



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 07:15 PM BST

PDB ID : 2BBN  
Title : SOLUTION STRUCTURE OF A CALMODULIN-TARGET PEPTIDE  
COMPLEX BY MULTIDIMENSIONAL NMR  
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Deposited on : 1992-07-16

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

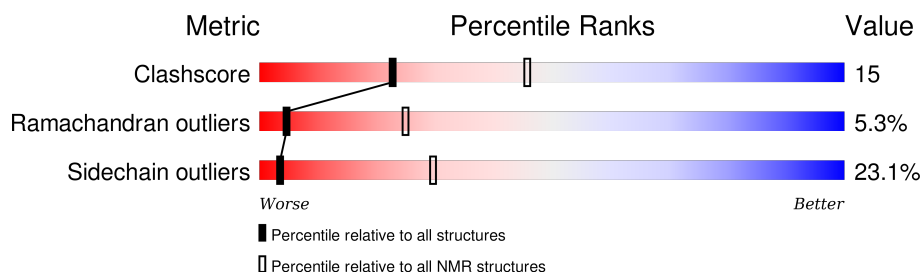
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment was not calculated.

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  $\geq 3$ , 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	148	
2	B	26	

## 2 Ensemble composition and analysis

This entry contains 21 models. Model 17 is the overall representative, medoid model (most similar to other models).

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:5-A:74, A:81-A:145, B:3-B:21 (154)	0.67	17

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	1, 2, 3, 5, 7, 9, 10, 11, 15, 17, 20
2	8, 12, 13, 18
3	4, 19, 21
Single-model clusters	6; 14; 16

### 3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 2704 atoms, of which 1326 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called CALMODULIN.

Mol	Chain	Residues	Atoms						Trace
1	A	148	Total	C	H	N	O	S	0
			2259	713	1095	187	255	9	

- Molecule 2 is a protein called MYOSIN LIGHT CHAIN KINASE.

Mol	Chain	Residues	Atoms					Trace
2	B	26	Total	C	H	N	O	0
			441	134	231	43	33	

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

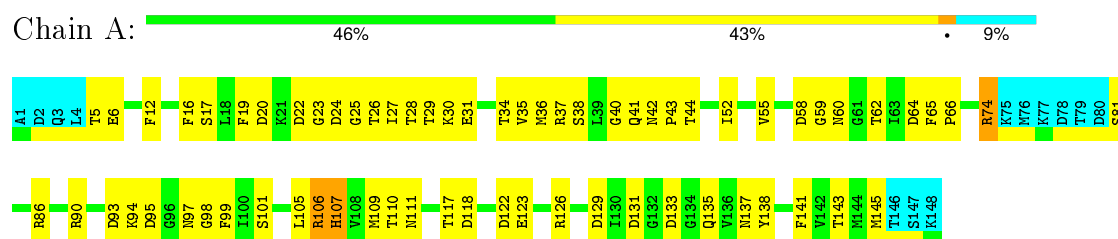
Mol	Chain	Residues	Atoms	
3	A	4	Total	Ca
			4	4

## 4 Residue-property plots [i](#)

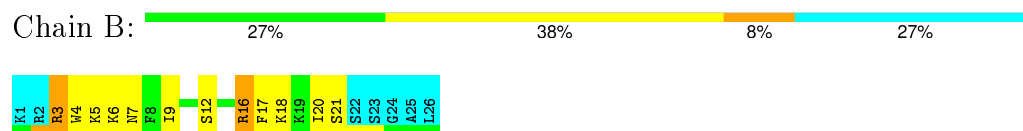
### 4.1 Average score per residue in the NMR ensemble

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: CALMODULIN



#### • Molecule 2: MYOSIN LIGHT CHAIN KINASE

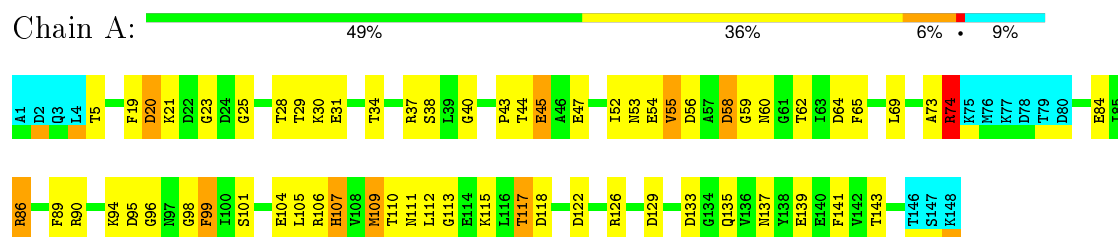


### 4.2 Scores per residue for each member of the ensemble

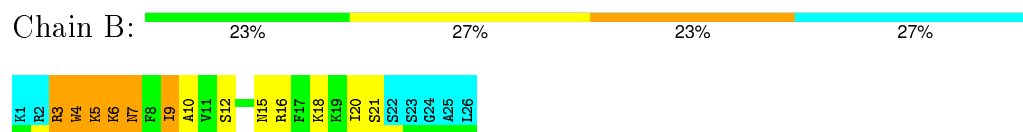
Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

#### • Molecule 1: CALMODULIN

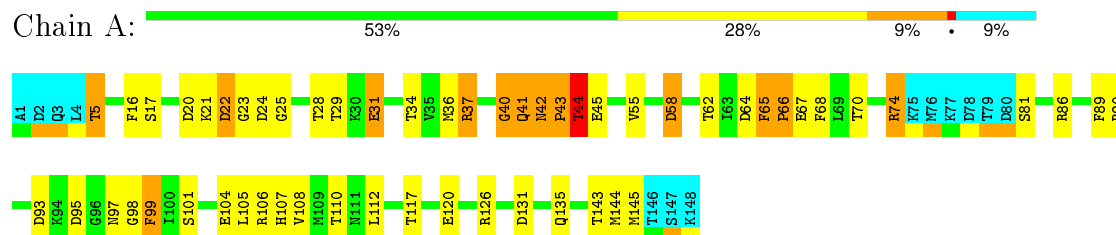


#### • Molecule 2: MYOSIN LIGHT CHAIN KINASE

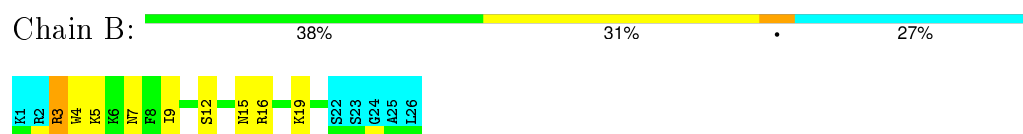


#### 4.2.2 Score per residue for model 2

- Molecule 1: CALMODULIN

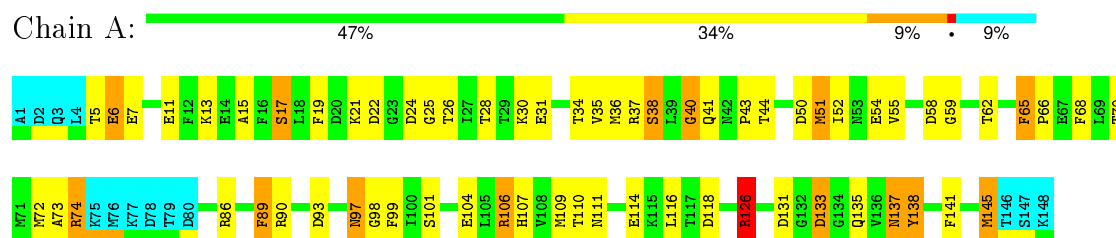


- Molecule 2: MYOSIN LIGHT CHAIN KINASE

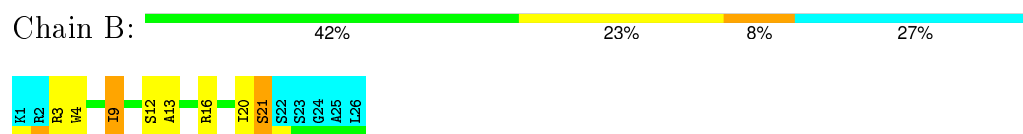


#### 4.2.3 Score per residue for model 3

- Molecule 1: CALMODULIN



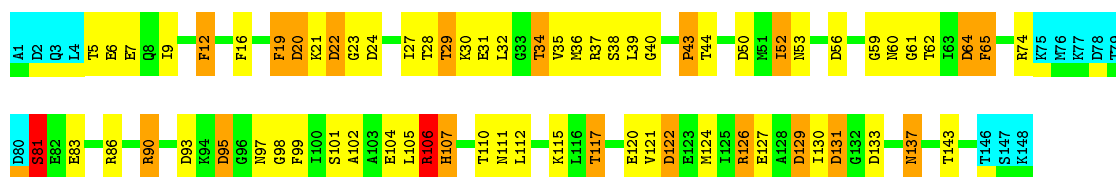
- Molecule 2: MYOSIN LIGHT CHAIN KINASE



#### 4.2.4 Score per residue for model 4

- Molecule 1: CALMODULIN





- Molecule 2: MYOSIN LIGHT CHAIN KINASE

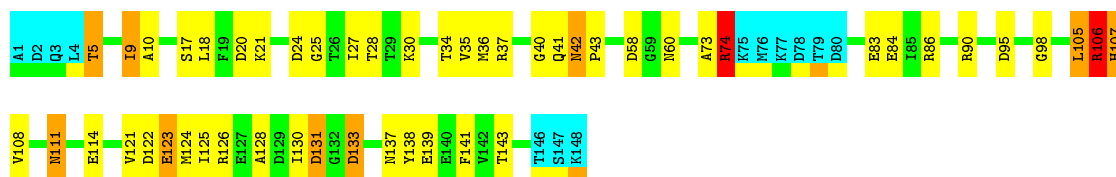
Chain B: 35% 27% 8% • 27%



#### 4.2.5 Score per residue for model 5

- Molecule 1: CALMODULIN

Chain A: 57% 27% 6% • 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

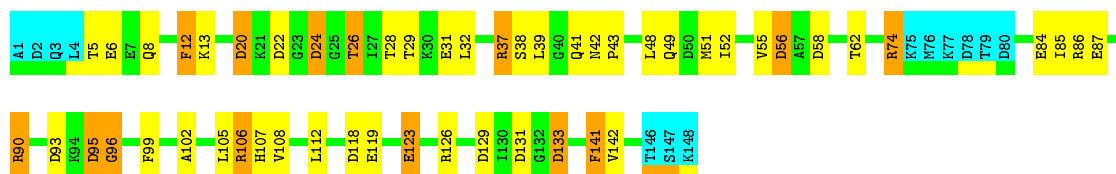
Chain B: 31% 31% 12% 27%



#### 4.2.6 Score per residue for model 6

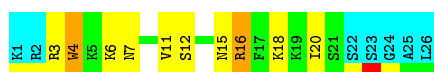
- Molecule 1: CALMODULIN

Chain A: 56% 26% 9% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

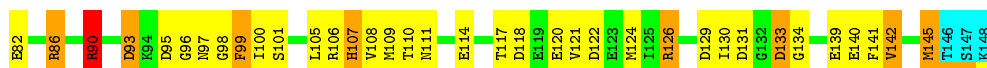
Chain B: 35% 31% 8% 27%



#### 4.2.7 Score per residue for model 7

- Molecule 1: CALMODULIN

Chain A: 44% 37% 9% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

Chain B: 27% 31% 15% 27%



#### 4.2.8 Score per residue for model 8

- Molecule 1: CALMODULIN

Chain A: 53% 32% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

Chain B: 35% 27% 12% 27%

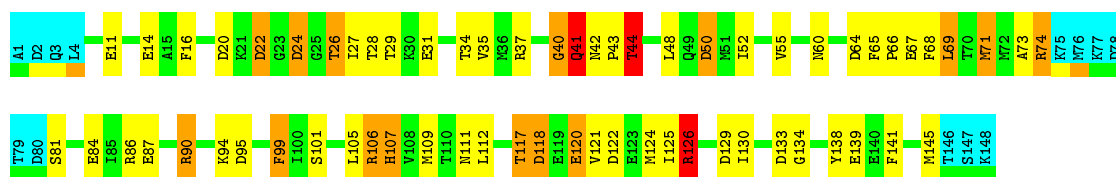


#### 4.2.9 Score per residue for model 9

- Molecule 1: CALMODULIN

Chain A: 48% 31% 10% 9%



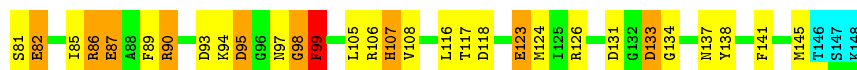
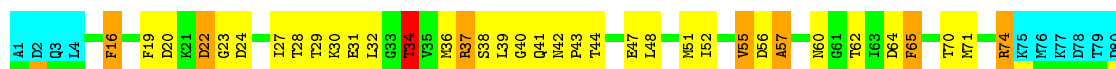


- Molecule 2: MYOSIN LIGHT CHAIN KINASE



#### 4.2.10 Score per residue for model 10

- Molecule 1: CALMODULIN

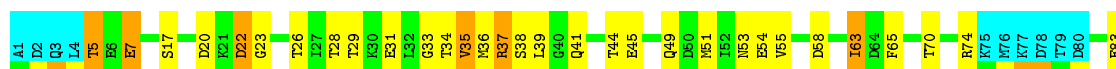


- Molecule 2: MYOSIN LIGHT CHAIN KINASE



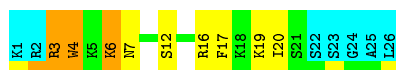
#### 4.2.11 Score per residue for model 11

- Molecule 1: CALMODULIN



- Molecule 2: MYOSIN LIGHT CHAIN KINASE





#### 4.2.12 Score per residue for model 12

- Molecule 1: CALMODULIN

Chain A: 49% 34% 7% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

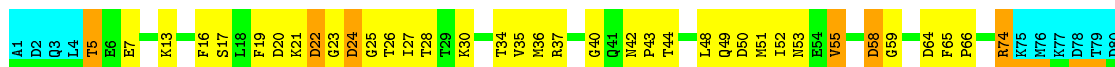
Chain B: 35% 27% 12% 27%



#### 4.2.13 Score per residue for model 13

- Molecule 1: CALMODULIN

Chain A: 47% 38% 7% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

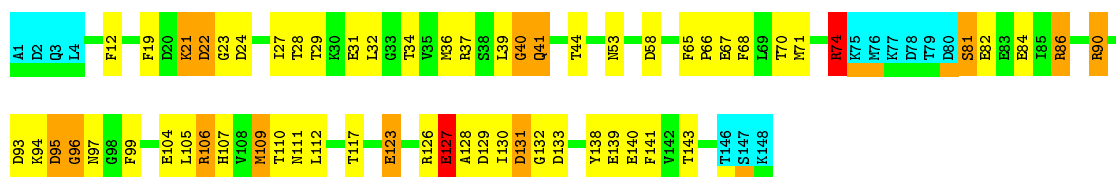
Chain B: 31% 31% 12% 27%



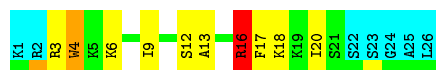
#### 4.2.14 Score per residue for model 14

- Molecule 1: CALMODULIN

Chain A: 50% 31% 9% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

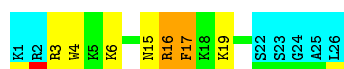


#### 4.2.15 Score per residue for model 15

- Molecule 1: CALMODULIN

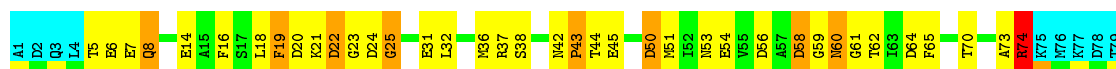


- Molecule 2: MYOSIN LIGHT CHAIN KINASE



#### 4.2.16 Score per residue for model 16

- Molecule 1: CALMODULIN



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

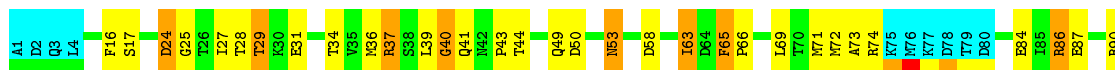




#### 4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: CALMODULIN

Chain A: 56% 25% 10% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

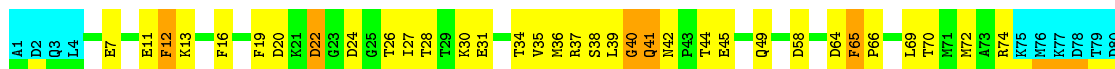
Chain B: 31% 27% 12% 27%



#### 4.2.18 Score per residue for model 18

- Molecule 1: CALMODULIN

Chain A: 51% 31% 8% 9%



- Molecule 2: MYOSIN LIGHT CHAIN KINASE

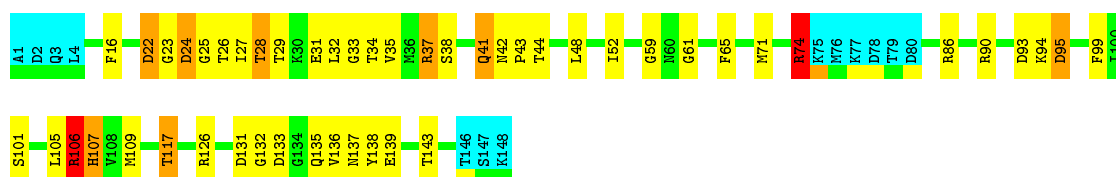
Chain B: 38% 23% 8% 27%



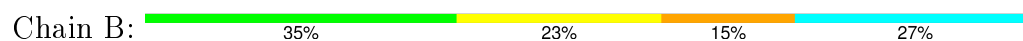
#### 4.2.19 Score per residue for model 19

- Molecule 1: CALMODULIN

Chain A: 58% 26% 5% 9%

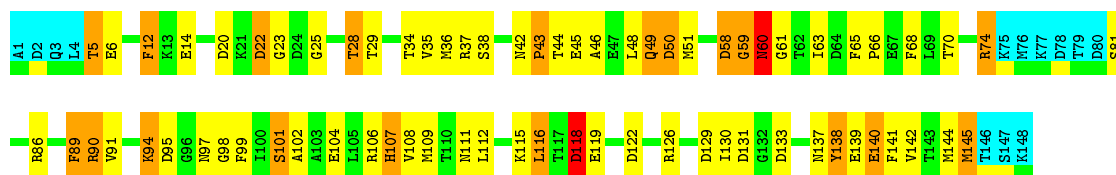


- Molecule 2: MYOSIN LIGHT CHAIN KINASE



#### 4.2.20 Score per residue for model 20

- Molecule 1: CALMODULIN

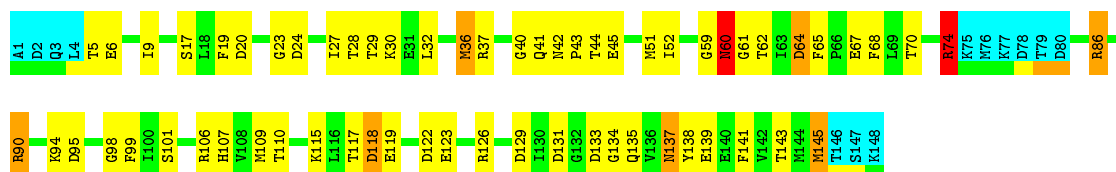


- Molecule 2: MYOSIN LIGHT CHAIN KINASE



#### 4.2.21 Score per residue for model 21

- Molecule 1: CALMODULIN



- Molecule 2: MYOSIN LIGHT CHAIN KINASE





## 5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: ?.

Of the ? calculated structures, 21 were deposited, based on the following criterion: ?.

The authors did not provide any information on software used for structure solution, optimization or refinement.

No chemical shift data was provided. 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	1.14±0.00	1±0/1075 (0.1±0.0%)	1.10±0.00	0±0/1446 (0.0±0.0%)
2	B	1.09±0.01	1±0/164 (0.6±0.0%)	1.42±0.02	5±0/218 (2.2±0.2%)
All	All	1.13	42/26019 (0.2%)	1.15	101/34944 (0.3%)

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	5.7±0.5
2	B	0.0±0.0	1.9±0.3
All	All	0	159

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
2	B	4	TRP	CG-CD2	-6.39	1.32	1.43	4	21
1	A	107	HIS	CG-ND1	-5.93	1.25	1.38	4	21

All unique angle 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(°)	Ideal(°)	Models	
								Worst	Total
2	B	4	TRP	NE1-CE2-CZ2	8.13	139.34	130.40	4	21
2	B	4	TRP	NE1-CE2-CD2	-6.95	100.35	107.30	4	21
2	B	4	TRP	CD1-NE1-CE2	6.36	114.72	109.00	18	21
2	B	4	TRP	CG-CD1-NE1	-6.33	103.77	110.10	11	21

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
2	B	4	TRP	CD1-CG-CD2	5.62	110.80	106.30	9	17

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)
2	B	3	ARG	Sidechain	21
1	A	37	ARG	Sidechain	21
1	A	126	ARG	Sidechain	20
1	A	90	ARG	Sidechain	20
1	A	86	ARG	Sidechain	20
1	A	106	ARG	Sidechain	19
2	B	16	ARG	Sidechain	19
1	A	74	ARG	Sidechain	19

## 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	1062	990	990	32±7
2	B	160	174	174	5±3
3	A	4	0	0	0±0
All	All	25746	24444	24441	741

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 15.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:85:ILE:HD12	1:A:85:ILE:H	0.75	1.39	6	1
1:A:27:ILE:HG21	2:B:17:PHE:CE2	0.73	2.17	9	8
1:A:28:THR:HG22	1:A:29:THR:H	0.71	1.45	8	6
1:A:85:ILE:HD12	1:A:85:ILE:N	0.68	2.03	6	1
1:A:117:THR:HG23	1:A:118:ASP:N	0.67	2.05	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:LEU:O	1:A:73:ALA:HB3	0.67	1.90	17	1
1:A:105:LEU:HD22	2:B:4:TRP:CH2	0.67	2.25	14	1
1:A:5:THR:HG23	1:A:6:GLU:H	0.66	1.50	20	2
1:A:22:ASP:OD2	3:A:181:CA:CA	0.65	1.73	19	1
1:A:28:THR:HG22	1:A:29:THR:N	0.65	2.07	8	8
1:A:65:PHE:N	1:A:65:PHE:CD1	0.65	2.65	17	1
1:A:5:THR:HG23	1:A:6:GLU:N	0.65	2.06	16	3
1:A:30:LYS:O	1:A:34:THR:HG23	0.64	1.92	13	5
1:A:65:PHE:CD1	1:A:65:PHE:N	0.64	2.66	18	1
1:A:99:PHE:CD1	1:A:99:PHE:N	0.63	2.66	1	3
1:A:99:PHE:N	1:A:99:PHE:CD1	0.63	2.67	9	2
1:A:117:THR:HG23	1:A:118:ASP:H	0.63	1.53	9	1
1:A:137:ASN:N	1:A:137:ASN:HD22	0.62	1.92	3	1
1:A:97:ASN:ND2	1:A:98:GLY:N	0.62	2.47	7	1
1:A:137:ASN:ND2	1:A:138:TYR:N	0.62	2.48	21	2
1:A:29:THR:HG23	1:A:52:ILE:HD12	0.61	1.71	4	1
1:A:42:ASN:ND2	2:B:18:LYS:NZ	0.61	2.48	16	1
1:A:97:ASN:ND2	1:A:99:PHE:N	0.61	2.48	7	1
1:A:99:PHE:CZ	1:A:137:ASN:ND2	0.61	2.69	17	1
1:A:124:MET:SD	2:B:4:TRP:CE2	0.60	2.95	9	1
1:A:48:LEU:N	1:A:48:LEU:HD12	0.60	2.12	10	2
1:A:65:PHE:N	1:A:66:PRO:CD	0.60	2.64	13	6
1:A:42:ASN:HD21	2:B:18:LYS:NZ	0.59	1.95	16	1
2:B:6:LYS:CB	2:B:6:LYS:NZ	0.59	2.65	4	1
1:A:91:VAL:HG23	1:A:92:PHE:N	0.59	2.12	8	1
1:A:85:ILE:CD1	1:A:85:ILE:H	0.59	2.11	6	1
1:A:7:GLU:O	1:A:10:ALA:HB3	0.59	1.98	12	1
1:A:145:MET:SD	1:A:145:MET:N	0.59	2.75	20	1
1:A:141:PHE:CD1	1:A:145:MET:SD	0.59	2.96	21	1
1:A:85:ILE:N	1:A:85:ILE:HD12	0.58	2.13	10	4
1:A:12:PHE:CD1	1:A:12:PHE:N	0.58	2.69	4	1
1:A:135:GLN:NE2	1:A:135:GLN:H	0.57	1.97	17	1
1:A:89:PHE:CD2	1:A:138:TYR:CZ	0.57	2.91	3	1
1:A:32:LEU:HD11	2:B:17:PHE:CG	0.56	2.34	12	1
2:B:15:ASN:OD1	2:B:16:ARG:N	0.56	2.38	16	1
1:A:145:MET:N	1:A:145:MET:SD	0.56	2.78	11	2
1:A:89:PHE:CD2	1:A:138:TYR:CE1	0.56	2.94	3	1
1:A:24:ASP:N	1:A:24:ASP:OD1	0.56	2.39	4	8
1:A:137:ASN:ND2	1:A:138:TYR:H	0.56	1.98	21	1
1:A:144:MET:SD	1:A:145:MET:SD	0.56	3.03	2	2
1:A:97:ASN:ND2	1:A:99:PHE:CD2	0.56	2.74	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:12:PHE:CG	1:A:13:LYS:N	0.55	2.75	6	2
1:A:106:ARG:O	1:A:110:THR:HG23	0.55	2.01	3	2
1:A:97:ASN:HD22	1:A:99:PHE:H	0.55	1.44	7	2
1:A:135:GLN:NE2	1:A:135:GLN:N	0.55	2.54	17	1
1:A:25:GLY:O	1:A:26:THR:HG23	0.55	2.02	12	3
1:A:141:PHE:CZ	1:A:145:MET:SD	0.55	2.99	3	1
1:A:69:LEU:O	1:A:73:ALA:N	0.54	2.40	9	2
1:A:141:PHE:CE1	1:A:145:MET:SD	0.54	3.00	21	2
1:A:16:PHE:CZ	1:A:64:ASP:O	0.54	2.61	13	1
1:A:12:PHE:CD1	1:A:68:PHE:CE2	0.54	2.95	20	1
1:A:36:MET:O	1:A:40:GLY:N	0.54	2.40	2	10
1:A:60:ASN:H	1:A:60:ASN:ND2	0.54	2.01	21	2
1:A:105:LEU:HD21	1:A:109:MET:SD	0.54	2.43	13	1
1:A:22:ASP:OD1	1:A:23:GLY:N	0.54	2.40	4	1
1:A:60:ASN:ND2	1:A:60:ASN:N	0.54	2.54	16	1
1:A:105:LEU:O	1:A:107:HIS:N	0.54	2.41	9	5
1:A:22:ASP:N	1:A:22:ASP:OD1	0.53	2.42	16	3
1:A:41:GLN:HE22	1:A:42:ASN:ND2	0.53	2.02	2	1
1:A:32:LEU:HD11	1:A:36:MET:SD	0.53	2.43	4	1
1:A:60:ASN:ND2	1:A:62:THR:H	0.53	2.01	10	1
2:B:13:ALA:O	2:B:17:PHE:CD2	0.53	2.61	14	2
1:A:16:PHE:CD2	1:A:25:GLY:O	0.53	2.61	17	2
1:A:98:GLY:O	1:A:99:PHE:CD2	0.53	2.62	10	2
1:A:58:ASP:OD1	1:A:58:ASP:N	0.53	2.42	6	1
1:A:141:PHE:CE2	1:A:145:MET:SD	0.53	3.02	12	1
1:A:123:GLU:OE1	1:A:123:GLU:N	0.52	2.42	6	2
1:A:59:GLY:O	1:A:61:GLY:N	0.52	2.42	20	5
1:A:137:ASN:ND2	1:A:139:GLU:H	0.52	2.02	11	1
1:A:28:THR:OG1	1:A:29:THR:N	0.52	2.42	20	3
1:A:63:ILE:HD11	2:B:17:PHE:CZ	0.52	2.40	15	1
1:A:16:PHE:O	1:A:20:ASP:N	0.52	2.43	16	2
1:A:56:ASP:OD1	1:A:59:GLY:N	0.52	2.42	4	1
1:A:107:HIS:O	1:A:111:ASN:ND2	0.52	2.43	7	2
1:A:117:THR:OG1	1:A:118:ASP:N	0.52	2.42	9	1
1:A:90:ARG:O	1:A:94:LYS:N	0.52	2.42	21	1
1:A:53:ASN:O	1:A:53:ASN:ND2	0.52	2.42	17	1
1:A:41:GLN:NE2	1:A:42:ASN:ND2	0.52	2.56	2	1
1:A:64:ASP:OD1	1:A:65:PHE:CD2	0.52	2.62	9	1
2:B:19:LYS:CB	2:B:19:LYS:NZ	0.52	2.73	17	1
1:A:137:ASN:HD21	1:A:139:GLU:H	0.52	1.45	11	1
1:A:72:MET:SD	1:A:72:MET:N	0.52	2.81	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:ASN:HD21	2:B:18:LYS:HZ3	0.52	1.44	16	1
1:A:16:PHE:CD2	1:A:65:PHE:CE1	0.52	2.98	8	2
1:A:65:PHE:CD1	1:A:65:PHE:C	0.52	2.83	10	2
1:A:95:ASP:O	1:A:97:ASN:N	0.52	2.42	14	1
1:A:53:ASN:O	1:A:55:VAL:N	0.52	2.43	11	1
1:A:105:LEU:HD11	1:A:109:MET:SD	0.52	2.44	14	2
1:A:20:ASP:CG	1:A:25:GLY:H	0.52	2.08	20	4
1:A:36:MET:SD	2:B:18:LYS:NZ	0.52	2.76	16	1
1:A:14:GLU:OE2	2:B:6:LYS:NZ	0.52	2.42	9	1
2:B:19:LYS:HZ3	2:B:19:LYS:CB	0.52	2.18	17	1
1:A:106:ARG:O	1:A:110:THR:N	0.52	2.43	17	1
1:A:99:PHE:O	1:A:99:PHE:CG	0.52	2.62	19	1
1:A:98:GLY:O	1:A:99:PHE:CD1	0.52	2.63	11	2
1:A:24:ASP:OD1	1:A:24:ASP:N	0.51	2.42	18	2
1:A:40:GLY:O	1:A:41:GLN:CB	0.51	2.57	7	4
1:A:137:ASN:OD1	1:A:139:GLU:N	0.51	2.42	5	1
1:A:12:PHE:CE2	1:A:69:LEU:HD11	0.51	2.40	18	1
1:A:31:GLU:CD	1:A:31:GLU:H	0.51	2.09	2	1
1:A:64:ASP:OD1	1:A:64:ASP:N	0.51	2.42	21	1
1:A:81:SER:OG	1:A:82:GLU:N	0.51	2.42	14	2
1:A:58:ASP:OD1	1:A:59:GLY:N	0.51	2.43	3	1
1:A:5:THR:OG1	1:A:6:GLU:N	0.51	2.41	4	5
1:A:55:VAL:HG13	1:A:56:ASP:N	0.51	2.21	10	1
1:A:64:ASP:OD1	1:A:65:PHE:CE2	0.51	2.63	13	1
1:A:6:GLU:OE1	1:A:9:ILE:HD12	0.51	2.06	21	1
1:A:126:ARG:O	1:A:128:ALA:N	0.51	2.43	14	1
1:A:65:PHE:H	1:A:66:PRO:CD	0.51	2.17	13	2
1:A:117:THR:CG2	1:A:118:ASP:N	0.51	2.74	18	3
2:B:5:LYS:O	2:B:7:ASN:N	0.51	2.44	1	3
2:B:16:ARG:O	2:B:18:LYS:N	0.51	2.44	17	2
1:A:137:ASN:OD1	1:A:138:TYR:N	0.51	2.44	5	1
1:A:22:ASP:CG	1:A:23:GLY:N	0.51	2.63	4	3
1:A:97:ASN:OD1	1:A:97:ASN:N	0.50	2.44	2	2
1:A:64:ASP:CG	1:A:65:PHE:H	0.50	2.10	9	4
1:A:48:LEU:N	1:A:48:LEU:CD1	0.50	2.74	10	1
1:A:139:GLU:O	1:A:141:PHE:N	0.50	2.45	20	2
1:A:28:THR:CG2	1:A:29:THR:H	0.50	2.19	8	2
1:A:133:ASP:OD1	1:A:134:GLY:N	0.50	2.45	7	2
1:A:64:ASP:OD2	1:A:65:PHE:CD2	0.50	2.64	13	1
1:A:99:PHE:CE2	1:A:137:ASN:OD1	0.50	2.65	3	1
1:A:97:ASN:N	1:A:97:ASN:HD22	0.50	2.04	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:121:VAL:O	1:A:124:MET:N	0.50	2.45	15	7
1:A:138:TYR:O	1:A:142:VAL:HG23	0.50	2.07	15	1
1:A:106:ARG:O	1:A:110:THR:HG22	0.50	2.07	7	2
1:A:12:PHE:CE1	1:A:68:PHE:CD1	0.50	3.00	12	1
1:A:141:PHE:O	1:A:145:MET:SD	0.50	2.70	11	2
1:A:51:MET:SD	2:B:17:PHE:O	0.49	2.70	21	5
1:A:12:PHE:CE1	1:A:68:PHE:CD2	0.49	2.99	14	1
1:A:94:LYS:O	1:A:96:GLY:N	0.49	2.45	14	2
1:A:92:PHE:O	1:A:108:VAL:HG21	0.49	2.06	15	1
1:A:20:ASP:OD2	1:A:23:GLY:N	0.49	2.44	1	1
1:A:24:ASP:OD1	1:A:25:GLY:N	0.49	2.44	3	3
1:A:9:ILE:CG2	1:A:10:ALA:N	0.49	2.75	5	1
1:A:125:ILE:O	1:A:128:ALA:HB3	0.49	2.08	5	1
1:A:64:ASP:OD1	1:A:65:PHE:CZ	0.49	2.66	13	1
1:A:5:THR:O	1:A:6:GLU:CG	0.49	2.61	15	1
1:A:9:ILE:HG23	1:A:10:ALA:N	0.49	2.23	5	1
1:A:86:ARG:HE	1:A:90:ARG:NH2	0.49	2.05	7	1
1:A:55:VAL:CG1	1:A:56:ASP:N	0.49	2.75	10	1
1:A:137:ASN:CG	1:A:138:TYR:N	0.49	2.65	21	2
1:A:16:PHE:CE1	1:A:25:GLY:O	0.49	2.66	2	1
1:A:135:GLN:CD	1:A:135:GLN:H	0.49	2.11	21	1
1:A:28:THR:CG2	1:A:29:THR:N	0.49	2.76	1	7
1:A:70:THR:O	1:A:74:ARG:N	0.49	2.46	21	5
1:A:84:GLU:OE1	1:A:84:GLU:N	0.49	2.46	8	1
1:A:126:ARG:C	1:A:128:ALA:N	0.49	2.66	14	1
1:A:142:VAL:O	1:A:142:VAL:HG12	0.49	2.08	20	1
2:B:6:LYS:CG	2:B:7:ASN:N	0.49	2.76	19	1
1:A:19:PHE:O	1:A:21:LYS:N	0.49	2.45	1	1
1:A:135:GLN:CD	1:A:135:GLN:N	0.49	2.66	15	2
1:A:64:ASP:OD1	1:A:65:PHE:N	0.49	2.45	1	2
1:A:16:PHE:CE2	1:A:65:PHE:CE1	0.48	3.00	8	1
1:A:16:PHE:CE2	1:A:25:GLY:O	0.48	2.65	7	1
1:A:105:LEU:C	1:A:107:HIS:N	0.48	2.66	12	4
1:A:31:GLU:N	1:A:31:GLU:CD	0.48	2.66	18	1
1:A:97:ASN:ND2	1:A:99:PHE:H	0.48	2.05	7	1
1:A:117:THR:CG2	1:A:118:ASP:H	0.48	2.17	9	1
1:A:31:GLU:H	1:A:31:GLU:CD	0.48	2.11	18	1
1:A:84:GLU:H	1:A:84:GLU:CD	0.48	2.08	5	1
1:A:94:LYS:NZ	1:A:94:LYS:CB	0.48	2.76	13	2
1:A:65:PHE:CE1	1:A:69:LEU:HD11	0.48	2.43	7	1
1:A:64:ASP:CG	1:A:65:PHE:N	0.48	2.66	13	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:16:PHE:O	1:A:19:PHE:N	0.48	2.47	10	1
1:A:34:THR:CG2	1:A:35:VAL:N	0.48	2.76	12	3
1:A:95:ASP:OD1	1:A:96:GLY:N	0.48	2.46	1	2
2:B:3:ARG:O	2:B:6:LYS:NZ	0.48	2.46	11	1
1:A:137:ASN:OD1	1:A:137:ASN:N	0.48	2.46	4	1
1:A:120:GLU:N	1:A:120:GLU:OE1	0.48	2.47	16	1
1:A:71:MET:SD	1:A:71:MET:O	0.48	2.71	9	1
1:A:101:SER:OG	1:A:102:ALA:N	0.48	2.42	20	1
1:A:131:ASP:OD1	1:A:131:ASP:N	0.48	2.44	18	1
1:A:93:ASP:OD1	1:A:96:GLY:N	0.48	2.47	11	2
2:B:19:LYS:C	2:B:21:SER:N	0.48	2.67	17	2
1:A:137:ASN:ND2	1:A:137:ASN:N	0.48	2.60	3	2
1:A:98:GLY:C	1:A:99:PHE:CG	0.48	2.86	1	2
1:A:20:ASP:OD2	1:A:25:GLY:N	0.48	2.47	5	2
2:B:16:ARG:C	2:B:18:LYS:N	0.48	2.65	17	5
1:A:105:LEU:HD22	1:A:109:MET:SD	0.48	2.48	17	1
1:A:93:ASP:OD2	1:A:98:GLY:CA	0.48	2.62	3	2
1:A:116:LEU:O	1:A:117:THR:C	0.48	2.52	11	1
1:A:35:VAL:O	1:A:38:SER:N	0.48	2.47	20	5
1:A:94:LYS:O	1:A:94:LYS:CG	0.48	2.62	12	1
1:A:131:ASP:N	1:A:131:ASP:OD1	0.47	2.47	10	1
1:A:97:ASN:N	1:A:97:ASN:ND2	0.47	2.61	12	1
1:A:87:GLU:O	1:A:91:VAL:HG23	0.47	2.08	18	1
1:A:50:ASP:CG	1:A:51:MET:N	0.47	2.68	20	2
1:A:59:GLY:C	1:A:61:GLY:N	0.47	2.67	21	5
1:A:45:GLU:N	1:A:45:GLU:OE2	0.47	2.47	21	2
1:A:133:ASP:CG	1:A:134:GLY:N	0.47	2.68	21	2
1:A:58:ASP:CG	1:A:59:GLY:N	0.47	2.66	13	1
1:A:141:PHE:CE2	1:A:145:MET:CE	0.47	2.97	3	1
1:A:56:ASP:OD2	1:A:60:ASN:N	0.47	2.47	10	1
1:A:14:GLU:CD	2:B:6:LYS:HZ1	0.47	2.13	9	1
1:A:113:GLY:O	1:A:115:LYS:N	0.47	2.46	12	1
1:A:99:PHE:O	1:A:99:PHE:CD1	0.47	2.67	19	1
1:A:85:ILE:CD1	1:A:85:ILE:N	0.47	2.77	10	3
1:A:18:LEU:O	1:A:21:LYS:NZ	0.47	2.43	5	1
1:A:45:GLU:CG	1:A:46:ALA:N	0.47	2.77	20	2
1:A:55:VAL:O	1:A:57:ALA:N	0.47	2.47	8	1
1:A:86:ARG:O	1:A:89:PHE:N	0.47	2.48	10	3
2:B:9:ILE:O	2:B:12:SER:CB	0.47	2.63	4	3
2:B:9:ILE:O	2:B:12:SER:N	0.47	2.47	5	5
1:A:22:ASP:OD1	1:A:22:ASP:N	0.47	2.47	7	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:126:ARG:HH11	1:A:126:ARG:CG	0.47	2.22	3	1
1:A:28:THR:OG1	1:A:62:THR:CG2	0.47	2.62	2	2
1:A:28:THR:HG23	1:A:62:THR:HG22	0.47	1.86	1	2
1:A:95:ASP:CG	1:A:96:GLY:N	0.47	2.67	6	2
1:A:28:THR:O	1:A:30:LYS:N	0.47	2.48	10	1
1:A:84:GLU:N	1:A:84:GLU:CD	0.47	2.69	5	1
1:A:122:ASP:CG	1:A:123:GLU:N	0.47	2.68	16	1
1:A:82:GLU:O	1:A:84:GLU:N	0.46	2.48	14	1
2:B:19:LYS:O	2:B:21:SER:N	0.46	2.48	17	2
1:A:93:ASP:OD2	1:A:98:GLY:N	0.46	2.48	17	1
1:A:91:VAL:CG2	1:A:92:PHE:N	0.46	2.78	8	1
1:A:37:ARG:N	1:A:42:ASN:OD1	0.46	2.48	10	1
1:A:45:GLU:CD	1:A:45:GLU:N	0.46	2.68	2	5
1:A:105:LEU:O	1:A:109:MET:N	0.46	2.49	1	1
1:A:44:THR:O	1:A:48:LEU:CD1	0.46	2.63	9	1
1:A:87:GLU:OE1	1:A:88:ALA:N	0.46	2.48	15	1
1:A:129:ASP:OD1	1:A:130:ILE:N	0.46	2.49	20	1
1:A:31:GLU:N	1:A:31:GLU:OE1	0.46	2.48	2	1
1:A:12:PHE:CD1	1:A:13:LYS:N	0.46	2.84	6	1
1:A:117:THR:HG22	1:A:118:ASP:N	0.46	2.24	18	1
1:A:110:THR:CG2	1:A:111:ASN:N	0.46	2.79	8	1
1:A:58:ASP:N	1:A:58:ASP:OD1	0.46	2.45	2	2
2:B:6:LYS:CB	2:B:6:LYS:HZ2	0.46	2.24	4	1
1:A:106:ARG:O	1:A:110:THR:CG2	0.46	2.64	8	3
1:A:54:GLU:O	1:A:54:GLU:CG	0.46	2.63	16	1
2:B:4:TRP:N	2:B:4:TRP:CD1	0.46	2.84	6	2
1:A:53:ASN:C	1:A:55:VAL:N	0.46	2.67	11	2
1:A:126:ARG:O	1:A:129:ASP:N	0.46	2.49	4	1
1:A:42:ASN:ND2	1:A:42:ASN:H	0.46	2.08	2	1
1:A:135:GLN:OE1	1:A:135:GLN:N	0.46	2.48	19	1
1:A:5:THR:O	1:A:6:GLU:CB	0.46	2.63	15	1
1:A:105:LEU:O	1:A:108:VAL:N	0.46	2.48	5	4
1:A:82:GLU:C	1:A:84:GLU:N	0.46	2.67	14	1
1:A:44:THR:O	1:A:48:LEU:HD13	0.46	2.11	20	1
2:B:3:ARG:H	2:B:6:LYS:NZ	0.46	2.07	17	1
1:A:35:VAL:O	1:A:37:ARG:N	0.46	2.48	11	2
1:A:94:LYS:CG	1:A:95:ASP:N	0.46	2.79	9	1
1:A:120:GLU:CA	1:A:120:GLU:OE1	0.45	2.64	16	1
1:A:36:MET:CG	1:A:42:ASN:HD21	0.45	2.25	20	1
1:A:32:LEU:HD22	1:A:36:MET:SD	0.45	2.52	7	1
1:A:99:PHE:CZ	1:A:137:ASN:OD1	0.45	2.69	20	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:84:GLU:OE2	2:B:16:ARG:NH1	0.45	2.49	9	1
1:A:5:THR:C	1:A:7:GLU:N	0.45	2.69	12	5
1:A:56:ASP:OD2	1:A:60:ASN:ND2	0.45	2.49	16	1
1:A:141:PHE:CD1	1:A:141:PHE:C	0.45	2.88	17	3
1:A:8:GLN:H	1:A:8:GLN:HE21	0.45	1.52	16	1
1:A:5:THR:C	1:A:7:GLU:H	0.45	2.14	4	5
1:A:113:GLY:C	1:A:115:LYS:N	0.45	2.69	12	1
2:B:5:LYS:HG2	2:B:9:ILE:HD12	0.45	1.87	10	1
1:A:56:ASP:OD1	1:A:60:ASN:N	0.45	2.49	4	1
1:A:56:ASP:OD2	1:A:62:THR:N	0.45	2.50	4	3
1:A:43:PRO:O	1:A:44:THR:O	0.45	2.35	9	2
1:A:94:LYS:C	1:A:96:GLY:N	0.45	2.70	13	1
2:B:4:TRP:CD1	2:B:4:TRP:N	0.45	2.85	1	3
1:A:50:ASP:C	1:A:52:ILE:N	0.45	2.70	9	2
1:A:26:THR:O	1:A:31:GLU:OE1	0.45	2.35	3	5
1:A:32:LEU:CD1	2:B:17:PHE:CD1	0.45	2.99	19	1
1:A:85:ILE:N	1:A:85:ILE:CD1	0.45	2.79	13	1
1:A:5:THR:CG2	1:A:6:GLU:H	0.45	2.18	16	1
2:B:7:ASN:CG	2:B:8:PHE:N	0.45	2.70	7	1
2:B:4:TRP:O	2:B:7:ASN:N	0.45	2.50	9	1
1:A:41:GLN:CG	1:A:42:ASN:N	0.45	2.79	18	1
1:A:9:ILE:HD12	1:A:9:ILE:N	0.45	2.27	4	1
1:A:65:PHE:CZ	1:A:69:LEU:HD11	0.45	2.47	7	1
1:A:42:ASN:C	1:A:42:ASN:ND2	0.45	2.70	5	1
1:A:93:ASP:OD2	1:A:95:ASP:O	0.45	2.35	19	1
1:A:39:LEU:HD12	1:A:39:LEU:N	0.45	2.27	11	1
1:A:23:GLY:H	1:A:31:GLU:CD	0.45	2.14	4	1
1:A:99:PHE:CD1	1:A:99:PHE:O	0.45	2.70	4	1
1:A:56:ASP:OD1	1:A:57:ALA:N	0.44	2.50	10	1
1:A:130:ILE:O	1:A:130:ILE:HG22	0.44	2.11	9	1
1:A:36:MET:O	1:A:39:LEU:N	0.44	2.49	12	2
1:A:5:THR:O	1:A:7:GLU:N	0.44	2.50	12	3
1:A:52:ILE:C	1:A:54:GLU:N	0.44	2.70	3	1
1:A:30:LYS:O	1:A:34:THR:OG1	0.44	2.34	4	1
2:B:5:LYS:C	2:B:7:ASN:N	0.44	2.69	1	2
1:A:131:ASP:OD1	1:A:132:GLY:N	0.44	2.50	14	2
1:A:53:ASN:C	1:A:55:VAL:H	0.44	2.15	1	3
1:A:9:ILE:N	1:A:9:ILE:CD1	0.44	2.80	4	1
1:A:87:GLU:OE1	1:A:87:GLU:CA	0.44	2.65	10	1
1:A:89:PHE:CZ	1:A:98:GLY:O	0.44	2.70	2	1
1:A:99:PHE:CE2	1:A:137:ASN:ND2	0.44	2.86	17	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:ASN:OD1	1:A:62:THR:O	0.44	2.36	10	1
1:A:121:VAL:O	1:A:122:ASP:C	0.44	2.56	5	4
1:A:68:PHE:CZ	1:A:72:MET:SD	0.44	3.10	3	1
1:A:128:ALA:O	1:A:140:GLU:OE1	0.44	2.36	16	1
1:A:139:GLU:O	1:A:143:THR:N	0.44	2.50	5	1
1:A:93:ASP:OD1	1:A:93:ASP:O	0.44	2.36	12	1
1:A:48:LEU:HD13	1:A:51:MET:SD	0.44	2.53	6	1
1:A:56:ASP:OD1	1:A:56:ASP:O	0.44	2.36	4	1
1:A:89:PHE:CG	1:A:138:TYR:CE1	0.44	3.06	20	1
2:B:20:ILE:O	2:B:21:SER:O	0.44	2.36	7	2
1:A:95:ASP:OD2	1:A:97:ASN:OD1	0.44	2.36	11	3
1:A:114:GLU:CD	1:A:114:GLU:N	0.43	2.72	7	1
1:A:107:HIS:O	1:A:110:THR:OG1	0.43	2.36	18	1
1:A:56:ASP:OD2	1:A:62:THR:O	0.43	2.36	4	1
1:A:22:ASP:OD2	1:A:31:GLU:OE1	0.43	2.35	14	1
1:A:63:ILE:HD13	2:B:17:PHE:CZ	0.43	2.47	20	1
1:A:130:ILE:CG2	1:A:131:ASP:N	0.43	2.80	7	1
1:A:55:VAL:O	1:A:67:GLU:OE2	0.43	2.36	2	1
1:A:22:ASP:OD2	1:A:31:GLU:OE2	0.43	2.36	15	1
1:A:20:ASP:OD1	1:A:22:ASP:OD1	0.43	2.37	10	1
2:B:17:PHE:HA	2:B:20:ILE:HD12	0.43	1.90	7	2
1:A:43:PRO:O	1:A:45:GLU:OE2	0.43	2.37	7	1
1:A:117:THR:OG1	1:A:120:GLU:OE1	0.43	2.36	2	1
1:A:129:ASP:OD1	1:A:140:GLU:OE1	0.43	2.36	17	1
1:A:62:THR:O	1:A:67:GLU:OE2	0.43	2.35	21	1
1:A:83:GLU:O	1:A:87:GLU:OE1	0.43	2.37	11	1
2:B:3:ARG:C	2:B:5:LYS:N	0.43	2.71	8	1
1:A:19:PHE:O	1:A:31:GLU:OE1	0.43	2.36	16	1
1:A:27:ILE:HG21	2:B:17:PHE:CD2	0.43	2.47	14	1
1:A:58:ASP:OD2	1:A:60:ASN:OD1	0.43	2.37	20	2
1:A:69:LEU:O	1:A:73:ALA:CB	0.43	2.65	17	1
2:B:16:ARG:C	2:B:18:LYS:H	0.43	2.16	17	1
1:A:35:VAL:C	1:A:37:ARG:N	0.43	2.71	11	2
1:A:20:ASP:OD2	1:A:24:ASP:OD1	0.43	2.36	6	1
1:A:50:ASP:O	1:A:52:ILE:N	0.43	2.51	3	1
1:A:105:LEU:O	1:A:106:ARG:C	0.43	2.56	5	5
1:A:66:PRO:O	1:A:68:PHE:N	0.43	2.51	12	1
1:A:117:THR:C	1:A:119:GLU:H	0.43	2.16	21	1
1:A:71:MET:C	1:A:72:MET:SD	0.43	2.96	15	1
1:A:129:ASP:OD2	1:A:133:ASP:N	0.43	2.50	7	2
1:A:105:LEU:O	1:A:105:LEU:HD23	0.43	2.14	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:ASP:OD2	1:A:67:GLU:OE1	0.43	2.37	2	1
1:A:126:ARG:O	1:A:129:ASP:O	0.43	2.37	9	1
1:A:106:ARG:O	1:A:110:THR:OG1	0.43	2.35	18	1
2:B:4:TRP:O	2:B:7:ASN:OD1	0.43	2.36	11	2
1:A:82:GLU:N	1:A:82:GLU:OE2	0.43	2.52	10	1
1:A:118:ASP:OD1	1:A:122:ASP:OD2	0.43	2.37	11	2
1:A:20:ASP:OD1	1:A:31:GLU:OE2	0.43	2.37	12	2
1:A:20:ASP:OD1	1:A:24:ASP:N	0.43	2.52	4	1
1:A:37:ARG:C	1:A:39:LEU:N	0.43	2.72	6	2
1:A:133:ASP:OD1	1:A:135:GLN:O	0.43	2.37	16	1
1:A:119:GLU:O	1:A:123:GLU:OE2	0.43	2.37	6	1
2:B:5:LYS:CB	2:B:5:LYS:NZ	0.43	2.82	13	1
1:A:118:ASP:O	1:A:118:ASP:OD1	0.43	2.37	21	1
1:A:28:THR:C	1:A:30:LYS:N	0.43	2.71	10	2
1:A:21:LYS:NZ	1:A:21:LYS:CB	0.43	2.82	14	1
1:A:94:LYS:O	1:A:95:ASP:O	0.43	2.36	18	1
1:A:98:GLY:C	1:A:99:PHE:CD1	0.43	2.92	13	1
1:A:15:ALA:C	1:A:17:SER:N	0.43	2.73	3	1
1:A:95:ASP:OD1	1:A:97:ASN:OD1	0.43	2.37	11	1
1:A:12:PHE:C	1:A:12:PHE:CD1	0.42	2.88	20	1
1:A:72:MET:SD	2:B:16:ARG:NH1	0.42	2.92	17	1
1:A:24:ASP:OD2	1:A:26:THR:OG1	0.42	2.34	6	1
1:A:51:MET:C	1:A:51:MET:SD	0.42	2.97	3	1
1:A:65:PHE:CB	1:A:66:PRO:CD	0.42	2.96	8	1
1:A:129:ASP:OD2	1:A:133:ASP:OD1	0.42	2.37	16	3
1:A:107:HIS:N	1:A:107:HIS:CD2	0.42	2.86	16	1
1:A:95:ASP:N	1:A:95:ASP:OD1	0.42	2.52	11	2
1:A:14:GLU:CD	2:B:6:LYS:NZ	0.42	2.73	9	1
1:A:120:GLU:O	1:A:120:GLU:OE1	0.42	2.37	9	1
1:A:12:PHE:CD2	1:A:13:LYS:N	0.42	2.87	18	1
1:A:117:THR:O	1:A:118:ASP:OD2	0.42	2.36	21	1
1:A:22:ASP:OD2	1:A:24:ASP:OD1	0.42	2.37	14	2
1:A:137:ASN:CG	1:A:138:TYR:H	0.42	2.17	20	1
1:A:97:ASN:ND2	1:A:98:GLY:H	0.42	2.11	7	1
1:A:93:ASP:OD1	1:A:104:GLU:OE1	0.42	2.37	2	1
1:A:25:GLY:O	1:A:26:THR:CG2	0.42	2.67	12	1
1:A:95:ASP:OD2	1:A:104:GLU:OE1	0.42	2.36	18	1
1:A:95:ASP:CG	1:A:96:GLY:H	0.42	2.17	11	1
1:A:139:GLU:C	1:A:141:PHE:N	0.42	2.70	20	2
2:B:18:LYS:CD	2:B:18:LYS:C	0.42	2.88	20	1
2:B:8:PHE:O	2:B:12:SER:OG	0.42	2.37	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:22:ASP:OD2	1:A:24:ASP:OD2	0.42	2.37	19	1
2:B:5:LYS:O	2:B:6:LYS:C	0.42	2.57	10	2
1:A:138:TYR:O	1:A:141:PHE:N	0.42	2.52	12	2
2:B:4:TRP:O	2:B:5:LYS:C	0.42	2.58	9	1
1:A:40:GLY:O	1:A:41:GLN:O	0.42	2.37	9	1
1:A:13:LYS:O	1:A:17:SER:OG	0.42	2.37	3	1
1:A:136:VAL:HG12	1:A:137:ASN:N	0.42	2.28	19	1
1:A:65:PHE:N	1:A:66:PRO:HD2	0.42	2.30	18	3
1:A:19:PHE:CZ	1:A:35:VAL:HG11	0.42	2.49	4	1
2:B:9:ILE:HG22	2:B:10:ALA:N	0.42	2.29	16	7
1:A:93:ASP:OD2	1:A:95:ASP:OD1	0.42	2.37	10	1
1:A:139:GLU:O	1:A:143:THR:OG1	0.42	2.36	5	1
1:A:49:GLN:O	1:A:49:GLN:OE1	0.42	2.37	20	1
1:A:20:ASP:C	1:A:22:ASP:N	0.42	2.72	12	2
1:A:5:THR:CG2	1:A:6:GLU:N	0.42	2.82	3	1
1:A:123:GLU:OE1	1:A:123:GLU:CA	0.42	2.65	10	2
1:A:126:ARG:C	1:A:128:ALA:H	0.42	2.18	14	1
1:A:129:ASP:OD1	1:A:131:ASP:OD1	0.42	2.38	7	1
1:A:33:GLY:O	1:A:37:ARG:CB	0.42	2.68	11	2
1:A:45:GLU:OE1	1:A:45:GLU:N	0.42	2.52	1	1
1:A:87:GLU:N	1:A:87:GLU:OE1	0.42	2.53	10	1
1:A:34:THR:OG1	1:A:35:VAL:N	0.42	2.53	5	1
1:A:131:ASP:OD1	1:A:133:ASP:OD1	0.42	2.37	5	2
1:A:141:PHE:CD2	1:A:142:VAL:N	0.41	2.88	6	1
1:A:142:VAL:HG12	1:A:142:VAL:O	0.41	2.15	13	1
1:A:19:PHE:CE2	2:B:13:ALA:HB3	0.41	2.50	3	1
1:A:21:LYS:CB	1:A:21:LYS:NZ	0.41	2.83	4	1
1:A:142:VAL:O	1:A:142:VAL:CG1	0.41	2.68	20	1
1:A:89:PHE:CE2	1:A:138:TYR:CE1	0.41	3.09	3	1
1:A:130:ILE:HG22	1:A:130:ILE:O	0.41	2.14	4	1
1:A:95:ASP:OD2	1:A:104:GLU:OE2	0.41	2.37	4	1
1:A:101:SER:O	1:A:103:ALA:N	0.41	2.54	8	1
1:A:92:PHE:CZ	2:B:7:ASN:OD1	0.41	2.73	17	1
1:A:91:VAL:HG23	1:A:92:PHE:H	0.41	1.73	8	1
2:B:10:ALA:O	2:B:13:ALA:HB3	0.41	2.15	7	1
1:A:125:ILE:O	1:A:129:ASP:CB	0.41	2.68	9	1
1:A:130:ILE:O	1:A:130:ILE:CG2	0.41	2.68	9	1
1:A:47:GLU:O	1:A:47:GLU:OE2	0.41	2.37	8	1
1:A:97:ASN:O	1:A:98:GLY:O	0.41	2.38	10	1
1:A:117:THR:OG1	1:A:120:GLU:OE2	0.41	2.38	2	1
1:A:12:PHE:CD1	1:A:12:PHE:O	0.41	2.73	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:23:GLY:O	1:A:24:ASP:C	0.41	2.59	4	1
1:A:31:GLU:O	1:A:34:THR:OG1	0.41	2.37	17	2
1:A:130:ILE:HG23	1:A:131:ASP:N	0.41	2.30	7	1
1:A:20:ASP:OD2	1:A:22:ASP:OD2	0.41	2.39	2	2
1:A:114:GLU:CD	1:A:114:GLU:H	0.41	2.17	17	1
1:A:84:GLU:O	2:B:15:ASN:ND2	0.41	2.54	12	1
2:B:7:ASN:O	2:B:11:VAL:HG23	0.41	2.15	6	1
1:A:99:PHE:CD1	1:A:99:PHE:C	0.41	2.94	4	1
1:A:93:ASP:C	1:A:95:ASP:H	0.41	2.18	12	1
1:A:131:ASP:CG	1:A:132:GLY:N	0.41	2.73	13	1
1:A:52:ILE:O	1:A:55:VAL:HG22	0.41	2.16	3	1
1:A:95:ASP:OD1	1:A:104:GLU:OE2	0.41	2.38	1	1
1:A:129:ASP:OD1	1:A:135:GLN:O	0.41	2.39	1	1
1:A:37:ARG:C	1:A:39:LEU:H	0.41	2.19	7	2
1:A:20:ASP:OD1	1:A:22:ASP:OD2	0.41	2.39	9	1
1:A:63:ILE:N	1:A:63:ILE:HD13	0.41	2.31	11	2
1:A:107:HIS:O	1:A:111:ASN:OD1	0.41	2.38	16	2
1:A:123:GLU:O	1:A:127:GLU:OE1	0.41	2.39	14	1
1:A:20:ASP:C	1:A:22:ASP:H	0.41	2.19	18	1
1:A:93:ASP:O	1:A:93:ASP:OD1	0.41	2.37	4	1
1:A:95:ASP:O	1:A:97:ASN:OD1	0.41	2.38	8	1
1:A:89:PHE:CE1	1:A:141:PHE:CG	0.41	3.09	10	1
1:A:93:ASP:O	1:A:94:LYS:C	0.41	2.60	14	1
1:A:36:MET:CE	2:B:14:ALA:O	0.41	2.69	21	1
1:A:137:ASN:ND2	1:A:139:GLU:N	0.41	2.69	11	1
1:A:52:ILE:O	1:A:56:ASP:N	0.41	2.54	1	1
1:A:16:PHE:O	1:A:18:LEU:N	0.40	2.54	16	1
1:A:66:PRO:O	1:A:70:THR:OG1	0.40	2.35	14	1
2:B:16:ARG:O	2:B:20:ILE:N	0.40	2.54	9	1
1:A:67:GLU:O	1:A:68:PHE:C	0.40	2.59	21	2
1:A:35:VAL:O	1:A:36:MET:C	0.40	2.60	13	2
1:A:97:ASN:N	1:A:97:ASN:OD1	0.40	2.54	11	1
1:A:33:GLY:O	1:A:34:THR:C	0.40	2.60	11	1
1:A:26:THR:CG2	1:A:62:THR:OG1	0.40	2.69	15	1
1:A:97:ASN:OD1	1:A:104:GLU:OE2	0.40	2.39	12	1
1:A:59:GLY:C	1:A:61:GLY:H	0.40	2.19	4	1
1:A:81:SER:C	1:A:83:GLU:H	0.40	2.20	4	1
1:A:138:TYR:C	1:A:140:GLU:N	0.40	2.74	14	1
1:A:66:PRO:O	1:A:67:GLU:C	0.40	2.60	14	1
2:B:7:ASN:OD1	2:B:7:ASN:C	0.40	2.60	7	1
1:A:93:ASP:OD1	1:A:95:ASP:OD2	0.40	2.39	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:LYS:O	1:A:16:PHE:N	0.40	2.54	13	1
1:A:39:LEU:CD1	1:A:39:LEU:N	0.40	2.85	11	1
1:A:110:THR:C	1:A:112:LEU:H	0.40	2.19	16	1
1:A:139:GLU:O	1:A:140:GLU:C	0.40	2.59	7	1
1:A:32:LEU:HD13	2:B:17:PHE:CD2	0.40	2.51	21	1
1:A:22:ASP:OD1	1:A:31:GLU:CD	0.40	2.60	4	1
1:A:84:GLU:OE1	2:B:16:ARG:NH1	0.40	2.53	16	1
1:A:32:LEU:HD23	1:A:48:LEU:CD1	0.40	2.47	6	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	135/148 (91%)	99±5 (73±3%)	29±5 (21±4%)	8±3 (6±2%)	4	23
2	B	19/26 (73%)	16±2 (82±8%)	3±1 (15±8%)	1±1 (3±4%)	8	39
All	All	3234/3654 (89%)	2398 (74%)	663 (21%)	173 (5%)	4	25

All 54 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	43	PRO	14
1	A	40	GLY	12
1	A	23	GLY	8
1	A	41	GLN	8
1	A	95	ASP	7
1	A	5	THR	6
1	A	112	LEU	6
1	A	117	THR	6
1	A	132	GLY	5
2	B	21	SER	5
1	A	74	ARG	5
1	A	131	ASP	4
1	A	66	PRO	4

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Mol	Chain	Res	Type	Models (Total)
1	A	59	GLY	4
1	A	64	ASP	4
2	B	5	LYS	4
1	A	96	GLY	4
1	A	58	ASP	4
1	A	81	SER	4
1	A	55	VAL	4
1	A	104	GLU	4
1	A	114	GLU	4
1	A	98	GLY	3
1	A	106	ARG	3
1	A	44	THR	2
1	A	94	LYS	2
1	A	6	GLU	2
1	A	139	GLU	2
1	A	118	ASP	2
1	A	113	GLY	2
1	A	60	ASN	2
1	A	54	GLU	2
1	A	116	LEU	2
2	B	3	ARG	2
1	A	102	ALA	2
1	A	36	MET	1
1	A	133	ASP	1
1	A	93	ASP	1
1	A	35	VAL	1
1	A	24	ASP	1
1	A	29	THR	1
1	A	84	GLU	1
1	A	140	GLU	1
1	A	99	PHE	1
2	B	17	PHE	1
1	A	57	ALA	1
1	A	20	ASP	1
1	A	122	ASP	1
1	A	25	GLY	1
2	B	6	LYS	1
1	A	127	GLU	1
1	A	34	THR	1
1	A	115	LYS	1
1	A	56	ASP	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	115/127 (91%)	89±4 (78±3%)	26±4 (22±3%)	4	31
2	B	16/21 (76%)	12±1 (72±9%)	4±1 (28±9%)	2	21
All	All	2751/3108 (89%)	2116 (77%)	635 (23%)	3	30

All 118 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	16
1	A	22	ASP	15
1	A	65	PHE	14
1	A	133	ASP	13
1	A	101	SER	13
2	B	20	ILE	13
1	A	118	ASP	12
1	A	99	PHE	12
1	A	131	ASP	11
1	A	109	MET	11
1	A	143	THR	11
1	A	17	SER	10
2	B	6	LYS	10
1	A	24	ASP	10
2	B	12	SER	10
1	A	19	PHE	10
1	A	74	ARG	9
1	A	111	ASN	9
2	B	9	ILE	9
1	A	58	ASP	9
1	A	42	ASN	8
2	B	15	ASN	8
1	A	95	ASP	8
1	A	52	ILE	8
1	A	138	TYR	8
2	B	19	LYS	8
1	A	34	THR	8
1	A	38	SER	8

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Mol	Chain	Res	Type	Models (Total)
1	A	41	GLN	8
1	A	90	ARG	7
2	B	3	ARG	7
2	B	17	PHE	7
1	A	28	THR	7
1	A	145	MET	7
1	A	106	ARG	7
1	A	107	HIS	7
2	B	16	ARG	6
1	A	5	THR	6
2	B	7	ASN	6
1	A	137	ASN	6
1	A	71	MET	6
1	A	50	ASP	6
1	A	110	THR	6
1	A	122	ASP	6
1	A	60	ASN	6
1	A	123	GLU	6
1	A	49	GLN	6
1	A	94	LYS	6
1	A	87	GLU	6
1	A	108	VAL	5
1	A	81	SER	5
1	A	16	PHE	5
1	A	97	ASN	5
1	A	12	PHE	5
1	A	120	GLU	5
1	A	21	LYS	5
1	A	105	LEU	5
1	A	129	ASP	5
1	A	126	ARG	5
1	A	47	GLU	4
1	A	32	LEU	4
1	A	117	THR	4
2	B	18	LYS	4
1	A	116	LEU	4
1	A	27	ILE	4
1	A	70	THR	4
1	A	53	ASN	4
1	A	31	GLU	4
1	A	43	PRO	4
1	A	115	LYS	4

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Mol	Chain	Res	Type	Models (Total)
1	A	20	ASP	4
1	A	29	THR	4
1	A	39	LEU	4
1	A	135	GLN	4
1	A	26	THR	4
1	A	127	GLU	4
1	A	72	MET	3
2	B	5	LYS	3
1	A	55	VAL	3
1	A	114	GLU	3
1	A	45	GLU	3
1	A	37	ARG	3
1	A	84	GLU	3
1	A	7	GLU	3
1	A	141	PHE	3
1	A	8	GLN	3
1	A	62	THR	3
1	A	86	ARG	3
1	A	11	GLU	3
1	A	139	GLU	3
1	A	112	LEU	3
1	A	100	ILE	3
1	A	63	ILE	3
1	A	30	LYS	3
1	A	119	GLU	3
1	A	48	LEU	2
1	A	130	ILE	2
1	A	36	MET	2
1	A	68	PHE	2
1	A	6	GLU	2
1	A	91	VAL	2
1	A	89	PHE	2
1	A	13	LYS	2
1	A	93	ASP	2
1	A	14	GLU	2
2	B	21	SER	2
1	A	69	LEU	1
1	A	9	ILE	1
1	A	64	ASP	1
1	A	144	MET	1
1	A	124	MET	1
1	A	104	GLU	1

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Mol	Chain	Res	Type	Models (Total)
1	A	140	GLU	1
1	A	83	GLU	1
1	A	82	GLU	1
1	A	51	MET	1
1	A	142	VAL	1
1	A	56	ASP	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 carbohydrates in this entry.

## 6.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 4 are 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

No chemical shift data were provided