



# Full wwPDB NMR Structure Validation Report ⓘ

May 28, 2020 – 10:49 pm BST

PDB ID : 2KZK  
Title : Solution structure of alpha-mannosidase binding domain of Atg34  
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Deposited on : 2010-06-18

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.

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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  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : 2.11  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

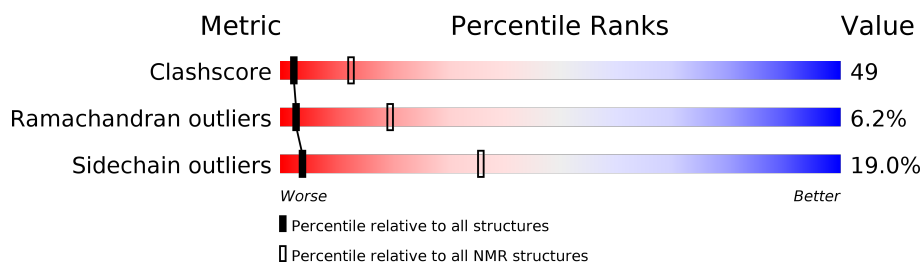
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLUTION NMR*

The overall completeness of chemical shifts assignment is 94%.

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	107	

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 20 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:249-A:283, A:288-A:348 (96)	0.40	20

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 1 single-model cluster was found.

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

### 3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1617 atoms, of which 807 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Uncharacterized protein YOL083W.

Mol	Chain	Residues	Atoms						Trace
1	A	103	Total	C	H	N	O	S	0
			1617	520	807	129	157	4	

There are 4 discrepancies between the modelled and reference sequences:

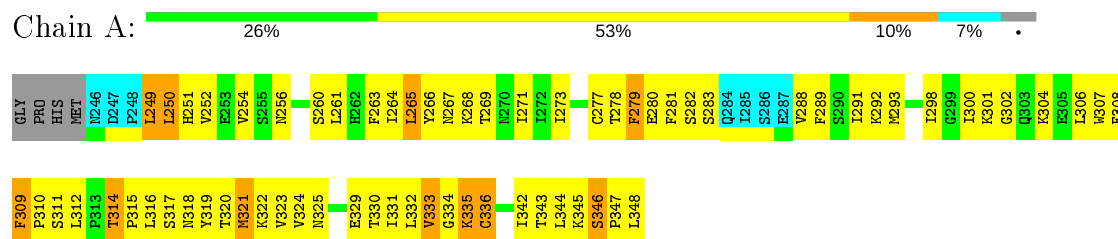
Chain	Residue	Modelled	Actual	Comment	Reference
A	242	GLY	-	expression tag	UNP Q12292
A	243	PRO	-	expression tag	UNP Q12292
A	244	HIS	-	expression tag	UNP Q12292
A	245	MET	-	expression tag	UNP Q12292

## 4 Residue-property plots

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

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

- Molecule 1: Uncharacterized protein YOL083W

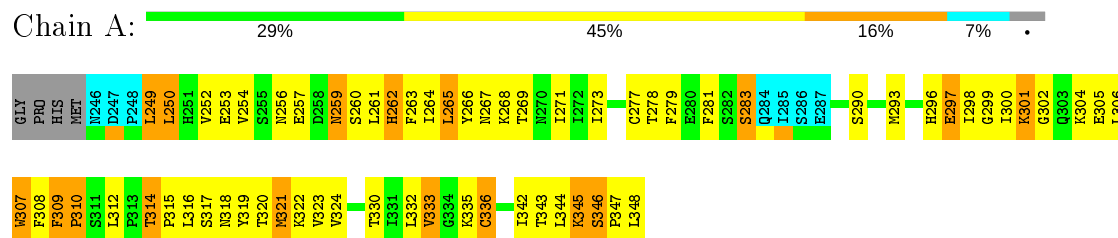


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

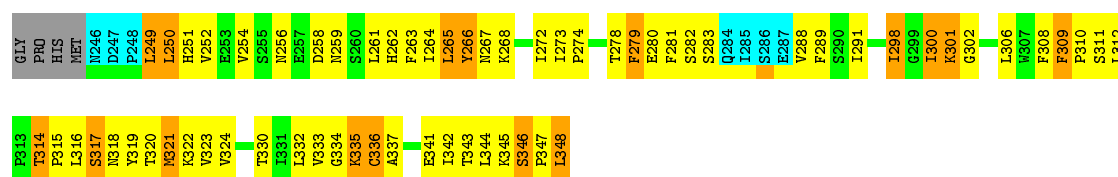
- Molecule 1: Uncharacterized protein YOL083W



#### 4.2.2 Score per residue for model 2

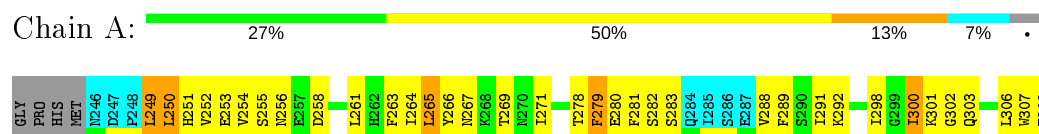
- Molecule 1: Uncharacterized protein YOL083W





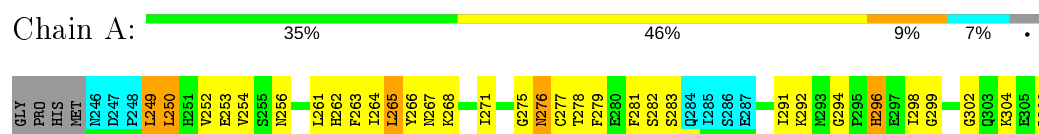
### 4.2.3 Score per residue for model 3

- Molecule 1: Uncharacterized protein YOL083W



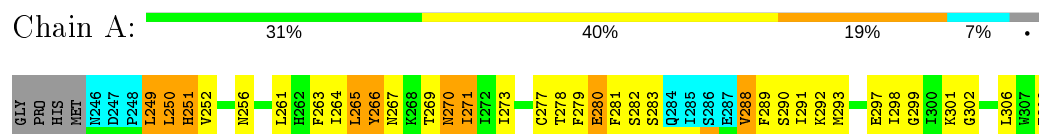
### 4.2.4 Score per residue for model 4

- Molecule 1: Uncharacterized protein YOL083W



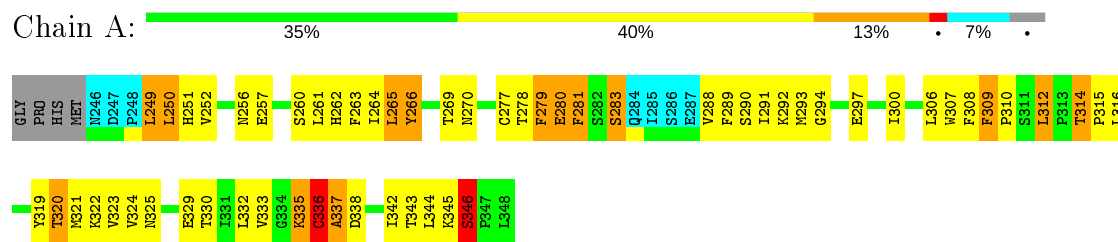
### 4.2.5 Score per residue for model 5

- Molecule 1: Uncharacterized protein YOL083W



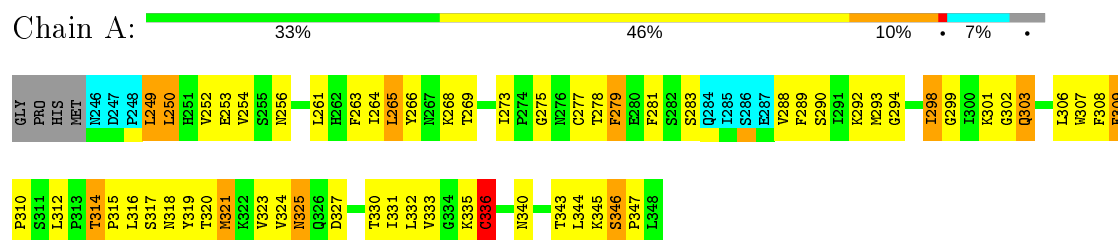
### 4.2.6 Score per residue for model 6

- Molecule 1: Uncharacterized protein YOL083W



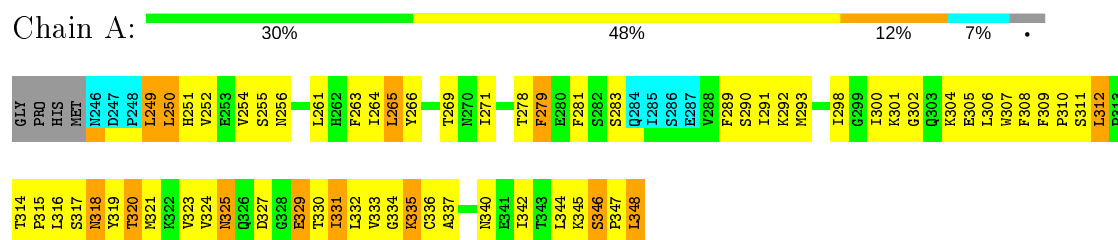
#### 4.2.7 Score per residue for model 7

- Molecule 1: Uncharacterized protein YOL083W



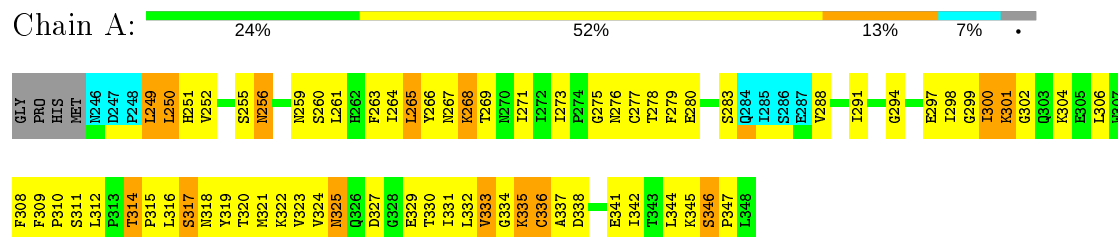
#### 4.2.8 Score per residue for model 8

- Molecule 1: Uncharacterized protein YOL083W



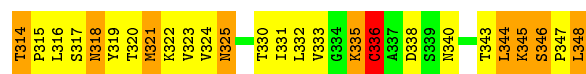
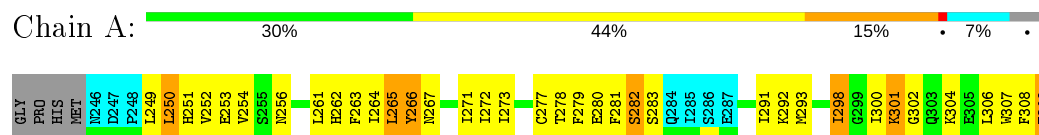
#### 4.2.9 Score per residue for model 9

- Molecule 1: Uncharacterized protein YOL083W



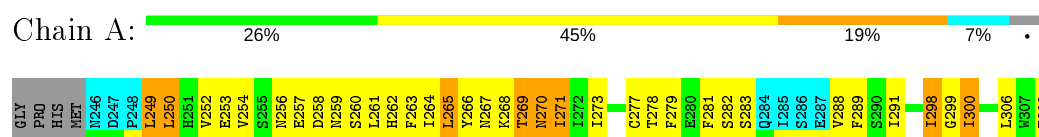
#### 4.2.10 Score per residue for model 10

- Molecule 1: Uncharacterized protein YOL083W



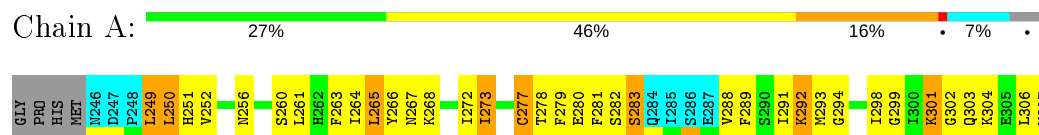
#### 4.2.11 Score per residue for model 11

- Molecule 1: Uncharacterized protein YOL083W



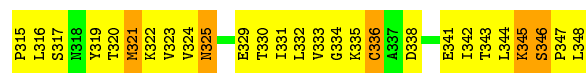
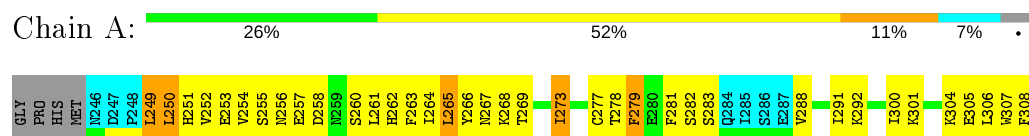
#### 4.2.12 Score per residue for model 12

- Molecule 1: Uncharacterized protein YOL083W



#### 4.2.13 Score per residue for model 13

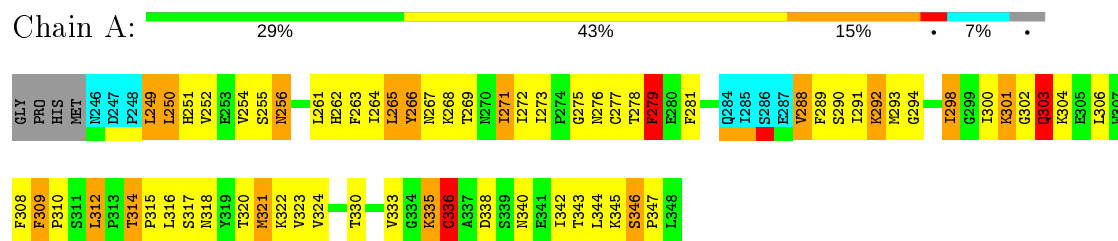
- Molecule 1: Uncharacterized protein YOL083W





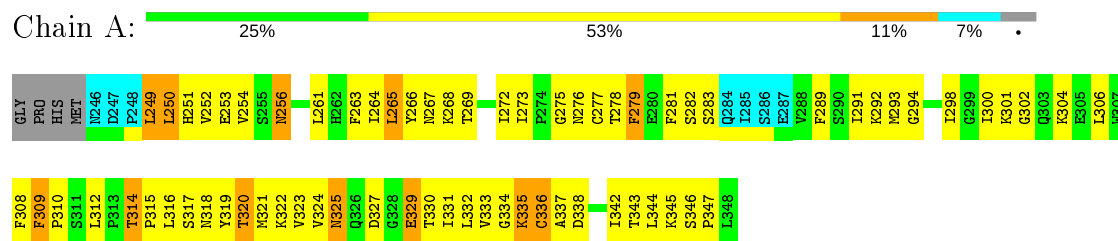
## 4.2.14 Score per residue for model 14

- Molecule 1: Uncharacterized protein YOL083W



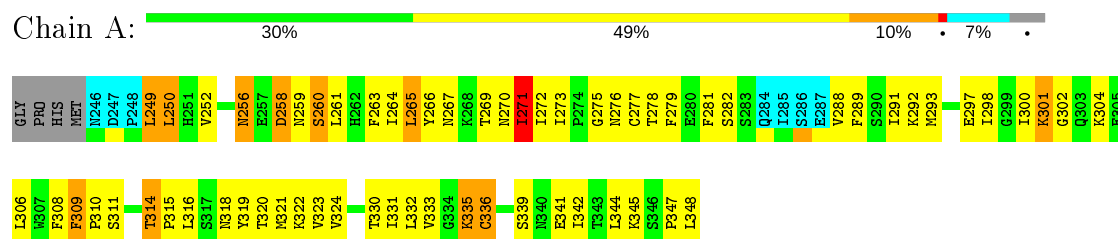
## 4.2.18 Score per residue for model 18

- Molecule 1: Uncharacterized protein YOL083W



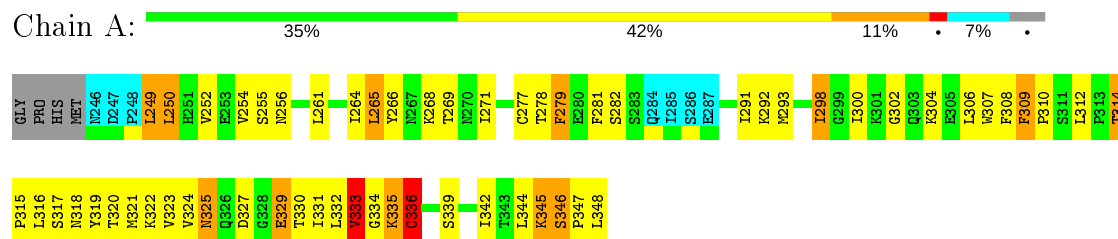
## 4.2.19 Score per residue for model 19

- Molecule 1: Uncharacterized protein YOL083W



## 4.2.20 Score per residue for model 20 (medoid)

- Molecule 1: Uncharacterized protein YOL083W



## 5 Refinement protocol and experimental data overview

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

The following table shows the software used for structure solution, optimisation and refinement.

Software name	Classification	Version
CYANA	structure solution	
CYANA	refinement	

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)	input_cs.cif
Number of chemical shift lists	1
Total number of shifts	1303
Number of shifts mapped to atoms	1303
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	94%

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

## 6 Model quality ⓘ

### 6.1 Standard geometry ⓘ

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 6.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	755	758	755	74±8
All	All	15100	15160	15100	1471

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 49.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:265:LEU:HD11	1:A:306:LEU:HD12	1.05	1.28	20	11
1:A:252:VAL:HG13	1:A:265:LEU:HD23	0.97	1.36	11	3
1:A:261:LEU:CD1	1:A:312:LEU:HD12	0.94	1.92	12	7
1:A:279:PHE:CG	1:A:306:LEU:HD13	0.92	2.00	15	12
1:A:316:LEU:HD13	1:A:321:MET:SD	0.91	2.05	9	5
1:A:249:LEU:O	1:A:249:LEU:HD23	0.91	1.65	3	2
1:A:283:SER:O	1:A:312:LEU:HD22	0.91	1.66	8	2
1:A:249:LEU:O	1:A:249:LEU:HD13	0.88	1.69	19	2
1:A:291:ILE:HD11	1:A:308:PHE:CD1	0.86	2.06	18	4
1:A:249:LEU:HD13	1:A:249:LEU:O	0.85	1.69	7	3
1:A:335:LYS:HZ3	1:A:337:ALA:H	0.85	1.04	18	1
1:A:278:THR:O	1:A:324:VAL:HG22	0.84	1.72	9	18
1:A:265:LEU:HD11	1:A:306:LEU:CD1	0.83	2.03	20	7
1:A:252:VAL:CG2	1:A:265:LEU:HD23	0.81	2.05	5	7

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:263:PHE:CE1	1:A:308:PHE:CD2	0.81	2.68	12	3
1:A:256:ASN:HA	1:A:261:LEU:HD23	0.81	1.53	11	20
1:A:279:PHE:CD1	1:A:323:VAL:HG22	0.81	2.11	12	7
1:A:250:LEU:HD22	1:A:344:LEU:HD22	0.80	1.53	19	7
1:A:298:ILE:HG23	1:A:302:GLY:O	0.80	1.75	15	4
1:A:278:THR:HG22	1:A:290:SER:OG	0.79	1.78	6	5
1:A:332:LEU:HB3	1:A:344:LEU:HD23	0.79	1.54	17	18
1:A:281:PHE:CE2	1:A:308:PHE:CD2	0.79	2.70	11	5
1:A:321:MET:SD	1:A:342:ILE:HD13	0.79	2.18	19	5
1:A:298:ILE:HG22	1:A:299:GLY:N	0.78	1.93	15	3
1:A:261:LEU:HD11	1:A:312:LEU:HG	0.78	1.54	14	1
1:A:252:VAL:HG21	1:A:265:LEU:HD23	0.78	1.55	5	8
1:A:261:LEU:HD11	1:A:312:LEU:HB2	0.77	1.54	7	6
1:A:293:MET:HG2	1:A:306:LEU:HD21	0.77	1.57	15	13
1:A:264:ILE:HG22	1:A:266:TYR:CZ	0.76	2.15	12	17
1:A:300:ILE:HG22	1:A:301:LYS:HD3	0.76	1.58	2	3
1:A:324:VAL:HG12	1:A:330:THR:N	0.75	1.97	20	12
1:A:250:LEU:CD2	1:A:344:LEU:HD22	0.75	2.12	2	5
1:A:316:LEU:HD23	1:A:319:TYR:CE2	0.75	2.15	1	10
1:A:279:PHE:CD1	1:A:306:LEU:HD13	0.75	2.15	5	4
1:A:325:ASN:OD1	1:A:331:ILE:HG21	0.75	1.82	10	3
1:A:264:ILE:HG22	1:A:266:TYR:CE1	0.74	2.16	20	4
1:A:321:MET:HE3	1:A:342:ILE:CD1	0.74	2.10	2	6
1:A:308:PHE:CE2	1:A:312:LEU:HD11	0.74	2.17	16	2
1:A:281:PHE:CZ	1:A:308:PHE:CG	0.74	2.75	3	4
1:A:264:ILE:HG22	1:A:266:TYR:CE2	0.74	2.18	13	10
1:A:325:ASN:ND2	1:A:331:ILE:HG23	0.74	1.97	3	1
1:A:265:LEU:HD12	1:A:265:LEU:N	0.74	1.97	15	1
1:A:283:SER:HB2	1:A:312:LEU:HD23	0.73	1.60	11	1
1:A:271:ILE:HD13	1:A:271:ILE:C	0.73	2.03	19	1
1:A:252:VAL:CG1	1:A:265:LEU:HD23	0.73	2.14	11	2
1:A:254:VAL:HG23	1:A:340:ASN:O	0.73	1.84	10	3
1:A:335:LYS:HZ2	1:A:337:ALA:HB2	0.72	1.44	9	7
1:A:251:HIS:CD2	1:A:343:THR:HG22	0.71	2.20	10	5
1:A:273:ILE:HG21	1:A:298:ILE:HD12	0.71	1.61	7	1
1:A:249:LEU:N	1:A:249:LEU:HD12	0.71	1.99	5	2
1:A:249:LEU:HD22	1:A:343:THR:HB	0.71	1.62	5	1
1:A:291:ILE:CD1	1:A:308:PHE:CD1	0.71	2.74	6	11
1:A:249:LEU:HD22	1:A:249:LEU:C	0.69	2.07	11	3
1:A:320:THR:HG22	1:A:322:LYS:HG2	0.69	1.64	16	1
1:A:281:PHE:CD1	1:A:308:PHE:CE2	0.69	2.81	8	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:332:LEU:CB	1:A:344:LEU:HD23	0.69	2.17	15	14
1:A:314:THR:HG22	1:A:316:LEU:HD12	0.69	1.63	13	5
1:A:254:VAL:CG1	1:A:314:THR:HG21	0.69	2.18	4	10
1:A:348:LEU:HD13	1:A:348:LEU:O	0.69	1.87	13	2
1:A:300:ILE:HG22	1:A:301:LYS:CD	0.68	2.17	14	2
1:A:273:ILE:HG13	1:A:298:ILE:HD12	0.68	1.64	18	2
1:A:254:VAL:HG22	1:A:263:PHE:CE2	0.68	2.24	15	1
1:A:250:LEU:C	1:A:250:LEU:HD12	0.67	2.10	11	7
1:A:316:LEU:HD13	1:A:321:MET:CE	0.67	2.18	18	6
1:A:309:PHE:CD1	1:A:309:PHE:N	0.67	2.63	1	7
1:A:293:MET:CG	1:A:306:LEU:HD21	0.67	2.19	20	8
1:A:249:LEU:HD22	1:A:251:HIS:NE2	0.67	2.04	6	2
1:A:348:LEU:C	1:A:348:LEU:HD22	0.67	2.11	3	2
1:A:281:PHE:CZ	1:A:308:PHE:CD2	0.67	2.82	10	9
1:A:334:GLY:CA	1:A:344:LEU:HD12	0.66	2.19	12	4
1:A:320:THR:HG23	1:A:322:LYS:HD3	0.66	1.65	13	1
1:A:263:PHE:CE2	1:A:308:PHE:CD2	0.66	2.83	3	4
1:A:249:LEU:HD12	1:A:249:LEU:O	0.66	1.91	4	6
1:A:249:LEU:C	1:A:249:LEU:HD22	0.66	2.11	1	2
1:A:249:LEU:O	1:A:249:LEU:HD12	0.66	1.91	14	3
1:A:279:PHE:CD1	1:A:306:LEU:CD1	0.66	2.80	12	6
1:A:252:VAL:HG22	1:A:265:LEU:HD23	0.66	1.67	20	2
1:A:321:MET:HE1	1:A:342:ILE:HD11	0.65	1.66	15	2
1:A:249:LEU:C	1:A:249:LEU:HD23	0.65	2.11	3	2
1:A:266:TYR:CD1	1:A:266:TYR:N	0.65	2.64	14	6
1:A:261:LEU:HD12	1:A:312:LEU:HD12	0.65	1.67	1	4
1:A:323:VAL:CG2	1:A:344:LEU:HD21	0.65	2.21	1	4
1:A:265:LEU:CD1	1:A:306:LEU:HD12	0.65	2.15	20	2
1:A:252:VAL:HG22	1:A:265:LEU:HB3	0.65	1.67	6	4
1:A:309:PHE:N	1:A:309:PHE:CD1	0.65	2.64	16	8
1:A:300:ILE:HG22	1:A:301:LYS:N	0.64	2.07	9	2
1:A:264:ILE:CG2	1:A:266:TYR:CZ	0.64	2.80	4	14
1:A:321:MET:HE3	1:A:342:ILE:HD13	0.64	1.67	2	1
1:A:316:LEU:O	1:A:319:TYR:CD1	0.64	2.51	11	2
1:A:273:ILE:HD13	1:A:273:ILE:N	0.64	2.07	2	1
1:A:264:ILE:CG2	1:A:266:TYR:CE2	0.64	2.81	13	9
1:A:251:HIS:NE2	1:A:343:THR:HG22	0.64	2.07	10	1
1:A:264:ILE:CG2	1:A:266:TYR:CE1	0.64	2.81	19	4
1:A:321:MET:HE1	1:A:342:ILE:CD1	0.64	2.23	15	5
1:A:325:ASN:OD1	1:A:331:ILE:HD13	0.64	1.93	16	1
1:A:261:LEU:CD1	1:A:312:LEU:CD1	0.63	2.77	6	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:263:PHE:CD2	1:A:308:PHE:CE2	0.63	2.87	2	3
1:A:291:ILE:CD1	1:A:308:PHE:CE1	0.63	2.81	17	6
1:A:281:PHE:CE1	1:A:308:PHE:CD2	0.63	2.87	8	1
1:A:283:SER:OG	1:A:312:LEU:HD22	0.63	1.94	12	1
1:A:264:ILE:HG23	1:A:304:LYS:O	0.63	1.94	10	3
1:A:324:VAL:HG12	1:A:330:THR:HA	0.62	1.68	6	8
1:A:281:PHE:CE1	1:A:308:PHE:CE2	0.62	2.87	8	4
1:A:316:LEU:HD12	1:A:321:MET:CE	0.62	2.25	4	2
1:A:336:CYS:O	1:A:337:ALA:HB2	0.62	1.94	6	1
1:A:267:ASN:HB2	1:A:273:ILE:HD13	0.62	1.70	1	2
1:A:325:ASN:ND2	1:A:331:ILE:HD13	0.62	2.09	17	1
1:A:249:LEU:HD22	1:A:343:THR:CB	0.61	2.24	5	1
1:A:314:THR:HG22	1:A:316:LEU:CD1	0.61	2.25	13	3
1:A:261:LEU:HD11	1:A:312:LEU:CG	0.61	2.26	14	1
1:A:324:VAL:HG12	1:A:330:THR:CA	0.61	2.26	6	12
1:A:281:PHE:N	1:A:281:PHE:CD1	0.61	2.68	6	5
1:A:321:MET:CE	1:A:342:ILE:CD1	0.61	2.79	1	8
1:A:316:LEU:HD23	1:A:319:TYR:CD2	0.61	2.30	19	6
1:A:251:HIS:O	1:A:266:TYR:CD2	0.61	2.54	10	1
1:A:316:LEU:HD12	1:A:321:MET:HE2	0.60	1.72	3	2
1:A:265:LEU:HD12	1:A:265:LEU:H	0.60	1.56	15	3
1:A:264:ILE:O	1:A:266:TYR:CE1	0.60	2.54	14	9
1:A:282:SER:O	1:A:319:TYR:CD2	0.60	2.55	4	9
1:A:301:LYS:N	1:A:301:LYS:CD	0.60	2.64	2	2
1:A:254:VAL:HG22	1:A:263:PHE:CE1	0.60	2.31	13	2
1:A:291:ILE:HD12	1:A:308:PHE:CE1	0.60	2.32	13	8
1:A:264:ILE:O	1:A:266:TYR:CE2	0.60	2.54	20	2
1:A:279:PHE:CD2	1:A:306:LEU:HD13	0.60	2.29	15	3
1:A:291:ILE:HD12	1:A:308:PHE:CD1	0.60	2.31	19	7
1:A:256:ASN:CA	1:A:261:LEU:HD23	0.60	2.27	15	6
1:A:306:LEU:O	1:A:308:PHE:CE1	0.60	2.55	10	7
1:A:298:ILE:CG2	1:A:299:GLY:N	0.60	2.64	15	2
1:A:256:ASN:OD1	1:A:314:THR:HG23	0.60	1.96	9	4
1:A:282:SER:OG	1:A:319:TYR:CD2	0.60	2.53	5	2
1:A:261:LEU:HD13	1:A:263:PHE:CZ	0.60	2.32	18	4
1:A:308:PHE:CE2	1:A:312:LEU:CD1	0.60	2.83	16	2
1:A:308:PHE:CE2	1:A:309:PHE:O	0.60	2.55	16	1
1:A:298:ILE:HG23	1:A:302:GLY:C	0.60	2.16	15	5
1:A:300:ILE:HD13	1:A:300:ILE:N	0.60	2.10	20	2
1:A:291:ILE:HD13	1:A:308:PHE:CE1	0.59	2.32	17	3
1:A:282:SER:O	1:A:319:TYR:CE2	0.59	2.55	11	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:267:ASN:HB3	1:A:298:ILE:HG22	0.59	1.73	4	1
1:A:254:VAL:HG11	1:A:314:THR:CG2	0.59	2.27	1	4
1:A:271:ILE:C	1:A:272:ILE:HD12	0.59	2.17	14	1
1:A:261:LEU:HD12	1:A:308:PHE:CD1	0.59	2.32	7	1
1:A:263:PHE:CE1	1:A:321:MET:SD	0.59	2.96	2	1
1:A:307:TRP:CD1	1:A:307:TRP:O	0.59	2.55	8	2
1:A:317:SER:O	1:A:318:ASN:CB	0.58	2.51	12	15
1:A:291:ILE:HD13	1:A:308:PHE:CD1	0.58	2.34	17	4
1:A:335:LYS:HZ2	1:A:337:ALA:CB	0.58	2.12	2	6
1:A:291:ILE:HD11	1:A:308:PHE:HD1	0.57	1.58	5	3
1:A:254:VAL:HG13	1:A:263:PHE:CE1	0.57	2.33	11	1
1:A:308:PHE:CE1	1:A:312:LEU:HD11	0.57	2.33	1	1
1:A:252:VAL:HG13	1:A:265:LEU:CD2	0.57	2.24	11	2
1:A:316:LEU:HD22	1:A:321:MET:HE3	0.57	1.76	17	1
1:A:345:LYS:O	1:A:346:SER:CB	0.56	2.52	17	17
1:A:329:GLU:O	1:A:329:GLU:CG	0.56	2.53	17	3
1:A:254:VAL:HG11	1:A:314:THR:HG21	0.56	1.75	1	7
1:A:320:THR:O	1:A:321:MET:C	0.56	2.44	11	20
1:A:250:LEU:C	1:A:250:LEU:CD1	0.56	2.73	11	8
1:A:261:LEU:HD13	1:A:263:PHE:HE2	0.56	1.58	7	2
1:A:249:LEU:N	1:A:249:LEU:CD2	0.56	2.68	12	1
1:A:250:LEU:HD12	1:A:250:LEU:C	0.56	2.21	10	3
1:A:296:HIS:CE1	1:A:297:GLU:OE1	0.56	2.58	1	1
1:A:320:THR:HG23	1:A:322:LYS:HD2	0.56	1.77	18	1
1:A:294:GLY:HA3	1:A:304:LYS:HZ2	0.56	1.61	18	1
1:A:267:ASN:ND2	1:A:273:ILE:HD11	0.56	2.15	2	1
1:A:283:SER:OG	1:A:319:TYR:CE2	0.56	2.55	6	1
1:A:334:GLY:HA2	1:A:344:LEU:HD12	0.55	1.76	5	3
1:A:308:PHE:CE1	1:A:312:LEU:CD1	0.55	2.89	1	1
1:A:251:HIS:O	1:A:252:VAL:HG23	0.55	2.02	14	2
1:A:332:LEU:HD21	1:A:345:LYS:O	0.55	2.01	20	1
1:A:250:LEU:CD1	1:A:250:LEU:C	0.55	2.75	17	2
1:A:261:LEU:HD13	1:A:312:LEU:HD12	0.55	1.73	12	2
1:A:262:HIS:NE2	1:A:264:ILE:CD1	0.55	2.70	13	1
1:A:267:ASN:CG	1:A:273:ILE:HD13	0.55	2.22	13	1
1:A:262:HIS:NE2	1:A:307:TRP:CD1	0.55	2.74	4	2
1:A:308:PHE:CD2	1:A:312:LEU:CD1	0.55	2.89	16	1
1:A:281:PHE:HE1	1:A:291:ILE:HD12	0.55	1.61	3	1
1:A:322:LYS:HZ2	1:A:333:VAL:HB	0.55	1.62	4	2
1:A:294:GLY:CA	1:A:304:LYS:NZ	0.55	2.70	18	1
1:A:279:PHE:CE1	1:A:323:VAL:HG22	0.55	2.36	3	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:332:LEU:HD23	1:A:346:SER:HA	0.55	1.78	4	5
1:A:308:PHE:CZ	1:A:309:PHE:O	0.55	2.59	16	3
1:A:308:PHE:C	1:A:309:PHE:CD1	0.54	2.81	10	4
1:A:335:LYS:HZ3	1:A:337:ALA:N	0.54	1.88	18	1
1:A:324:VAL:HG23	1:A:329:GLU:H	0.54	1.61	16	1
1:A:335:LYS:C	1:A:336:CYS:SG	0.54	2.86	20	1
1:A:281:PHE:CZ	1:A:308:PHE:CE2	0.53	2.96	6	2
1:A:263:PHE:O	1:A:265:LEU:HD23	0.53	2.03	9	1
1:A:298:ILE:HG22	1:A:298:ILE:O	0.53	2.04	4	1
1:A:252:VAL:CG1	1:A:265:LEU:CD2	0.53	2.86	11	1
1:A:308:PHE:CG	1:A:309:PHE:N	0.53	2.76	7	6
1:A:269:THR:O	1:A:270:ASN:CB	0.53	2.57	11	2
1:A:292:LYS:CD	1:A:292:LYS:N	0.53	2.72	14	1
1:A:324:VAL:HG23	1:A:329:GLU:N	0.53	2.18	16	1
1:A:252:VAL:HG13	1:A:265:LEU:HB3	0.53	1.80	9	1
1:A:262:HIS:CD2	1:A:307:TRP:CD1	0.52	2.97	4	1
1:A:320:THR:CG2	1:A:321:MET:N	0.52	2.72	8	2
1:A:325:ASN:OD1	1:A:331:ILE:HG22	0.52	2.04	8	2
1:A:325:ASN:ND2	1:A:325:ASN:N	0.52	2.57	3	3
1:A:325:ASN:CG	1:A:331:ILE:HD13	0.52	2.25	16	2
1:A:279:PHE:HD1	1:A:323:VAL:HG22	0.52	1.59	12	1
1:A:261:LEU:HD13	1:A:263:PHE:CE2	0.52	2.39	7	3
1:A:298:ILE:CG2	1:A:302:GLY:O	0.52	2.58	14	7
1:A:251:HIS:CD2	1:A:341:GLU:OE1	0.52	2.62	5	1
1:A:263:PHE:CD1	1:A:308:PHE:CE2	0.52	2.98	19	4
1:A:270:ASN:O	1:A:300:ILE:HD11	0.52	2.04	19	2
1:A:252:VAL:HG13	1:A:265:LEU:HG	0.52	1.80	16	1
1:A:279:PHE:CG	1:A:306:LEU:CD1	0.52	2.85	15	3
1:A:278:THR:HG23	1:A:291:ILE:O	0.52	2.05	16	3
1:A:333:VAL:HG11	1:A:347:PRO:HA	0.52	1.80	15	2
1:A:283:SER:CB	1:A:312:LEU:HD23	0.52	2.35	9	5
1:A:251:HIS:ND1	1:A:343:THR:HG22	0.52	2.19	2	1
1:A:281:PHE:CZ	1:A:308:PHE:HB3	0.51	2.40	3	2
1:A:265:LEU:HD21	1:A:306:LEU:HD12	0.51	1.82	9	3
1:A:316:LEU:HD23	1:A:319:TYR:HD2	0.51	1.65	15	2
1:A:316:LEU:HD22	1:A:319:TYR:CE2	0.51	2.40	2	2
1:A:278:THR:HG22	1:A:290:SER:HB3	0.51	1.82	7	1
1:A:325:ASN:ND2	1:A:325:ASN:H	0.51	2.03	9	3
1:A:336:CYS:SG	1:A:342:ILE:CD1	0.51	2.98	17	1
1:A:336:CYS:SG	1:A:342:ILE:HD13	0.51	2.45	8	2
1:A:335:LYS:NZ	1:A:337:ALA:HB2	0.51	2.18	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:269:THR:OG1	1:A:271:ILE:CD1	0.51	2.59	11	1
1:A:269:THR:O	1:A:300:ILE:HD12	0.51	2.05	20	1
1:A:258:ASP:O	1:A:259:ASN:CB	0.51	2.59	11	2
1:A:312:LEU:HD12	1:A:312:LEU:O	0.51	2.04	14	1
1:A:332:LEU:C	1:A:333:VAL:HG12	0.51	2.26	20	1
1:A:316:LEU:CD2	1:A:319:TYR:CD2	0.51	2.94	7	3
1:A:280:GLU:CG	1:A:288:VAL:HG21	0.51	2.36	2	2
1:A:294:GLY:CA	1:A:304:LYS:HZ2	0.51	2.18	18	1
1:A:325:ASN:OD1	1:A:331:ILE:CG2	0.50	2.60	18	6
1:A:261:LEU:HD22	1:A:263:PHE:CE1	0.50	2.42	10	1
1:A:280:GLU:HG3	1:A:288:VAL:HG21	0.50	1.83	2	4
1:A:266:TYR:N	1:A:266:TYR:CD1	0.50	2.79	15	4
1:A:280:GLU:HG2	1:A:288:VAL:HG21	0.50	1.82	5	1
1:A:271:ILE:CD1	1:A:271:ILE:C	0.50	2.74	19	1
1:A:325:ASN:H	1:A:325:ASN:ND2	0.50	2.04	18	2
1:A:306:LEU:O	1:A:308:PHE:CD1	0.50	2.64	12	2
1:A:316:LEU:CD2	1:A:319:TYR:CE2	0.50	2.93	1	5
1:A:251:HIS:O	1:A:252:VAL:CG2	0.50	2.59	14	2
1:A:263:PHE:CE1	1:A:308:PHE:CE2	0.50	3.00	9	3
1:A:329:GLU:CG	1:A:329:GLU:O	0.50	2.60	15	3
1:A:320:THR:HG23	1:A:322:LYS:HZ3	0.50	1.67	20	1
1:A:281:PHE:CD1	1:A:281:PHE:N	0.50	2.80	5	4
1:A:320:THR:HG22	1:A:322:LYS:HG3	0.50	1.83	2	5
1:A:256:ASN:OD1	1:A:314:THR:CG2	0.50	2.60	9	3
1:A:308:PHE:C	1:A:309:PHE:CG	0.49	2.86	10	1
1:A:275:GLY:O	1:A:276:ASN:CB	0.49	2.60	18	3
1:A:332:LEU:CD2	1:A:345:LYS:C	0.49	2.80	20	1
1:A:268:LYS:CE	1:A:300:ILE:O	0.49	2.60	1	2
1:A:261:LEU:HD13	1:A:263:PHE:HZ	0.49	1.67	5	2
1:A:316:LEU:C	1:A:319:TYR:CD1	0.49	2.85	17	2
1:A:282:SER:HB3	1:A:288:VAL:HG23	0.49	1.84	15	1
1:A:267:ASN:CG	1:A:298:ILE:CG2	0.49	2.79	18	1
1:A:316:LEU:HD22	1:A:321:MET:CE	0.49	2.38	6	3
1:A:321:MET:CE	1:A:342:ILE:HD11	0.49	2.37	16	2
1:A:322:LYS:HG2	1:A:333:VAL:HG23	0.49	1.85	12	1
1:A:320:THR:HG23	1:A:322:LYS:CD	0.49	2.38	18	1
1:A:252:VAL:HG12	1:A:253:GLU:N	0.49	2.23	11	10
1:A:348:LEU:HD22	1:A:348:LEU:C	0.49	2.27	2	2
1:A:316:LEU:O	1:A:319:TYR:HB2	0.49	2.07	12	2
1:A:261:LEU:HD21	1:A:312:LEU:CD1	0.49	2.38	14	1
1:A:322:LYS:HG2	1:A:333:VAL:HG12	0.49	1.84	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:283:SER:HA	1:A:319:TYR:CE2	0.49	2.42	4	8
1:A:251:HIS:CD2	1:A:252:VAL:N	0.49	2.81	5	2
1:A:335:LYS:O	1:A:336:CYS:CB	0.49	2.60	6	1
1:A:249:LEU:O	1:A:249:LEU:CD1	0.49	2.60	14	4
1:A:249:LEU:HD23	1:A:249:LEU:N	0.49	2.22	12	1
1:A:249:LEU:HD22	1:A:250:LEU:N	0.49	2.23	7	2
1:A:288:VAL:HG22	1:A:289:PHE:N	0.49	2.23	11	8
1:A:294:GLY:N	1:A:304:LYS:NZ	0.49	2.60	18	2
1:A:305:GLU:HB2	1:A:307:TRP:CZ2	0.49	2.43	1	1
1:A:267:ASN:OD1	1:A:273:ILE:CD1	0.49	2.60	16	3
1:A:294:GLY:H	1:A:304:LYS:NZ	0.49	2.06	4	2
1:A:249:LEU:CD1	1:A:249:LEU:O	0.49	2.61	6	5
1:A:267:ASN:OD1	1:A:273:ILE:HD13	0.49	2.08	13	1
1:A:254:VAL:CG2	1:A:340:ASN:O	0.49	2.61	14	1
1:A:279:PHE:CD1	1:A:322:LYS:O	0.49	2.66	16	1
1:A:335:LYS:NZ	1:A:337:ALA:CB	0.48	2.76	5	5
1:A:281:PHE:CE1	1:A:291:ILE:HD12	0.48	2.43	3	1
1:A:316:LEU:HD13	1:A:321:MET:HE3	0.48	1.85	12	5
1:A:283:SER:O	1:A:319:TYR:CE2	0.48	2.66	9	1
1:A:321:MET:CE	1:A:336:CYS:SG	0.48	3.01	16	2
1:A:279:PHE:CD2	1:A:281:PHE:CD1	0.48	3.02	7	5
1:A:277:CYS:SG	1:A:293:MET:CE	0.48	3.01	12	1
1:A:324:VAL:HG12	1:A:329:GLU:C	0.48	2.28	20	2
1:A:336:CYS:O	1:A:337:ALA:CB	0.48	2.60	6	1
1:A:252:VAL:HG22	1:A:265:LEU:CD2	0.48	2.35	20	1
1:A:279:PHE:CE2	1:A:321:MET:HG2	0.48	2.43	4	3
1:A:316:LEU:HD13	1:A:321:MET:HE1	0.48	1.85	18	2
1:A:307:TRP:O	1:A:307:TRP:CE3	0.48	2.67	16	2
1:A:281:PHE:CD2	1:A:312:LEU:HD11	0.48	2.44	8	2
1:A:273:ILE:HG22	1:A:274:PRO:HD2	0.48	1.85	2	1
1:A:306:LEU:HB3	1:A:308:PHE:CE1	0.48	2.43	2	12
1:A:312:LEU:HD12	1:A:312:LEU:H	0.48	1.69	11	1
1:A:251:HIS:CE1	1:A:341:GLU:CD	0.48	2.87	9	1
1:A:332:LEU:C	1:A:333:VAL:CG1	0.48	2.82	3	9
1:A:271:ILE:HD13	1:A:271:ILE:O	0.48	2.09	19	1
1:A:298:ILE:CG2	1:A:302:GLY:C	0.47	2.82	1	6
1:A:298:ILE:HG22	1:A:299:GLY:H	0.47	1.63	15	2
1:A:249:LEU:CD1	1:A:249:LEU:C	0.47	2.82	9	1
1:A:259:ASN:ND2	1:A:260:SER:N	0.47	2.63	9	1
1:A:281:PHE:CZ	1:A:308:PHE:CB	0.47	2.97	3	1
1:A:296:HIS:CE1	1:A:304:LYS:HD3	0.47	2.44	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:267:ASN:OD1	1:A:271:ILE:HD13	0.47	2.09	11	1
1:A:263:PHE:N	1:A:263:PHE:CD1	0.47	2.78	14	1
1:A:292:LYS:N	1:A:292:LYS:CD	0.47	2.78	12	1
1:A:305:GLU:CB	1:A:307:TRP:CZ2	0.47	2.97	1	1
1:A:281:PHE:CE2	1:A:308:PHE:HB3	0.47	2.45	3	2
1:A:279:PHE:CD2	1:A:308:PHE:CZ	0.47	3.02	12	1
1:A:310:PRO:O	1:A:311:SER:CB	0.47	2.63	17	1
1:A:321:MET:HE3	1:A:342:ILE:HD11	0.47	1.84	18	1
1:A:314:THR:CB	1:A:315:PRO:HA	0.47	2.39	14	10
1:A:252:VAL:N	1:A:342:ILE:O	0.47	2.48	14	2
1:A:316:LEU:HD13	1:A:321:MET:HE2	0.47	1.84	18	2
1:A:312:LEU:C	1:A:312:LEU:CD1	0.47	2.83	14	1
1:A:322:LYS:CG	1:A:333:VAL:HG12	0.47	2.40	19	2
1:A:323:VAL:HG21	1:A:344:LEU:HD21	0.47	1.83	1	1
1:A:270:ASN:C	1:A:271:ILE:CG2	0.47	2.83	11	1
1:A:330:THR:HG22	1:A:347:PRO:HG3	0.47	1.86	12	1
1:A:267:ASN:O	1:A:267:ASN:CG	0.47	2.51	15	2
1:A:316:LEU:CD1	1:A:321:MET:CE	0.47	2.93	12	1
1:A:277:CYS:SG	1:A:331:ILE:CD1	0.47	3.03	19	1
1:A:306:LEU:HB3	1:A:308:PHE:CZ	0.47	2.45	17	8
1:A:267:ASN:ND2	1:A:271:ILE:O	0.46	2.48	11	2
1:A:278:THR:HG23	1:A:292:LYS:HA	0.46	1.87	8	1
1:A:272:ILE:N	1:A:272:ILE:HD12	0.46	2.25	18	2
1:A:336:CYS:SG	1:A:337:ALA:N	0.46	2.88	6	1
1:A:261:LEU:HD21	1:A:312:LEU:HD12	0.46	1.87	14	1
1:A:254:VAL:HG12	1:A:314:THR:HG21	0.46	1.87	2	1
1:A:294:GLY:H	1:A:304:LYS:HZ1	0.46	1.54	4	2
1:A:278:THR:CG2	1:A:290:SER:OG	0.46	2.60	8	2
1:A:252:VAL:HG13	1:A:265:LEU:CB	0.46	2.40	9	1
1:A:316:LEU:O	1:A:319:TYR:CG	0.46	2.69	11	2
1:A:269:THR:O	1:A:300:ILE:CD1	0.46	2.64	19	1
1:A:314:THR:HA	1:A:315:PRO:C	0.46	2.31	8	20
1:A:348:LEU:HD13	1:A:348:LEU:C	0.46	2.30	13	1
1:A:278:THR:O	1:A:324:VAL:CG2	0.46	2.64	5	6
1:A:267:ASN:ND2	1:A:299:GLY:O	0.46	2.49	9	1
1:A:325:ASN:HB3	1:A:331:ILE:HG21	0.46	1.87	11	1
1:A:305:GLU:HG2	1:A:307:TRP:CZ3	0.46	2.46	13	1
1:A:320:THR:O	1:A:322:LYS:N	0.46	2.49	2	2
1:A:325:ASN:ND2	1:A:329:GLU:O	0.46	2.49	3	1
1:A:288:VAL:CG2	1:A:289:PHE:N	0.46	2.79	19	4
1:A:298:ILE:HD11	1:A:304:LYS:HB2	0.46	1.88	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:272:ILE:HD12	1:A:272:ILE:N	0.46	2.26	14	1
1:A:267:ASN:CG	1:A:273:ILE:CD1	0.46	2.85	19	1
1:A:251:HIS:CE1	1:A:341:GLU:HG2	0.46	2.46	2	2
1:A:261:LEU:HD22	1:A:263:PHE:CZ	0.45	2.46	18	1
1:A:300:ILE:CG2	1:A:301:LYS:N	0.45	2.76	9	2
1:A:252:VAL:CG1	1:A:253:GLU:N	0.45	2.79	17	6
1:A:260:SER:CB	1:A:310:PRO:O	0.45	2.64	12	1
1:A:263:PHE:CD1	1:A:263:PHE:N	0.45	2.83	17	1
1:A:251:HIS:CD2	1:A:341:GLU:CD	0.45	2.89	5	1
1:A:281:PHE:CE2	1:A:312:LEU:HD11	0.45	2.47	8	2
1:A:249:LEU:O	1:A:269:THR:CG2	0.45	2.64	11	1
1:A:298:ILE:N	1:A:298:ILE:HD13	0.45	2.25	14	1
1:A:309:PHE:HA	1:A:310:PRO:C	0.45	2.32	10	20
1:A:279:PHE:CZ	1:A:321:MET:HG2	0.45	2.47	4	2
1:A:312:LEU:HD22	1:A:316:LEU:HD21	0.45	1.89	14	1
1:A:312:LEU:CD2	1:A:316:LEU:HD21	0.45	2.40	14	1
1:A:323:VAL:HG23	1:A:344:LEU:HD21	0.45	1.88	2	2
1:A:267:ASN:ND2	1:A:267:ASN:O	0.45	2.50	4	1
1:A:333:VAL:O	1:A:333:VAL:CG2	0.45	2.64	17	3
1:A:283:SER:CB	1:A:319:TYR:OH	0.45	2.65	6	1
1:A:300:ILE:C	1:A:302:GLY:N	0.45	2.70	8	1
1:A:249:LEU:N	1:A:249:LEU:CD1	0.45	2.70	5	2
1:A:267:ASN:ND2	1:A:300:ILE:O	0.45	2.50	9	1
1:A:266:TYR:O	1:A:268:LYS:N	0.45	2.50	12	3
1:A:265:LEU:O	1:A:304:LYS:N	0.44	2.50	13	6
1:A:263:PHE:CE2	1:A:308:PHE:CE2	0.44	3.05	3	3
1:A:254:VAL:O	1:A:340:ASN:ND2	0.44	2.50	3	2
1:A:262:HIS:CD2	1:A:264:ILE:HG13	0.44	2.46	13	1
1:A:275:GLY:O	1:A:276:ASN:ND2	0.44	2.49	4	1
1:A:256:ASN:HB2	1:A:314:THR:HG21	0.44	1.88	8	1
1:A:280:GLU:O	1:A:321:MET:N	0.44	2.50	2	2
1:A:281:PHE:CE1	1:A:289:PHE:HB3	0.44	2.47	2	1
1:A:322:LYS:C	1:A:323:VAL:CG2	0.44	2.86	6	6
1:A:335:LYS:NZ	1:A:336:CYS:O	0.44	2.49	6	1
1:A:335:LYS:O	1:A:336:CYS:SG	0.44	2.76	6	3
1:A:265:LEU:CD1	1:A:265:LEU:N	0.44	2.69	15	1
1:A:278:THR:N	1:A:293:MET:SD	0.44	2.91	16	2
1:A:283:SER:HB2	1:A:312:LEU:HD21	0.44	1.89	5	1
1:A:273:ILE:O	1:A:297:GLU:CG	0.44	2.65	9	2
1:A:305:GLU:HG2	1:A:307:TRP:CH2	0.44	2.47	13	1
1:A:335:LYS:CE	1:A:336:CYS:O	0.44	2.65	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:291:ILE:CG2	1:A:306:LEU:HD23	0.44	2.42	16	1
1:A:267:ASN:OD1	1:A:273:ILE:HD12	0.44	2.12	1	1
1:A:281:PHE:O	1:A:281:PHE:CG	0.44	2.70	2	1
1:A:316:LEU:C	1:A:336:CYS:HG	0.44	2.16	11	1
1:A:282:SER:OG	1:A:288:VAL:N	0.44	2.51	13	1
1:A:267:ASN:OD1	1:A:299:GLY:O	0.44	2.36	15	1
1:A:305:GLU:HB3	1:A:307:TRP:CE2	0.44	2.48	17	2
1:A:264:ILE:HG21	1:A:266:TYR:CE2	0.44	2.48	17	1
1:A:325:ASN:ND2	1:A:331:ILE:CG2	0.43	2.76	3	1
1:A:250:LEU:HD12	1:A:267:ASN:HA	0.43	1.90	2	2
1:A:281:PHE:CZ	1:A:308:PHE:CD1	0.43	3.06	11	1
1:A:299:GLY:O	1:A:300:ILE:O	0.43	2.36	15	1
1:A:316:LEU:HB3	1:A:319:TYR:CG	0.43	2.48	17	1
1:A:275:GLY:C	1:A:277:CYS:N	0.43	2.71	4	2
1:A:275:GLY:O	1:A:294:GLY:O	0.43	2.37	7	1
1:A:251:HIS:NE2	1:A:341:GLU:CG	0.43	2.81	9	1
1:A:299:GLY:O	1:A:300:ILE:C	0.43	2.57	15	2
1:A:296:HIS:NE2	1:A:297:GLU:OE1	0.43	2.51	1	1
1:A:254:VAL:HG22	1:A:263:PHE:CD1	0.43	2.47	2	1
1:A:316:LEU:HD22	1:A:321:MET:HE2	0.43	1.89	15	1
1:A:333:VAL:CG1	1:A:347:PRO:HA	0.43	2.43	17	2
1:A:320:THR:HG23	1:A:322:LYS:HG3	0.43	1.90	20	7
1:A:302:GLY:O	1:A:303:GLN:O	0.43	2.37	15	3
1:A:259:ASN:N	1:A:259:ASN:OD1	0.43	2.50	1	1
1:A:334:GLY:C	1:A:336:CYS:N	0.43	2.72	8	9
1:A:334:GLY:CA	1:A:344:LEU:CD1	0.43	2.96	5	1
1:A:300:ILE:HG22	1:A:301:LYS:HG2	0.43	1.90	19	1
1:A:330:THR:HG23	1:A:332:LEU:O	0.43	2.14	20	1
1:A:283:SER:CB	1:A:312:LEU:HD21	0.43	2.43	5	1
1:A:293:MET:O	1:A:294:GLY:C	0.43	2.57	18	1
1:A:269:THR:OG1	1:A:270:ASN:N	0.43	2.52	5	1
1:A:280:GLU:O	1:A:322:LYS:N	0.43	2.52	6	1
1:A:249:LEU:HD13	1:A:249:LEU:C	0.43	2.31	7	1
1:A:261:LEU:HD11	1:A:312:LEU:CB	0.43	2.37	7	1
1:A:335:LYS:O	1:A:336:CYS:C	0.43	2.57	17	4
1:A:268:LYS:HZ1	1:A:301:LYS:HA	0.43	1.73	13	1
1:A:333:VAL:HG22	1:A:346:SER:C	0.43	2.34	14	1
1:A:272:ILE:CG2	1:A:273:ILE:N	0.43	2.82	18	1
1:A:265:LEU:HD21	1:A:279:PHE:CE1	0.43	2.49	2	1
1:A:288:VAL:HG22	1:A:289:PHE:H	0.43	1.74	14	1
1:A:249:LEU:C	1:A:249:LEU:CD2	0.43	2.83	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:278:THR:CA	1:A:293:MET:SD	0.43	3.07	16	1
1:A:283:SER:OG	1:A:319:TYR:CZ	0.42	2.65	8	1
1:A:251:HIS:NE2	1:A:343:THR:CG2	0.42	2.82	10	1
1:A:257:GLU:N	1:A:260:SER:O	0.42	2.52	6	1
1:A:307:TRP:O	1:A:307:TRP:CD1	0.42	2.73	20	1
1:A:308:PHE:CD1	1:A:308:PHE:N	0.42	2.83	2	2
1:A:338:ASP:N	1:A:338:ASP:OD2	0.42	2.50	12	1
1:A:338:ASP:CG	1:A:338:ASP:O	0.42	2.57	14	1
1:A:289:PHE:CD2	1:A:308:PHE:CE1	0.42	3.07	18	1
1:A:270:ASN:O	1:A:271:ILE:O	0.42	2.37	19	1
1:A:257:GLU:O	1:A:260:SER:O	0.42	2.38	15	3
1:A:316:LEU:O	1:A:336:CYS:SG	0.42	2.78	17	3
1:A:343:THR:O	1:A:344:LEU:C	0.42	2.58	13	8
1:A:256:ASN:CG	1:A:314:THR:HG1	0.42	2.17	9	1
1:A:324:VAL:CG1	1:A:330:THR:N	0.42	2.82	17	1
1:A:283:SER:HB2	1:A:312:LEU:CD2	0.42	2.44	1	1
1:A:252:VAL:CG2	1:A:265:LEU:CD2	0.42	2.98	10	2
1:A:278:THR:HB	1:A:324:VAL:HG13	0.42	1.90	16	1
1:A:265:LEU:CD1	1:A:306:LEU:CD1	0.42	2.89	20	1
1:A:275:GLY:O	1:A:277:CYS:N	0.42	2.53	4	1
1:A:249:LEU:O	1:A:269:THR:HG23	0.42	2.15	11	1
1:A:269:THR:OG1	1:A:271:ILE:HD12	0.42	2.13	11	1
1:A:250:LEU:HD21	1:A:265:LEU:HB3	0.42	1.92	14	1
1:A:335:LYS:O	1:A:336:CYS:O	0.42	2.38	14	2
1:A:250:LEU:O	1:A:342:ILE:O	0.42	2.38	19	3
1:A:316:LEU:HD13	1:A:319:TYR:CD2	0.42	2.49	2	1
1:A:256:ASN:O	1:A:256:ASN:CG	0.42	2.58	12	2
1:A:327:ASP:N	1:A:327:ASP:OD2	0.42	2.51	7	1
1:A:308:PHE:N	1:A:308:PHE:CD1	0.42	2.87	8	1
1:A:325:ASN:N	1:A:325:ASN:ND2	0.42	2.67	9	1
1:A:271:ILE:HG12	1:A:272:ILE:N	0.42	2.29	19	1
1:A:277:CYS:C	1:A:278:THR:OG1	0.42	2.59	13	10
1:A:273:ILE:CD1	1:A:273:ILE:N	0.42	2.75	2	1
1:A:261:LEU:HD12	1:A:312:LEU:HG	0.42	1.92	8	1
1:A:281:PHE:CE1	1:A:308:PHE:CZ	0.42	3.08	11	1
1:A:266:TYR:CD1	1:A:303:GLN:HG2	0.42	2.49	14	1
1:A:348:LEU:HD12	1:A:348:LEU:C	0.42	2.34	20	1
1:A:252:VAL:HG12	1:A:253:GLU:H	0.41	1.75	3	1
1:A:278:THR:HB	1:A:324:VAL:CG2	0.41	2.45	8	1
1:A:300:ILE:O	1:A:302:GLY:N	0.41	2.53	8	1
1:A:249:LEU:HD22	1:A:251:HIS:CE1	0.41	2.50	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:339:SER:C	1:A:341:GLU:N	0.41	2.72	19	3
1:A:268:LYS:O	1:A:269:THR:O	0.41	2.38	15	1
1:A:277:CYS:CB	1:A:293:MET:SD	0.41	3.08	15	2
1:A:321:MET:SD	1:A:342:ILE:CD1	0.41	3.08	15	1
1:A:261:LEU:CD1	1:A:312:LEU:HG	0.41	2.45	8	1
1:A:283:SER:OG	1:A:312:LEU:CD2	0.41	2.67	12	1
1:A:299:GLY:C	1:A:301:LYS:N	0.41	2.73	1	2
1:A:301:LYS:HD3	1:A:301:LYS:N	0.41	2.30	7	1
1:A:347:PRO:O	1:A:348:LEU:C	0.41	2.58	12	2
1:A:270:ASN:O	1:A:271:ILE:C	0.41	2.58	19	1
1:A:335:LYS:HB3	1:A:345:LYS:CE	0.41	2.46	5	2
1:A:294:GLY:HA3	1:A:304:LYS:HZ3	0.41	1.75	12	1
1:A:267:ASN:CG	1:A:298:ILE:HG21	0.41	2.34	18	1
1:A:256:ASN:ND2	1:A:312:LEU:O	0.41	2.53	2	1
1:A:348:LEU:C	1:A:348:LEU:HD13	0.41	2.36	2	1
1:A:320:THR:C	1:A:322:LYS:N	0.41	2.73	17	2
1:A:316:LEU:HD22	1:A:319:TYR:CD2	0.41	2.49	12	1
1:A:298:ILE:CD1	1:A:304:LYS:HB2	0.41	2.46	14	1
1:A:267:ASN:ND2	1:A:298:ILE:CG2	0.41	2.83	18	1
1:A:298:ILE:CG2	1:A:302:GLY:HA3	0.41	2.45	18	1
1:A:316:LEU:HA	1:A:319:TYR:CD1	0.41	2.50	8	1
1:A:281:PHE:O	1:A:288:VAL:HG23	0.41	2.15	6	1
1:A:261:LEU:CD1	1:A:312:LEU:CG	0.41	2.98	6	1
1:A:336:CYS:H	1:A:342:ILE:HG23	0.41	1.76	17	1
1:A:283:SER:CB	1:A:312:LEU:CD2	0.41	2.99	1	1
1:A:258:ASP:O	1:A:259:ASN:C	0.41	2.59	17	3
1:A:275:GLY:O	1:A:276:ASN:C	0.41	2.59	4	2
1:A:277:CYS:SG	1:A:324:VAL:O	0.41	2.79	7	2
1:A:277:CYS:O	1:A:278:THR:OG1	0.41	2.39	9	1
1:A:252:VAL:HG22	1:A:265:LEU:CB	0.41	2.46	14	1
1:A:256:ASN:OD1	1:A:312:LEU:O	0.41	2.39	18	1
1:A:319:TYR:O	1:A:320:THR:C	0.41	2.59	18	1
1:A:316:LEU:HB3	1:A:319:TYR:CD2	0.41	2.51	19	1
1:A:308:PHE:O	1:A:309:PHE:O	0.41	2.39	3	1
1:A:251:HIS:C	1:A:252:VAL:CG2	0.41	2.90	8	1
1:A:257:GLU:O	1:A:258:ASP:C	0.41	2.60	13	1
1:A:279:PHE:CE1	1:A:323:VAL:CG2	0.40	3.04	12	1
1:A:301:LYS:HG2	1:A:301:LYS:O	0.40	2.16	15	1
1:A:317:SER:OG	1:A:337:ALA:C	0.40	2.60	5	1
1:A:317:SER:OG	1:A:338:ASP:OD2	0.40	2.39	12	1
1:A:251:HIS:C	1:A:252:VAL:HG23	0.40	2.36	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:283:SER:HB3	1:A:312:LEU:CD2	0.40	2.46	2	3
1:A:256:ASN:OD1	1:A:314:THR:OG1	0.40	2.40	4	1
1:A:259:ASN:C	1:A:260:SER:OG	0.40	2.60	19	1
1:A:267:ASN:O	1:A:300:ILE:O	0.40	2.40	3	1
1:A:314:THR:CG2	1:A:340:ASN:OD1	0.40	2.69	5	1
1:A:273:ILE:O	1:A:297:GLU:CD	0.40	2.60	9	1
1:A:267:ASN:HB3	1:A:298:ILE:CG2	0.40	2.46	10	1
1:A:272:ILE:O	1:A:273:ILE:C	0.40	2.59	12	2
1:A:298:ILE:CD1	1:A:304:LYS:HD3	0.40	2.47	14	1
1:A:267:ASN:OD1	1:A:267:ASN:O	0.40	2.39	18	1
1:A:343:THR:O	1:A:343:THR:OG1	0.40	2.40	1	1
1:A:275:GLY:C	1:A:276:ASN:CG	0.40	2.81	4	1
1:A:267:ASN:HB3	1:A:273:ILE:CD1	0.40	2.47	9	1
1:A:269:THR:C	1:A:270:ASN:CG	0.40	2.80	11	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	95/107 (89%)	68±2 (71±3%)	21±4 (23±4%)	6±2 (6±2%)	3	19
All	All	1900/2140 (89%)	1355 (71%)	428 (23%)	117 (6%)	3	19

All 27 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	346	SER	17
1	A	347	PRO	15
1	A	298	ILE	9
1	A	311	SER	9
1	A	321	MET	8
1	A	336	CYS	8
1	A	300	ILE	5
1	A	271	ILE	5

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Mol	Chain	Res	Type	Models (Total)
1	A	280	GLU	4
1	A	310	PRO	4
1	A	262	HIS	3
1	A	344	LEU	3
1	A	318	ASN	3
1	A	303	GLN	3
1	A	279	PHE	3
1	A	270	ASN	2
1	A	267	ASN	2
1	A	288	VAL	2
1	A	330	THR	2
1	A	269	THR	2
1	A	294	GLY	2
1	A	333	VAL	1
1	A	296	HIS	1
1	A	302	GLY	1
1	A	309	PHE	1
1	A	337	ALA	1
1	A	299	GLY	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	89/99 (90%)	72±2 (81±3%)	17±2 (19±3%)	4	36
All	All	1780/1980 (90%)	1442 (81%)	338 (19%)	4	36

All 52 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	335	LYS	20
1	A	249	LEU	20
1	A	265	LEU	20
1	A	250	LEU	20
1	A	314	THR	19
1	A	336	CYS	16

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Mol	Chain	Res	Type	Models (Total)
1	A	309	PHE	16
1	A	333	VAL	14
1	A	301	LYS	13
1	A	292	LYS	12
1	A	325	ASN	12
1	A	345	LYS	11
1	A	279	PHE	9
1	A	271	ILE	9
1	A	338	ASP	8
1	A	268	LYS	8
1	A	348	LEU	7
1	A	307	TRP	7
1	A	255	SER	7
1	A	312	LEU	6
1	A	321	MET	6
1	A	318	ASN	6
1	A	266	TYR	6
1	A	317	SER	5
1	A	329	GLU	5
1	A	262	HIS	4
1	A	327	ASP	4
1	A	256	ASN	4
1	A	258	ASP	3
1	A	346	SER	3
1	A	341	GLU	3
1	A	283	SER	3
1	A	260	SER	3
1	A	297	GLU	3
1	A	303	GLN	3
1	A	320	THR	3
1	A	282	SER	2
1	A	339	SER	2
1	A	324	VAL	2
1	A	273	ILE	2
1	A	305	GLU	1
1	A	276	ASN	1
1	A	278	THR	1
1	A	300	ILE	1
1	A	296	HIS	1
1	A	277	CYS	1
1	A	251	HIS	1
1	A	269	THR	1

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Mol	Chain	Res	Type	Models (Total)
1	A	311	SER	1
1	A	259	ASN	1
1	A	281	PHE	1
1	A	331	ILE	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](#)

There are no ligands in this entry.

### 6.7 Other polymers [i](#)

There are no such molecules in this entry.

### 6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 7 Chemical shift validation

The completeness of assignment taking into account all chemical shift lists is 94% for the well-defined parts and 94% for the entire structure.

### 7.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: *assigned\_chem\_shift\_list\_1*

#### 7.1.1 Bookkeeping

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1303
Number of shifts mapped to atoms	1303
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	102	$-0.14 \pm 0.23$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}_\beta$	97	$-0.09 \pm 0.13$	None needed ( $< 0.5$ ppm)
$^{13}\text{C}'$	92	$0.36 \pm 0.16$	None needed ( $< 0.5$ ppm)
$^{15}\text{N}$	95	$0.66 \pm 0.88$	None needed (imprecise)

#### 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 94%, i.e. 1095 atoms were assigned a chemical shift out of a possible 1171. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	455/468 (97%)	184/186 (99%)	181/192 (94%)	90/90 (100%)
Sidechain	564/600 (94%)	343/352 (97%)	212/231 (92%)	9/17 (53%)

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	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Aromatic	76/103 (74%)	40/56 (71%)	36/43 (84%)	0/4 (0%)
Overall	1095/1171 (94%)	567/594 (95%)	429/466 (92%)	99/111 (89%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 94%, i.e. 1172 atoms were assigned a chemical shift out of a possible 1253. 0 out of 16 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	<sup>1</sup> H	<sup>13</sup> C	<sup>15</sup> N
Backbone	485/501 (97%)	196/199 (98%)	194/206 (94%)	95/96 (99%)
Sidechain	611/649 (94%)	372/381 (98%)	228/249 (92%)	11/19 (58%)
Aromatic	76/103 (74%)	40/56 (71%)	36/43 (84%)	0/4 (0%)
Overall	1172/1253 (94%)	608/636 (96%)	458/498 (92%)	106/119 (89%)

#### 7.1.4 Statistically unusual chemical shifts ⓘ

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

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	289	PHE	HB2	1.00	4.85 – 1.15	-5.4

#### 7.1.5 Random Coil Index (RCI) plots ⓘ

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.

Random coil index (RCI) for chain A:

