



Full wwPDB NMR Structure Validation Report ⓘ

Mar 28, 2026 – 08:07 PM UTC

PDB ID : 7UWY / pdb_00007uwy
BMRB ID : 31017
Title : NMR solution structure of the De novo designed small beta-barrel protein
29_bp_sh3
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B.F.; Baker, D.
Deposited on : 2022-05-04

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 types of validation reports are described at

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

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

MolProbity : 4-5-2 with Phenix2.0
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
wwPDB-RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
wwPDB-ShiftChecker : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

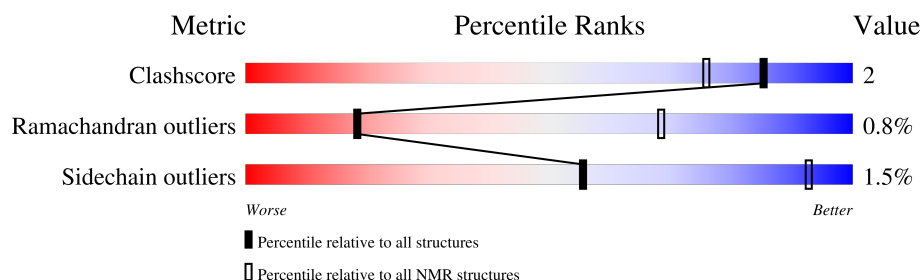
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

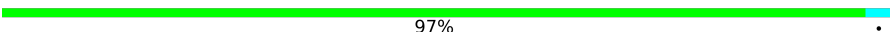
The overall completeness of chemical shifts assignment is 91%.

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	229148	14424
Ramachandran outliers	224038	12848
Sidechain outliers	223484	12823

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	61	 97%

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *target function*.

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:3-A:61 (59)	0.45	3

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. No single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 980 atoms, of which 497 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called De novo designed small beta-barrel protein 29_bp_sh3.

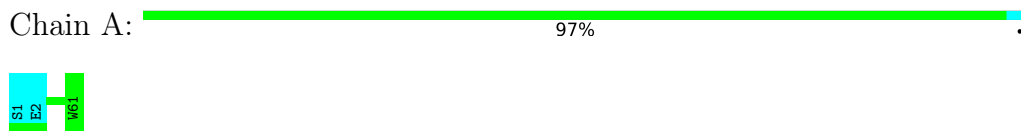
Mol	Chain	Residues	Atoms					Trace
1	A	61	Total 980	C 293	H 497	N 92	O 98	0

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: De novo designed small beta-barrel protein 29_bp_sh3

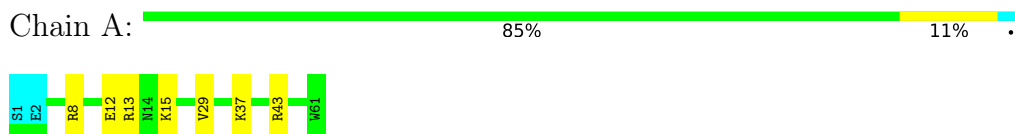


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

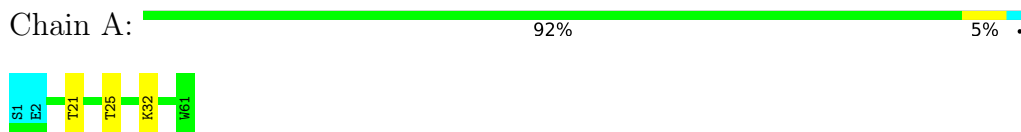
4.2.1 Score per residue for model 1

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



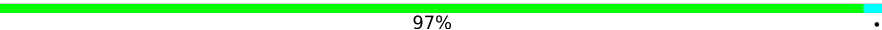
4.2.2 Score per residue for model 2

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



4.2.3 Score per residue for model 3 (medoid)

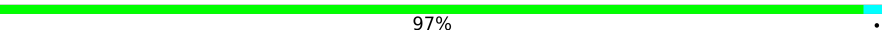
- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

Chain A:  97% .



4.2.4 Score per residue for model 4

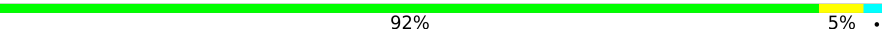
- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

Chain A:  97% .



4.2.5 Score per residue for model 5

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

Chain A:  92% 5% .



4.2.6 Score per residue for model 6

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

Chain A:  89% 8% .



4.2.7 Score per residue for model 7

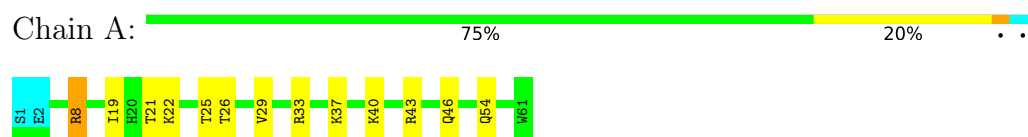
- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

Chain A:  90% 7% .



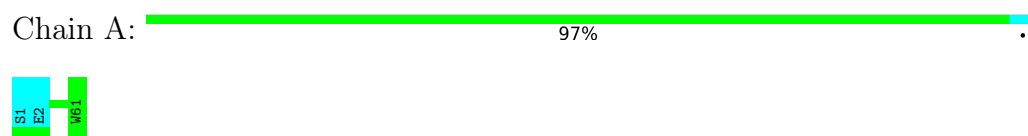
4.2.8 Score per residue for model 8

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



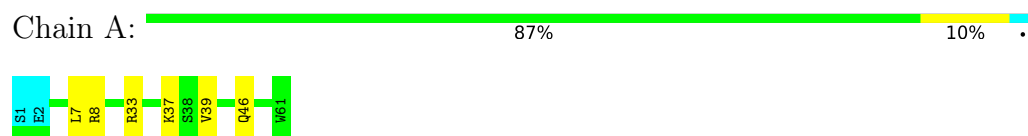
4.2.9 Score per residue for model 9

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



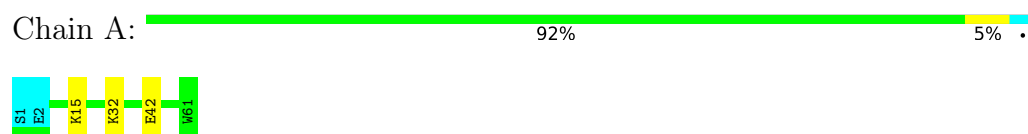
4.2.10 Score per residue for model 10

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



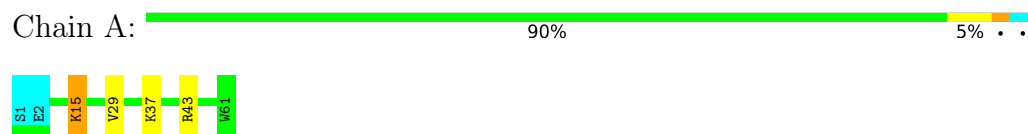
4.2.11 Score per residue for model 11

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



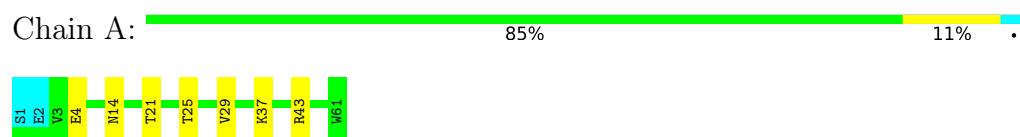
4.2.12 Score per residue for model 12

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



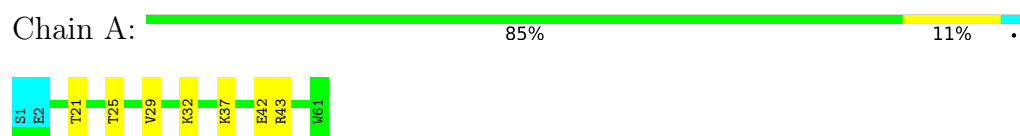
4.2.13 Score per residue for model 13

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



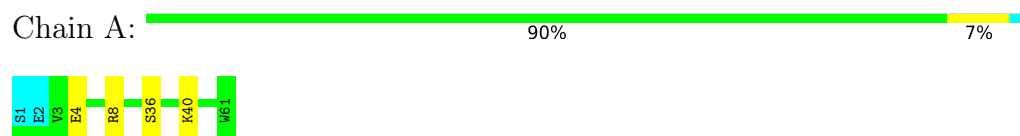
4.2.14 Score per residue for model 14

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



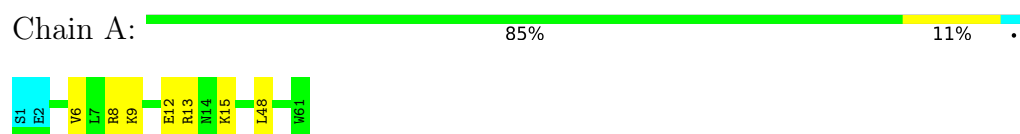
4.2.15 Score per residue for model 15

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



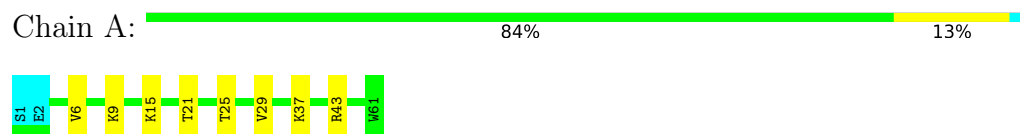
4.2.16 Score per residue for model 16

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



4.2.17 Score per residue for model 17

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3



4.2.18 Score per residue for model 18

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

Chain A:  92% 5% .



4.2.19 Score per residue for model 19

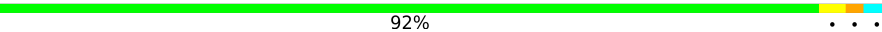
- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

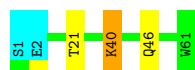
Chain A:  90% 5% . .



4.2.20 Score per residue for model 20

- Molecule 1: De novo designed small beta-barrel protein 29_bp_sh3

Chain A:  92% . . .



5 Refinement protocol and experimental data overview

The models were refined using the following method: *torsion angle dynamics, molecular dynamics*.

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function*.

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

Software name	Classification	Version
CYANA	refinement	3.98.13
X-PLOR NIH	refinement	
CYANA	structure calculation	3.98.13
X-PLOR NIH	geometry optimization	

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	760
Number of shifts mapped to atoms	760
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	91%

6 Model quality [i](#)

6.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.09±0.04	0±0/471 (0.0± 0.1%)	0.89±0.03	0±0/633 (0.0± 0.0%)
All	All	1.10	2/9420 (0.0%)	0.89	0/12660 (0.0%)

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	21	THR	N-CA	-5.27	1.39	1.45	20	1
1	A	40	LYS	C-N	-5.13	1.27	1.33	18	1

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts [i](#)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	468	484	482	2±2
All	All	9360	9680	9640	41

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 2.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:LYS:HE2	1:A:15:LYS:HA	0.52	1.80	11	5
1:A:33:ARG:HB3	1:A:40:LYS:HB3	0.52	1.81	6	2
1:A:8:ARG:O	1:A:12:GLU:HG3	0.50	2.06	1	2
1:A:32:LYS:HD2	1:A:42:GLU:HB2	0.50	1.82	14	1
1:A:21:THR:OG1	1:A:25:THR:HB	0.50	2.06	14	5
1:A:29:VAL:HG12	1:A:43:ARG:HB3	0.48	1.83	13	6
1:A:6:VAL:O	1:A:9:LYS:HB3	0.48	2.08	16	2
1:A:4:GLU:OE2	1:A:36:SER:HA	0.48	2.09	7	1
1:A:8:ARG:C	1:A:8:ARG:HD3	0.48	2.33	8	2
1:A:22:LYS:CD	1:A:54:GLN:HA	0.45	2.41	8	1
1:A:8:ARG:O	1:A:12:GLU:HG2	0.44	2.13	16	1
1:A:40:LYS:HB2	1:A:40:LYS:NZ	0.44	2.28	20	1
1:A:13:ARG:HB2	1:A:15:LYS:HG2	0.44	1.89	1	2
1:A:21:THR:HA	1:A:54:GLN:O	0.43	2.12	8	1
1:A:4:GLU:O	1:A:8:ARG:HG3	0.43	2.13	15	1
1:A:32:LYS:HE2	1:A:32:LYS:HA	0.43	1.91	2	1
1:A:4:GLU:OE1	1:A:36:SER:HA	0.42	2.14	15	1
1:A:15:LYS:HA	1:A:15:LYS:HE3	0.42	1.91	12	1
1:A:7:LEU:HD13	1:A:39:VAL:HG21	0.41	1.91	10	1
1:A:32:LYS:CG	1:A:42:GLU:HB2	0.41	2.45	11	1
1:A:17:VAL:O	1:A:28:ARG:HA	0.41	2.15	19	1
1:A:19:ILE:O	1:A:26:THR:HA	0.41	2.15	5	2

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	58/61 (95%)	57±1 (98±1%)	1±1 (1±1%)	0±0 (1±1%)	18	68
All	All	1160/1220 (95%)	1140 (98%)	11 (1%)	9 (1%)	18	68

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	37	LYS	9

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	54/56 (96%)	53±1 (99±2%)	1±1 (1±2%)	55	93
All	All	1080/1120 (96%)	1064 (99%)	16 (1%)	55	93

All 9 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	46	GLN	4
1	A	15	LYS	2
1	A	14	ASN	2
1	A	40	LYS	2
1	A	48	LEU	2
1	A	8	ARG	1
1	A	33	ARG	1
1	A	4	GLU	1
1	A	37	LYS	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 oligosaccharides 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 91% for the well-defined parts and 90% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: 29_bp_sh3.star

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	760
Number of shifts mapped to atoms	760
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

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction $\pm$ precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	60	-0.39 ± 0.21	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	57	-0.12 ± 0.18	None needed (< 0.5 ppm)
$^{13}\text{C}'$	58	0.00 ± 0.22	None needed (< 0.5 ppm)
^{15}N	59	0.64 ± 0.38	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 91%, i.e. 751 atoms were assigned a chemical shift out of a possible 826. 0 out of 13 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	296/298 (99%)	121/121 (100%)	116/118 (98%)	59/59 (100%)
Sidechain	435/500 (87%)	296/321 (92%)	134/153 (88%)	5/26 (19%)

Continued on next page...

	Total	¹H	¹³C	¹⁵N
Aromatic	20/28 (71%)	10/14 (71%)	9/9 (100%)	1/5 (20%)
Overall	751/826 (91%)	427/456 (94%)	259/280 (92%)	65/90 (72%)

	Total	¹H	¹³C	¹⁵N
Backbone	299/308 (97%)	122/125 (98%)	118/122 (97%)	59/61 (97%)
Sidechain	441/510 (86%)	300/327 (92%)	136/157 (87%)	5/26 (19%)
Aromatic	20/28 (71%)	10/14 (71%)	9/9 (100%)	1/5 (20%)
Overall	760/846 (90%)	432/466 (93%)	263/288 (91%)	65/92 (71%)

Auth seq ID	RCI
2:GLU	0.022
3:GLU	0.019
4:GLU	0.015
5:VAL	0.014
6:VAL	0.015
7:ARG	0.017
8:ARG	0.019
9:ALA	0.020
10:ALA	0.023
11:GLU	0.027
12:GLU	0.034
13:ASN	0.041
14:ASN	0.038
15:THR	0.031
16:THR	0.023
17:ASP	0.030
18:ASP	0.030
19:HIS	0.028
20:HIS	0.020
21:LYS	0.027
22:LYS	0.042
23:GLY	0.053
24:GLY	0.048
25:THR	0.035
26:THR	0.022
27:ARG	0.018
28:ARG	0.017
29:ASN	0.028
30:ASN	0.035
31:LYS	0.041
32:LYS	0.036
33:VAL	0.034
34:VAL	0.035
35:SER	0.033
36:SER	0.028
37:SER	0.019
38:SER	0.014
39:LYS	0.013
40:LYS	0.018
41:GLU	0.027
42:GLU	0.034
43:ASN	0.038
44:ASN	0.033
45:GLN	0.029
46:GLN	0.027
47:LEU	0.029
48:LEU	0.031
49:ILE	0.031
50:ILE	0.028
51:LEU	0.032
52:LEU	0.048
53:GLN	0.058
54:GLN	0.052
55:THR	0.038
56:THR	0.033
57:VAL	0.038
58:VAL	0.046
59:GLY	0.049
60:GLY	0.049