Full wwPDB NMR Structure Validation Report (i)

Apr 21, 2024 – 07:36 AM EDT

PDB ID	:	2LTX
BMRB ID	:	18500
Title	:	Smurf1 WW2 domain in complex with a Smad7 derived peptide
Authors	:	Macias, M.J.; Aragon, E.; Goerner, N.; Xi, Q.; Lopes, T.; Gao, S.; Massague, J.
Deposited on	:	2012-06-04

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:

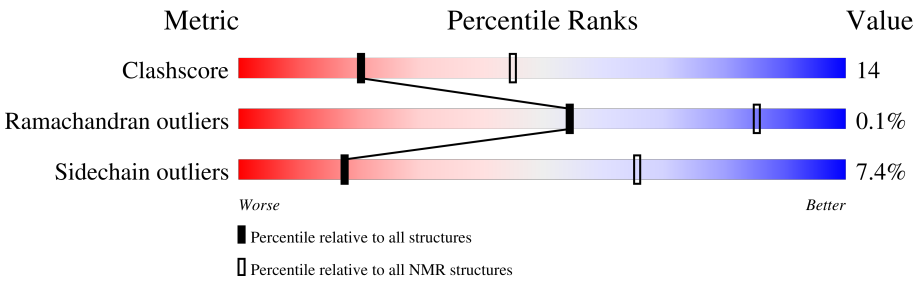
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson 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 43%.

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	35	66% 17% 17%
2	B	15	47% 13% 40%

2 Ensemble composition and analysis (i)

This entry contains 25 models. Model 11 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:283-A:311, B:207-B:215 (38)	0.40	11

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

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

The models can be grouped into 5 clusters and 2 single-model clusters were found.

Cluster number	Models
1	1, 2, 3, 6, 9, 11, 12, 13, 21, 23, 24, 25
2	7, 14, 18, 20
3	8, 15, 16
4	5, 19
5	4, 22
Single-model clusters	10; 17

3 Entry composition (i)

There are 2 unique types of molecules in this entry. The entry contains 803 atoms, of which 390 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called E3 ubiquitin-protein ligase SMURF1.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
1	A	35	564	181	276	55	52	0

- Molecule 2 is a protein called Smad7 derived peptide.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
2	B	15	239	80	114	18	26	1	0

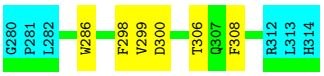
4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

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

• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 66% 17% 17%



• Molecule 2: Smad7 derived peptide

Chain B: 47% 13% 40%

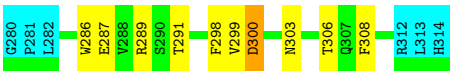
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

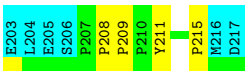
• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 54% 26% • 17%



• Molecule 2: Smad7 derived peptide

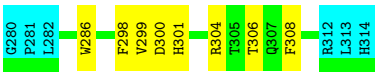
Chain B: 33% 27% 40%



4.2.2 Score per residue for model 2

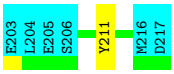
• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 60% 23% 17%



• Molecule 2: Smad7 derived peptide

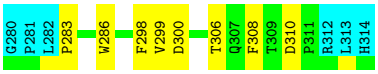
Chain B: 53% 7% 40%



4.2.3 Score per residue for model 3

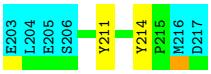
• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 60% 23% 17%



• Molecule 2: Smad7 derived peptide

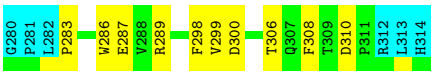
Chain B: 47% 13% 40%



4.2.4 Score per residue for model 4

• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 54% 29% 17%



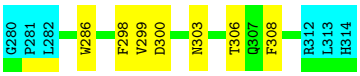
• Molecule 2: Smad7 derived peptide

Chain B: 40% 20% 40%

4.2.5 Score per residue for model 5

• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 63% 20% 17%



• Molecule 2: Smad7 derived peptide

Chain B: 47% 13% 40%

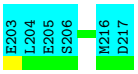
4.2.6 Score per residue for model 6

• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 60% 23% 17%

• Molecule 2: Smad7 derived peptide

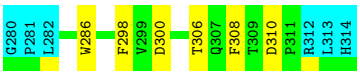
Chain B: 60% 40%



4.2.7 Score per residue for model 7

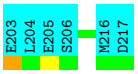
• Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 66% 17% 17%



• Molecule 2: Smad7 derived peptide

Chain B: 60% 40%

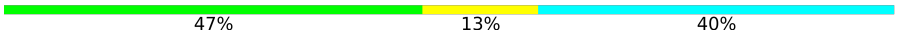


4.2.8 Score per residue for model 8

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A:

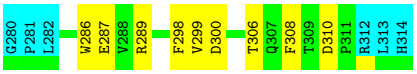
- Molecule 2: Smad7 derived peptide

Chain B: 

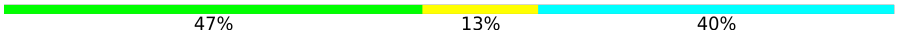
4.2.9 Score per residue for model 9

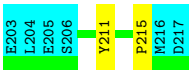
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A:



- Molecule 2: Smad7 derived peptide

Chain B: 

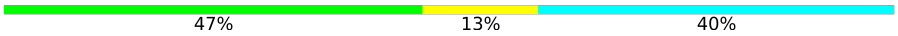


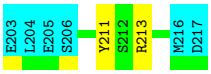
4.2.10 Score per residue for model 10

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A:

- Molecule 2: Smad7 derived peptide

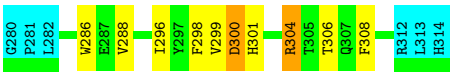
Chain B: 



4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 54% 23% 6% 17%



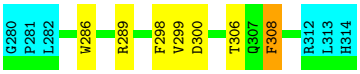
- Molecule 2: Smad7 derived peptide

Chain B: 47% 13% 40%

4.2.12 Score per residue for model 12

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 63% 17% • 17%



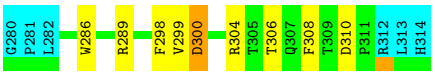
- Molecule 2: Smad7 derived peptide

Chain B: 47% 13% 40%

4.2.13 Score per residue for model 13

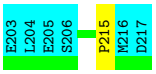
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 57% 23% • 17%



- Molecule 2: Smad7 derived peptide

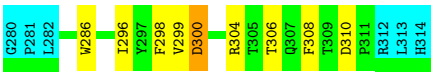
Chain B: 53% 7% 40%



4.2.14 Score per residue for model 14

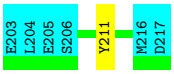
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 57% 23% • 17%



- Molecule 2: Smad7 derived peptide

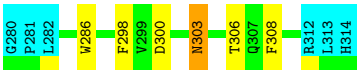
Chain B: 53% 7% 40%



4.2.15 Score per residue for model 15

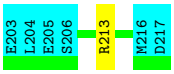
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 66% 14% • 17%



- Molecule 2: Smad7 derived peptide

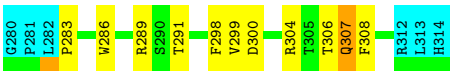
Chain B: 53% 7% 40%



4.2.16 Score per residue for model 16

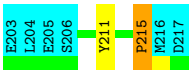
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 51% 29% • 17%



- Molecule 2: Smad7 derived peptide

Chain B: 47% 7% 7% 40%



4.2.17 Score per residue for model 17

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 63% 20% 17%

G280 P281 L282 W286 F298 V299 D300 T306 Q307 F308 R312 L313 H314

- Molecule 2: Smad7 derived peptide

Chain B: 53% 7% 40%

E203 L204 E205 S206 Y211 M216 D217

4.2.18 Score per residue for model 18

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 63% 20% 17%

G280 P281 L282 W286 E287 F298 V299 D300 T306 Q307 F308 R312 L313 H314

- Molecule 2: Smad7 derived peptide

Chain B: 53% 7% 40%

E203 L204 E205 S206 Y211 M216 D217

4.2.19 Score per residue for model 19

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 54% 29% 17%

G280 P281 L282 W286 E287 V288 R295 I296 Y297 F298 V299 D300 T306 Q307 F308 T309 D310 P311 R312 L313 H314

- Molecule 2: Smad7 derived peptide

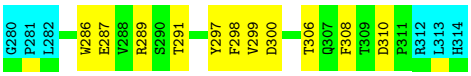
Chain B: 53% 7% 40%

E203 L204 E205 S206 P215 M216 D217

4.2.20 Score per residue for model 20

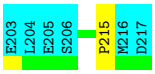
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 51% 31% 17%



- Molecule 2: Smad7 derived peptide

Chain B: 53% 7% 40%



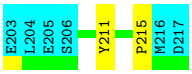
4.2.21 Score per residue for model 21

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 54% 26% • 17%

- Molecule 2: Smad7 derived peptide

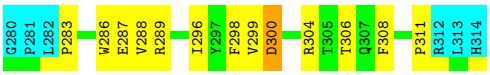
Chain B: 47% 13% 40%



4.2.22 Score per residue for model 22

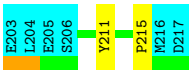
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 46% 34% • 17%



- Molecule 2: Smad7 derived peptide

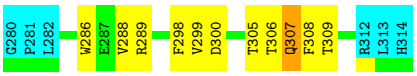
Chain B: 47% 13% 40%



4.2.23 Score per residue for model 23

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 51% 29% • 17%



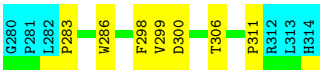
- Molecule 2: Smad7 derived peptide

Chain B: 47% 13% 40%

4.2.24 Score per residue for model 24

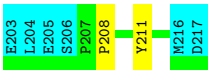
- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 63% 20% 17%



- Molecule 2: Smad7 derived peptide

Chain B: 47% 13% 40%



4.2.25 Score per residue for model 25

- Molecule 1: E3 ubiquitin-protein ligase SMURF1

Chain A: 49% 31% • 17%

- Molecule 2: Smad7 derived peptide

Chain B: 47% 13% 40%

5 Refinement protocol and experimental data overview (i)

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

Of the 300 calculated structures, 25 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
CNSSOLVE	structure solution	
CNSSOLVE	refinement	

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	281
Number of shifts mapped to atoms	281
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	43%

6 Model quality (i)

6.1 Standard geometry (i)

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	239	221	220	8±2
2	B	76	71	71	2±1
All	All	7875	7300	7275	208

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 14.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:299:VAL:HB	2:B:211:TYR:CD1	0.72	2.20	3	15
1:A:286:TRP:HE3	1:A:298:PHE:CE1	0.70	2.04	10	25
1:A:298:PHE:O	1:A:306:THR:HA	0.64	1.93	22	25
1:A:299:VAL:HB	2:B:211:TYR:CE1	0.63	2.28	14	5
1:A:286:TRP:HE3	1:A:298:PHE:CZ	0.61	2.13	17	25
1:A:288:VAL:HB	1:A:298:PHE:CZ	0.61	2.31	10	1
1:A:307:GLN:HE21	1:A:307:GLN:HA	0.59	1.57	23	2
1:A:289:ARG:HG3	2:B:215:PRO:HG2	0.59	1.73	20	5
1:A:299:VAL:HG21	2:B:215:PRO:HG3	0.58	1.74	12	7
1:A:286:TRP:CE3	1:A:298:PHE:CE1	0.56	2.92	10	25
1:A:287:GLU:HB3	1:A:299:VAL:O	0.55	2.01	9	4
1:A:286:TRP:CE3	1:A:298:PHE:CZ	0.53	2.95	1	25
1:A:300:ASP:O	1:A:304:ARG:HA	0.53	2.03	25	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:289:ARG:HB3	1:A:297:TYR:CZ	0.51	2.40	21	1
1:A:288:VAL:CG2	1:A:296:ILE:HD11	0.51	2.35	6	2
1:A:289:ARG:CG	2:B:215:PRO:HG2	0.49	2.38	23	1
1:A:306:THR:HG23	2:B:208:PRO:HB2	0.49	1.83	24	1
1:A:299:VAL:HB	2:B:211:TYR:HD1	0.48	1.66	3	5
1:A:288:VAL:HG23	1:A:296:ILE:HD11	0.48	1.84	11	3
1:A:306:THR:CG2	2:B:208:PRO:HB2	0.47	2.38	4	3
1:A:289:ARG:HG3	2:B:215:PRO:HB2	0.47	1.85	4	4
1:A:288:VAL:HB	1:A:298:PHE:CE1	0.47	2.44	10	1
1:A:306:THR:HG22	2:B:208:PRO:HB2	0.46	1.88	1	1
1:A:299:VAL:HA	1:A:305:THR:O	0.46	2.11	23	1
1:A:288:VAL:O	1:A:289:ARG:HD2	0.45	2.12	23	1
1:A:291:THR:HG23	1:A:297:TYR:CE1	0.43	2.49	20	2
1:A:288:VAL:HG22	1:A:296:ILE:HD11	0.43	1.91	22	1
1:A:286:TRP:CZ3	1:A:298:PHE:CE2	0.43	3.07	12	2
2:B:211:TYR:CE1	2:B:213:ARG:HA	0.42	2.49	10	1
1:A:301:HIS:ND1	2:B:211:TYR:OH	0.42	2.53	2	2
1:A:300:ASP:OD2	1:A:303:ASN:HB2	0.42	2.14	1	1
1:A:306:THR:HG21	2:B:209:PRO:O	0.41	2.16	1	1
1:A:296:ILE:HG21	1:A:310:ASP:HB2	0.41	1.92	14	1
1:A:303:ASN:N	1:A:303:ASN:HD22	0.40	2.15	15	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	29/35 (83%)	28±1 (97±3%)	1±1 (3±3%)	0±0 (0±0%)	100	100
2	B	9/15 (60%)	7±1 (81±8%)	2±1 (18±8%)	0±0 (0±2%)	38	78
All	All	950/1250 (76%)	888 (93%)	61 (6%)	1 (0%)	54	85

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
2	B	215	PRO	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	27/32 (84%)	24±1 (90±3%)	3±1 (10±3%)	11	57
2	B	9/15 (60%)	9±0 (100±2%)	0±0 (0±2%)	91	98
All	All	900/1175 (77%)	833 (93%)	67 (7%)	17	65

All 9 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	300	ASP	25
1	A	308	PHE	24
1	A	291	THR	5
1	A	304	ARG	3
1	A	287	GLU	3
1	A	307	GLN	3
1	A	303	ASN	2
2	B	213	ARG	1
1	A	309	THR	1

6.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

6.5 Carbohydrates (i)

There are no monosaccharides in this entry.

6.6 Ligand geometry (i)

There are no ligands in this entry.

6.7 Other polymers (i)

There are no such molecules in this entry.

6.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

7 Chemical shift validation (i)

The completeness of assignment taking into account all chemical shift lists is 43% for the well-defined parts and 40% 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	281
Number of shifts mapped to atoms	281
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

7.1.2 Chemical shift referencing (i)

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

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 43%, i.e. 224 atoms were assigned a chemical shift out of a possible 523. 0 out of 3 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	**^{1}H**	**^{13}C**	**^{15}N**
Backbone	66/176 (38%)	66/70 (94%)	0/76 (0%)	0/30 (0%)
Sidechain	134/280 (48%)	134/180 (74%)	0/85 (0%)	0/15 (0%)
Aromatic	24/67 (36%)	24/32 (75%)	0/32 (0%)	0/3 (0%)
Overall	224/523 (43%)	224/282 (79%)	0/193 (0%)	0/48 (0%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 40%, i.e. 279 atoms were assigned a chemical shift out of a possible 690. 0 out of 6 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	84/235 (36%)	84/94 (89%)	0/100 (0%)	0/41 (0%)
Sidechain	171/380 (45%)	171/245 (70%)	0/117 (0%)	0/18 (0%)
Aromatic	24/75 (32%)	24/36 (67%)	0/34 (0%)	0/5 (0%)
Overall	279/690 (40%)	279/375 (74%)	0/251 (0%)	0/64 (0%)

7.1.4 Statistically unusual chemical shifts (i)

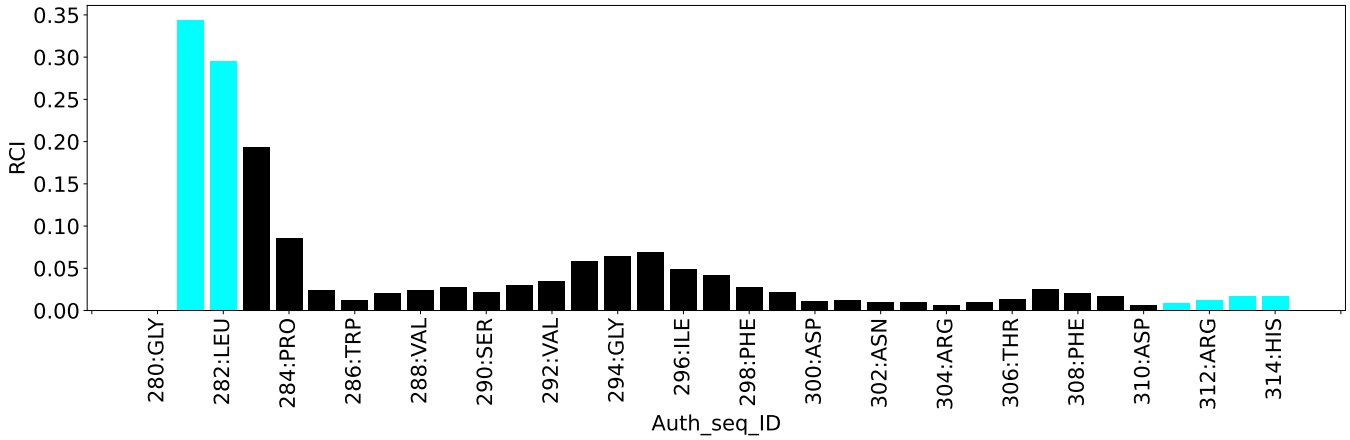
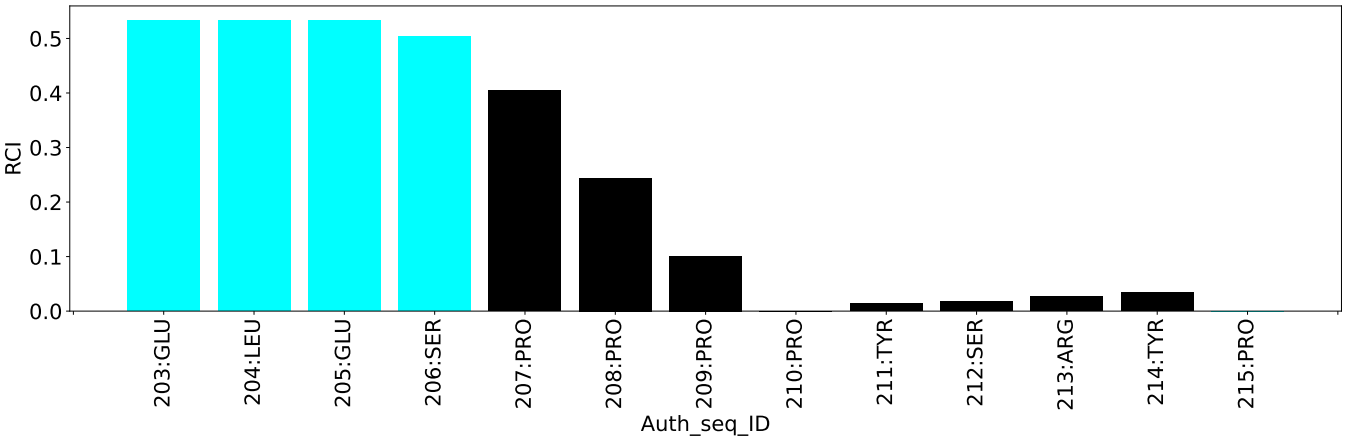
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	300	ASP	HB3	-0.23	1.32 – 4.00	-10.8
1	A	310	ASP	HA	2.51	3.04 – 6.12	-6.7
1	A	311	PRO	HG3	-0.03	0.33 – 3.48	-6.2
1	A	289	ARG	HG3	-0.10	0.15 – 2.94	-5.9
1	A	311	PRO	HG2	0.28	0.41 – 3.45	-5.4
1	B	208	PRO	HD3	1.66	1.76 – 5.48	-5.3
1	A	304	ARG	HA	2.00	2.06 – 6.51	-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.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:



Random coil index (RCI) for chain B: