



Full wwPDB NMR Structure Validation Report ⓘ

Jan 16, 2018 – 08:38 PM EST

PDB ID : 2MBC
Title : Solution Structure of human holo-PRL-3 in complex with vanadate
Authors : Jeong, K.; Kang, D.; Kim, J.; Shin, S.; Jin, B.; Lee, C.; Kim, E.; Jeon, Y.H.;
Kim, Y.
Deposited on : 2013-07-29

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 ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20030736
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030736

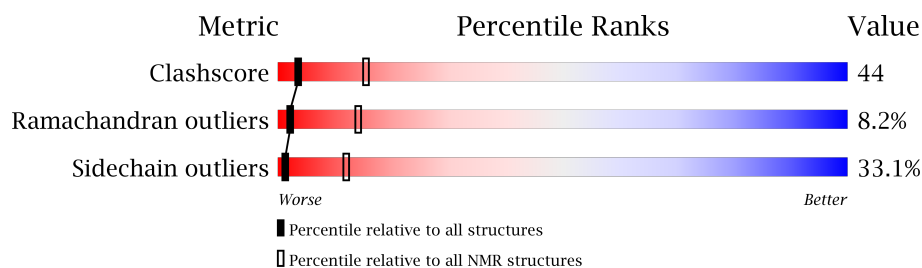
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 69%.

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	162	<div> <div></div> <div>35%</div> <div>36%</div> <div>16%</div> <div>13%</div> </div>

2 Ensemble composition and analysis

This entry contains 20 models. Model 2 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:7-A:22, A:30-A:70, A:79-A:162 (141)	0.32	2

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 5 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2595 atoms, of which 1314 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein tyrosine phosphatase type IVA 3.

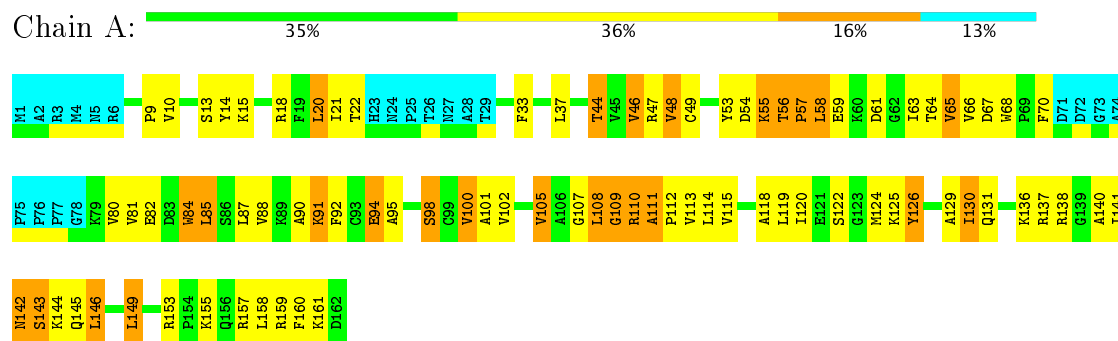
Mol	Chain	Residues	Atoms						Trace
1	A	162	Total	C	H	N	O	S	0
			2595	820	1314	225	228	8	

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: Protein tyrosine phosphatase type IVA 3

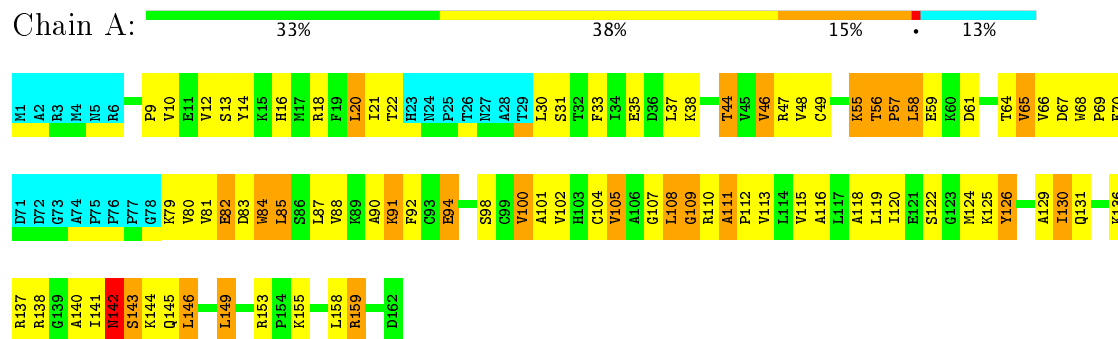


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

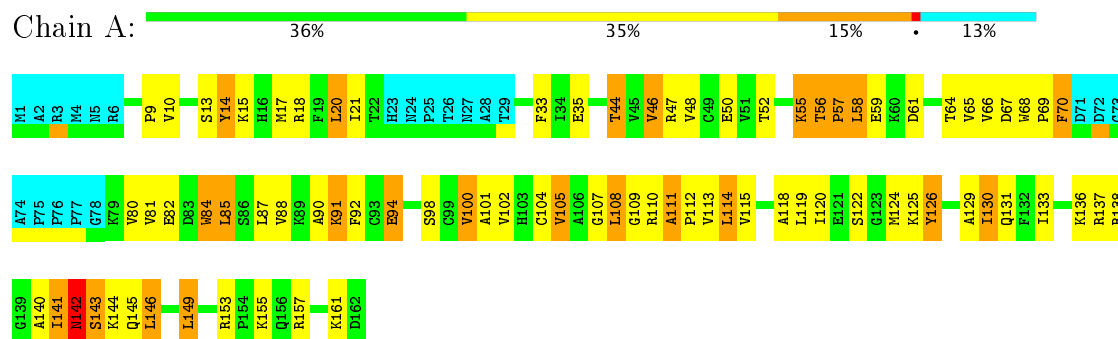
4.2.1 Score per residue for model 1

- Molecule 1: Protein tyrosine phosphatase type IVA 3



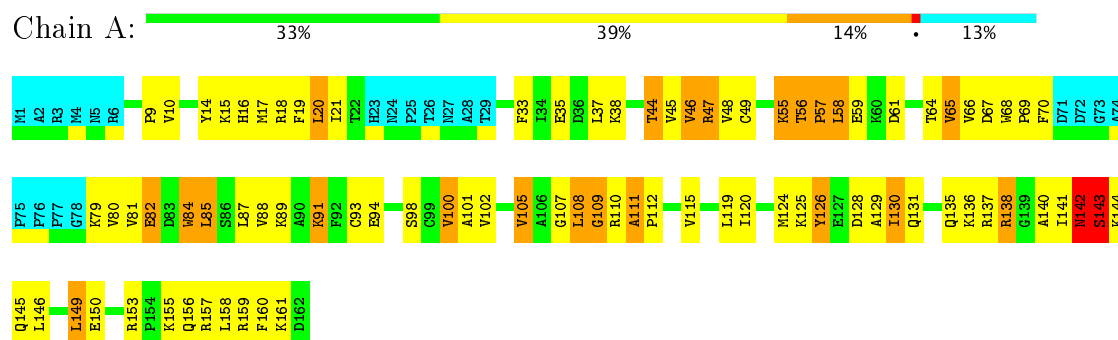
4.2.2 Score per residue for model 2 (medoid)

- Molecule 1: Protein tyrosine phosphatase type IVA 3



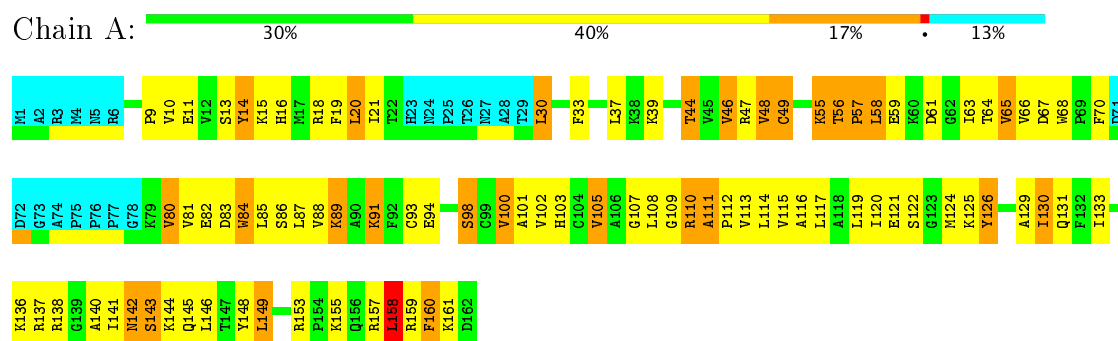
4.2.3 Score per residue for model 3

- Molecule 1: Protein tyrosine phosphatase type IVA 3



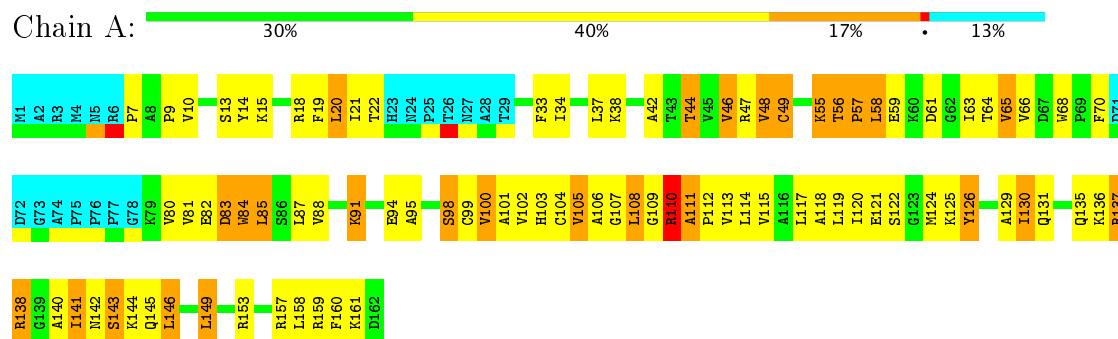
4.2.4 Score per residue for model 4

- Molecule 1: Protein tyrosine phosphatase type IVA 3



4.2.5 Score per residue for model 5

- Molecule 1: Protein tyrosine phosphatase type IVA 3



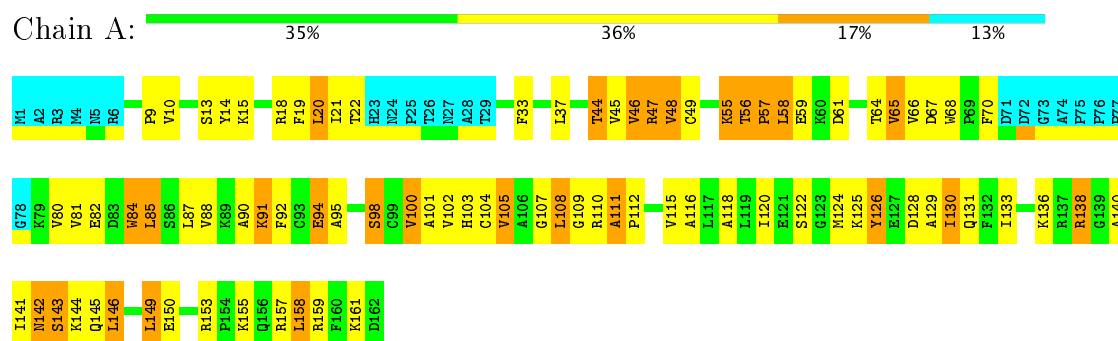
4.2.6 Score per residue for model 6

- Molecule 1: Protein tyrosine phosphatase type IVA 3



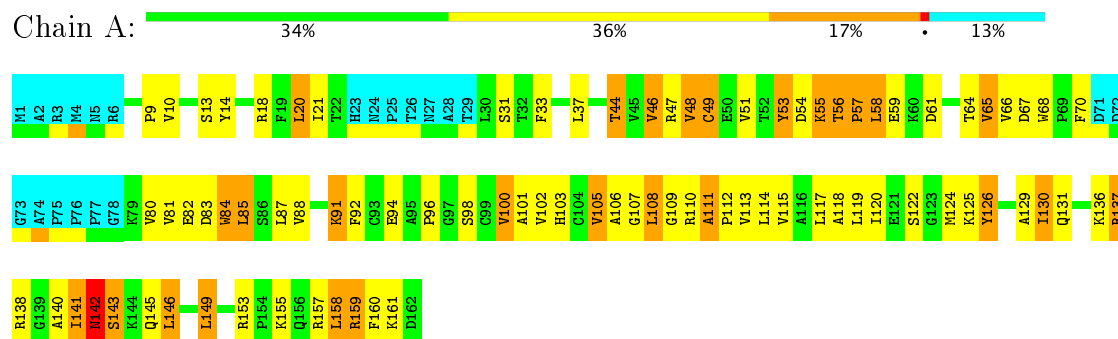
4.2.7 Score per residue for model 7

- Molecule 1: Protein tyrosine phosphatase type IVA 3



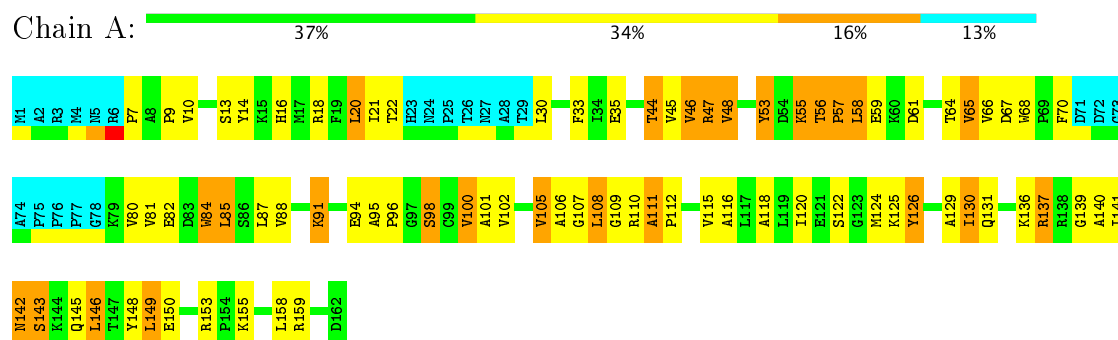
4.2.8 Score per residue for model 8

- Molecule 1: Protein tyrosine phosphatase type IVA 3



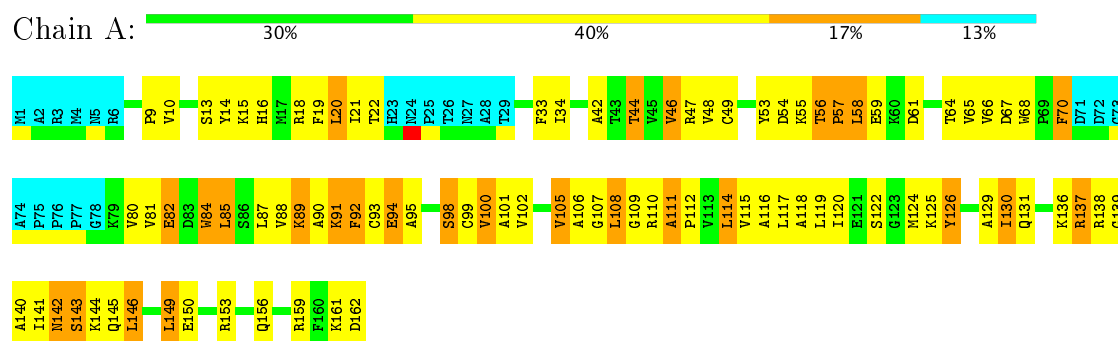
4.2.9 Score per residue for model 9

- Molecule 1: Protein tyrosine phosphatase type IVA 3



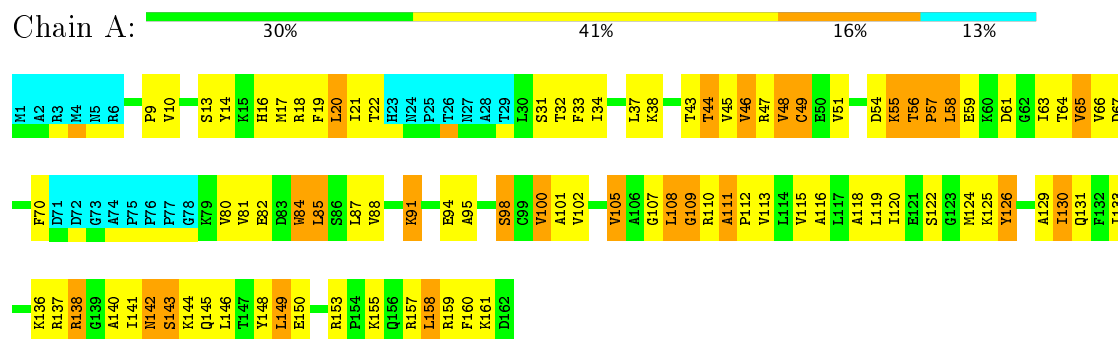
4.2.10 Score per residue for model 10

- Molecule 1: Protein tyrosine phosphatase type IVA 3



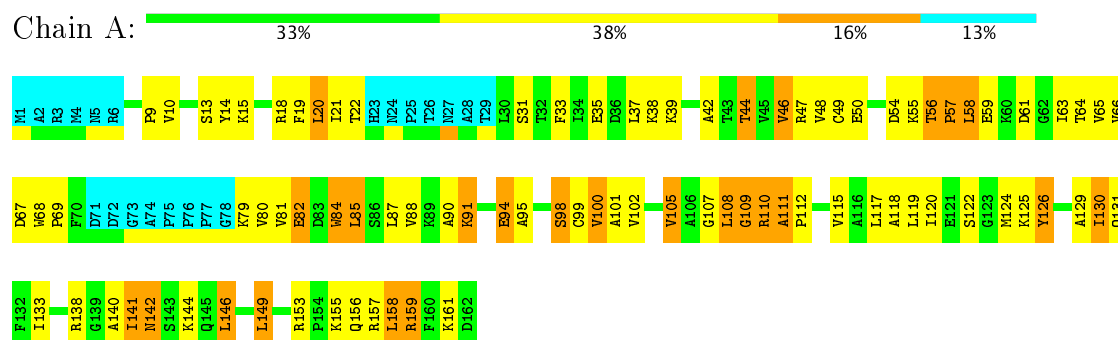
4.2.11 Score per residue for model 11

- Molecule 1: Protein tyrosine phosphatase type IVA 3



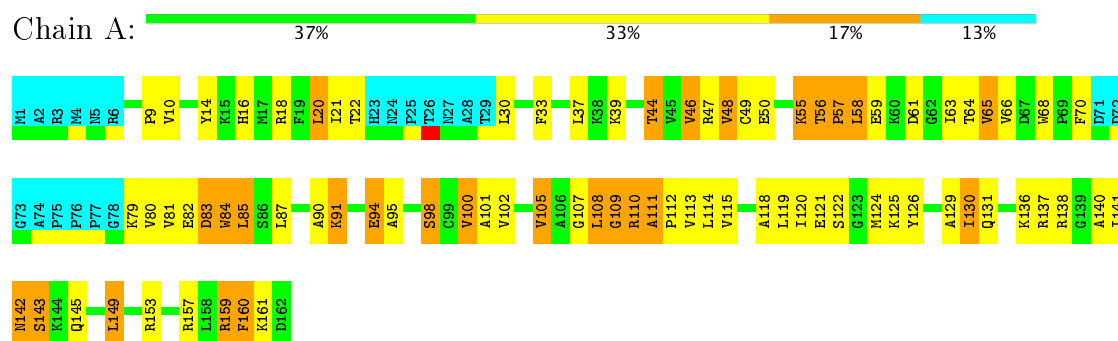
4.2.12 Score per residue for model 12

- Molecule 1: Protein tyrosine phosphatase type IVA 3



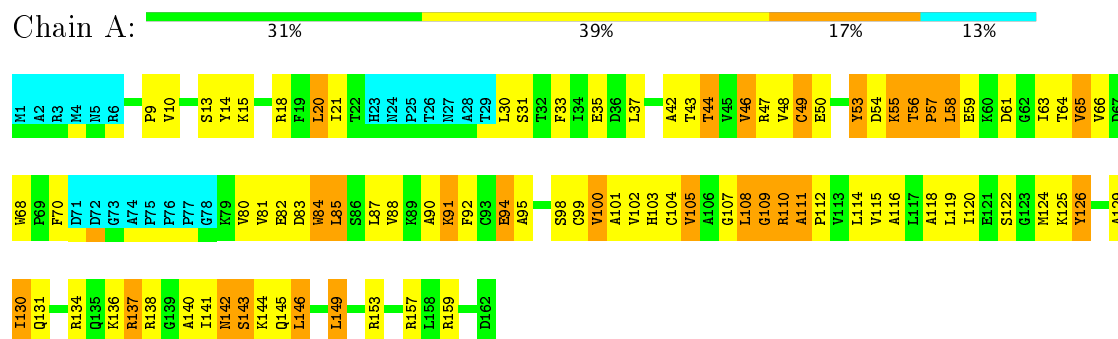
4.2.13 Score per residue for model 13

- Molecule 1: Protein tyrosine phosphatase type IVA 3



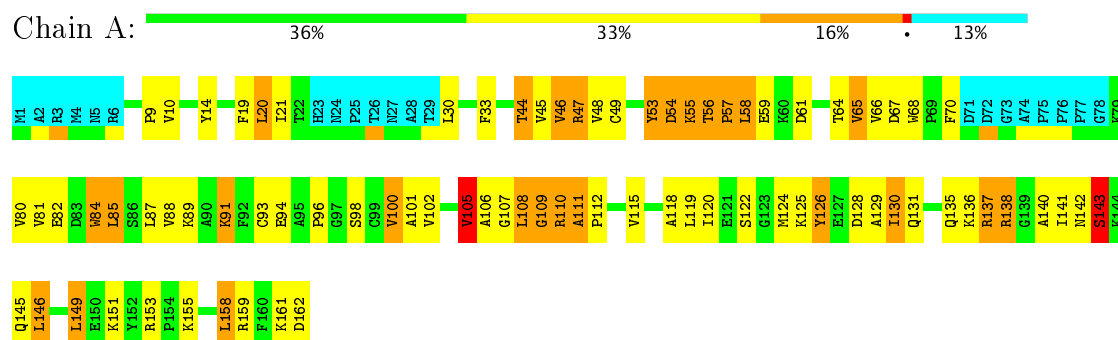
4.2.14 Score per residue for model 14

- Molecule 1: Protein tyrosine phosphatase type IVA 3



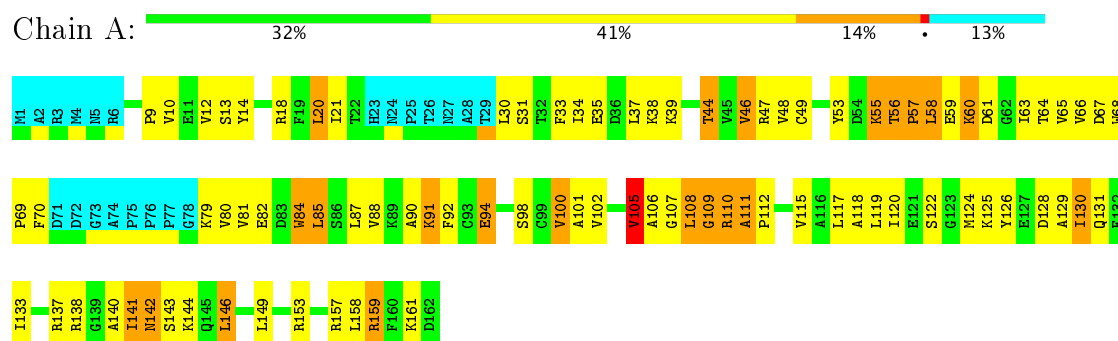
4.2.15 Score per residue for model 15

- Molecule 1: Protein tyrosine phosphatase type IVA 3



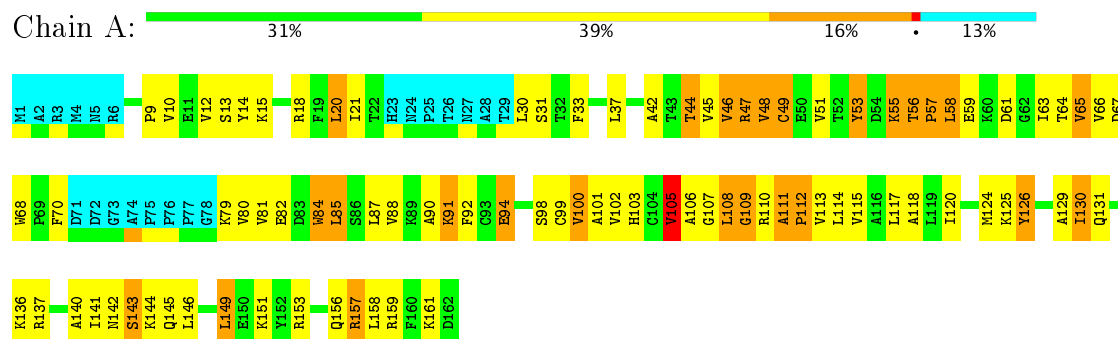
4.2.16 Score per residue for model 16

- Molecule 1: Protein tyrosine phosphatase type IVA 3



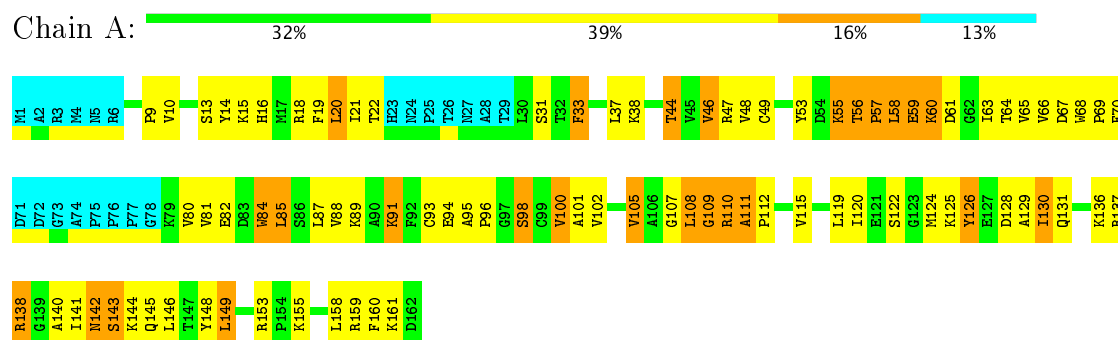
4.2.17 Score per residue for model 17

- Molecule 1: Protein tyrosine phosphatase type IVA 3



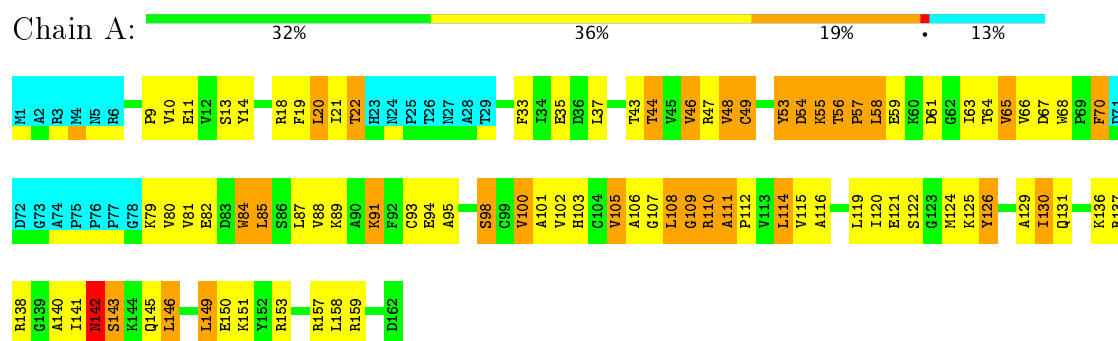
4.2.18 Score per residue for model 18

- Molecule 1: Protein tyrosine phosphatase type IVA 3



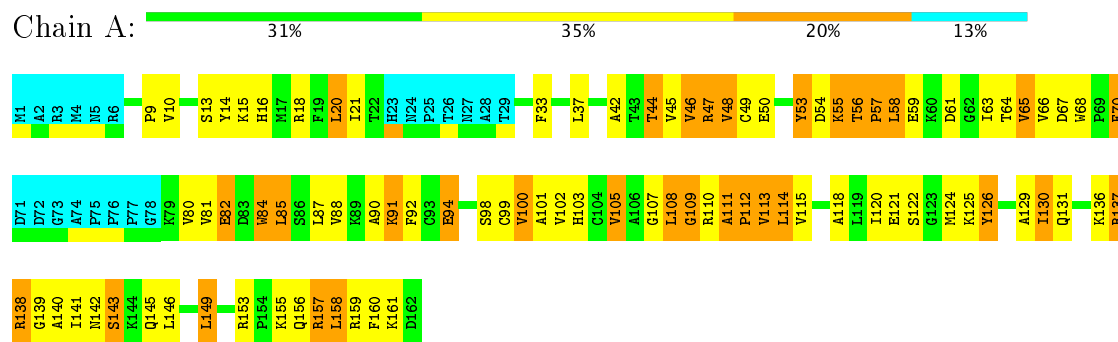
4.2.19 Score per residue for model 19

- Molecule 1: Protein tyrosine phosphatase type IVA 3



4.2.20 Score per residue for model 20

- Molecule 1: Protein tyrosine phosphatase type IVA 3



5 Refinement protocol and experimental data overview

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

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
CYANA	structure solution	
CYANA	refinement	
CYANA	structure solution	
XPLOR NIH	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)	2mbc_cs.cif
Number of chemical shift lists	1
Total number of shifts	1470
Number of shifts mapped to atoms	1470
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	69%

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	A	1128	1174	1174	101±6
All	All	22560	23480	23480	2019

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 44.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:111:ALA:HB3	1:A:112:PRO:CD	0.95	1.92	16	20
1:A:111:ALA:HB3	1:A:112:PRO:HD3	0.88	1.45	16	20
1:A:46:VAL:CG1	1:A:101:ALA:HB1	0.85	2.02	9	20
1:A:108:LEU:O	1:A:112:PRO:HD2	0.84	1.73	20	12
1:A:70:PHE:CE2	1:A:80:VAL:HG11	0.79	2.13	5	6
1:A:46:VAL:HG23	1:A:46:VAL:O	0.78	1.77	17	9
1:A:107:GLY:CA	1:A:111:ALA:HB2	0.77	2.10	4	11
1:A:20:LEU:N	1:A:100:VAL:O	0.77	2.18	7	8
1:A:46:VAL:HG12	1:A:101:ALA:HB1	0.77	1.56	20	20
1:A:107:GLY:O	1:A:108:LEU:O	0.77	2.02	20	12
1:A:46:VAL:O	1:A:46:VAL:HG23	0.76	1.79	14	11
1:A:44:THR:O	1:A:101:ALA:HB3	0.76	1.80	5	20
1:A:47:ARG:CD	1:A:65:VAL:HG23	0.76	2.11	8	18
1:A:142:ASN:O	1:A:143:SER:CB	0.76	2.34	11	15

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:LEU:HD13	1:A:158:LEU:HD23	0.75	1.59	4	1
1:A:44:THR:OG1	1:A:100:VAL:HA	0.74	1.81	17	20
1:A:107:GLY:O	1:A:109:GLY:N	0.74	2.21	10	8
1:A:141:ILE:HG23	1:A:146:LEU:CD1	0.74	2.12	3	15
1:A:58:LEU:HD22	1:A:58:LEU:C	0.73	2.03	11	13
1:A:58:LEU:C	1:A:58:LEU:HD22	0.72	2.04	5	7
1:A:111:ALA:CB	1:A:112:PRO:CD	0.72	2.67	8	20
1:A:130:ILE:HD12	1:A:141:ILE:HG21	0.72	1.61	18	11
1:A:44:THR:HG22	1:A:66:VAL:CG2	0.72	2.15	10	20
1:A:112:PRO:HG3	1:A:140:ALA:HB1	0.71	1.62	2	20
1:A:105:VAL:HG13	1:A:106:ALA:H	0.71	1.46	19	4
1:A:141:ILE:HG23	1:A:146:LEU:HD12	0.71	1.60	15	11
1:A:105:VAL:HG22	1:A:106:ALA:H	0.70	1.46	8	4
1:A:70:PHE:CZ	1:A:80:VAL:HG13	0.69	2.22	15	4
1:A:142:ASN:HA	1:A:146:LEU:HD13	0.69	1.65	10	16
1:A:48:VAL:HG21	1:A:102:VAL:HG22	0.69	1.65	10	1
1:A:109:GLY:O	1:A:112:PRO:HD2	0.68	1.88	6	20
1:A:107:GLY:HA2	1:A:111:ALA:HB2	0.68	1.66	5	7
1:A:81:VAL:O	1:A:85:LEU:HD22	0.68	1.89	16	18
1:A:108:LEU:O	1:A:109:GLY:C	0.67	2.32	1	12
1:A:105:VAL:HG22	1:A:106:ALA:N	0.67	2.04	19	5
1:A:112:PRO:CG	1:A:140:ALA:HB1	0.67	2.20	9	13
1:A:47:ARG:HD3	1:A:65:VAL:HG23	0.67	1.66	1	10
1:A:58:LEU:HD22	1:A:59:GLU:N	0.67	2.05	14	20
1:A:108:LEU:O	1:A:111:ALA:N	0.66	2.28	12	12
1:A:70:PHE:CE1	1:A:80:VAL:HG13	0.66	2.26	6	7
1:A:46:VAL:HA	1:A:102:VAL:HA	0.65	1.67	8	20
1:A:141:ILE:O	1:A:141:ILE:HG13	0.65	1.90	3	7
1:A:37:LEU:HD11	1:A:63:ILE:HD13	0.65	1.67	18	11
1:A:48:VAL:HG12	1:A:48:VAL:O	0.65	1.90	8	3
1:A:110:ARG:O	1:A:114:LEU:HB2	0.65	1.92	20	3
1:A:47:ARG:HD2	1:A:65:VAL:HG23	0.64	1.69	19	18
1:A:141:ILE:HG23	1:A:142:ASN:H	0.64	1.52	16	2
1:A:48:VAL:HG22	1:A:66:VAL:HG12	0.64	1.69	1	15
1:A:81:VAL:HG12	1:A:117:LEU:HD21	0.64	1.67	16	3
1:A:46:VAL:HA	1:A:101:ALA:O	0.64	1.93	16	20
1:A:141:ILE:O	1:A:142:ASN:C	0.63	2.35	13	8
1:A:48:VAL:CG2	1:A:102:VAL:HG22	0.63	2.22	10	1
1:A:55:LYS:HE3	1:A:65:VAL:HG11	0.63	1.71	10	2
1:A:107:GLY:O	1:A:108:LEU:C	0.63	2.37	20	13
1:A:44:THR:HG23	1:A:64:THR:HB	0.63	1.69	8	20

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:PHE:CD2	1:A:114:LEU:HD11	0.63	2.29	2	5
1:A:46:VAL:HB	1:A:102:VAL:C	0.62	2.14	17	19
1:A:120:ILE:HG21	1:A:149:LEU:HD21	0.62	1.70	13	1
1:A:85:LEU:HD21	1:A:121:GLU:OE2	0.62	1.94	13	4
1:A:141:ILE:O	1:A:145:GLN:HB2	0.62	1.94	7	13
1:A:66:VAL:CG1	1:A:87:LEU:HD22	0.62	2.24	4	20
1:A:14:TYR:OH	1:A:119:LEU:HD13	0.61	1.94	4	2
1:A:105:VAL:HG13	1:A:106:ALA:N	0.61	2.10	5	5
1:A:141:ILE:HG13	1:A:141:ILE:O	0.61	1.96	20	2
1:A:70:PHE:CZ	1:A:80:VAL:HG11	0.61	2.30	20	3
1:A:112:PRO:HA	1:A:115:VAL:HG22	0.60	1.73	5	13
1:A:66:VAL:HG11	1:A:87:LEU:HD22	0.60	1.72	4	10
1:A:30:LEU:HD23	1:A:57:PRO:CG	0.60	2.27	13	2
1:A:47:ARG:CD	1:A:65:VAL:HG12	0.60	2.25	11	1
1:A:30:LEU:HD21	1:A:57:PRO:HG3	0.60	1.72	14	1
1:A:55:LYS:CB	1:A:58:LEU:HD11	0.60	2.26	2	20
1:A:46:VAL:HG13	1:A:101:ALA:HB1	0.60	1.72	10	20
1:A:10:VAL:O	1:A:20:LEU:HD13	0.60	1.96	9	20
1:A:111:ALA:CB	1:A:112:PRO:HD3	0.60	2.26	7	19
1:A:46:VAL:CG2	1:A:46:VAL:O	0.60	2.50	17	5
1:A:33:PHE:CE1	1:A:37:LEU:HD23	0.59	2.32	1	8
1:A:33:PHE:CZ	1:A:46:VAL:HG22	0.59	2.32	6	18
1:A:46:VAL:HG12	1:A:101:ALA:C	0.59	2.18	9	20
1:A:111:ALA:O	1:A:115:VAL:HG13	0.58	1.99	5	13
1:A:47:ARG:C	1:A:66:VAL:O	0.58	2.41	8	20
1:A:85:LEU:HD11	1:A:121:GLU:HB3	0.58	1.75	4	1
1:A:105:VAL:HG13	1:A:107:GLY:H	0.58	1.59	9	4
1:A:95:ALA:HB1	1:A:98:SER:OG	0.58	1.98	10	8
1:A:87:LEU:O	1:A:91:LYS:HG3	0.57	1.98	13	14
1:A:47:ARG:CB	1:A:66:VAL:O	0.57	2.52	10	14
1:A:141:ILE:O	1:A:142:ASN:CB	0.57	2.52	6	2
1:A:48:VAL:HG13	1:A:70:PHE:CE2	0.57	2.34	8	1
1:A:88:VAL:O	1:A:91:LYS:HE2	0.57	1.99	18	18
1:A:105:VAL:HG23	1:A:107:GLY:H	0.57	1.60	4	4
1:A:34:ILE:HG22	1:A:38:LYS:HE3	0.57	1.77	5	2
1:A:48:VAL:HG12	1:A:110:ARG:NH1	0.57	2.14	20	1
1:A:66:VAL:HG22	1:A:87:LEU:HD13	0.57	1.77	14	14
1:A:109:GLY:O	1:A:113:VAL:HG22	0.57	1.99	20	3
1:A:48:VAL:HG13	1:A:68:TRP:HB2	0.57	1.75	14	3
1:A:141:ILE:CG1	1:A:145:GLN:HB2	0.57	2.29	6	3
1:A:141:ILE:HG12	1:A:146:LEU:HD12	0.57	1.76	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:44:THR:HG22	1:A:66:VAL:HG23	0.56	1.77	13	18
1:A:44:THR:CG2	1:A:66:VAL:CG2	0.56	2.83	3	20
1:A:85:LEU:HG	1:A:158:LEU:HD23	0.56	1.76	20	1
1:A:46:VAL:HG12	1:A:101:ALA:CB	0.56	2.28	15	19
1:A:113:VAL:HG13	1:A:145:GLN:CD	0.56	2.21	2	3
1:A:45:VAL:HG21	1:A:58:LEU:HG	0.56	1.76	11	1
1:A:88:VAL:CG1	1:A:158:LEU:HD21	0.56	2.30	20	2
1:A:47:ARG:HD3	1:A:65:VAL:HG12	0.56	1.78	11	1
1:A:142:ASN:O	1:A:143:SER:HB2	0.56	2.00	14	6
1:A:56:THR:H	1:A:57:PRO:HD2	0.55	1.61	9	20
1:A:67:ASP:O	1:A:68:TRP:CE3	0.55	2.60	19	11
1:A:48:VAL:O	1:A:48:VAL:HG12	0.55	2.01	14	2
1:A:70:PHE:CD2	1:A:80:VAL:HG11	0.55	2.36	8	3
1:A:66:VAL:HG13	1:A:87:LEU:HD22	0.55	1.78	14	2
1:A:91:LYS:CB	1:A:100:VAL:HG13	0.55	2.32	20	12
1:A:47:ARG:HB2	1:A:66:VAL:C	0.55	2.23	20	6
1:A:48:VAL:HG12	1:A:70:PHE:HB2	0.54	1.77	1	3
1:A:112:PRO:CB	1:A:140:ALA:HB1	0.54	2.32	17	1
1:A:46:VAL:O	1:A:46:VAL:CG2	0.54	2.52	14	5
1:A:48:VAL:HG21	1:A:102:VAL:HG12	0.54	1.79	19	3
1:A:110:ARG:HA	1:A:113:VAL:CG2	0.54	2.31	5	3
1:A:88:VAL:HG23	1:A:91:LYS:NZ	0.54	2.18	10	1
1:A:58:LEU:CD2	1:A:58:LEU:C	0.54	2.77	12	14
1:A:55:LYS:CE	1:A:65:VAL:HG11	0.53	2.32	10	2
1:A:48:VAL:O	1:A:49:CYS:HB3	0.53	2.03	8	1
1:A:130:ILE:CG2	1:A:146:LEU:HD11	0.53	2.34	14	8
1:A:56:THR:OG1	1:A:57:PRO:HD3	0.53	2.04	11	20
1:A:141:ILE:HG23	1:A:146:LEU:HD11	0.53	1.80	11	2
1:A:112:PRO:HB2	1:A:133:ILE:HD12	0.53	1.78	12	6
1:A:81:VAL:HG11	1:A:148:TYR:OH	0.53	2.04	4	4
1:A:58:LEU:C	1:A:58:LEU:CD2	0.53	2.77	16	6
1:A:9:PRO:HB3	1:A:22:THR:HG22	0.53	1.79	18	2
1:A:109:GLY:O	1:A:112:PRO:CD	0.52	2.56	20	20
1:A:84:TRP:NE1	1:A:114:LEU:HD13	0.52	2.18	19	4
1:A:119:LEU:CD2	1:A:129:ALA:HB1	0.52	2.34	13	8
1:A:19:PHE:CD2	1:A:100:VAL:HG21	0.52	2.39	12	8
1:A:113:VAL:HG22	1:A:145:GLN:HG2	0.52	1.80	8	2
1:A:22:THR:HG22	1:A:103:HIS:HA	0.52	1.81	5	1
1:A:9:PRO:HB2	1:A:20:LEU:HD12	0.52	1.81	5	20
1:A:68:TRP:CZ2	1:A:87:LEU:HD23	0.52	2.39	14	3
1:A:109:GLY:O	1:A:110:ARG:C	0.52	2.48	15	18

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:PHE:CG	1:A:80:VAL:HG11	0.52	2.40	8	1
1:A:58:LEU:N	1:A:58:LEU:HD13	0.52	2.20	14	10
1:A:55:LYS:CB	1:A:58:LEU:HD21	0.51	2.35	14	3
1:A:88:VAL:HG13	1:A:89:LYS:N	0.51	2.20	10	1
1:A:110:ARG:O	1:A:111:ALA:C	0.51	2.49	20	10
1:A:91:LYS:HD2	1:A:100:VAL:CG2	0.51	2.35	4	10
1:A:110:ARG:CA	1:A:113:VAL:HG22	0.51	2.35	17	3
1:A:84:TRP:CE3	1:A:118:ALA:HB2	0.51	2.39	7	13
1:A:65:VAL:O	1:A:65:VAL:HG22	0.51	2.04	3	3
1:A:55:LYS:HB3	1:A:58:LEU:HD21	0.51	1.83	14	1
1:A:22:THR:HG21	1:A:46:VAL:HG21	0.51	1.82	10	1
1:A:126:TYR:OH	1:A:146:LEU:HD23	0.51	2.04	6	2
1:A:88:VAL:HG12	1:A:158:LEU:HD11	0.51	1.82	6	1
1:A:45:VAL:HG21	1:A:58:LEU:HD23	0.51	1.82	7	3
1:A:48:VAL:HG21	1:A:102:VAL:CG1	0.51	2.35	19	9
1:A:120:ILE:HD11	1:A:129:ALA:HB3	0.50	1.83	3	20
1:A:84:TRP:O	1:A:88:VAL:HG23	0.50	2.06	19	4
1:A:19:PHE:HZ	1:A:88:VAL:HG22	0.50	1.65	4	5
1:A:45:VAL:HB	1:A:47:ARG:CG	0.50	2.36	9	6
1:A:12:VAL:O	1:A:12:VAL:HG13	0.50	2.06	6	2
1:A:95:ALA:HB1	1:A:96:PRO:HD2	0.50	1.83	6	2
1:A:58:LEU:HD13	1:A:58:LEU:N	0.50	2.21	3	9
1:A:10:VAL:C	1:A:20:LEU:HD13	0.50	2.27	8	20
1:A:85:LEU:HD13	1:A:85:LEU:N	0.50	2.20	19	8
1:A:112:PRO:HA	1:A:115:VAL:CG2	0.50	2.37	11	10
1:A:85:LEU:HD12	1:A:158:LEU:HD23	0.50	1.83	7	7
1:A:120:ILE:HG21	1:A:149:LEU:HD11	0.49	1.84	17	5
1:A:126:TYR:HB2	1:A:149:LEU:HD12	0.49	1.84	6	18
1:A:47:ARG:HB2	1:A:66:VAL:O	0.49	2.07	3	15
1:A:18:ARG:O	1:A:100:VAL:HG23	0.49	2.07	4	11
1:A:85:LEU:HD23	1:A:157:ARG:HD3	0.49	1.85	17	2
1:A:141:ILE:O	1:A:145:GLN:HB3	0.49	2.07	8	2
1:A:68:TRP:CH2	1:A:87:LEU:HD23	0.49	2.42	13	1
1:A:65:VAL:HG22	1:A:65:VAL:O	0.49	2.06	7	5
1:A:48:VAL:N	1:A:66:VAL:O	0.49	2.46	8	11
1:A:113:VAL:HG22	1:A:145:GLN:HG3	0.49	1.82	11	4
1:A:70:PHE:CE1	1:A:114:LEU:HD21	0.49	2.43	19	3
1:A:130:ILE:HD13	1:A:130:ILE:N	0.49	2.23	13	8
1:A:68:TRP:CE3	1:A:70:PHE:CE2	0.49	3.01	13	1
1:A:105:VAL:CG2	1:A:106:ALA:N	0.49	2.76	16	1
1:A:85:LEU:HD21	1:A:121:GLU:CD	0.49	2.28	20	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:LEU:HD23	1:A:57:PRO:HG3	0.48	1.83	15	3
1:A:56:THR:O	1:A:60:LYS:HD2	0.48	2.08	16	2
1:A:116:ALA:CB	1:A:141:ILE:HD12	0.48	2.38	14	6
1:A:142:ASN:O	1:A:143:SER:HB3	0.48	2.07	19	3
1:A:19:PHE:CD1	1:A:100:VAL:CG1	0.48	2.96	3	8
1:A:119:LEU:HD23	1:A:129:ALA:HB1	0.48	1.84	6	8
1:A:56:THR:N	1:A:57:PRO:HD2	0.48	2.23	9	20
1:A:48:VAL:HG22	1:A:66:VAL:CG1	0.48	2.38	11	2
1:A:130:ILE:HG21	1:A:146:LEU:HD11	0.48	1.85	5	6
1:A:141:ILE:HG23	1:A:142:ASN:N	0.48	2.22	13	1
1:A:70:PHE:O	1:A:70:PHE:CD1	0.48	2.67	8	1
1:A:130:ILE:HG23	1:A:141:ILE:CG2	0.48	2.38	17	1
1:A:47:ARG:O	1:A:67:ASP:HA	0.48	2.08	8	14
1:A:81:VAL:HG23	1:A:82:GLU:N	0.48	2.24	19	18
1:A:85:LEU:N	1:A:85:LEU:HD13	0.48	2.23	6	7
1:A:33:PHE:HZ	1:A:46:VAL:HG22	0.48	1.67	6	2
1:A:65:VAL:HG22	1:A:67:ASP:OD1	0.48	2.09	10	1
1:A:142:ASN:CA	1:A:146:LEU:HD13	0.48	2.38	8	5
1:A:19:PHE:HA	1:A:100:VAL:HG13	0.48	1.86	7	8
1:A:49:CYS:SG	1:A:51:VAL:HG13	0.48	2.49	11	2
1:A:48:VAL:CG2	1:A:66:VAL:HG12	0.48	2.39	10	3
1:A:34:ILE:HG22	1:A:38:LYS:HE2	0.47	1.86	16	1
1:A:90:ALA:O	1:A:93:CYS:N	0.47	2.47	6	1
1:A:141:ILE:CG1	1:A:141:ILE:O	0.47	2.62	2	1
1:A:58:LEU:CD1	1:A:58:LEU:N	0.47	2.77	3	10
1:A:55:LYS:HB3	1:A:58:LEU:HD11	0.47	1.85	14	2
1:A:30:LEU:HD21	1:A:53:TYR:OH	0.47	2.10	9	1
1:A:70:PHE:CD1	1:A:70:PHE:N	0.47	2.82	6	2
1:A:70:PHE:CE2	1:A:114:LEU:HD11	0.47	2.44	20	1
1:A:85:LEU:HD11	1:A:121:GLU:CB	0.47	2.39	4	1
1:A:108:LEU:O	1:A:112:PRO:CD	0.47	2.63	8	2
1:A:130:ILE:CD1	1:A:141:ILE:HG21	0.47	2.38	18	2
1:A:46:VAL:O	1:A:103:HIS:HB2	0.47	2.10	20	1
1:A:130:ILE:N	1:A:130:ILE:HD13	0.47	2.25	18	11
1:A:91:LYS:HD2	1:A:100:VAL:HG22	0.47	1.87	20	7
1:A:84:TRP:CZ3	1:A:118:ALA:HB2	0.47	2.45	2	7
1:A:88:VAL:CG1	1:A:158:LEU:HD11	0.47	2.39	6	1
1:A:45:VAL:HG21	1:A:58:LEU:CG	0.47	2.40	11	1
1:A:87:LEU:O	1:A:90:ALA:N	0.46	2.48	13	3
1:A:91:LYS:CG	1:A:100:VAL:HG11	0.46	2.40	9	5
1:A:58:LEU:N	1:A:58:LEU:CD1	0.46	2.78	7	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:158:LEU:O	1:A:159:ARG:CB	0.46	2.63	12	2
1:A:89:LYS:O	1:A:93:CYS:CB	0.46	2.64	3	6
1:A:141:ILE:O	1:A:142:ASN:O	0.46	2.33	16	3
1:A:70:PHE:HB3	1:A:114:LEU:HD21	0.46	1.87	6	1
1:A:19:PHE:CD2	1:A:100:VAL:CG2	0.46	2.99	5	8
1:A:88:VAL:HG13	1:A:91:LYS:NZ	0.46	2.25	15	1
1:A:119:LEU:HD12	1:A:119:LEU:O	0.46	2.11	4	3
1:A:56:THR:OG1	1:A:57:PRO:CD	0.45	2.64	11	20
1:A:81:VAL:CG2	1:A:82:GLU:N	0.45	2.79	4	17
1:A:108:LEU:O	1:A:112:PRO:CG	0.45	2.64	9	6
1:A:142:ASN:O	1:A:143:SER:OG	0.45	2.35	4	2
1:A:12:VAL:HG13	1:A:12:VAL:O	0.45	2.11	17	2
1:A:33:PHE:CE1	1:A:46:VAL:HG22	0.45	2.46	9	4
1:A:143:SER:O	1:A:144:LYS:C	0.45	2.55	6	2
1:A:18:ARG:O	1:A:100:VAL:HG13	0.45	2.11	3	8
1:A:70:PHE:HE1	1:A:80:VAL:HG22	0.45	1.71	6	1
1:A:42:ALA:HB2	1:A:99:CYS:HB2	0.45	1.88	20	3
1:A:107:GLY:C	1:A:111:ALA:HB2	0.45	2.31	1	4
1:A:90:ALA:O	1:A:94:GLU:N	0.45	2.50	1	11
1:A:88:VAL:HG13	1:A:158:LEU:HD11	0.45	1.88	9	1
1:A:113:VAL:HG13	1:A:145:GLN:HG3	0.45	1.88	13	1
1:A:141:ILE:HG13	1:A:145:GLN:HB2	0.45	1.87	5	1
1:A:70:PHE:CE1	1:A:80:VAL:HG22	0.45	2.46	6	1
1:A:112:PRO:O	1:A:113:VAL:C	0.45	2.55	20	1
1:A:47:ARG:NE	1:A:65:VAL:HG23	0.45	2.27	1	1
1:A:91:LYS:HG2	1:A:100:VAL:HG11	0.45	1.88	9	4
1:A:70:PHE:CD1	1:A:114:LEU:HD21	0.45	2.46	19	1
1:A:112:PRO:O	1:A:116:ALA:HB2	0.44	2.12	7	6
1:A:109:GLY:O	1:A:111:ALA:N	0.44	2.50	5	1
1:A:68:TRP:CZ3	1:A:114:LEU:HD13	0.44	2.47	14	1
1:A:70:PHE:N	1:A:70:PHE:CD1	0.44	2.85	3	3
1:A:19:PHE:CE1	1:A:100:VAL:HG11	0.44	2.48	3	8
1:A:141:ILE:O	1:A:141:ILE:CG1	0.44	2.65	7	1
1:A:82:GLU:CG	1:A:83:ASP:N	0.44	2.79	4	3
1:A:45:VAL:HG11	1:A:47:ARG:CZ	0.44	2.43	9	1
1:A:85:LEU:HA	1:A:88:VAL:HG12	0.44	1.90	9	1
1:A:67:ASP:O	1:A:68:TRP:CD2	0.44	2.71	7	6
1:A:111:ALA:HB3	1:A:112:PRO:HD2	0.44	1.84	14	3
1:A:107:GLY:O	1:A:110:ARG:HG2	0.44	2.13	19	1
1:A:113:VAL:HG13	1:A:145:GLN:CG	0.44	2.43	13	1
1:A:137:ARG:NE	1:A:138:ARG:H	0.44	2.11	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:84:TRP:HE1	1:A:114:LEU:HD13	0.44	1.71	19	2
1:A:117:LEU:C	1:A:117:LEU:HD13	0.44	2.34	6	4
1:A:55:LYS:HB2	1:A:58:LEU:HD11	0.44	1.88	18	3
1:A:56:THR:HG23	1:A:57:PRO:CD	0.43	2.43	11	16
1:A:91:LYS:CE	1:A:92:PHE:CB	0.43	2.96	1	9
1:A:68:TRP:CE2	1:A:83:ASP:HB3	0.43	2.48	8	1
1:A:48:VAL:HB	1:A:102:VAL:HG13	0.43	1.90	10	1
1:A:111:ALA:O	1:A:115:VAL:HG22	0.43	2.13	16	3
1:A:14:TYR:HB2	1:A:17:MET:O	0.43	2.14	6	1
1:A:70:PHE:CE2	1:A:114:LEU:CD1	0.43	3.02	13	1
1:A:46:VAL:HA	1:A:102:VAL:CA	0.43	2.41	8	3
1:A:66:VAL:HG11	1:A:87:LEU:CD2	0.43	2.44	10	3
1:A:110:ARG:O	1:A:114:LEU:CB	0.43	2.66	17	1
1:A:53:TYR:CD1	1:A:53:TYR:C	0.43	2.91	17	1
1:A:37:LEU:HD12	1:A:37:LEU:C	0.43	2.34	18	1
1:A:34:ILE:HD13	1:A:57:PRO:HB2	0.43	1.91	10	1
1:A:141:ILE:HG13	1:A:145:GLN:CG	0.42	2.44	8	2
1:A:113:VAL:HG23	1:A:114:LEU:N	0.42	2.29	5	2
1:A:51:VAL:HG21	1:A:67:ASP:CB	0.42	2.44	8	1
1:A:58:LEU:HD21	1:A:65:VAL:HG22	0.42	1.90	11	1
1:A:19:PHE:CD1	1:A:19:PHE:N	0.42	2.87	18	4
1:A:91:LYS:HD3	1:A:100:VAL:HG21	0.42	1.91	13	1
1:A:119:LEU:O	1:A:119:LEU:HD12	0.42	2.15	8	2
1:A:105:VAL:CG1	1:A:106:ALA:N	0.42	2.78	5	2
1:A:53:TYR:CZ	1:A:54:ASP:O	0.42	2.73	15	5
1:A:43:THR:C	1:A:63:ILE:HG23	0.42	2.34	11	1
1:A:113:VAL:HG23	1:A:114:LEU:HD23	0.42	1.91	20	1
1:A:43:THR:HG21	1:A:95:ALA:HB2	0.42	1.92	14	2
1:A:19:PHE:N	1:A:19:PHE:CD1	0.42	2.88	3	2
1:A:56:THR:CB	1:A:57:PRO:CD	0.42	2.98	7	11
1:A:107:GLY:HA3	1:A:111:ALA:HB2	0.42	1.91	7	2
1:A:81:VAL:HG12	1:A:117:LEU:CD2	0.42	2.43	16	1
1:A:126:TYR:O	1:A:130:ILE:HG12	0.41	2.14	10	2
1:A:42:ALA:HA	1:A:99:CYS:O	0.41	2.15	5	3
1:A:55:LYS:CA	1:A:58:LEU:HD11	0.41	2.45	2	2
1:A:33:PHE:C	1:A:33:PHE:CD1	0.41	2.94	6	1
1:A:70:PHE:CD1	1:A:114:LEU:CD1	0.41	3.04	8	1
1:A:105:VAL:CG1	1:A:106:ALA:H	0.41	2.20	19	1
1:A:66:VAL:CG2	1:A:87:LEU:HD13	0.41	2.45	9	3
1:A:19:PHE:CD1	1:A:100:VAL:HG13	0.41	2.50	19	2
1:A:48:VAL:HG23	1:A:66:VAL:CG1	0.41	2.46	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:46:VAL:CG1	1:A:101:ALA:CB	0.41	2.91	14	1
1:A:107:GLY:C	1:A:108:LEU:O	0.41	2.58	18	1
1:A:109:GLY:C	1:A:113:VAL:HG22	0.41	2.36	20	1
1:A:70:PHE:HB3	1:A:80:VAL:HG21	0.41	1.92	8	1
1:A:34:ILE:HG22	1:A:38:LYS:CE	0.41	2.44	5	1
1:A:47:ARG:O	1:A:49:CYS:N	0.41	2.53	5	1
1:A:91:LYS:CE	1:A:92:PHE:N	0.41	2.84	10	2
1:A:55:LYS:HD2	1:A:65:VAL:HG21	0.41	1.92	11	1
1:A:117:LEU:HD13	1:A:117:LEU:C	0.41	2.36	8	1
1:A:44:THR:O	1:A:101:ALA:CB	0.41	2.66	10	1
1:A:30:LEU:HD23	1:A:57:PRO:HG2	0.41	1.92	13	1
1:A:51:VAL:HG21	1:A:67:ASP:HB3	0.41	1.93	17	1
1:A:53:TYR:CE2	1:A:54:ASP:O	0.41	2.74	15	1
1:A:47:ARG:HD2	1:A:65:VAL:CG2	0.40	2.45	3	1
1:A:46:VAL:HG12	1:A:102:VAL:N	0.40	2.30	10	1
1:A:88:VAL:HG13	1:A:89:LYS:H	0.40	1.76	10	1
1:A:85:LEU:HD23	1:A:157:ARG:CB	0.40	2.45	20	1
1:A:142:ASN:HA	1:A:146:LEU:HD22	0.40	1.93	4	1
1:A:43:THR:HG21	1:A:95:ALA:CB	0.40	2.47	19	1
1:A:53:TYR:O	1:A:53:TYR:CD1	0.40	2.75	20	1

6.3 Torsion angles ⓘ

6.3.1 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	140/162 (86%)	103±3 (73±2%)	26±2 (18±2%)	11±1 (8±1%)	2	14
All	All	2800/3240 (86%)	2055 (73%)	516 (18%)	229 (8%)	2	14

All 25 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	98	SER	20
1	A	111	ALA	20

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Mol	Chain	Res	Type	Models (Total)
1	A	46	VAL	20
1	A	105	VAL	20
1	A	108	LEU	20
1	A	57	PRO	20
1	A	49	CYS	18
1	A	143	SER	16
1	A	142	ASN	12
1	A	109	GLY	12
1	A	48	VAL	11
1	A	138	ARG	10
1	A	137	ARG	8
1	A	139	GLY	4
1	A	159	ARG	3
1	A	96	PRO	3
1	A	112	PRO	2
1	A	160	PHE	2
1	A	54	ASP	2
1	A	113	VAL	1
1	A	22	THR	1
1	A	158	LEU	1
1	A	110	ARG	1
1	A	14	TYR	1
1	A	52	THR	1

6.3.2 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	123/139 (88%)	82±2 (67±2%)	41±2 (33±2%)	1	12
All	All	2460/2780 (88%)	1645 (67%)	815 (33%)	1	12

All 78 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	44	THR	20
1	A	84	TRP	20

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Mol	Chain	Res	Type	Models (Total)
1	A	94	GLU	20
1	A	124	MET	20
1	A	131	GLN	20
1	A	20	LEU	20
1	A	130	ILE	20
1	A	61	ASP	20
1	A	100	VAL	20
1	A	14	TYR	20
1	A	21	ILE	20
1	A	149	LEU	20
1	A	126	TYR	20
1	A	153	ARG	20
1	A	91	LYS	20
1	A	58	LEU	20
1	A	56	THR	20
1	A	125	LYS	20
1	A	159	ARG	19
1	A	85	LEU	19
1	A	55	LYS	18
1	A	136	LYS	18
1	A	13	SER	17
1	A	137	ARG	17
1	A	122	SER	17
1	A	161	LYS	16
1	A	138	ARG	15
1	A	65	VAL	14
1	A	157	ARG	14
1	A	155	LYS	13
1	A	146	LEU	13
1	A	144	LYS	12
1	A	158	LEU	11
1	A	105	VAL	11
1	A	15	LYS	11
1	A	53	TYR	10
1	A	110	ARG	10
1	A	16	HIS	9
1	A	79	LYS	8
1	A	31	SER	8
1	A	35	GLU	8
1	A	160	PHE	8
1	A	142	ASN	8
1	A	103	HIS	7

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Mol	Chain	Res	Type	Models (Total)
1	A	82	GLU	6
1	A	114	LEU	6
1	A	141	ILE	6
1	A	150	GLU	6
1	A	115	VAL	6
1	A	47	ARG	6
1	A	143	SER	6
1	A	128	ASP	6
1	A	22	THR	5
1	A	39	LYS	5
1	A	50	GLU	5
1	A	104	CYS	5
1	A	156	GLN	5
1	A	83	ASP	4
1	A	70	PHE	4
1	A	17	MET	4
1	A	54	ASP	4
1	A	49	CYS	4
1	A	38	LYS	4
1	A	98	SER	3
1	A	135	GLN	3
1	A	11	GLU	3
1	A	151	LYS	3
1	A	60	LYS	2
1	A	89	LYS	2
1	A	162	ASP	2
1	A	92	PHE	2
1	A	59	GLU	1
1	A	86	SER	1
1	A	30	LEU	1
1	A	33	PHE	1
1	A	67	ASP	1
1	A	134	ARG	1
1	A	80	VAL	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 [i](#)

There are no carbohydrates 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

The completeness of assignment taking into account all chemical shift lists is 69% for the well-defined parts and 63% for the entire structure.

7.1 Chemical shift list 1

File name: 2mbc_cs.cif

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	1470
Number of shifts mapped to atoms	1470
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	136	-0.33 ± 0.20	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	130	0.33 ± 0.09	None needed (< 0.5 ppm)
$^{13}\text{C}'$	0	—	None (insufficient data)
^{15}N	126	-0.20 ± 0.21	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 69%, i.e. 1250 atoms were assigned a chemical shift out of a possible 1800. 13 out of 29 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	508/691 (74%)	255/275 (93%)	131/282 (46%)	122/134 (91%)
Sidechain	715/969 (74%)	440/568 (77%)	273/355 (77%)	2/46 (4%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	27/140 (19%)	25/74 (34%)	0/62 (0%)	2/4 (50%)
Overall	1250/1800 (69%)	720/917 (79%)	404/699 (58%)	126/184 (68%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 63%, i.e. 1292 atoms were assigned a chemical shift out of a possible 2038. 13 out of 29 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	528/788 (67%)	266/313 (85%)	136/324 (42%)	126/151 (83%)
Sidechain	737/1103 (67%)	452/649 (70%)	283/399 (71%)	2/55 (4%)
Aromatic	27/147 (18%)	25/78 (32%)	0/64 (0%)	2/5 (40%)
Overall	1292/2038 (63%)	743/1040 (71%)	419/787 (53%)	130/211 (62%)

7.1.4 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	18	ARG	NE	7.22	92.63 – 76.73	-48.7
1	A	134	ARG	HE	3.05	10.48 – 4.28	-7.0
1	A	114	LEU	HB3	-0.53	3.34 – -0.26	-5.8
1	A	124	MET	CE	27.04	26.97 – 7.37	5.0

7.1.5 Random Coil Index (RCI) plots ⓘ

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:

