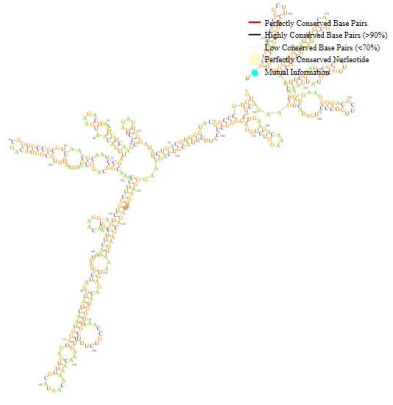
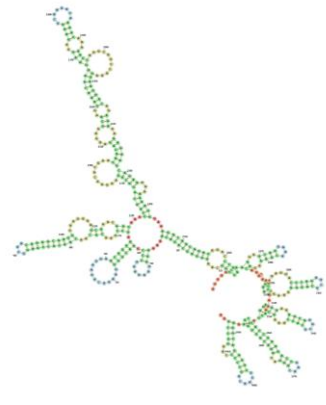
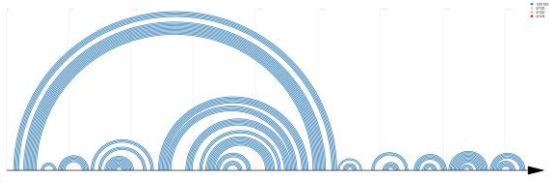
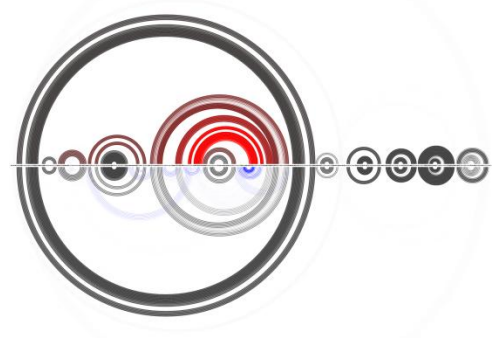

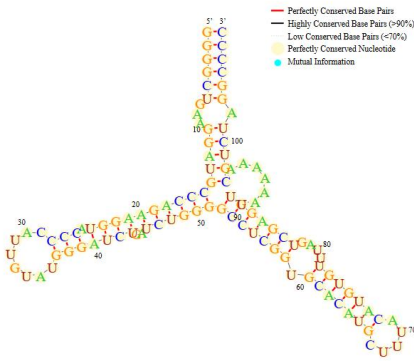
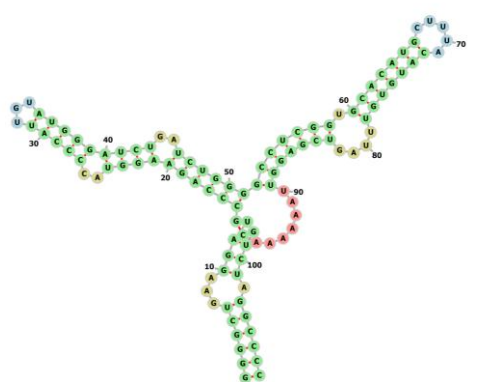
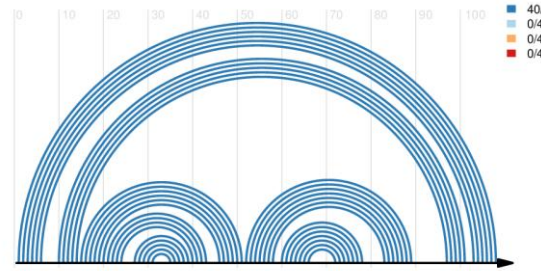
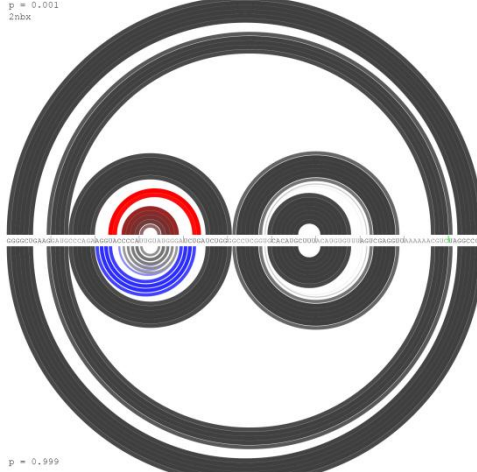
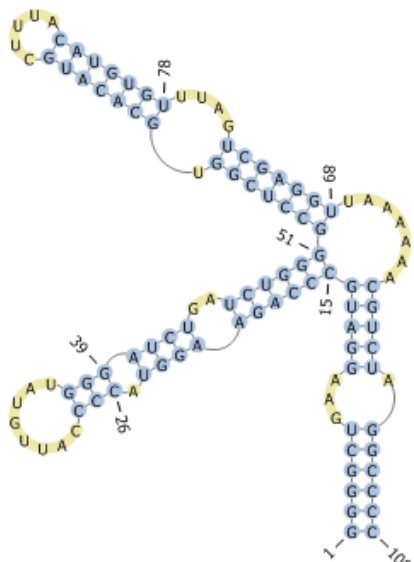
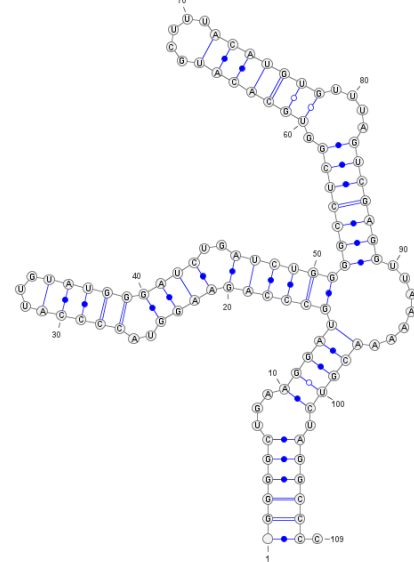


Zestawienie otrzymanych wyników

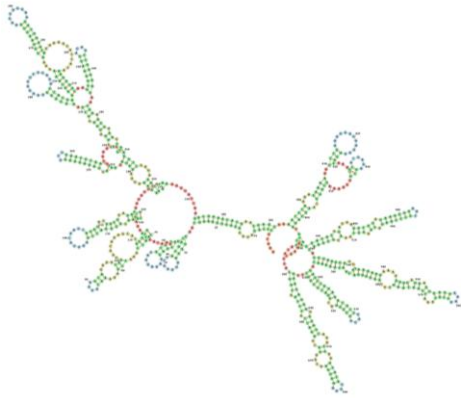
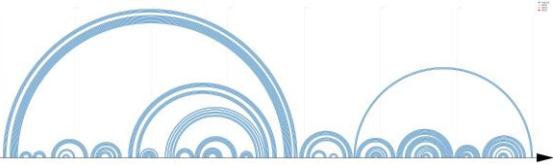
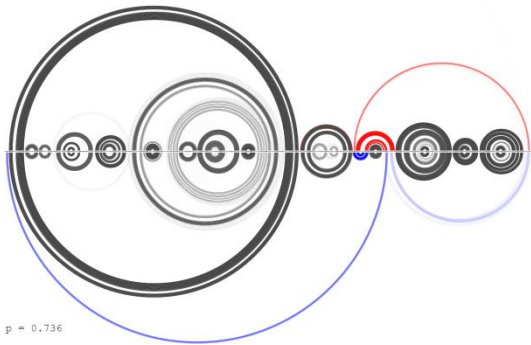
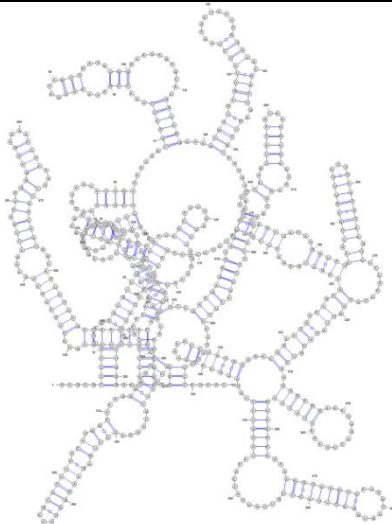
5J01

RNALogo	forna
<p>► The RNALogo graph:</p> <p>5J01</p> 	
RNAChIE	RNAbows
	<p>p = 0.735</p> <p>5J01</p>  <p>p = 0.265</p>
PseudoViewer	VARNA
<p>błąd</p>	 <p>User file #57</p>

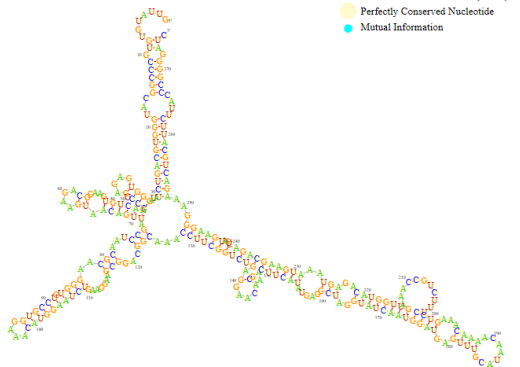
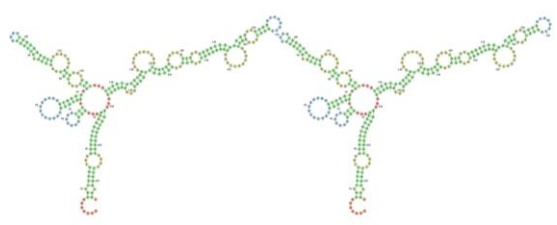
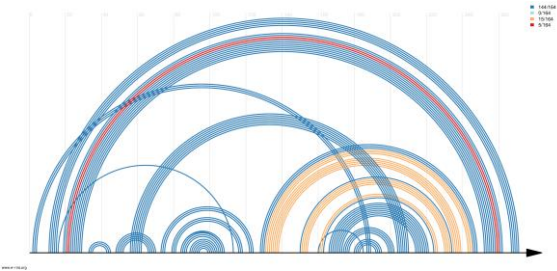
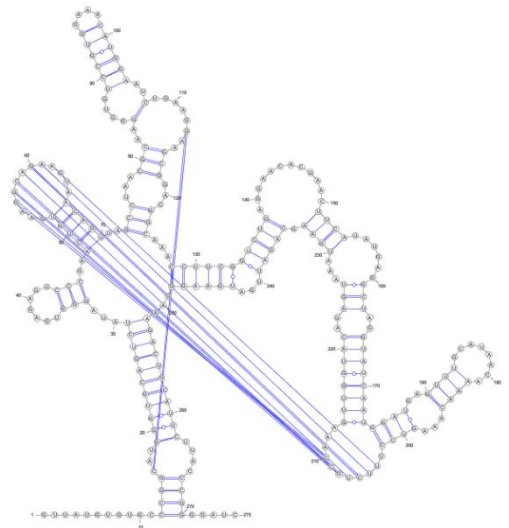
2NBX

RNALogo	forna
<p>► The RNALogo graph:</p> <p>2NBX</p> 	
RCHIE	RNAbows
 <p>www.e-ma.org</p>	 <p>p = 0.001 2nbx</p> <p>p = 0.999</p>
PseudoViewer	VARNA
	 <p>User file #4</p>

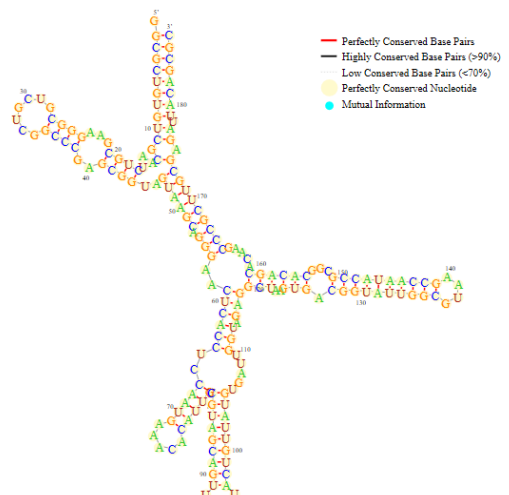
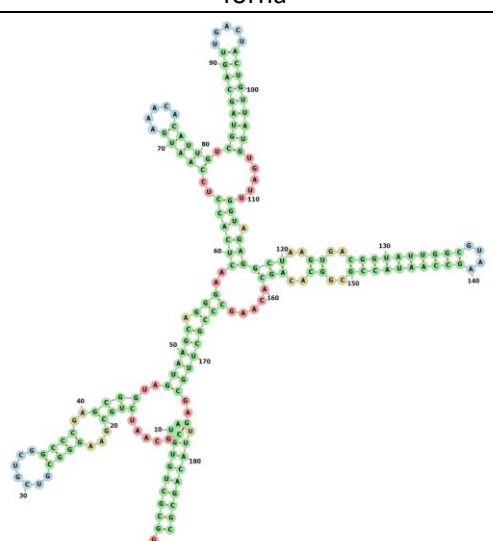
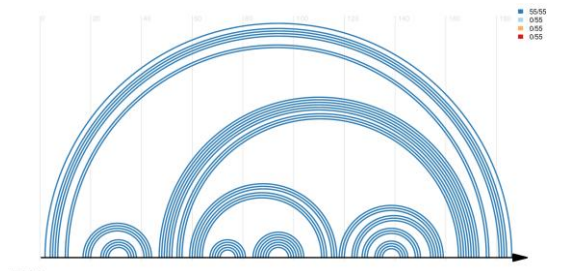
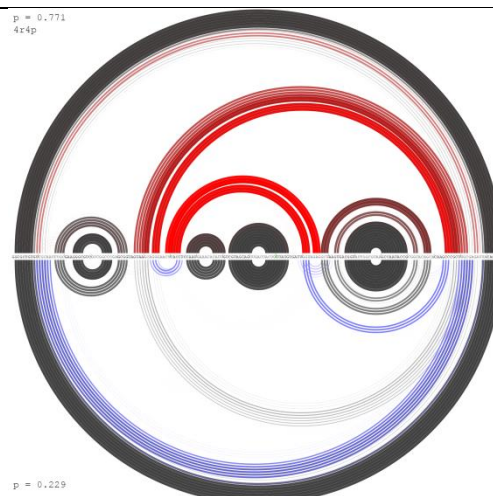
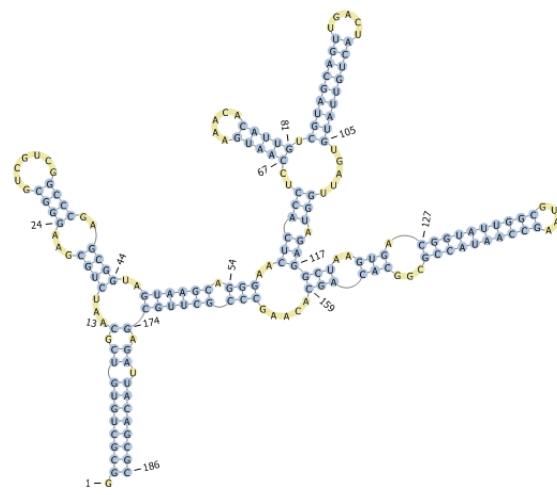
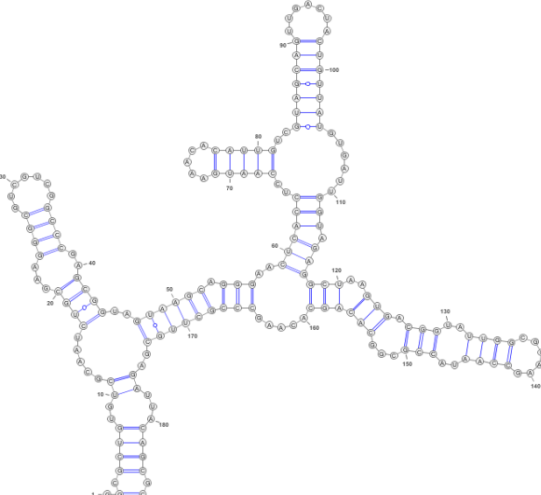
5G2Y

RNALogo	forna
długość sekwencji przekracza 600 pz	
RCHIE	RNAbows
	
PseudoViewer	VARNA
błąd	 User file #56

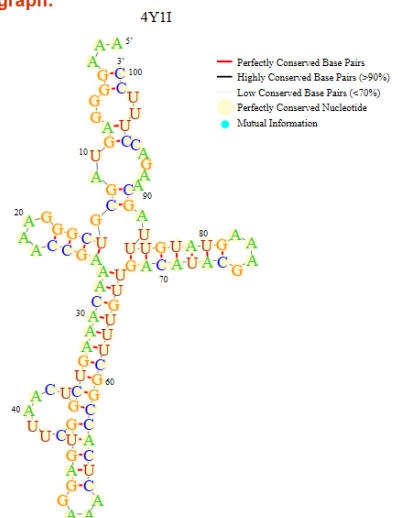
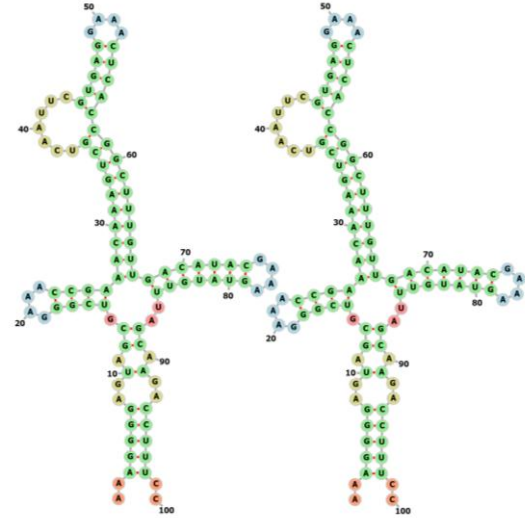
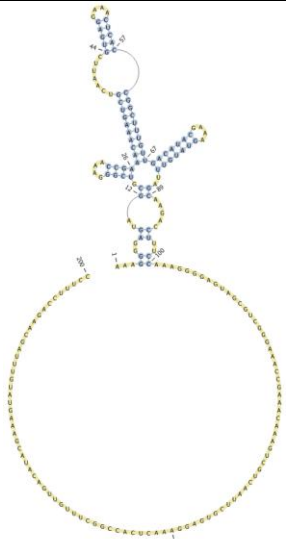
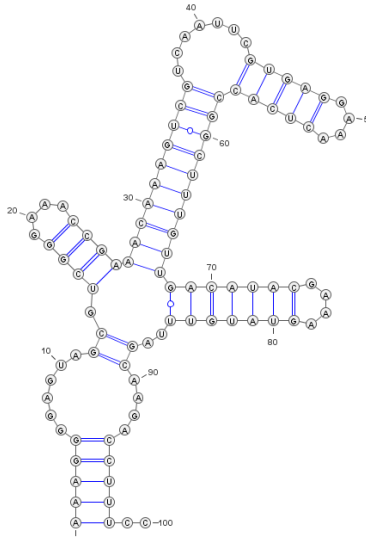
4Y1N

RNALogo	forna
<p>► The RNALogo graph:</p> <p>4Y1N</p> <ul style="list-style-type: none"> Perfectly Conserved Base Pairs Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<70%) Perfectly Conserved Nucleotide Mutual Information 	
RCHIE	RNAbows
	<p>błąd dla metody Clusters (pusty plik)</p>
PseudoViewer	VARNA
<p>błąd</p>	 <p>User file #54</p>

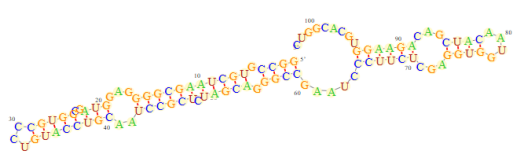
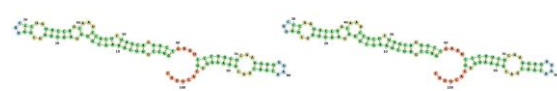
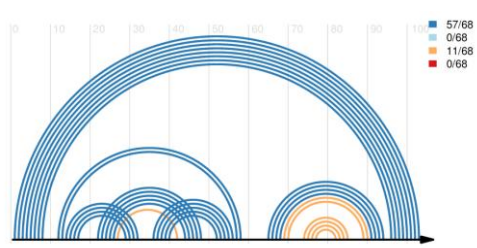
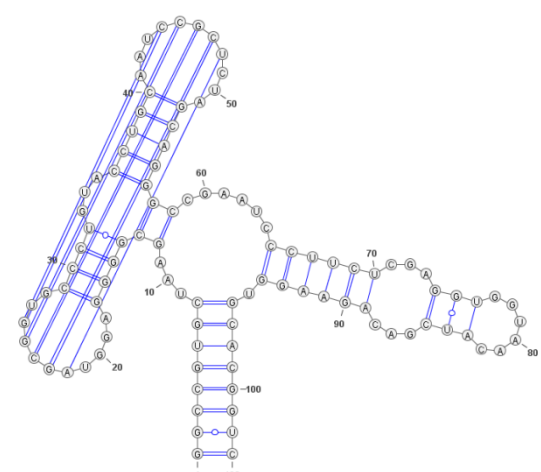
4R4P

RNALogo	forna
<p>► The RNALogo graph:</p> <p>4R4P</p>  <ul style="list-style-type: none"> Perfectly Conserved Base Pairs Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<70%) Perfectly Conserved Nucleotide Mutual Information 	
RCHIE	RNAbows
	
PseudoViewer	VARNA
	 <p>User file #40</p>

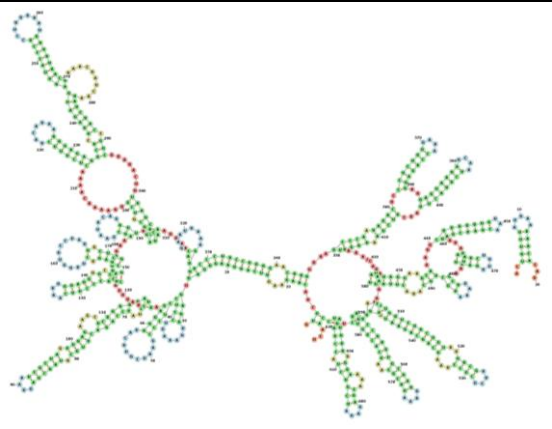
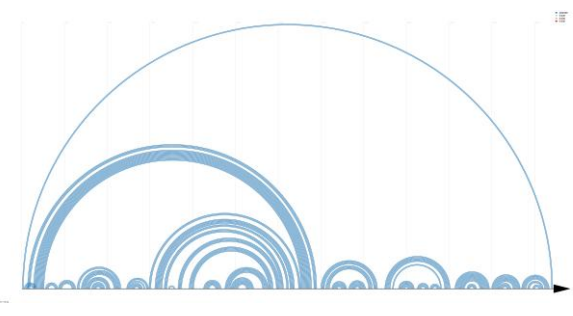
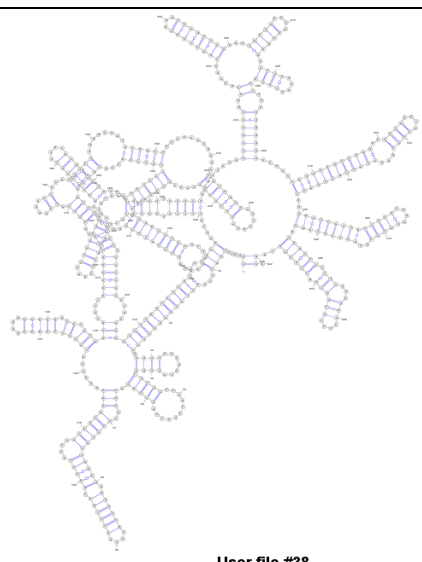
4Y1I

RNALogo	forna
<p>► The RNALogo graph:</p> 	
RCHIE	RNAbows
<p>błąd</p>	<p>błąd (pusty plik)</p>
PseudoViewer	VARNA
	 <p>User file #52</p>

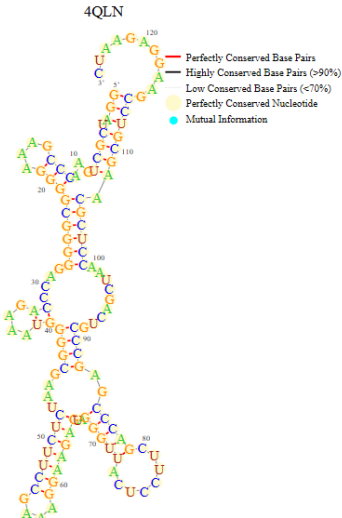
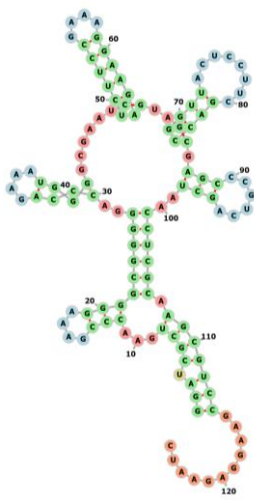
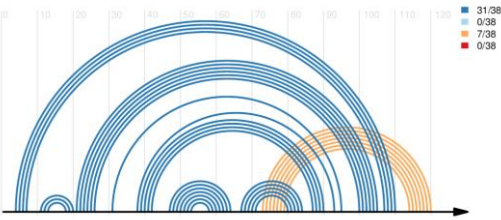
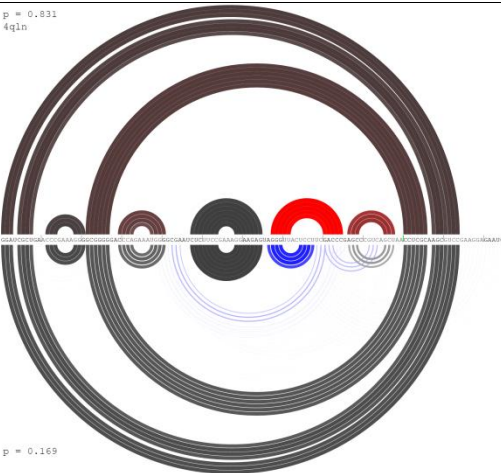
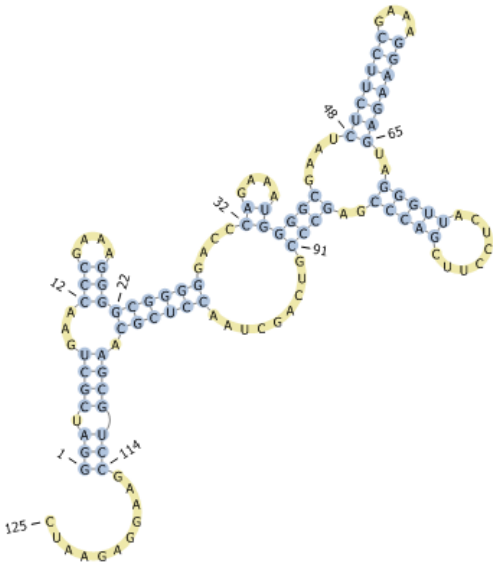
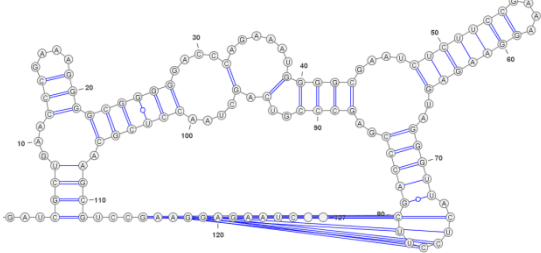
4WFM

RNALogo	forna
<p>► The RNALogo graph:</p> <p>4WFM</p> <ul style="list-style-type: none"> Perfectly Conserved Base Pairs Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<70%) Perfectly Conserved Nucleotide Mutual Information 	
RCHIE	RNAbows
 <p>www.e-ribo.org</p>	<p>błąd dla metody Clusters (pusty plik)</p>
PseudoViewer	VARNA
<p>błąd</p>	 <p>User file #41</p>

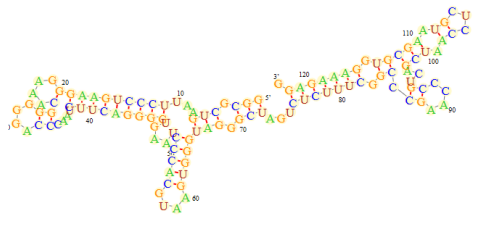
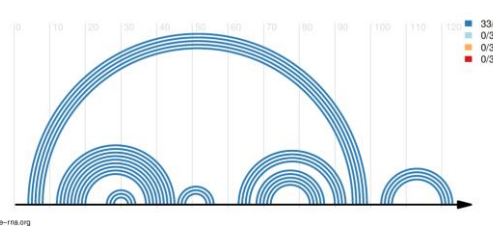
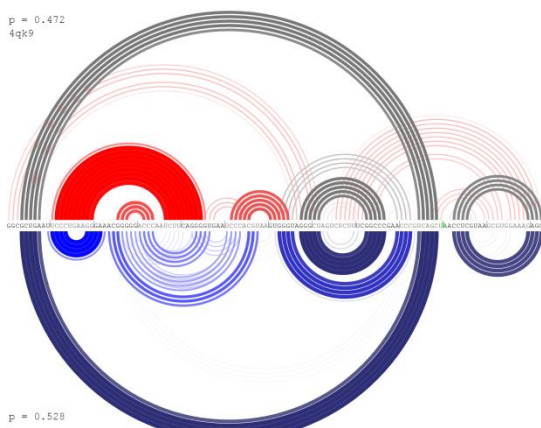
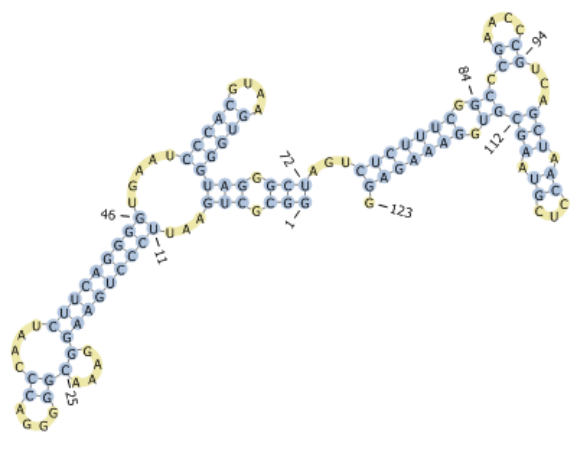
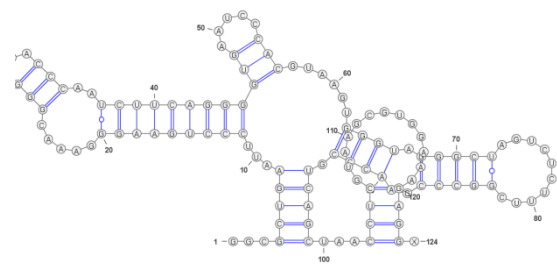
4R0D

RNALogo	forna
długość sekwencji przekracza 600 pz	
RCHIE	RNAbows
	błąd (pusty plik)
PseudoViewer	VARNA
błąd	 User file #38

4QLN

RNALogo	forna
<p>► The RNALogo graph:</p>  <p>4QLN</p> <ul style="list-style-type: none"> Perfectly Conserved Base Pairs Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<70%) Perfectly Conserved Nucleotide Mutual Information 	
RCHIE	RNAbows
 <p>www.e-rib.org</p>	 <p>p = 0.832 4qln</p> <p>p = 0.169</p>
PseudoViewer	VARNA
	 <p>User file #37</p>

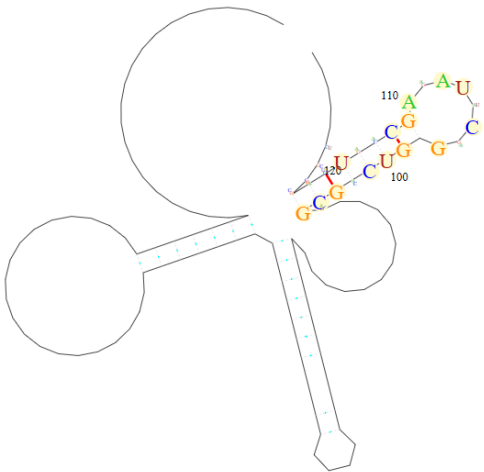
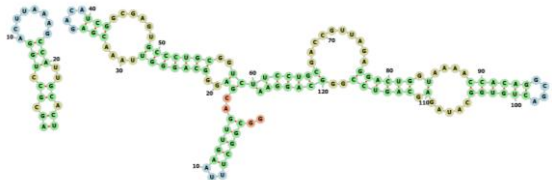
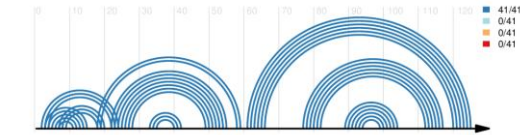
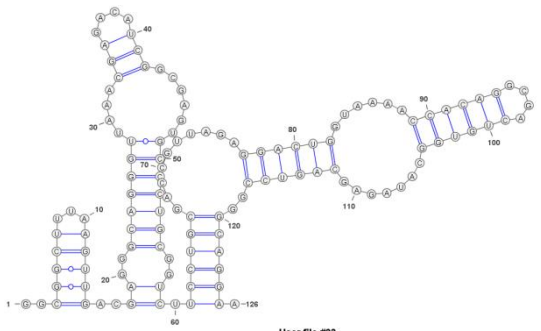
4QK9

RNALogo	forna
<p>► The RNALogo graph:</p> <p>4QK9</p> <ul style="list-style-type: none"> Perfectly Conserved Base Pairs Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<70%) Perfectly Conserved Nucleotide Mutual Information 	<p>błąd</p>
RCHIE	RNAbows
 <p>www.rna.org</p>	<p>p = 0.472 4qk9</p>  <p>p = 0.528</p>
PseudoViewer	VARNA
	 <p>User file #36</p>


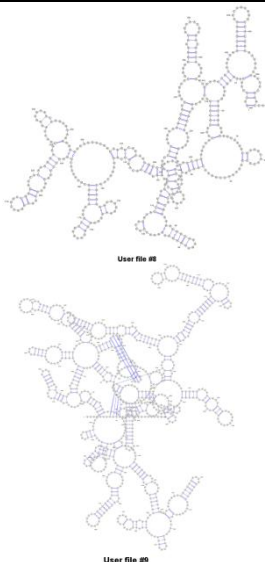
4P9R

RNAlogo	forna
<p>► The RNAlogo graph:</p> <p>4P9R</p> <p> — Perfectly Conserved Base Pairs — Highly Conserved Base Pairs (>90%) — Low Conserved Base Pairs (<70%) ● Perfectly Conserved Nucleotide ● Mutual Information </p>	
RNAIE	RNAbows
	<p>p = 0.375 4p9r</p> <p>p = 0.625</p>
PseudoViewer	VARNA
	<p>User file #34</p>

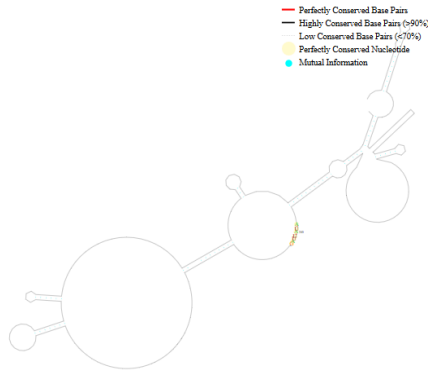
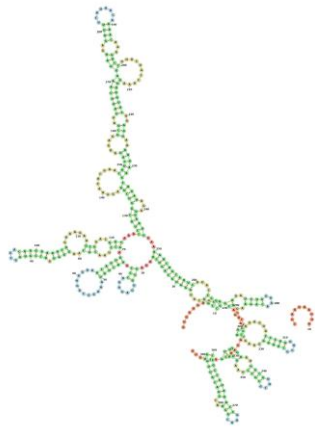
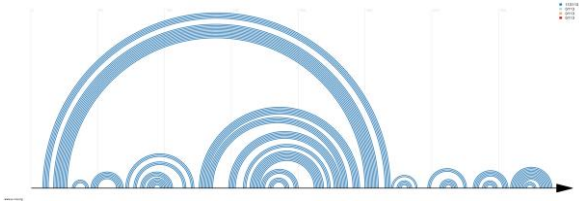
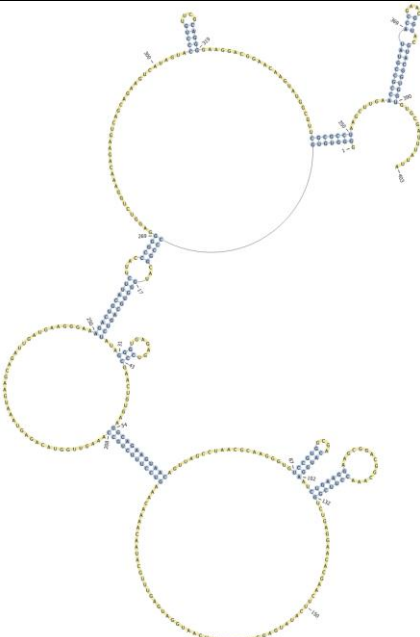
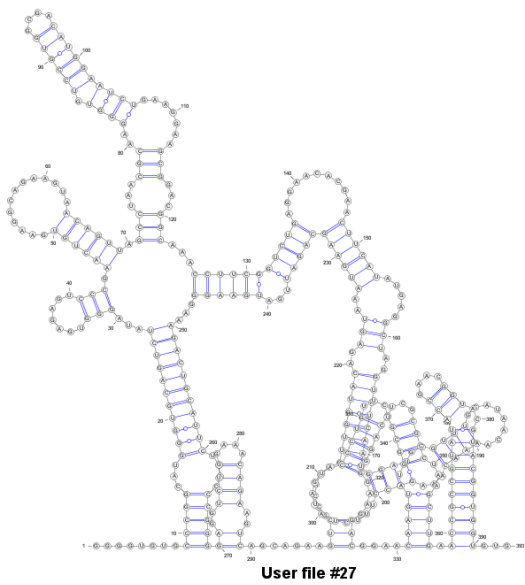
4MEH

RNALogo	forna
<p>► The RNALogo graph:</p> <p>4MEH</p> 	
RCHIE	RNAbows
 <p>www.e-rib.org</p>	<p>błąd dla metody Clusters (pusty plik)</p>
PseudoViewer	VARNA
<p>błąd</p>	 <p>User file #33</p>

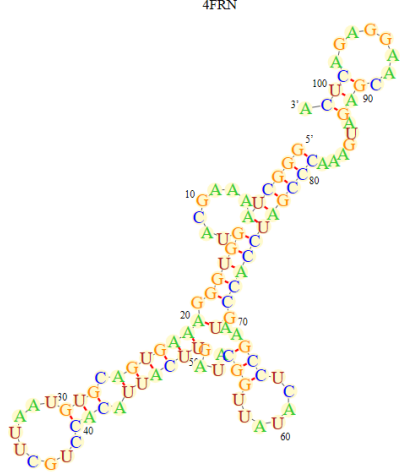
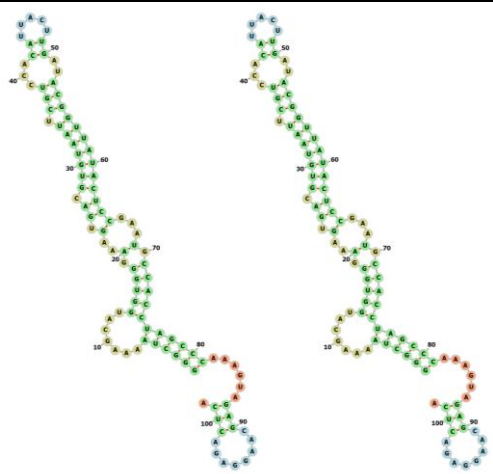
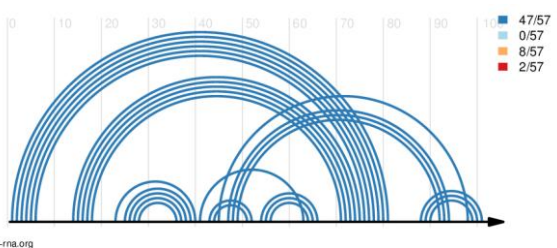

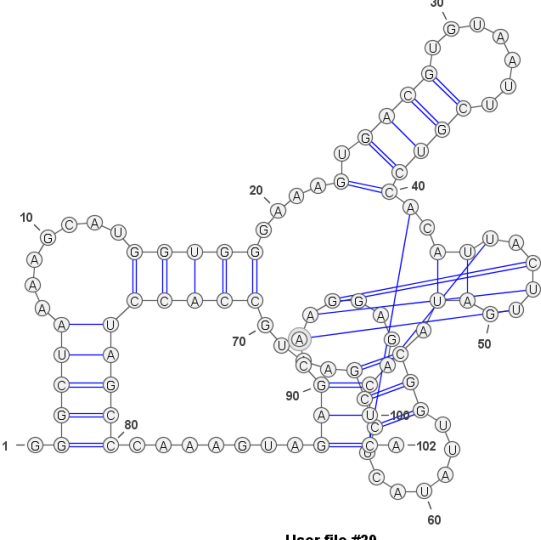
3J2C

RNALogo	forna
długość sekwencji przekracza 600 pz	
RCHIE	RNAbows
błąd	błąd (pusty plik)
PseudoViewer	VARNA
błąd	

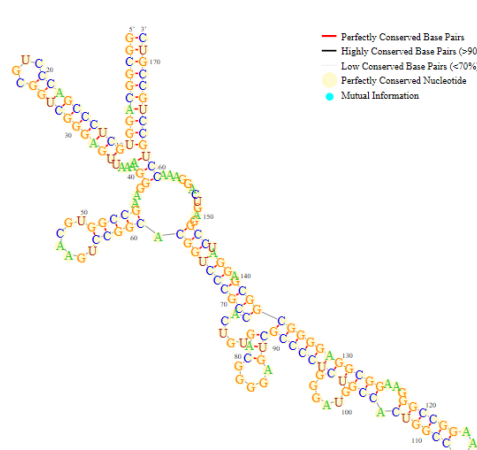
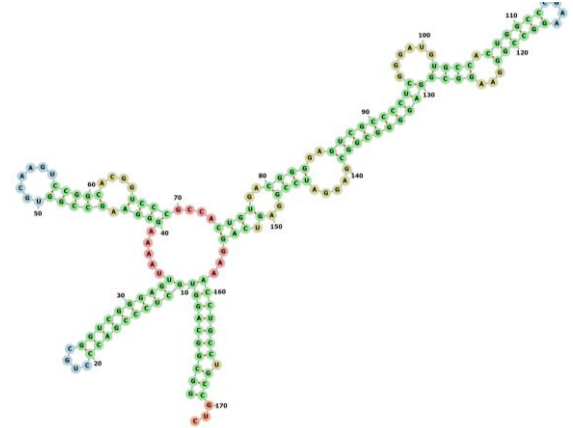
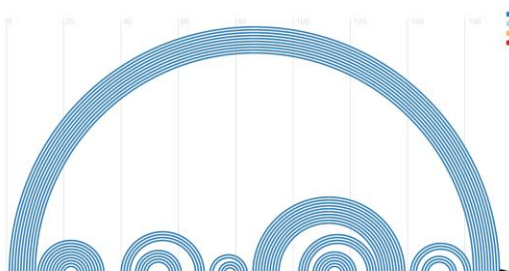
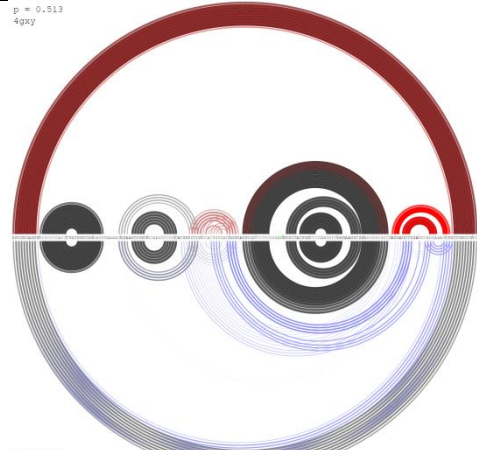
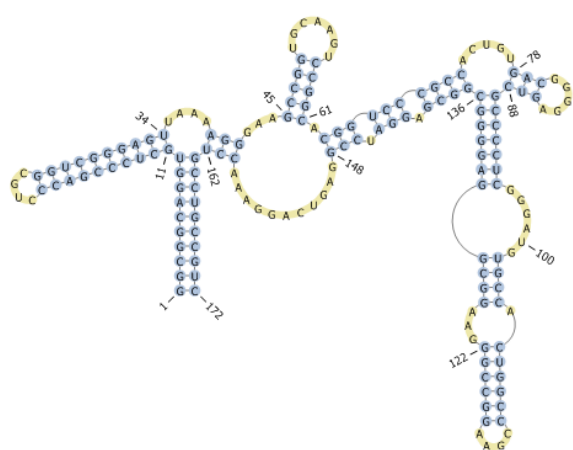
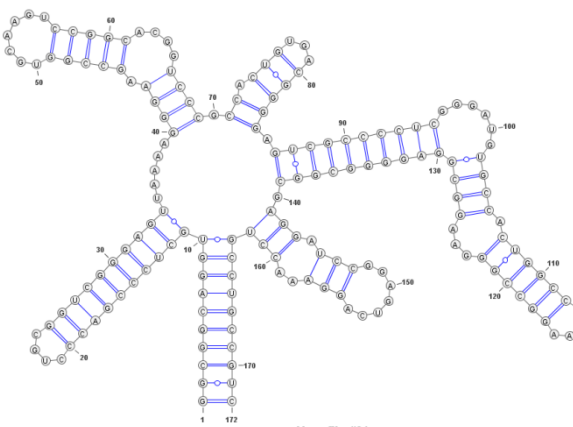
4E8K

RNALogo	forna
<p>► The RNALogo graph: 4E8K</p> <ul style="list-style-type: none"> Perfectly Conserved Base Pair Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<70%) Perfectly Conserved Nucleotide Mutual Information 	
RNAIE	RNAbows
	<p>błąd dla metody Clusters (pusty plik)</p>
PseudoViewer	VARNA
	 <p>User file #27</p>

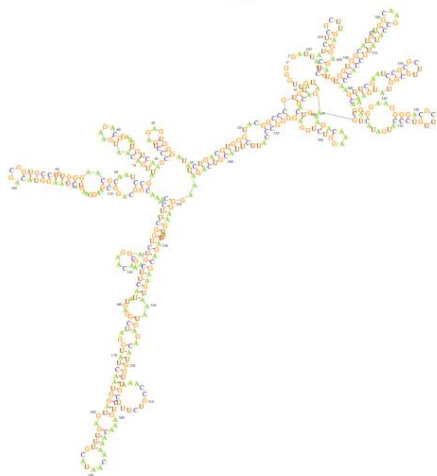
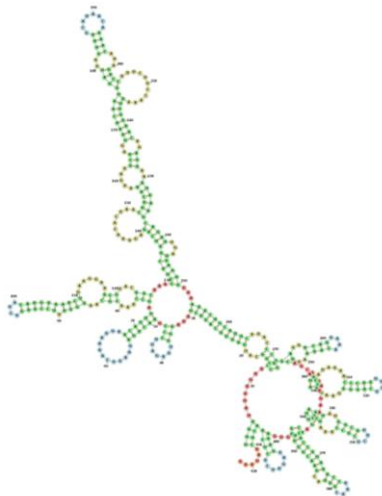
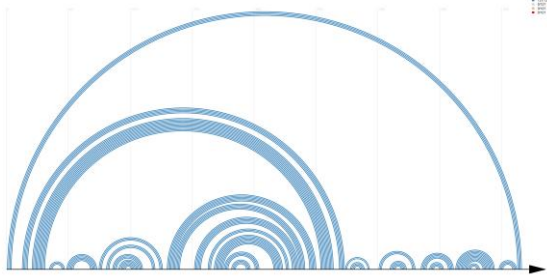
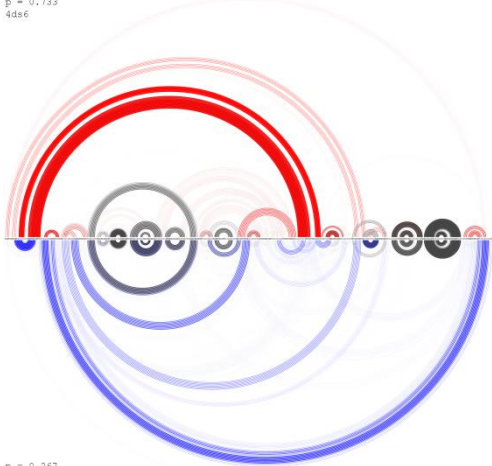
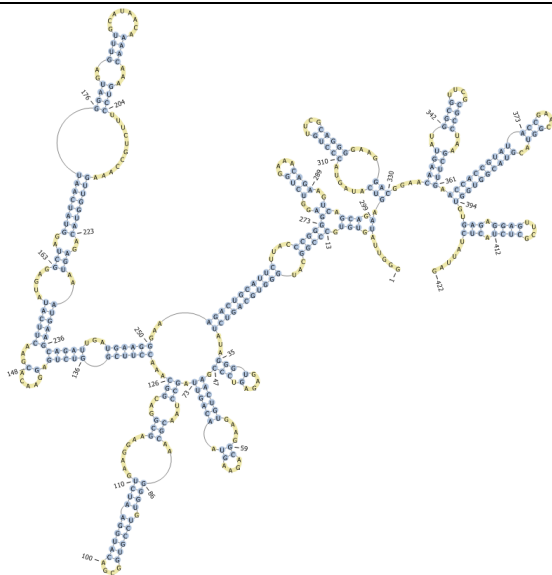
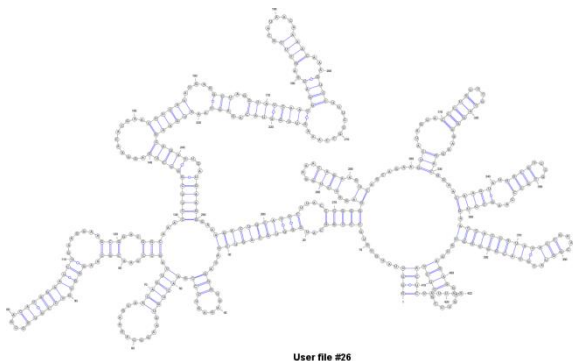
4FRN

RNALogo	forna
<p>► The RNALogo graph:</p> 	
RNAHIE	RNAbows
	<p>błąd dla metody Clusters (pusty plik)</p>
PseudoViewer	VARNA
	 <p>User file #29</p>

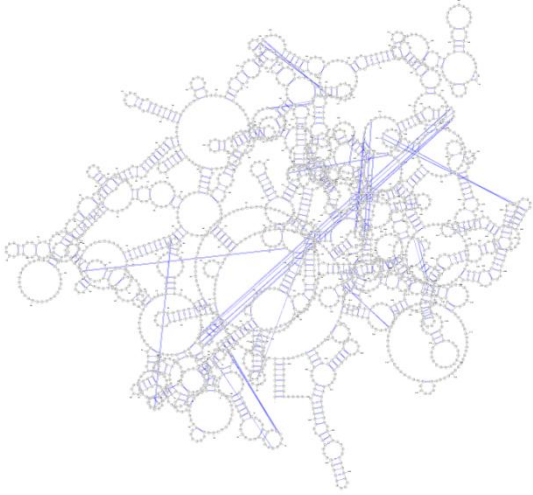
4GXY

RNAlogo	forna
<p>► The RNAlogo graph:</p> <p>4GXY</p>  <ul style="list-style-type: none"> Perfectly Conserved Base Pairs Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<10%) Perfectly Conserved Nucleotide Mutual Information 	
RCHIE	RNAbows
 <p>www.rch.ie</p>	 <p>p = 0.513 4gxy</p> <p>p = 0.487</p>
PseudoViewer	VARNA
	 <p>User file #31</p>

4DS6

RNALogo	forna
<p>► The RNALogo graph: 4DS6</p> 	
RCHE	RNAbows
	<p>p = 0.733 4ds6</p>  <p>p = 0.267</p>
PseudoViewer	VARNA
	 <p>User file #26</p>

3JQ4

RNALogo	forna
długość sekwencji przekracza 600 pz	błąd
RCHIE	RNAbows
błąd	błąd (pusty plik)
PseudoViewer	VARNA
błąd	 <p>User file #23</p>

3IZD

RNALogo	forna
<p>► The RNALogo graph:</p> <p>3IZD</p> <ul style="list-style-type: none"> Perfectly Conserved Base Pairs Highly Conserved Base Pairs (>90%) Low Conserved Base Pairs (<70%) Perfectly Conserved Nucleotide Mutual Information 	
RCHE	RNAbows
<p>www.rche.org</p>	<p>p = 0.757 3izd</p> <p>p = 0.243</p>
PseudoViewer	VARNA
	<p>User file #7</p>