



# Full wwPDB NMR Structure Validation Report ⓘ

Jun 17, 2020 – 06:43 am BST

PDB ID : 6QEB  
Title : Assessment of a large enzyme-drug complex by proton-detected solid-state NMR without deuteration  
Authors : Vasa, S.K.  
Deposited on : 2019-01-07

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  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
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

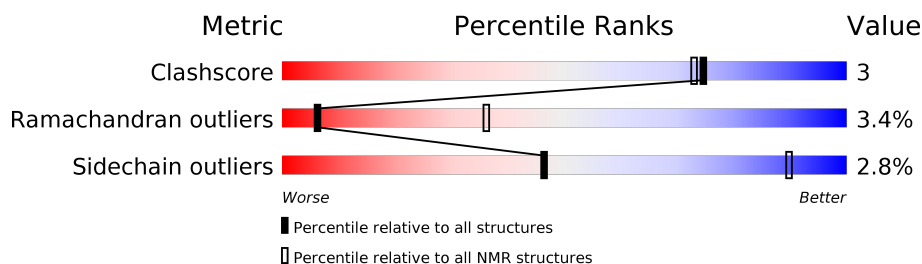
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*SOLID-STATE NMR*

The overall completeness of chemical shifts assignment is 72%.

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	260	

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 1 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:29-A:196, A:203-A:231, A:239-A:260 (219)	1.45	1

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 2 clusters and 9 single-model clusters were found.

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

### 3 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4122 atoms, of which 2035 are hydrogens and 0 are deuteriums.

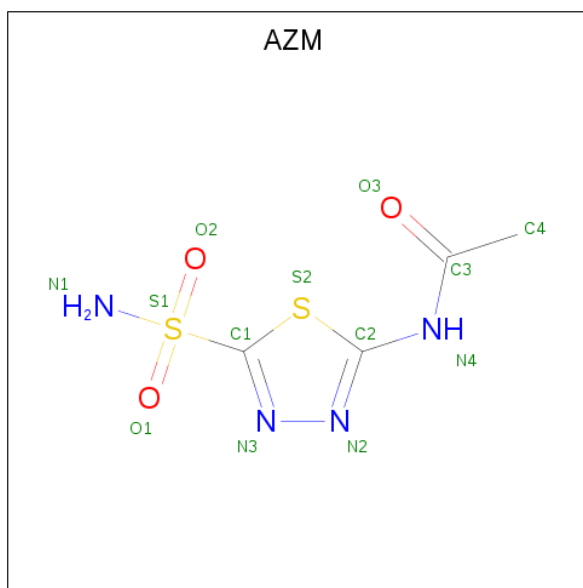
- Molecule 1 is a protein called Carbonic anhydrase 2.

Mol	Chain	Residues	Atoms						Trace
1	A	260	Total	C	H	N	O	S	0
			4108	1329	2035	357	384	3	

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	
2	A	1	Total	Zn
			1	1

- Molecule 3 is 5-ACETAMIDO-1,3,4-THIADIAZOLE-2-SULFONAMIDE (three-letter code: AZM) (formula: C<sub>4</sub>H<sub>6</sub>N<sub>4</sub>O<sub>3</sub>S<sub>2</sub>).



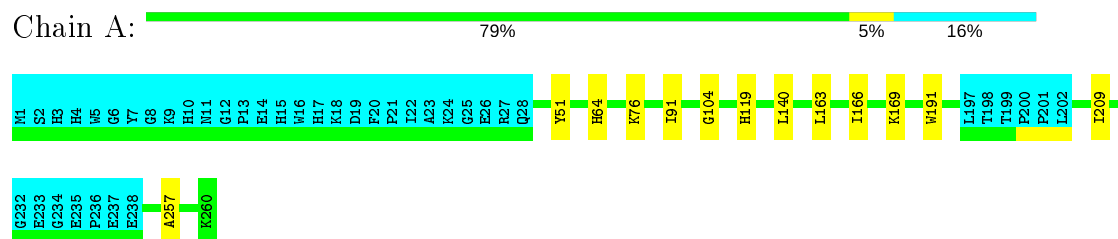
Mol	Chain	Residues	Atoms				
3	A	1	Total	C	N	O	S
			13	4	4	3	2

## 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: Carbonic anhydrase 2

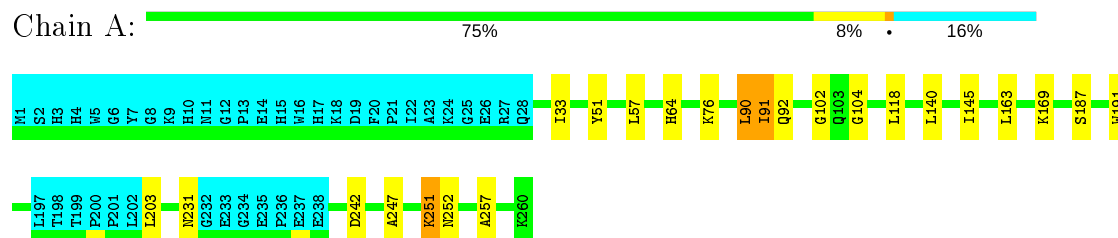


### 4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1 (medoid)

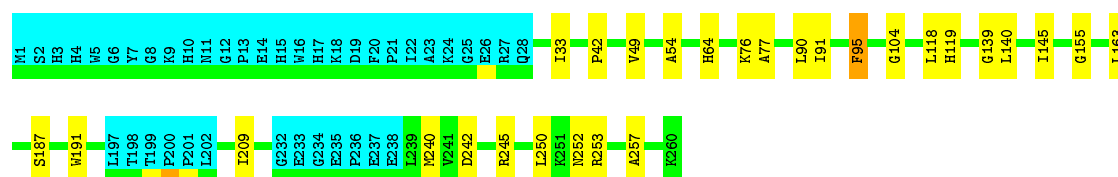
- Molecule 1: Carbonic anhydrase 2



#### 4.2.2 Score per residue for model 2

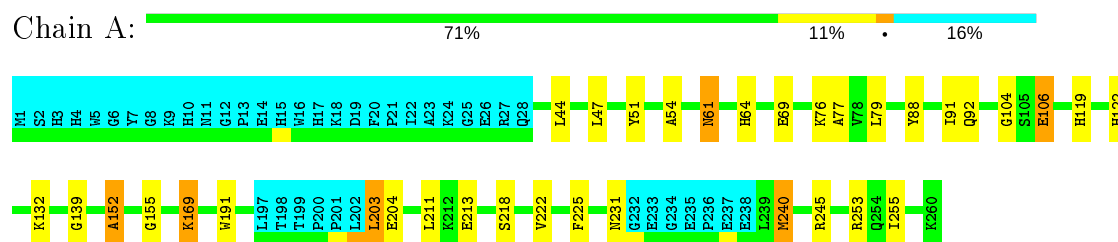
- Molecule 1: Carbonic anhydrase 2





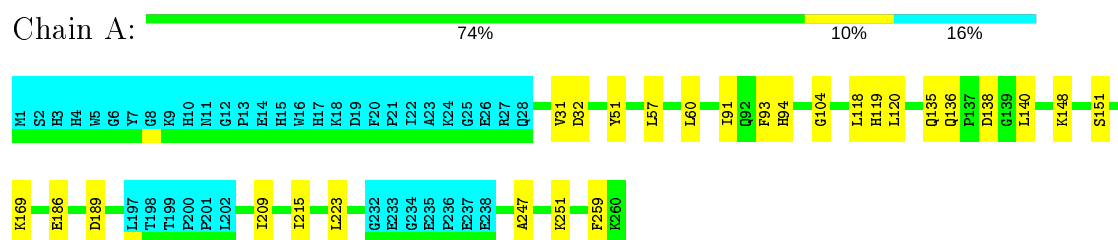
### 4.2.3 Score per residue for model 3

- Molecule 1: Carbonic anhydrase 2



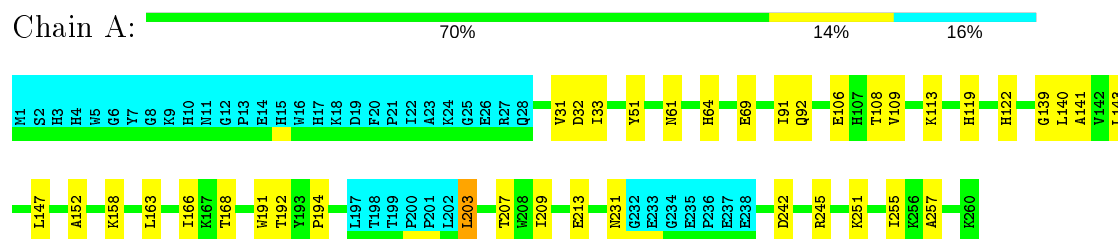
### 4.2.4 Score per residue for model 4

- Molecule 1: Carbonic anhydrase 2



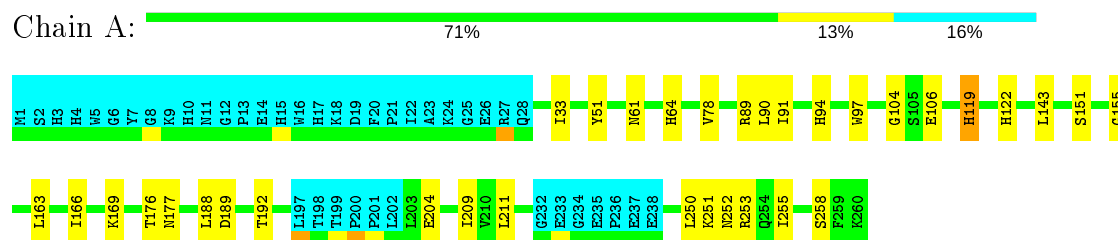
### 4.2.5 Score per residue for model 5

- Molecule 1: Carbonic anhydrase 2



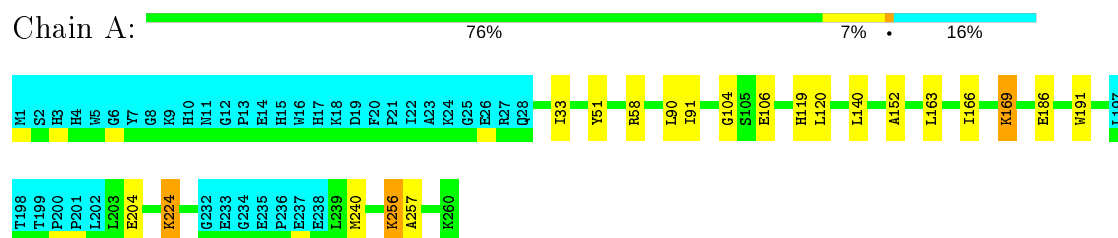
### 4.2.6 Score per residue for model 6

- Molecule 1: Carbonic anhydrase 2



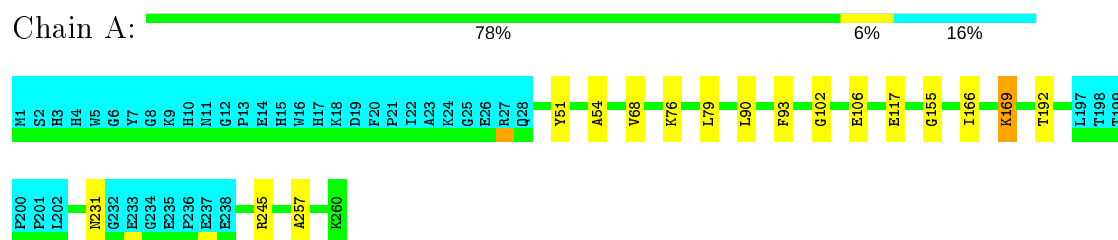
#### 4.2.7 Score per residue for model 7

- Molecule 1: Carbonic anhydrase 2



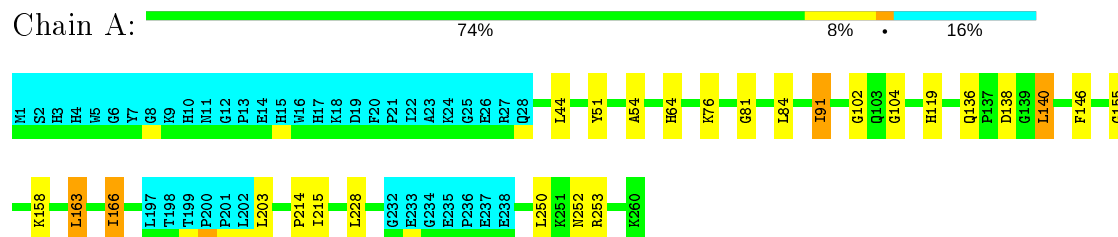
#### 4.2.8 Score per residue for model 8

- Molecule 1: Carbonic anhydrase 2



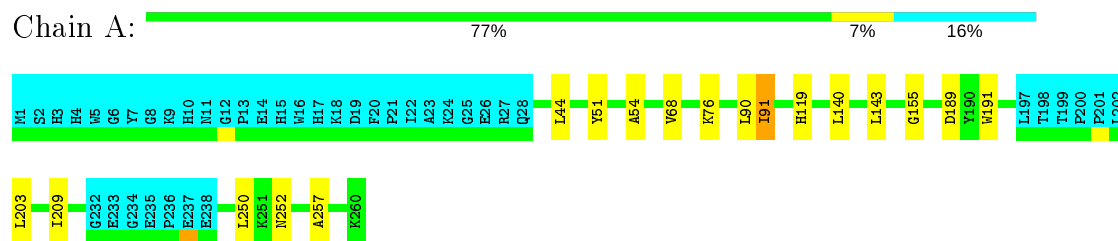
#### 4.2.9 Score per residue for model 9

- Molecule 1: Carbonic anhydrase 2



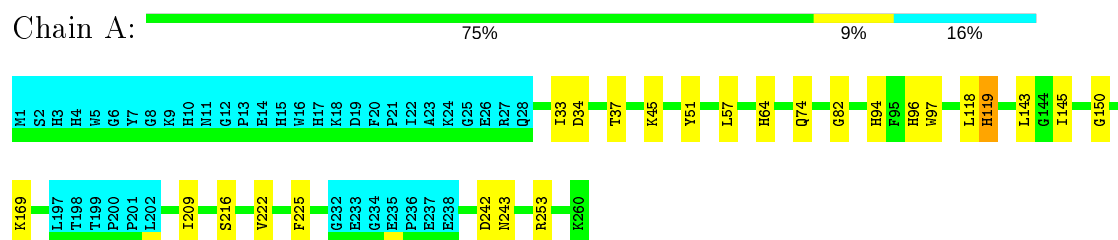
### 4.2.10 Score per residue for model 10

- Molecule 1: Carbonic anhydrase 2



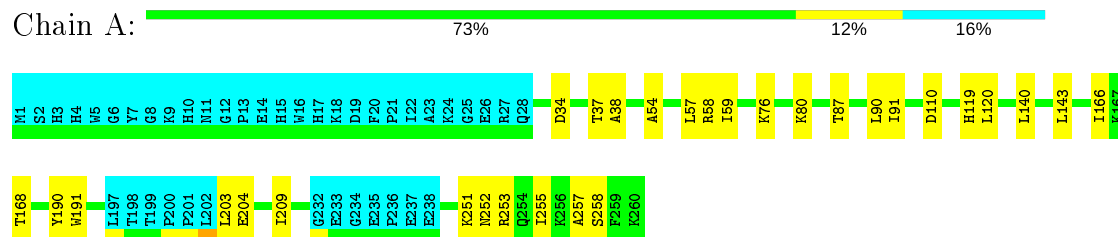
### 4.2.11 Score per residue for model 11

- Molecule 1: Carbonic anhydrase 2



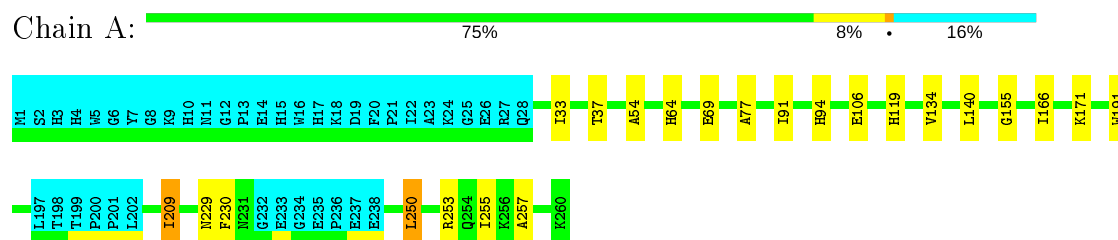
### 4.2.12 Score per residue for model 12

- Molecule 1: Carbonic anhydrase 2



### 4.2.13 Score per residue for model 13

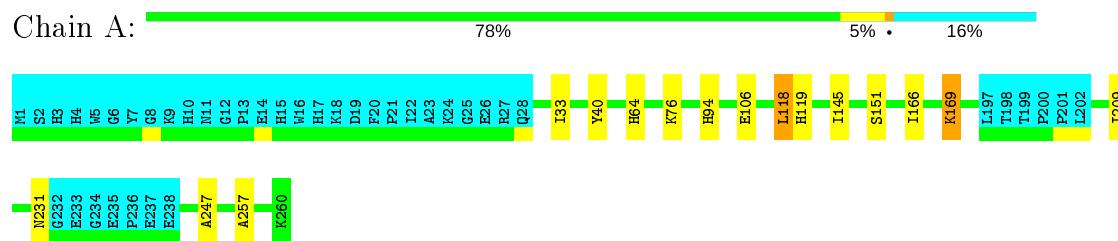
- Molecule 1: Carbonic anhydrase 2





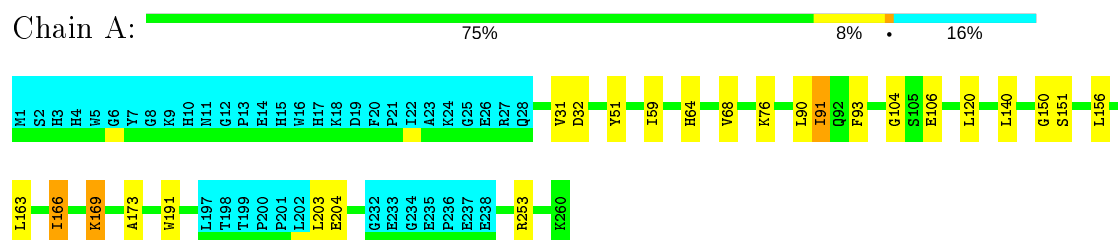
## 4.2.14 Score per residue for model 14

- Molecule 1: Carbonic anhydrase 2



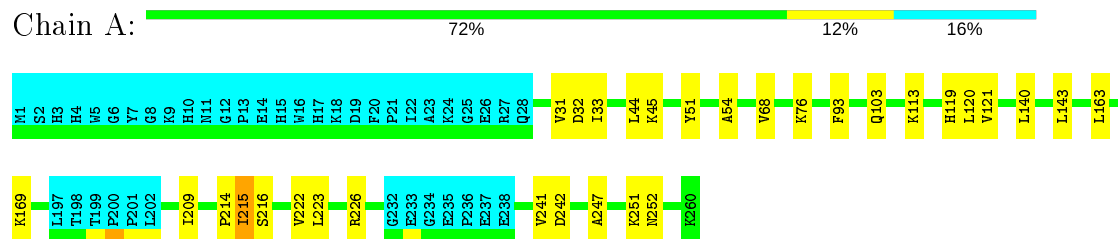
## 4.2.15 Score per residue for model 15

- Molecule 1: Carbonic anhydrase 2



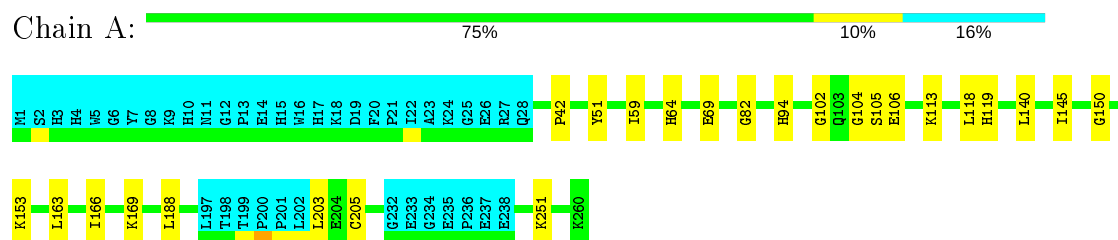
## 4.2.16 Score per residue for model 16

- Molecule 1: Carbonic anhydrase 2



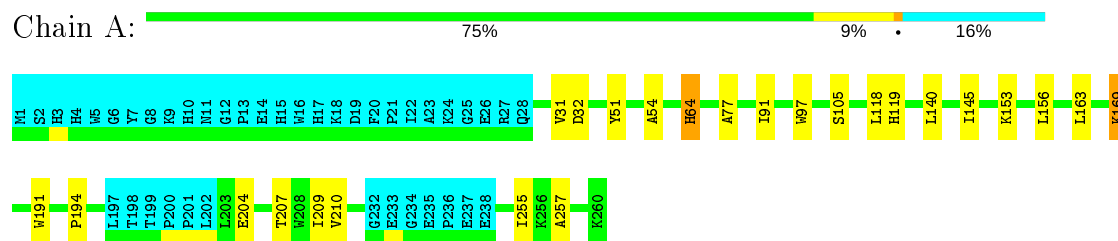
## 4.2.17 Score per residue for model 17

- Molecule 1: Carbonic anhydrase 2



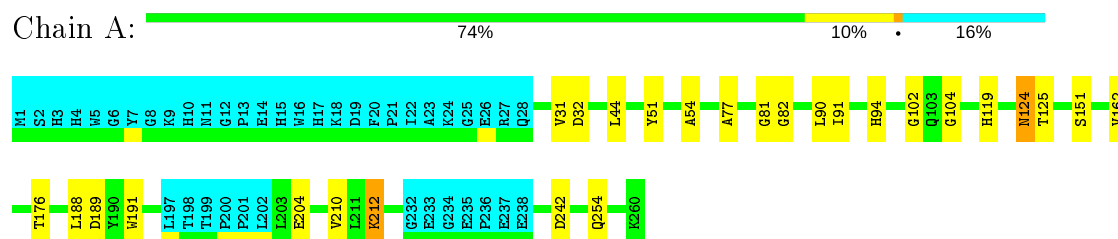
### 4.2.18 Score per residue for model 18

- Molecule 1: Carbonic anhydrase 2



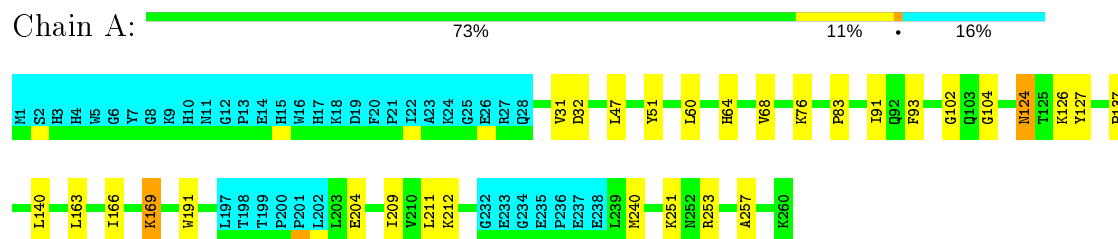
### 4.2.19 Score per residue for model 19

- Molecule 1: Carbonic anhydrase 2



### 4.2.20 Score per residue for model 20

- Molecule 1: Carbonic anhydrase 2



## 5 Refinement protocol and experimental data overview

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

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

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

Software name	Classification	Version
ARIA	refinement	
ARIA	structure calculation	

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	2450
Number of shifts mapped to atoms	2450
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	72%

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

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

## 6 Model quality ⓘ

### 6.1 Standard geometry ⓘ

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

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	1739	1730	1726	10±3
3	A	13	0	6	1±0
All	All	35060	34600	34625	220

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 3.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
3:A:302:AZM:S2	3:A:302:AZM:C1	1.48	2.01	12	12
3:A:302:AZM:C1	3:A:302:AZM:S2	1.48	2.01	10	5
1:A:90:LEU:H	1:A:90:LEU:HD23	0.62	1.54	12	1
1:A:118:LEU:HD21	1:A:145:ILE:HB	0.60	1.72	14	1
1:A:215:ILE:HD13	1:A:215:ILE:H	0.58	1.58	16	1
1:A:191:TRP:HA	1:A:257:ALA:HB1	0.54	1.77	10	9
1:A:176:THR:HG23	1:A:177:ASN:HD22	0.54	1.63	6	1
1:A:59:ILE:HB	1:A:166:ILE:HD12	0.53	1.79	17	1
1:A:250:LEU:HD23	1:A:250:LEU:H	0.53	1.63	2	1
1:A:166:ILE:HG23	1:A:173:ALA:HB2	0.53	1.80	15	1
1:A:54:ALA:HB2	1:A:77:ALA:HB2	0.52	1.80	18	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:93:PHE:HB3	1:A:120:LEU:HD13	0.52	1.81	15	1
1:A:90:LEU:N	1:A:90:LEU:HD13	0.52	2.20	1	1
1:A:212:LYS:H	1:A:212:LYS:HD2	0.52	1.65	19	1
1:A:143:LEU:HD13	1:A:209:ILE:HB	0.50	1.82	16	1
1:A:141:ALA:HB1	1:A:209:ILE:HD13	0.50	1.82	5	1
1:A:124:ASN:HD22	1:A:124:ASN:N	0.50	2.04	20	1
1:A:91:ILE:HG22	1:A:92:GLN:HG3	0.49	1.83	3	2
1:A:68:VAL:HG21	1:A:93:PHE:CE1	0.49	2.43	15	1
1:A:118:LEU:HB2	1:A:145:ILE:HB	0.48	1.84	2	4
1:A:134:VAL:HA	1:A:140:LEU:HD22	0.48	1.84	13	1
1:A:209:ILE:HD12	1:A:209:ILE:N	0.48	2.24	5	3
1:A:140:LEU:N	1:A:140:LEU:HD22	0.48	2.23	17	2
1:A:140:LEU:HD23	1:A:140:LEU:H	0.48	1.68	16	1
1:A:169:LYS:HD2	1:A:169:LYS:N	0.48	2.23	3	3
1:A:91:ILE:N	1:A:91:ILE:HD12	0.48	2.23	12	6
1:A:79:LEU:N	1:A:79:LEU:HD22	0.47	2.24	3	1
1:A:31:VAL:HG22	1:A:32:ASP:H	0.47	1.69	18	4
1:A:47:LEU:HD23	1:A:47:LEU:H	0.47	1.69	3	1
1:A:94:HIS:NE2	1:A:119:HIS:HB2	0.47	2.25	19	7
1:A:31:VAL:HG12	1:A:32:ASP:N	0.47	2.25	19	3
1:A:54:ALA:HA	1:A:76:LYS:HB3	0.46	1.87	10	5
1:A:136:GLN:HE21	1:A:138:ASP:HB2	0.46	1.69	9	1
1:A:192:THR:H	1:A:257:ALA:HA	0.46	1.70	8	1
1:A:90:LEU:HD23	1:A:122:HIS:HA	0.46	1.88	6	1
1:A:91:ILE:HD13	1:A:91:ILE:N	0.46	2.26	9	2
1:A:140:LEU:H	1:A:140:LEU:HD23	0.46	1.71	18	1
1:A:203:LEU:HD12	1:A:203:LEU:O	0.46	2.10	5	1
1:A:78:VAL:HA	1:A:89:ARG:HG3	0.45	1.88	6	1
1:A:169:LYS:HE3	1:A:169:LYS:N	0.45	2.26	7	1
1:A:54:ALA:HA	1:A:76:LYS:HG3	0.45	1.87	2	1
1:A:90:LEU:N	1:A:90:LEU:HD22	0.45	2.26	2	1
1:A:103:GLN:HA	1:A:113:LYS:HD2	0.45	1.89	16	1
1:A:34:ASP:HB2	1:A:37:THR:HG22	0.45	1.87	11	2
1:A:81:GLY:HA3	1:A:84:LEU:HD21	0.45	1.87	9	1
1:A:211:LEU:HG	1:A:212:LYS:H	0.45	1.72	20	1
1:A:209:ILE:N	1:A:209:ILE:HD12	0.44	2.27	6	4
1:A:61:ASN:ND2	1:A:166:ILE:HG21	0.44	2.26	5	1
1:A:90:LEU:N	1:A:90:LEU:HD12	0.44	2.28	10	4
1:A:44:LEU:HD22	1:A:44:LEU:N	0.44	2.28	9	2
1:A:106:GLU:HA	1:A:245:ARG:HB3	0.44	1.90	3	1
1:A:37:THR:HG23	1:A:255:ILE:HG22	0.44	1.89	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:33:ILE:N	1:A:33:ILE:HD12	0.44	2.28	6	5
1:A:240:MET:N	1:A:240:MET:SD	0.44	2.91	3	1
1:A:152:ALA:HB2	1:A:218:SER:HB3	0.44	1.89	3	1
1:A:105:SER:H	1:A:113:LYS:HE2	0.43	1.73	17	1
1:A:120:LEU:HD23	1:A:121:VAL:N	0.43	2.28	16	1
1:A:106:GLU:HA	1:A:245:ARG:HB2	0.43	1.89	5	1
1:A:69:GLU:HA	1:A:92:GLN:HG2	0.43	1.89	3	2
1:A:255:ILE:HD12	1:A:255:ILE:N	0.43	2.29	3	1
1:A:68:VAL:HG12	1:A:93:PHE:CD2	0.43	2.49	8	1
1:A:33:ILE:HD12	1:A:33:ILE:N	0.43	2.29	1	2
1:A:91:ILE:HD12	1:A:91:ILE:N	0.43	2.29	18	3
1:A:44:LEU:HD23	1:A:45:LYS:N	0.43	2.29	16	1
1:A:194:PRO:HA	1:A:207:THR:HG23	0.43	1.90	5	2
1:A:91:ILE:N	1:A:91:ILE:HD13	0.43	2.29	10	1
1:A:192:THR:HG22	1:A:258:SER:N	0.43	2.29	6	1
1:A:60:LEU:HD22	1:A:60:LEU:N	0.43	2.29	4	1
1:A:203:LEU:HD13	1:A:204:GLU:H	0.43	1.73	3	1
1:A:61:ASN:N	1:A:61:ASN:HD22	0.43	2.12	3	1
1:A:122:HIS:NE2	1:A:143:LEU:HG	0.43	2.27	5	1
1:A:191:TRP:HB2	1:A:211:LEU:HD22	0.43	1.90	3	1
1:A:88:TYR:HB3	1:A:122:HIS:HB3	0.43	1.90	3	1
1:A:153:LYS:HB3	1:A:156:LEU:HB2	0.43	1.91	18	1
1:A:222:VAL:HB	1:A:225:PHE:HB2	0.43	1.90	11	1
1:A:44:LEU:N	1:A:44:LEU:HD12	0.43	2.29	3	1
1:A:250:LEU:HD22	1:A:250:LEU:N	0.42	2.28	6	3
1:A:256:LYS:HD2	1:A:256:LYS:H	0.42	1.73	7	1
1:A:146:PHE:H	1:A:214:PRO:HG2	0.42	1.74	9	1
1:A:91:ILE:HG12	1:A:92:GLN:N	0.42	2.28	1	1
1:A:124:ASN:HD22	1:A:125:THR:N	0.42	2.11	19	1
1:A:44:LEU:HD11	1:A:81:GLY:HA3	0.42	1.91	19	1
1:A:190:TYR:HB2	1:A:258:SER:HB3	0.42	1.91	12	1
1:A:169:LYS:N	1:A:169:LYS:HD2	0.42	2.30	1	2
1:A:209:ILE:N	1:A:209:ILE:HD13	0.42	2.30	13	1
1:A:80:LYS:HD2	1:A:87:THR:HB	0.42	1.90	12	1
1:A:118:LEU:HD21	1:A:145:ILE:HD12	0.42	1.90	11	1
1:A:203:LEU:HD22	1:A:203:LEU:N	0.42	2.29	17	1
1:A:68:VAL:HG23	1:A:93:PHE:O	0.42	2.15	15	2
1:A:59:ILE:HD12	1:A:59:ILE:N	0.42	2.30	15	1
1:A:143:LEU:HA	1:A:209:ILE:HB	0.42	1.92	10	1
1:A:245:ARG:HE	1:A:245:ARG:HA	0.42	1.75	8	1
1:A:163:LEU:HD12	1:A:228:LEU:HD11	0.42	1.92	9	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:188:LEU:HG	1:A:189:ASP:H	0.42	1.73	19	1
1:A:203:LEU:N	1:A:203:LEU:HD23	0.42	2.30	10	1
1:A:68:VAL:HG22	1:A:93:PHE:O	0.42	2.15	16	1
1:A:58:ARG:HG3	1:A:59:ILE:N	0.42	2.30	12	1
1:A:137:PRO:HB3	1:A:204:GLU:HG3	0.42	1.90	20	1
1:A:108:THR:HG23	1:A:113:LYS:N	0.41	2.31	5	1
1:A:140:LEU:N	1:A:140:LEU:HD23	0.41	2.30	12	1
1:A:57:LEU:N	1:A:57:LEU:HD12	0.41	2.30	12	1
1:A:96:HIS:ND1	1:A:243:ASN:HB3	0.41	2.31	11	1
1:A:90:LEU:H	1:A:90:LEU:HD22	0.41	1.75	1	1
1:A:33:ILE:HG23	1:A:255:ILE:HG12	0.41	1.92	5	1
1:A:40:TYR:HA	1:A:257:ALA:HA	0.41	1.91	14	1
1:A:192:THR:HG22	1:A:257:ALA:HA	0.41	1.93	5	1
1:A:191:TRP:HB3	1:A:210:VAL:HB	0.41	1.92	18	1
1:A:136:GLN:HG2	1:A:138:ASP:H	0.41	1.75	4	1
1:A:169:LYS:N	1:A:169:LYS:HE2	0.41	2.30	15	1
1:A:31:VAL:O	1:A:33:ILE:HD12	0.41	2.16	16	1
1:A:255:ILE:N	1:A:255:ILE:HD12	0.41	2.30	18	1
1:A:166:ILE:N	1:A:166:ILE:HD13	0.41	2.30	9	1
1:A:95:PHE:N	1:A:95:PHE:CD1	0.41	2.88	2	1
1:A:93:PHE:HB3	1:A:120:LEU:HA	0.41	1.93	4	1
1:A:64:HIS:HA	1:A:169:LYS:HG2	0.41	1.93	18	1
1:A:156:LEU:HD23	1:A:156:LEU:N	0.41	2.31	15	1
1:A:222:VAL:HB	1:A:225:PHE:HB3	0.41	1.92	3	1
1:A:33:ILE:HB	1:A:109:VAL:HG12	0.41	1.91	5	1
1:A:211:LEU:N	1:A:211:LEU:HD22	0.41	2.31	6	1
1:A:166:ILE:HG22	1:A:171:LYS:CB	0.41	2.46	13	1
1:A:33:ILE:HG23	1:A:255:ILE:HG21	0.41	1.93	6	1
1:A:188:LEU:HD23	1:A:189:ASP:N	0.41	2.31	6	1
1:A:38:ALA:HA	1:A:255:ILE:HG22	0.41	1.91	12	1
1:A:189:ASP:HB3	1:A:259:PHE:HB2	0.41	1.92	4	1
1:A:54:ALA:HA	1:A:76:LYS:HG2	0.41	1.93	3	1
1:A:140:LEU:HD23	1:A:140:LEU:N	0.41	2.31	9	1
1:A:224:LYS:N	1:A:224:LYS:HD2	0.40	2.31	7	1
1:A:143:LEU:HD23	1:A:209:ILE:HB	0.40	1.92	11	1
1:A:215:ILE:HD12	1:A:215:ILE:H	0.40	1.76	4	1
3:A:302:AZM:N2	3:A:302:AZM:O3	0.40	2.52	17	2
1:A:90:LEU:HD23	1:A:120:LEU:HD21	0.40	1.92	7	1
1:A:97:TRP:H	1:A:243:ASN:HB2	0.40	1.76	11	1
1:A:245:ARG:NE	1:A:245:ARG:HA	0.40	2.31	2	1
1:A:162:VAL:HG11	1:A:176:THR:HG21	0.40	1.92	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:120:LEU:HD23	1:A:143:LEU:HB3	0.40	1.93	12	1
1:A:191:TRP:HB2	1:A:210:VAL:HB	0.40	1.93	19	1
1:A:143:LEU:N	1:A:143:LEU:HD22	0.40	2.32	6	1
1:A:61:ASN:HD22	1:A:169:LYS:HA	0.40	1.76	6	1
3:A:302:AZM:O3	3:A:302:AZM:N2	0.40	2.52	7	1
1:A:250:LEU:H	1:A:250:LEU:HD23	0.40	1.75	13	1
1:A:223:LEU:HD12	1:A:226:ARG:HD2	0.40	1.93	16	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	218/260 (84%)	190±4 (87±2%)	21±3 (9±2%)	7±3 (3±1%)	6	36
All	All	4360/5200 (84%)	3799 (87%)	413 (9%)	148 (3%)	6	36

All 39 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	51	TYR	16
1	A	64	HIS	13
1	A	104	GLY	11
1	A	106	GLU	8
1	A	253	ARG	8
1	A	251	LYS	8
1	A	155	GLY	7
1	A	252	ASN	7
1	A	242	ASP	6
1	A	102	GLY	6
1	A	151	SER	5
1	A	247	ALA	4
1	A	76	LYS	4
1	A	231	ASN	4
1	A	166	ILE	4

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Mol	Chain	Res	Type	Models (Total)
1	A	152	ALA	3
1	A	82	GLY	3
1	A	139	GLY	3
1	A	150	GLY	3
1	A	187	SER	2
1	A	42	PRO	2
1	A	97	TRP	2
1	A	69	GLU	2
1	A	216	SER	2
1	A	49	VAL	1
1	A	91	ILE	1
1	A	188	LEU	1
1	A	105	SER	1
1	A	214	PRO	1
1	A	205	CYS	1
1	A	74	GLN	1
1	A	240	MET	1
1	A	215	ILE	1
1	A	147	LEU	1
1	A	189	ASP	1
1	A	222	VAL	1
1	A	47	LEU	1
1	A	241	VAL	1
1	A	83	PRO	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	191/225 (85%)	186±2 (97±1%)	5±2 (3±1%)	46	90
All	All	3820/4500 (85%)	3713 (97%)	107 (3%)	46	90

All 43 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	169	LYS	11

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Mol	Chain	Res	Type	Models (Total)
1	A	119	HIS	11
1	A	163	LEU	11
1	A	140	LEU	8
1	A	91	ILE	5
1	A	204	GLU	5
1	A	203	LEU	5
1	A	166	ILE	4
1	A	209	ILE	3
1	A	240	MET	3
1	A	57	LEU	3
1	A	124	ASN	2
1	A	90	LEU	2
1	A	118	LEU	2
1	A	186	GLU	2
1	A	213	GLU	2
1	A	158	LYS	2
1	A	229	ASN	1
1	A	135	GLN	1
1	A	68	VAL	1
1	A	223	LEU	1
1	A	224	LYS	1
1	A	110	ASP	1
1	A	212	LYS	1
1	A	256	LYS	1
1	A	117	GLU	1
1	A	126	LYS	1
1	A	215	ILE	1
1	A	95	PHE	1
1	A	61	ASN	1
1	A	79	LEU	1
1	A	153	LYS	1
1	A	253	ARG	1
1	A	251	LYS	1
1	A	148	LYS	1
1	A	132	LYS	1
1	A	58	ARG	1
1	A	127	TYR	1
1	A	45	LYS	1
1	A	250	LEU	1
1	A	254	GLN	1
1	A	191	TRP	1
1	A	60	LEU	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 carbohydrates in this entry.

## 6.6 Ligand geometry ⓘ

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
3	AZM	A	302	2	8,13,13	5.89±0.02	1±0 (12±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
3	AZM	A	302	2	9,19,19	2.22±0.01	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means

no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AZM	A	302	2	-	0±0,2,10,10	0±0,1,1,1

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
3	A	302	AZM	N3-N2	16.24	1.05	1.37	12	20

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 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 72% for the well-defined parts and 69% for the entire structure.

### 7.1 Chemical shift list 1

File name: input\_cs.cif

Chemical shift list name: *starch\_output*

#### 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	2450
Number of shifts mapped to atoms	2450
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	10

#### 7.1.2 Chemical shift referencing

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	254	$0.78 \pm 0.12$	Should be applied
$^{13}\text{C}_\beta$	213	$0.71 \pm 0.19$	Should be applied
$^{13}\text{C}'$	221	$0.61 \pm 0.10$	Should be applied
$^{15}\text{N}$	237	$1.16 \pm 0.20$	Should be applied

#### 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 72%, i.e. 1966 atoms were assigned a chemical shift out of a possible 2718. 33 out of 41 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	$^1\text{H}$	$^{13}\text{C}$	$^{15}\text{N}$
Backbone	1016/1071 (95%)	400/426 (94%)	409/438 (93%)	207/207 (100%)
Sidechain	950/1379 (69%)	556/810 (69%)	394/511 (77%)	0/58 (0%)

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	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Aromatic	0/268 (0%)	0/141 (0%)	0/111 (0%)	0/16 (0%)
Overall	1966/2718 (72%)	956/1377 (69%)	803/1060 (76%)	207/281 (74%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 69%, i.e. 2247 atoms were assigned a chemical shift out of a possible 3234. 33 out of 43 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	<b>Total</b>	<b><sup>1</sup>H</b>	<b><sup>13</sup>C</b>	<b><sup>15</sup>N</b>
Backbone	1170/1266 (92%)	458/503 (91%)	475/520 (91%)	237/243 (98%)
Sidechain	1077/1619 (67%)	629/956 (66%)	448/597 (75%)	0/66 (0%)
Aromatic	0/349 (0%)	0/182 (0%)	0/139 (0%)	0/28 (0%)
Overall	2247/3234 (69%)	1087/1641 (66%)	923/1256 (73%)	237/337 (70%)

Note: This is a solid-state NMR structure, where hydrogen atoms are typically not assigned a chemical shift value, which may lead to lower completeness of assignment measure.

#### 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	27	ARG	CZ	60.10	176.59 – 143.59	-30.3
1	A	153	LYS	CD	58.40	34.86 – 23.06	24.9
1	A	194	PRO	CA	45.76	71.13 – 55.53	-11.3
1	A	108	THR	CG2	29.34	27.15 – 15.95	7.0
1	A	147	LEU	CB	29.66	51.69 – 32.89	-6.7
1	A	254	GLN	CB	40.82	38.36 – 19.96	6.3
1	A	242	ASP	CB	30.78	49.06 – 32.66	-6.1
1	A	197	LEU	CG	33.20	32.55 – 21.05	5.6
1	A	118	LEU	HB2	3.37	3.32 – -0.08	5.1
1	A	118	LEU	HB3	3.37	3.34 – -0.26	5.1

#### 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:

