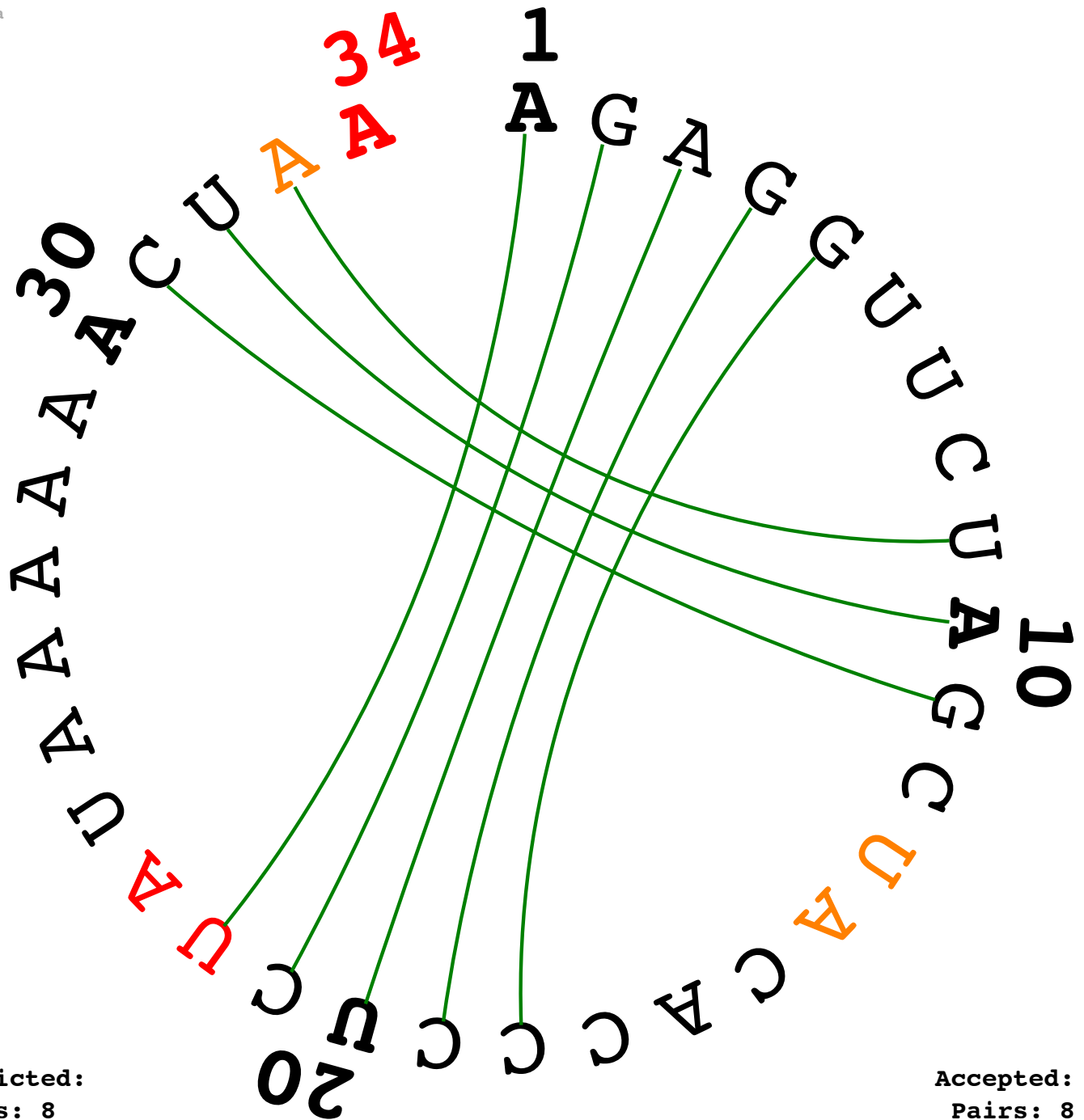


Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

Sensitivity: 8 / 8 = 100.00%
PPV: 8 / 8 = 100.00%



Accepted:
Pairs: 8
Pseudoknotted Pairs: 3

Telomerase pseudoknot, human ENERGY = -37.2

Green: Pair in both structures

Red: Pair in Accepted Structure only

Purple: Pair in Predicted Structure only

.85 >= SHAPE

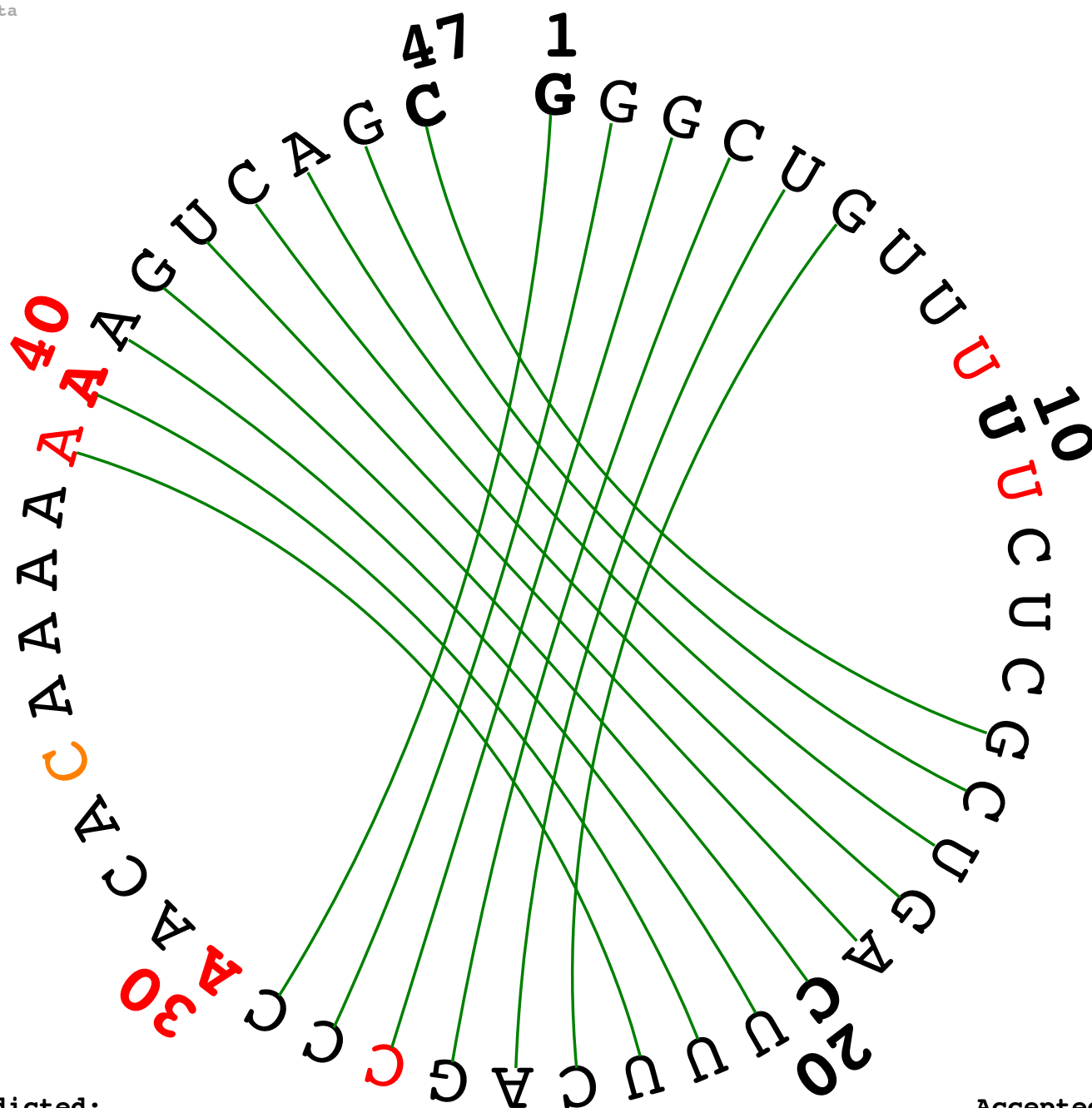
.85 > SHAPE >= .4

.4 > SHAPE

No Data

Sensitivity: 15 / 15 = 100.00%

PPV: 15 / 15 = 100.00%



Predicted:

Pairs: 15

Pseudoknotted Pairs: 6

Accepted:

Pairs: 15

Pseudoknotted Pairs: 6

tRNA(asp), yeast ENERGY = -46.9

Green: Pair in both structures

Red: Pair in Accepted Structure only

Purple: Pair in Predicted Structure only

.85 >= SHAPE

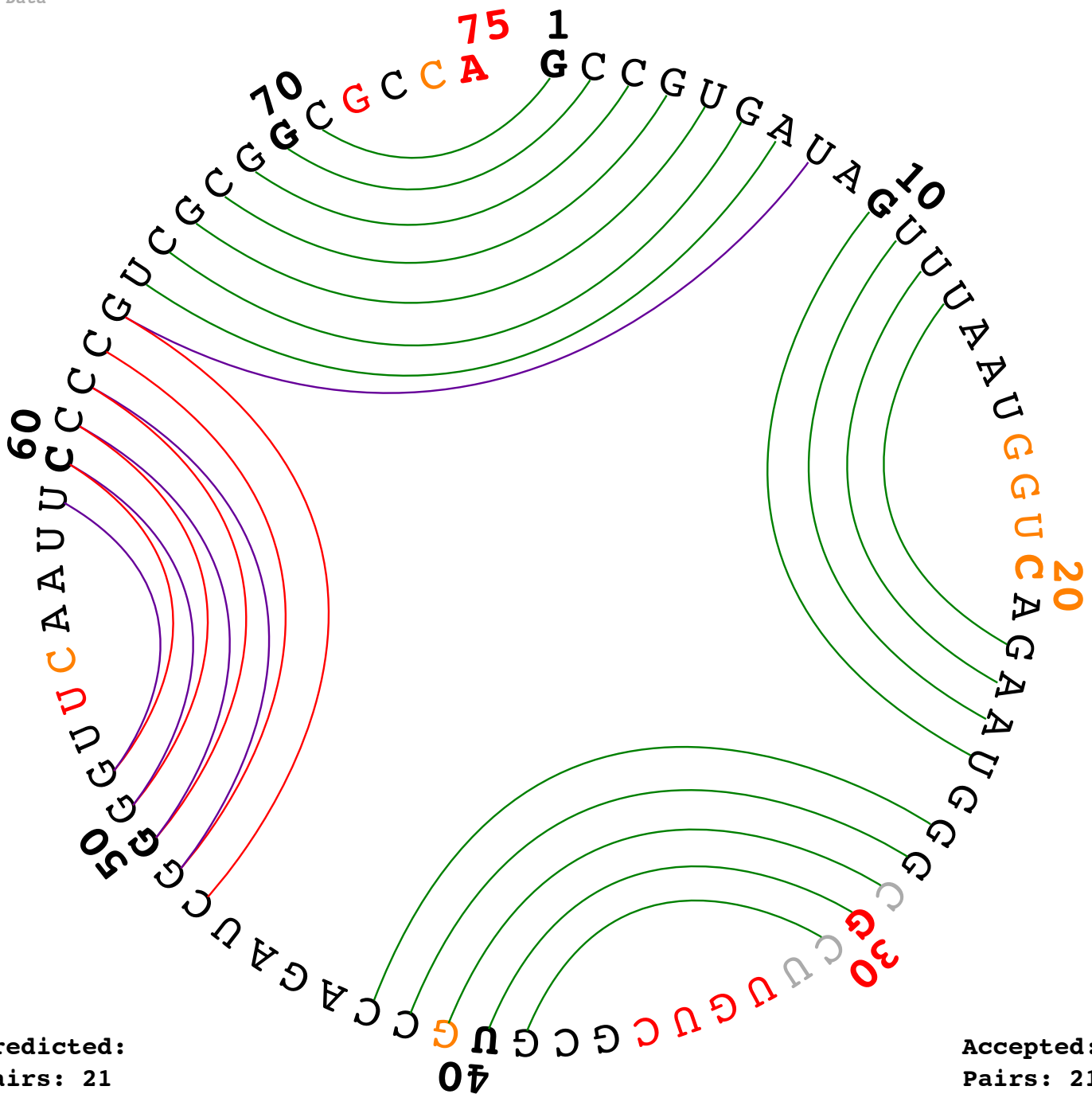
```
.85 > SHAPE >= .4
```

```
.4 > SHAPE
```

No Data

Sensitivity: $20 / 21 = 95.24\%$

PPV: 20 / 21 = 95.24%



Predicted:

Pairs: 21

Pseudoknotted Pairs: 0

Accepted:

Pairs: 21

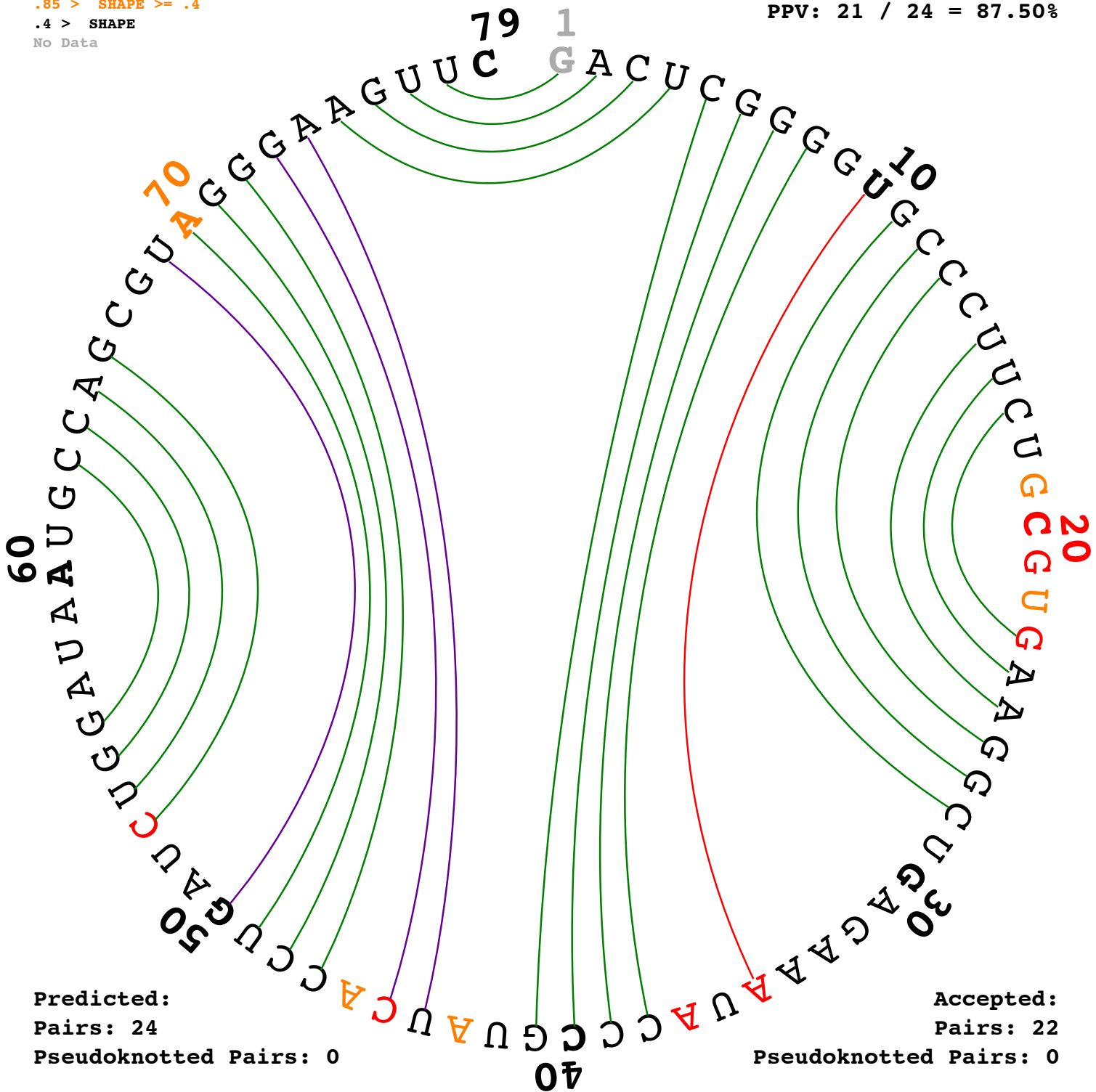
Pseudoknotted Pairs: 0

TPP riboswitch, *E. coli* ENERGY = -45.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 21 / 22 = 95.45%
PPV: 21 / 24 = 87.50%

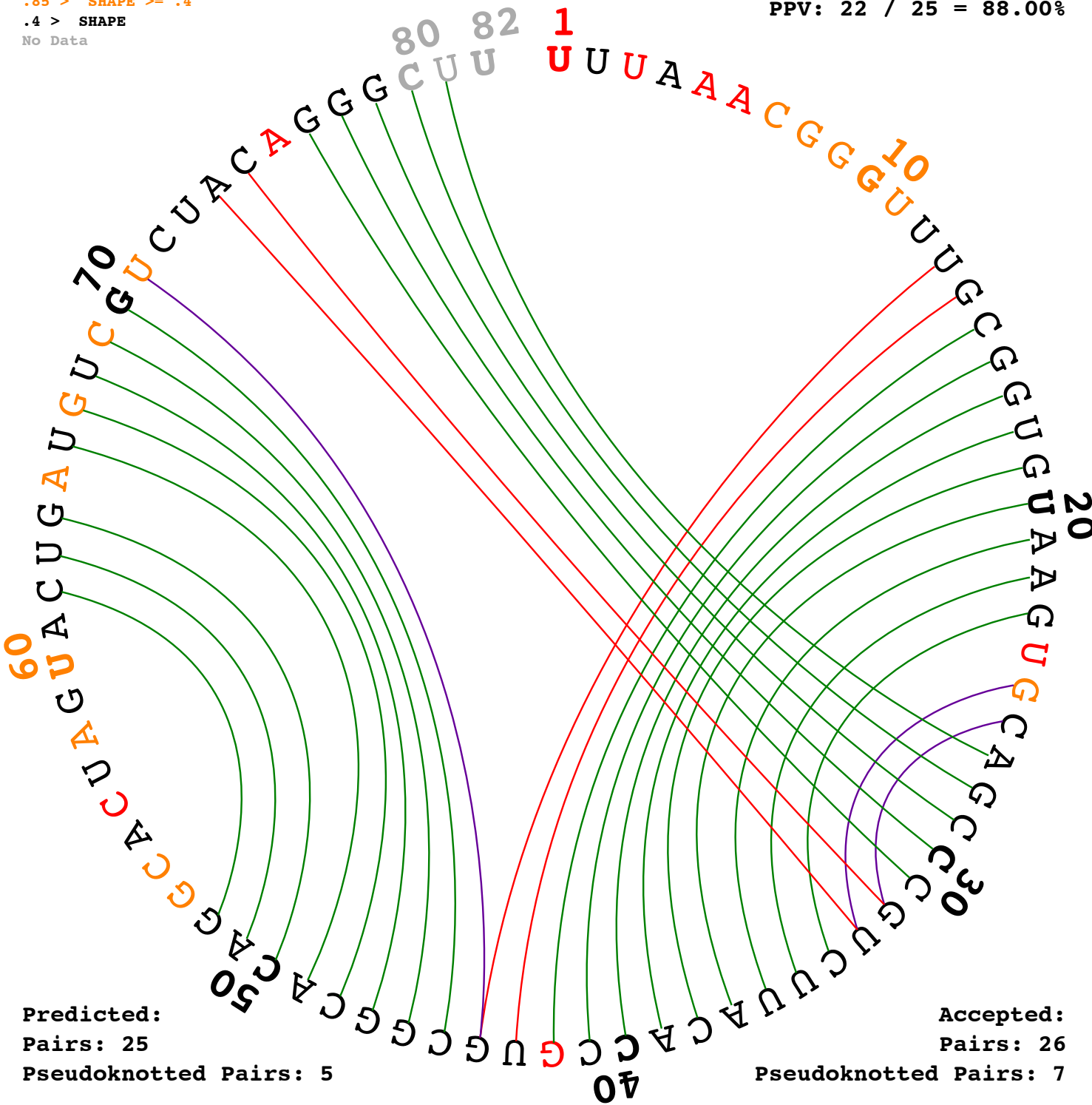


SARS corona virus pseudoknot ENERGY = -55.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 22 / 26 = 84.62%
PPV: 22 / 25 = 88.00%



cyclic-di-GMP riboswitch, *V. cholerae* ENERGY = -66.3

Green: Pair in both structures

Red: Pair in Accepted Structure only

Purple: Pair in Predicted Structure only

.85 >= SHAPE

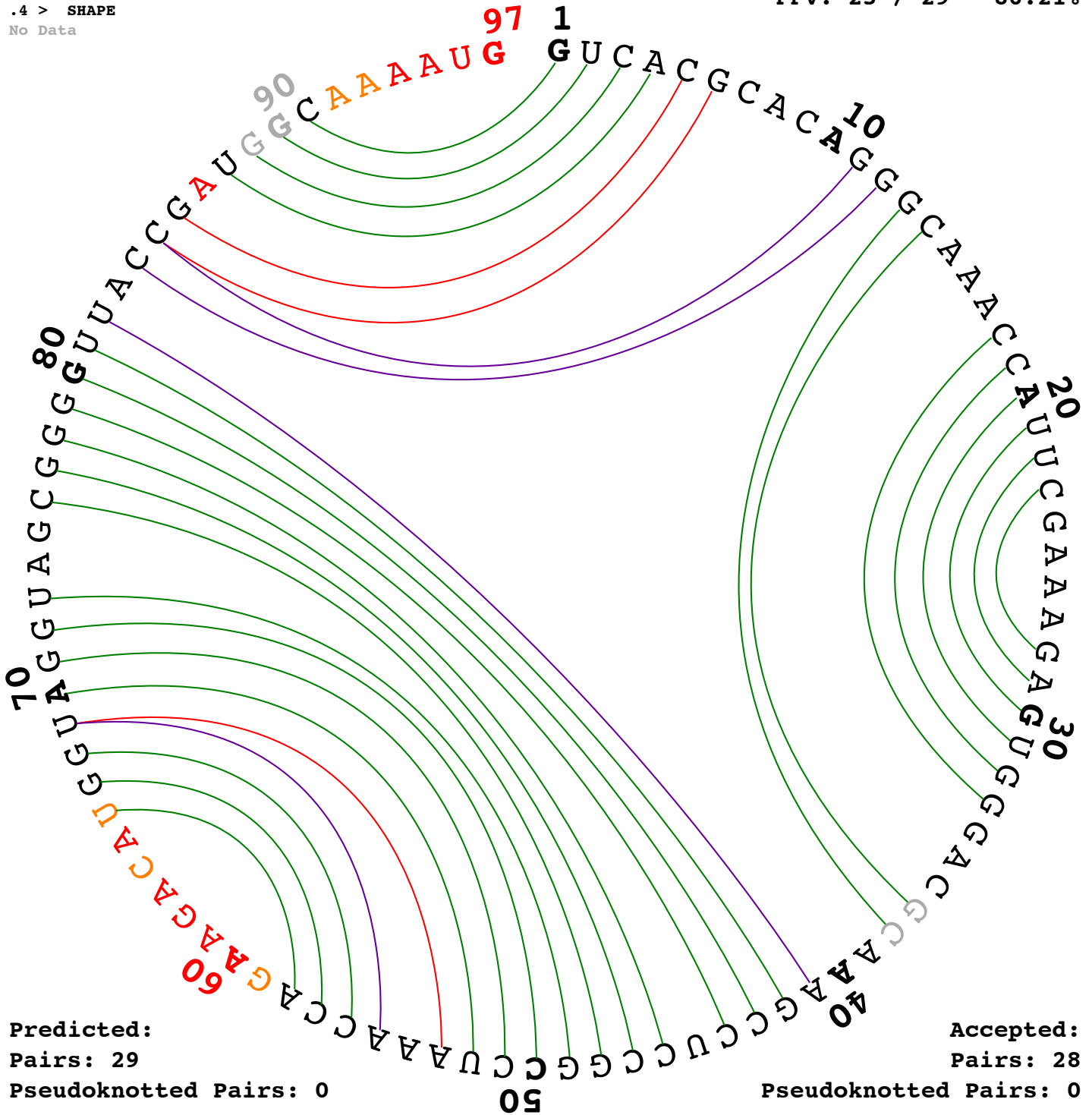
.85 > SHAPE >= .4

```
.4 > SHAPE
```

No Data

Sensitivity: $25 / 28 = 89.29\%$

PPV: 25 / 29 = 86.21%



Predicted:

Pairs: 29

Pseudoknotted Pairs: 0

Accepted:

Pairs: 28

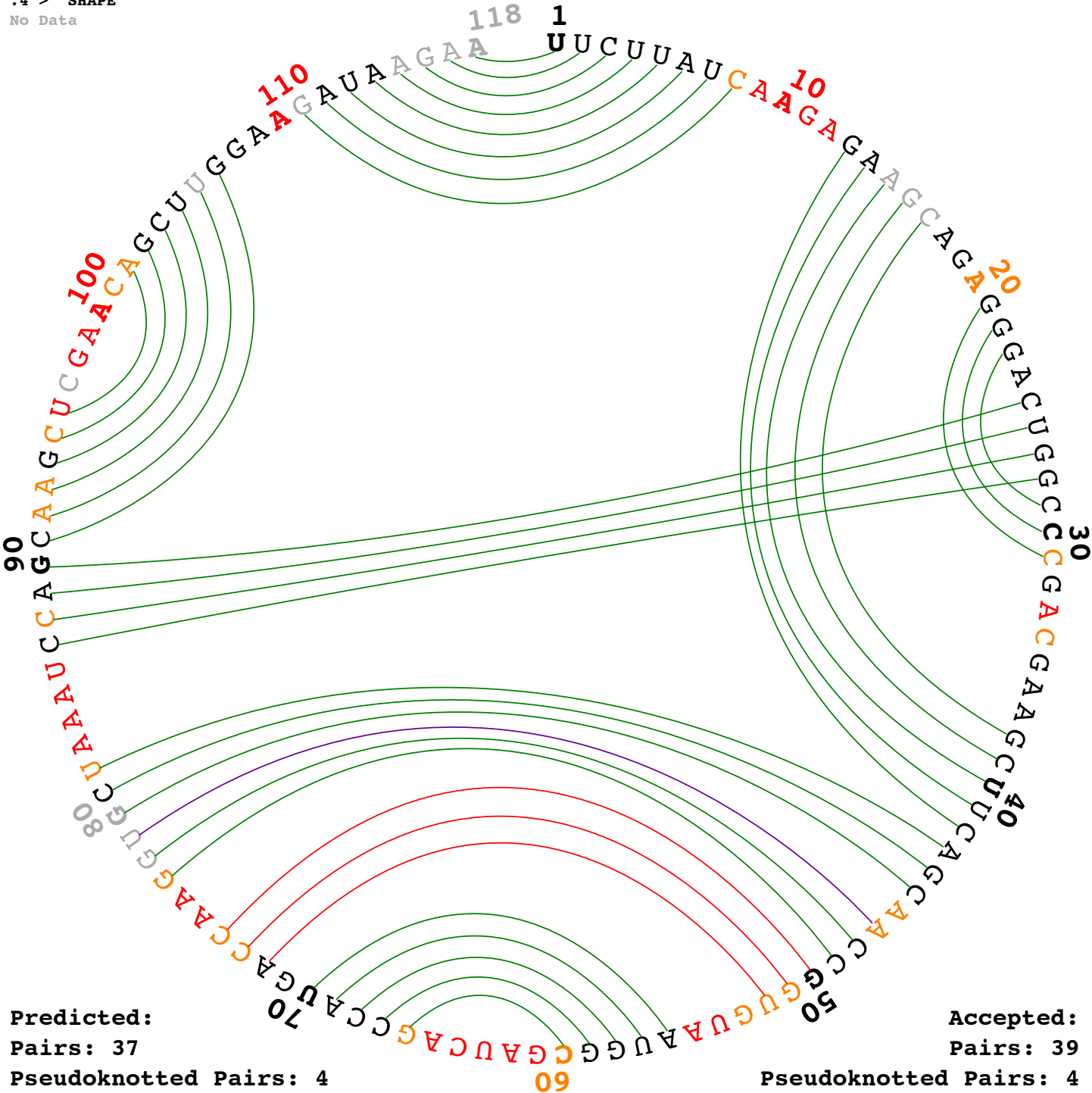
Pseudoknotted Pairs: 0

SAM I riboswitch, *T. tengcongensis* ENERGY = -65.6

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 36 / 39 = 92.31%
PPV: 36 / 37 = 97.30%

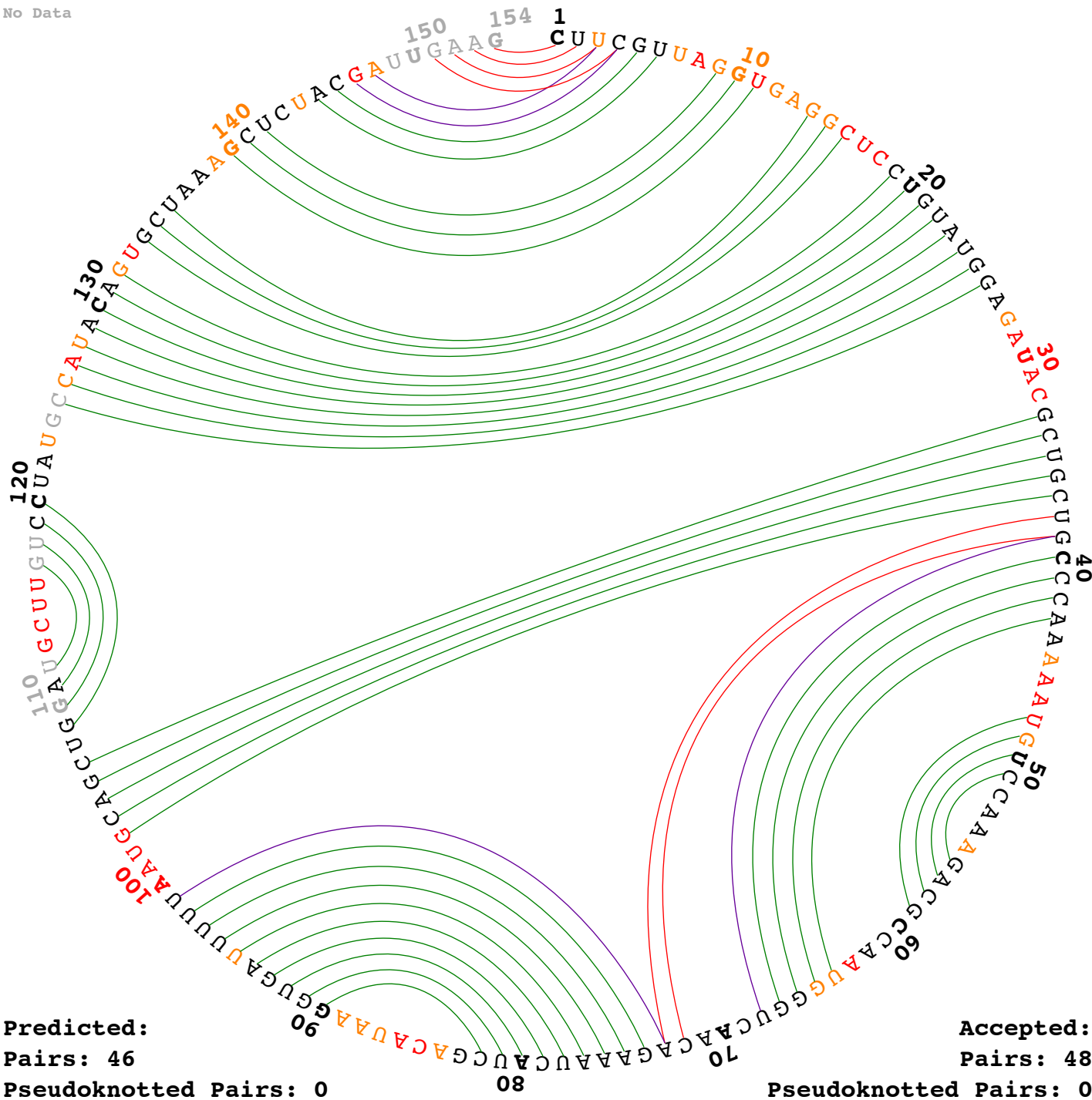


M-Box riboswitch, *B. subtilis* ENERGY = -80.5

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 42 / 48 = 87.50%
PPV: 42 / 46 = 91.30%



P546 domain, bI3 group I intron ENERGY = -81.0

Green: Pair in both structures

Red: Pair in Accepted Structure only

Purple: Pair in Predicted Structure only

.85 >= SHAPE

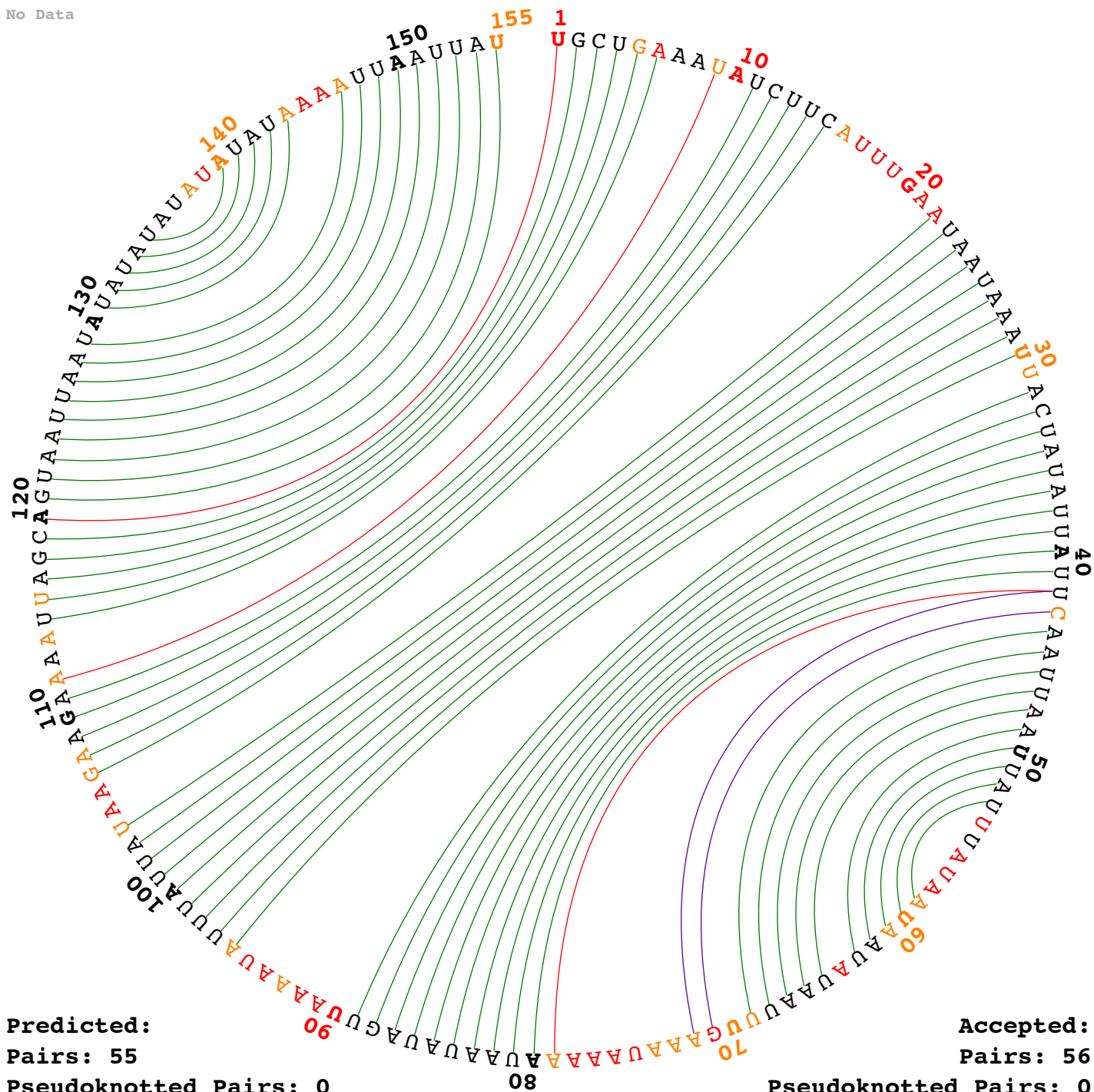
.85 > SHAPE >= .4

```
.4 > SHAPE
```

No Data

Sensitivity: 53 / 56 = 94.64%

PPV: 53 / 55 = 96.36%

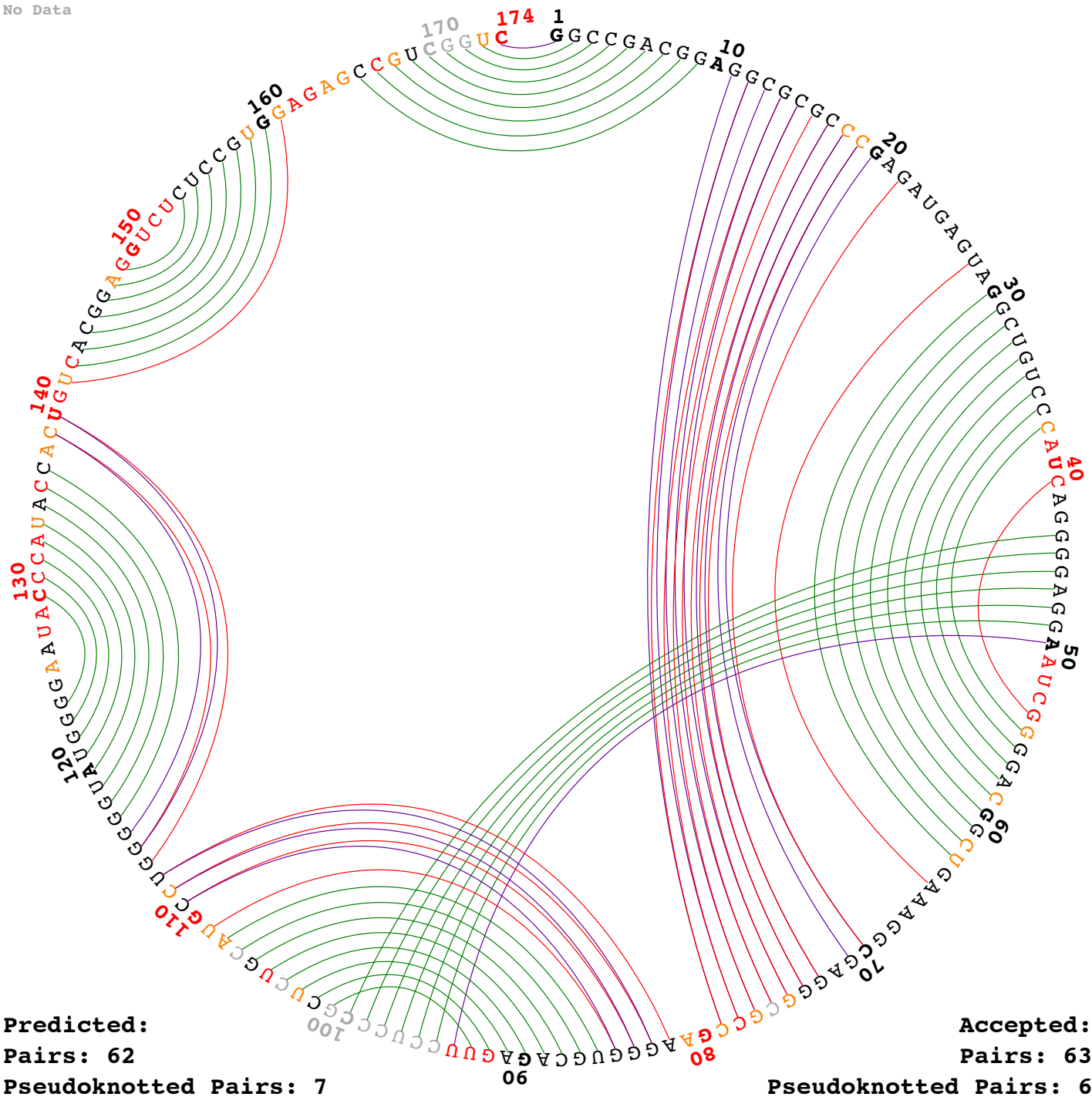


Lysine riboswitch, *T. maritima* ENERGY = -119.8

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 55 / 63 = 87.30%
PPV: 55 / 62 = 88.71%

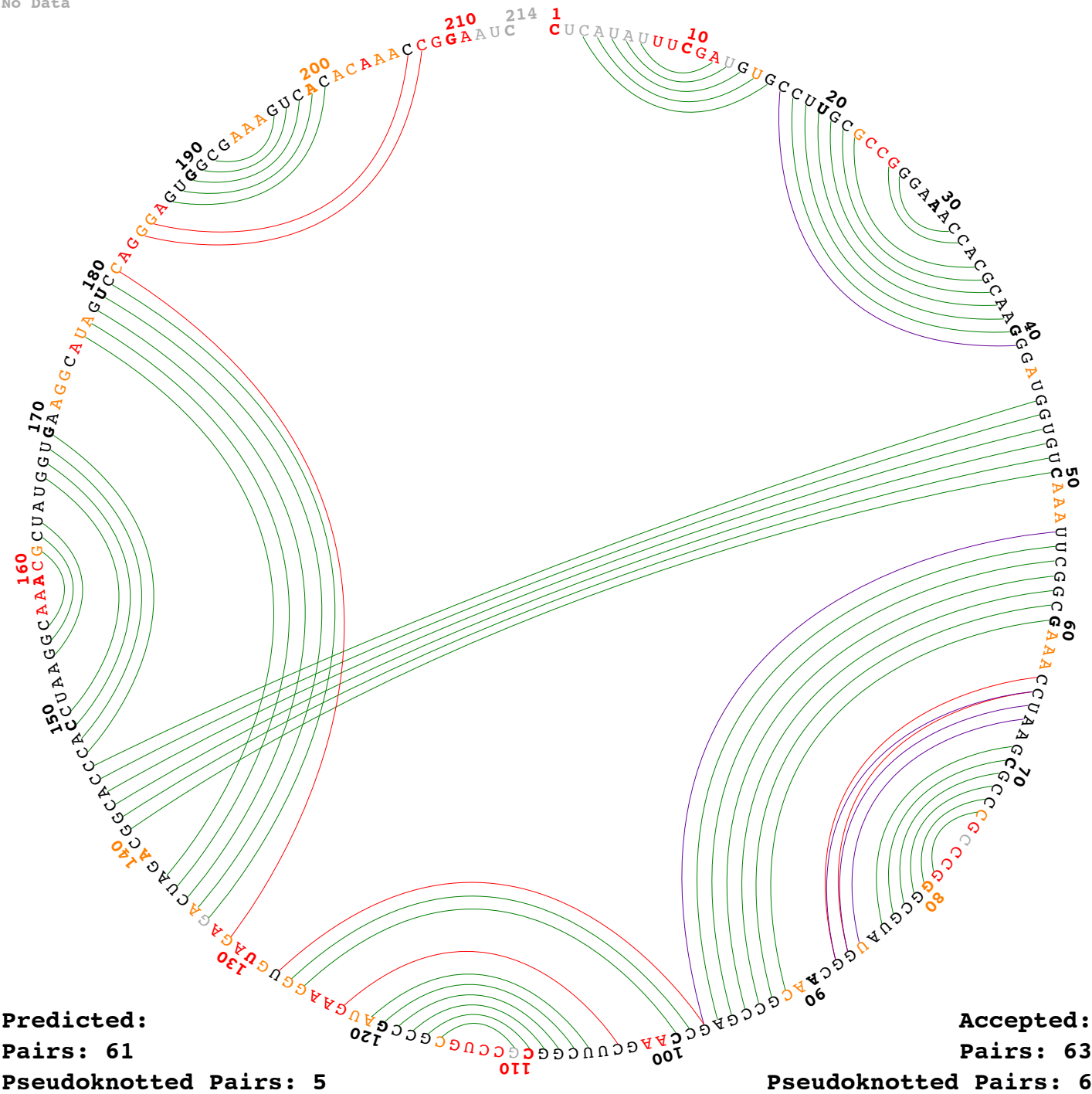


Group I intron, *Azoarcus* sp. ENERGY = -123.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 58 / 63 = 92.06%
PPV: 58 / 61 = 95.08%

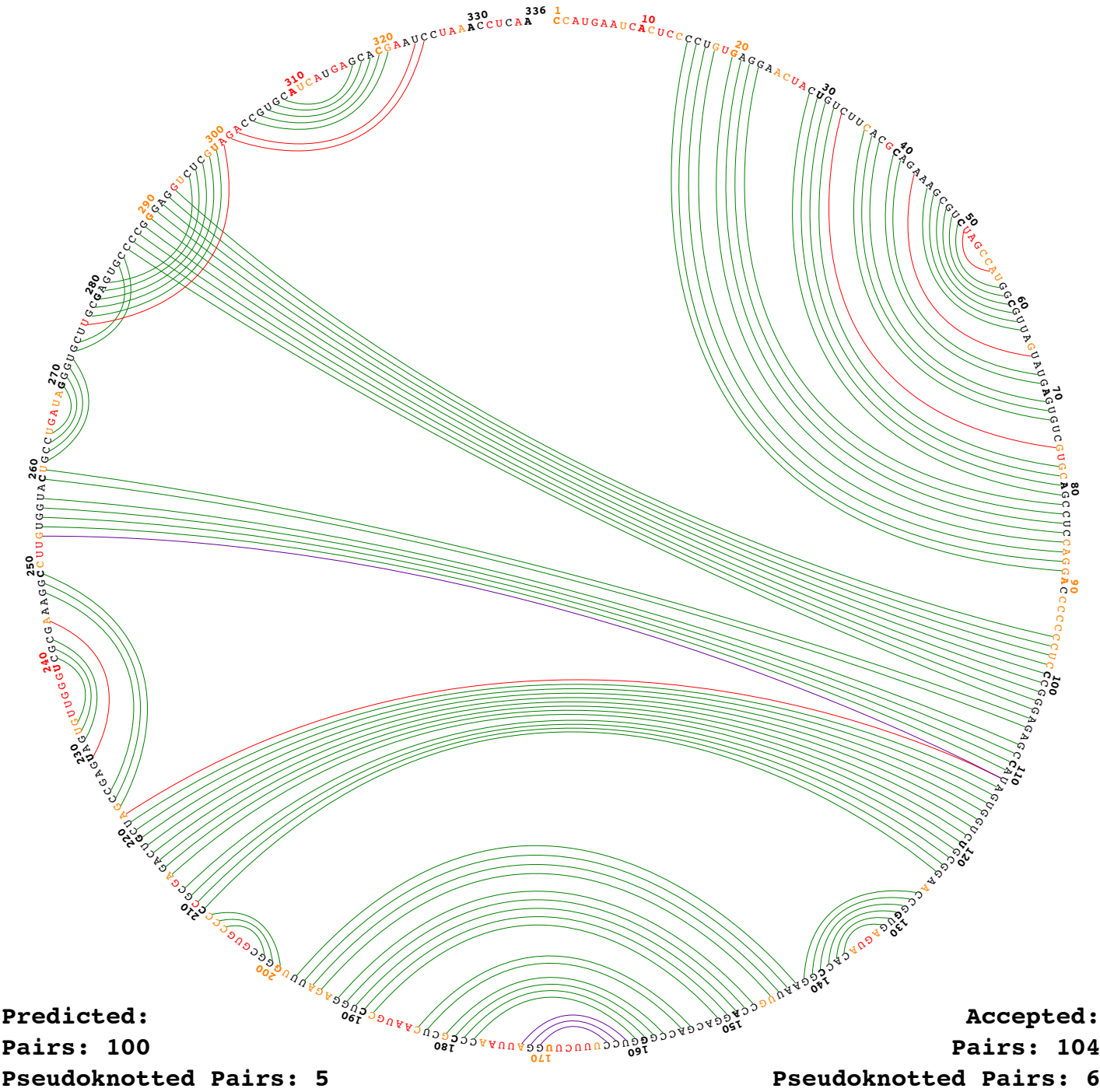


Hepatitis C virus IRES domain ENERGY = -190.7

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 96 / 104 = 92.31%
PPV: 96 / 100 = 96.00%

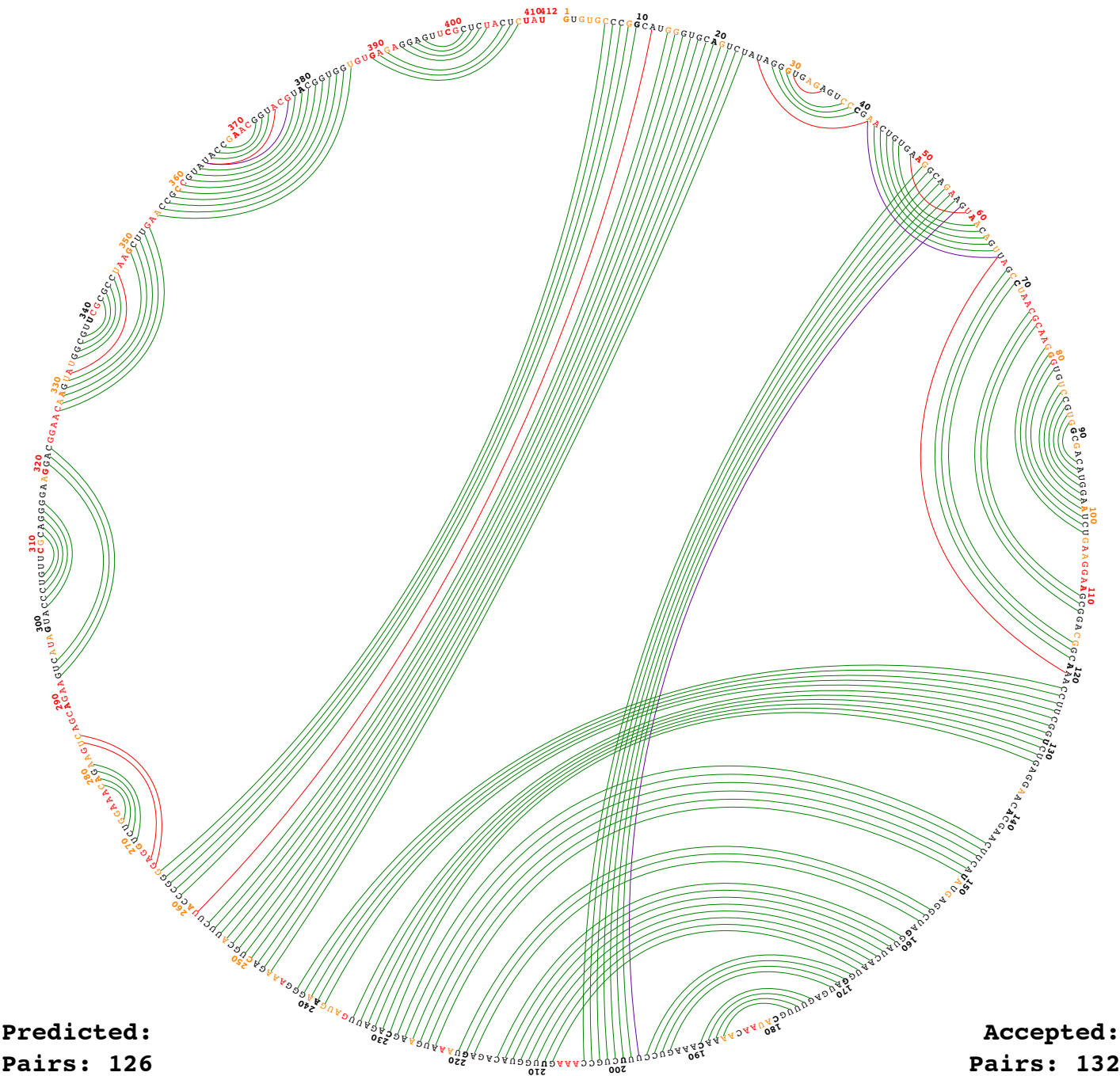


Group II intron, *O. iheyensis* ENERGY = -240.4

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 123 / 132 = 93.18%
PPV: 123 / 126 = 97.62%



Predicted:
Pairs: 126
Pseudoknotted Pairs: 8

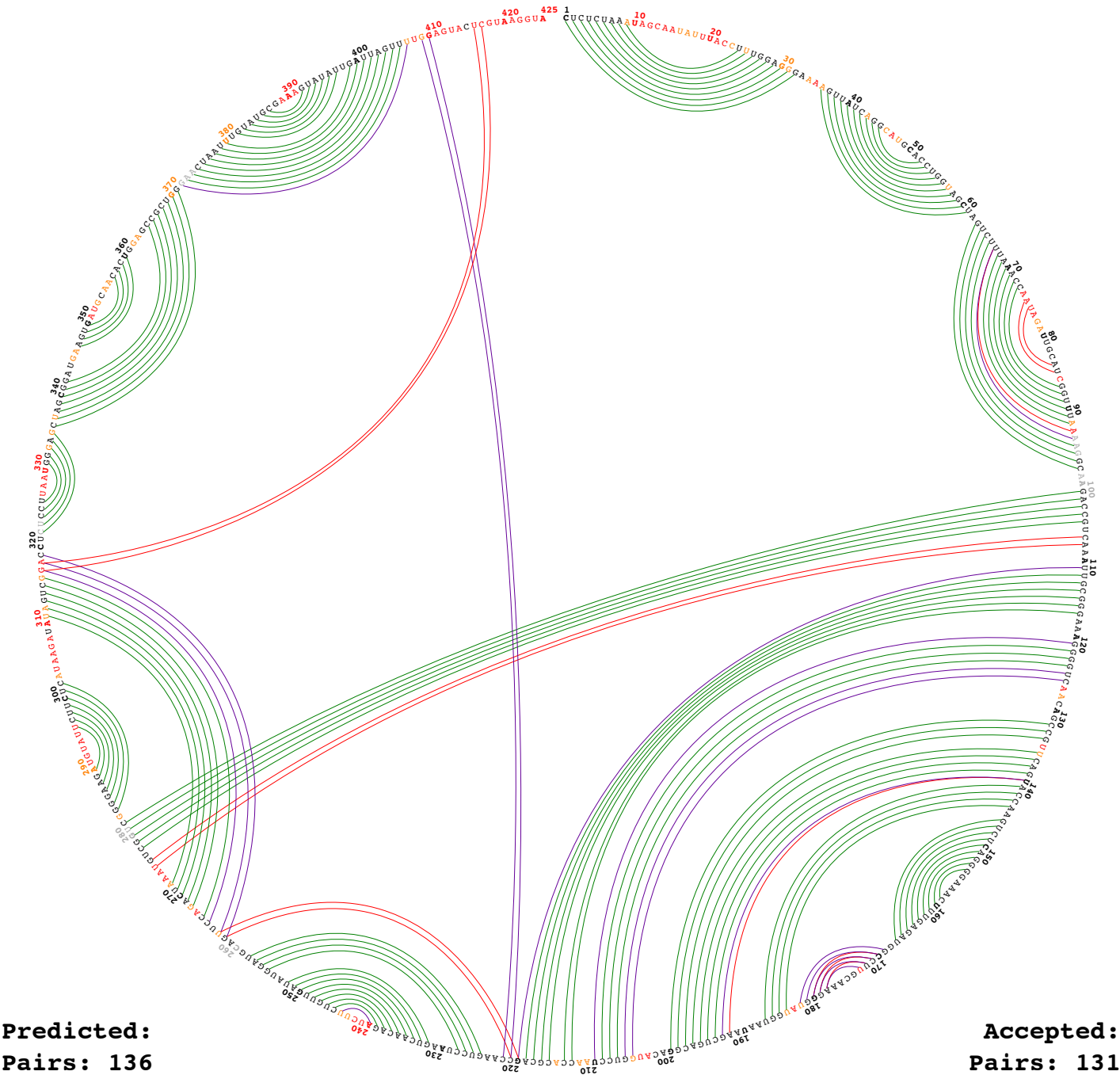
Accepted:
Pairs: 132
Pseudoknotted Pairs: 7

Group I Intron, *T. thermophila* ENERGY = -302.3

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 123 / 131 = 93.89%
PPV: 124 / 136 = 91.18%



Predicted:
Pairs: 136
Pseudoknotted Pairs: 5

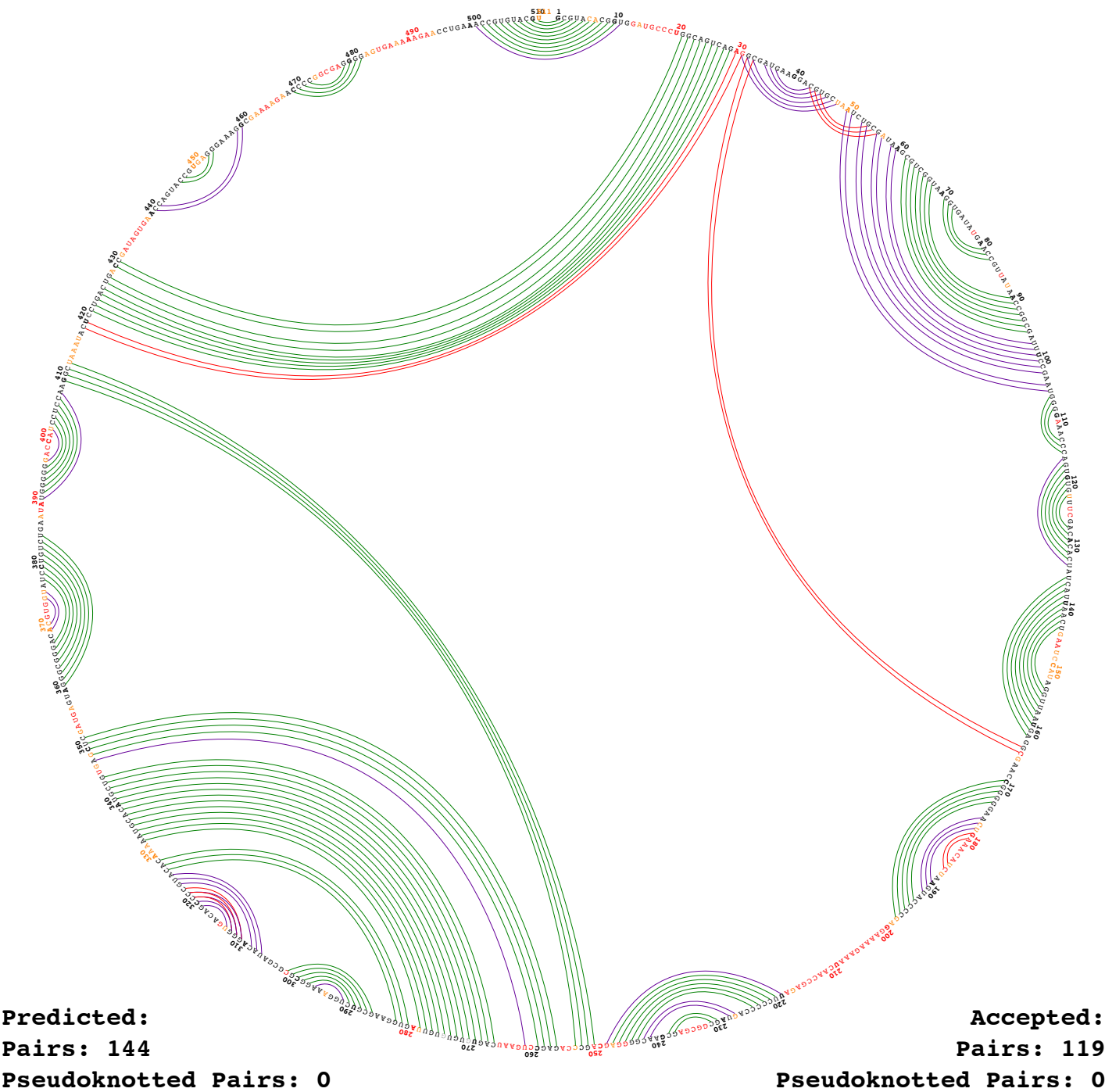
Accepted:
Pairs: 131
Pseudoknotted Pairs: 6

5' domain of 23S rRNA, *E. coli* ENERGY = -328.2

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 110 / 119 = 92.44%
PPV: 110 / 144 = 76.39%

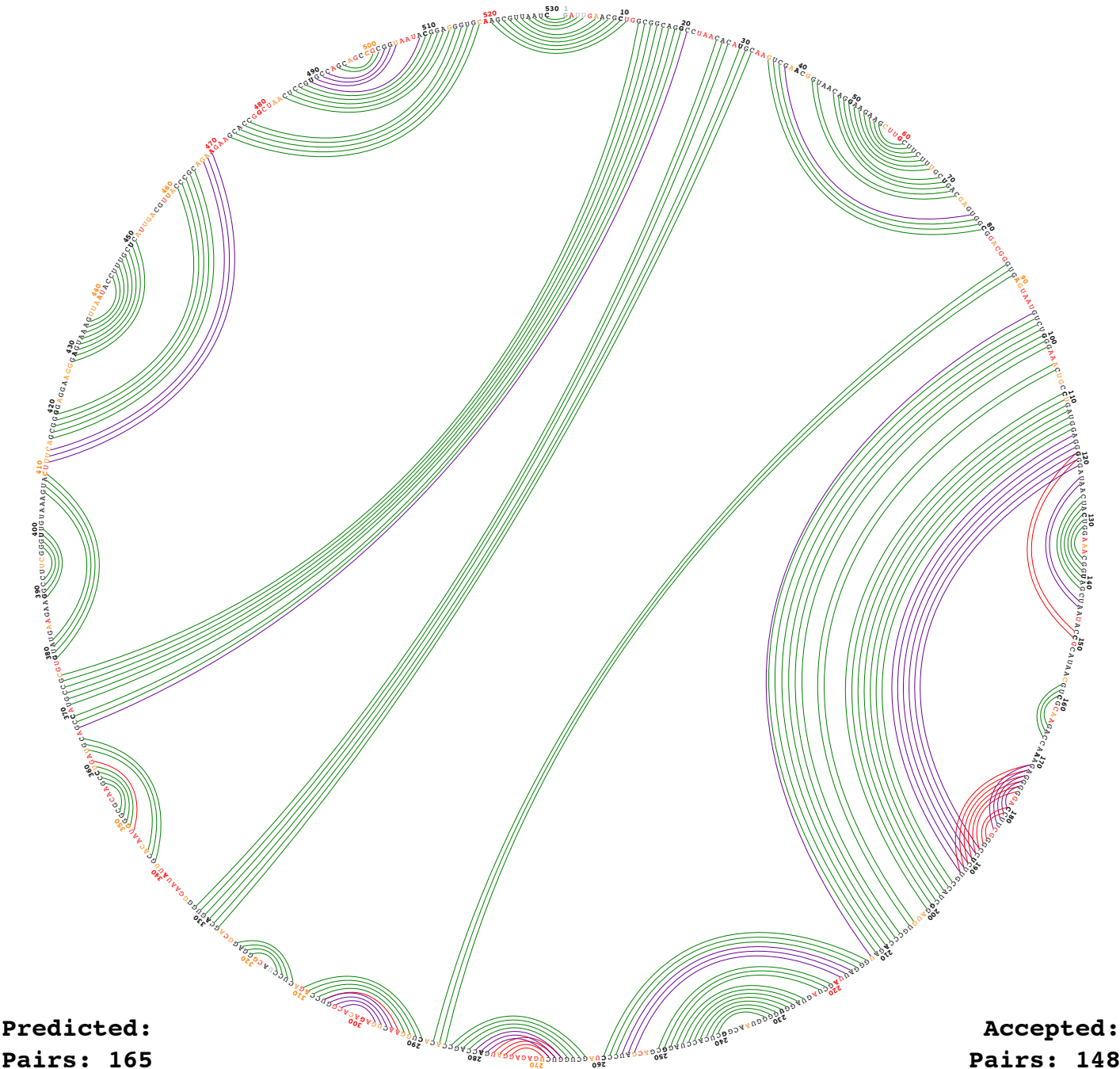


5' domain of 16S rRNA, *E. coli* ENERGY = -371.0

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 133 / 148 = 89.86%
PPV: 133 / 165 = 80.61%



Predicted:
Pairs: 165
Pseudoknotted Pairs: 0

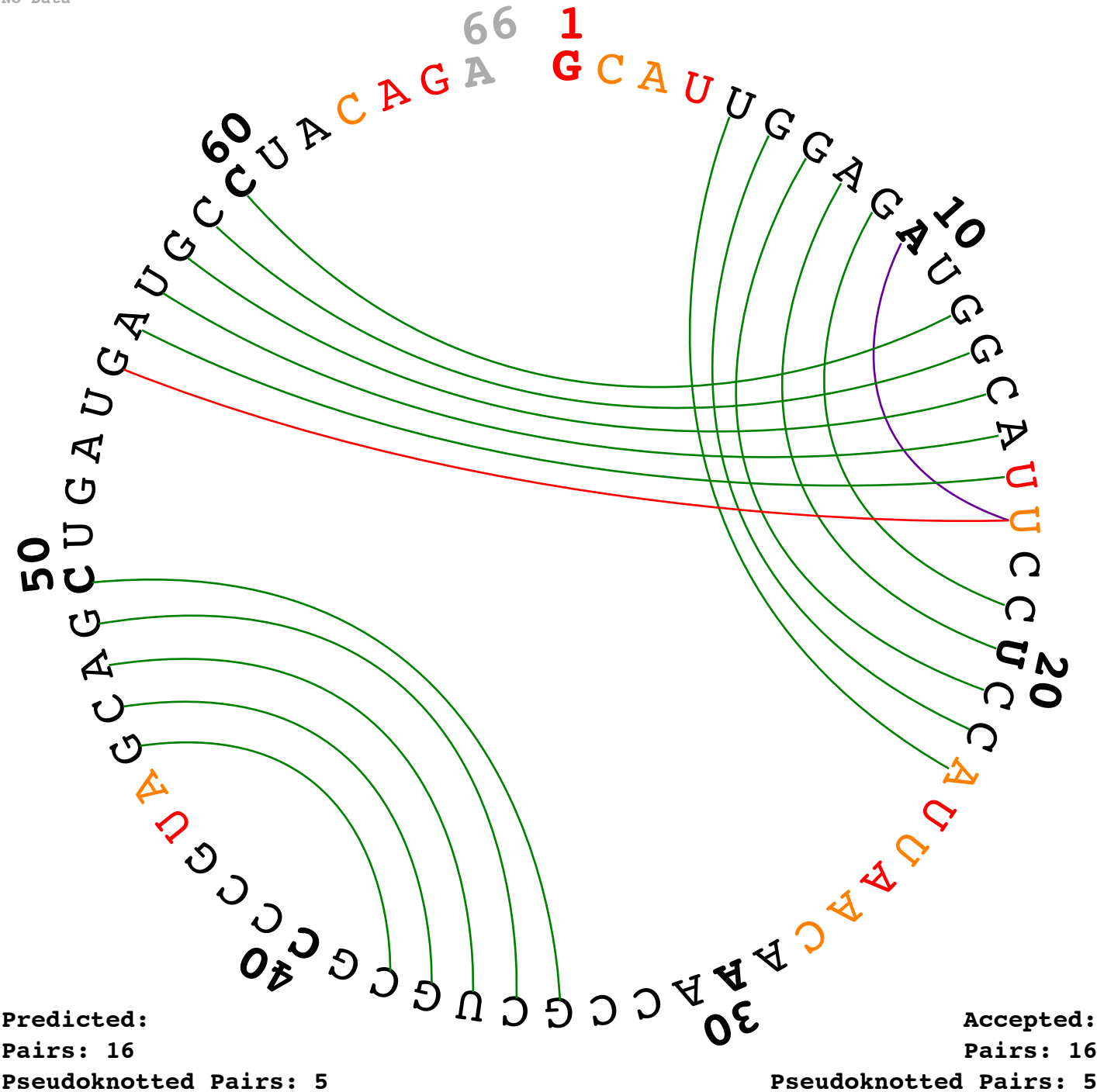
Accepted:
Pairs: 148
Pseudoknotted Pairs: 0

Fluoride riboswitch, *P. syringae* ENERGY = -40.5

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

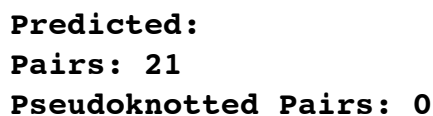
.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 15 / 16 = 93.75%
PPV: 15 / 16 = 93.75%



Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

Sensitivity: 21 / 21 = 100.00%
PPV: 21 / 21 = 100.00%



Accepted:
Pairs: 21
Pseudoknotted Pairs: 0

tRNA(phe), *E. coli* ENERGY = -64.4

Green: Pair in both structures

Red: Pair in Accepted Structure only

Purple: Pair in Predicted Structure only

.85 >= SHAPE

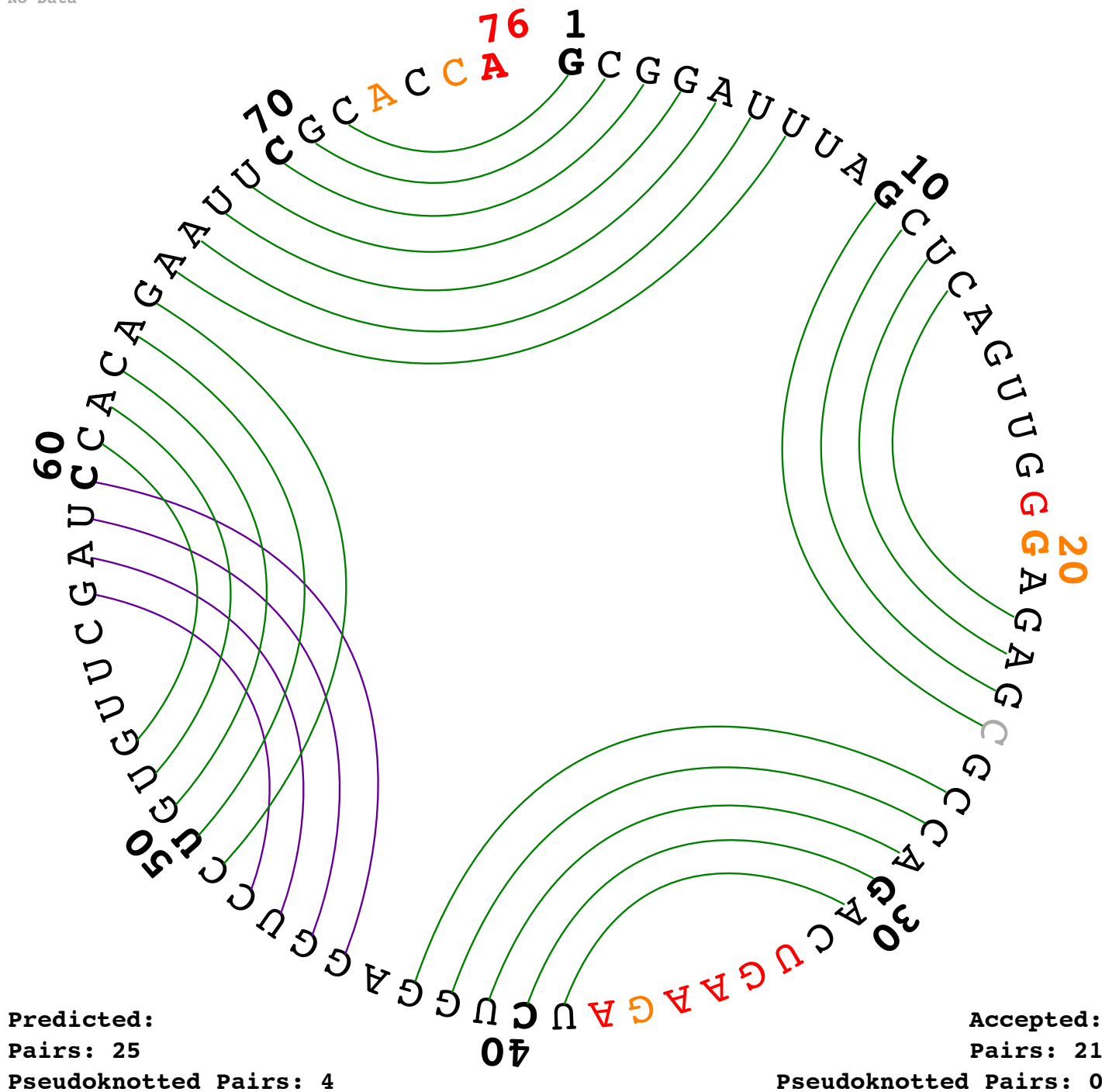
```
.85 > SHAPE >= .4
```

```
.4 > SHAPE
```

No Data

Sensitivity: 21 / 21 = 100.00%

PPV: 21 / 25 = 84.00%

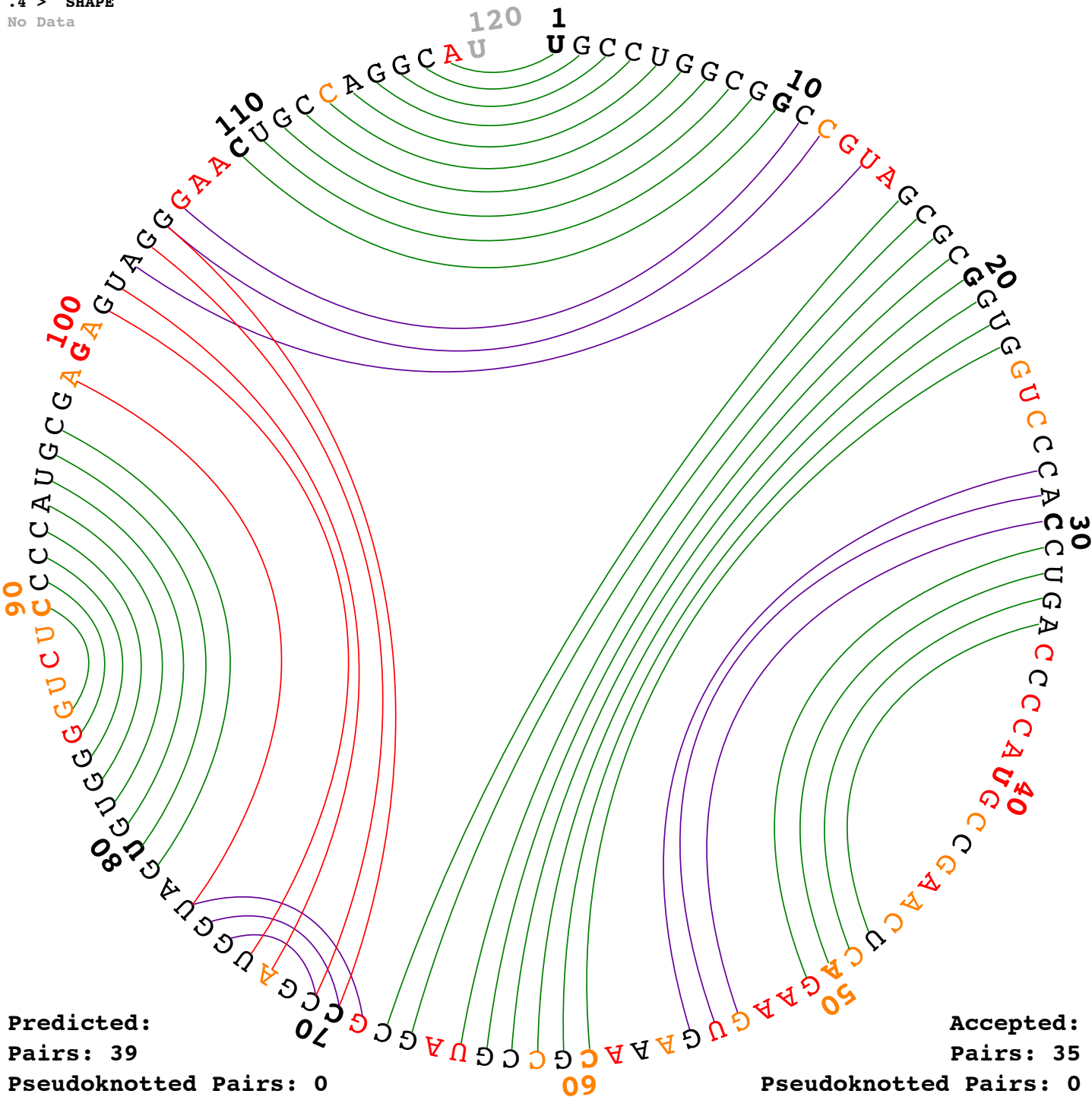


5S rRNA, *E. coli* ENERGY = -76.7

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 30 / 35 = 85.71%
PPV: 30 / 39 = 76.92%



5' domain of 16S rRNA, *H. volcanii* ENERGY = -368.9

Green: Pair in both structures

Red: Pair in Accepted Structure only

Purple: Pair in Predicted Structure only

```
.85 >= SHAPE
```

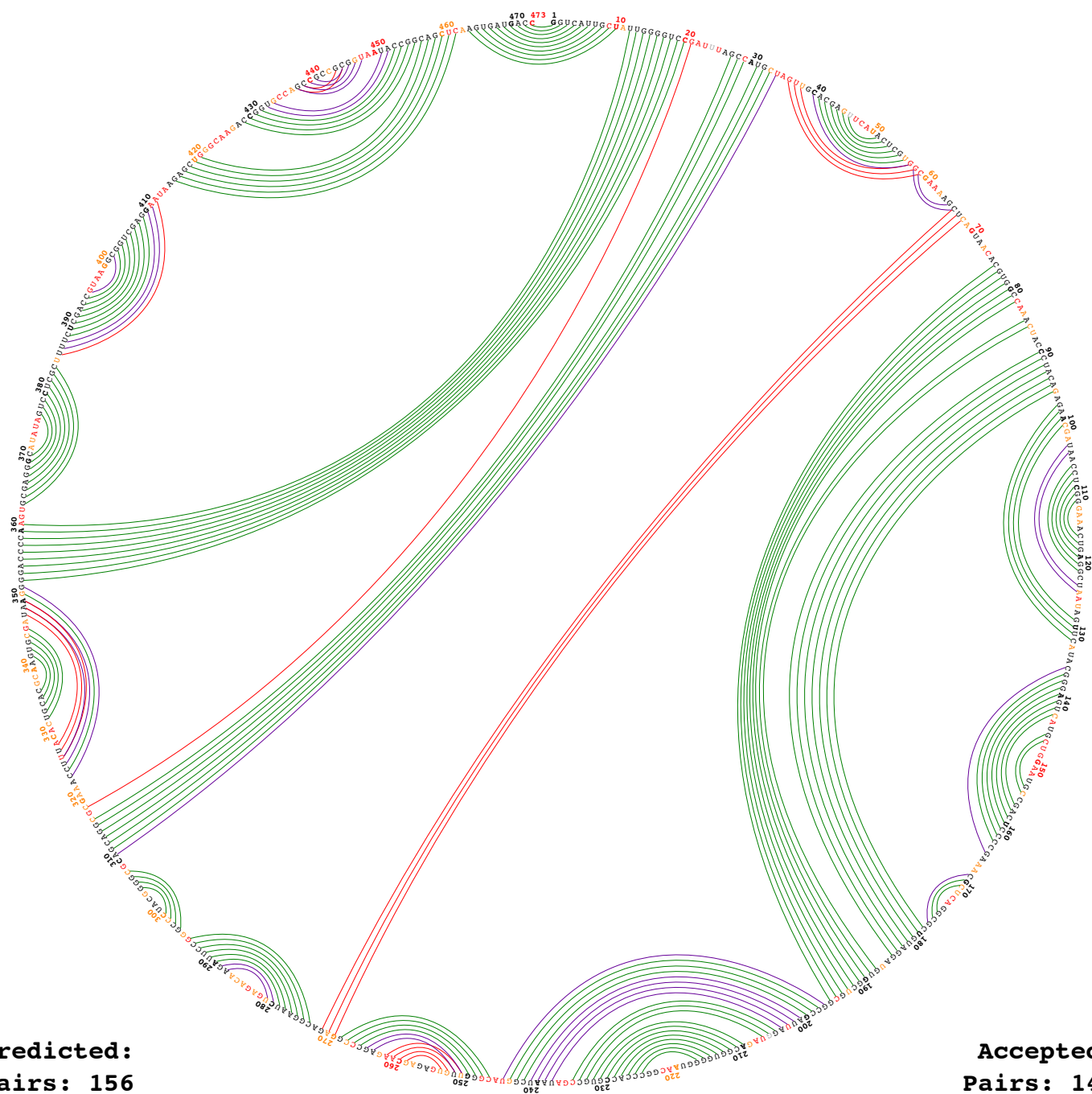
```
.85 > SHAPE >= .4
```

```
.4 > SHAPE
```

No Data

Sensitivity: 129 / 144 = 89.58%

PPV: 129 / 156 = 82.69%



Predicted:

Pairs: 156

Pseudoknotted Pairs: 0

Accepted:

Pairs: 144

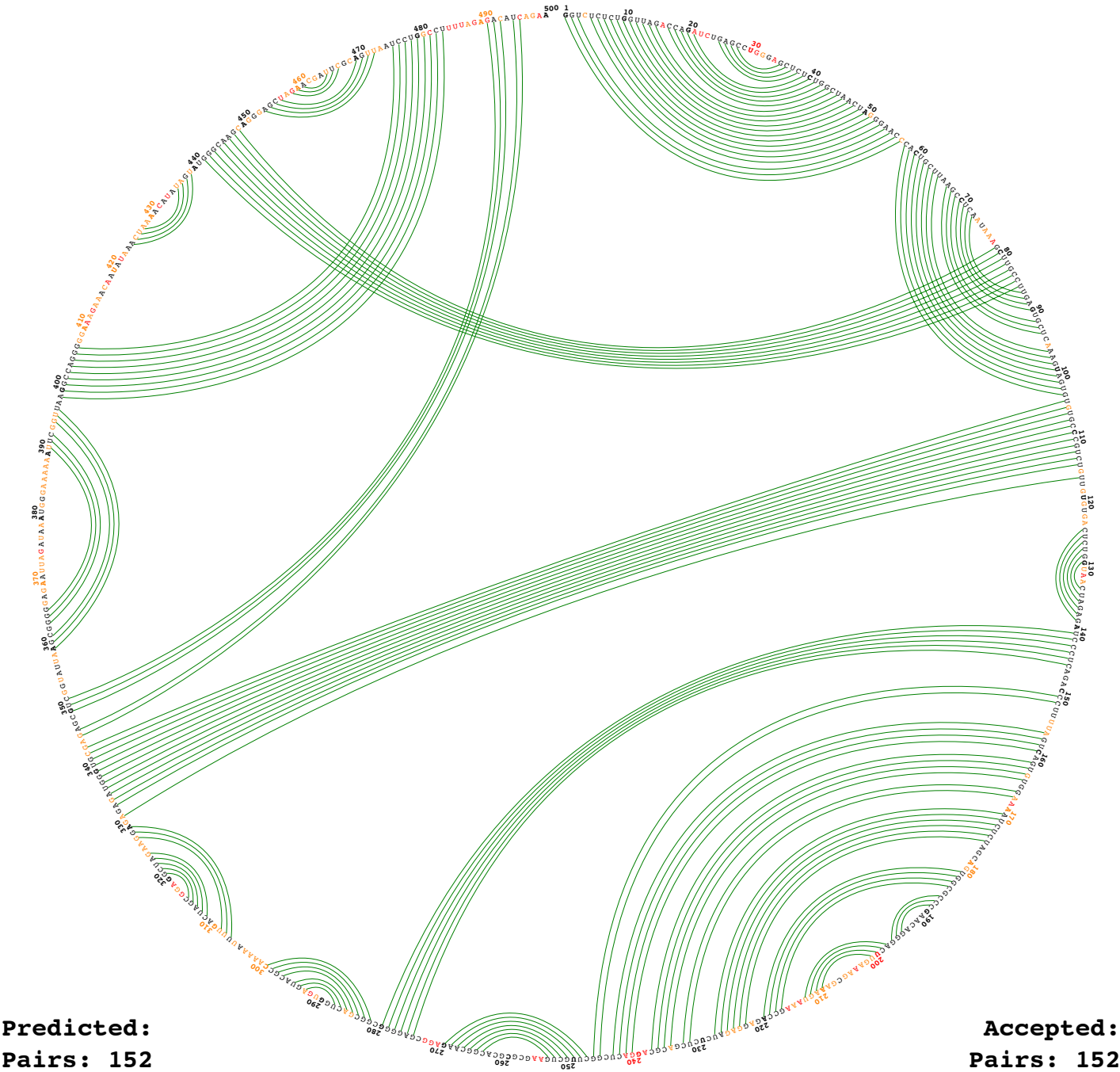
Pseudoknotted Pairs: 0

HIV-1 5' pseudoknot domain ENERGY = -292.2

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 152 / 152 = 100.00%
PPV: 152 / 152 = 100.00%



Predicted:
Pairs: 152
Pseudoknotted Pairs: 8

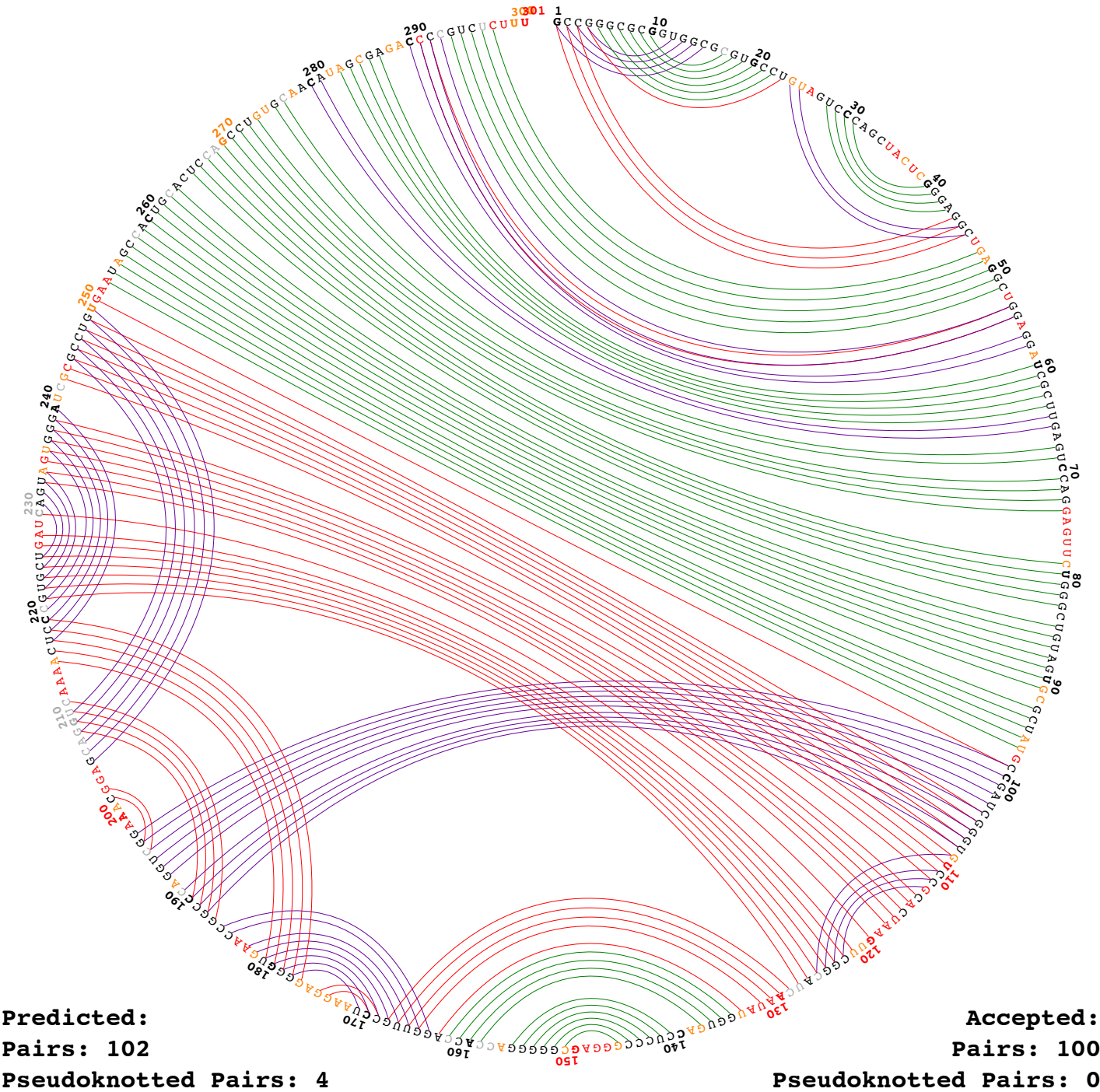
Accepted:
Pairs: 152
Pseudoknotted Pairs: 8

Signal recognition particle RNA, human ENERGY = -202.6

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 55 / 100 = 55.00%
PPV: 55 / 102 = 53.92%

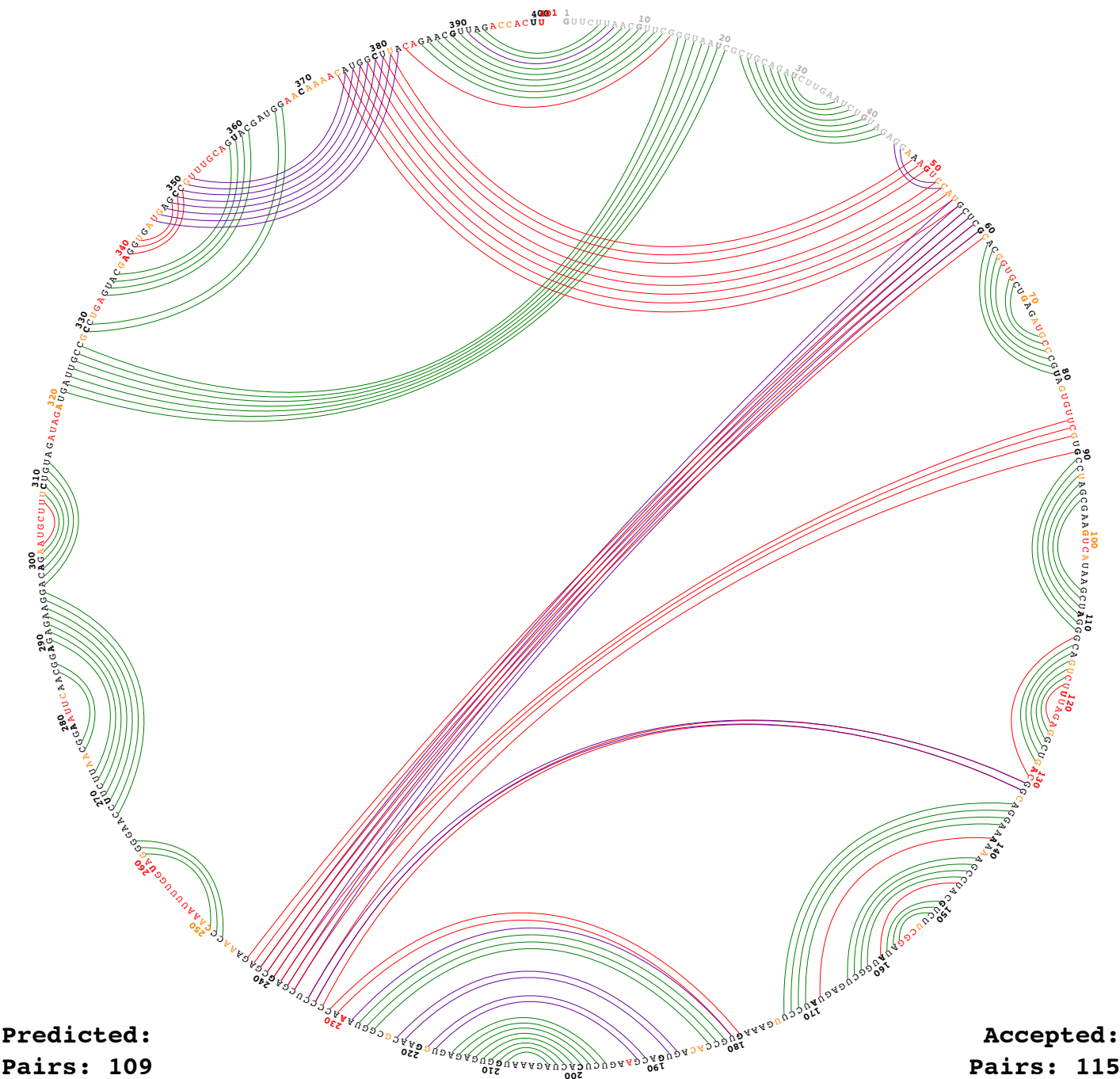


RNase P, *B. subtilis* ENERGY = -201.7

Green: Pair in both structures
Red: Pair in Accepted Structure only
Purple: Pair in Predicted Structure only

.85 >= SHAPE
.85 > SHAPE >= .4
.4 > SHAPE
No Data

Sensitivity: 87 / 115 = 75.65%
PPV: 87 / 109 = 79.82%



Predicted:
Pairs: 109
Pseudoknotted Pairs: 6

Accepted:
Pairs: 115
Pseudoknotted Pairs: 7