



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 10:29 PM BST

PDB ID : 2JXC
Title : Structure of the EPS15-EH2 Stonin2 Complex
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Groemping, Y.
Deposited on : 2007-11-12

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
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

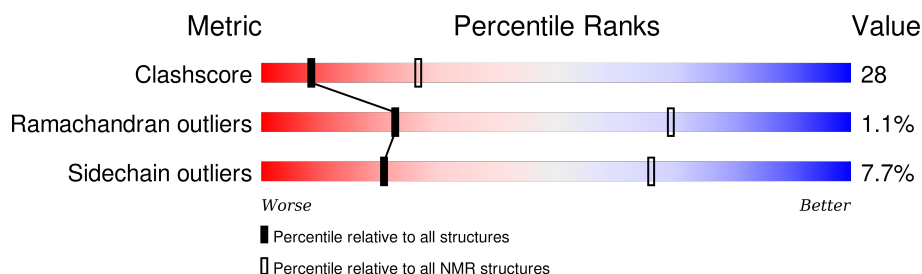
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 86%.

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



Metric	Whole archive (#Entries)	NMR archive (#Entries)
Clashscore	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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

Mol	Chain	Length	Quality of chain
1	A	100	
2	B	45	

2 Ensemble composition and analysis

This entry contains 10 models. Model 7 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:121-A:212, B:309-B:317, B:325-B:332 (109)	0.27	7

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 3 clusters and 3 single-model clusters were found.

Cluster number	Models
1	3, 5, 6
2	7, 9
3	1, 2
Single-model clusters	4; 8; 10

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2119 atoms, of which 1050 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Epidermal growth factor receptor substrate 15.

Mol	Chain	Residues	Atoms						Trace
1	A	95	Total	C	H	N	O	S	0
			1496	484	753	118	137	4	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	116	GLY	-	EXPRESSION TAG	UNP P42566
A	117	PRO	-	EXPRESSION TAG	UNP P42566
A	118	LEU	-	EXPRESSION TAG	UNP P42566
A	119	GLY	-	EXPRESSION TAG	UNP P42566
A	120	SER	-	EXPRESSION TAG	UNP P42566

- Molecule 2 is a protein called Stonin-2.

Mol	Chain	Residues	Atoms					Trace
2	B	40	Total	C	H	N	O	0
			622	206	297	53	66	

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	296	GLY	-	EXPRESSION TAG	UNP Q8WXE9
B	297	PRO	-	EXPRESSION TAG	UNP Q8WXE9
B	298	LEU	-	EXPRESSION TAG	UNP Q8WXE9
B	299	GLY	-	EXPRESSION TAG	UNP Q8WXE9
B	300	SER	-	EXPRESSION TAG	UNP Q8WXE9

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

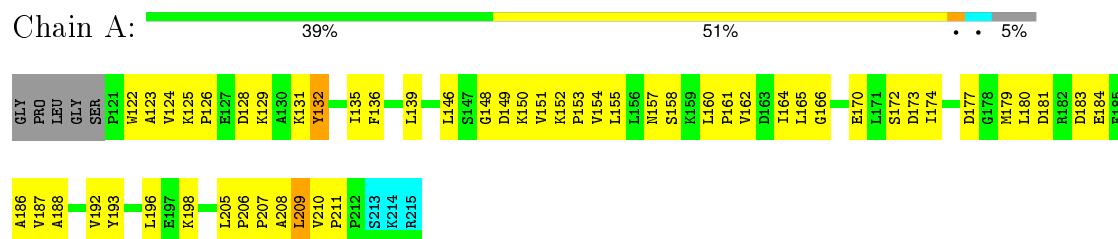
Mol	Chain	Residues	Atoms	
3	A	1	Total	Ca
			1	1

4 Residue-property plots [i](#)

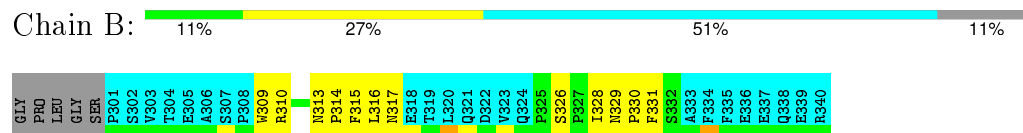
4.1 Average score per residue in the NMR ensemble

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

- Molecule 1: Epidermal growth factor receptor substrate 15



- Molecule 2: Stonin-2

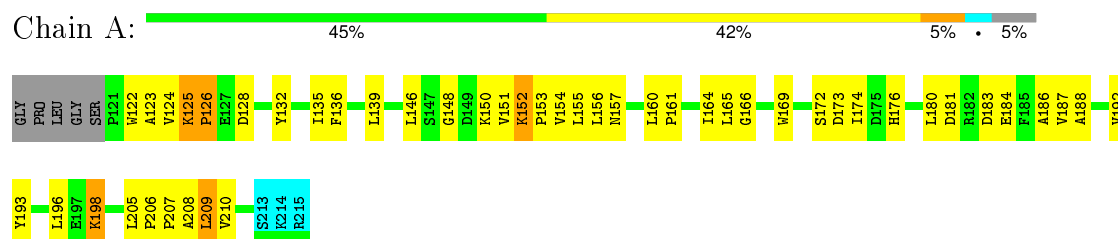


4.2 Scores per residue for each member of the ensemble

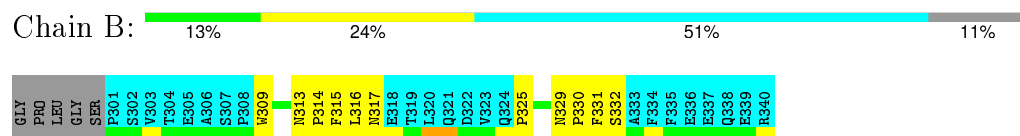
Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

- Molecule 1: Epidermal growth factor receptor substrate 15

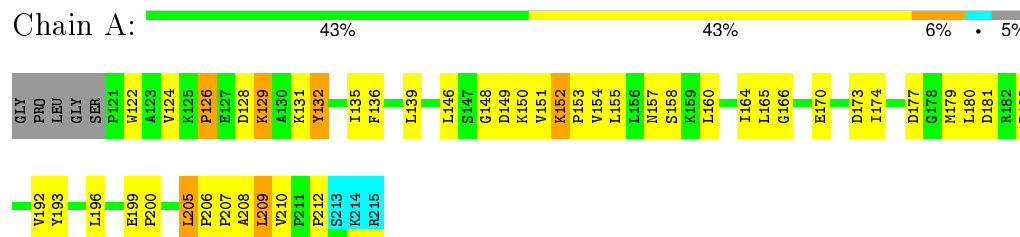


- Molecule 2: Stonin-2

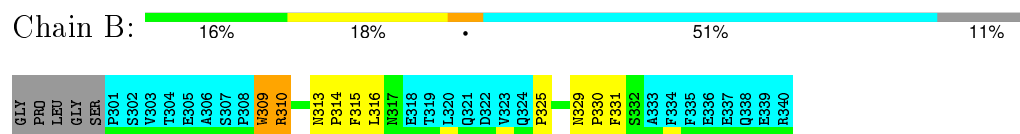


4.2.2 Score per residue for model 2

- Molecule 1: Epidermal growth factor receptor substrate 15

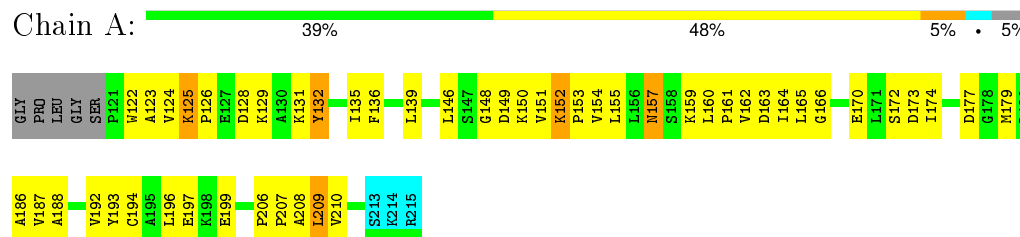


- Molecule 2: Stonin-2

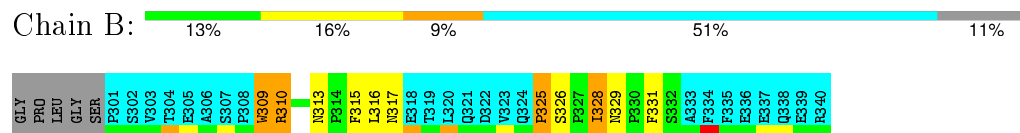


4.2.3 Score per residue for model 3

- Molecule 1: Epidermal growth factor receptor substrate 15

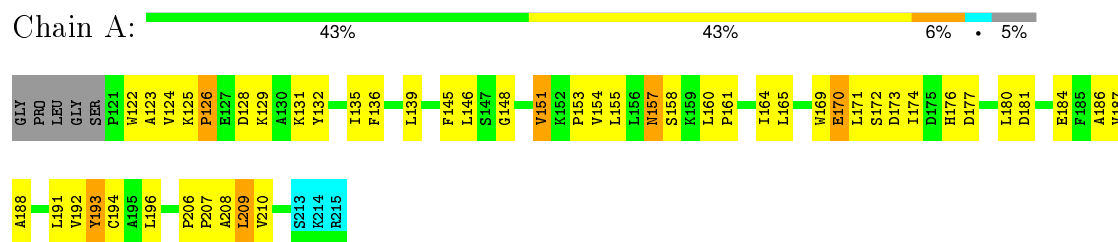


- Molecule 2: Stonin-2

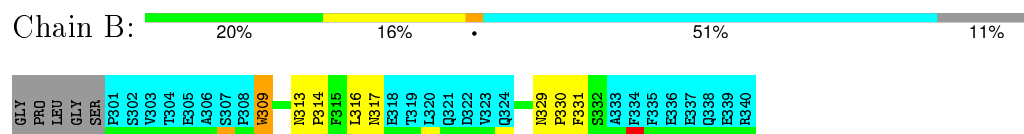


4.2.4 Score per residue for model 4

- Molecule 1: Epidermal growth factor receptor substrate 15

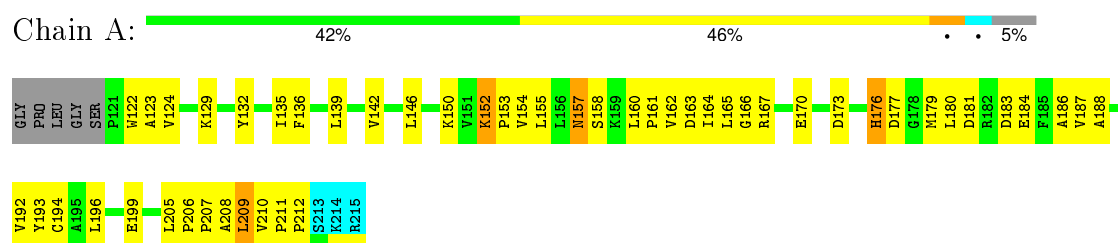


- Molecule 2: Stonin-2

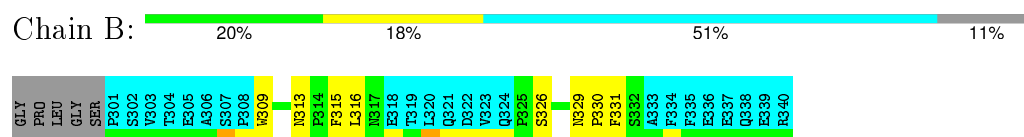


4.2.5 Score per residue for model 5

- Molecule 1: Epidermal growth factor receptor substrate 15

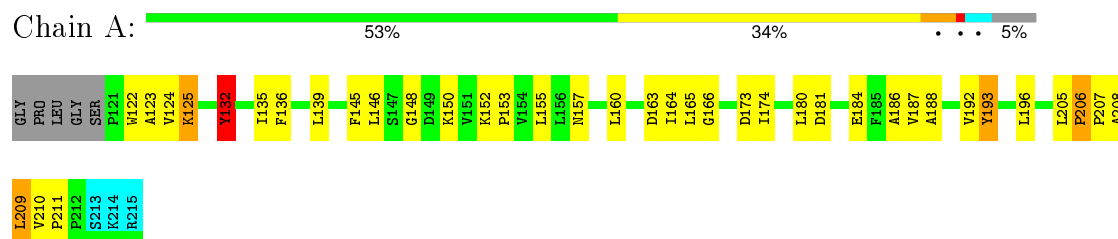


- Molecule 2: Stonin-2

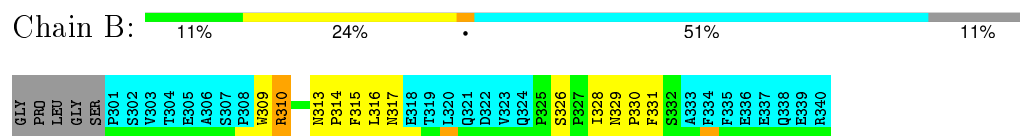


4.2.6 Score per residue for model 6

- Molecule 1: Epidermal growth factor receptor substrate 15

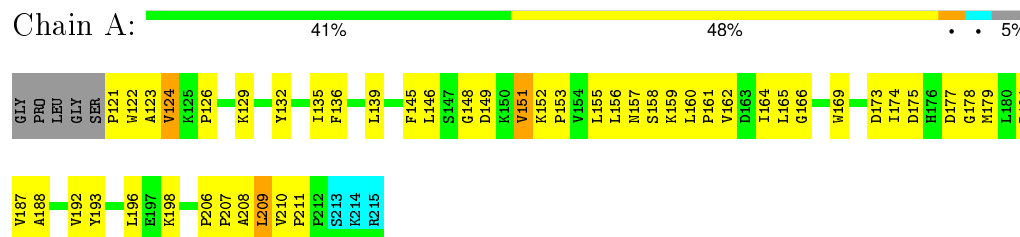


- Molecule 2: Stonin-2

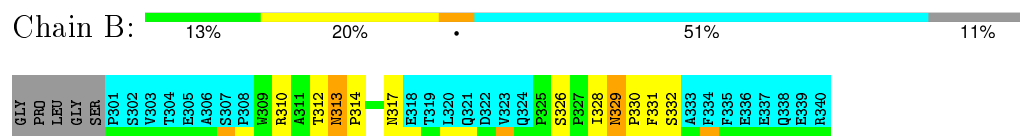


4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Epidermal growth factor receptor substrate 15

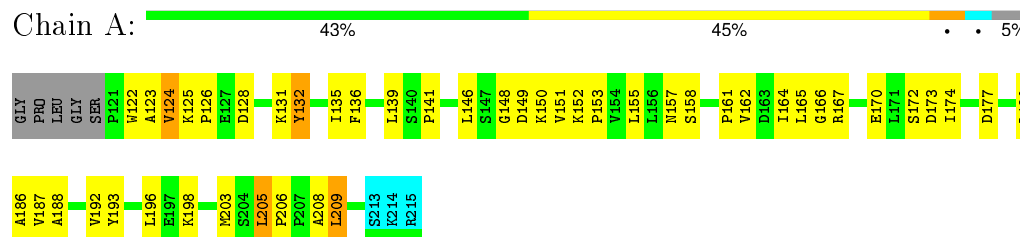


- Molecule 2: Stonin-2

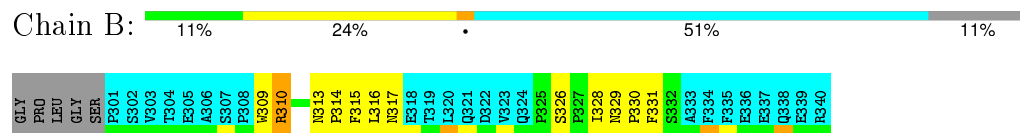


4.2.8 Score per residue for model 8

- Molecule 1: Epidermal growth factor receptor substrate 15

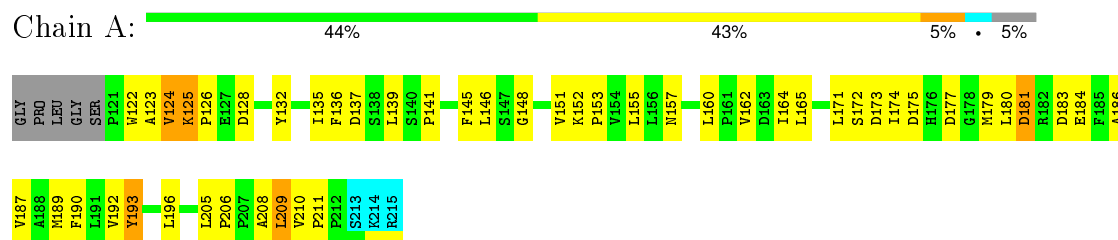


- Molecule 2: Stonin-2

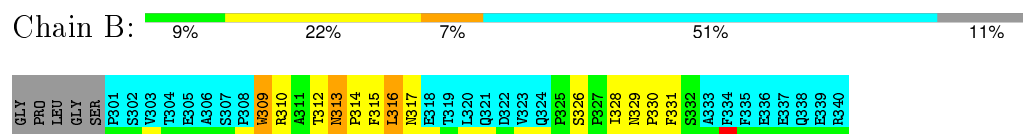


4.2.9 Score per residue for model 9

- Molecule 1: Epidermal growth factor receptor substrate 15

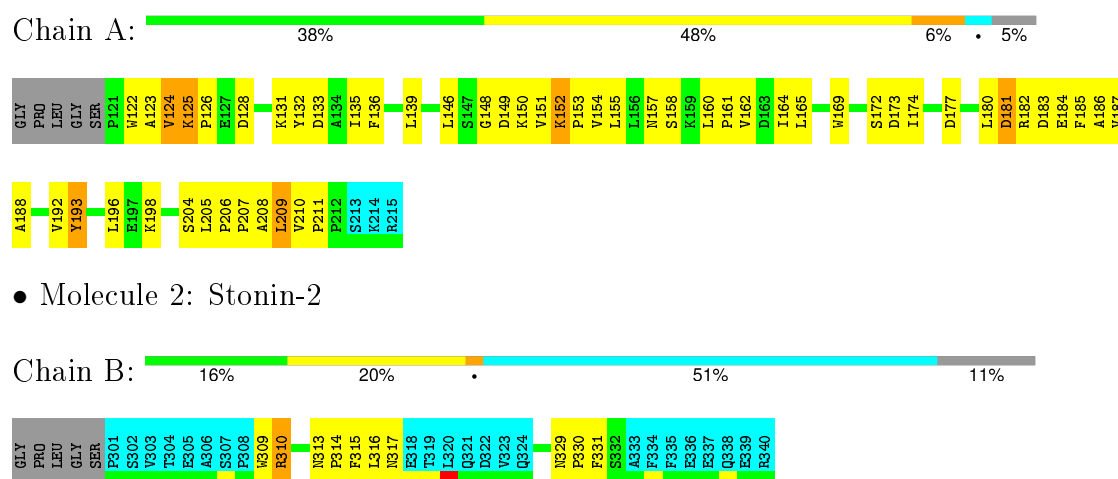


- Molecule 2: Stonin-2



4.2.10 Score per residue for model 10

- Molecule 1: Epidermal growth factor receptor substrate 15



- Molecule 2: Stonin-2

5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 10 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
CNS	refinement	1.1
ARIA	structure solution	1.2

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

Chemical shift file(s)	BMRB entry 15554
Number of chemical shift lists	1
Total number of shifts	1609
Number of shifts mapped to atoms	1609
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	86%

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

6 Model quality (i)

6.1 Standard geometry (i)

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

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.55±0.13	2±1/738 (0.2±0.2%)	0.57±0.03	0±0/1009 (0.0±0.0%)
2	B	0.47±0.08	0±0/147 (0.0±0.0%)	0.56±0.03	0±0/204 (0.0±0.0%)
All	All	0.55	16/8850 (0.2%)	0.57	0/12130 (0.0%)

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

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	0.2±0.4
All	All	0	2

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	132	TYR	CE2-CZ	10.36	1.52	1.38	8	4
1	A	132	TYR	CE1-CZ	-9.98	1.25	1.38	8	4
1	A	193	TYR	CE1-CZ	-6.63	1.29	1.38	9	4
1	A	193	TYR	CE2-CZ	6.59	1.47	1.38	9	4

There are no bond-angle outliers.

There are no chirality outliers.

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

Mol	Chain	Res	Type	Group	Models (Total)
1	A	132	TYR	Sidechain	1

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Mol	Chain	Res	Type	Group	Models (Total)
1	A	193	TYR	Sidechain	1

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	716	722	721	44±4
2	B	139	131	131	14±5
3	A	1	0	0	2±0
All	All	8560	8530	8520	478

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 28.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:160:LEU:HB3	1:A:164:ILE:HD11	1.04	1.28	2	9
1:A:155:LEU:HB3	1:A:165:LEU:HD22	0.92	1.39	5	10
1:A:124:VAL:HG11	1:A:186:ALA:HB1	0.91	1.41	1	10
1:A:206:PRO:HD2	1:A:209:LEU:HD11	0.88	1.43	8	1
1:A:157:ASN:HB2	2:B:330:PRO:HD2	0.79	1.53	9	2
1:A:151:VAL:HG13	1:A:155:LEU:HD23	0.78	1.55	7	4
1:A:122:TRP:HA	1:A:208:ALA:O	0.77	1.79	6	10
2:B:309:TRP:HB2	2:B:316:LEU:HB3	0.76	1.55	4	8
1:A:135:ILE:HD11	1:A:189:MET:SD	0.75	2.21	9	1
1:A:158:SER:HB2	1:A:196:LEU:HD21	0.75	1.56	2	3
1:A:157:ASN:HB3	2:B:330:PRO:HD2	0.73	1.59	7	6
1:A:193:TYR:OH	2:B:330:PRO:HB2	0.72	1.84	8	4
1:A:152:LYS:HB3	1:A:153:PRO:HD3	0.71	1.63	8	6
1:A:207:PRO:HA	1:A:210:VAL:HG12	0.70	1.64	10	6
1:A:196:LEU:HG	2:B:331:PHE:HD2	0.70	1.46	5	4
1:A:207:PRO:HA	1:A:210:VAL:HG23	0.70	1.63	3	1
1:A:167:ARG:NH2	1:A:203:MET:HA	0.69	2.02	8	1
1:A:174:ILE:HD12	1:A:184:GLU:HG2	0.69	1.63	2	1
1:A:151:VAL:HG11	1:A:169:TRP:CZ3	0.69	2.22	4	3
1:A:160:LEU:CB	1:A:164:ILE:HD11	0.69	2.13	2	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:181:ASP:HB3	1:A:184:GLU:HG3	0.68	1.64	1	7
2:B:326:SER:HB2	2:B:328:ILE:HD12	0.68	1.64	6	2
1:A:196:LEU:HG	2:B:331:PHE:CD2	0.67	2.24	5	4
1:A:148:GLY:HA2	1:A:151:VAL:HG12	0.67	1.64	4	1
1:A:157:ASN:HD21	1:A:192:VAL:HG11	0.67	1.49	5	1
1:A:139:LEU:HD12	1:A:146:LEU:HD13	0.67	1.67	1	9
1:A:123:ALA:HB2	1:A:209:LEU:HD22	0.66	1.65	6	6
1:A:173:ASP:OD1	3:A:1000:CA:CA	0.65	1.74	1	10
1:A:153:PRO:HB2	2:B:326:SER:OG	0.65	1.92	9	3
1:A:154:VAL:HA	1:A:157:ASN:ND2	0.65	2.05	3	1
2:B:330:PRO:HG2	2:B:331:PHE:CE1	0.65	2.26	8	3
1:A:160:LEU:HD12	1:A:192:VAL:HG13	0.65	1.67	9	3
1:A:160:LEU:HB3	1:A:164:ILE:CD1	0.65	2.17	2	8
1:A:205:LEU:HD11	1:A:210:VAL:HB	0.65	1.69	1	4
1:A:181:ASP:OD2	1:A:184:GLU:HG3	0.63	1.94	10	2
1:A:170:GLU:OE2	2:B:310:ARG:HD3	0.63	1.93	2	1
1:A:170:GLU:HA	2:B:310:ARG:NH1	0.63	2.07	8	1
1:A:177:ASP:OD1	3:A:1000:CA:CA	0.63	1.75	9	5
1:A:123:ALA:HB3	1:A:209:LEU:HB3	0.63	1.70	8	1
1:A:128:ASP:HA	1:A:131:LYS:HE2	0.63	1.70	8	5
1:A:157:ASN:HD22	1:A:158:SER:N	0.63	1.92	5	1
1:A:207:PRO:HA	1:A:210:VAL:CG2	0.61	2.25	3	1
1:A:170:GLU:HG3	2:B:309:TRP:CD1	0.61	2.30	5	1
1:A:139:LEU:HD22	1:A:146:LEU:HD13	0.61	1.72	4	1
1:A:174:ILE:HD11	1:A:211:PRO:HG2	0.60	1.72	7	1
1:A:170:GLU:HA	2:B:310:ARG:HH11	0.60	1.55	8	1
2:B:310:ARG:HD2	2:B:310:ARG:H	0.60	1.56	3	1
1:A:157:ASN:HA	2:B:329:ASN:HB3	0.60	1.72	5	4
1:A:206:PRO:HG2	1:A:209:LEU:HD11	0.59	1.73	10	8
1:A:166:GLY:HA2	2:B:313:ASN:HD21	0.59	1.56	8	7
1:A:161:PRO:HB2	1:A:163:ASP:OD1	0.59	1.97	3	1
1:A:148:GLY:HA3	2:B:314:PRO:HG3	0.59	1.75	6	5
1:A:184:GLU:O	1:A:187:VAL:HB	0.59	1.97	4	10
1:A:174:ILE:HG12	1:A:211:PRO:HD2	0.58	1.74	6	2
1:A:158:SER:OG	1:A:160:LEU:HG	0.58	1.99	4	2
1:A:170:GLU:HG3	2:B:309:TRP:HD1	0.58	1.57	5	1
1:A:181:ASP:OD1	1:A:184:GLU:HG3	0.58	1.99	9	1
1:A:192:VAL:O	1:A:196:LEU:HD12	0.57	2.00	9	2
1:A:157:ASN:HA	2:B:329:ASN:CB	0.57	2.30	8	4
1:A:157:ASN:HA	2:B:329:ASN:ND2	0.57	2.14	10	1
1:A:135:ILE:O	1:A:139:LEU:HG	0.57	2.00	8	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:161:PRO:O	1:A:164:ILE:HG13	0.56	1.99	7	7
1:A:157:ASN:O	2:B:331:PHE:HB2	0.56	2.00	5	4
2:B:331:PHE:CD1	2:B:331:PHE:N	0.56	2.73	5	1
1:A:151:VAL:HG11	1:A:180:LEU:HD22	0.56	1.76	10	2
1:A:157:ASN:HB3	2:B:331:PHE:CD1	0.56	2.36	8	1
1:A:164:ILE:HD12	1:A:165:LEU:N	0.56	2.16	2	3
1:A:196:LEU:HD13	2:B:331:PHE:CD1	0.55	2.36	9	3
1:A:139:LEU:HD21	2:B:328:ILE:HG21	0.55	1.76	3	3
1:A:132:TYR:O	1:A:136:PHE:HB2	0.55	2.02	5	10
1:A:180:LEU:HD23	1:A:184:GLU:HB3	0.55	1.79	9	6
1:A:196:LEU:HD13	2:B:331:PHE:CE1	0.55	2.37	9	1
2:B:313:ASN:HB3	2:B:316:LEU:HD23	0.54	1.77	8	4
1:A:152:LYS:HG3	2:B:315:PHE:CE2	0.54	2.37	6	2
1:A:172:SER:O	1:A:174:ILE:HD12	0.53	2.03	10	6
1:A:126:PRO:HA	1:A:129:LYS:HB3	0.53	1.80	4	2
1:A:167:ARG:HH22	1:A:203:MET:HA	0.53	1.61	8	1
1:A:151:VAL:HG11	1:A:180:LEU:HD12	0.53	1.81	8	2
1:A:206:PRO:HD2	1:A:209:LEU:CD1	0.53	2.24	8	1
1:A:139:LEU:HD11	1:A:154:VAL:HG21	0.53	1.79	4	5
1:A:157:ASN:CB	2:B:330:PRO:HD2	0.53	2.33	10	4
1:A:188:ALA:O	1:A:192:VAL:HG23	0.53	2.04	10	9
1:A:152:LYS:HG2	2:B:315:PHE:CE2	0.53	2.39	8	1
1:A:161:PRO:HD2	1:A:164:ILE:HG12	0.53	1.81	1	2
1:A:145:PHE:CE2	1:A:181:ASP:HB3	0.52	2.39	6	1
2:B:309:TRP:CZ3	2:B:316:LEU:HA	0.52	2.38	9	1
1:A:145:PHE:CE2	1:A:181:ASP:HB2	0.52	2.40	4	2
1:A:157:ASN:HA	2:B:329:ASN:HB2	0.52	1.82	8	2
1:A:169:TRP:CH2	1:A:180:LEU:HD13	0.52	2.40	1	2
1:A:154:VAL:O	1:A:157:ASN:HB2	0.51	2.05	10	3
2:B:330:PRO:HG2	2:B:331:PHE:CD1	0.51	2.40	2	2
1:A:152:LYS:HG2	2:B:315:PHE:CE1	0.51	2.41	2	1
1:A:157:ASN:CG	2:B:329:ASN:HA	0.51	2.26	2	3
1:A:157:ASN:HB3	2:B:330:PRO:CD	0.51	2.35	1	1
2:B:316:LEU:HD12	2:B:317:ASN:N	0.50	2.22	10	1
1:A:123:ALA:HB2	1:A:209:LEU:CD2	0.50	2.37	3	3
1:A:148:GLY:HA2	1:A:151:VAL:CG1	0.50	2.34	4	1
1:A:151:VAL:HG13	1:A:155:LEU:CD2	0.49	2.33	7	4
1:A:163:ASP:O	1:A:167:ARG:HG3	0.49	2.07	5	1
1:A:196:LEU:HD11	2:B:331:PHE:CE2	0.49	2.42	4	1
1:A:154:VAL:HG13	1:A:157:ASN:ND2	0.49	2.23	1	1
1:A:150:LYS:O	1:A:153:PRO:HD2	0.49	2.08	1	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:122:TRP:CZ3	1:A:124:VAL:HB	0.49	2.43	1	2
1:A:123:ALA:O	1:A:125:LYS:HD3	0.48	2.07	3	2
1:A:160:LEU:CD1	1:A:192:VAL:HG13	0.48	2.39	9	1
1:A:193:TYR:CZ	2:B:331:PHE:HE1	0.48	2.27	6	1
1:A:155:LEU:HD12	2:B:315:PHE:CZ	0.47	2.45	10	2
1:A:177:ASP:OD2	1:A:179:MET:HB2	0.47	2.10	3	5
1:A:205:LEU:HD21	1:A:210:VAL:HB	0.47	1.85	2	1
1:A:183:ASP:O	1:A:187:VAL:HG23	0.47	2.10	10	8
1:A:206:PRO:O	1:A:209:LEU:HG	0.47	2.10	9	4
1:A:194:CYS:SG	1:A:199:GLU:HB2	0.46	2.50	3	2
1:A:157:ASN:HA	2:B:329:ASN:HD22	0.46	1.69	10	1
1:A:152:LYS:HA	2:B:315:PHE:CZ	0.46	2.45	10	7
1:A:173:ASP:OD2	1:A:176:HIS:HA	0.46	2.10	5	3
1:A:171:LEU:HB3	1:A:205:LEU:HD23	0.46	1.87	9	1
1:A:193:TYR:O	1:A:197:GLU:HG3	0.46	2.11	3	1
1:A:174:ILE:HD12	1:A:174:ILE:H	0.46	1.70	10	2
1:A:133:ASP:OD2	1:A:182:ARG:HD2	0.46	2.10	10	1
1:A:154:VAL:HG13	1:A:157:ASN:OD1	0.45	2.11	2	1
1:A:157:ASN:C	2:B:331:PHE:HD2	0.45	2.15	3	2
1:A:148:GLY:CA	2:B:314:PRO:HG3	0.45	2.41	9	4
2:B:310:ARG:HD2	2:B:310:ARG:N	0.45	2.27	7	3
1:A:193:TYR:CE1	2:B:331:PHE:HE1	0.45	2.30	6	1
1:A:152:LYS:O	1:A:155:LEU:HB2	0.45	2.12	1	1
1:A:178:GLY:HA2	2:B:312:THR:HB	0.45	1.89	7	1
2:B:313:ASN:HD21	2:B:315:PHE:HD1	0.44	1.54	3	1
1:A:141:PRO:HA	1:A:146:LEU:HD23	0.44	1.89	9	2
1:A:156:LEU:HD12	1:A:165:LEU:HD13	0.44	1.88	1	1
1:A:145:PHE:CD2	1:A:181:ASP:HB3	0.44	2.47	6	1
1:A:193:TYR:HH	2:B:330:PRO:HB2	0.44	1.70	8	1
1:A:145:PHE:HA	1:A:181:ASP:HA	0.44	1.89	9	2
1:A:125:LYS:NZ	1:A:125:LYS:HB2	0.44	2.28	6	1
1:A:198:LYS:N	1:A:198:LYS:HD2	0.44	2.28	1	1
2:B:313:ASN:HD21	2:B:315:PHE:HD2	0.44	1.54	10	1
1:A:175:ASP:HB2	1:A:177:ASP:OD1	0.44	2.13	9	1
1:A:151:VAL:HG22	1:A:185:PHE:CE1	0.43	2.48	10	1
1:A:125:LYS:O	1:A:128:ASP:N	0.43	2.51	10	3
1:A:209:LEU:O	1:A:211:PRO:HD3	0.43	2.14	7	1
1:A:155:LEU:C	1:A:157:ASN:H	0.43	2.15	8	1
1:A:157:ASN:HB3	2:B:331:PHE:HD1	0.43	1.73	8	1
1:A:192:VAL:HG12	2:B:331:PHE:CE2	0.43	2.48	5	1
1:A:122:TRP:CH2	1:A:129:LYS:HD3	0.43	2.48	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:170:GLU:HG3	1:A:171:LEU:N	0.43	2.27	4	1
1:A:151:VAL:O	1:A:155:LEU:HD23	0.43	2.14	1	1
1:A:207:PRO:O	1:A:210:VAL:HG12	0.43	2.14	4	1
1:A:157:ASN:CA	2:B:329:ASN:HB2	0.43	2.42	8	1
1:A:191:LEU:O	1:A:194:CYS:HB3	0.43	2.14	4	1
1:A:132:TYR:CG	1:A:189:MET:SD	0.42	3.12	9	1
1:A:132:TYR:HA	1:A:135:ILE:HG12	0.42	1.90	4	1
2:B:329:ASN:OD1	2:B:332:SER:HB3	0.42	2.14	7	1
2:B:313:ASN:ND2	2:B:315:PHE:HD1	0.42	2.11	3	1
2:B:310:ARG:N	2:B:310:ARG:HD2	0.42	2.30	10	2
1:A:169:TRP:CE2	2:B:314:PRO:HD3	0.42	2.50	10	1
1:A:181:ASP:CG	1:A:184:GLU:HG3	0.42	2.35	6	1
1:A:199:GLU:OE2	1:A:200:PRO:HD2	0.42	2.14	2	1
1:A:122:TRP:O	1:A:125:LYS:HE3	0.42	2.15	9	1
1:A:159:LYS:O	1:A:159:LYS:HG2	0.42	2.14	3	1
1:A:123:ALA:HB1	1:A:190:PHE:CE1	0.42	2.50	9	1
1:A:196:LEU:O	1:A:198:LYS:HD2	0.42	2.15	1	1
1:A:175:ASP:OD2	1:A:177:ASP:HB3	0.42	2.15	7	1
1:A:148:GLY:O	1:A:152:LYS:HB3	0.41	2.15	3	1
1:A:207:PRO:HA	1:A:210:VAL:CG1	0.41	2.42	10	1
1:A:125:LYS:HA	1:A:126:PRO:HD2	0.41	1.69	1	1
1:A:125:LYS:N	1:A:125:LYS:HD3	0.41	2.30	6	1
2:B:330:PRO:HG2	2:B:331:PHE:CE2	0.41	2.50	9	1
2:B:313:ASN:ND2	2:B:314:PRO:HD2	0.41	2.29	10	1
1:A:160:LEU:HD13	1:A:164:ILE:HD13	0.41	1.91	2	1
1:A:139:LEU:HD12	1:A:146:LEU:CD1	0.41	2.44	6	1
2:B:313:ASN:HB3	2:B:316:LEU:CD2	0.41	2.45	4	1
2:B:329:ASN:HA	2:B:330:PRO:HD2	0.41	1.78	5	1
1:A:132:TYR:CD2	1:A:186:ALA:HA	0.41	2.51	4	1
2:B:313:ASN:ND2	2:B:315:PHE:HD2	0.41	2.14	10	1
1:A:151:VAL:HG11	1:A:169:TRP:CE3	0.41	2.50	4	1
1:A:205:LEU:HA	1:A:206:PRO:HD3	0.40	1.81	8	1
1:A:165:LEU:HB3	2:B:315:PHE:CE2	0.40	2.51	8	1
1:A:142:VAL:HB	1:A:179:MET:HE1	0.40	1.92	5	1
2:B:313:ASN:O	2:B:316:LEU:HD23	0.40	2.15	9	1
2:B:309:TRP:CE3	2:B:316:LEU:HA	0.40	2.51	3	1
1:A:207:PRO:CA	1:A:210:VAL:HG12	0.40	2.43	10	1
1:A:205:LEU:HD12	1:A:210:VAL:HB	0.40	1.94	9	1
1:A:151:VAL:HG13	1:A:155:LEU:HD12	0.40	1.91	4	1
1:A:135:ILE:O	1:A:139:LEU:HD13	0.40	2.17	4	1
2:B:326:SER:HB3	2:B:328:ILE:HG13	0.40	1.93	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:157:ASN:CG	2:B:330:PRO:HD2	0.40	2.37	10	1
1:A:148:GLY:HA3	2:B:314:PRO:CG	0.40	2.47	4	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	91/100 (91%)	86±1 (94±1%)	4±1 (5±2%)	1±1 (1±1%)	24	71
2	B	17/45 (38%)	11±1 (65±8%)	6±1 (33±8%)	0±1 (2±4%)	15	58
All	All	1080/1450 (74%)	969 (90%)	99 (9%)	12 (1%)	23	69

All 4 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	126	PRO	8
2	B	328	ILE	2
2	B	325	PRO	1
1	A	123	ALA	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	81/87 (93%)	75±2 (93±2%)	6±2 (7±2%)	23	69
2	B	16/40 (40%)	14±1 (89±9%)	2±1 (11±9%)	12	55
All	All	970/1270 (76%)	895 (92%)	75 (8%)	21	66

All 29 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	209	LEU	10
1	A	125	LYS	7
2	B	310	ARG	6
1	A	149	ASP	5
1	A	152	LYS	5
1	A	124	VAL	4
2	B	309	TRP	4
1	A	198	LYS	4
1	A	157	ASN	3
1	A	129	LYS	3
1	A	181	ASP	2
1	A	170	GLU	2
1	A	205	LEU	2
2	B	313	ASN	2
1	A	151	VAL	2
1	A	163	ASP	1
2	B	332	SER	1
2	B	329	ASN	1
1	A	156	LEU	1
1	A	206	PRO	1
2	B	317	ASN	1
1	A	159	LYS	1
2	B	312	THR	1
2	B	326	SER	1
1	A	121	PRO	1
1	A	204	SER	1
1	A	176	HIS	1
2	B	316	LEU	1
1	A	137	ASP	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](#)

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 86% for the well-defined parts and 85% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 15554

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	1609
Number of shifts mapped to atoms	1609
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	2

7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	142	-0.07 ± 0.20	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	133	0.57 ± 0.14	Should be applied
$^{13}\text{C}'$	0	—	—
^{15}N	121	0.45 ± 0.23	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 86%, i.e. 1150 atoms were assigned a chemical shift out of a possible 1339. 1 out of 23 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	401/515 (78%)	201/203 (99%)	108/218 (50%)	92/94 (98%)
Sidechain	641/710 (90%)	399/421 (95%)	238/268 (89%)	4/21 (19%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	108/114 (95%)	57/60 (95%)	48/49 (98%)	3/5 (60%)
Overall	1150/1339 (86%)	657/684 (96%)	394/535 (74%)	99/120 (82%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 85%, i.e. 1412 atoms were assigned a chemical shift out of a possible 1667. 1 out of 26 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	499/641 (78%)	250/253 (99%)	134/270 (50%)	115/118 (97%)
Sidechain	787/894 (88%)	494/530 (93%)	287/333 (86%)	6/31 (19%)
Aromatic	126/132 (95%)	67/70 (96%)	56/57 (98%)	3/5 (60%)
Overall	1412/1667 (85%)	811/853 (95%)	477/660 (72%)	124/154 (81%)

7.1.4 Statistically unusual chemical shifts [i](#)

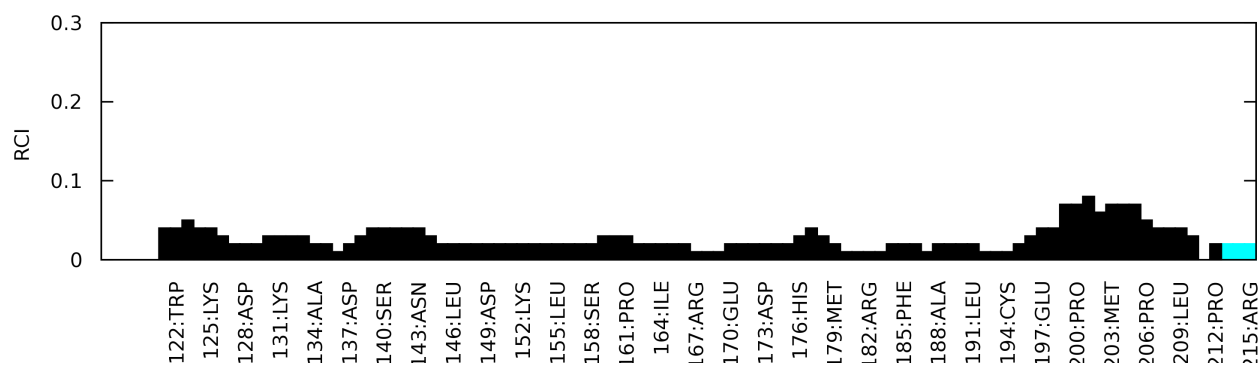
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	124	VAL	HB	-0.53	3.59 – 0.39	-7.9
2	B	314	PRO	HD3	1.71	5.52 – 1.72	-5.0

7.1.5 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:

