



Full wwPDB NMR Structure Validation Report ⓘ

Aug 9, 2020 – 11:18 PM BST

PDB ID : 2LI0
Title : Mono-O-GalNAc glycosylated Mucin sequence based on MUC2 Mucin glycoprotein tandem repeat
Authors : Borgert, A.; Heimbürg-Molinaro, J.; Lasanajak, Y.; Ju, T.; Liu, M.; Thompson, P.; Ragupathi, G.; Barany, G.; Cummings, R.; Smith, D.; Live, D.
Deposited on : 2011-08-18

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

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 : 2.13.1
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

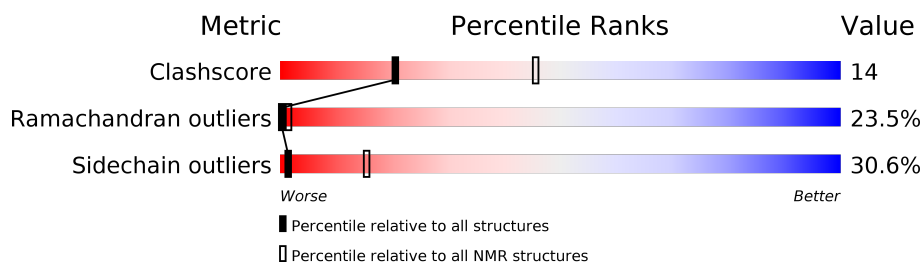
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 83%.

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 ≥ 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	9	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA and RNA chains that are outliers for geometric criteria:

Mol	Chain	Compound	Res	Total models with violations	
				Chirality	Geometry
2	A	A2G	10	1	-

2 Ensemble composition and analysis ⓘ

This entry contains 62 models.

Cyrange was unable to find well-defined residues.

Error message: The number of core atoms (3) was below the domain threshold value (8).

NmrClust was unable to cluster the ensemble.

Error message: Wrapper check: not enough residues in core to run NmrClust

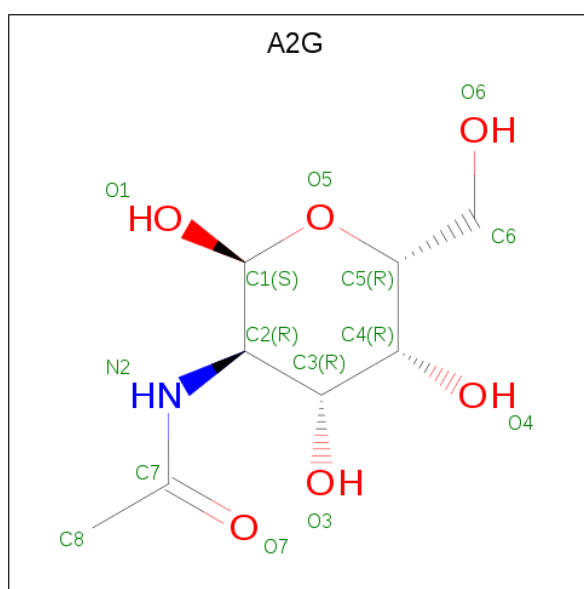
3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 147 atoms, of which 77 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MUC2 Mucin Domain Peptide.

Mol	Chain	Residues	Atoms					Trace
1	A	9	Total	C	H	N	O	1
			119	36	63	9	11	

- Molecule 2 is 2-acetamido-2-deoxy- α -D-galactopyranose (three-letter code: A2G) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				
2	A	1	Total	C	H	N	O
			28	8	14	1	5

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: MUC2 Mucin Domain Peptide

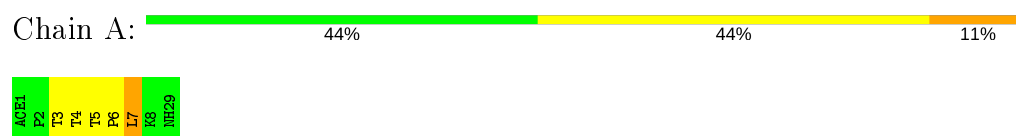


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

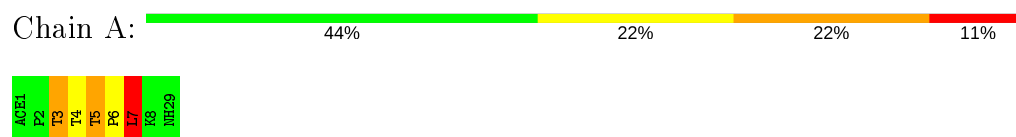
4.2.1 Score per residue for model 1

- Molecule 1: MUC2 Mucin Domain Peptide



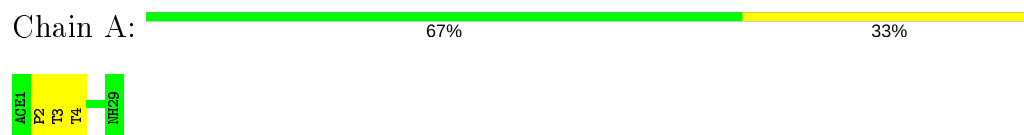
4.2.2 Score per residue for model 2

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.3 Score per residue for model 3

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.4 Score per residue for model 4

- Molecule 1: MUC2 Mucin Domain Peptide



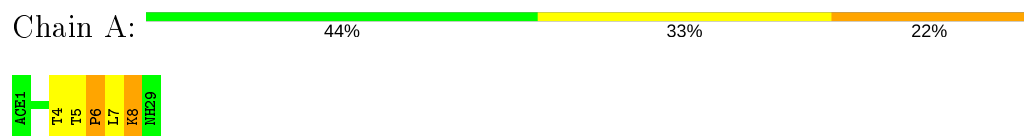
4.2.5 Score per residue for model 5

- Molecule 1: MUC2 Mucin Domain Peptide



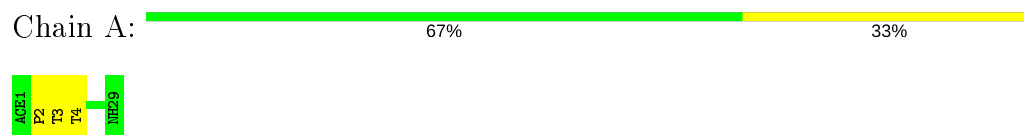
4.2.6 Score per residue for model 6

- Molecule 1: MUC2 Mucin Domain Peptide



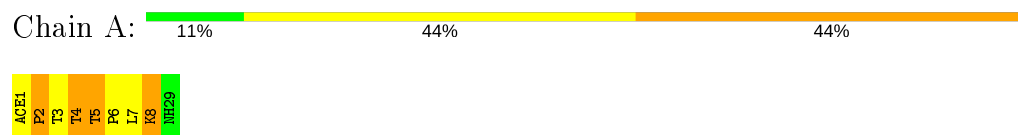
4.2.7 Score per residue for model 7

- Molecule 1: MUC2 Mucin Domain Peptide



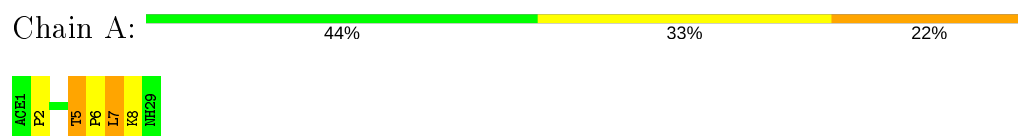
4.2.8 Score per residue for model 8

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.9 Score per residue for model 9

- Molecule 1: MUC2 Mucin Domain Peptide



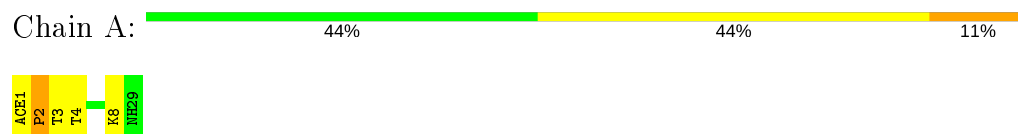
4.2.10 Score per residue for model 10

- Molecule 1: MUC2 Mucin Domain Peptide



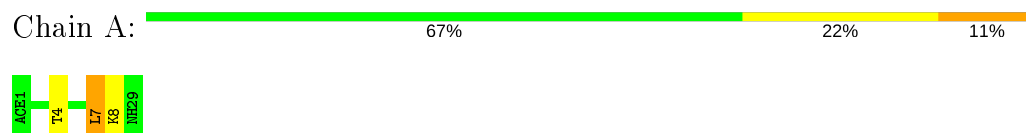
4.2.11 Score per residue for model 11

- Molecule 1: MUC2 Mucin Domain Peptide



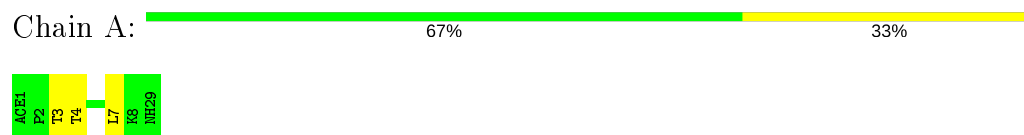
4.2.12 Score per residue for model 12

- Molecule 1: MUC2 Mucin Domain Peptide



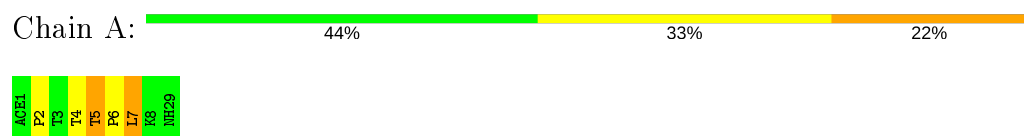
4.2.13 Score per residue for model 13

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.14 Score per residue for model 14

- Molecule 1: MUC2 Mucin Domain Peptide



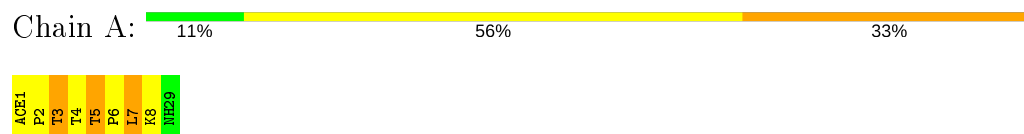
4.2.15 Score per residue for model 15

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.16 Score per residue for model 16

- Molecule 1: MUC2 Mucin Domain Peptide



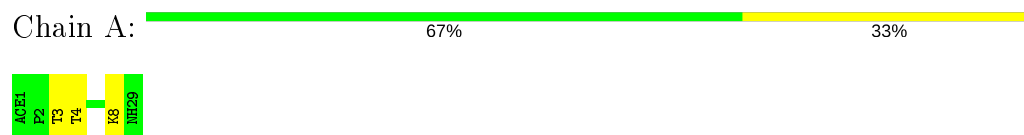
4.2.17 Score per residue for model 17

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.18 Score per residue for model 18

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.19 Score per residue for model 19

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.20 Score per residue for model 20

- Molecule 1: MUC2 Mucin Domain Peptide



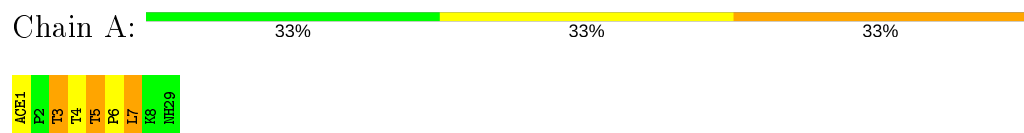
4.2.21 Score per residue for model 21

- Molecule 1: MUC2 Mucin Domain Peptide



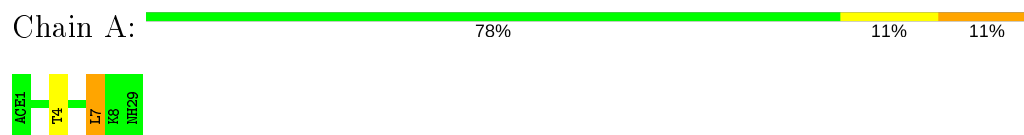
4.2.22 Score per residue for model 22

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.23 Score per residue for model 23

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.24 Score per residue for model 24

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.25 Score per residue for model 25

- Molecule 1: MUC2 Mucin Domain Peptide



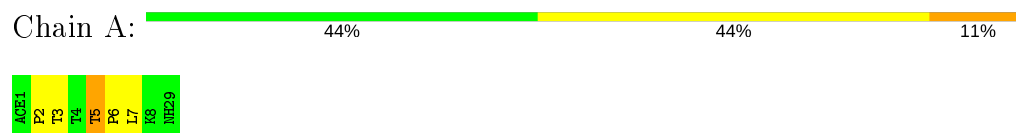
4.2.26 Score per residue for model 26

- Molecule 1: MUC2 Mucin Domain Peptide



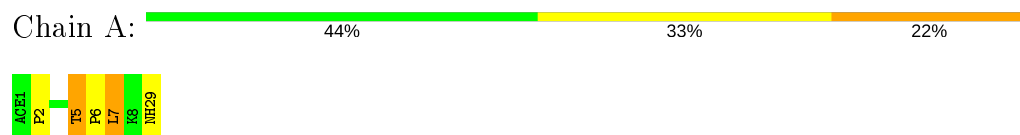
4.2.27 Score per residue for model 27

- Molecule 1: MUC2 Mucin Domain Peptide



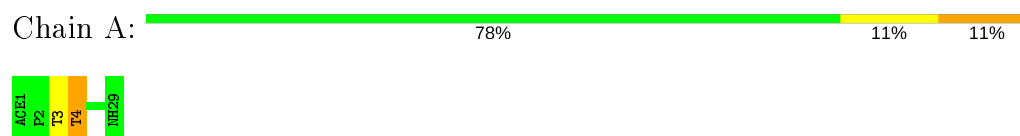
4.2.28 Score per residue for model 28

- Molecule 1: MUC2 Mucin Domain Peptide



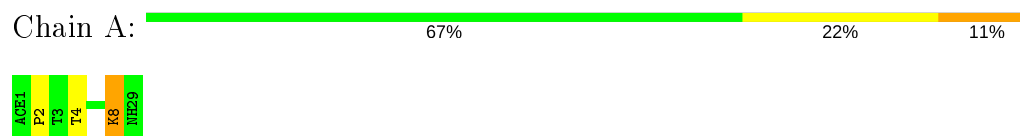
4.2.29 Score per residue for model 29

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.30 Score per residue for model 30

- Molecule 1: MUC2 Mucin Domain Peptide



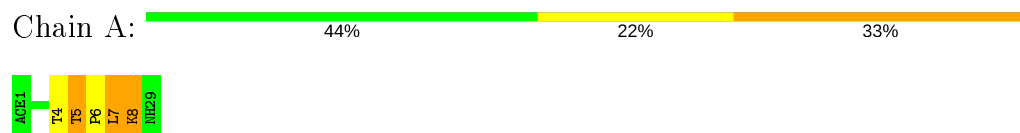
4.2.31 Score per residue for model 31

- Molecule 1: MUC2 Mucin Domain Peptide



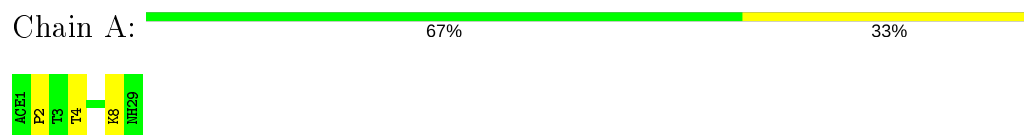
4.2.32 Score per residue for model 32

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.33 Score per residue for model 33

- Molecule 1: MUC2 Mucin Domain Peptide



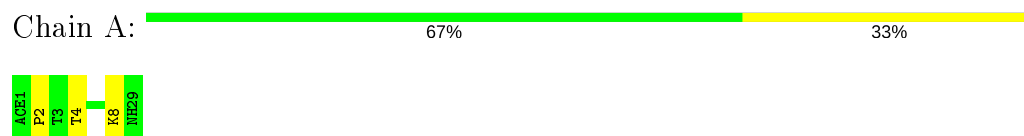
4.2.34 Score per residue for model 34

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.35 Score per residue for model 35

- Molecule 1: MUC2 Mucin Domain Peptide



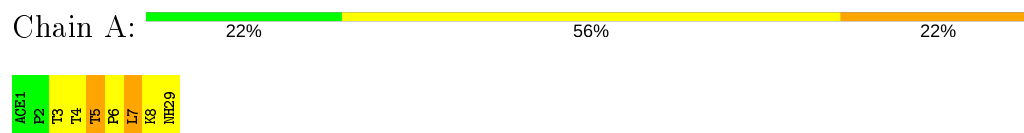
4.2.36 Score per residue for model 36

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.37 Score per residue for model 37

- Molecule 1: MUC2 Mucin Domain Peptide



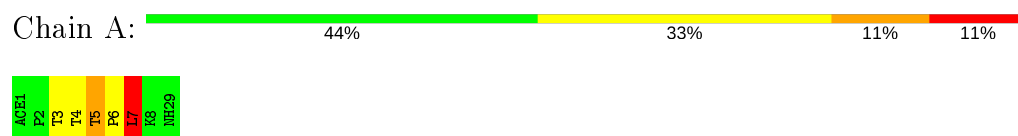
4.2.38 Score per residue for model 38

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.39 Score per residue for model 39

- Molecule 1: MUC2 Mucin Domain Peptide



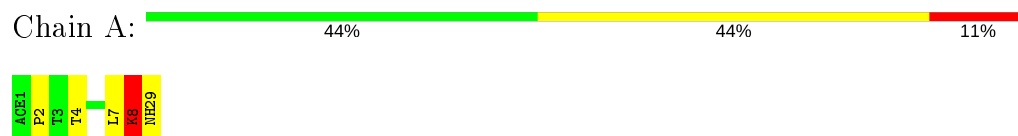
4.2.40 Score per residue for model 40

- Molecule 1: MUC2 Mucin Domain Peptide



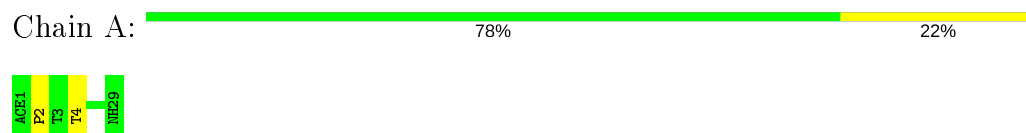
4.2.41 Score per residue for model 41

- Molecule 1: MUC2 Mucin Domain Peptide



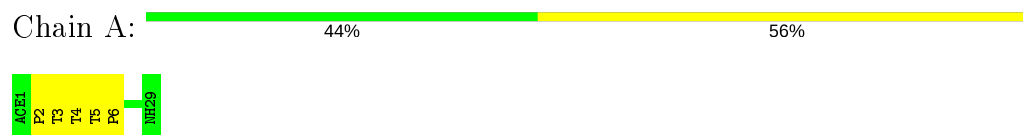
4.2.42 Score per residue for model 42

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.43 Score per residue for model 43

- Molecule 1: MUC2 Mucin Domain Peptide



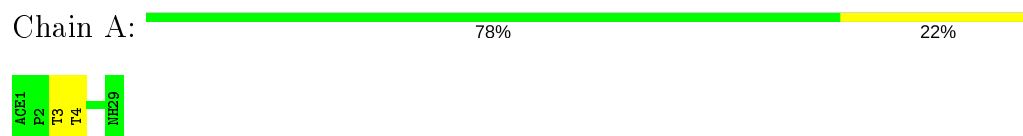
4.2.44 Score per residue for model 44

- Molecule 1: MUC2 Mucin Domain Peptide



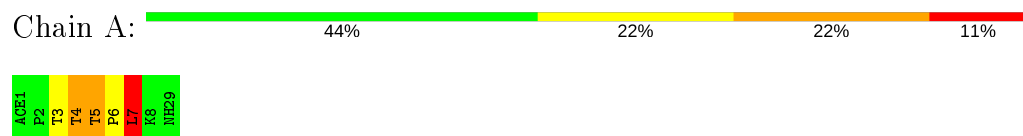
4.2.45 Score per residue for model 45

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.46 Score per residue for model 46

- Molecule 1: MUC2 Mucin Domain Peptide



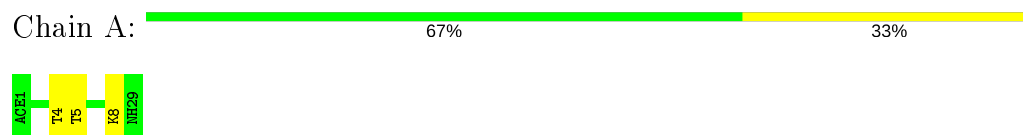
4.2.47 Score per residue for model 47

- Molecule 1: MUC2 Mucin Domain Peptide



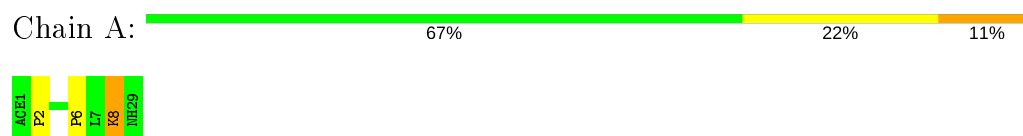
4.2.48 Score per residue for model 48

- Molecule 1: MUC2 Mucin Domain Peptide



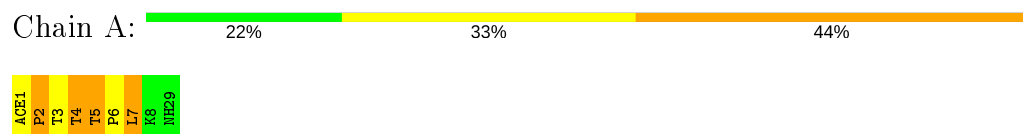
4.2.49 Score per residue for model 49

- Molecule 1: MUC2 Mucin Domain Peptide



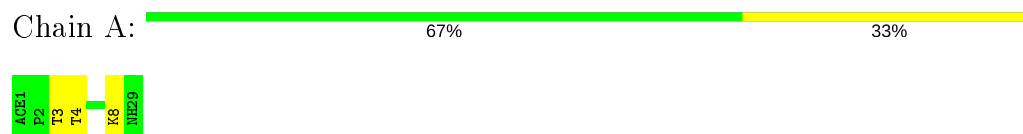
4.2.50 Score per residue for model 50

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.51 Score per residue for model 51

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.52 Score per residue for model 52

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.53 Score per residue for model 53

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.54 Score per residue for model 54

- Molecule 1: MUC2 Mucin Domain Peptide



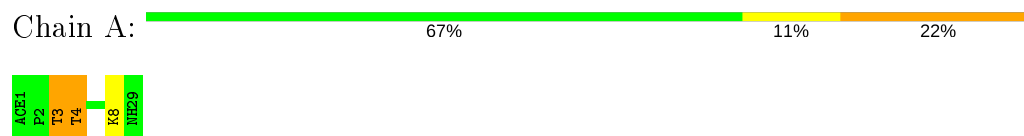
4.2.55 Score per residue for model 55

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.56 Score per residue for model 56

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.57 Score per residue for model 57

- Molecule 1: MUC2 Mucin Domain Peptide



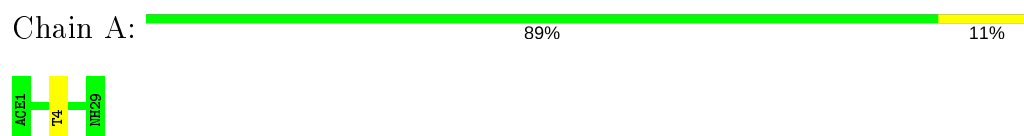
4.2.58 Score per residue for model 58

- Molecule 1: MUC2 Mucin Domain Peptide



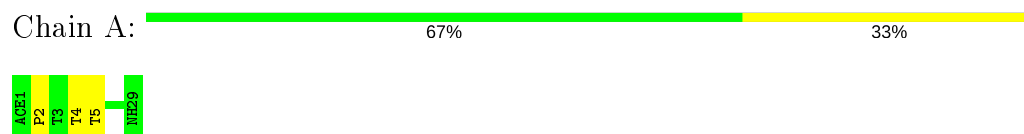
4.2.59 Score per residue for model 59

- Molecule 1: MUC2 Mucin Domain Peptide



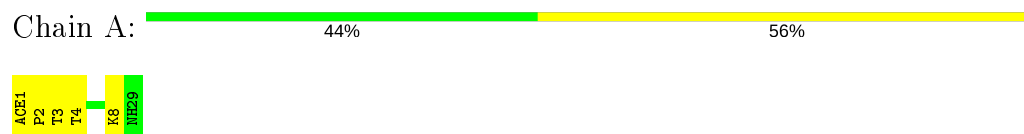
4.2.60 Score per residue for model 60

- Molecule 1: MUC2 Mucin Domain Peptide



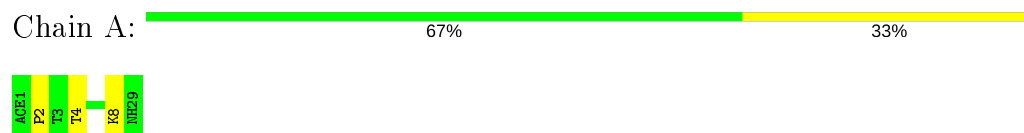
4.2.61 Score per residue for model 61

- Molecule 1: MUC2 Mucin Domain Peptide



4.2.62 Score per residue for model 62

- Molecule 1: MUC2 Mucin Domain Peptide



5 Refinement protocol and experimental data overview

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

Of the 100 calculated structures, 62 were deposited, based on the following criterion: *structures with the least restraint violations*.

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

Software name	Classification	Version
CNS	structure solution	
XPLOR-NIH	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)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	99
Number of shifts mapped to atoms	99
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	83%

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: NH2, ACE, A2G

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	56	63	61	2±2
2	A	14	14	12	0±1
All	All	4340	4774	4526	120

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 14.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:LEU:HD13	1:A:7:LEU:H	0.97	1.10	12	1
1:A:5:THR:O	1:A:7:LEU:N	0.92	2.02	53	27
1:A:7:LEU:HD13	1:A:7:LEU:N	0.82	1.88	12	1
1:A:7:LEU:HD13	2:A:10:A2G:O7	0.81	1.73	16	3
1:A:7:LEU:CD1	1:A:7:LEU:H	0.77	1.84	12	1
1:A:7:LEU:HD22	2:A:10:A2G:O7	0.75	1.82	55	1
1:A:7:LEU:HD12	1:A:7:LEU:H	0.74	1.43	23	1
1:A:7:LEU:H	1:A:7:LEU:HD12	0.72	1.42	57	1
1:A:7:LEU:H	1:A:7:LEU:CD1	0.64	2.02	57	2
1:A:7:LEU:N	1:A:7:LEU:HD22	0.63	2.09	12	1
1:A:3:THR:O	1:A:3:THR:HG23	0.61	1.94	39	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:7:LEU:HD22	2:A:10:A2G:H8	0.59	1.72	16	2
1:A:9:NH2:N	2:A:10:A2G:H8	0.59	2.13	37	1
1:A:3:THR:HG23	1:A:4:THR:N	0.58	2.13	29	2
1:A:3:THR:HG22	1:A:4:THR:N	0.58	2.13	4	4
1:A:4:THR:HG23	1:A:5:THR:N	0.55	2.17	47	5
1:A:7:LEU:HD23	1:A:7:LEU:N	0.54	2.17	47	1
1:A:7:LEU:N	1:A:7:LEU:HD23	0.54	2.17	40	1
1:A:7:LEU:CD2	1:A:7:LEU:N	0.52	2.71	6	2
1:A:7:LEU:CD1	1:A:7:LEU:N	0.52	2.71	41	3
1:A:1:ACE:O	1:A:3:THR:N	0.51	2.43	16	5
1:A:7:LEU:N	1:A:7:LEU:CD2	0.51	2.74	47	2
1:A:6:PRO:O	2:A:10:A2G:C7	0.51	2.59	6	1
1:A:7:LEU:HD22	1:A:7:LEU:N	0.51	2.19	6	1
1:A:7:LEU:N	1:A:7:LEU:HD12	0.51	2.20	41	2
1:A:7:LEU:HD12	1:A:7:LEU:N	0.50	2.19	23	1
1:A:3:THR:HG22	1:A:4:THR:H	0.50	1.66	4	3
1:A:3:THR:OG1	1:A:4:THR:N	0.50	2.45	1	4
1:A:7:LEU:HD23	2:A:10:A2G:O7	0.49	2.07	10	1
1:A:7:LEU:HD23	1:A:8:LYS:N	0.49	2.21	44	1
1:A:7:LEU:O	1:A:7:LEU:CD1	0.48	2.62	2	1
1:A:7:LEU:C	1:A:7:LEU:HD13	0.47	2.29	52	2
1:A:8:LYS:CG	1:A:9:NH2:N	0.47	2.77	41	1
1:A:7:LEU:H	1:A:7:LEU:CD2	0.47	2.23	40	1
1:A:3:THR:CG2	1:A:4:THR:N	0.47	2.77	4	4
1:A:5:THR:O	1:A:6:PRO:O	0.47	2.33	6	1
1:A:7:LEU:CD1	1:A:7:LEU:C	0.47	2.84	52	2
1:A:7:LEU:N	1:A:7:LEU:CD1	0.46	2.78	57	1
1:A:7:LEU:CD2	2:A:10:A2G:O7	0.46	2.60	55	1
1:A:7:LEU:CD2	1:A:7:LEU:H	0.46	2.23	47	1
1:A:7:LEU:HD13	1:A:7:LEU:O	0.45	2.11	31	1
1:A:7:LEU:O	1:A:8:LYS:CG	0.45	2.65	36	1
1:A:7:LEU:C	1:A:7:LEU:CD2	0.45	2.85	12	1
1:A:8:LYS:CD	1:A:8:LYS:H	0.45	2.23	30	1
1:A:9:NH2:N	2:A:10:A2G:H8A	0.45	2.27	28	1
1:A:1:ACE:C	1:A:3:THR:N	0.44	2.71	16	5
1:A:7:LEU:CD1	2:A:10:A2G:O7	0.43	2.60	55	1
1:A:3:THR:CG2	1:A:4:THR:H	0.43	2.25	4	2
1:A:8:LYS:O	2:A:10:A2G:O7	0.43	2.37	8	2
1:A:1:ACE:O	1:A:2:PRO:O	0.42	2.38	8	3
1:A:7:LEU:CD2	1:A:8:LYS:H	0.42	2.28	9	1
1:A:9:NH2:N	2:A:10:A2G:O7	0.42	2.53	38	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:PRO:C	1:A:8:LYS:H	0.41	2.19	6	1
1:A:1:ACE:C	1:A:3:THR:H	0.41	2.19	16	1
1:A:7:LEU:HD22	2:A:10:A2G:C8	0.40	2.46	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	7/9 (78%)	4±1 (54±15%)	2±1 (23±13%)	2±1 (24±14%)	0	1
All	All	434/558 (78%)	234 (54%)	98 (23%)	102 (24%)	0	1

All 5 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	6	PRO	36
1	A	2	PRO	30
1	A	7	LEU	19
1	A	8	LYS	15
1	A	3	THR	2

6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	7/7 (100%)	5±1 (69±14%)	2±1 (31±14%)	1	15
All	All	434/434 (100%)	301 (69%)	133 (31%)	1	15

All 5 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	4	THR	47
1	A	5	THR	27
1	A	3	THR	23
1	A	8	LYS	19
1	A	7	LEU	17

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 monosaccharides in this entry.

6.6 Ligand geometry [i](#)

1 ligand is modelled in this entry.

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
2	A2G	A	10	1	14,14,15	0.56±0.00	0±0 (0±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
2	A2G	A	10	1	17,19,21	0.90±0.00	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
2	A2G	A	10	1	-	0±0,6,23,26	0±0,1,1,1

There are no bond-length outliers.

There are no bond-angle outliers.

All unique chiral outliers are listed below.

Mol	Chain	Res	Type	Atoms	Models (Total)
2	A	10	A2G	C1	1

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 83% for the well-defined parts and 83% for the entire structure.

7.1 Chemical shift list 1

File name: working_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	99
Number of shifts mapped to atoms	99
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	0

7.1.2 Chemical shift referencing

No chemical shift referencing corrections were calculated (not enough data).

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 83%, i.e. 69 atoms were assigned a chemical shift out of a possible 83. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹ H	¹³ C	¹⁵ N
Backbone	24/31 (77%)	12/12 (100%)	7/14 (50%)	5/5 (100%)
Sidechain	45/52 (87%)	28/31 (90%)	17/20 (85%)	0/1 (0%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	69/83 (83%)	40/43 (93%)	24/34 (71%)	5/6 (83%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 83%, i.e. 69 atoms were assigned a chemical shift out of a possible 83. 0 out of 1 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	24/31 (77%)	12/12 (100%)	7/14 (50%)	5/5 (100%)
Sidechain	45/52 (87%)	28/31 (90%)	17/20 (85%)	0/1 (0%)
Aromatic	0/0 (—%)	0/0 (—%)	0/0 (—%)	0/0 (—%)
Overall	69/83 (83%)	40/43 (93%)	24/34 (71%)	5/6 (83%)

7.1.4 Statistically unusual chemical shifts ⓘ

There are no statistically unusual chemical shifts.

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:

