:ALA:HA	0.66	1.68
1:A:142:ILE:HA	1:A:176:GLY:O	0.59	1.96
1:A:148:VAL:HG22	1:A:149:ARG:H	0.59	1.56
1:A:112:ALA:HA	1:A:188:LYS:CE	0.58	2.28
1:A:200:ALA:HB1	1:A:218:LEU:HD21	0.56	1.77
1:A:176:GLY:HA2	1:A:206:SER:HB3	0.55	1.77
1:A:169:ALA:HB3	1:A:170:PRO:HD3	0.54	1.79
1:A:158:ASP:OD2	1:A:161:GLY:HA3	0.54	2.03
1:A:220:TYR:CD1	1:A:221:PRO:HD2	0.54	2.37
1:A:98:THR:HG22	1:A:133:SER:HB2	0.52	1.82
1:A:112:ALA:HA	1:A:188:LYS:HE3	0.50	1.83

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:108:LEU:HB3	1:A:109:PRO:HD2	0.50	1.84
1:A:212:SER:HB3	1:A:237:ASP:OD2	0.48	2.08
1:A:184:GLU:HG2	1:A:193:THR:OG1	0.47	2.09
1:A:220:TYR:CE2	1:A:222:LEU:HB2	0.46	2.45
1:A:209:LEU:HD23	1:A:219:MET:HG3	0.45	1.89
1:A:148:VAL:HG13	1:A:150:GLU:HG2	0.44	1.88
4:A:1:JT5:H33	4:A:1:JT5:H30	0.44	1.89
1:A:124:TRP:CZ2	1:A:218:LEU:HD23	0.43	2.49
1:A:119:LYS:O	1:A:123:VAL:HB	0.43	2.13
1:A:121:LEU:HD11	1:A:132:PHE:CB	0.43	2.44
1:A:164:LEU:HD12	4:A:1:JT5:H36	0.42	1.92
1:A:119:LYS:HB3	1:A:196:PHE:CE1	0.41	2.51
1:A:122:LYS:HB2	1:A:122:LYS:HZ3	0.41	1.76
1:A:188:LYS:O	1:A:188:LYS:HG3	0.40	2.16

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	159/161 (99%)	127 (80%)	27 (17%)	5 (3%)	7 39
All	All	159/161 (99%)	127 (80%)	27 (17%)	5 (3%)	7 39

All 5 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	137	GLU
1	A	138	GLY
1	A	154	PHE
1	A	169	ALA
1	A	174	ILE

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	135/135 (100%)	104 (77%)	31 (23%)	3 28
All	All	135/135 (100%)	104 (77%)	31 (23%)	3 28

All 31 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	100	ARG
1	A	102	VAL
1	A	105	THR
1	A	110	LYS
1	A	111	ASP
1	A	114	ASP
1	A	118	GLU
1	A	119	LYS
1	A	122	LYS
1	A	123	VAL
1	A	131	THR
1	A	134	ARG
1	A	135	LEU
1	A	137	GLU
1	A	145	SER
1	A	149	ARG
1	A	154	PHE
1	A	157	PHE
1	A	164	LEU
1	A	182	ASP
1	A	187	THR
1	A	189	ASP
1	A	190	THR
1	A	191	THR
1	A	193	THR
1	A	195	LEU
1	A	215	THR
1	A	224	HIS
1	A	225	SER

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Mol	Chain	Res	Type
1	A	227	THR
1	A	230	THR

6.3.3 RNA (i)

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains (i)

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
4	JT5	A	1	2	24,25,25	2.55	5 (20%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
4	JT5	A	1	2	29,34,34	1.88	5 (17%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	JT5	A	1	2	-	0,21,25,25	0,2,2,2

All bond outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1	JT5	C3-N2	8.72	1.41	1.32
4	A	1	JT5	O1-N2	5.92	1.25	1.40
4	A	1	JT5	C12-S7	3.62	1.71	1.76
4	A	1	JT5	C8-N6	2.68	1.44	1.48
4	A	1	JT5	C4-C3	2.07	1.55	1.52

All angle outliers are listed below. They are sorted according to the Z-score.

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	1	JT5	O13-S7-N6	5.05	111.29	106.69
4	A	1	JT5	O11-S7-N6	4.70	110.97	106.69
4	A	1	JT5	O1-N2-C3	3.87	125.52	119.79
4	A	1	JT5	O13-S7-O11	3.51	113.83	119.52
4	A	1	JT5	O13-S7-C12	2.56	104.81	108.05

There are no chirality outliers.

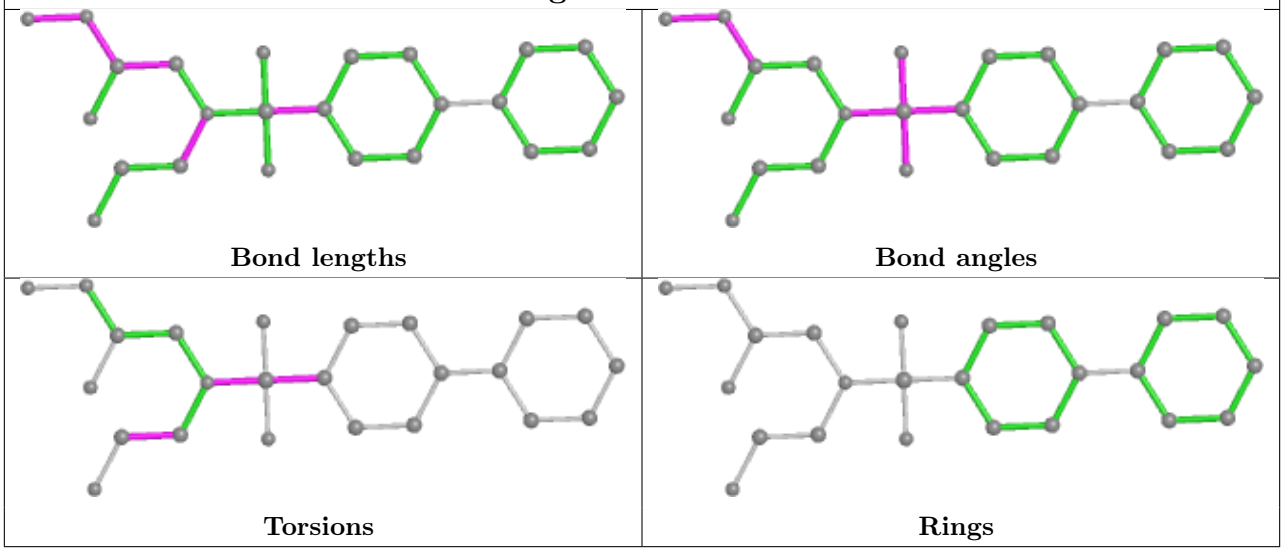
There are no torsion outliers.

There are no ring outliers.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand JT5 A 1



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 14% for the well-defined parts and 14% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

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	300
Number of shifts mapped to atoms	298
Number of unparsed shifts	0
Number of shifts with mapping errors	2
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

The following assigned chemical shifts were not mapped to the molecules present in the coordinate file.

- No matching atom found in the structure. All 2 occurrences are reported below.

List ID	Chain	Res	Type	Atom	Shift Data		
					Value	Uncertainty	Ambiguity
1	A	67	ASP	H	7.76	.	.
1	A	67	ASP	N	115.788	.	.

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	None (insufficient data)
$^{13}C_{\beta}$	0	—	None (insufficient data)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	150	0.17 ± 0.31	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 14%, i.e. 298 atoms were assigned a chemical shift out of a possible 2152. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	298/798 (37%)	149/325 (46%)	0/322 (0%)	149/151 (99%)
Sidechain	0/1108 (0%)	0/723 (0%)	0/352 (0%)	0/33 (0%)
Aromatic	0/246 (0%)	0/122 (0%)	0/111 (0%)	0/13 (0%)
Overall	298/2152 (14%)	149/1170 (13%)	0/785 (0%)	149/197 (76%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 14%, i.e. 298 atoms were assigned a chemical shift out of a possible 2152. 0 out of 24 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	298/798 (37%)	149/325 (46%)	0/322 (0%)	149/151 (99%)
Sidechain	0/1108 (0%)	0/723 (0%)	0/352 (0%)	0/33 (0%)
Aromatic	0/246 (0%)	0/122 (0%)	0/111 (0%)	0/13 (0%)
Overall	298/2152 (14%)	149/1170 (13%)	0/785 (0%)	149/197 (76%)

7.1.4 Statistically unusual chemical shifts (i)

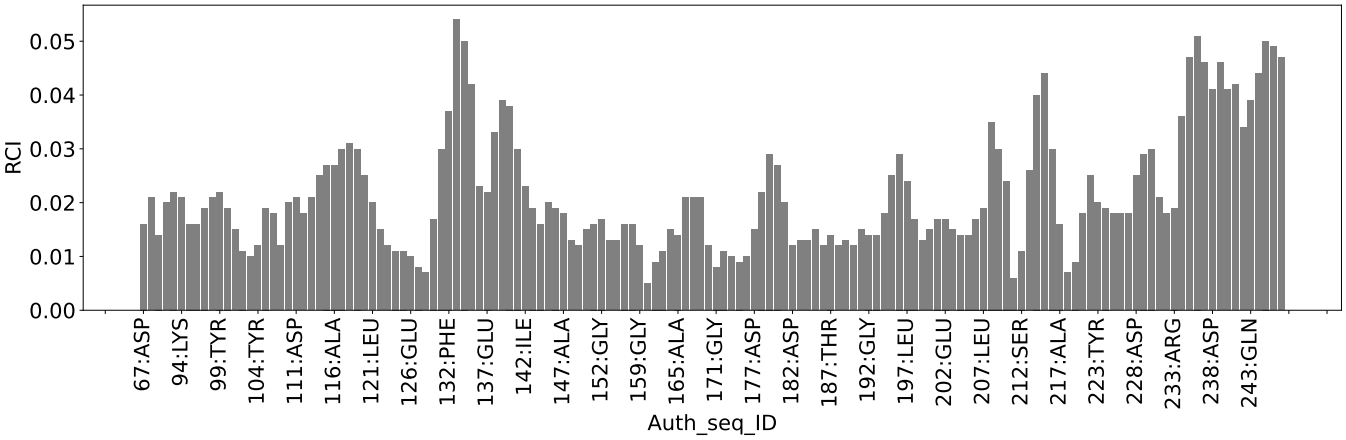
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	218	LEU	H	11.51	5.09 – 11.34	5.3

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.If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:


RCI
0.00
0.01
0.02
0.03
0.04
0.05
67:ASP
94:LYS
99:TYR
104:TYR
111:ASP
116:ALA
121:LEU
126:GLU
132:PHE
137:GLU
142:ILE
147:ALA
152:GLY
159:GLY
165:ALA
171:GLY
177:ASP
182:ASP
187:THR
192:GLY
197:LEU
202:GLU
207:LEU
212:SER
217:ALA
223:TYR
228:ASP
233:ARG
238:ASP
243:GLN
Auth_seq_ID