Full wwPDB NMR Structure Validation Report (i)

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PDB ID	:	2MP0
Title	:	Protein Phosphorylation upon a Fleeting Encounter
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Deposited on	:	2014-05-08

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 following versions of software and data (see references (1)) were used in the production of this report:

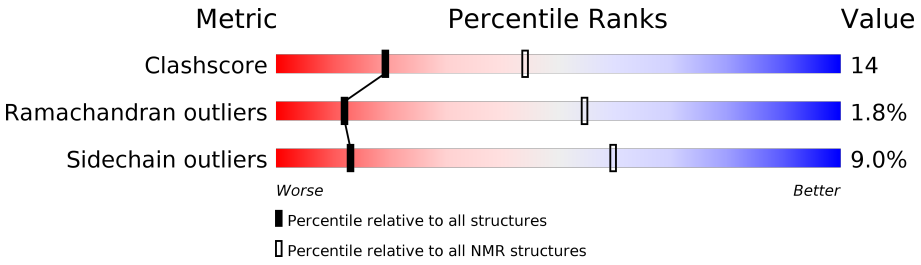
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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 15%.

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	258	75% 19% • •
2	B	168	55% 27% 7% 11%

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

There are 3 unique types of molecules in this entry. The entry contains 6156 atoms, of which 3117 are hydrogens and 0 are deuteriums.

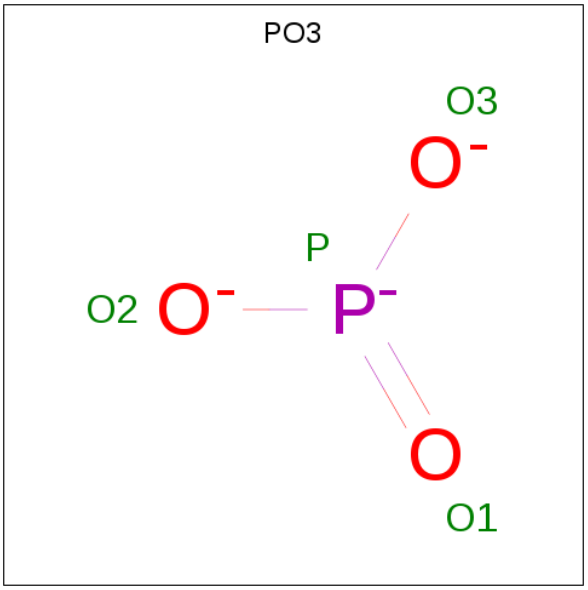
- Molecule 1 is a protein called Phosphoenolpyruvate-protein phosphotransferase.

Mol	Chain	Residues	Atoms						Trace
1	A	249	Total	C	H	N	O	S	0
			3857	1192	1950	322	388	5	

- Molecule 2 is a protein called Glucose-specific phosphotransferase enzyme IIA component.

Mol	Chain	Residues	Atoms						Trace
2	B	149	Total	C	H	N	O	S	0
			2295	723	1167	179	224	2	

- Molecule 3 is PHOSPHITE ION (three-letter code: PO3) (formula: O_3P).



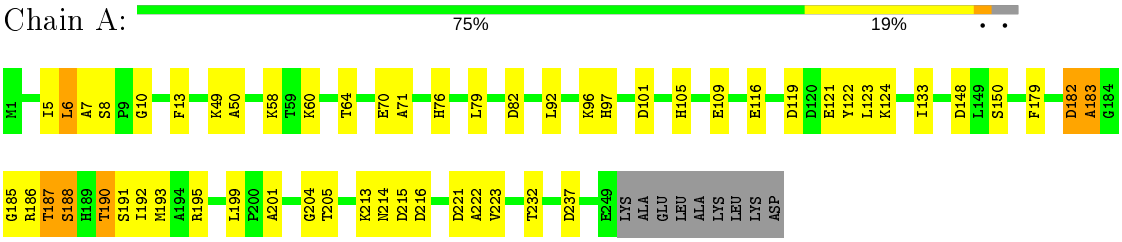
Mol	Chain	Residues	Atoms			
3	B	1	Total	O	P	
			4	3	1	

4 Residue-property plots (i)

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.

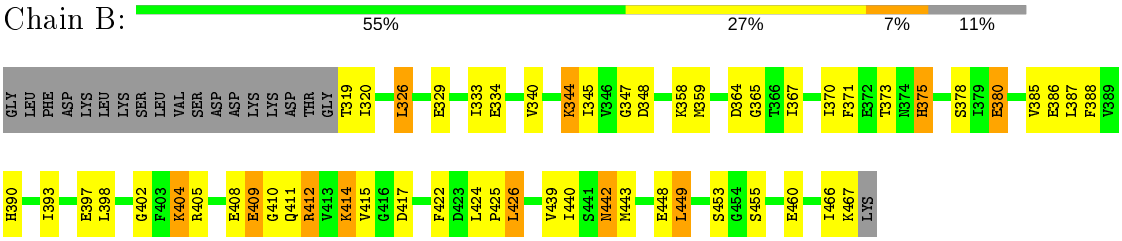
- Molecule 1: Phosphoenolpyruvate-protein phosphotransferase

Chain A:



- Molecule 2: Glucose-specific phosphotransferase enzyme IIA component

Chain B:



5 Refinement protocol and experimental data overview

The models were refined using the following method: *simulated annealing.*

Of the 90 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
NMRPipe	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 6 of this report.

Chemical shift file(s)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	694
Number of shifts mapped to atoms	694
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	15%

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

COVALENT-GEOMETRY INFOmissingINFO

5.1 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	A	1907	1950	1947	44
2	B	1128	1167	1165	51
3	B	4	0	0	1
All	All	3039	3117	3112	87

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 clashes are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:122:TYR:CG	2:B:397:GLU:OE1	0.76	2.38
2:B:386:GLU:H	2:B:442:ASN:ND2	0.73	1.81
1:A:71:ALA:HB1	2:B:345:ILE:HG22	0.72	1.59
2:B:405:ARG:NH1	2:B:409:GLU:OE2	0.71	2.24
2:B:364:ASP:OD1	2:B:415:VAL:HG23	0.71	1.86
2:B:385:VAL:HG21	2:B:466:ILE:CD1	0.71	2.14
1:A:122:TYR:CD1	2:B:397:GLU:OE1	0.70	2.43
2:B:320:ILE:HB	2:B:466:ILE:CG1	0.70	2.16
2:B:367:ILE:HG21	2:B:408:GLU:O	0.70	1.85
1:A:190:THR:O	1:A:193:MET:N	0.69	2.25
2:B:373:THR:OG1	2:B:375:HIS:CD2	0.67	2.48
1:A:122:TYR:CD2	2:B:397:GLU:OE1	0.66	2.48
2:B:367:ILE:HD12	2:B:378:SER:O	0.66	1.90
1:A:10:GLY:O	1:A:222:ALA:HB3	0.64	1.92
2:B:440:ILE:HD13	2:B:449:LEU:HD11	0.63	1.70
1:A:60:LYS:O	1:A:64:THR:HG23	0.61	1.96
2:B:348:ASP:OD2	2:B:443:MET:SD	0.60	2.59
1:A:79:LEU:HD12	1:A:82:ASP:OD2	0.60	1.95
2:B:385:VAL:HG21	2:B:466:ILE:HD11	0.60	1.73
2:B:340:VAL:HA	2:B:345:ILE:HD12	0.59	1.74
1:A:182:ASP:OD1	1:A:182:ASP:N	0.59	2.35
1:A:187:THR:O	1:A:188:SER:O	0.58	2.20
2:B:426:LEU:O	2:B:426:LEU:HD12	0.58	1.97
1:A:122:TYR:CD1	1:A:122:TYR:N	0.57	2.67
2:B:367:ILE:CG2	2:B:411:GLN:N	0.56	2.68
1:A:190:THR:O	1:A:191:SER:C	0.56	2.40
1:A:122:TYR:CE1	2:B:397:GLU:OE1	0.56	2.58
2:B:370:ILE:HD12	2:B:409:GLU:OE1	0.56	2.01
2:B:367:ILE:HG23	2:B:410:GLY:N	0.55	2.17
1:A:186:ARG:O	1:A:187:THR:O	0.55	2.23
1:A:101:ASP:OD1	1:A:101:ASP:N	0.55	2.39
1:A:13:PHE:N	1:A:13:PHE:CD1	0.55	2.74
1:A:58:LYS:NZ	1:A:70:GLU:O	0.55	2.39
2:B:386:GLU:N	2:B:442:ASN:ND2	0.54	2.54
1:A:122:TYR:CD1	2:B:397:GLU:CD	0.53	2.81
2:B:402:GLY:O	2:B:404:LYS:NZ	0.53	2.36
2:B:367:ILE:CG2	2:B:411:GLN:H	0.52	2.17
1:A:105:HIS:NE2	1:A:109:GLU:OE1	0.52	2.42
1:A:122:TYR:CE2	2:B:397:GLU:OE1	0.52	2.63
2:B:426:LEU:C	2:B:426:LEU:HD12	0.50	2.27
1:A:60:LYS:O	1:A:64:THR:CG2	0.50	2.58
1:A:105:HIS:CD2	1:A:109:GLU:OE1	0.50	2.64
2:B:409:GLU:H	2:B:409:GLU:CD	0.50	2.10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
1:A:122:TYR:CZ	2:B:397:GLU:OE1	0.48	2.67
2:B:412:ARG:CG	2:B:412:ARG:NH1	0.48	2.77
2:B:424:LEU:HB3	2:B:425:PRO:HD3	0.48	1.84
1:A:221:ASP:C	1:A:223:VAL:N	0.48	2.66
1:A:10:GLY:O	1:A:221:ASP:O	0.48	2.32
2:B:333:ILE:CD1	2:B:439:VAL:CG1	0.48	2.92
1:A:7:ALA:O	1:A:195:ARG:NE	0.47	2.46
2:B:364:ASP:OD1	2:B:415:VAL:N	0.47	2.40
1:A:221:ASP:O	1:A:223:VAL:N	0.47	2.48
2:B:344:LYS:HB2	2:B:347:GLY:O	0.47	2.09
2:B:375:HIS:CE1	2:B:390:HIS:CE1	0.47	3.03
1:A:123:LEU:N	1:A:123:LEU:CD2	0.47	2.78
1:A:190:THR:O	1:A:192:ILE:N	0.46	2.48
1:A:5:ILE:O	1:A:6:LEU:O	0.46	2.34
2:B:380:GLU:CD	2:B:380:GLU:N	0.46	2.66
1:A:121:GLU:OE1	1:A:121:GLU:N	0.46	2.45
2:B:344:LYS:CB	2:B:348:ASP:OD1	0.45	2.64
2:B:409:GLU:N	2:B:409:GLU:CD	0.45	2.70
1:A:92:LEU:O	1:A:96:LYS:N	0.44	2.50
2:B:320:ILE:HB	2:B:466:ILE:HG13	0.44	1.87
2:B:412:ARG:CG	2:B:412:ARG:HH11	0.44	2.24
2:B:367:ILE:HG23	2:B:410:GLY:H	0.43	1.71
1:A:116:GLU:O	1:A:124:LYS:NZ	0.43	2.50
2:B:442:ASN:O	2:B:443:MET:C	0.43	2.56
2:B:388:PHE:CE2	2:B:390:HIS:HB2	0.43	2.49
2:B:402:GLY:O	2:B:422:PHE:HA	0.43	2.13
1:A:49:LYS:O	1:A:50:ALA:C	0.43	2.57
2:B:424:LEU:N	2:B:425:PRO:CD	0.43	2.80
1:A:182:ASP:O	1:A:183:ALA:O	0.43	2.37
1:A:8:SER:CB	1:A:199:LEU:O	0.42	2.67
1:A:190:THR:C	1:A:192:ILE:N	0.42	2.71
1:A:179:PHE:O	1:A:201:ALA:HB1	0.42	2.15
2:B:371:PHE:CE2	3:B:500:PO3:O3	0.42	2.73
2:B:398:LEU:HD12	2:B:398:LEU:N	0.42	2.29
2:B:380:GLU:CA	2:B:380:GLU:OE1	0.41	2.68
1:A:214:ASN:O	1:A:214:ASN:OD1	0.41	2.38
1:A:5:ILE:HG22	1:A:5:ILE:O	0.41	2.15
2:B:367:ILE:HG22	2:B:411:GLN:O	0.41	2.15
1:A:76:HIS:CG	1:A:133:ILE:HD11	0.41	2.51
1:A:119:ASP:OD1	1:A:119:ASP:O	0.40	2.38
1:A:204:GLY:O	1:A:205:THR:C	0.40	2.60
2:B:414:LYS:HE3	2:B:417:ASP:OD2	0.40	2.16

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Atom-1	Atom-2	Clash(Å)	Distance(Å)
2:B:365:GLY:HA3	2:B:380:GLU:O	0.40	2.16
1:A:221:ASP:C	1:A:223:VAL:H	0.40	2.19

5.2 Torsion angles

5.2.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the backbone conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	247/258 (96%)	229 (93%)	11 (4%)	7 (3%)	8 42
2	B	147/168 (88%)	140 (95%)	7 (5%)	0 (0%)	100 100
All	All	394/426 (92%)	369 (94%)	18 (5%)	7 (2%)	12 54

All 7 Ramachandran outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
1	A	190	THR
1	A	185	GLY
1	A	148	ASP
1	A	183	ALA
1	A	188	SER
1	A	6	LEU
1	A	187	THR

5.2.2 Protein sidechains

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	206/213 (97%)	198 (96%)	8 (4%)	36 84
2	B	128/145 (88%)	106 (83%)	22 (17%)	5 39

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	334/358 (93%)	304 (91%)	30 (9%)	13 60

All 30 residues with a non-rotameric sidechain are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type
2	B	326	LEU
1	A	182	ASP
2	B	460	GLU
2	B	467	LYS
2	B	414	LYS
2	B	393	ILE
2	B	358	LYS
1	A	237	ASP
1	A	150	SER
2	B	455	SER
2	B	334	GLU
2	B	387	LEU
2	B	319	THR
1	A	216	ASP
1	A	213	LYS
2	B	412	ARG
2	B	426	LEU
2	B	375	HIS
1	A	232	THR
2	B	448	GLU
2	B	359	MET
2	B	329	GLU
2	B	404	LYS
2	B	449	LEU
2	B	344	LYS
2	B	409	GLU
2	B	453	SER
2	B	380	GLU
1	A	215	ASP
1	A	97	HIS

5.2.3 RNA

There are no RNA molecules in this entry.

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

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

5.4 Carbohydrates (i)

There are no carbohydrates in this entry.

5.5 Ligand geometry (i)

1 ligand is modelled in this entry.

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
3	PO3	B	500	-	0,3,3	0.00	-

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
3	PO3	B	500	-	0,3,3	0.00	-

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5.6 Other polymers

There are no such molecules in this entry.

5.7 Polymer linkage issues

There are no chain breaks in this entry.

6 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 15% for the well-defined parts and 15% for the entire structure.

6.1 Chemical shift list 1

File name: input_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

6.1.1 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	694
Number of shifts mapped to atoms	694
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

6.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	0	—	None (insufficient data)
$^{13}C_{\beta}$	0	—	None (insufficient data)
$^{13}C'$	0	—	None (insufficient data)
^{15}N	347	0.35 ± 0.27	None needed (< 0.5 ppm)

6.1.3 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 15%, i.e. 692 atoms were assigned a chemical shift out of a possible 4737. 0 out of 71 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	692/1968 (35%)	346/785 (44%)	0/796 (0%)	346/387 (89%)
Sidechain	0/2591 (0%)	0/1489 (0%)	0/1011 (0%)	0/91 (0%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	0/178 (0%)	0/96 (0%)	0/72 (0%)	0/10 (0%)
Overall	692/4737 (15%)	346/2370 (15%)	0/1879 (0%)	346/488 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 15%, i.e. 692 atoms were assigned a chemical shift out of a possible 4737. 0 out of 71 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	692/1968 (35%)	346/785 (44%)	0/796 (0%)	346/387 (89%)
Sidechain	0/2591 (0%)	0/1489 (0%)	0/1011 (0%)	0/91 (0%)
Aromatic	0/178 (0%)	0/96 (0%)	0/72 (0%)	0/10 (0%)
Overall	692/4737 (15%)	346/2370 (15%)	0/1879 (0%)	346/488 (71%)

6.1.4 Statistically unusual chemical shifts (i)

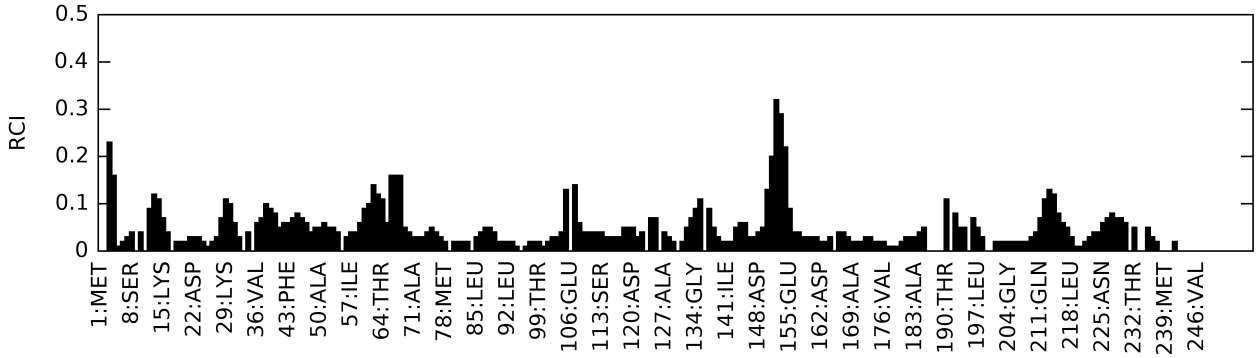
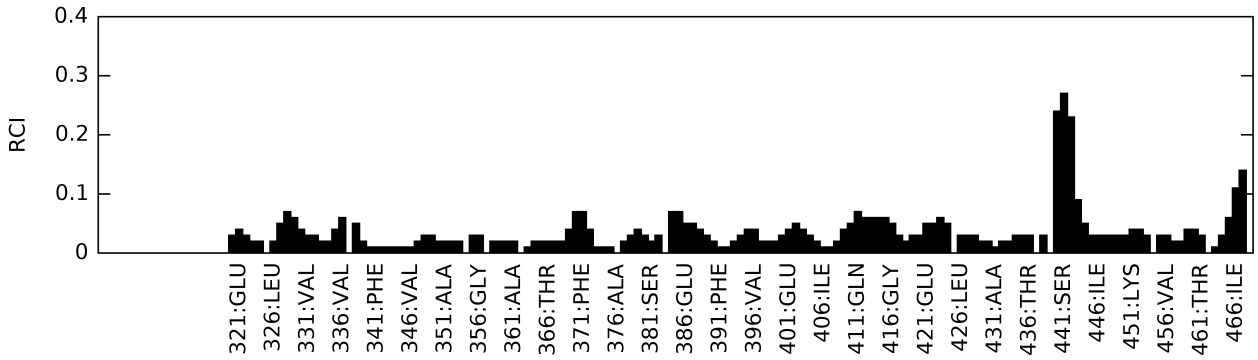
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	178	GLY	N	129.37	129.07 – 90.27	5.1

6.1.5 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: