



# Full wwPDB NMR Structure Validation Report ⓘ

Jun 16, 2024 – 01:51 AM EDT

PDB ID : 2L2C  
Title : NMR Structure of mosquito odorant binding protein bound to MOP pheromone  
Authors : Ames, J.  
Deposited on : 2010-08-16

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

<https://www.wwpdb.org/validation/2017/NMRValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.37.1

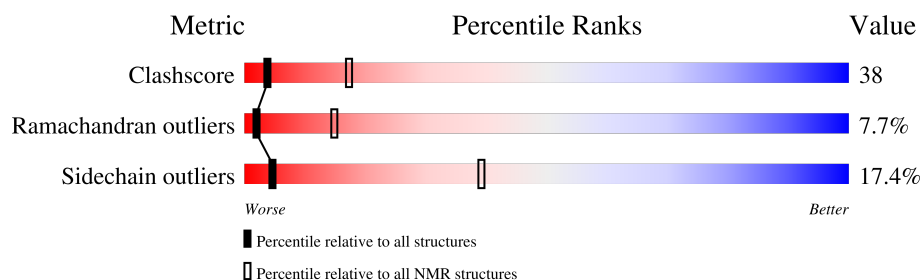
# 1 Overall quality at a glance

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

The table below summarises the geometric issues observed across the polymeric chains and their fit to the experimental data. The red, orange, yellow and green segments indicate the fraction of residues that contain outliers for  $\geq 3$ , 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	125	<div> <div></div> <div>34%</div> <div>46%</div> <div>18%</div> <div>.</div> </div>

## 2 Ensemble composition and analysis

This entry contains 15 models. Model 4 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:4-A:124 (121)	1.11	4

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 1 single-model cluster was found.

Cluster number	Models
1	2, 5, 14, 15
2	3, 4, 11, 13
3	6, 9, 12
4	1, 7, 10
Single-model clusters	8

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 2001 atoms, of which 985 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Odorant-binding protein.

Mol	Chain	Residues	Atoms						Trace
1	A	125	Total	C	H	N	O	S	0
			2001	644	985	173	189	10	

There is a discrepancy between the modelled and reference sequences:

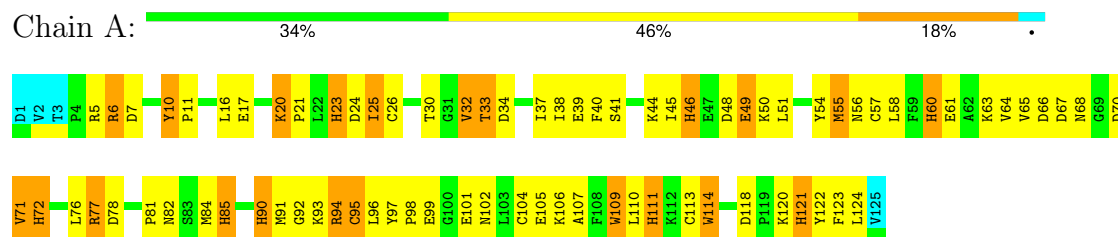
Chain	Residue	Modelled	Actual	Comment	Reference
A	77	ARG	HIS	SEE REMARK 999	UNP Q8T6I2

## 4 Residue-property plots

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

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

- Molecule 1: Odorant-binding protein

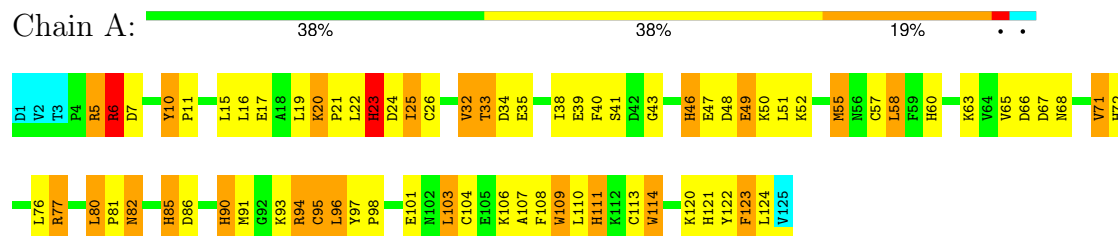


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

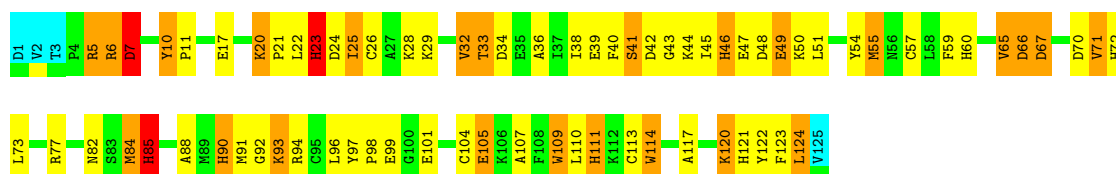
- Molecule 1: Odorant-binding protein



#### 4.2.2 Score per residue for model 2

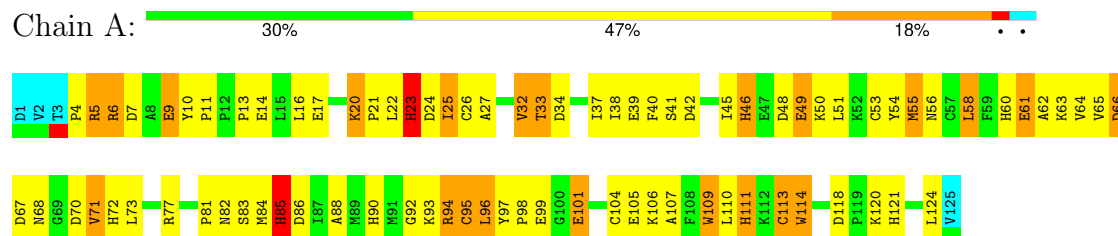
- Molecule 1: Odorant-binding protein





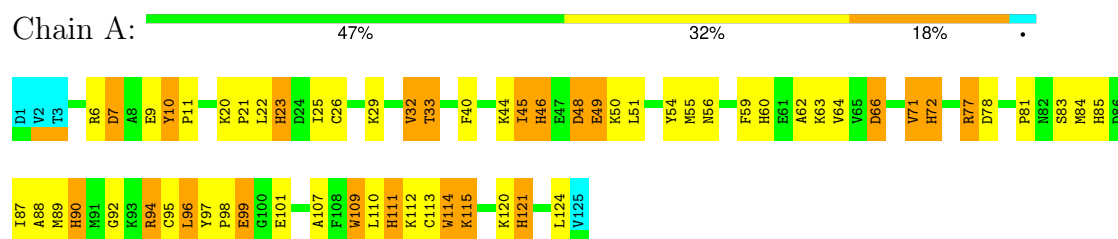
#### 4.2.3 Score per residue for model 3

- Molecule 1: Odorant-binding protein



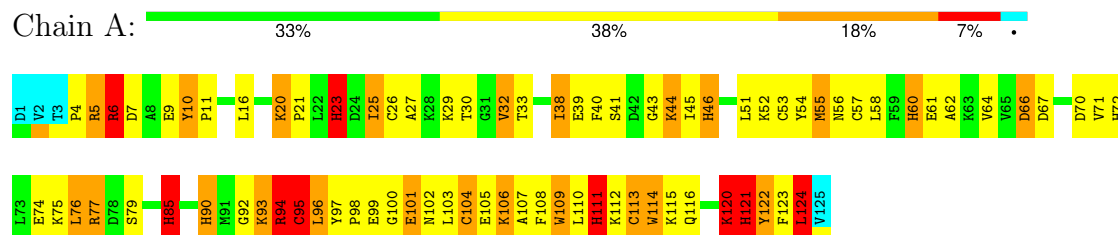
#### 4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Odorant-binding protein



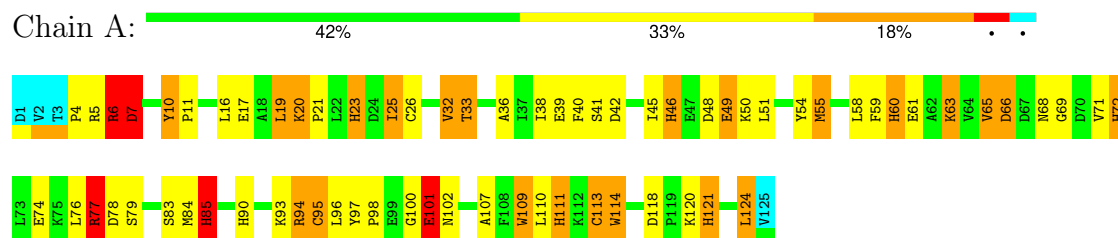
#### 4.2.5 Score per residue for model 5

- Molecule 1: Odorant-binding protein



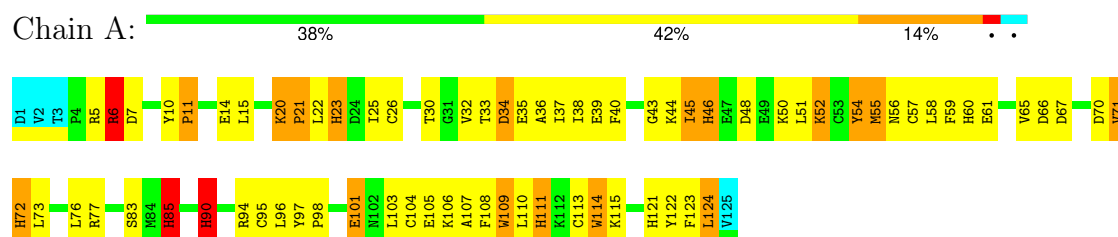
#### 4.2.6 Score per residue for model 6

- Molecule 1: Odorant-binding protein



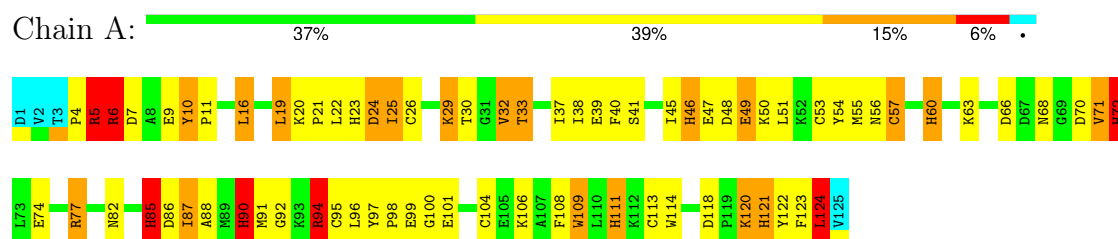
#### 4.2.7 Score per residue for model 7

- Molecule 1: Odorant-binding protein



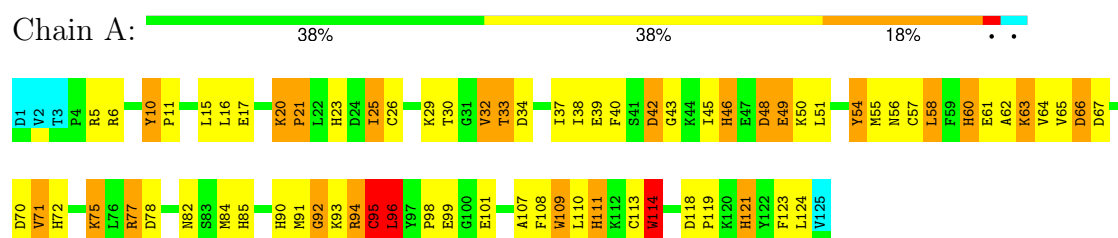
#### 4.2.8 Score per residue for model 8

- Molecule 1: Odorant-binding protein



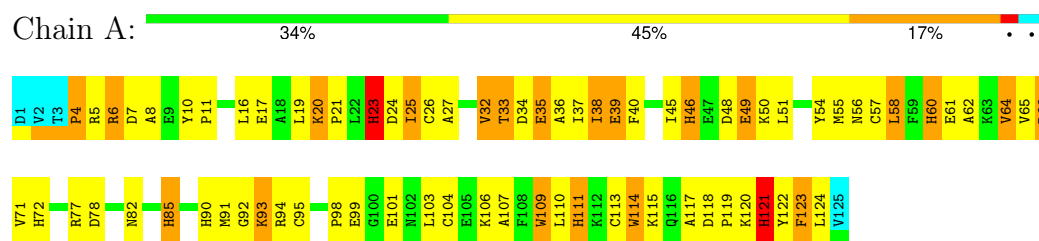
#### 4.2.9 Score per residue for model 9

- Molecule 1: Odorant-binding protein



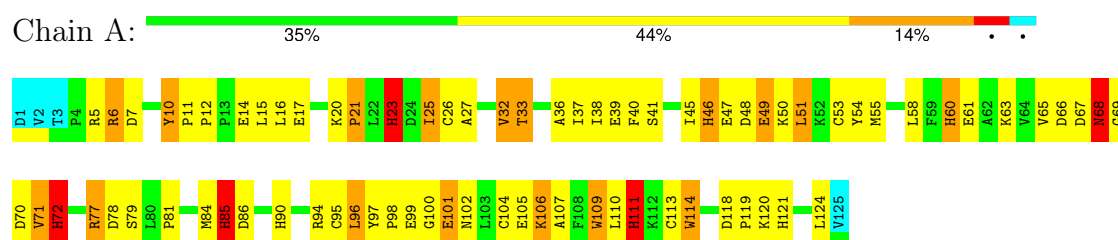
### 4.2.10 Score per residue for model 10

- Molecule 1: Odorant-binding protein



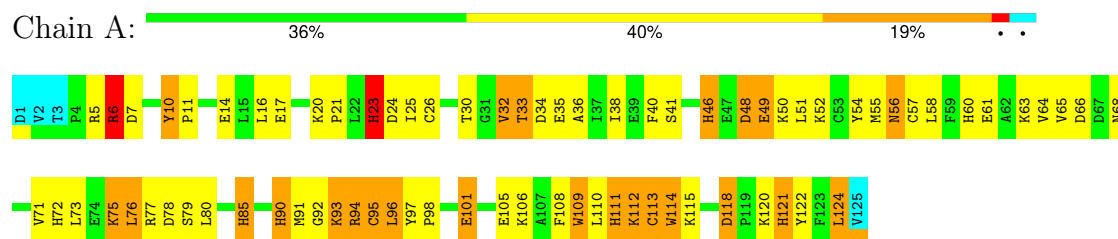
### 4.2.11 Score per residue for model 11

- Molecule 1: Odorant-binding protein



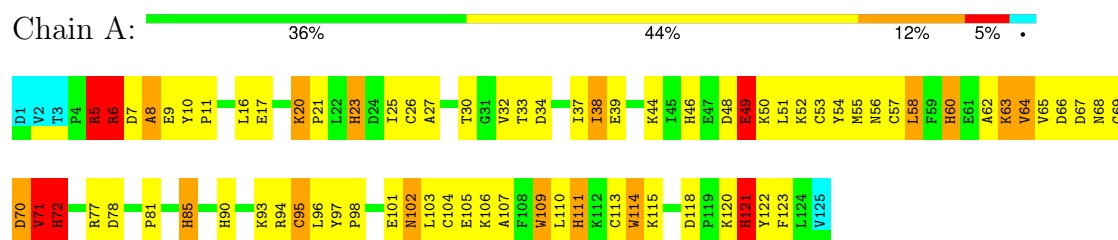
### 4.2.12 Score per residue for model 12

- Molecule 1: Odorant-binding protein



### 4.2.13 Score per residue for model 13

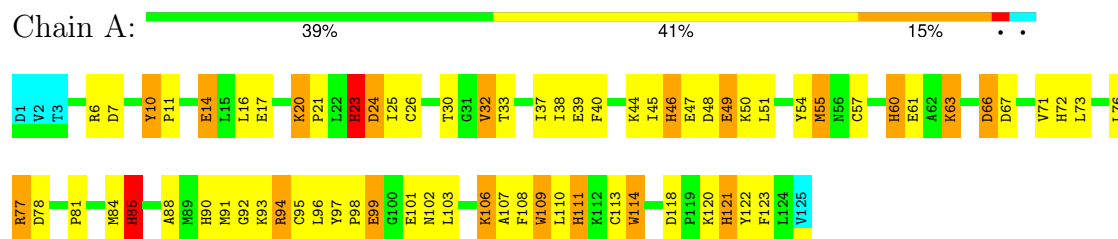
- Molecule 1: Odorant-binding protein





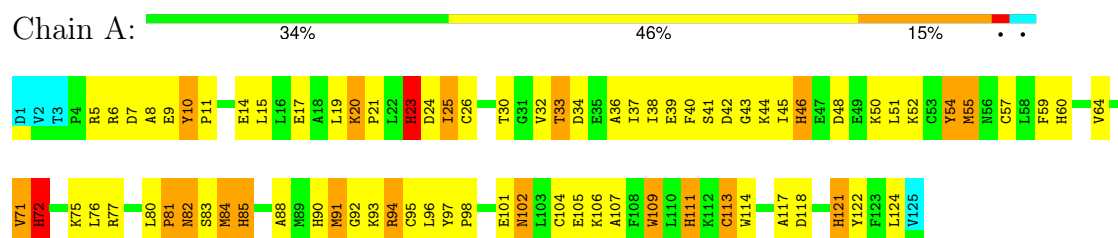
#### 4.2.14 Score per residue for model 14

- Molecule 1: Odorant-binding protein



#### 4.2.15 Score per residue for model 15

- Molecule 1: Odorant-binding protein



## 5 Refinement protocol and experimental data overview ⓘ

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

Of the 30 calculated structures, 15 were deposited, based on the following criterion: *structures with the lowest energy*.

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

No chemical shift data was provided.

## 6 Model quality

### 6.1 Standard geometry

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	1.19±0.00	10±0/1014 ( 1.0± 0.0%)	1.29±0.00	11±0/1368 ( 0.8± 0.0%)
All	All	1.19	150/15210 ( 1.0%)	1.29	163/20520 ( 0.8%)

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	3.7±0.6
All	All	0	55

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	109	TRP	CG-CD2	-7.17	1.31	1.43	13	15
1	A	114	TRP	CG-CD2	-6.58	1.32	1.43	1	15
1	A	111	HIS	CG-ND1	-6.46	1.24	1.38	1	15
1	A	85	HIS	CG-ND1	-6.37	1.24	1.38	13	15
1	A	46	HIS	CG-ND1	-6.33	1.24	1.38	2	15
1	A	121	HIS	CG-ND1	-6.22	1.25	1.38	12	15
1	A	72	HIS	CG-ND1	-6.21	1.25	1.38	2	15
1	A	60	HIS	CG-ND1	-6.19	1.25	1.38	5	15
1	A	23	HIS	CG-ND1	-6.17	1.25	1.38	7	15
1	A	90	HIS	CG-ND1	-6.14	1.25	1.38	2	15

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( $^{\circ}$ )	Ideal( $^{\circ}$ )	Models	
								Worst	Total
1	A	109	TRP	NE1-CE2-CZ2	8.81	140.10	130.40	5	15
1	A	114	TRP	NE1-CE2-CZ2	8.27	139.50	130.40	15	15
1	A	109	TRP	NE1-CE2-CD2	-7.43	99.87	107.30	5	15
1	A	114	TRP	NE1-CE2-CD2	-7.14	100.16	107.30	9	15
1	A	109	TRP	CG-CD1-NE1	-6.71	103.39	110.10	3	15
1	A	114	TRP	CG-CD1-NE1	-6.42	103.67	110.10	10	15
1	A	109	TRP	CD1-CG-CD2	6.12	111.19	106.30	7	15
1	A	114	TRP	CD1-NE1-CE2	5.99	114.39	109.00	2	15
1	A	109	TRP	CD1-NE1-CE2	5.98	114.38	109.00	2	15
1	A	114	TRP	CD1-CG-CD2	5.89	111.01	106.30	15	15
1	A	109	TRP	CG-CD2-CE3	-5.70	128.77	133.90	13	12
1	A	109	TRP	CE2-CD2-CG	5.09	111.37	107.30	13	1

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	6	ARG	Sidechain	15
1	A	77	ARG	Sidechain	15
1	A	94	ARG	Sidechain	13
1	A	5	ARG	Sidechain	12

## 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	986	957	957	74 $\pm$ 8
All	All	14790	14355	14355	1112

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 38.

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

Atom-1	Atom-2	Clash( $\text{\AA}$ )	Distance( $\text{\AA}$ )	Models	
				Worst	Total
1:A:40:PHE:CE2	1:A:45:ILE:HG23	0.91	2.00	5	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:26:CYS:HG	1:A:57:CYS:HG	0.91	1.08	1	1
1:A:32:VAL:HG22	1:A:33:THR:H	0.81	1.35	5	9
1:A:26:CYS:SG	1:A:54:TYR:CD1	0.80	2.75	2	3
1:A:55:MET:SD	1:A:111:HIS:CG	0.80	2.74	11	5
1:A:55:MET:SD	1:A:111:HIS:CD2	0.79	2.75	9	6
1:A:26:CYS:SG	1:A:54:TYR:CD2	0.79	2.76	8	1
1:A:109:TRP:CH2	1:A:113:CYS:SG	0.78	2.76	4	10
1:A:109:TRP:CZ2	1:A:113:CYS:SG	0.78	2.77	13	8
1:A:80:LEU:HD23	1:A:80:LEU:N	0.77	1.94	1	1
1:A:10:TYR:N	1:A:11:PRO:CD	0.76	2.47	7	13
1:A:109:TRP:CZ3	1:A:113:CYS:SG	0.76	2.78	11	7
1:A:76:LEU:HD13	1:A:76:LEU:O	0.75	1.81	7	1
1:A:95:CYS:SG	1:A:96:LEU:N	0.73	2.61	1	3
1:A:32:VAL:HG22	1:A:33:THR:N	0.72	1.99	1	11
1:A:40:PHE:CD2	1:A:51:LEU:CD2	0.72	2.73	8	4
1:A:95:CYS:SG	1:A:114:TRP:NE1	0.71	2.64	3	1
1:A:23:HIS:ND1	1:A:24:ASP:N	0.70	2.39	1	6
1:A:109:TRP:CE3	1:A:113:CYS:SG	0.70	2.84	7	8
1:A:5:ARG:HE	1:A:6:ARG:H	0.70	1.29	3	1
1:A:23:HIS:NE2	1:A:37:ILE:CD1	0.70	2.55	3	3
1:A:22:LEU:O	1:A:22:LEU:HD13	0.69	1.88	1	2
1:A:124:LEU:HD22	1:A:124:LEU:N	0.69	2.02	3	1
1:A:10:TYR:HH	1:A:121:HIS:CE1	0.69	2.06	14	3
1:A:40:PHE:CE1	1:A:45:ILE:HG23	0.68	2.23	14	5
1:A:55:MET:HB3	1:A:107:ALA:HB1	0.68	1.66	2	6
1:A:69:GLY:O	1:A:103:LEU:HD11	0.68	1.88	10	1
1:A:69:GLY:O	1:A:71:VAL:HG23	0.67	1.88	11	1
1:A:23:HIS:ND1	1:A:23:HIS:C	0.67	2.48	5	9
1:A:71:VAL:HG22	1:A:71:VAL:O	0.67	1.90	3	3
1:A:109:TRP:CE2	1:A:113:CYS:SG	0.67	2.88	13	5
1:A:124:LEU:N	1:A:124:LEU:CD2	0.67	2.57	3	1
1:A:64:VAL:HG13	1:A:65:VAL:N	0.66	2.05	10	1
1:A:123:PHE:CG	1:A:124:LEU:N	0.65	2.62	7	2
1:A:40:PHE:CE2	1:A:115:LYS:NZ	0.65	2.64	12	1
1:A:30:THR:HG21	1:A:54:TYR:N	0.65	2.06	7	4
1:A:10:TYR:C	1:A:10:TYR:CD1	0.65	2.70	1	10
1:A:109:TRP:CD2	1:A:113:CYS:SG	0.65	2.90	7	5
1:A:72:HIS:CD2	1:A:74:GLU:CD	0.65	2.70	8	1
1:A:97:TYR:N	1:A:109:TRP:CH2	0.65	2.65	1	7
1:A:103:LEU:HD22	1:A:103:LEU:H	0.65	1.52	1	1
1:A:64:VAL:HG13	1:A:65:VAL:H	0.64	1.52	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:71:VAL:O	1:A:71:VAL:HG13	0.64	1.90	2	1
1:A:40:PHE:CD1	1:A:51:LEU:CD2	0.64	2.81	15	3
1:A:41:SER:OG	1:A:42:ASP:N	0.64	2.30	15	3
1:A:45:ILE:HG12	1:A:115:LYS:HZ3	0.64	1.53	4	1
1:A:124:LEU:CD2	1:A:124:LEU:N	0.64	2.61	15	1
1:A:102:ASN:HD21	1:A:105:GLU:CG	0.63	2.06	13	2
1:A:46:HIS:CE1	1:A:51:LEU:HD12	0.63	2.27	9	2
1:A:97:TYR:N	1:A:98:PRO:CD	0.63	2.60	11	8
1:A:85:HIS:ND1	1:A:85:HIS:C	0.63	2.52	11	7
1:A:10:TYR:OH	1:A:121:HIS:ND1	0.63	2.32	6	1
1:A:32:VAL:CG1	1:A:33:THR:N	0.62	2.62	3	2
1:A:99:GLU:OE1	1:A:100:GLY:N	0.62	2.32	5	1
1:A:66:ASP:OD2	1:A:72:HIS:CD2	0.62	2.53	11	1
1:A:102:ASN:N	1:A:102:ASN:ND2	0.62	2.48	13	2
1:A:123:PHE:CD1	1:A:123:PHE:N	0.62	2.66	1	4
1:A:25:ILE:HG22	1:A:26:CYS:N	0.62	2.10	9	14
1:A:34:ASP:OD1	1:A:35:GLU:N	0.62	2.33	10	3
1:A:73:LEU:CD2	1:A:73:LEU:N	0.62	2.62	3	1
1:A:10:TYR:OH	1:A:121:HIS:CE1	0.62	2.53	10	4
1:A:23:HIS:NE2	1:A:37:ILE:HD13	0.62	2.10	13	3
1:A:16:LEU:C	1:A:16:LEU:HD13	0.61	2.15	10	1
1:A:66:ASP:N	1:A:66:ASP:OD1	0.61	2.32	4	2
1:A:104:CYS:SG	1:A:105:GLU:N	0.61	2.73	7	2
1:A:66:ASP:OD2	1:A:72:HIS:NE2	0.61	2.33	13	1
1:A:10:TYR:OH	1:A:121:HIS:NE2	0.61	2.33	14	1
1:A:104:CYS:SG	1:A:105:GLU:OE1	0.61	2.59	2	1
1:A:23:HIS:HD1	1:A:24:ASP:N	0.61	1.94	3	2
1:A:7:ASP:OD1	1:A:8:ALA:N	0.61	2.33	13	2
1:A:40:PHE:CD2	1:A:115:LYS:NZ	0.61	2.66	12	1
1:A:23:HIS:ND1	1:A:54:TYR:OH	0.61	2.34	4	3
1:A:74:GLU:CG	1:A:75:LYS:N	0.60	2.64	5	1
1:A:39:GLU:OE1	1:A:46:HIS:CD2	0.60	2.54	14	1
1:A:99:GLU:OE2	1:A:100:GLY:N	0.60	2.34	8	2
1:A:26:CYS:CB	1:A:57:CYS:HG	0.60	2.09	1	4
1:A:91:MET:SD	1:A:118:ASP:OD2	0.60	2.59	10	1
1:A:66:ASP:OD2	1:A:72:HIS:CG	0.60	2.55	11	1
1:A:123:PHE:CD2	1:A:124:LEU:N	0.60	2.69	7	2
1:A:14:GLU:CG	1:A:15:LEU:N	0.60	2.65	11	1
1:A:7:ASP:C	1:A:9:GLU:N	0.60	2.55	15	2
1:A:5:ARG:NE	1:A:6:ARG:H	0.60	1.93	3	1
1:A:91:MET:SD	1:A:118:ASP:OD1	0.60	2.59	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:104:CYS:SG	1:A:105:GLU:OE2	0.59	2.59	2	1
1:A:79:SER:OG	1:A:80:LEU:N	0.59	2.33	12	1
1:A:51:LEU:HG	1:A:55:MET:HE1	0.59	1.74	2	2
1:A:14:GLU:N	1:A:14:GLU:CD	0.59	2.56	14	1
1:A:19:LEU:C	1:A:19:LEU:HD13	0.59	2.17	15	1
1:A:54:TYR:CD1	1:A:54:TYR:C	0.58	2.72	9	4
1:A:35:GLU:CG	1:A:36:ALA:N	0.58	2.65	12	1
1:A:26:CYS:SG	1:A:54:TYR:CE1	0.58	2.93	2	3
1:A:22:LEU:HD13	1:A:22:LEU:C	0.58	2.19	3	2
1:A:85:HIS:CG	1:A:86:ASP:N	0.58	2.72	3	3
1:A:55:MET:CG	1:A:111:HIS:CD2	0.58	2.87	1	9
1:A:104:CYS:SG	1:A:105:GLU:CD	0.58	2.82	2	1
1:A:32:VAL:O	1:A:33:THR:HG23	0.58	1.98	12	1
1:A:46:HIS:CE1	1:A:51:LEU:HD22	0.57	2.34	4	4
1:A:102:ASN:ND2	1:A:105:GLU:OE1	0.57	2.37	11	1
1:A:82:ASN:ND2	1:A:82:ASN:N	0.57	2.51	2	2
1:A:16:LEU:HD13	1:A:16:LEU:O	0.57	1.98	10	1
1:A:66:ASP:CG	1:A:67:ASP:N	0.57	2.57	1	6
1:A:124:LEU:C	1:A:124:LEU:HD13	0.57	2.20	1	1
1:A:25:ILE:CG2	1:A:26:CYS:N	0.57	2.67	3	4
1:A:121:HIS:O	1:A:123:PHE:N	0.57	2.38	10	2
1:A:7:ASP:C	1:A:9:GLU:H	0.57	2.03	15	2
1:A:82:ASN:ND2	1:A:83:SER:N	0.57	2.53	15	1
1:A:59:PHE:CD2	1:A:71:VAL:CG2	0.56	2.87	4	1
1:A:32:VAL:CG2	1:A:33:THR:N	0.56	2.67	2	9
1:A:32:VAL:HG12	1:A:33:THR:N	0.56	2.13	7	2
1:A:80:LEU:N	1:A:80:LEU:CD2	0.56	2.61	1	1
1:A:5:ARG:CG	1:A:6:ARG:N	0.56	2.68	13	3
1:A:23:HIS:C	1:A:23:HIS:HD1	0.56	2.03	3	1
1:A:7:ASP:O	1:A:9:GLU:N	0.56	2.39	15	5
1:A:73:LEU:N	1:A:73:LEU:HD22	0.56	2.16	3	1
1:A:10:TYR:OH	1:A:121:HIS:CD2	0.55	2.59	14	2
1:A:32:VAL:CG2	1:A:33:THR:H	0.55	2.15	1	7
1:A:107:ALA:O	1:A:111:HIS:ND1	0.55	2.38	1	4
1:A:101:GLU:N	1:A:105:GLU:OE1	0.55	2.40	5	2
1:A:65:VAL:HG12	1:A:71:VAL:HA	0.55	1.78	3	2
1:A:52:LYS:NZ	1:A:108:PHE:CD2	0.55	2.75	12	1
1:A:38:ILE:HG22	1:A:39:GLU:N	0.55	2.16	11	12
1:A:96:LEU:O	1:A:97:TYR:CD2	0.55	2.60	14	6
1:A:71:VAL:HG12	1:A:71:VAL:O	0.55	1.99	9	1
1:A:77:ARG:NH2	1:A:78:ASP:OD1	0.55	2.40	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:ASP:N	1:A:7:ASP:OD1	0.54	2.40	4	2
1:A:124:LEU:C	1:A:124:LEU:HD23	0.54	2.22	12	3
1:A:48:ASP:O	1:A:50:LYS:N	0.54	2.41	12	14
1:A:5:ARG:HE	1:A:6:ARG:N	0.54	2.00	3	1
1:A:23:HIS:CE1	1:A:27:ALA:CB	0.54	2.90	5	2
1:A:96:LEU:O	1:A:97:TYR:CG	0.54	2.61	4	11
1:A:26:CYS:SG	1:A:61:GLU:OE1	0.54	2.59	5	1
1:A:19:LEU:HD13	1:A:19:LEU:O	0.54	2.03	15	1
1:A:96:LEU:O	1:A:97:TYR:CD1	0.54	2.61	15	3
1:A:82:ASN:N	1:A:82:ASN:HD22	0.54	1.99	2	1
1:A:30:THR:HG21	1:A:54:TYR:HB2	0.54	1.80	8	3
1:A:46:HIS:O	1:A:48:ASP:N	0.54	2.41	8	3
1:A:42:ASP:N	1:A:42:ASP:OD1	0.54	2.38	9	1
1:A:55:MET:SD	1:A:107:ALA:O	0.54	2.66	11	1
1:A:89:MET:SD	1:A:89:MET:C	0.53	2.87	4	1
1:A:40:PHE:CD2	1:A:51:LEU:HD21	0.53	2.38	5	2
1:A:92:GLY:O	1:A:94:ARG:N	0.53	2.41	12	2
1:A:124:LEU:HD13	1:A:124:LEU:O	0.53	2.04	1	1
1:A:113:CYS:SG	1:A:114:TRP:N	0.53	2.82	5	3
1:A:40:PHE:CZ	1:A:45:ILE:HG23	0.53	2.36	5	2
1:A:102:ASN:N	1:A:106:LYS:HZ3	0.53	2.00	5	1
1:A:60:HIS:NE2	1:A:103:LEU:HD13	0.53	2.19	13	1
1:A:76:LEU:HD23	1:A:76:LEU:O	0.53	2.03	1	3
1:A:120:LYS:O	1:A:122:TYR:N	0.53	2.42	5	4
1:A:95:CYS:HG	1:A:114:TRP:HE1	0.53	1.38	3	1
1:A:23:HIS:CE1	1:A:37:ILE:HD13	0.53	2.38	13	2
1:A:97:TYR:N	1:A:98:PRO:HD3	0.53	2.17	12	7
1:A:66:ASP:CG	1:A:67:ASP:H	0.53	2.07	2	5
1:A:66:ASP:OD2	1:A:67:ASP:N	0.53	2.42	7	1
1:A:69:GLY:C	1:A:71:VAL:H	0.53	2.06	11	1
1:A:75:LYS:O	1:A:79:SER:N	0.53	2.42	12	1
1:A:61:GLU:N	1:A:61:GLU:OE1	0.53	2.42	3	1
1:A:94:ARG:O	1:A:95:CYS:SG	0.53	2.66	14	3
1:A:91:MET:SD	1:A:117:ALA:HB3	0.53	2.44	15	1
1:A:54:TYR:O	1:A:57:CYS:N	0.53	2.42	9	1
1:A:55:MET:O	1:A:58:LEU:N	0.52	2.43	10	6
1:A:40:PHE:CD1	1:A:51:LEU:HD21	0.52	2.40	1	1
1:A:67:ASP:O	1:A:68:ASN:ND2	0.52	2.42	1	2
1:A:110:LEU:O	1:A:113:CYS:N	0.52	2.42	2	7
1:A:109:TRP:O	1:A:113:CYS:SG	0.52	2.67	14	7
1:A:7:ASP:O	1:A:11:PRO:CD	0.52	2.57	8	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:36:ALA:O	1:A:46:HIS:NE2	0.52	2.41	12	7
1:A:118:ASP:C	1:A:120:LYS:H	0.52	2.07	10	4
1:A:23:HIS:CD2	1:A:37:ILE:HD13	0.52	2.39	10	1
1:A:69:GLY:O	1:A:71:VAL:N	0.52	2.43	11	1
1:A:95:CYS:O	1:A:96:LEU:CB	0.52	2.56	4	5
1:A:84:MET:O	1:A:88:ALA:N	0.52	2.41	15	3
1:A:46:HIS:O	1:A:46:HIS:ND1	0.52	2.43	11	1
1:A:51:LEU:O	1:A:55:MET:SD	0.52	2.67	3	8
1:A:118:ASP:O	1:A:120:LYS:N	0.52	2.43	10	3
1:A:23:HIS:C	1:A:23:HIS:CD2	0.52	2.83	6	3
1:A:55:MET:SD	1:A:107:ALA:C	0.52	2.87	11	1
1:A:51:LEU:CG	1:A:55:MET:HE1	0.52	2.34	3	2
1:A:95:CYS:SG	1:A:95:CYS:O	0.52	2.67	3	3
1:A:122:TYR:O	1:A:123:PHE:CB	0.52	2.56	10	1
1:A:80:LEU:O	1:A:85:HIS:CE1	0.52	2.62	15	1
1:A:26:CYS:O	1:A:29:LYS:N	0.52	2.42	9	3
1:A:111:HIS:ND1	1:A:122:TYR:OH	0.52	2.41	15	3
1:A:65:VAL:HG23	1:A:66:ASP:N	0.52	2.20	6	1
1:A:76:LEU:HD13	1:A:76:LEU:C	0.52	2.25	7	1
1:A:101:GLU:CG	1:A:105:GLU:OE2	0.52	2.58	3	1
1:A:64:VAL:O	1:A:72:HIS:N	0.52	2.43	15	2
1:A:85:HIS:ND1	1:A:85:HIS:O	0.52	2.43	5	1
1:A:60:HIS:O	1:A:63:LYS:N	0.52	2.42	14	4
1:A:124:LEU:N	1:A:124:LEU:HD22	0.52	2.19	15	1
1:A:38:ILE:O	1:A:41:SER:N	0.51	2.42	2	6
1:A:76:LEU:C	1:A:76:LEU:HD23	0.51	2.25	15	1
1:A:66:ASP:C	1:A:68:ASN:H	0.51	2.07	13	3
1:A:60:HIS:O	1:A:62:ALA:N	0.51	2.43	9	2
1:A:110:LEU:O	1:A:113:CYS:SG	0.51	2.69	12	3
1:A:62:ALA:CB	1:A:64:VAL:HG13	0.51	2.34	5	1
1:A:66:ASP:OD1	1:A:72:HIS:CG	0.51	2.61	6	1
1:A:26:CYS:SG	1:A:54:TYR:O	0.51	2.69	14	2
1:A:66:ASP:O	1:A:68:ASN:N	0.51	2.44	13	2
1:A:48:ASP:OD2	1:A:51:LEU:N	0.51	2.41	1	1
1:A:97:TYR:O	1:A:109:TRP:CZ2	0.51	2.64	1	2
1:A:95:CYS:SG	1:A:114:TRP:CD1	0.51	3.00	3	1
1:A:59:PHE:CD2	1:A:71:VAL:HG21	0.51	2.39	4	1
1:A:102:ASN:OD1	1:A:104:CYS:SG	0.51	2.68	5	1
1:A:95:CYS:SG	1:A:117:ALA:HB2	0.51	2.46	10	1
1:A:102:ASN:ND2	1:A:102:ASN:H	0.51	2.03	13	1
1:A:110:LEU:O	1:A:114:TRP:N	0.51	2.40	1	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:ARG:O	1:A:11:PRO:CD	0.51	2.59	6	1
1:A:99:GLU:CD	1:A:99:GLU:C	0.51	2.68	8	2
1:A:87:ILE:O	1:A:91:MET:SD	0.51	2.68	8	1
1:A:99:GLU:CD	1:A:100:GLY:N	0.51	2.64	8	1
1:A:66:ASP:C	1:A:68:ASN:N	0.51	2.64	13	3
1:A:91:MET:O	1:A:93:LYS:N	0.51	2.44	9	3
1:A:45:ILE:HD13	1:A:112:LYS:HG3	0.51	1.82	4	1
1:A:91:MET:SD	1:A:118:ASP:CG	0.51	2.89	10	1
1:A:69:GLY:C	1:A:71:VAL:N	0.51	2.64	11	1
1:A:49:GLU:N	1:A:49:GLU:OE1	0.51	2.44	13	1
1:A:102:ASN:N	1:A:106:LYS:NZ	0.50	2.59	5	1
1:A:92:GLY:C	1:A:94:ARG:H	0.50	2.09	8	1
1:A:124:LEU:C	1:A:124:LEU:CD2	0.50	2.80	12	3
1:A:95:CYS:SG	1:A:113:CYS:SG	0.50	3.09	12	1
1:A:84:MET:SD	1:A:84:MET:N	0.50	2.84	2	1
1:A:95:CYS:SG	1:A:113:CYS:C	0.50	2.90	7	1
1:A:122:TYR:CE1	1:A:123:PHE:O	0.50	2.65	7	1
1:A:60:HIS:C	1:A:62:ALA:N	0.50	2.65	9	2
1:A:64:VAL:CG1	1:A:65:VAL:N	0.50	2.74	10	1
1:A:58:LEU:O	1:A:58:LEU:HD13	0.50	2.06	13	1
1:A:66:ASP:OD1	1:A:72:HIS:N	0.50	2.45	4	1
1:A:95:CYS:O	1:A:95:CYS:SG	0.50	2.69	9	1
1:A:17:GLU:O	1:A:21:PRO:CD	0.50	2.60	2	11
1:A:10:TYR:N	1:A:11:PRO:HD3	0.50	2.22	3	3
1:A:25:ILE:CG2	1:A:61:GLU:OE2	0.50	2.60	14	2
1:A:13:PRO:O	1:A:16:LEU:N	0.50	2.43	3	1
1:A:55:MET:HG3	1:A:111:HIS:CD2	0.50	2.42	1	3
1:A:10:TYR:N	1:A:11:PRO:HD2	0.50	2.20	11	11
1:A:120:LYS:C	1:A:122:TYR:N	0.50	2.64	5	4
1:A:45:ILE:H	1:A:115:LYS:HZ1	0.50	1.48	4	1
1:A:96:LEU:C	1:A:97:TYR:CG	0.50	2.85	15	3
1:A:95:CYS:SG	1:A:113:CYS:O	0.50	2.70	7	1
1:A:108:PHE:CE2	1:A:112:LYS:CE	0.50	2.95	12	1
1:A:10:TYR:CE1	1:A:121:HIS:CD2	0.50	3.00	4	1
1:A:101:GLU:C	1:A:102:ASN:ND2	0.49	2.65	6	1
1:A:107:ALA:O	1:A:111:HIS:CD2	0.49	2.65	10	1
1:A:39:GLU:O	1:A:43:GLY:CA	0.49	2.60	7	4
1:A:77:ARG:CD	1:A:77:ARG:C	0.49	2.81	6	1
1:A:40:PHE:CE2	1:A:115:LYS:CE	0.49	2.94	12	1
1:A:91:MET:C	1:A:93:LYS:N	0.49	2.65	1	3
1:A:124:LEU:N	1:A:124:LEU:HD12	0.49	2.21	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:40:PHE:HB2	1:A:46:HIS:HE2	0.49	1.67	1	2
1:A:100:GLY:C	1:A:105:GLU:OE1	0.49	2.51	5	1
1:A:121:HIS:CG	1:A:122:TYR:N	0.49	2.79	10	1
1:A:95:CYS:O	1:A:97:TYR:CE2	0.49	2.66	13	1
1:A:102:ASN:N	1:A:102:ASN:HD22	0.49	2.04	15	1
1:A:20:LYS:N	1:A:21:PRO:HD2	0.49	2.22	12	15
1:A:48:ASP:O	1:A:51:LEU:N	0.49	2.46	1	5
1:A:55:MET:HG2	1:A:111:HIS:CD2	0.49	2.43	1	11
1:A:54:TYR:CD1	1:A:54:TYR:O	0.49	2.65	11	1
1:A:20:LYS:N	1:A:21:PRO:CD	0.49	2.75	7	14
1:A:82:ASN:O	1:A:85:HIS:CD2	0.49	2.66	3	1
1:A:103:LEU:N	1:A:103:LEU:CD1	0.49	2.75	5	1
1:A:101:GLU:O	1:A:102:ASN:ND2	0.49	2.46	6	1
1:A:66:ASP:O	1:A:67:ASP:CB	0.49	2.61	11	2
1:A:62:ALA:O	1:A:63:LYS:CB	0.48	2.61	13	4
1:A:63:LYS:C	1:A:65:VAL:H	0.48	2.11	13	2
1:A:45:ILE:CG1	1:A:115:LYS:NZ	0.48	2.76	4	1
1:A:70:ASP:O	1:A:71:VAL:C	0.48	2.51	2	5
1:A:112:LYS:O	1:A:116:GLN:NE2	0.48	2.46	5	1
1:A:90:HIS:O	1:A:94:ARG:CZ	0.48	2.62	4	1
1:A:50:LYS:C	1:A:52:LYS:N	0.48	2.64	7	3
1:A:34:ASP:OD1	1:A:34:ASP:N	0.48	2.46	9	3
1:A:16:LEU:HD23	1:A:16:LEU:O	0.48	2.07	14	2
1:A:14:GLU:CD	1:A:14:GLU:C	0.48	2.72	12	2
1:A:71:VAL:O	1:A:71:VAL:CG1	0.48	2.61	2	1
1:A:99:GLU:O	1:A:99:GLU:CG	0.48	2.61	9	2
1:A:20:LYS:CB	1:A:21:PRO:CD	0.48	2.91	2	1
1:A:39:GLU:O	1:A:43:GLY:N	0.48	2.47	2	2
1:A:85:HIS:O	1:A:88:ALA:HB3	0.48	2.08	2	1
1:A:10:TYR:H	1:A:11:PRO:CD	0.48	2.20	8	5
1:A:94:ARG:O	1:A:96:LEU:N	0.48	2.45	3	1
1:A:94:ARG:C	1:A:95:CYS:SG	0.48	2.91	5	1
1:A:25:ILE:HG21	1:A:61:GLU:OE2	0.48	2.09	12	1
1:A:92:GLY:O	1:A:93:LYS:C	0.48	2.51	12	5
1:A:90:HIS:O	1:A:94:ARG:NH2	0.48	2.47	4	1
1:A:35:GLU:HG2	1:A:36:ALA:N	0.48	2.24	12	1
1:A:86:ASP:OD1	1:A:90:HIS:CE1	0.47	2.66	1	1
1:A:23:HIS:NE2	1:A:37:ILE:HD11	0.47	2.23	3	1
1:A:30:THR:HG21	1:A:54:TYR:CA	0.47	2.39	7	1
1:A:68:ASN:HD22	1:A:68:ASN:C	0.47	2.12	11	1
1:A:50:LYS:O	1:A:53:CYS:N	0.47	2.48	8	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:27:ALA:HB2	1:A:54:TYR:CZ	0.47	2.44	11	1
1:A:56:ASN:ND2	1:A:56:ASN:C	0.47	2.65	12	1
1:A:7:ASP:CG	1:A:8:ALA:N	0.47	2.67	13	1
1:A:99:GLU:CG	1:A:99:GLU:O	0.47	2.62	14	1
1:A:120:LYS:C	1:A:122:TYR:H	0.47	2.13	5	2
1:A:59:PHE:O	1:A:64:VAL:HG22	0.47	2.09	15	1
1:A:6:ARG:HH22	1:A:42:ASP:CG	0.47	2.12	2	1
1:A:110:LEU:HD23	1:A:114:TRP:CH2	0.47	2.44	9	1
1:A:97:TYR:O	1:A:109:TRP:CE2	0.47	2.67	1	2
1:A:87:ILE:HG21	1:A:121:HIS:CE1	0.47	2.44	4	1
1:A:34:ASP:O	1:A:38:ILE:HD13	0.47	2.08	13	2
1:A:82:ASN:ND2	1:A:82:ASN:H	0.47	2.07	1	1
1:A:119:PRO:C	1:A:121:HIS:H	0.47	2.14	9	1
1:A:32:VAL:HG22	1:A:50:LYS:HB3	0.47	1.85	12	1
1:A:98:PRO:HA	1:A:109:TRP:CD2	0.46	2.45	3	12
1:A:64:VAL:CG1	1:A:65:VAL:H	0.46	2.22	10	1
1:A:91:MET:SD	1:A:117:ALA:HB1	0.46	2.51	2	1
1:A:85:HIS:ND1	1:A:86:ASP:N	0.46	2.62	3	1
1:A:59:PHE:CD1	1:A:59:PHE:N	0.46	2.83	7	2
1:A:88:ALA:O	1:A:92:GLY:N	0.46	2.42	15	3
1:A:124:LEU:HD22	1:A:124:LEU:H	0.46	1.69	3	2
1:A:106:LYS:O	1:A:109:TRP:N	0.46	2.47	8	2
1:A:45:ILE:CG1	1:A:115:LYS:HZ3	0.46	2.21	4	1
1:A:85:HIS:C	1:A:85:HIS:HD1	0.46	2.12	6	1
1:A:55:MET:CE	1:A:111:HIS:CG	0.46	2.98	12	2
1:A:32:VAL:HG12	1:A:33:THR:H	0.46	1.69	12	1
1:A:40:PHE:CD1	1:A:51:LEU:HD22	0.46	2.44	15	1
1:A:21:PRO:O	1:A:24:ASP:N	0.46	2.49	8	1
1:A:40:PHE:CD2	1:A:51:LEU:HD23	0.46	2.45	8	1
1:A:92:GLY:C	1:A:94:ARG:N	0.46	2.68	8	1
1:A:102:ASN:HD22	1:A:102:ASN:H	0.46	1.54	15	1
1:A:6:ARG:HH21	1:A:41:SER:CB	0.46	2.24	2	1
1:A:45:ILE:HD11	1:A:115:LYS:HD2	0.46	1.87	5	1
1:A:90:HIS:ND1	1:A:90:HIS:N	0.46	2.64	7	1
1:A:17:GLU:O	1:A:21:PRO:CG	0.46	2.63	15	6
1:A:74:GLU:HG3	1:A:75:LYS:N	0.46	2.26	5	1
1:A:108:PHE:CD1	1:A:108:PHE:O	0.46	2.68	8	1
1:A:7:ASP:O	1:A:11:PRO:CG	0.46	2.64	12	2
1:A:20:LYS:O	1:A:24:ASP:N	0.46	2.45	10	1
1:A:55:MET:CE	1:A:111:HIS:ND1	0.46	2.79	12	2
1:A:56:ASN:ND2	1:A:56:ASN:O	0.46	2.47	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:65:VAL:CG2	1:A:66:ASP:N	0.46	2.79	2	1
1:A:41:SER:CB	1:A:124:LEU:O	0.46	2.64	11	1
1:A:63:LYS:C	1:A:65:VAL:N	0.46	2.68	3	1
1:A:94:ARG:O	1:A:95:CYS:CB	0.45	2.63	5	1
1:A:91:MET:SD	1:A:117:ALA:CB	0.45	3.05	15	2
1:A:99:GLU:HG2	1:A:109:TRP:CD1	0.45	2.47	3	3
1:A:103:LEU:N	1:A:103:LEU:HD23	0.45	2.26	7	2
1:A:65:VAL:C	1:A:67:ASP:H	0.45	2.14	9	1
1:A:123:PHE:O	1:A:123:PHE:CD2	0.45	2.69	8	1
1:A:44:LYS:O	1:A:45:ILE:C	0.45	2.54	4	3
1:A:100:GLY:O	1:A:101:GLU:CB	0.45	2.64	6	1
1:A:73:LEU:HD22	1:A:73:LEU:N	0.45	2.27	12	1
1:A:109:TRP:C	1:A:109:TRP:CE3	0.45	2.90	2	1
1:A:43:GLY:O	1:A:44:LYS:CB	0.45	2.63	5	1
1:A:27:ALA:N	1:A:54:TYR:CE1	0.45	2.85	13	3
1:A:45:ILE:HG12	1:A:115:LYS:NZ	0.45	2.25	4	1
1:A:14:GLU:CD	1:A:15:LEU:N	0.45	2.70	15	1
1:A:19:LEU:C	1:A:19:LEU:CD1	0.45	2.85	15	1
1:A:91:MET:C	1:A:93:LYS:H	0.45	2.15	9	3
1:A:61:GLU:OE1	1:A:61:GLU:CA	0.45	2.64	3	1
1:A:71:VAL:O	1:A:71:VAL:CG2	0.45	2.63	8	2
1:A:14:GLU:HG2	1:A:15:LEU:N	0.45	2.27	11	1
1:A:110:LEU:CD2	1:A:114:TRP:CH2	0.45	2.99	12	1
1:A:10:TYR:CG	1:A:11:PRO:HD3	0.44	2.47	1	3
1:A:54:TYR:O	1:A:55:MET:C	0.44	2.53	9	1
1:A:17:GLU:CD	1:A:17:GLU:C	0.44	2.76	11	1
1:A:124:LEU:C	1:A:124:LEU:CD1	0.44	2.85	1	1
1:A:99:GLU:OE2	1:A:100:GLY:CA	0.44	2.65	8	1
1:A:103:LEU:N	1:A:103:LEU:HD13	0.44	2.27	1	1
1:A:71:VAL:HG11	1:A:110:LEU:CD1	0.44	2.41	2	1
1:A:55:MET:HG2	1:A:111:HIS:NE2	0.44	2.27	10	4
1:A:29:LYS:HZ2	1:A:29:LYS:HB3	0.44	1.72	2	1
1:A:98:PRO:HA	1:A:109:TRP:CG	0.44	2.48	12	3
1:A:10:TYR:CD2	1:A:11:PRO:HD3	0.44	2.48	1	6
1:A:101:GLU:O	1:A:101:GLU:CG	0.44	2.65	12	2
1:A:54:TYR:O	1:A:57:CYS:CB	0.44	2.66	9	1
1:A:46:HIS:NE2	1:A:51:LEU:HD22	0.44	2.28	4	2
1:A:48:ASP:O	1:A:49:GLU:C	0.44	2.56	1	12
1:A:10:TYR:H	1:A:11:PRO:HD3	0.44	1.73	3	2
1:A:6:ARG:O	1:A:6:ARG:CG	0.44	2.64	12	1
1:A:108:PHE:CE2	1:A:112:LYS:HE3	0.44	2.46	12	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:56:ASN:OD1	1:A:60:HIS:NE2	0.44	2.51	5	1
1:A:103:LEU:N	1:A:103:LEU:HD12	0.44	2.27	5	1
1:A:51:LEU:HD22	1:A:55:MET:CE	0.44	2.43	9	1
1:A:37:ILE:CG2	1:A:124:LEU:HD22	0.44	2.43	11	1
1:A:66:ASP:OD2	1:A:67:ASP:OD1	0.44	2.36	7	1
1:A:5:ARG:HD3	1:A:6:ARG:N	0.44	2.28	8	1
1:A:19:LEU:O	1:A:19:LEU:HD13	0.44	2.13	8	1
1:A:66:ASP:OD2	1:A:67:ASP:CG	0.44	2.57	5	1
1:A:48:ASP:CG	1:A:51:LEU:H	0.44	2.14	7	1
1:A:106:LYS:O	1:A:107:ALA:C	0.43	2.57	10	7
1:A:82:ASN:O	1:A:85:HIS:N	0.43	2.51	3	1
1:A:77:ARG:CD	1:A:78:ASP:N	0.43	2.81	6	1
1:A:96:LEU:O	1:A:96:LEU:HD13	0.43	2.13	9	1
1:A:51:LEU:HD23	1:A:51:LEU:O	0.43	2.13	11	1
1:A:10:TYR:CB	1:A:11:PRO:HD3	0.43	2.44	6	5
1:A:22:LEU:C	1:A:22:LEU:CD1	0.43	2.87	3	1
1:A:63:LYS:O	1:A:65:VAL:N	0.43	2.51	3	1
1:A:60:HIS:C	1:A:62:ALA:H	0.43	2.17	10	2
1:A:40:PHE:O	1:A:115:LYS:NZ	0.43	2.50	12	2
1:A:6:ARG:O	1:A:7:ASP:C	0.43	2.55	6	1
1:A:23:HIS:CG	1:A:54:TYR:OH	0.43	2.72	13	1
1:A:85:HIS:O	1:A:88:ALA:N	0.43	2.50	8	1
1:A:5:ARG:HG3	1:A:6:ARG:N	0.43	2.29	13	1
1:A:34:ASP:HA	1:A:37:ILE:HD12	0.43	1.91	13	1
1:A:48:ASP:OD1	1:A:48:ASP:C	0.43	2.57	6	3
1:A:121:HIS:O	1:A:121:HIS:CD2	0.43	2.72	15	1
1:A:26:CYS:SG	1:A:57:CYS:CB	0.43	3.07	8	1
1:A:52:LYS:NZ	1:A:108:PHE:CG	0.43	2.84	12	1
1:A:76:LEU:C	1:A:76:LEU:CD1	0.43	2.87	12	1
1:A:102:ASN:CG	1:A:104:CYS:SG	0.43	2.97	13	1
1:A:77:ARG:C	1:A:79:SER:N	0.43	2.72	5	2
1:A:118:ASP:C	1:A:120:LYS:N	0.43	2.72	10	2
1:A:55:MET:CE	1:A:111:HIS:CD2	0.43	3.02	11	1
1:A:73:LEU:N	1:A:73:LEU:CD2	0.43	2.82	12	1
1:A:20:LYS:CB	1:A:21:PRO:HD3	0.43	2.43	2	2
1:A:26:CYS:SG	1:A:57:CYS:HB3	0.43	2.54	8	3
1:A:120:LYS:N	1:A:120:LYS:HD3	0.43	2.28	5	1
1:A:64:VAL:O	1:A:75:LYS:NZ	0.43	2.51	9	1
1:A:106:LYS:O	1:A:108:PHE:N	0.43	2.51	14	1
1:A:5:ARG:HG2	1:A:6:ARG:N	0.42	2.28	1	2
1:A:48:ASP:C	1:A:50:LYS:N	0.42	2.73	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:LYS:HB2	1:A:20:LYS:HZ3	0.42	1.74	14	1
1:A:77:ARG:CG	1:A:78:ASP:N	0.42	2.82	6	1
1:A:106:LYS:C	1:A:108:PHE:N	0.42	2.70	14	2
1:A:30:THR:HB	1:A:32:VAL:HG23	0.42	1.90	12	1
1:A:124:LEU:N	1:A:124:LEU:CD1	0.42	2.82	4	1
1:A:40:PHE:CE1	1:A:45:ILE:CG2	0.42	2.99	14	1
1:A:92:GLY:O	1:A:95:CYS:SG	0.42	2.68	14	1
1:A:6:ARG:O	1:A:7:ASP:CB	0.42	2.65	2	1
1:A:121:HIS:O	1:A:121:HIS:CG	0.42	2.72	6	1
1:A:110:LEU:HB3	1:A:114:TRP:CZ3	0.42	2.49	11	3
1:A:65:VAL:HG12	1:A:71:VAL:CA	0.42	2.44	3	2
1:A:86:ASP:O	1:A:90:HIS:ND1	0.42	2.53	8	1
1:A:50:LYS:O	1:A:51:LEU:C	0.42	2.58	9	6
1:A:37:ILE:HG23	1:A:124:LEU:HD13	0.42	1.90	9	1
1:A:6:ARG:CG	1:A:6:ARG:HH11	0.42	2.27	2	1
1:A:99:GLU:OE1	1:A:99:GLU:C	0.42	2.58	5	1
1:A:66:ASP:CG	1:A:67:ASP:OD1	0.42	2.58	7	1
1:A:10:TYR:CD1	1:A:11:PRO:N	0.42	2.88	8	1
1:A:120:LYS:O	1:A:121:HIS:C	0.42	2.58	13	1
1:A:73:LEU:HD13	1:A:96:LEU:HD11	0.42	1.92	2	1
1:A:16:LEU:C	1:A:16:LEU:CD1	0.42	2.86	10	1
1:A:70:ASP:C	1:A:71:VAL:CG2	0.42	2.88	13	1
1:A:102:ASN:H	1:A:102:ASN:HD22	0.42	1.57	13	1
1:A:59:PHE:CD2	1:A:71:VAL:CG1	0.42	3.03	15	1
1:A:50:LYS:O	1:A:52:LYS:N	0.42	2.53	15	2
1:A:16:LEU:HD12	1:A:16:LEU:N	0.42	2.30	12	1
1:A:7:ASP:CG	1:A:8:ALA:H	0.42	2.17	13	1
1:A:62:ALA:C	1:A:64:VAL:H	0.42	2.18	13	1
1:A:69:GLY:HA3	1:A:103:LEU:HD21	0.42	1.90	13	1
1:A:82:ASN:CG	1:A:83:SER:N	0.42	2.73	3	1
1:A:37:ILE:HD12	1:A:37:ILE:H	0.42	1.75	8	1
1:A:56:ASN:C	1:A:56:ASN:HD22	0.42	2.16	12	1
1:A:55:MET:CB	1:A:107:ALA:HB1	0.41	2.42	2	1
1:A:5:ARG:O	1:A:6:ARG:CB	0.41	2.68	5	1
1:A:12:PRO:HG2	1:A:84:MET:SD	0.41	2.55	11	1
1:A:115:LYS:HG3	1:A:122:TYR:CD1	0.41	2.50	7	1
1:A:121:HIS:O	1:A:123:PHE:CE2	0.41	2.73	9	1
1:A:123:PHE:O	1:A:124:LEU:C	0.41	2.58	5	1
1:A:51:LEU:HD21	1:A:55:MET:HE1	0.41	1.93	14	1
1:A:52:LYS:HG2	1:A:108:PHE:CD1	0.41	2.51	5	2
1:A:23:HIS:CE1	1:A:54:TYR:HH	0.41	2.27	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:ILE:O	1:A:40:PHE:N	0.41	2.54	3	1
1:A:55:MET:O	1:A:56:ASN:C	0.41	2.58	9	1
1:A:112:LYS:HZ2	1:A:112:LYS:CB	0.41	2.29	12	1
1:A:72:HIS:CD2	1:A:74:GLU:OE2	0.41	2.72	8	1
1:A:72:HIS:NE2	1:A:74:GLU:OE2	0.41	2.53	8	1
1:A:64:VAL:O	1:A:64:VAL:HG23	0.41	2.14	4	1
1:A:109:TRP:O	1:A:113:CYS:N	0.41	2.53	5	1
1:A:6:ARG:O	1:A:6:ARG:CD	0.41	2.69	12	1
1:A:55:MET:HG3	1:A:111:HIS:NE2	0.41	2.30	15	4
1:A:59:PHE:N	1:A:59:PHE:CD1	0.41	2.88	6	1
1:A:21:PRO:O	1:A:22:LEU:C	0.41	2.59	8	1
1:A:53:CYS:C	1:A:55:MET:N	0.41	2.72	11	1
1:A:24:ASP:O	1:A:28:LYS:CB	0.41	2.69	2	1
1:A:33:THR:O	1:A:34:ASP:C	0.41	2.59	2	1
1:A:10:TYR:CZ	1:A:121:HIS:CD2	0.41	3.09	4	2
1:A:39:GLU:O	1:A:43:GLY:C	0.41	2.60	5	2
1:A:115:LYS:HB2	1:A:122:TYR:CZ	0.41	2.51	5	1
1:A:14:GLU:HG3	1:A:15:LEU:N	0.41	2.31	7	1
1:A:22:LEU:HD11	1:A:61:GLU:OE1	0.41	2.16	7	1
1:A:26:CYS:SG	1:A:61:GLU:HB2	0.41	2.56	11	1
1:A:91:MET:SD	1:A:118:ASP:CB	0.41	3.09	12	1
1:A:58:LEU:HD13	1:A:58:LEU:C	0.41	2.35	13	1
1:A:14:GLU:N	1:A:14:GLU:OE2	0.41	2.53	14	1
1:A:102:ASN:O	1:A:106:LYS:CE	0.41	2.68	14	1
1:A:23:HIS:CE1	1:A:27:ALA:HB2	0.41	2.51	5	1
1:A:78:ASP:OD1	1:A:78:ASP:N	0.41	2.54	9	1
1:A:120:LYS:N	1:A:120:LYS:CD	0.40	2.85	5	1
1:A:72:HIS:C	1:A:74:GLU:N	0.40	2.74	6	1
1:A:101:GLU:CB	1:A:105:GLU:OE1	0.40	2.69	11	1
1:A:90:HIS:C	1:A:92:GLY:N	0.40	2.74	2	1
1:A:19:LEU:O	1:A:20:LYS:C	0.40	2.59	10	2
1:A:65:VAL:HG21	1:A:69:GLY:HA2	0.40	1.93	6	1
1:A:26:CYS:SG	1:A:61:GLU:OE2	0.40	2.79	3	1
1:A:38:ILE:CG2	1:A:39:GLU:N	0.40	2.83	5	1
1:A:51:LEU:CD2	1:A:55:MET:HE1	0.40	2.47	6	1
1:A:108:PHE:O	1:A:109:TRP:C	0.40	2.60	9	1
1:A:99:GLU:HG2	1:A:109:TRP:NE1	0.40	2.31	10	1
1:A:37:ILE:HG23	1:A:124:LEU:HD22	0.40	1.92	11	1
1:A:40:PHE:HB2	1:A:46:HIS:NE2	0.40	2.32	3	1
1:A:67:ASP:O	1:A:68:ASN:CG	0.40	2.60	3	1
1:A:94:ARG:O	1:A:95:CYS:C	0.40	2.60	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:118:ASP:O	1:A:118:ASP:CG	0.40	2.60	10	1
1:A:110:LEU:HD22	1:A:110:LEU:N	0.40	2.31	14	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	121/125 (97%)	89±3 (73±3%)	23±3 (19±3%)	9±2 (8±2%)	2	15
All	All	1815/1875 (97%)	1328 (73%)	347 (19%)	140 (8%)	2	15

All 35 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	71	VAL	15
1	A	101	GLU	15
1	A	32	VAL	13
1	A	49	GLU	12
1	A	93	LYS	7
1	A	96	LEU	6
1	A	120	LYS	6
1	A	66	ASP	6
1	A	124	LEU	5
1	A	6	ARG	4
1	A	64	VAL	4
1	A	81	PRO	4
1	A	95	CYS	4
1	A	94	ARG	3
1	A	47	GLU	3
1	A	121	HIS	3
1	A	65	VAL	3
1	A	7	ASP	2
1	A	45	ILE	2
1	A	63	LYS	2

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Mol	Chain	Res	Type	Models (Total)
1	A	21	PRO	2
1	A	61	GLU	2
1	A	119	PRO	2
1	A	123	PHE	2
1	A	8	ALA	2
1	A	72	HIS	2
1	A	43	GLY	1
1	A	9	GLU	1
1	A	122	TYR	1
1	A	11	PRO	1
1	A	92	GLY	1
1	A	68	ASN	1
1	A	70	ASP	1
1	A	5	ARG	1
1	A	67	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	108/112 (96%)	89±4 (83±3%)	19±4 (17±3%)	4	39
All	All	1620/1680 (96%)	1338 (83%)	282 (17%)	4	39

All 81 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	33	THR	12
1	A	85	HIS	12
1	A	10	TYR	11
1	A	20	LYS	11
1	A	25	ILE	10
1	A	23	HIS	9
1	A	58	LEU	9
1	A	6	ARG	8
1	A	55	MET	8
1	A	16	LEU	7

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Mol	Chain	Res	Type	Models (Total)
1	A	56	ASN	7
1	A	104	CYS	6
1	A	57	CYS	6
1	A	7	ASP	5
1	A	77	ARG	5
1	A	82	ASN	5
1	A	95	CYS	5
1	A	84	MET	5
1	A	124	LEU	5
1	A	113	CYS	5
1	A	78	ASP	5
1	A	106	LYS	5
1	A	63	LYS	4
1	A	81	PRO	4
1	A	94	ARG	4
1	A	38	ILE	4
1	A	44	LYS	4
1	A	90	HIS	4
1	A	72	HIS	4
1	A	118	ASP	4
1	A	19	LEU	3
1	A	48	ASP	3
1	A	83	SER	3
1	A	70	ASP	3
1	A	76	LEU	3
1	A	96	LEU	3
1	A	54	TYR	3
1	A	75	LYS	3
1	A	15	LEU	2
1	A	47	GLU	2
1	A	123	PHE	2
1	A	5	ARG	2
1	A	22	LEU	2
1	A	41	SER	2
1	A	65	VAL	2
1	A	14	GLU	2
1	A	61	GLU	2
1	A	66	ASP	2
1	A	99	GLU	2
1	A	115	LYS	2
1	A	29	LYS	2
1	A	111	HIS	2

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Models (Total)
1	A	68	ASN	2
1	A	34	ASP	2
1	A	73	LEU	2
1	A	24	ASP	2
1	A	114	TRP	2
1	A	51	LEU	2
1	A	102	ASN	2
1	A	91	MET	2
1	A	80	LEU	1
1	A	103	LEU	1
1	A	67	ASP	1
1	A	105	GLU	1
1	A	93	LYS	1
1	A	53	CYS	1
1	A	120	LYS	1
1	A	79	SER	1
1	A	101	GLU	1
1	A	52	LYS	1
1	A	9	GLU	1
1	A	87	ILE	1
1	A	21	PRO	1
1	A	42	ASP	1
1	A	4	PRO	1
1	A	35	GLU	1
1	A	39	GLU	1
1	A	121	HIS	1
1	A	112	LYS	1
1	A	49	GLU	1
1	A	71	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 ⓘ

There are no monosaccharides in this entry.

## 6.6 Ligand geometry

There are no ligands in this entry.

## 6.7 Other polymers

There are no such molecules in this entry.

## 6.8 Polymer linkage issues

There are no chain breaks in this entry.

## 7 Chemical shift validation

No chemical shift data were provided