

Cloud lab notes

As my switch diary got crowded, I decided to start a separate doc just for the cloud labs. Also most of the cloud labs are non switches. The idea however is the same. It is more about asking questions and wondering than getting it totally right first time. I will plot some of my thoughts in along as I watch the lab designs. I hope this will be inspirational for you to go and make your own lab data observations and find out things about RNA. Check [here](#) if you want an idea on how to get started with analysing the lab data?

Some of my analysis will be in the main doc here and not in the single lab docs I linked in below. I separated them out to make it a bit easier to find stuff on a specific lab. However if I get an idea while watching a lab, sometimes data from other labs will land in this document, as I go and explore from where I'm at.

Lately I have started adding pics of the main lab structure and link directly to the lab results. That way it is much easier to find the lab I'm interested in. [Lab overview](#) - clicking the link attached to the picture, will take you to the lab results in that lab. Later I will try link analysis for the labs below the pics, for the lab where it belongs. Note that I have a lot of my analysis in this main doc.

Also see my [Switch diary](#) & [Switch diary 2](#).

Eli Fisker

Cloud lab - first batch

[Cloud lab 2 - Triangle of Doom](#)

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[Cloud Lab 7 - 5 fold radial Asymmetrical Starfish Level 0 by Jieux](#)

[Cloud Lab 9 - Final Countdown](#)

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[Cloud Lab 13 - Alien party glasses](#)

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[Cloud lab 16 - Section from Water strider](#)

[Cloud Lab 17 - Oryza sativa 8 Elements Part 2 by merryskies](#)

[Cloud Lab 18 - Anaconda](#)

[Cloud lab 19 - Big hairpin Loop](#)

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Labs published the 27 June 2013

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[Single to switch try](#)

[Short stack](#)

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[The GAAA Loop](#)

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[RNA Bridge \(updated\)](#)

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[Two stacks](#)

Cloud lab - 5th batch

Cloud Labs published 17 July 2013

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Switch labs

[Bistable notes](#)

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[JR's Lets Break the barcode - Adjacent barcode version](#)

[FMN Binding Site Chemical Footprint - Round 2](#)

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[JR's Let's Break the Barcode](#)

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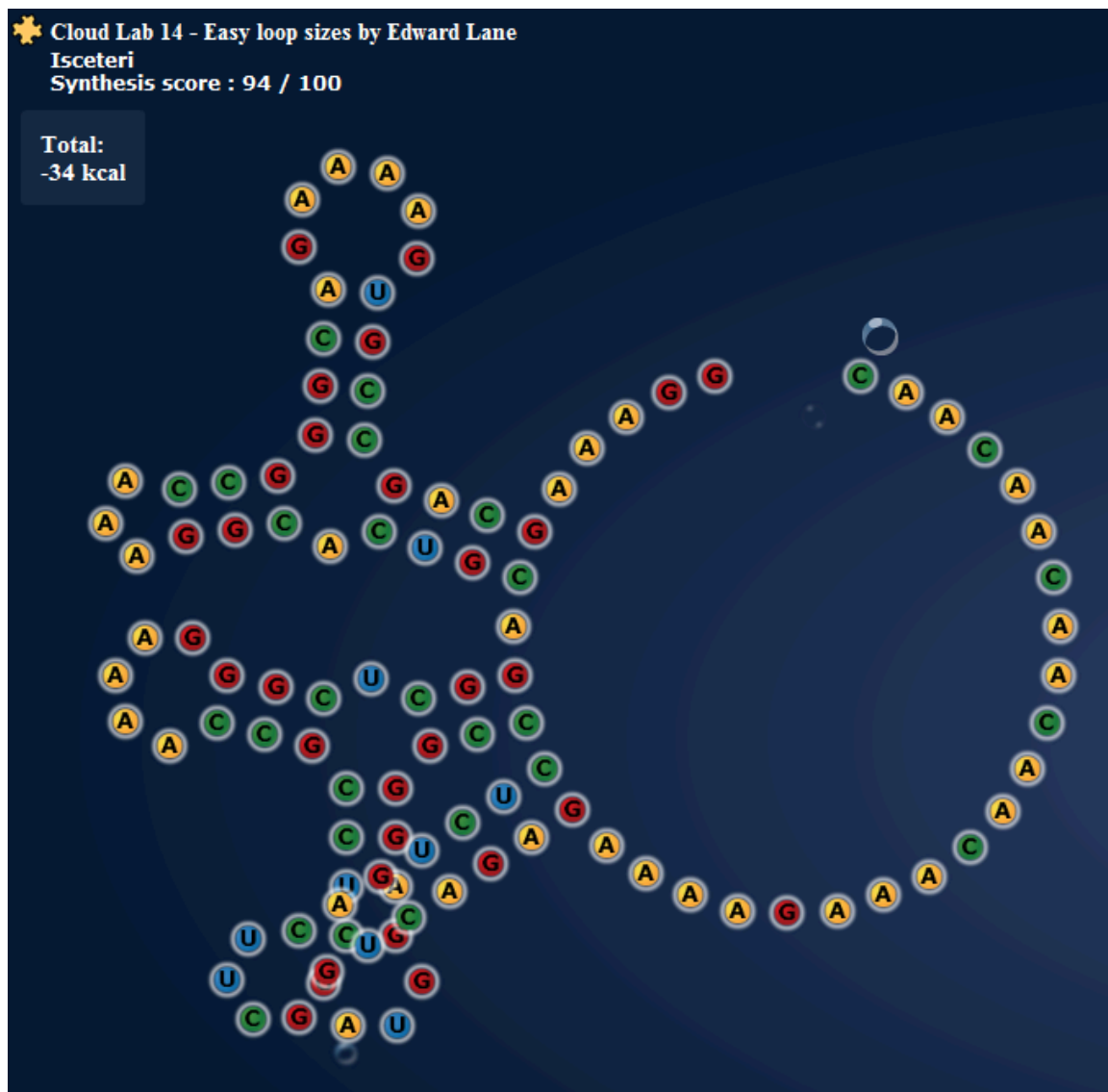
[5 June. 2014](#)

22 Mar, 2013

Cloud Lab 2 - Triangle of doom

Written after the new updated data for Cloud lab. Again a pressurized lab. Short strings of not too different length and only two winners.

Here is ViennaUTC's Design. This one of the winners had 79% GC-pairs.



The other winner also had an overweight of GC-pairs. 71%



All the high scorers had a relatively high GC-content, with a few exception. 61% is a rather normal GC-content in other designs.

Cloud Lab 14 - Easy loop sizes by Edward Lane

id	GC Pairs ▼		Synthesis score ▼	
	min	max	min	max
	22 (79%)		94 / 100	
	20 (71%)		94 / 100	
	27 (96%)		93 / 100	
	19 (68%)		93 / 100	
	28 (100%)		92 / 100	
	17 (61%)		92 / 100	
	25 (89%)		91 / 100	
	25 (89%)		91 / 100	
	20 (71%)		91 / 100	
	20 (71%)		91 / 100	
	19 (68%)		89 / 100	
	17 (61%)		89 / 100	
	17 (61%)		89 / 100	
	16 (57%)		89 / 100	
	28 (100%)		88 / 100	
	21 (75%)		88 / 100	
	20 (71%)		88 / 100	
	20 (71%)		88 / 100	
	19 (68%)		88 / 100	
	19 (68%)		88 / 100	
	18 (64%)		88 / 100	
	18 (64%)		88 / 100	
	18 (64%)		88 / 100	
	18 (64%)		88 / 100	
	18 (64%)		88 / 100	
	18 (64%)		88 / 100	
	16 (57%)		88 / 100	
	15 (54%)		88 / 100	
	14 (50%)		88 / 100	
	20 (71%)		87 / 100	
	19 (68%)		87 / 100	
	18 (64%)		87 / 100	
	18 (64%)		87 / 100	
	18 (64%)		87 / 100	
	17 (61%)		87 / 100	
	17 (61%)		87 / 100	
	17 (61%)		87 / 100	

+B17ut lower than 61 % GC-pairs and there is no real high scorer among.

2

17 (61%)	92 / 100
17 (61%)	89 / 100
17 (61%)	89 / 100
17 (61%)	87 / 100
17 (61%)	87 / 100
17 (61%)	87 / 100
17 (61%)	87 / 100
17 (61%)	86 / 100
17 (61%)	84 / 100
17 (61%)	77 / 100
16 (57%)	89 / 100
16 (57%)	88 / 100
16 (57%)	84 / 100
16 (57%)	84 / 100
16 (57%)	83 / 100
15 (54%)	88 / 100
15 (54%)	86 / 100
14 (50%)	88 / 100
14 (50%)	87 / 100
13 (46%)	79 / 100
12 (43%)	82 / 100

23 Mar, 2013

Cloud Lab 5 - The nonsuch

Seems sequence can vary but structure remains. Or in other words, different sequences can give the same structure. However there is a slight pattern for that closing base pairs remains the same, but just gets swapped around, so a C is interchangeable with a G and opposite. So for a particular base the alternating in the winning designs will most often be between a G or a C. Also middle of string section there seem to be the pattern that A is interchangeable with U and opposite. So for a particular base in middle string, it can be either A and U. G can be interchangeable with A and U or C can be interchangeable with A and U at that position too. Also A and U could interchangeable with a G and C at closing base pair position. But this is rarer than the other way around.

So though there are some differences there also are some overall similarities. Not for every base pair and in every case. But there seem to be a pattern.

Can I say that a base itself is sort of alternated to itself? So that base in a winning design if a U in one winner, can be also an A in another winner. Same if a base is G it will often be C in another winner and opposite.

I also find these two interesting. The top one scored 96% and the other one 93%. They are quite

[Unusual 27 July 2013] different in sequence.

✦ Cloud Lab 2 - Triangle of doom version 2 by dstea

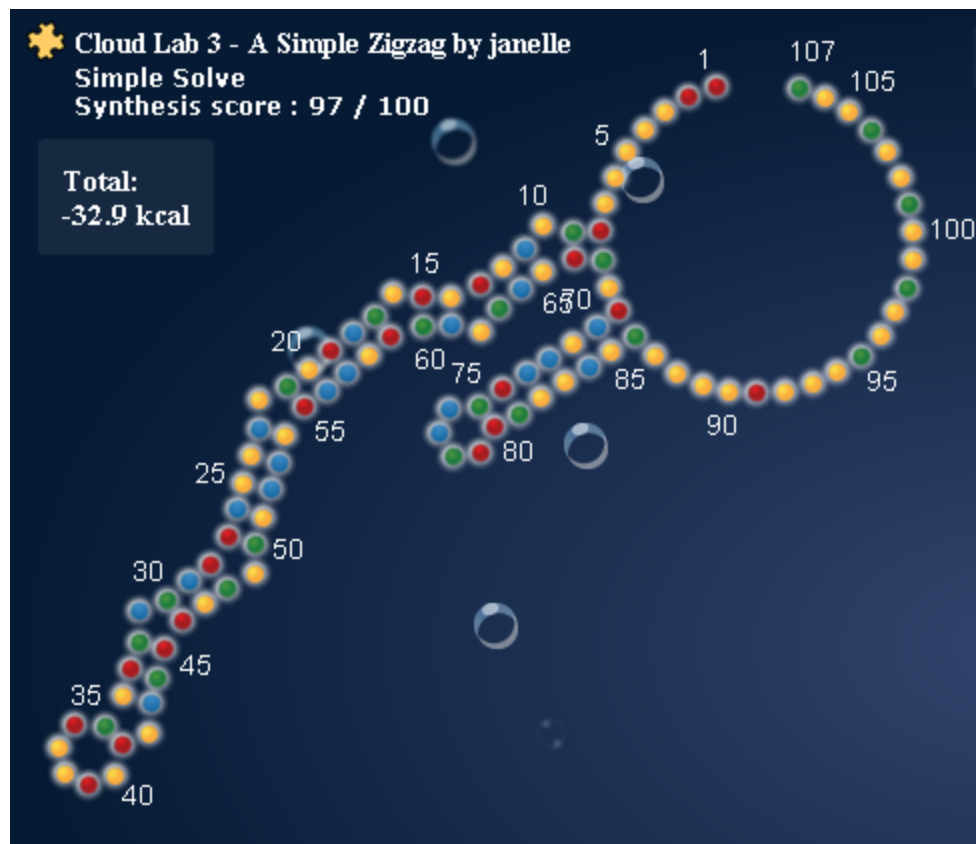
Roadmap Puzzle RN

Sequence

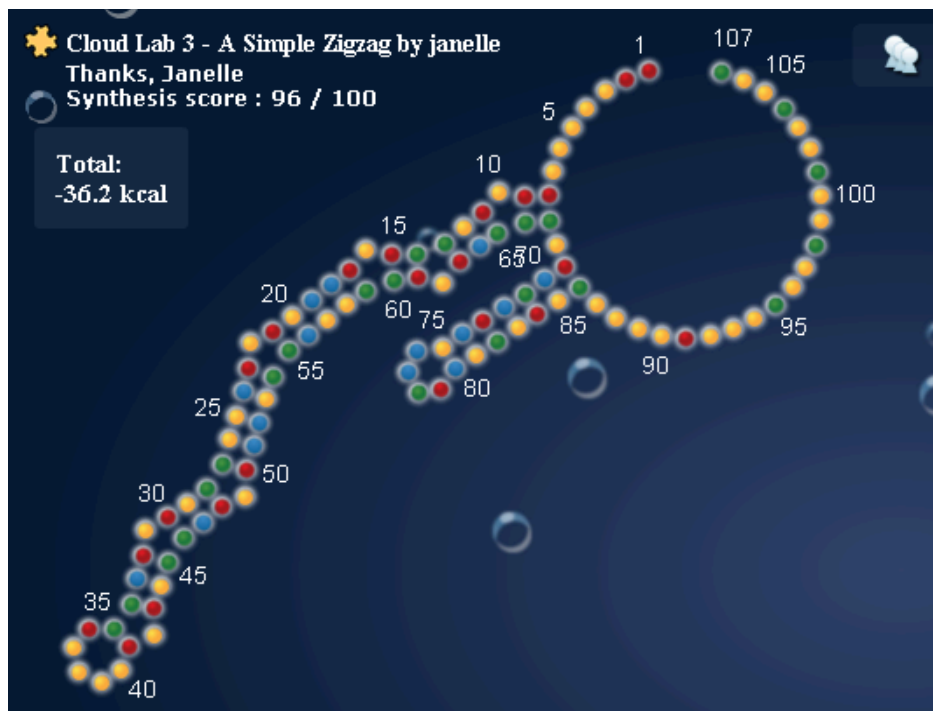
search

GGAAA GCUCAA CGAU AAACCA ACAAAU CGAAGCA CAACA AAAACA AAAGUGC
GGAAA GCGGA AGUCC UAAAG AGUAAC GGAACA AAGUG AAGA AAUAC GACCAAC

Apparently the new data for Cloud lab 3 tells that it don't mind having 1nt bulges closed by just one GC-pair.



This one has green at bottom of 1 nt bulges in an extreme. Only closing base pair at hook end and pentaloop (5 nt loop) is mispaired according to the SHAPE data.



27 Mar 2013

[Cloud Lab 4 - Random](#)

31 Mar, 2013

I see a tendency for the lowest melt temperatures for a lab (below 97) turning up along low scores too.

13 May, 2013

Cloud lab - round 2

Another thing I have noticed is that there is a surprising number of the winners that stay in the 97-107 melt temp range. There are also few 87. But they are rarer. I'm waiting to see if this is the overall pattern of all the cloud lab.

14 May, 2013

Cloud lab 20 is an exception from the above mentioned pattern. The absolute top scorer lands on a melt point of 77. And there are more 77 among the better designs. Cloud lab 19 is also an exception from that. Cloud lab 14 is an exception too. I look at designs on 94% and over as my cutting line. For labs with no winners, I look at designs on 90% and over.

Labs that doesn't follow pattern

Lab 20

Lab 19

Lab 14

Lab 12

Lab 8

Lab 5

Lab 3 Very different from pattern. Lower melt point in general

Labs that do follow pattern

Lab 18

Lab 17

Lab 16

Lab 15

Lab 13

Lab 11

Lab 10 (fits with one exception, ViennaUTC) Wonder if this is usual bot pattern. So perhaps this pattern trace we leave us for now, cant be used as I thought.

Lab 9 (fits except ViennaUTC)

Lab 7

Lab 6

Lab 4 (except for ViennaUTC)

Lab 2 (Vienna kicks in 1 outlier)

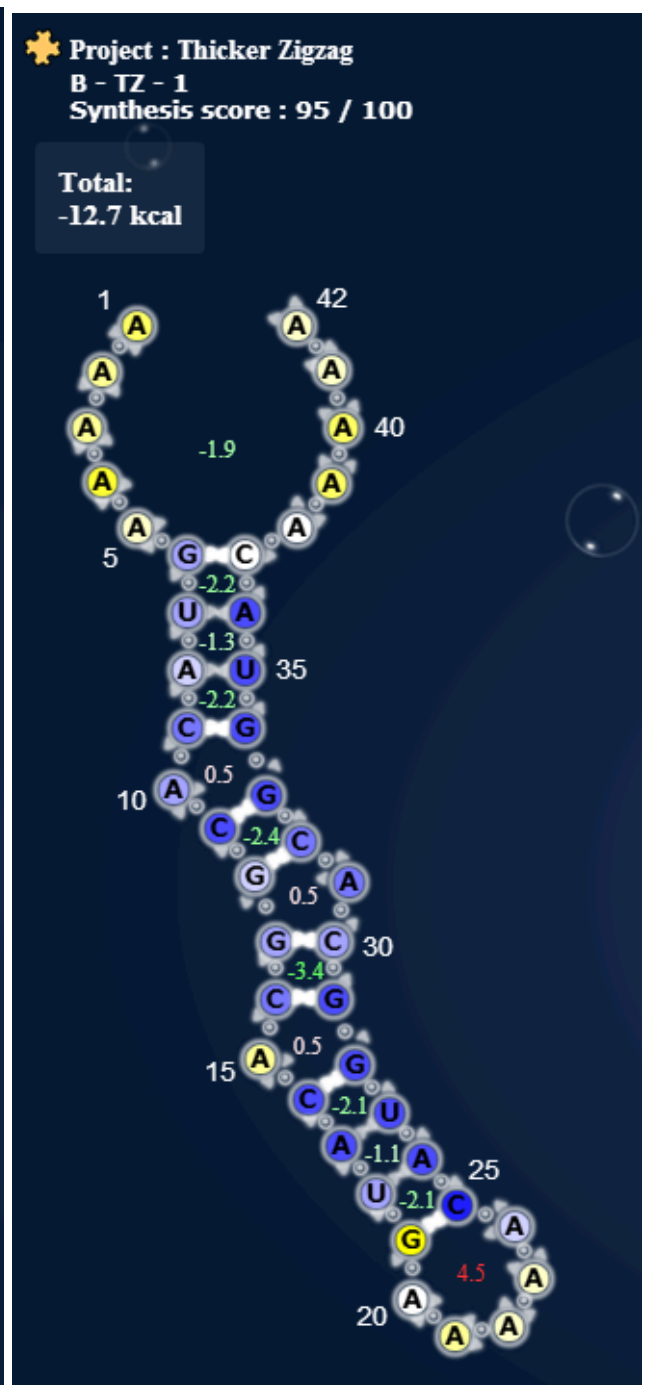
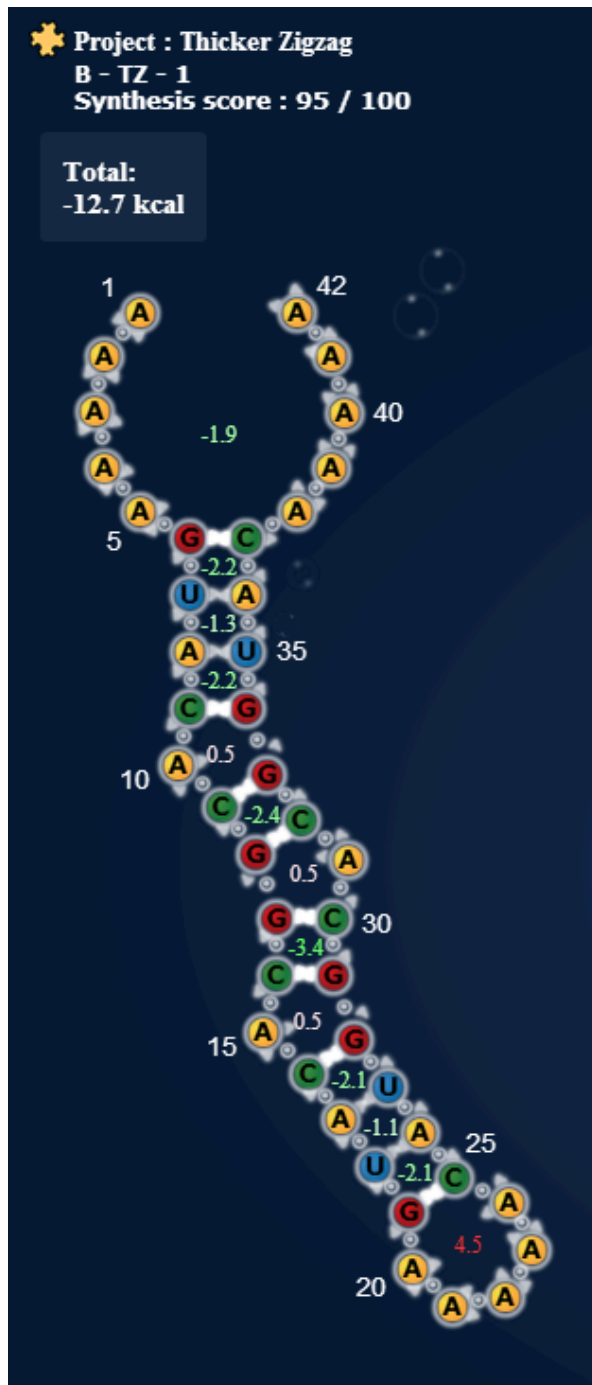
Lab 1

Funny that the labs that we have a harder time making winners in, seem to more often having meltplot below 87 too.

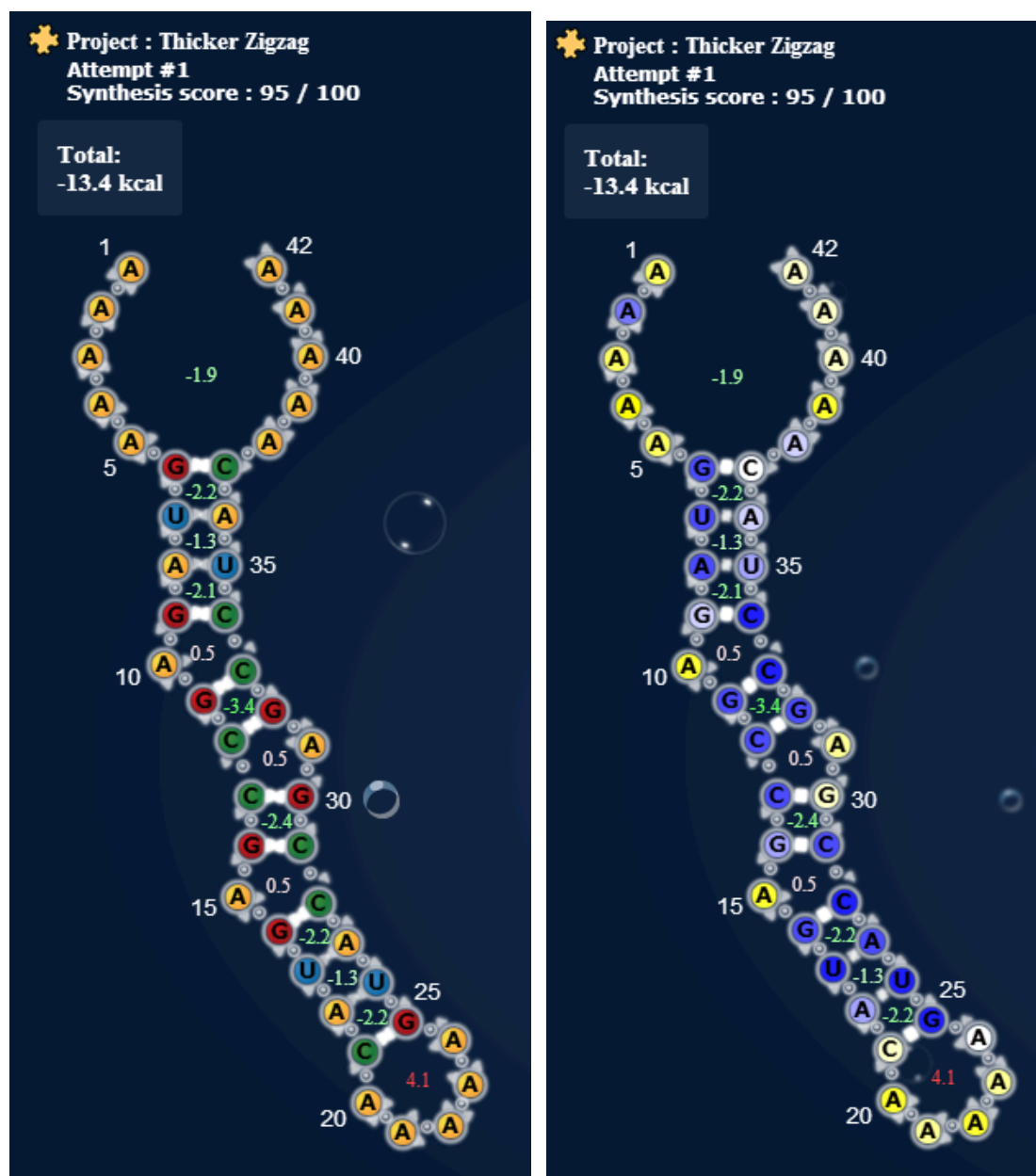
ViennaUTC almost always comes up with different melt temp to ours.

20 May, 2013

Find this one fascinating. I knew double red was strong too, and that double green seems stronger in lab than both double red or a mixture at bottom of the bulges.



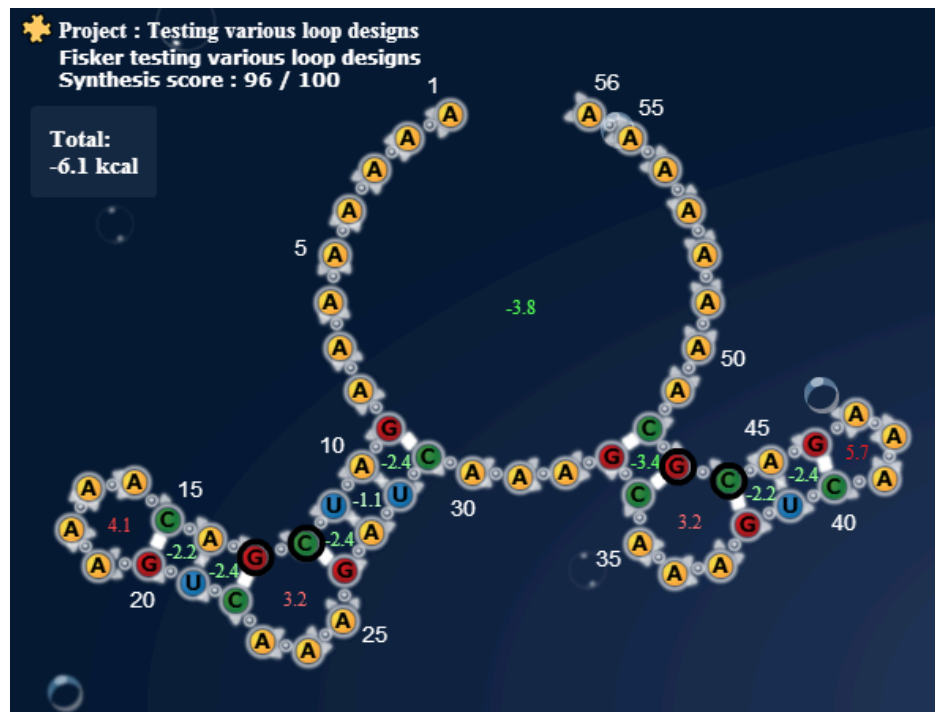
Its green bottom bulge twin does look more solid in the shape data, though they score the same.



Bulges

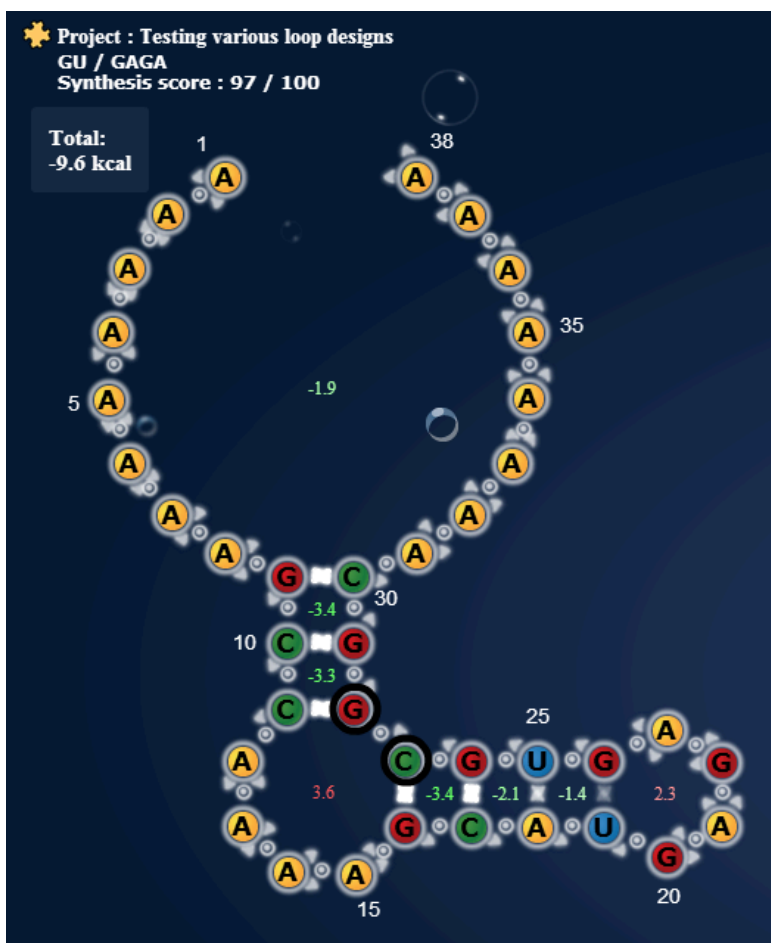
Looks like the bulge pattern I mentioned for 3 Nt bulges, continues to be pretty typical, though other are possible.

https://getsatisfaction.com/eternagame/topics/_strategy_market_2_and_3_nt_bulges



Testing various loop designs

Synthesis score ▼		Sequence
min	max	search
96 / 100		A A A A A A A A G A U C G A C A A A A G U C A A A G A U C A A A G C A A A G U C A A A G A C G C A A A A A A A
96 / 100		A A A A A A A A G A U C C A G G A A A G U C A A A G A U C A A A G C A A A G C G C A A A A A A A
94 / 100		A A A A A A A A G A U C G A C G A A A G U C A A A G A U C A A A G C A A A G A C G C A A A A A A A
92 / 100		A A A A A A A A G U A C G A C G A A A G U C A A A G A U C A A A G C A A A G A C G C A A A A A A A
92 / 100		A A A A A A A A G A U G G C G U G A G A G G C A A A C A U C A A A G C A A A G C G C A A A A A A A
91 / 100		A A A A A A A A G A U G G U C G A G A G A C A A A C A U C A A A G C A A A C G G G C A A A A A A A
89 / 100		A A A A A A A A U G U A C U G A A A A C A G A A A U A C A A G C G A A A G C G C A G A A A A A A
89 / 100		C A A U G U A U G C G C G C G U U A G U U C A G U C G A U A U G C G C U A U G C G C U A U U C A A U
89 / 100		A A A A A A A G G A C C U G G A A A C A G A A A G U C C A U U G C A A A G C G C A A A A A A A
78 / 100		U U U U U U U U G U A C C A C U U C G U G U U G U A C U U U G U U G C G U U U G C G C U U U U U U
73 / 100		U U U U U U U U G C G C G C G U U U G U G U U U G U G C U U U G C G C U U U G C G C U U U U U U



Synthesis score ▼		Sequence
min	max	search
97 / 100		A A A A A A A A G C C A A A A G C A U G A G A G U G C G G C A A A A A A A A
94 / 100		A A A A A A A A G C C A A A A G U A C G A A G G U A C G G C A A A A A A A A
94 / 100		A A A A A A A A G C C A A A A G U A C U U C G G U A C G G C A A A A A A A A
94 / 100		A A A A A A A A G A C A A A A G A G C G A A A G C U C G U C A A A A A A A A
86 / 100		A A A A A A A A G A G A A A A G U G A G A A A U C A C C U C G A A A A A A A A



25 May 2013

Brings memory of horse shoe pattern in puzzles and 1nt bulge pattern for lab, that shows a preference to have the green on the bottom of the bulge. Shaky shape pattern on the outside G's though.



The lowest scoring had reversed the pattern. However the reversed pattern with green on top went real fine.



And the green on the inside continues. When looking at the RNA lab results for the inside stretch base 6-27, it is quite clear that there is a tendency towards green.

★ 1-X bulge testing by Omei
Mas Vale Tarde Que Nunca
Synthesis score : 97 / 100

Total:
-35.7 kcal





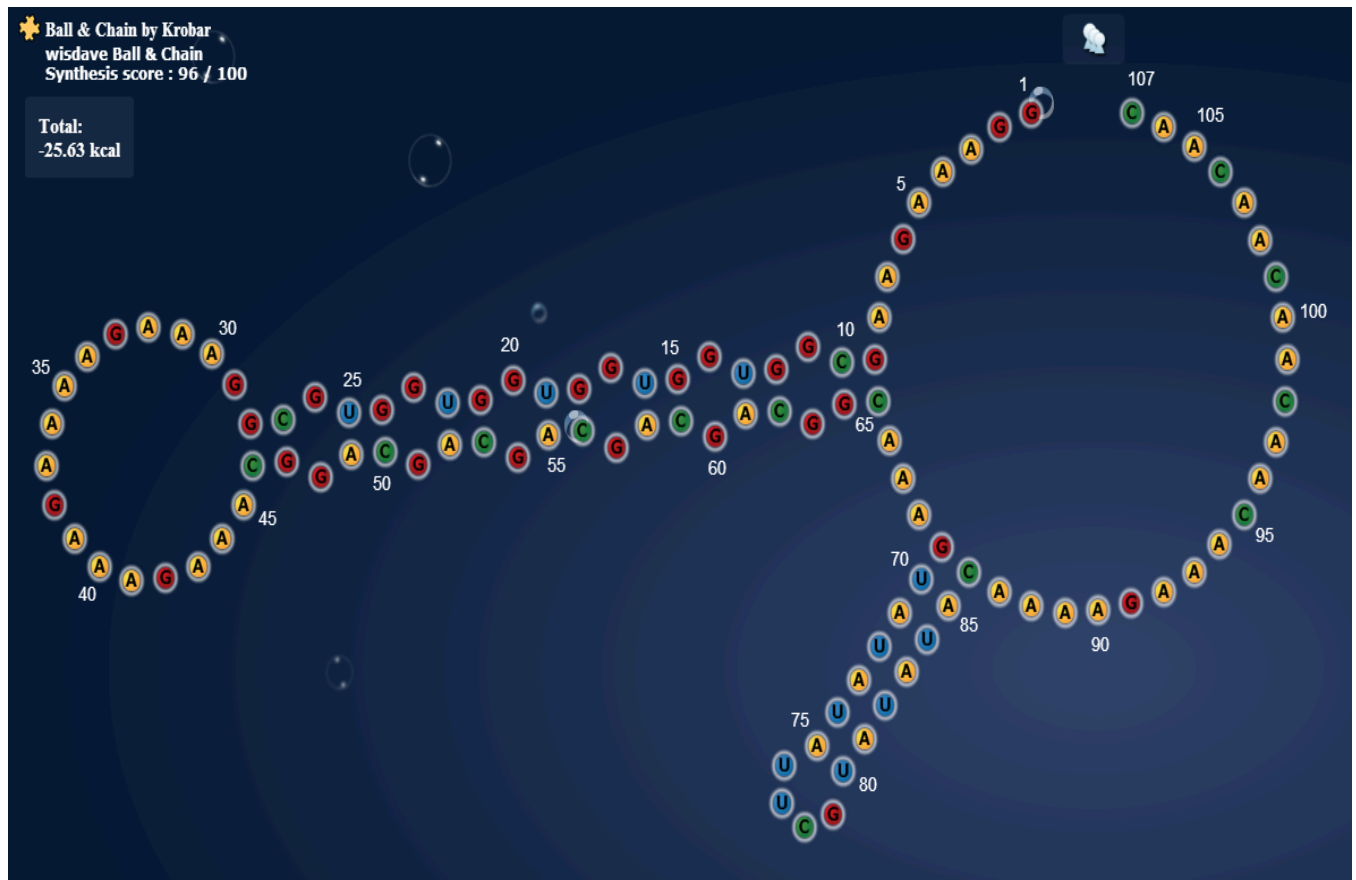
Text from my winner:

Here was the test I set out to find out with my design:

I generally have an idea that asymmetric internal loops likes to have their closing GC-pairs with the C on the inside of the bent. Also I think that asymmetric loops like to have their boost on the inside too. Perhaps except for 1-2 loops. But bigger and up. But for above size until perhaps really big. For really big assymettric loops, perhaps the picture seems to be turning a little when I watch the result from the lab Shape Test. From CC's on the inside towards GG's on the inside. I bought this a bit further this time. As this lab might qualify as an energetically pressured lab, due to it's many short and similar length strings, it makes it extra exciting. The difference is that I don't know how it will behave with this many big loops. I look forward to the results from this lab. With constraints too this time.

And I no longer believes that this lab qualifies as pressured. I shall mention more on that later. But in general it seems that internal loops do have a sort of stabilizing effect on a design, so a

design that would be otherwise viewed as pressured, due to short stem lengths, isn't as hard to get a winner in as expected. As example here is a short stacked one with 1-1 loops in between. It even solves with a way to repetitive pattern. Fascinating. And watch that barcode hairpin!



So do boost want to be on the outside or inside? Ok this lab clearly showed that it would do all together fine without. But checking anyway.

✦ 1-X bulge testing by Omei
 Make up a Test - Brourd - Lab '1-X bulge testing' - Sub 3 (Stable)
 Synthesis score : 100 / 100

Total:
 -24.2 kcal



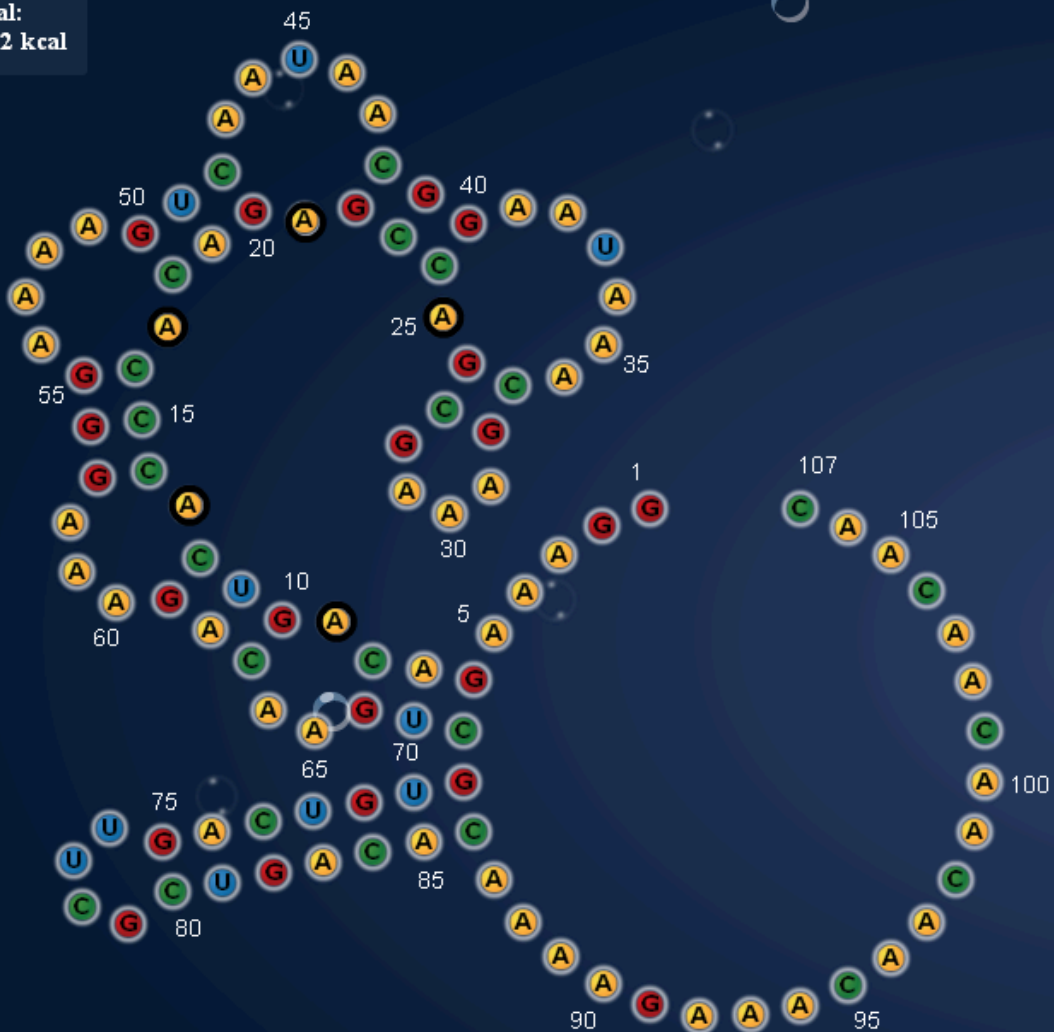


1-X bulge testing by Omei

Make up a Test - Brouard - Lab '1-X bulge testing' - Sub 3 (Stable)

Synthesis score : 100 / 100

Total:
-24.2 kcal



Riboswitch-based

Tendency for green on the inside of bend in this design too. Also general tendency for lab, but not in all of the winners. Some of the winners show a tendency for red.

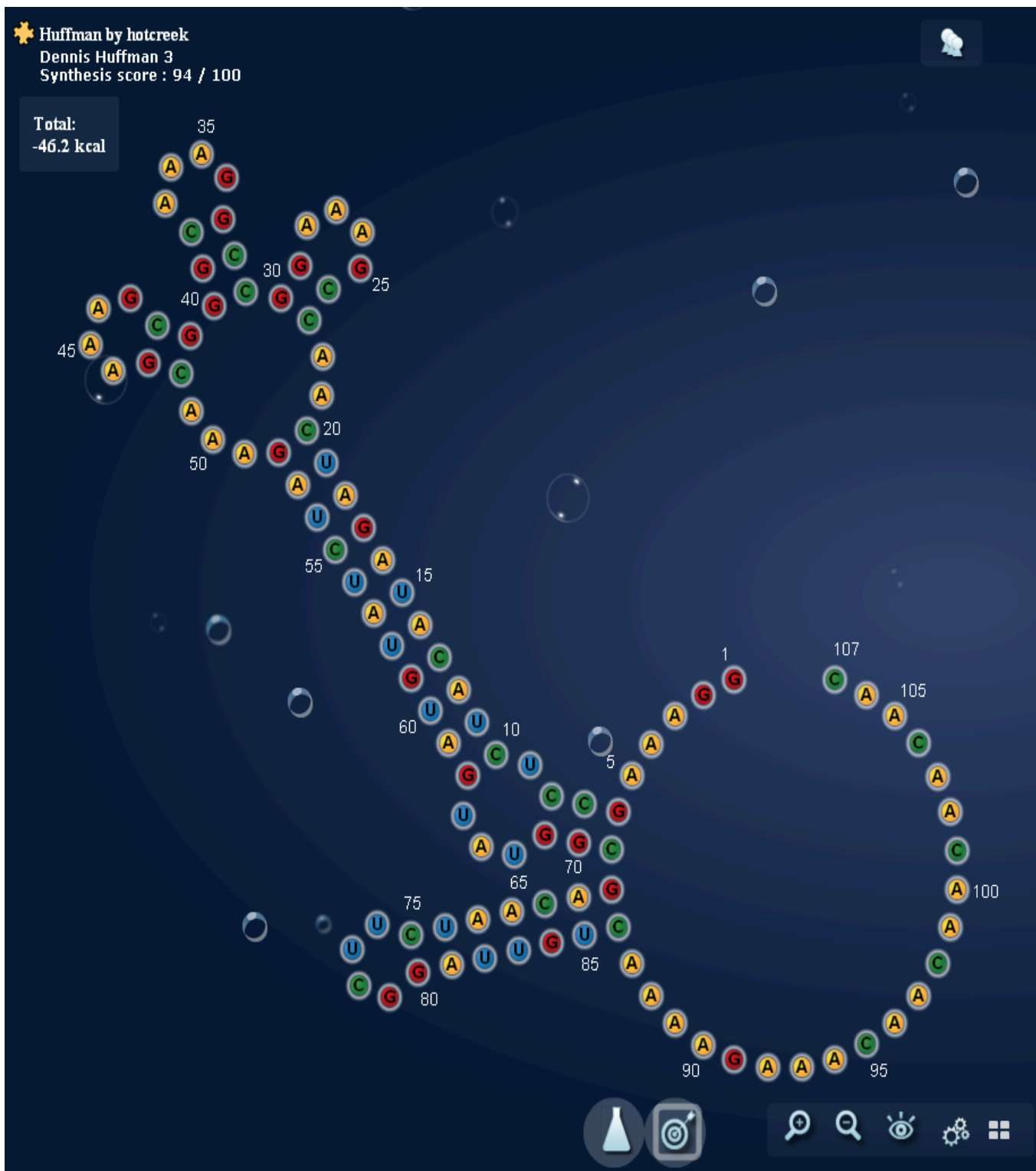


The same seems to be the case for the lab Thursday, base 59-54. Of course this is partly created by there being 1nt bulges present, which in themselves look green on the inside of the bend.

🌟 Thursday by DHammond
Thursday morning
Synthesis score : 94 / 100

Total:
-26.2 kcal



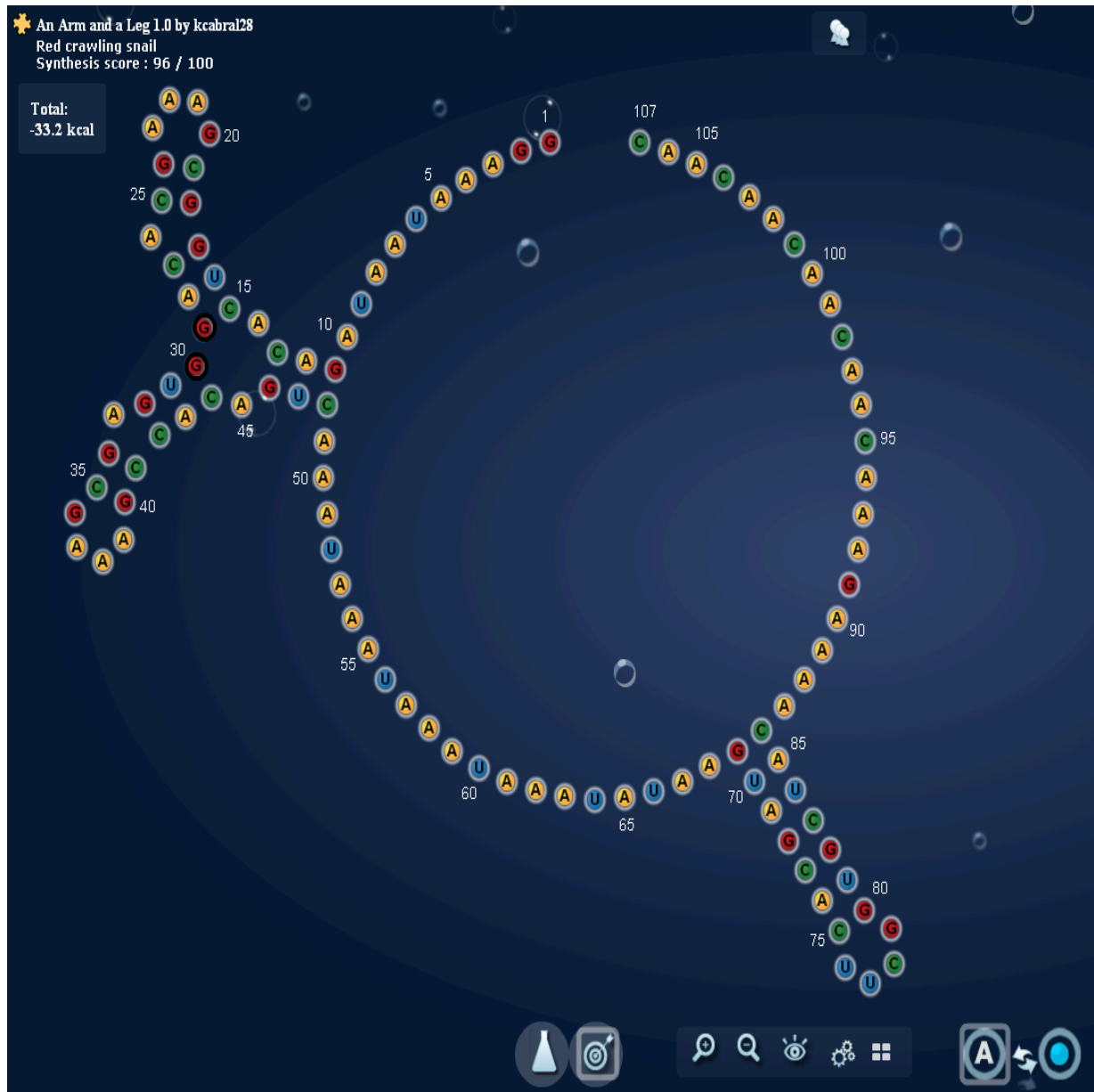


An arm and a leg

Text from my experiment:

I haven't seen much proof on it, but I have an idea that multiloops with adjacent stacks, have a tendency to behave slightly different to more symmetric multiloops. I think that GC-pairs facing each other instead of following orientation of GC-pairs in the multiloop, will be more prevalent here. I have seen both G and G facing each other in Kudzu that had a multiloop with adjacent stacks. And G and G. Both with success, as they held the near area together and the multiloop were stable.

Red facing red in adjacent stacks in multiloops turns out to be more successful than green facing green. I tried both and green facing green failed. The overall tendency is that red facing red and usual orientation in multiloops overall goes quite well.



I think I see a tendency for multiloops with a mixture of adjacent and non-adjacent stacks. While the closing base pairs for the adjacent stacks can follow usual orientation or have red facing each other and green too, the closing base pair for the non-adjacent stem seem to be following usual orientation.



Also if they occur as closing base pair in a neck. A place where the closing base pair have a tendency to be allowed to be flipped both ways. The lab An arm and a leg, is an example of a lab where the neck is also the non adjacent stem in a multiloop with adjacent stems.

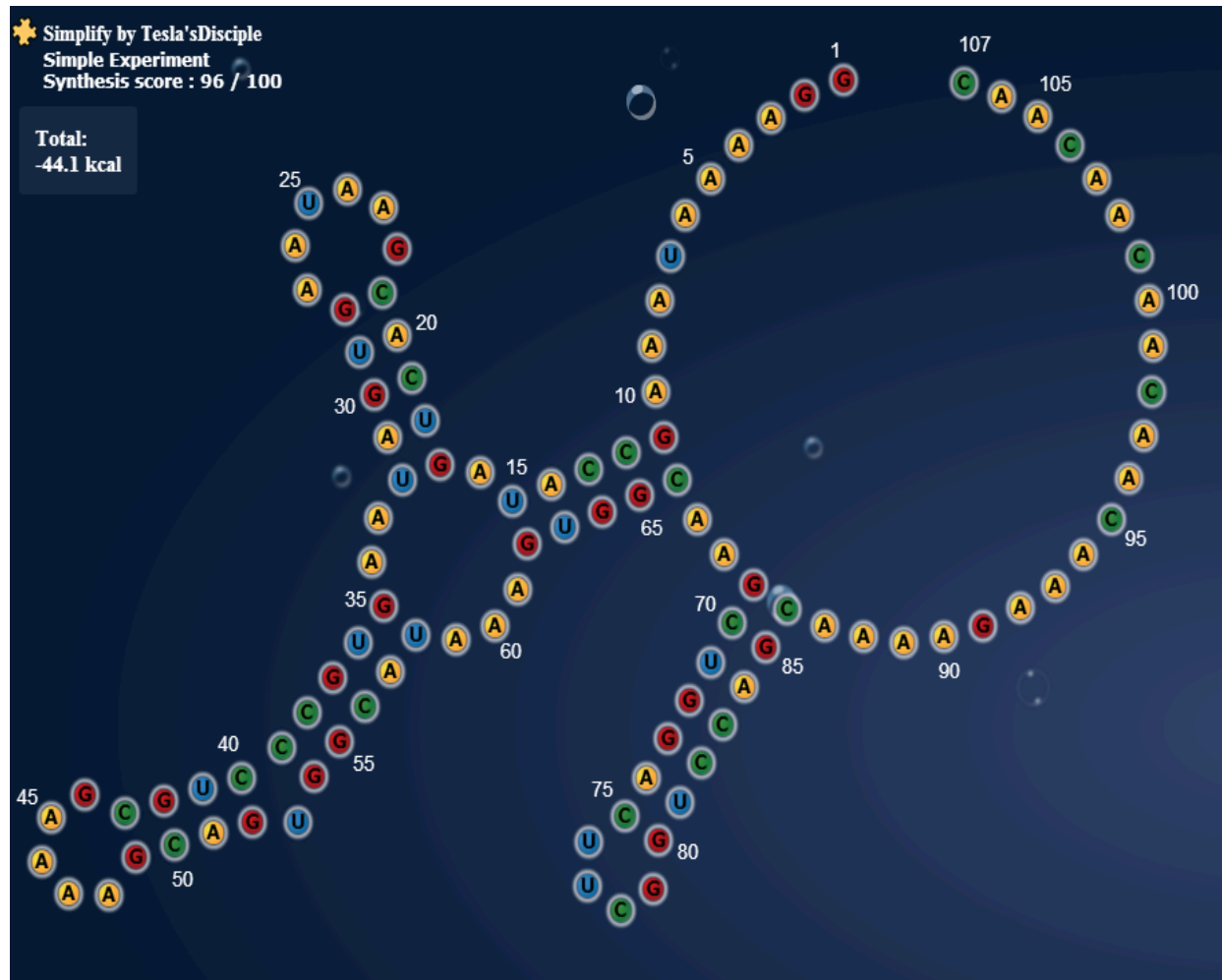
[illegible]

Simplify

Tendency for 1 nt bulges continue. Double green at bottom = favorite, double red at bottom, not bad and then a mixture.

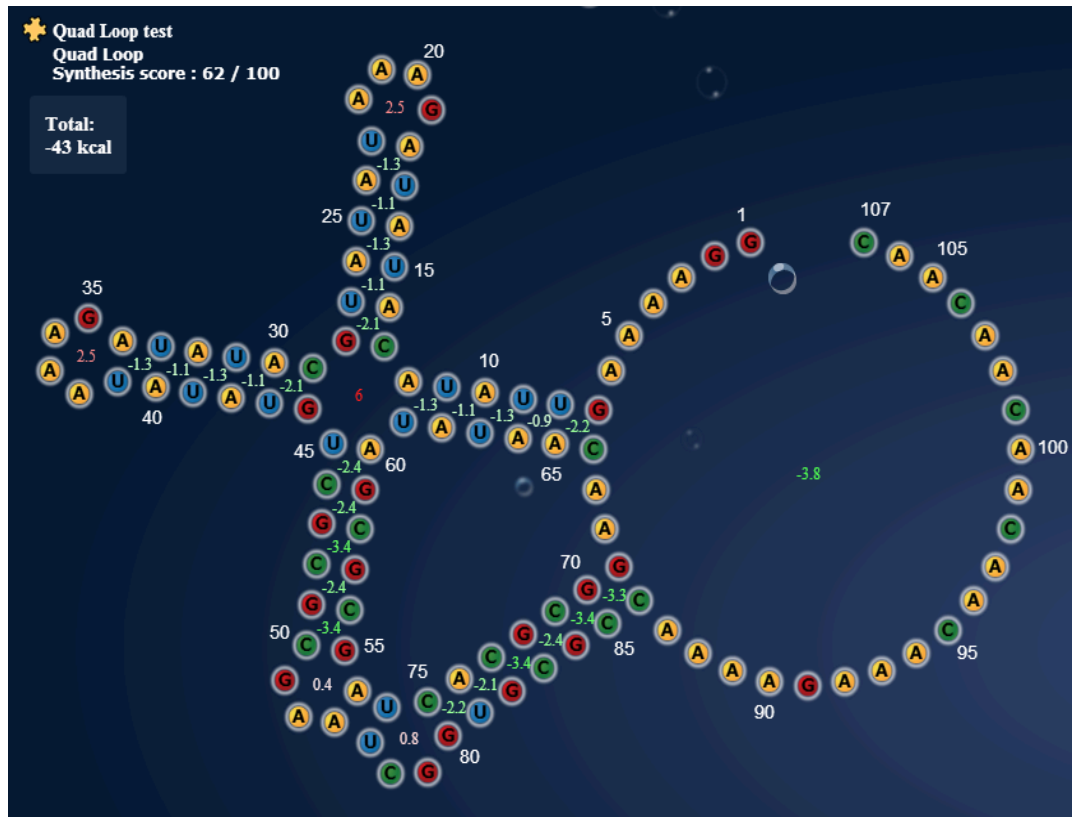
[illegible]

I like that Tesla's experiment succeeded. I doubt this will be possible in a more pressured design. However it went perfect in this easy to make happy lab. There was almost no losing designs in this lab. All except 9 designs made it to the winners. Only 3 scored in the lower end. And those were in the category Cub scouts and optical illusion.



28 June 2013

Here is a classic example on uneven energy distribution. Take note of the design score:



Notice that the 3 top stems have mainly AU and the bottom ones have GC-pairs. [Mainly GC for the barcode hairpin too]. The top ones are too weak to stay together, while the bottom one forms.

🌟 2-2 and 3-3 loops

Title	Synthesis score ▼	
	min	max
search		
Ultra-Clean	93 / 100	
JR_2-2/3-3_Rnd1...	93 / 100	
Starry's loops	91 / 100	
2-2/3-3 janders...	91 / 100	
2-2 #1	91 / 100	
32 Loops - Brou...	89 / 100	
Atarisorte	89 / 100	
JR_2-2/3-3_Rnd1...	89 / 100	
2-2-2	87 / 100	
Tu-Tu Trois-Trois	87 / 100	
2-2/3-3 - Brou...	87 / 100	
nature and model	87 / 100	
Bot mod 2 - 2-2...	86 / 100	
Tebeleenso	86 / 100	
Meechl 22 33 Loops	85 / 100	
janelle's design	85 / 100	
Victorious Vinnie	85 / 100	
22-Z1	85 / 100	
wisdave tu-tu	85 / 100	
2-2 3-3 Loops #3	83 / 100	
Mat 2-2 & 3-3 l...	83 / 100	
Mat 2-2 & 3-3 l...	83 / 100	
This is one	83 / 100	
Pidgenholed	83 / 100	
2-2/3-3 last an...	82 / 100	
Erlacear	82 / 100	
He	81 / 100	
Default title	81 / 100	
1 for 2 & 3	78 / 100	
Bot mod 3 - 2-2...	77 / 100	
A couple of loo...	77 / 100	
Tesloops	75 / 100	
Fiskers 2-2 and...	74 / 100	
22-Z2	74 / 100	
Bot mod 1 - 2-2...	73 / 100	
Blueper	70 / 100	
Lab 2-2 and 3-3...	66 / 100	
22-Z3	64 / 100	
2-2 and 3-3 Lower	63 / 100	
2-2 and 3-3 loo...	63 / 100	



[17 July 2013](#)

30 July 2013

I'm still thinking about the neck area. Apparently our new cloud lab data says it doesn't need those special patterns that arose a lot with our old synthesis method. I still think it is to some degree behaves differently. It is still there I have seen lowest energy compared to the main design. I mean, I have it is there I see uneven energy distribution, if I see it. Most commonly an rather AU filled neck, compared with a rather GC-heavy main design. Still this combo is getting rarer that it was before. I find it interesting and I'm also confused.

[Player project notes](#)

31 July 2013

Mixed adjacent multi loops

Generally it looks like adjacent multiloops like to hit most negative energy positive

There are different ways to lower energy in an adjacent multi loop.

One way to do this is to have single non adjacent stem, follow usual GC-pair orientation. Another way that also lowers energy, as it is built into our energy model is to have red face red in the closing basepairs of two adjacent stems. That is what lowers energy most.

Sometimes other solutions can get stable, though they will get higher energy, those can be following usual orientation

Also Green facing green, will be used, and sometimes stable. But will have a higher energy than red facing red, and usual orientation.

I'm thinking that small adjacent multiloops will be more dependant on having the most negative energy than the bigger ones, like in huffman with many single bases between some of the stems. However, I'm still not certain with the 0-0-0 and 0-0-0-0. They seem to be able to tolerate not having absolute lowest energy.

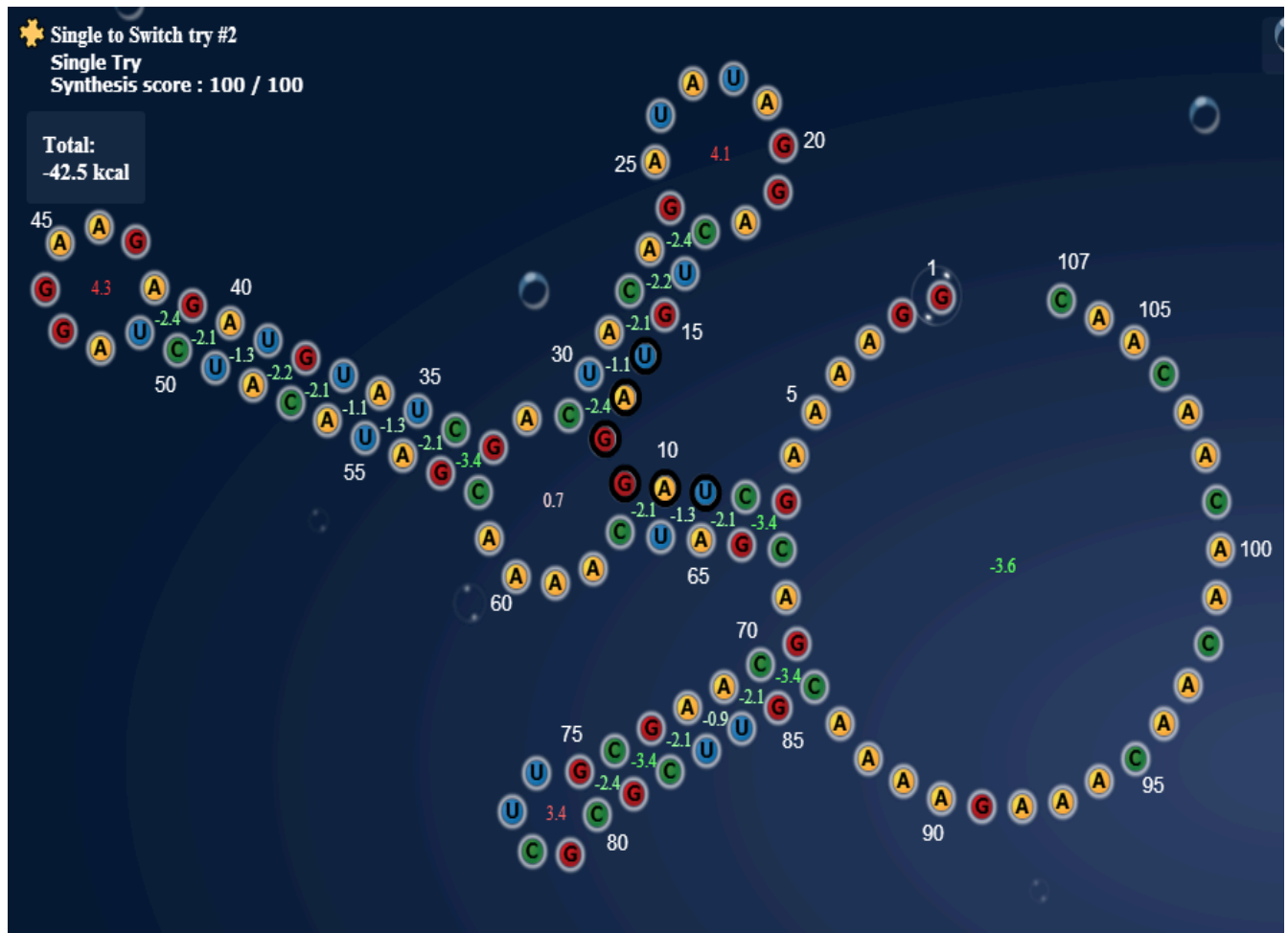
Trying to explore how an adjacent multi loop behaves if given the best possible conditions. In the lab Switch to try, the multi loop is big and has several single bases. and the stems are long. I know that I might not see true behaviour as less optimal solves will be allowed to pass, given that the lab is relaxed elsewhere, a local bad solution will not put as much strain on the design as the overall structure adds to stability in even a bad solve.

Yet the low energy causing multiloop stand out, GG version. Closely followed by usual orientation, but also more unusual two of the opposite orientation and a lonely CC among the top scorers.

🌟 Single to Switch try #2

Synthesis score ▼		Title	Sequence
min	max	search	search
100 / 100		Single Try	GGAAAAGCUGAGGAUGUCAG
100 / 100		Chitty Chitty B...	GGAAAAGCUGUGGGGACCGGA
100 / 100		Zabiorge	GGAAAAGUUGGGCGGCGAAG
98 / 100		Mod of Fiskers D3	GGAAAAGGAAGCGAGCUCAG
98 / 100		Switchingle -1	GGAAAAGAGCGGGCGAGUCAG
98 / 100		Dennis 9600 Mod	GGAAAAGAGUGGCGCAGACCA
98 / 100		Fiskers Single ...	GGAAAAGUCAGCGUGCGACCA
98 / 100		To Es, To Es - ...	GGAAAAGUAAGCGUGCAAGCA
98 / 100		S2S2 - Brourd -...	GGAAAAGUAUCCAUAGCA
98 / 100		janelle's Design 3	GGAAAAGCUGUGGCGAUGCA
98 / 100		Meechl SS2	GGAAAAGUCUGGUGUGACCA
98 / 100		3rdPass-SwitchTry#2	GGAAAAGUGUGGGAUGUCAG
97 / 100		Version 3	GGAAAAGAGAGCGAUCAACA
97 / 100		Based on PDB 2JL6	GGAAAAGUUGGCGCACCCCA
97 / 100		GU slip	GGAAAAGUAAGCGCAUUGA
97 / 100		Pretty Pretty P...	GGAAAAGCUGUAGCGUAUGCA
97 / 100		Fiskers Single ...	GGAAAAGGUGGCGUGCGACCA
97 / 100		Fiskers Single ...	GGAAAAGUCAGCGUGUGAACA
97 / 100		JR's Mt Everest	GGAAAAGUAAGCGUGCUACA
97 / 100		Give it a go	GGAAAAGAGUAAGGUAAGCA
97 / 100		randomness	GGAAAAGCUGUGGCGUUAACA
95 / 100		Single Omei 1	GGAAAAGAGUGGGAAGACCA
95 / 100		Single to Switc...	GGAAAAGUUGGGAUAAGA
95 / 100		Janelle #3 Mod	GGAAAAGCUGUGGGAUCCA
95 / 100		We the People o...	GGAAAAGCUCGCGGUGACA
95 / 100		Single Switch V.1	GGAAAAGCCAAGGCGAUACA
95 / 100		One	GGAAAAGUAUUGGUAUGCA
95 / 100		4thPass-SwitchTry#2	GGAAAAGUGAUGAUGUCAG
94 / 100		Switchingle -3	GGAAAAGCUGGCGCAGGGA
93 / 100		Single to Switc...	GGAAAAGUUGGGAAGAGA
93 / 100		janelle's Design	GGAAAAGCUAUGGCGAUGCA
93 / 100		wisdave switch	GGAAAAGUGAGCGUGAUGCA
93 / 100		Epsilon	GGAAAAGUGUGGUGUGAAGA
91 / 100		Single	GGAAAAGCGGCGCGAUAA
91 / 100		99.98% RNAsHapes	GGAAAAGAGUGGCGAUGCA
90 / 100		Single to Switc...	GGAAAAGUUGGGAUAAGA
89 / 100		Enatle	GGAAAAGGUGAAGAGGUGCA
89 / 100		Tionvedi	GGAAAAGGUGAAGAGGCGA
89 / 100		SS 1Z	GGAAAAGCUGUGGUGUGCA
77 / 100		JR Single2 Rnd1...	GGAAAAGAGGAGCAAGUGCA

Also note the fine mirroring between the adjacent stems.

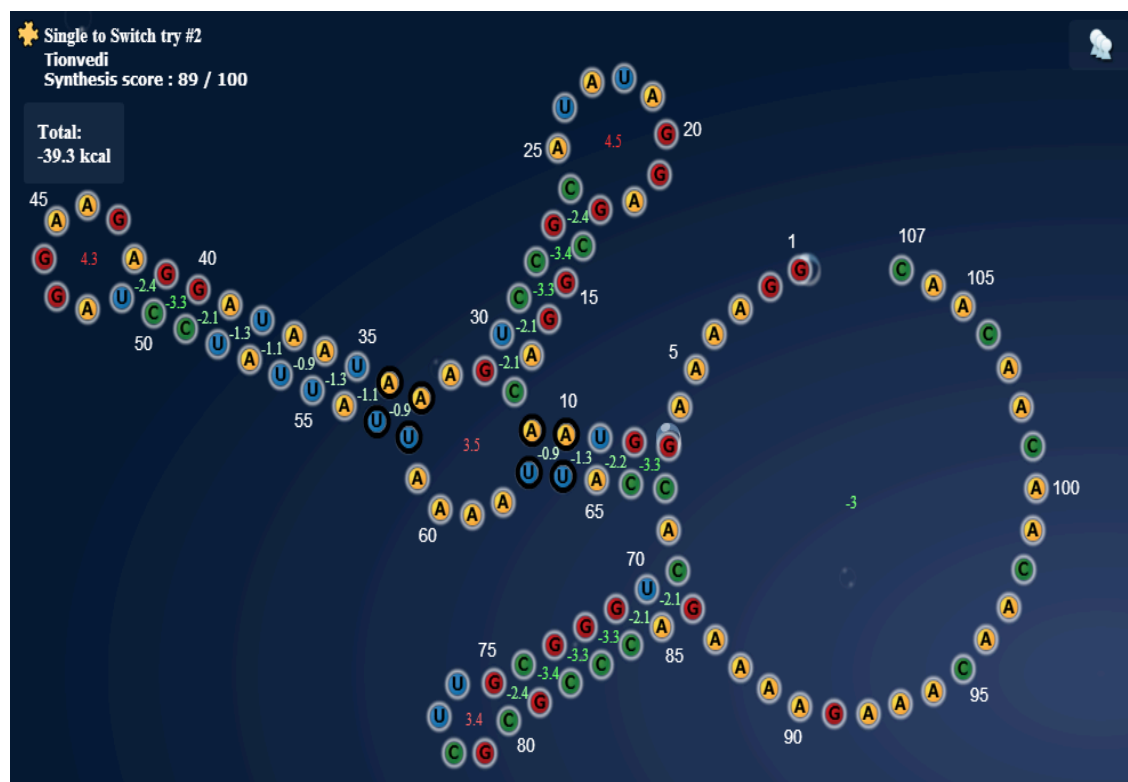


However many of the designs that had A's at the backing basepairs (10+13) didn't score too well.

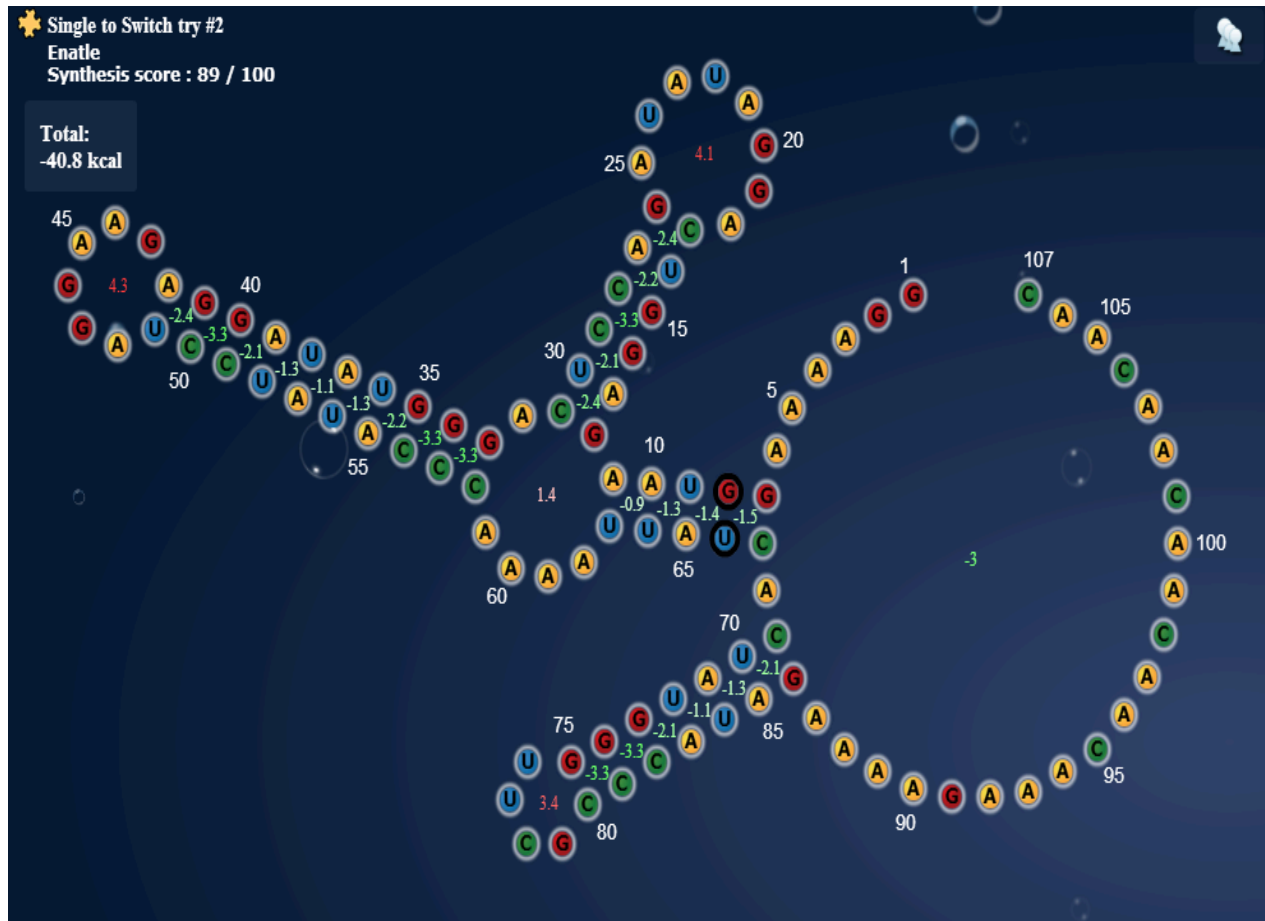
89 / 100	Enatle	GGA A A A G G U A A G A
89 / 100	Tionvedi	GGA A A A G G U A A C A
89 / 100	SS 1Z	GGA A A A C U G U G G G
77 / 100	JR Single2 Rnd1...	GGA A A G A G G A C C A

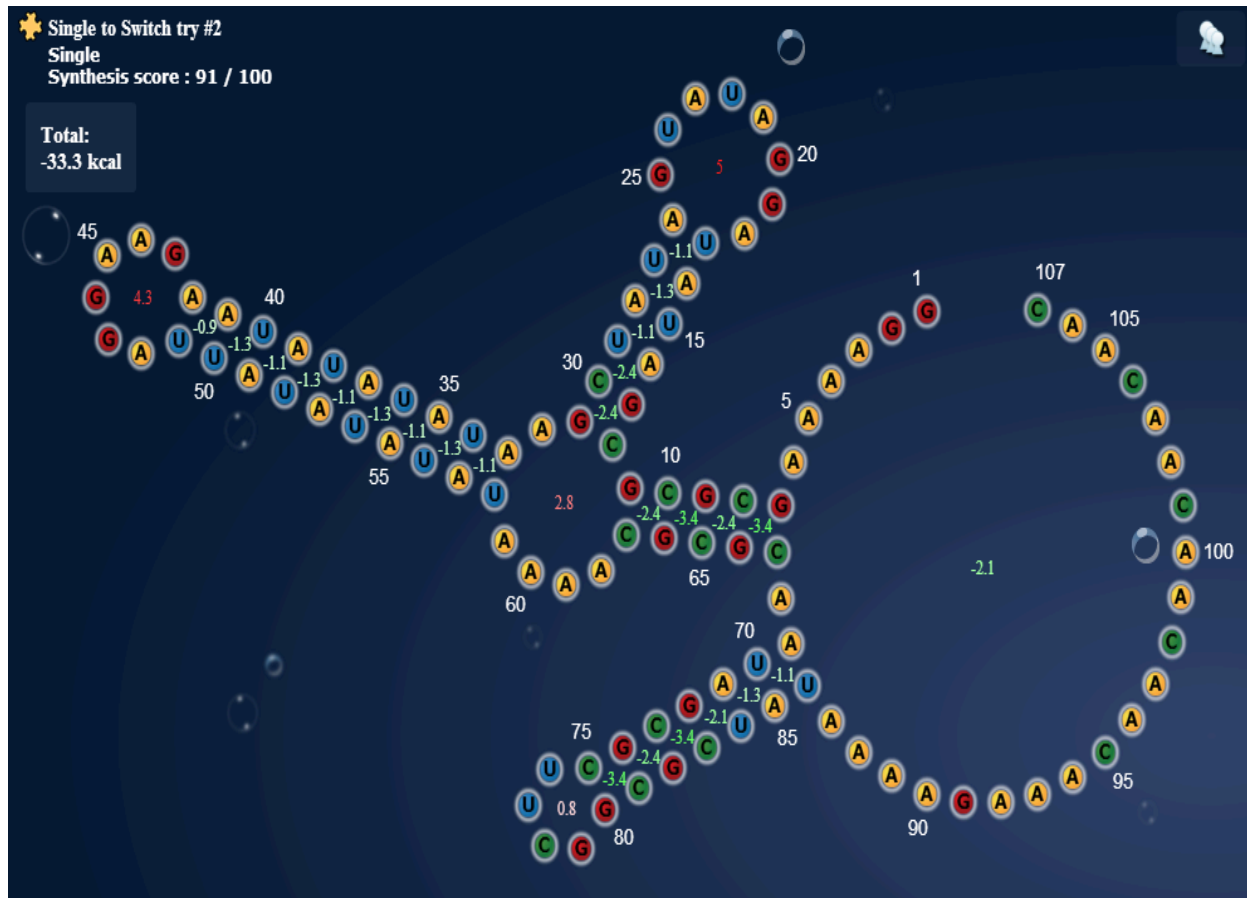
Where does GU-pairs makes least harm? What stem type needs GU the most? (Other than the switching area in a bound shape in a switch puzzle)

Also I found this design interesting. Apparently one can get stems to form without a defining/closing GC-pairs. But does double same turning AU pairs at closing position signals splitting?



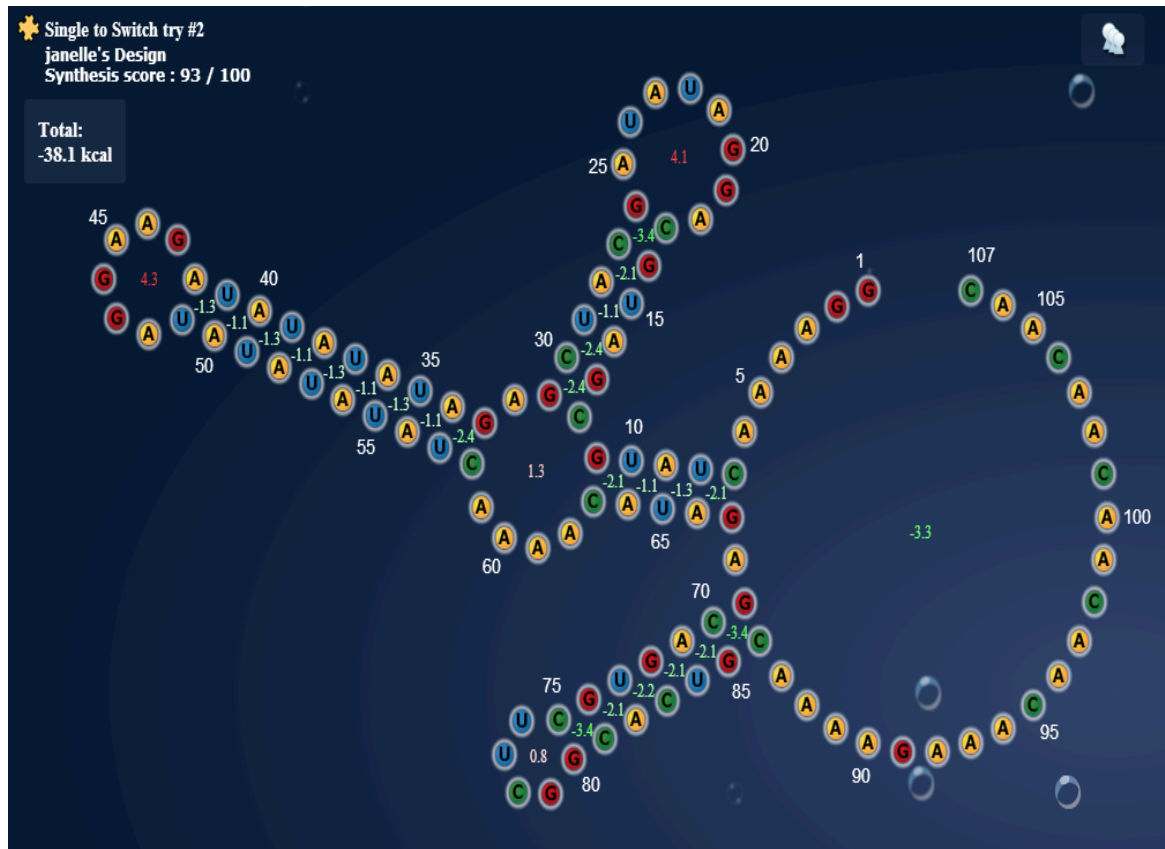
Estimate



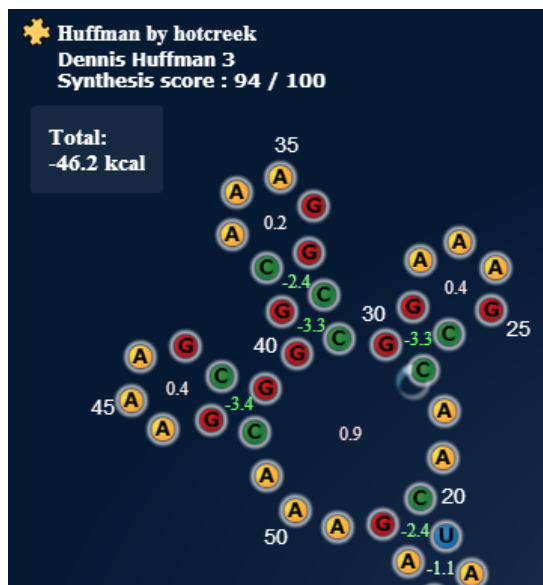


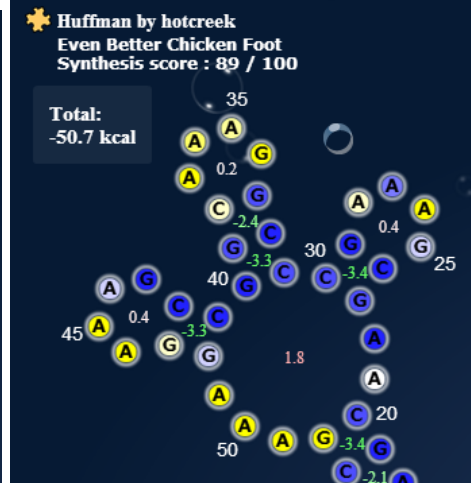
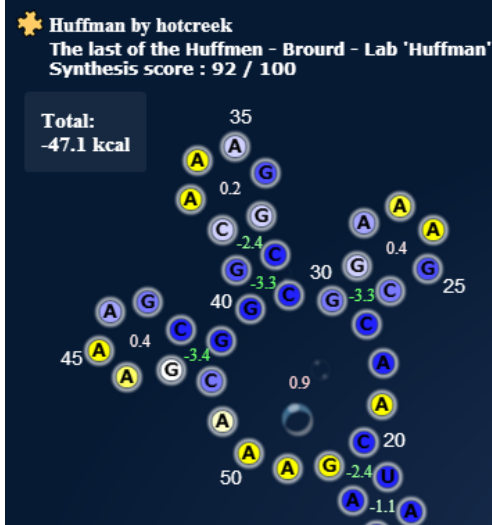
This one scores surprisingly well given its uneven energy distribution. Is relaxed designs more careless with energy distribution?

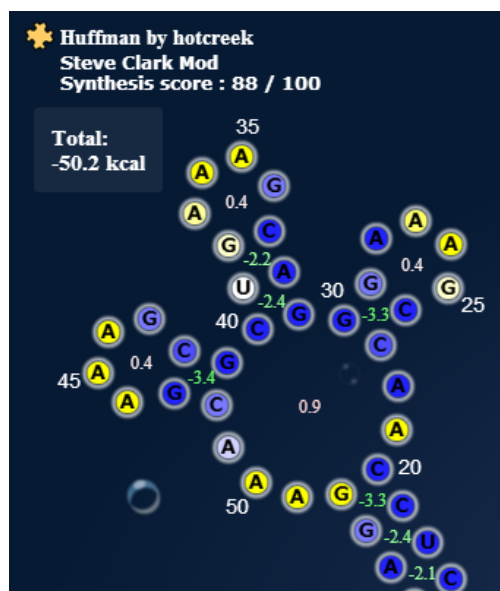
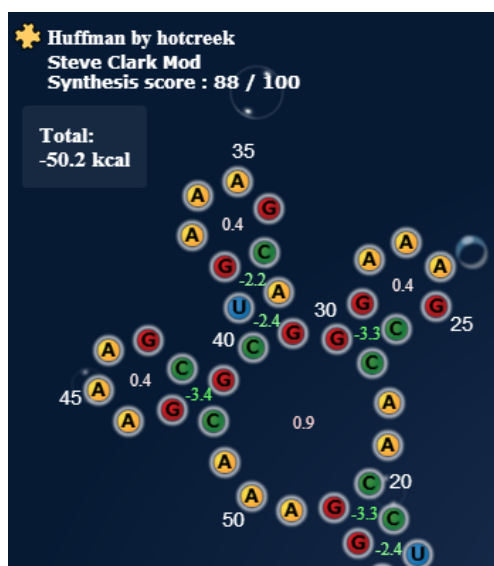
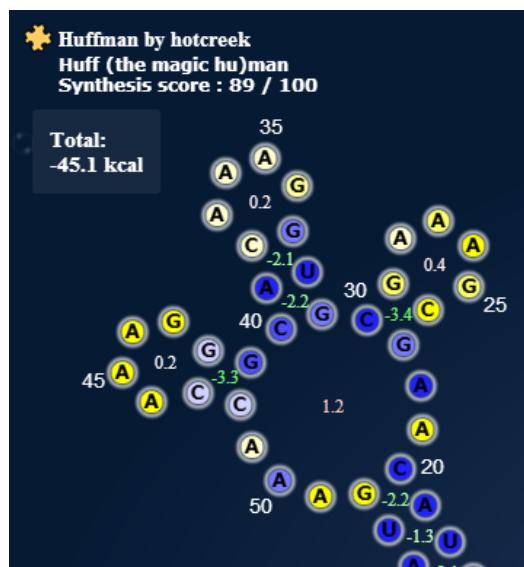
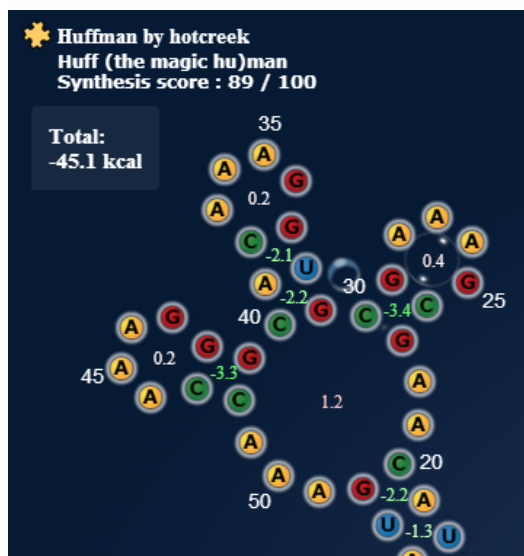
This one too: Do really long stems really not need GC-pairs to form? Is it more the smaller stems that more dependant on it? I have also seen some small form without GC-pairs.



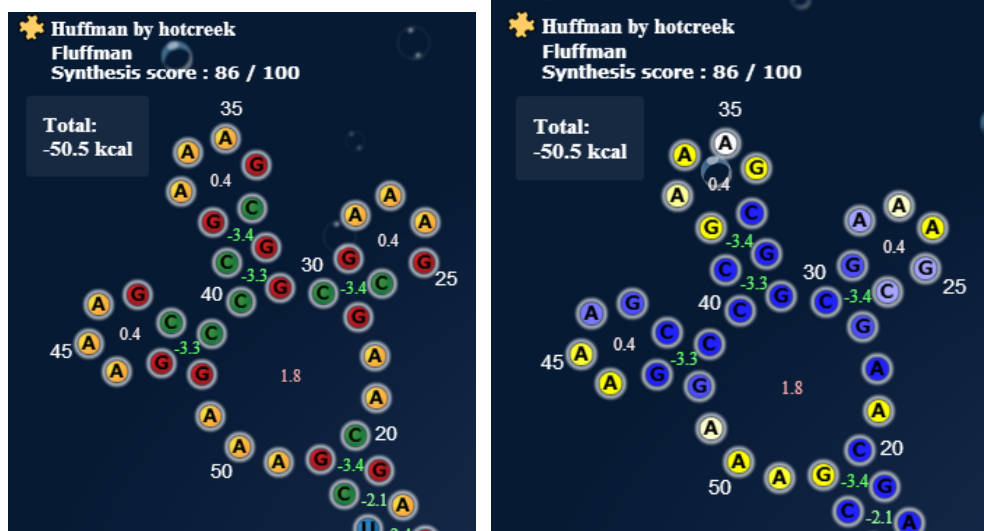
Stablest of huffman's







Except for this one, I see an interesting amount of double sameturning GC quads in the other solves.



[Huffman numbers](#)

3 Aug 2013

Actually now I think about it, I think the big multi loop ring side helped get winners in the lab series by Brouard, with Lonely Base Pair: 1-1, 2-2, 3-3. Those did had a distance of 4 single basepairs between the multi loop closing basepairs. When I add up the average for these labs, Bulged star, The star and Multiloop: 3 Branches, 12 unpaired Bases, I get a rather high solving rate (44.16%) compared to [our usual](#) overall average solving percentage. Now this is based on a rather small data sample. It will be great to have more data on how differently sized multiloops behaves.

I have [earlier](#) been speculating about that orientation of GC-pairs as closing basepairs in a multiloop, were handles that could be adjusted according to the situation. What if the size of the multiloop is one of the situations that calls for different solutions? And what if the other closing basepairs than GC-pairs, play a role in this game too? Also I have been seeing well placed boost in multiloops, that seems to help the multiloop form. I think there is an optimal energy range for each size and type of multiloop. If the energy inside a multi loop is either too negative or too positive for its size, the multi loop fails. Similarly if the energy in the quads surrounding the multiloop gets overall too negative or don't have energy enough, it will also break. There is a whole lot more to be found out here.

5 Aug 2013

I thought perhaps I could see something from the melt temperature when watching different kind of structures.

Another interesting tendency I see when I compare the melt plot for the winners in different labs is that designs with a stem average below around 2.8 basepairs, seems to have less melt temps of 107 degrees. There are a few labs having 2-2 loops that behaves as exceptions. Designs with longer stems have a higher amount of 107 degree. It is actually very logical. Designs with longer stems gain power by hydrogen bonding and are as such harder to make melting. However the many short stem designs, also have a general high amount of GC-pairs, that are the hardest ones to melt. I think we might be able to use our knowledge about what melt will be typical for a certain design. This is nice knowing when designing.

9 Aug 2013

Here is a fascinating misfold. It has the same zigzag like quality with asymmetric mirroring.

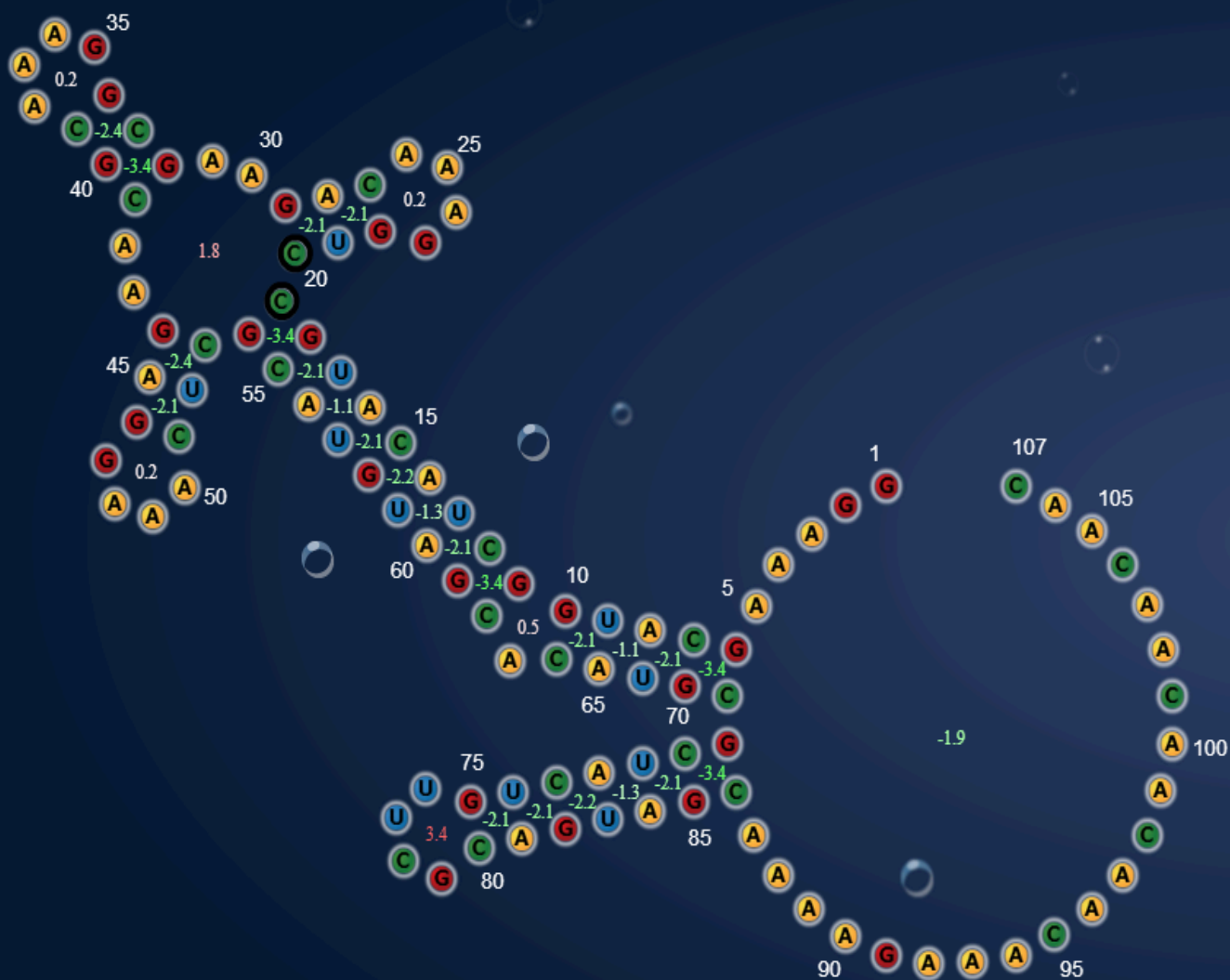




10 Aug 2013

Interesting enough there is a tendency for having CC at this spot, but GG at the other.

Total:
-49.7 kcal



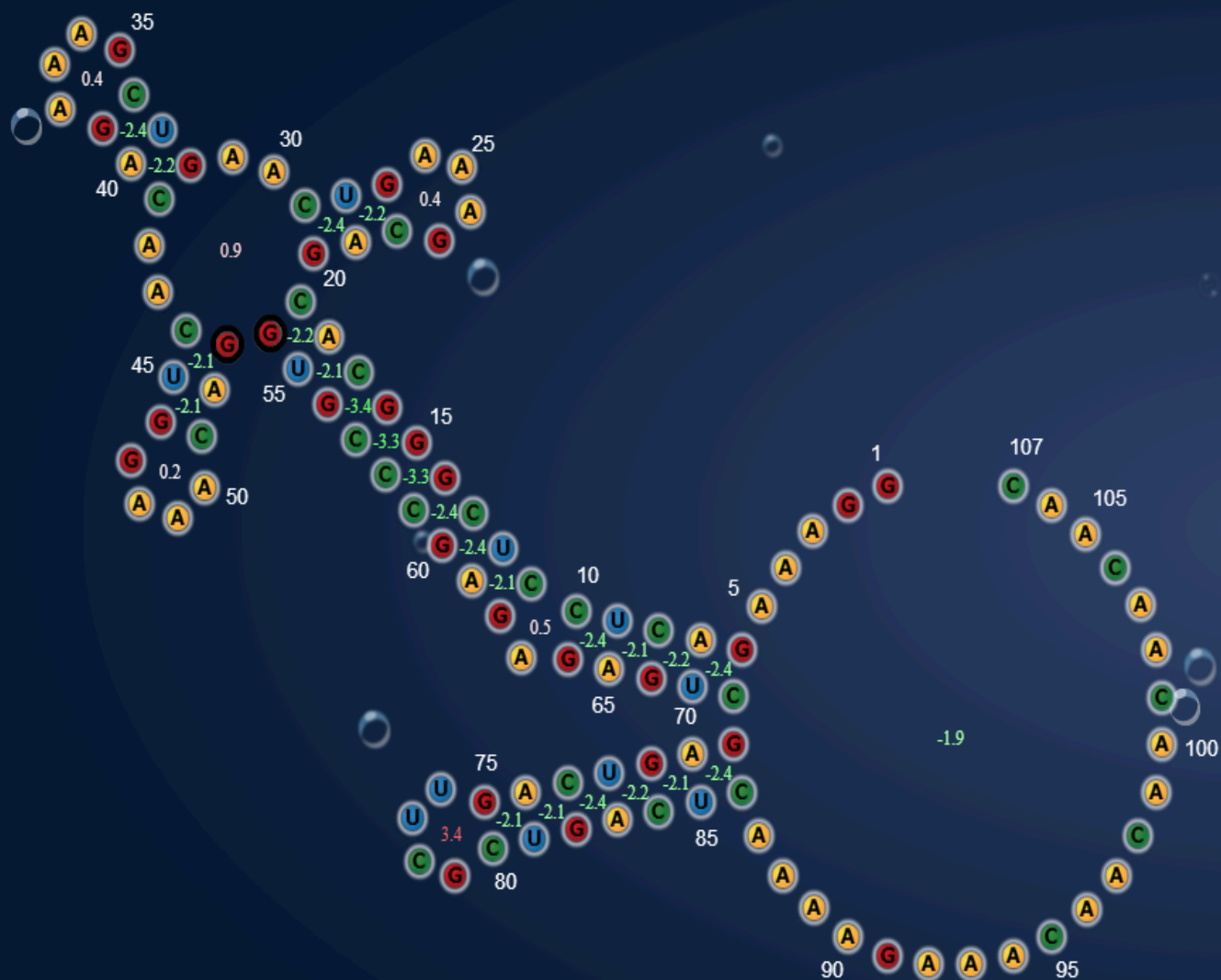
Chicken leg - Splayed

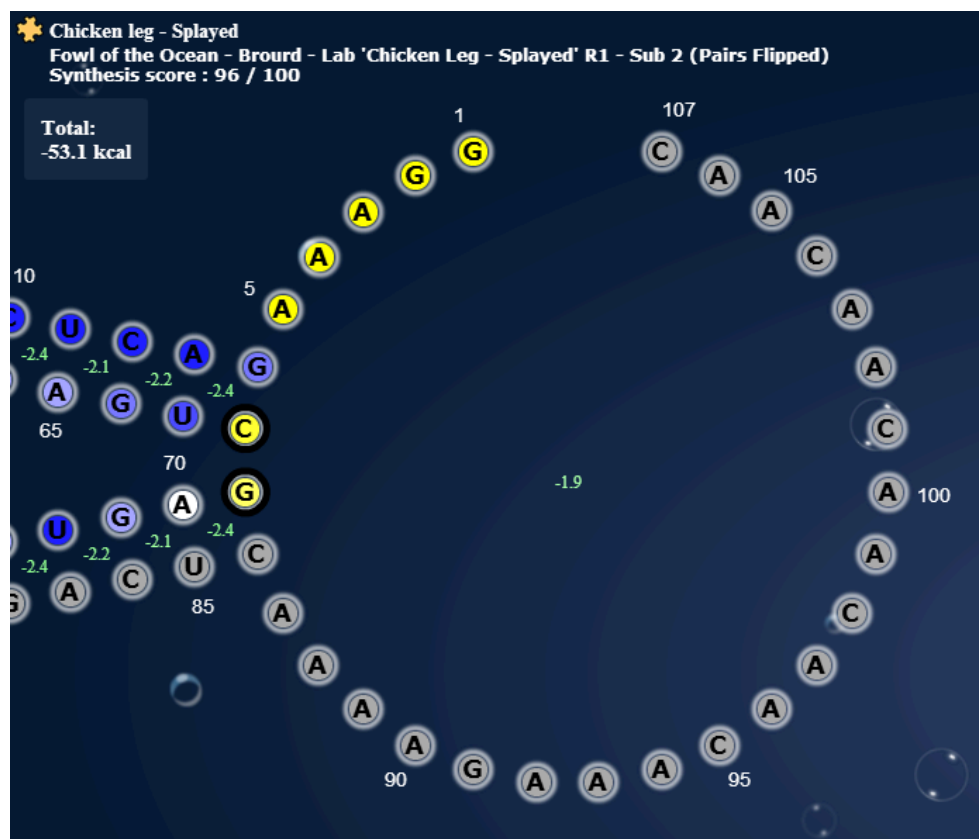
Fowl of the Ocean - Brouard - Lab 'Chicken Leg - Splayed' R1 - Sub 2 (Pairs Flipped)

Synthesis score : 96 / 100

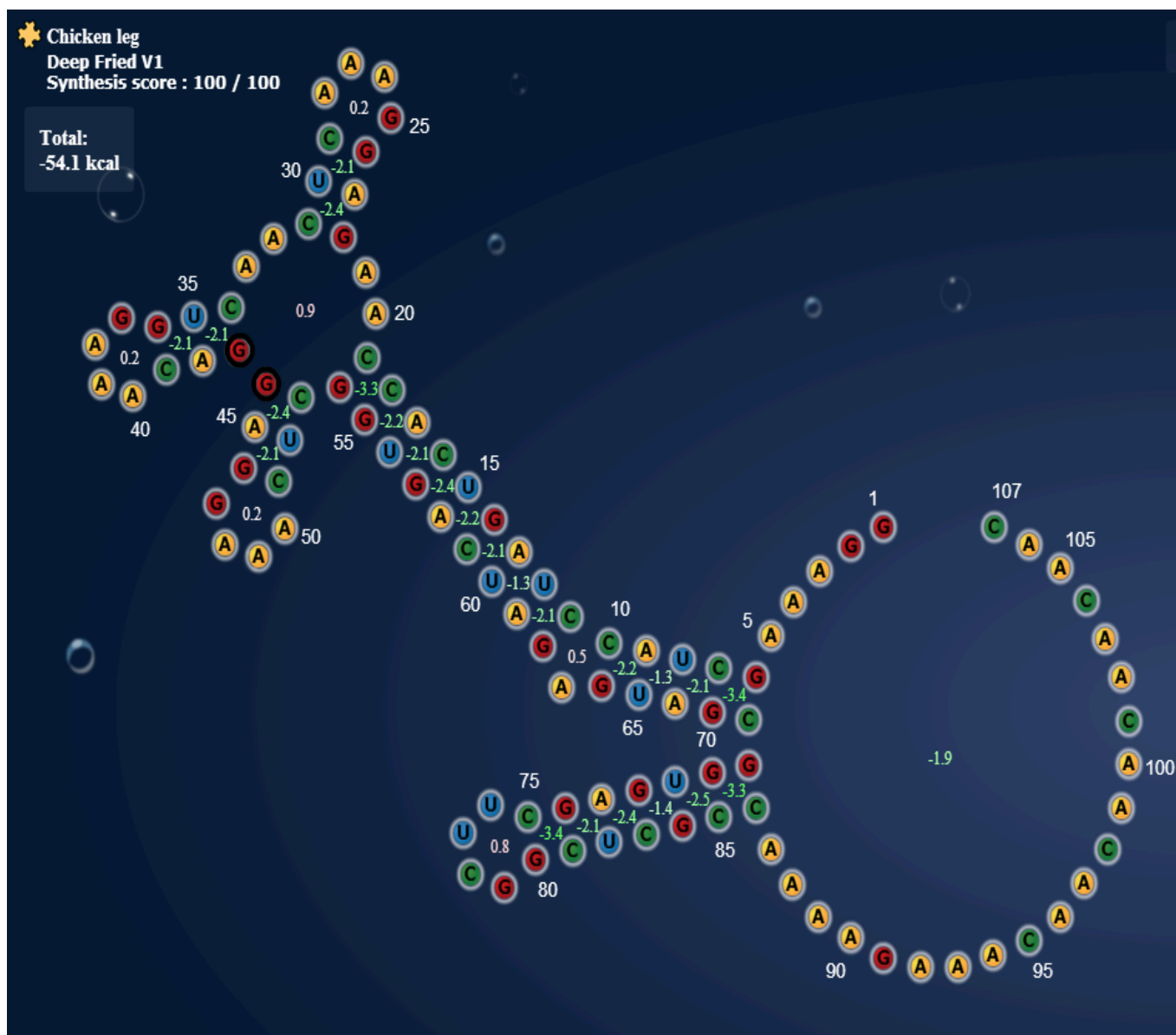
Total:

-53.1 kcal

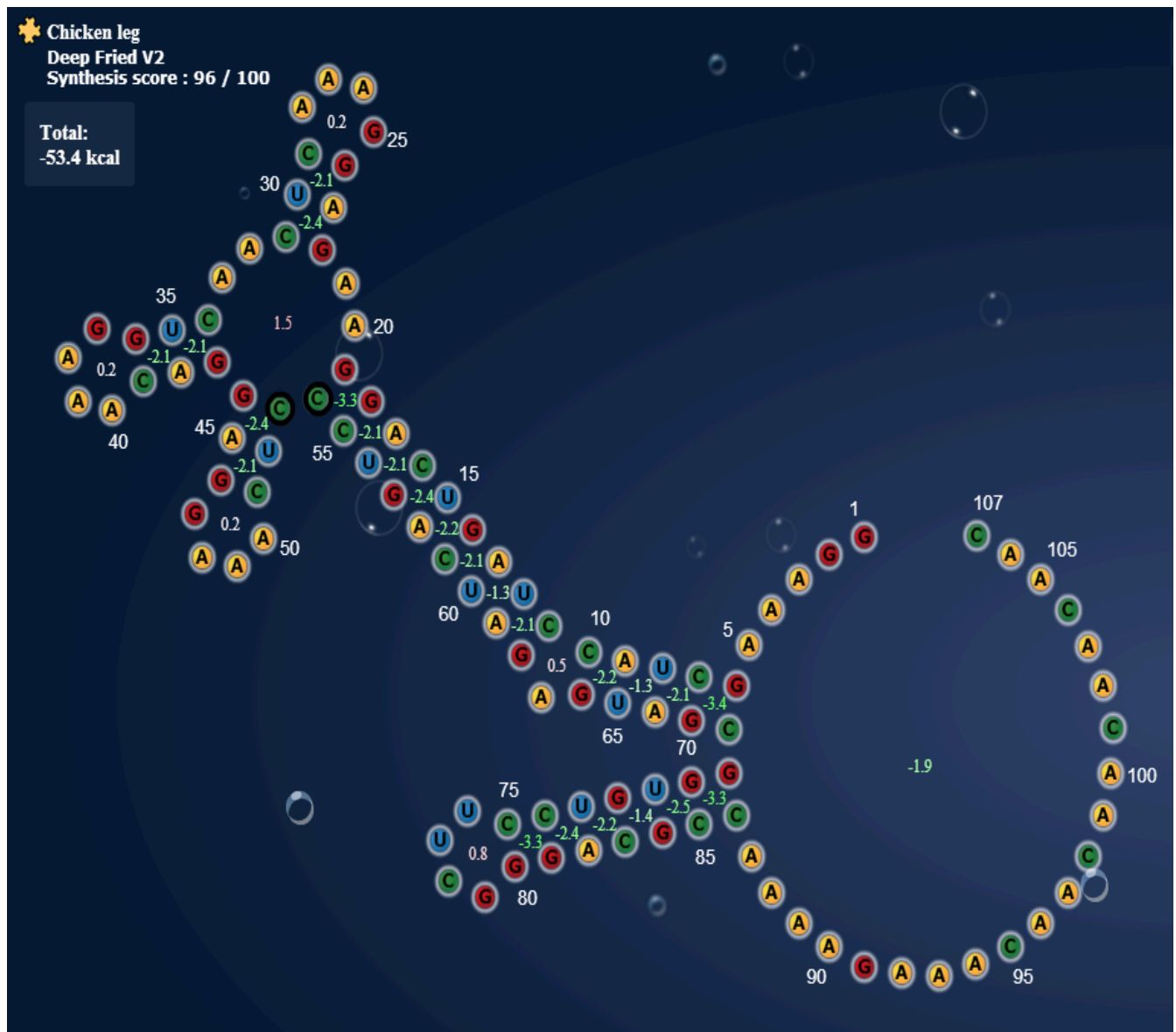




Similar it looks like this spot is favorite for GG in this lab



And this spot for CC. This design even have both patterns present at once.



For the SARS lab that is another bent shape, there seems to be a little overweight of red on the inside of the bend. However a short stretches is actually mainly green. Most of the designs agree on this. This was a lab with heavily locking of bases, so it is not too surprising. As it limited the numbers of ways to solve, without making the energy model too unhappy. Most still follow quite close to what Vienna says.

Synthesis score ▼		Title	Sequence
min	max	search	search
93 / 100		LROppy's SARS c...	G G A A A U U U A G G G A G C G C A G G C C G A G U A G G A U C C A G G C G A C A G U C C A A
93 / 100		steve's mod of ...	G G A A A U U U A G G G A G C A G A C C G C G A G U A G C A U G G A G C U G A C A G U C C A A
93 / 100		Plague (Full G-C)	G G A A A U U U A G G G A G C G C A C G C G G A G U A C G A U C G A G C G C A C A G U C C A A
92 / 100		SARS Sub2	G G A A A U U U A G G G A G C G C A C G C G G A G U A G C A U G C A G G G U A C A G U C A A A
92 / 100		Animal Balloon ...	G G A A A U U U A G G G A G G C A G C G C G A G U A G C A U G C A G G C C A C A G U G C A A
92 / 100		Corruption	G G A A A U U U A G G G A G G U C A G G G C G G A G U A G C A U C C A G G A C A C A G U G C A A
92 / 100		Try 2	G G A A A U U U A G G G A G A U C A G C G C G A G U A G C A U G C A G G A U A C A G U C C A A
90 / 100		SARS V1	G G A A A U U U A G G G A G G C C A C G C G G A G U A G C A U G C A G G G C A C A G U G C A A
90 / 100		Animal Balloon ...	G G A A A U U U A G G G A G G C C A C G C G G A G U A G C A U G C A G G G C A C A G U G C A A
90 / 100		TEST 2	G G A A A U U U A G A G A G G G C A G C C C G A G U A G G A U G C A G G G C C A C A G U U C A A
90 / 100		SARS viral 1	G G A A A U U U A G G G A G G U C A G C C C G G A G U A G G A U G C A G G A C A C A G U G C A A
90 / 100		SARS Z2	G G A A A U U U A G G G A G G C C A C C G C G A G U A G C A U G G A G G C G A C A G U G C A A
90 / 100		SARS	G G A A A U U U A G G G A G G G C A G G C G C G A G U A G C A U C C A G G C C A C A G U G C A A
90 / 100		modreds3	G G A A A U U U A G G G A G G G C A G C G C G A G U A G C A U G C A G G G C C A C A G U G C A A
90 / 100		modreds2	G G A A A U U U A G G G A G G C C A G C G C G A G U A G C A U G C A G G G C C A C A G U G C A A
90 / 100		Pestilence (2 A-U)	G G A A A U U U A U G G A G A G C A C G C G G A G U A G C A U G C A G G C U A C A G U G C A A
89 / 100		SARS	G G A A A U U U A G G G A G G U A G A G C G A G U A G C A U U C A G A C G A C A G U C C A A
89 / 100		SARS from MARS	G G A A A U U U A G G G A G G G C A C C G C G A G U A G C A U G G A G G C C A C A G U G C A A
89 / 100		Animal Balloon ...	G G A A A U U U A G G G A G G G C A C C G C G A G U A G G A U G G A G G C C A C A G U G C A A
89 / 100		SARS II	G G A A A U U U A G G G A G G U C A G C C C G A G U A G G A U G C A G G A C A C A G U G C A A
89 / 100		Mat - SARS coro...	G G A A A U U U A G G G A G G G C A C C G C G A G U A G C A U G G A G G G C C A C A G U G C A A
89 / 100		SARStenance - B...	G G A A A U U U A G G G A G A G C A C G C G G A G U A G G A U G C A G G U A C A G U G C A A
89 / 100		Hoopla	G G A A A U U U A G U G A G G G G A C C G C G A G U A G C A U G G A G G C G A C A G U A C A A
89 / 100		Try 1	G G A A A U U U A G G G A G A A U A G C G C G A G U A G C A U G C A G A U U A C A G U C C A A
88 / 100		LROppy's SARS c...	G G A A A U U U A G G G A G G C C A C G C G G A G U A G C A U G G A G G G G A C A G U G C A A
88 / 100		Keyfob	G G A A A U U U A G G G A G G A C A G C C C G A G U A G G A U G C A G G U C A C A G U G C A A
88 / 100		Mod of Real Seq...	G G A A A U U U A G G G A G A C C A C G C G G A G U A C G A U C G A G G G U A C A G U G C A A
88 / 100		shooting SARS	G G A A A U U U A G G G A G G G C A C C G C G A G U A G C A U G G A G G C C A C A G U A C A A
88 / 100		JR_SARS_Rnd1_Sub1	G G A A A U U U A G G G A G G C G A G G C G A G U A G C A U G C A G G G G A C A G U G G A A
88 / 100		Try 3	G G A A A U U U A A G G A G A U C A G C G C G A G U A G C A U G C A G G A U A C A G U C U A A
86 / 100		SARS III	G G A A A U U U A G G G A G G C C A C C G C G A G U A G C A U G G A G G G C C A C A G U G C A A
86 / 100		Fiskers SARS pi...	G G A A A U U U A G G G A G G C C A C C G C G A G U A G C A U G G A G G G C C A C A G U G C A A
86 / 100		modreds1	G G A A A U U U A G G G A G G C C A G C G C G A G U A G C A U G C A G G G U A C A G U G C A A
85 / 100		The Title of Ti...	G G A A A U U U A G A G A G U A C A G C G C G A G U A G C A U G C A G G U A A C A G U U C A A
85 / 100		Second Shot Sar...	G G A A A U U U A G G G A G G A C A G A G C G A G U A G C A U U C A G G U C A C A G U G C A A
82 / 100		SARS Sub1	G G A A A U U U A U G G A G G C C A C G C G G A G U A C G A U C G A G G G U A C A G U C A A A
80 / 100		Epidemic (1 A-U...	G G A A A U U U A U G G A G G C C A C G C G G A G U A C G A U C G A G G G U A C A G U C A A A
78 / 100		Mod of Real Seq...	G G A A A U U U A U G G A G G C C A C G C G G A G U A C G A U G C A G G G U A C A G U G A A A
76 / 100		JR_SARS_SARS_Co...	G G A A A U U U A G G G A G G C C A C G C G G A G U A C G A U G C A G G G U A C A G U G A A A
72 / 100		Mat - SARS coro...	G G A A A U U U A G G G A G G G C A G C G C G A G U A G C A U G C A G G G C C A C A G U G C A A

Interesting enough there was actually quite a lot of binding signal in the lab experiment FMN binding site chemical footprint, by Brouard. I think that means he hit bingo with his experiment, since it shows that there is actually quite a lot of reactivity, even though there shouldn't be anything to bind up with. Interesting.

FMN Binding Site Chemical Footprint			
Synthesis score ▾		Title	Sequence
min	max	search	search
98 / 100		Hepta 3	GGAAAGGUGUGUAUAAGGAUAUAGUGGUGGGGUAUAUGGCCACCACUAAGAGGAUUCGCCAC
98 / 100		Meechi FMN Foot...	GGAAAUAGAUUCUAUUAGGAUAUAGUCAUAACGAAAUAAAGUUAUUGAUAGAGGGAUAUGAUC
97 / 100		Footprint One	GGAAAGAAGCUGCAUUCAGGAUAUCUGGCAUUCGAAAGAAAGCAUUGCAGGAAGGSCAUAGCAGC
97 / 100		FMN Binding 2 (...)	GGAAAAAGUAUCUAGUAGGAUAUCUACUAUUCGAAAGAAAGAUUAGUAGAAGAGGSCUAGGUAC
97 / 100		FMNB - 1	GGAAACGAUAUAUAUAGGAUAUGAUUAUAUAGGAACAAAGUAUAUAUGAAGGAUAUAUAU
97 / 100		Hepta 1	GGAAAGAAUGAUAAUAGGAUAJAGGAGGGCCUCUCAAGGCCUCUUAAGAGGAUUAUCAU
97 / 100		Eninarus	GGAAAUAGUGGAGGAGAGGAUAJAGGGCGUGAAAGAAACACGCCCUUAAGAGGCUCCUCCAC
97 / 100		flick	GGAAAGCAAACGAUGAGGAUAJAUUAGAUGGGAAACAAACUAUUUAUAAGAGGCAUUGUUUG
97 / 100		Trail	GGAAACGACGAUCUUAAGGAUAUCGCGUACUGAAAGAAAGUGCAGCGGAAGAGGGAUUCGUC
96 / 100		Fiskers Footprint 3	GGAAAGAGUCAUCACGAGGAUAJGAUGGAUGCGAAUAAAGCAUCCAUCAAGGCGUGAUGAC
96 / 100		on your mark	GGAAAGAGCAUCAUACAGGAUAJUGAUUGGUGAAAGAAACCGGAUCAGAGAAGGUAUAGAUUGC
96 / 100			GGAAAUACUGGAGGUGAGGAUAJUGAUUGGUGAAAUAAACAUCCAUCCAGAGGGAUCUCCAG
96 / 100		I Printy the Fo...	GGAAAUACCAUGUAUCUAGGAUAUCUAUAUCUGGAUAAACAGAUUCUAGAAGAGGUACAUGG
96 / 100		JR FMNBinding_R...	GGAAAAACACGAUAUAGGAUAJUGUAUAAGCUUACACUCCUAUACACAGAGGCAUAUCGUG
96 / 100		JR FMNBinding_R...	GGAAAAACACUAUAGCAGGAUAJCAUCAUACCGCAACACACGUAUGAUGAGAAGGCUUAUGUG
94 / 100		boots made for ...	GGAAAGAGCAUCUAGCAGGAUAJCAUGCAUUCGAGAAAGGCAUGCAUGAGAAGGCUAGAUGC
94 / 100		Foot Binding 1	GGAAAGAGCGUAUAGCAGGAUAJCCGACACUCUAUAUAAGAGUGUGGGAAGAGGCUUAUACGC
94 / 100		Fiskers Footprint	GGAAAGAGGUCUAUAGCAGGAUAJCAUGGAUUCGAAUAAAGCAUCCAUAGAAGAGGCUACAAGAC
94 / 100		FMN Binding 3 (...)	GGAAAAAGUAUCUUGAGGAUAJUGACGUUAGGAAGAAAGAUUAGUACAGAGGJCAAGGUAC
94 / 100		FMN Binding 1 (...)	GGAAAAAGUAUCGACGAGGAUAJCAUCUAUUCGAAAGAAAGAUUAGAUGAGAAGGCGUUGAUAC
94 / 100		FMN BSC2	GGAAAGAGCCGAGUUCAGGAUAJGCGGAGUGCCAAAGAAAGGCAUCGGCAGAGGACAUUCGGC
94 / 100		Bigfoot, PhD	GGAAAGAGCAAGAUAGAGGAUAJUGAGCAAUUCGAAAGAAAGAUUGCUACAAGAGGCUAUCUUGC
94 / 100		BS Footprint - ...	GGAAAUAGCAUGUCUGAGGAUAJGAUCAUGACGAUAAAGGUCAUGAUCAJAGGUAGACAUUGC
94 / 100		Print Footing - ...	GGAAAUAGAUAGCAUGAGGAUAJUGAUAUCUGGAUAAACAGAUUCUAGAAGGCAUUCGUAUC
94 / 100		JR FMNBinding_R...	GGAAAAACACGAUAUAAGGAUAJAUUAUAUAGCUUACACUCCUAUAUAUAGAAGGUUAUUCGUG
94 / 100		FMN Z1	GGAAAUAGUGCGUACAGGAUAJUGUGCGUGUCGAAUUAAGAUUAGUACAGAGGUGUAUUGUAC
94 / 100		FMN R-G deck	GGAAAGAGCCGCGGUCAGGAUAJGCGCGCGCCAAAGAAAGCGGCGGCGAGAGGACCGCGGC
93 / 100		BS Footprint	GGAAAGAGCGUUCUGACAGGAUAJCAUGCAUUCGAAACAAAGCAUCCAUAGAAGGCUAGAAGC
93 / 100		Fiskers Footprint 2	GGAAAUAGGCUUAUCAGAGGAUAJGCGGGAUGCGAAUAAAGCAUCCAGCAGAGGCUGAUAGAC
93 / 100		duct tape	GGAAAUAGUAACUCCAGAGGAUAJUGAUCUGGGAUUAACCAUAUCAGAGAAGCTJCCAGUUAAC
93 / 100		Getting Off On ...	GGAAAGAGAUCAUAGGAGGAUAJGGAAGAGGCGUCUCAAGCCUUCUCCAGAGGCUUAUCAUC
93 / 100		Mat - FMN bindi...	GGAAAUAGCGUAUAGCAGGAUAJCAGAUAUUCGAAAUAAAGCAUAUCUGAAGAGGCUUAACGC
93 / 100		Mat - FMN bindi...	GGAAAUAGCGUAUAGCAGGAUAJCGUAUAUUCGAAAUAAAGUAUUAUCGAGAAGGCUUAUACGC
93 / 100		Hepta2	GGAAAGAUAGGAUUAGGAUAJAGAAAGGACGCUAACUGUCCUUCUAGAAGGUAGAUCCUAU
93 / 100		In a Bind 1	GGAAAGAGUUGGCAUGAGGAUAJUGUGACAUUCGAAUAAAGCAUUCACAGAGGCUAUCUAC
93 / 100		focus on free e...	GGAAAGGCGACCGGAGGAUAJCCGUAGGCGGAAAGAAAGGCCUAGGGGAAGGCGCGGUGCGC
93 / 100		hammer	GGAAAGAGAAUAGUAGAGGAUAJGUUAAGAUUGGAAACAAACUAUUUAACAAGAGGCUUAUUUG
93 / 100		Footprints in L...	GGAAAGAGUAGUAUGAGGAUAJGUUAAGACUGAAAUAAAGAGUCAUAGAAGGCUAUGACUAC
92 / 100		mod a la Eli	GGAAAGAGUUCUAUAGCAGGAUAJCAUGGAUUCGAGAAAGGCAUCCAUAGAAGAGGCUAUAAGC
92 / 100		Foot Binding 2	GGAAAGAGCGCAUAUUCAGGAUAJGGGUGUGAGUAUAUAUCUACACACCAAGAGGCGAUUUGC

It also looks like Nando's pseudoknot experiment didn't went too bad. Looks pretty well for the binding between the loop and the loop ring as intended.

10 Aug 2013

I was looking at my old spreadsheet and was thinking about how bigger multiloops behaved because I see a tendency of bigger multiloops being in designs with overall higher score. And I was playing with big multiloops in the puzzle maker.

<https://docs.google.com/spreadsheet/ccc?key=0AhJGPGrJ3fkKdFFLbm5OeIE5dDBOVEM1RWfjNUozZ3c#gid=0>

When JandersonLee was hacking the energy model for multiloops, I remember him saying something about there being no penalty if here were more than 2 bases between the stems.



There is literally no changes to the energy in the multi loop, if one prolongs the ring loop, if the orientation stays the same. So this has the same energy as the multi loop with only 2 bases between. Not why it is so. But the guys with Vienna decided that the amount of bases between stems didn't matter much, as long as there were 2 or more between. I agree with them on that. I'm not sure to what extent though. I mean how big the loop will get before it gets a problem, if it does.

This is from my article on hard designs and the numbers:

Designs with number of single bases between the stems.

0<1 = winner average of 9.62%

1<2 = winner average of 19.96%

2<3 = winner average of 25.84 %

3<4 = winner average of 44.16%

Bigger = even more relaxed?

[Optimal multi loop stem distance](#)

I have no idea how far this tendency continues.

Shape threshold

Brouard was talking about SHAPE threshold today and mentioned RMDB. (Chat log on [SHAPE threshold](#), also see [SHAPE lessons](#).) This thing with Shape min, max and threshold is that I have a hard time understanding, so till now I have ignored it. I got curious and went and looked.

I was checking into SHAPE threshold to see if I could make something from the numbers. I checked out this batch of Cloud labs:

http://rmdb.stanford.edu/repository/detail/ETERNA_R74_0000

I was looking at these labs:

<http://eterna.cmu.edu/game/browse/2892143/>

<http://eterna.cmu.edu/web/lab/2892143/>

.....((((((((((((((((.....)))))))))(((((((.....)))))))))(((((((.....)))))))))((((((((((((((((((((.....)))))))))(((((((.....)))))))))(((((((.....))))))))).....

The designs with a high score generally has a low shape threshold. It looks like one feature that causes higher SHAPE threshold than the average for a lab is uneven energy distribution. I was checking the lab Tetraloops and 0-0-0-0 Multiloop Phase 1. I wonder if it is the same for the other labs.

I think that lots of red in end loops causes high signal to noise numbers. Not totally. There are exceptions. But there seems to be a high rate of non yellow bases. I think a high rate of GU's can also disturb the signal to noise. Actually it looks uneven energy distribution is both disturbing shape threshold and signal to noise ratio. Perhaps even similar with lots of GU's. Yes, I think GU's have the power to disturb both SHAPE threshold and signal to noise ratio. Does many double same turning pairs cause lower signal to noise? There could be something to it. Yep, definitely seems to be something to it. Interesting. I would usually count many same turning pairs bad. But since this is a long stemmed design. Ok, is bad. Those designs with a signal to noise ratio much below 1 overall scored bad. And they had many double same turning or triple pairs.

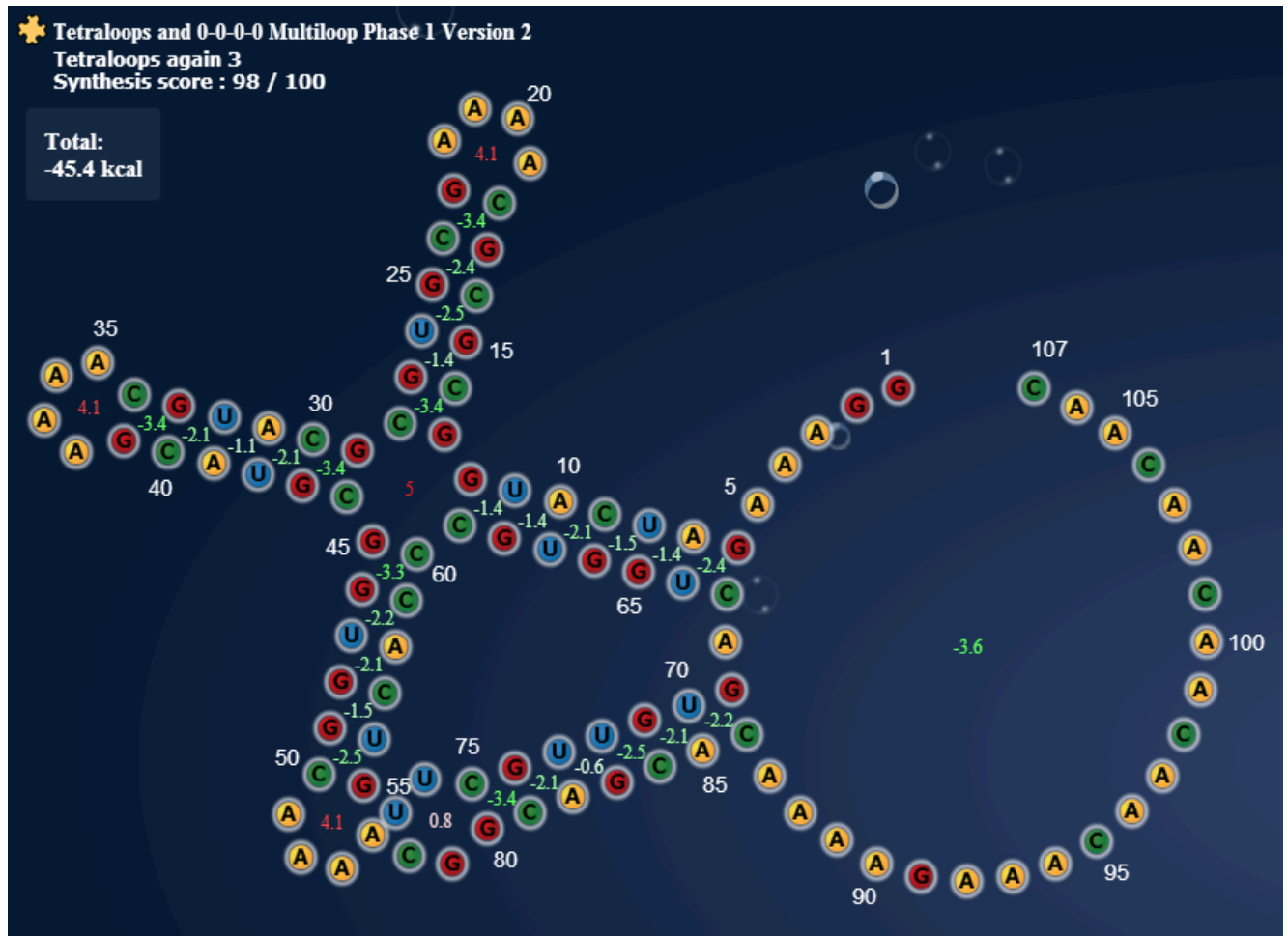
This one also has a very low signal to noise ratio. It has lots of same turning pairs and it is almost 100% GC. So very low threshold values aren't necessarily good, neither low signal to

229

sequence: **GGAAGCCCGGCGCGCCGAAAGGGCGCCGUGGGAACACGGCCGGCCGAAAGGCCGGCCGGGCACGCGGUCUUCGGACCGCGAAAAGAAACAACAACAAC**



66



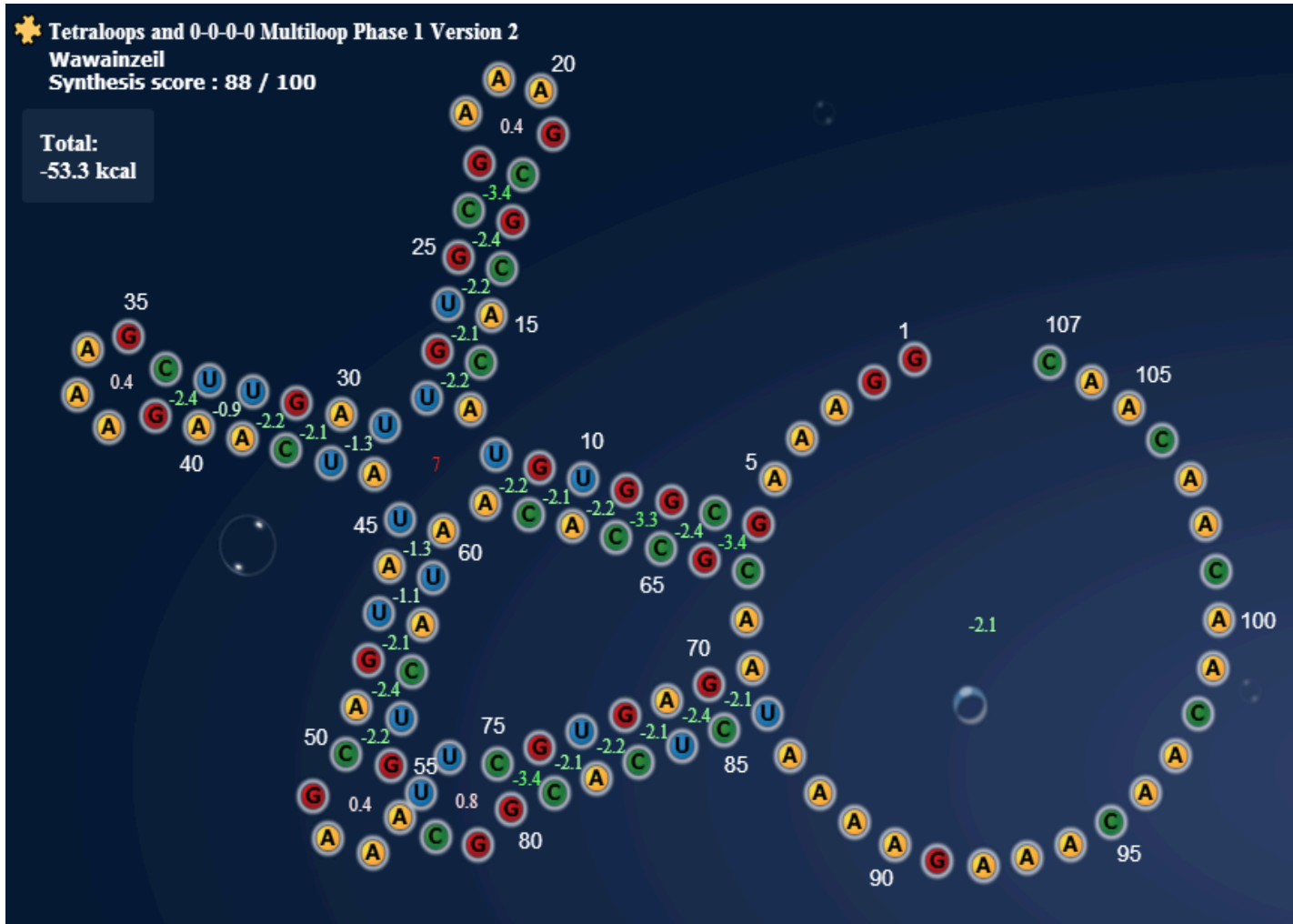
EteRNA:score:EteRNA_score:98.7, EteRNA:score:min_SHAPE:0.058, EteRNA:score:max_SHAPE:0.634, EteRNA:score:threshold_SHAPE:0.346, MAPseq:design_name:Tetraloops again 3, MAPseq:project_name:Tetraloops and 0-0-0-0 Multiloop Phase 1 Version 2, MAPseq:ID:3015799,
170 sequence:GGAAAGAUCAUGGCGCGCAAAGCGUGCGCAUGGCAAAAGCAUGCGGUGGCAAAAGUCACCCGUGGUCAGUGUUGCUUCGGCAGCACAAAAGAAACAACAACAAC,
signal_to_noise:good:5.692, structure:.....((((((((((((.....))))))((((.....))))))((((.....)))))).....((((.....)))))).....

Some design only has signal to noise ratio go high. What characterizes them? What about perhaps lots of red in the end loops? Yes, looks like there is something to it.

I think also bases of the same kind in line might add disturbance to shape threshold and signal to noise ratio. Is this so?

Uneven energy distribution doesn't always disturb signal to noise ratio - like make it go high, neither with SHAPE threshold. This one has a weak, but holding middle and it rather have lower than usual values than high

EteRNA:score:EteRNA_score:88.0, EteRNA:score:min_SHAPE:0.026, EteRNA:score:max_SHAPE:0.290, EteRNA:score:threshold_SHAPE:0.158, MAPseq:design_
 232 MAPseq:project_name:Tetraloops and 0-0-0-0 Multiloop Phase 1 Version 2, MAPseq:ID:3080415
 sequence:GGAAAGCGGUGUACACGCGAAAGCGUGUAGUUCGAAAGAUAUAUGACGAAAGUCAUAACACCGCAAGAGUGCUUCGGCACUCUAAAAGAAACAA
 signal_to_noise:weak:0.927, structure:.....((((((((((((.....))))))((((.....))))))((((.....)))))).....((((.....)))))).....



This should be useful for us when we make lab designs.

I have started to see what I could dig up on SHAPE threshold from my chat logs:

Getting hold of the shape numbers

Bround showed how to call shape data from the server. That way you can get those that are not uploaded yet.

<http://eterna.cmu.edu/get/?type=solutions&randvar=0.21552102267742157&puznid=2858258>

2858258 = Lab ID

You can add in any lab id on that numbers place.

And yes, they do artificially scale the SHAPE threshold (the divide between paired and unpaired) in order to enhance the structure that folded the most in the population
Brouard

Blasted all A-U stacks should fail, but it just so happens they have a reactivity around 0.6, well within range :) It's only *okay* when the rest of the design is similar otherwise, the threshold will be adjusted to low.
Brouard

I guess that I am saying something similar to Brouard, with that uneven energy distribution messes designs up.

The higher the threshold, the more amplified structural motifs in loops will become, the lower the threshold, the loop reactivities are less amplified, and the tendency for base pairing is a bit more amplified.
Brouard

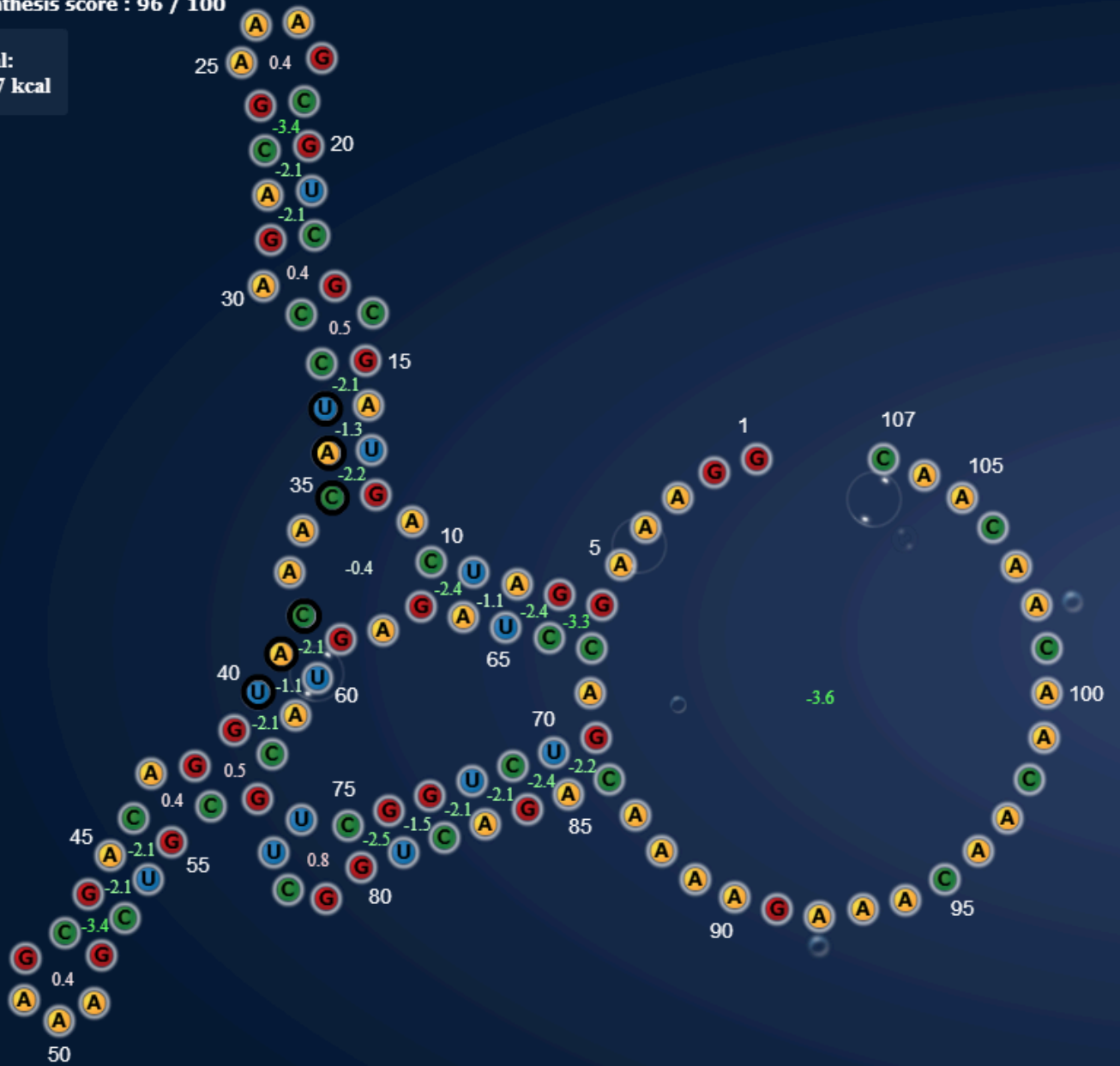
Also see [SHAPE lessons](#)

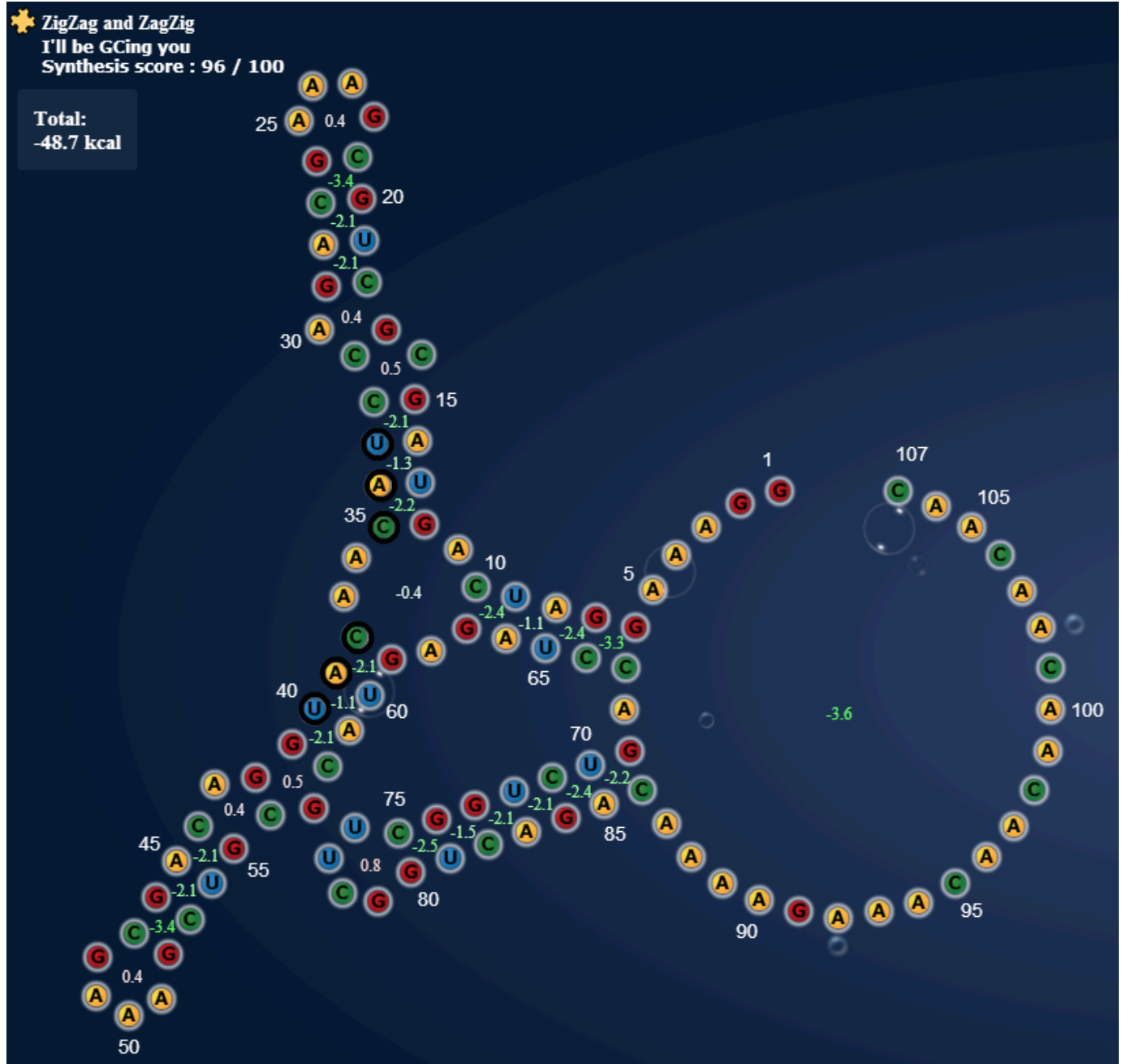
11 Aug 2013

I was looking for a zigzag element candidate for the lab Two bulge zigzag - both conformations, when I found this one. Notice the mirror pattern from the multiloop and out. Many of the lower scoring designs in this lab, had the two long arms fold pair up, as they were quite similar. This one found an alternative way around it, by mirroring the multiloop, which actually lowered the negative energy inside it. Yet it is a total winner. It did break in the multiloop, but the arms didn't mispair. There were one more of them among the winners, and a few more among the top scorers. Indicating that it is helpful to get around this similar arm problem.

✨ ZigZag and ZagZig
 I'll be GCing you
 Synthesis score : 96 / 100

Total:
 -48.7 kcal



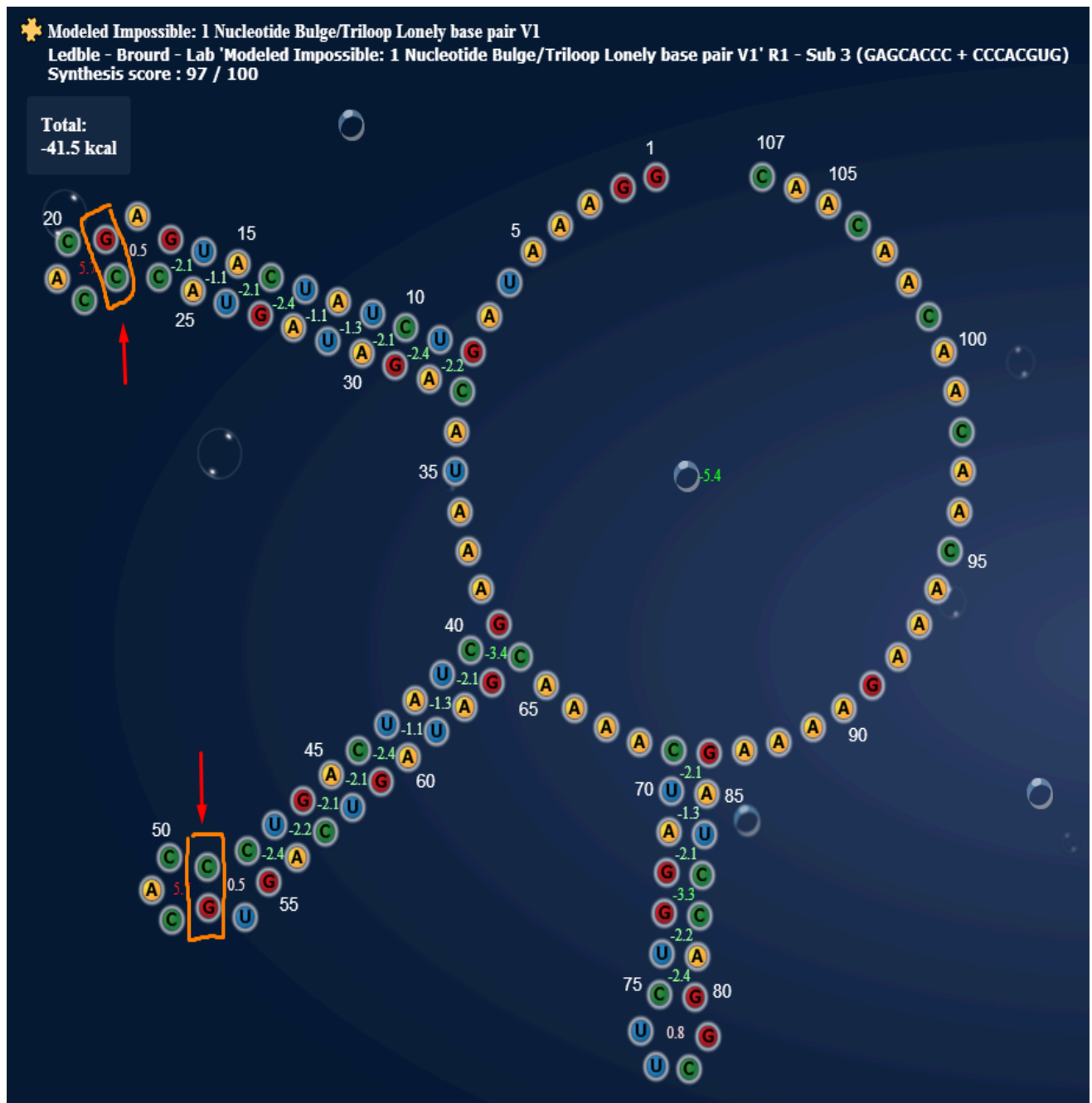


But generally it is still the best strategy of going with the more optimal orientation of the gc pairs in the multiloop.

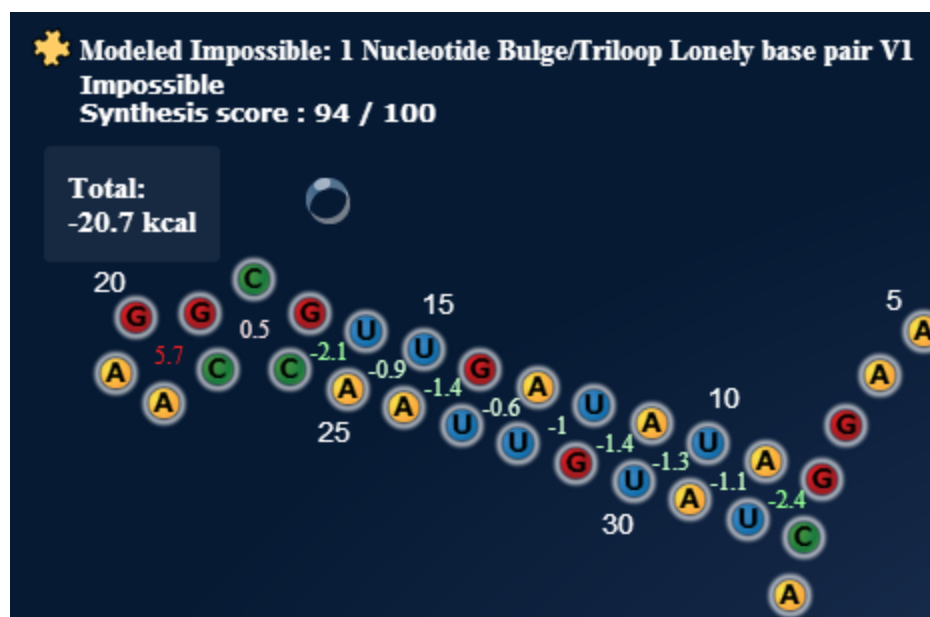
I found some interesting when I looked at modeled impossible. It looks like both these single base pair closing the triloop has a want for a certain orientation. When one look for the successful closings in the shape data, it appears they want C to be on the inside of bend. Not too surprising given that 1 nt bulges often have a preference for green on the inside of the bend. Still, I like it. :) I love when there is some consistency between what works. That means one got

a better chance of hitting it right and repeat it elsewhere.

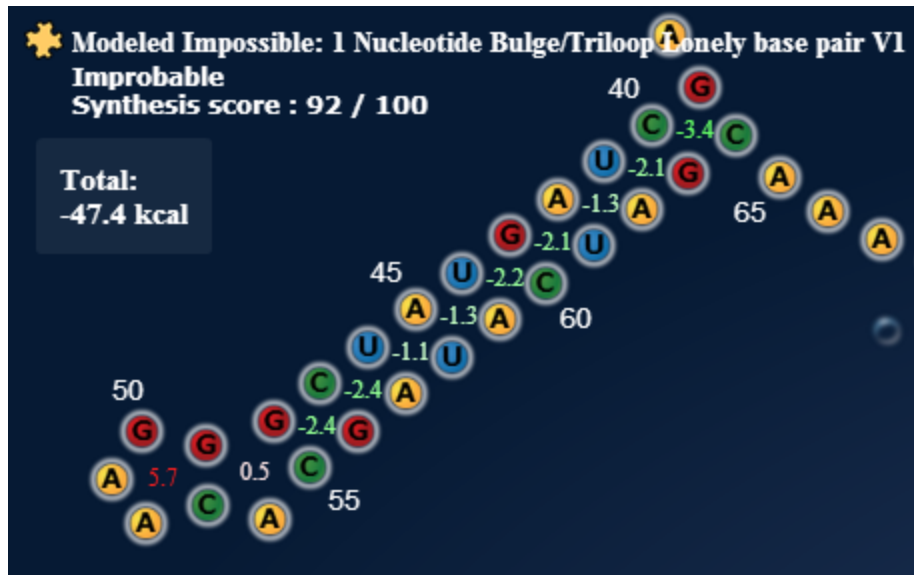
I knew that triloops had a love for uracil and green, but it looks like they have an even higher love for green than blue.



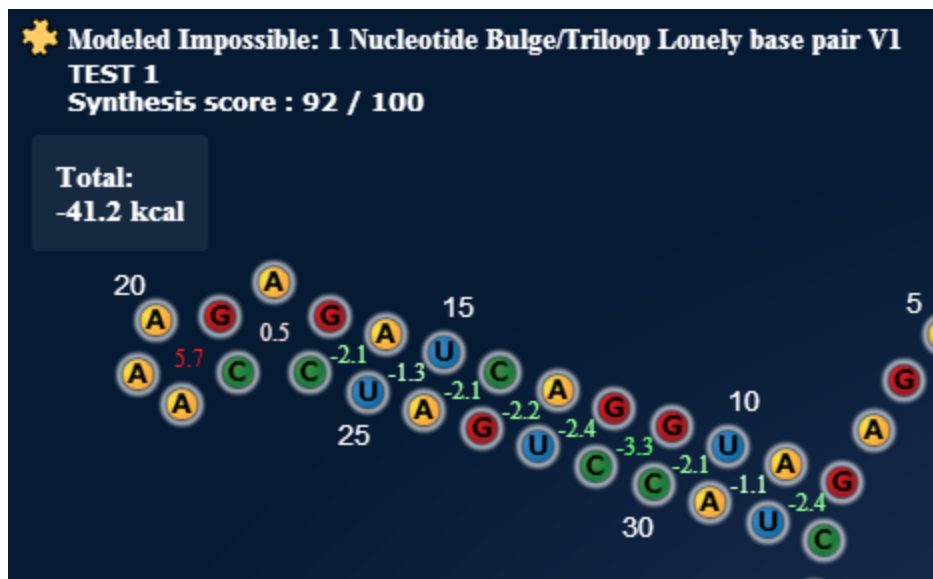
Here is a number of the stable ones. Interesting enough working ones among the top scorers are in agreement on the orientation of the backing AU base pair at base 16-25. This backing base pair if a GC, is flipped opposite the closing base pair of the long stem.



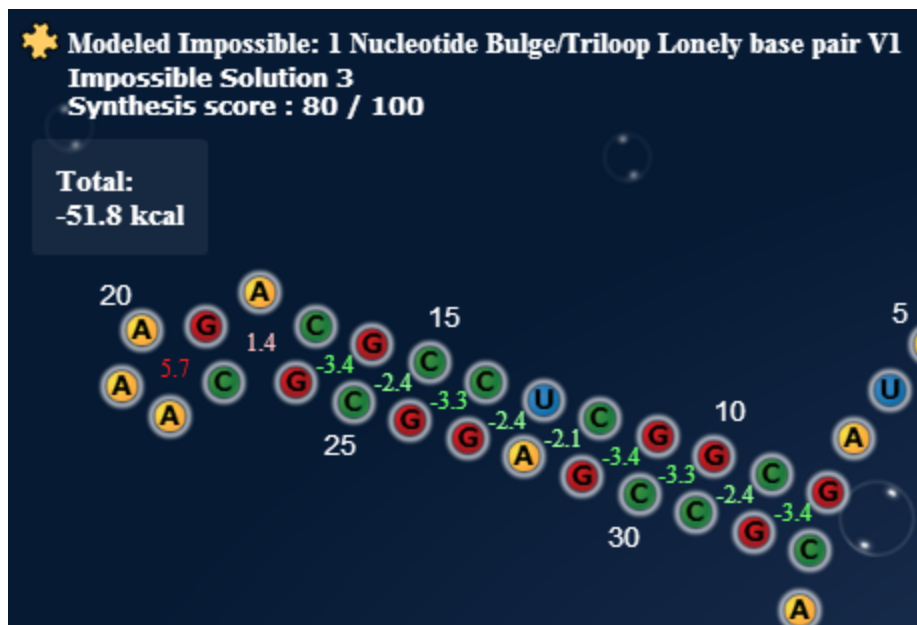
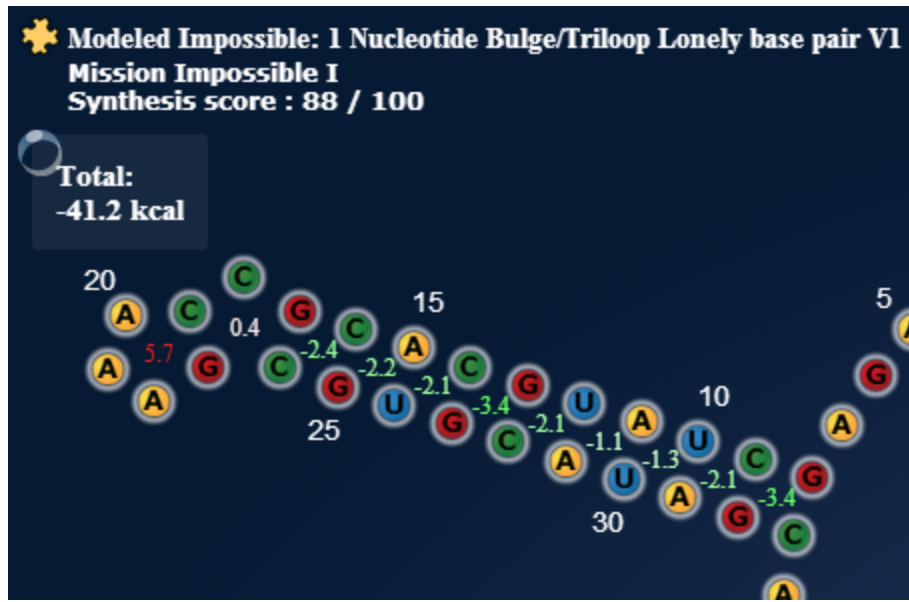
Oh, interesting. This one has the second strongest 1nt bulge formation, and no C at the bottom. This pattern seem to turn up more among the lower scoring designs.



It also appear in general that base spot 20 and 22 have biggest influence of the bulge and triloop forming. Often one of these spots is of same nature C/U or color as the bottom bulge base (23,49) [As often before U and C are quite interchangeable]

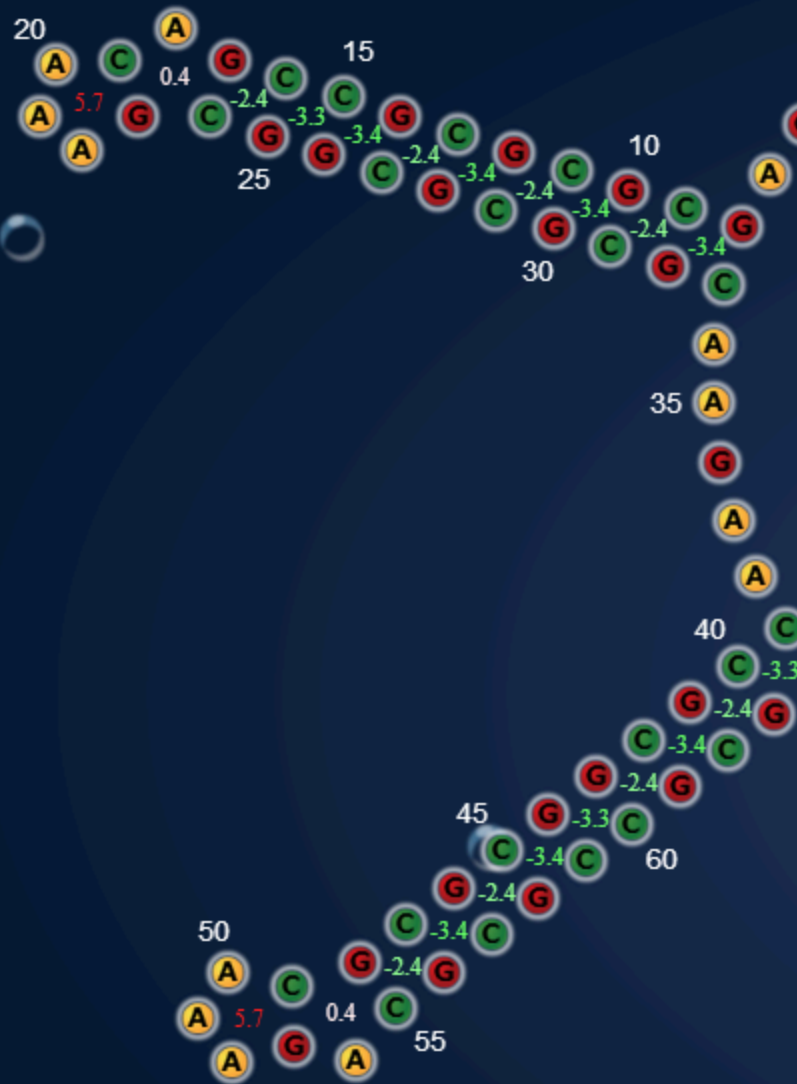


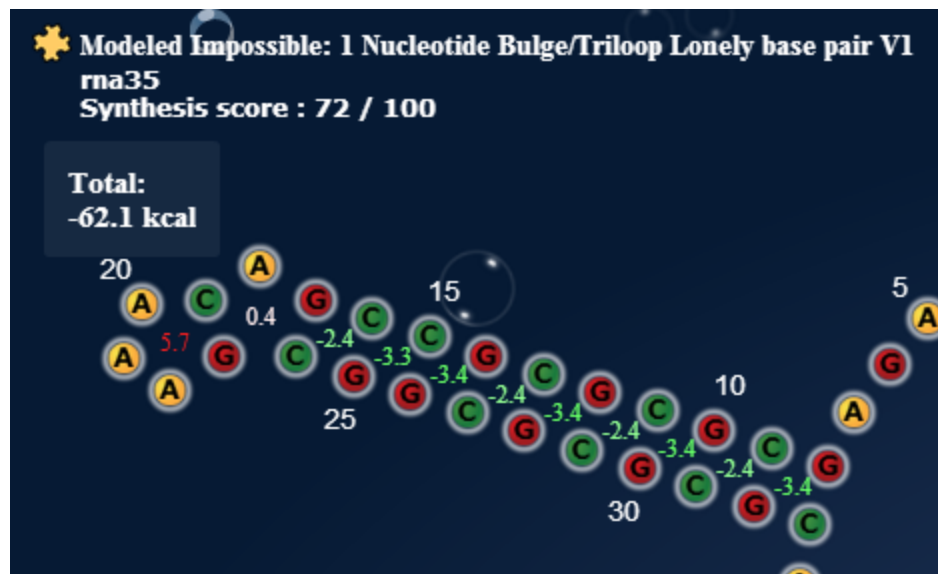
And one more with G on the inside



This one got both working, but isn't scoring high.

Total:
-61.9 kcal





I have noticed that where bulge misfolds occur spontaneously there is often same, but crossed bases in a stem.

Brouard mentioned that the motor protein labs might have some shape threshold problems in the areas of the adjacent multi loop due to the short stems. I'm still not totally sure how to read the shape raw numbers, but it looks like there is a raised SHAPE mix in exactly that area. Which also means the SHAPE threshold is raised.



<http://eterna.cmu.edu/get/?type=solutions&randvar=0.21552102267742157&puznid=3071343>

12 Aug 2013

I wonder if this is always the case with designs that has short stems or areas with short stems. And if so, can we really see how short stems fold? I mean, if the SHAPE data method won't let us see.

13 Aug 2013

Loose thought. Since the designs with longer stems in connection to adjacent multiloops do

better, like single to switch. Also the chicken/frog leg series did better than the shorter motor protein series. I'm thinking perhaps that the probe might have trouble gaining access to these short and sharp angled adjacent multiloops. So it could be that the less winners I'm seeing for the adjacent multiloops with short stems, is due to problems detecting a bind. However, nature also seems to find them hard, since Nando couldn't find a 5 branches one. So I think there is still something about adjacent stems being hard. Backbone doesn't like to be close to itself in space. But a weakness in the shape detection method for this specific area, might also play in.

16 Aug 2013

Again there is this funny tendency for really long stemmed design, that many of the best scoring have a rather high amount of GU-pairs. 4 of 5 of the highest scoring designs, have GU's and more than one. It could really look like longer stems crave GU's. What a weird world. :)

Also notice the overall high melt point. That is also often following longer and very long stems.

 **Motor Protein - Step 3**

Title	GU Pairs		Melting Point		Free Energy		Synthesis score ▼	
	min	max	min	max	min	max	min	max
search								
Title of epicness	7 (21%)		107 'C		-61 kcal		92 / 100	
Short Stacks Ad...	3 (9%)		107 'C		-53.9 kcal		92 / 100	
[Title]	7 (21%)		107 'C		-61.2 kcal		92 / 100	
Onerlebe	0 (0%)		98 'C		-55.84 kcal		92 / 100	
MP-3	2 (6%)		107 'C		-64.2 kcal		92 / 100	
Motor Protein - ...	0 (0%)		107 'C		-60.9 kcal		90 / 100	
Dynein 2	10 (30%)		107 'C		-62.6 kcal		90 / 100	
Dynein 1	1 (3%)		107 'C		-63.9 kcal		90 / 100	
Motor	6 (18%)		87 'C		-30.3 kcal		90 / 100	
JR_Motor3_Rnd1_Sub1	0 (0%)		97 'C		-52.2 kcal		90 / 100	

The winner doesn't have a GU, but most of all the other high scoring designs does. And the main part of the GU's are not just placed in the hairpin barcode.

Motor Protein - Step 2

Title	GU Pairs		Melting Point		Free Energy		Synthesis score ▼	
	min	max	min	max	min	max	min	max
search								
JR_Motor2_Rnd1_Sub2	0 (0%)		107 'C		-49.8 kcal		94 / 100	
Atisusti	6 (18%)		87 'C		-37.9 kcal		93 / 100	
Tesla Motor Protein	6 (18%)		97 'C		-49.8 kcal		93 / 100	
Motoring with S...	2 (6%)		107 'C		-53.6 kcal		93 / 100	
Kinesin 2	2 (6%)		107 'C		-55 kcal		93 / 100	
Malagezari	4 (12%)		87 'C		-32.5 kcal		92 / 100	
Default title	1 (3%)		107 'C		-58.4 kcal		92 / 100	
Fiskers Motor P...	1 (3%)		107 'C		-60.6 kcal		92 / 100	
motor2b	4 (12%)		87 'C		-36.7 kcal		92 / 100	
MP-Step2-Z3	8 (24%)		107 'C		-52.6 kcal		92 / 100	
Motopro 2	1 (3%)		107 'C		-60 kcal		90 / 100	
MOD Fiskers D3	1 (3%)		107 'C		-59.8 kcal		90 / 100	
Motoring with S...	2 (6%)		97 'C		-47.2 kcal		90 / 100	
'Title'	6 (18%)		107 'C		-62.2 kcal		90 / 100	
Kinesin 3	1 (3%)		107 'C		-55.7 kcal		90 / 100	
Kinesin 1	1 (3%)		107 'C		-53.8 kcal		90 / 100	
MP2 - GUGA hairpins	0 (0%)		107 'C		-59 kcal		90 / 100	
Fiskers Motor P...	2 (6%)		107 'C		-61.9 kcal		90 / 100	
Fiskers Motor P...	2 (6%)		107 'C		-62.5 kcal		90 / 100	
another step fo...	0 (0%)		107 'C		-56.6 kcal		90 / 100	
ProMo - Bround ...	0 (0%)		107 'C		-50.9 kcal		90 / 100	
Rotom Motor - B...	0 (0%)		107 'C		-55.7 kcal		90 / 100	
Motor Voter 2	0 (0%)		97 'C		-50.5 kcal		90 / 100	
motor2a	5 (15%)		87 'C		-36.7 kcal		90 / 100	
MP-Step2-Z2	3 (9%)		107 'C		-56.4 kcal		90 / 100	
JR_Motor2_Rnd1_Sub1	0 (0%)		97 'C		-51.7 kcal		90 / 100	
try 1	0 (0%)		97 'C		-44.5 kcal		90 / 100	

And it generally looks like it is energetically better to form a big end loop, than to form two small stems with each a loop.

Same pattern here. Lots of GU's in the long stem of the winners and high scorers.

Motor Protein - Step 2

Title	GU Pairs		Melting Point		Free Energy		Synthesis score ▼	
search	min	max	min	max	min	max	min	max
JR_Motor2_Rnd1_Sub2	0 (0%)		107 °C		-49.8 kcal		94 / 100	
Atisusti	6 (18%)		87 °C		-37.9 kcal		93 / 100	
Tesla Motor Protein	6 (18%)		97 °C		-49.8 kcal		93 / 100	
Motoring with S...	2 (6%)		107 °C		-53.6 kcal		93 / 100	
Kinesin 2	2 (6%)		107 °C		-55 kcal		93 / 100	
Malagezari	4 (12%)		87 °C		-32.5 kcal		92 / 100	
Default title	1 (3%)		107 °C		-58.4 kcal		92 / 100	
Fiskers Motor P...	1 (3%)		107 °C		-60.6 kcal		92 / 100	
motor2b	4 (12%)		87 °C		-36.7 kcal		92 / 100	
MP-Step2-Z3	8 (24%)		107 °C		-52.6 kcal		92 / 100	
Motopro 2	1 (3%)		107 °C		-60 kcal		90 / 100	
MOD Fiskers D3	1 (3%)		107 °C		-59.8 kcal		90 / 100	
Motoring with S...	2 (6%)		97 °C		-47.2 kcal		90 / 100	
'Title'	6 (18%)		107 °C		-62.2 kcal		90 / 100	
Kinesin 3	1 (3%)		107 °C		-55.7 kcal		90 / 100	
Kinesin 1	1 (3%)		107 °C		-53.8 kcal		90 / 100	
MP2 - GUGA hairpins	0 (0%)		107 °C		-59 kcal		90 / 100	
Fiskers Motor P...	2 (6%)		107 °C		-61.9 kcal		90 / 100	
Fiskers Motor P...	2 (6%)		107 °C		-62.5 kcal		90 / 100	
another step fo...	0 (0%)		107 °C		-56.6 kcal		90 / 100	
ProMo - Bround ...	0 (0%)		107 °C		-50.9 kcal		90 / 100	
Rotom Motor - B...	0 (0%)		107 °C		-55.7 kcal		90 / 100	
Motor Voter 2	0 (0%)		97 °C		-50.5 kcal		90 / 100	
motor2a	5 (15%)		87 °C		-36.7 kcal		90 / 100	
MP-Step2-Z2	3 (9%)		107 °C		-56.4 kcal		90 / 100	
JR_Motor2_Rnd1_Sub1	0 (0%)		97 °C		-51.7 kcal		90 / 100	
try 1	0 (0%)		97 °C		-44.5 kcal		90 / 100	

The GU overweight doesn't happen in the Chicken lab splayed lab. It seemingly favor happening in labs with extremely long stems.

Cloud Lab 18 - Anaconda About to Poop by SpaceFolder

Title	GU Pairs		Melting Point		Free Energy		Synthesis score ▼	
search	min	max	min	max	min	max	min	max
Snake Oil 4	8 (27%)		107 °C		-53.32 kcal		98 / 100	
Snakiest	3 (10%)		107 °C		-54.42 kcal		98 / 100	
The Key v.2	2 (7%)		97 °C		-44.92 kcal		98 / 100	
Combination Mod	2 (7%)		107 °C		-46.52 kcal		98 / 100	
Wacky Anaconda ...	2 (7%)		107 °C		-49.92 kcal		98 / 100	
Meechl's CL 18.2	0 (0%)		87 °C		-38.02 kcal		98 / 100	
The Key Revised	2 (7%)		97 °C		-47.42 kcal		98 / 100	
Janet's Lab 18	0 (0%)		97 °C		-43.72 kcal		98 / 100	
The Contender	6 (20%)		107 °C		-56.52 kcal		98 / 100	
CL18.2	5 (17%)		107 °C		-56.72 kcal		97 / 100	
LongUn - LROppy...	3 (10%)		107 °C		-54.42 kcal		97 / 100	
The other guy -...	5 (17%)		107 °C		-53.72 kcal		97 / 100	
Python	2 (7%)		107 °C		-60.12 kcal		97 / 100	
Flipped Contender	5 (17%)		107 °C		-54.22 kcal		97 / 100	
oneAAAA	0 (0%)		107 °C		-49.72 kcal		97 / 100	
design5	5 (17%)		107 °C		-51.72 kcal		97 / 100	
Design 2	2 (7%)		97 °C		-45.22 kcal		97 / 100	
Ergeiser	0 (0%)		99 °C		-45.8 kcal		97 / 100	
JR Lab mod	3 (10%)		107 °C		-49.12 kcal		97 / 100	
Wacky Blue/Gree...	0 (0%)		97 °C		-36.92 kcal		97 / 100	
Wacky Blue Anac...	0 (0%)		107 °C		-39.92 kcal		97 / 100	
Mod of my Anaco...	0 (0%)		97 °C		-41.32 kcal		97 / 100	
Default title	7 (23%)		97 °C		-31.72 kcal		97 / 100	
Mat - Mod of JR 97%	4 (13%)		107 °C		-47.42 kcal		97 / 100	
JR_Lab18_Submit3	3 (10%)		97 °C		-45.92 kcal		97 / 100	
JR_Lab18_Submit2	4 (13%)		97 °C		-45.42 kcal		97 / 100	
The Straight Poop	0 (0%)		107 °C		-49.72 kcal		96 / 100	
CL18P3v1	0 (0%)		87 °C		-29.32 kcal		96 / 100	
Double Flipped ...	5 (17%)		107 °C		-53.62 kcal		96 / 100	
My Contender +	5 (17%)		107 °C		-56.82 kcal		96 / 100	
Mod of The Cont...	5 (17%)		107 °C		-55.42 kcal		96 / 100	
My Contender	6 (20%)		107 °C		-56.32 kcal		96 / 100	
JR - The contender	2 (7%)		107 °C		-50.72 kcal		96 / 100	
Lab 18	6 (20%)		107 °C		-56.62 kcal		96 / 100	
Contender Mod 1	6 (20%)		107 °C		-53.82 kcal		96 / 100	
Snakeskin Const...	2 (7%)		107 °C		-55.82 kcal		96 / 100	
Dungeon #4	0 (0%)		97 °C		-43.32 kcal		96 / 100	

26 August 2013

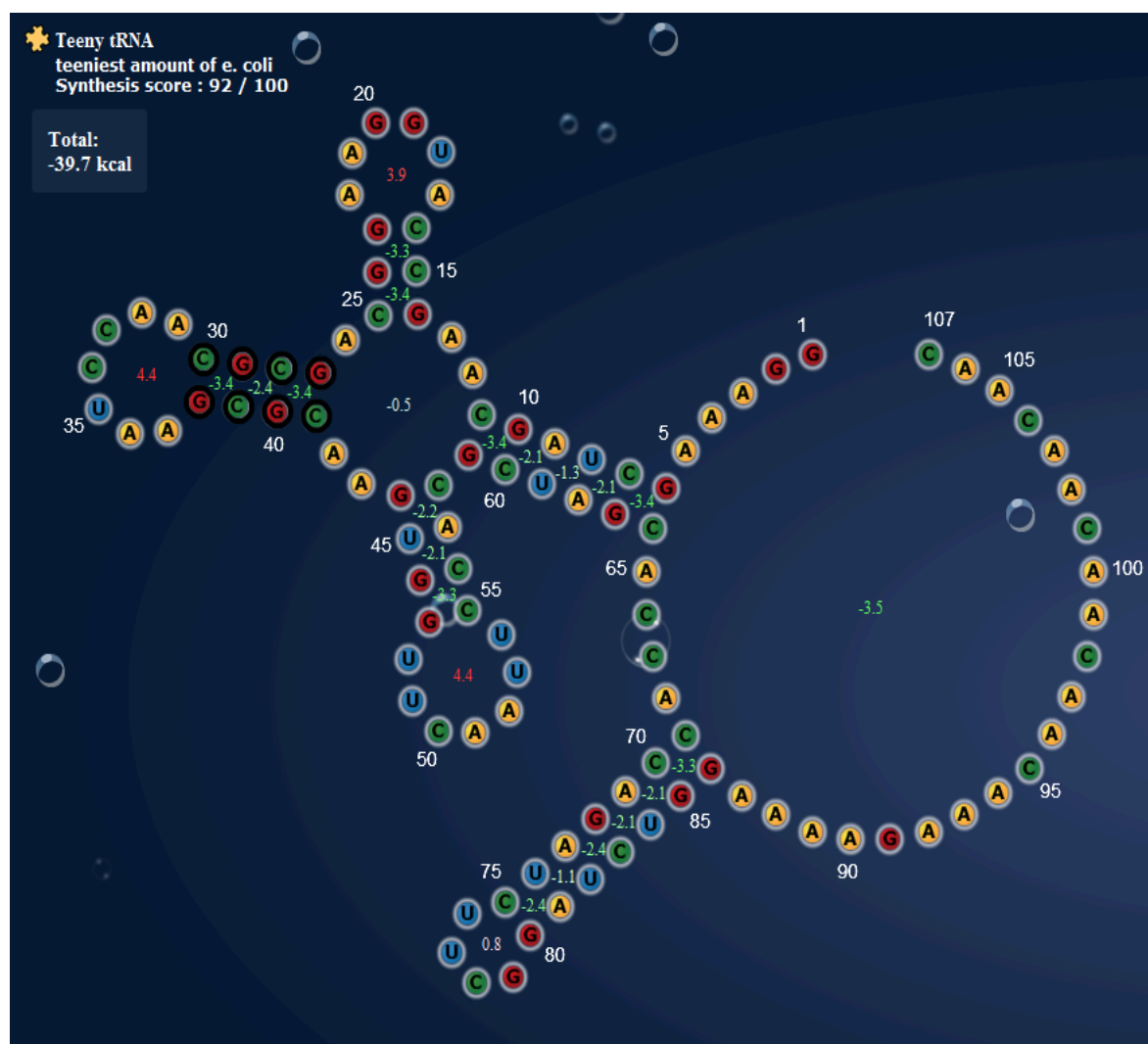
Teeny tRNA

Interesting enough it looks like this adjacent spot is more than content with following usual

[illegible]

Title	Synthesis score ▾		Sequence
search	min	max	search
teeny trouble	100 / 100		G G A A A G C A U G C A A G C C A U G G A A G G C A G C U C G A C C U A A G A G C A A G A G G U U C A A
Mod of Teeny tRNA	98 / 100		G G A A A G G A G C C A A G G C A U G G A A G C C A G U C G A C C U A A G G A C A A G C U U U C A A
Mat - Teeny tRNA	98 / 100		G G A A A G C A G U C A A G G C A U G G A A G C U C A G C U A A C C U A A G A U C A A G C A U U C A A
Teeny rRNA V2	96 / 100		G G A A A G A G A G C A A G U C A U G G A A G A C A G C U C A A C C U A A G A G C A A G C A G U U C A A
Teeny t V3	96 / 100		G G A A A G G A U C A A G G C A U G G A G C C C A G U G C G A C C U A A G G A C A A G U C U U C A A
spider	96 / 100		G G A A A G U A G A C A A G A G A U U G G A C C U C A G U U G C G A C C U A A G G A C A A G C C U U C A A
Turtle	96 / 100		G G A A A G A U A G C A A G U C A U G G U A G A C A G A C G U U C C U U A G U G C A A G C G G C U U C A A
Mini tRNA - Bro...	96 / 100		G G A A A G C G C A C A A G C C A U G G U A G G C A G C G C A A C C U A A G G C G A A G G C G U U C A A
Modification 2	94 / 100		G G A A A G C A G U C A A G A C A U G G A A G C U C A G C U A A C C U A A G A U C A A G C A C U U C A A
Mote	94 / 100		G G A A A G U G C U C A A G U C A U G G A A G A C A G U G C G A C C U A A G G A C A A G U G U U C A U
Christmas tRNA	94 / 100		G G A A A G U C U C A A A G C C A U G G U A G G G A G C G C G A A C C U A A G G C A A G A G C U U C A A
Itsy Bitsy Teen...	93 / 100		G G A A A G C A U G C A A G C C A U G G U A G G C A G U G C G A C C U A A G G A C A A G G C G U U C A C
teeniest amount...	92 / 100		G G A A A G C U A G C A A G C C A U G G A A G G C A G C G C A A C C U A A G G C A A G U G G U U C A A
Told U So	92 / 100		G G A A A G C U G A C A A G C C A U G G U A G G C A G G A C A A C C U A A G U C A A G U C G C U U C A A
Fiskers Teeny tRNA	90 / 100		G G A A A G C A G U C A A G C C A U G G A A G C C A G A G C G A C C U A A G G U C A A G C U G U U C A A
Bite Sized RNA ...	90 / 100		G G A A A G A C U A C A A G C C A U G G A A G G C A G A G C A A C C U A A G G U C A A C U C G U U C A A
Pygmy tRNA - Br...	89 / 100		G G A A A G U A A U A A G A C A U G G U A G U C A G U A C G A C C U A A G U A C A A C A C U U C U C A A
Not Pretty	88 / 100		G G A A A G C U A G C A A G C C A U G G A A G G C A G A G C A A C C U A A G G U C A A G G A C U U C A A
Crossroads III	86 / 100		G G A A A G C U G C A A G C G A U G G U A G C C A G C G C G A C C U A A G G C A A C G C C U U C A A
Teeny 13-19	85 / 100		G G A A A G C A U G C A A G G C A U G G A A G C C A G C A G A C C U A A C U G C A A C A C C U U C A A

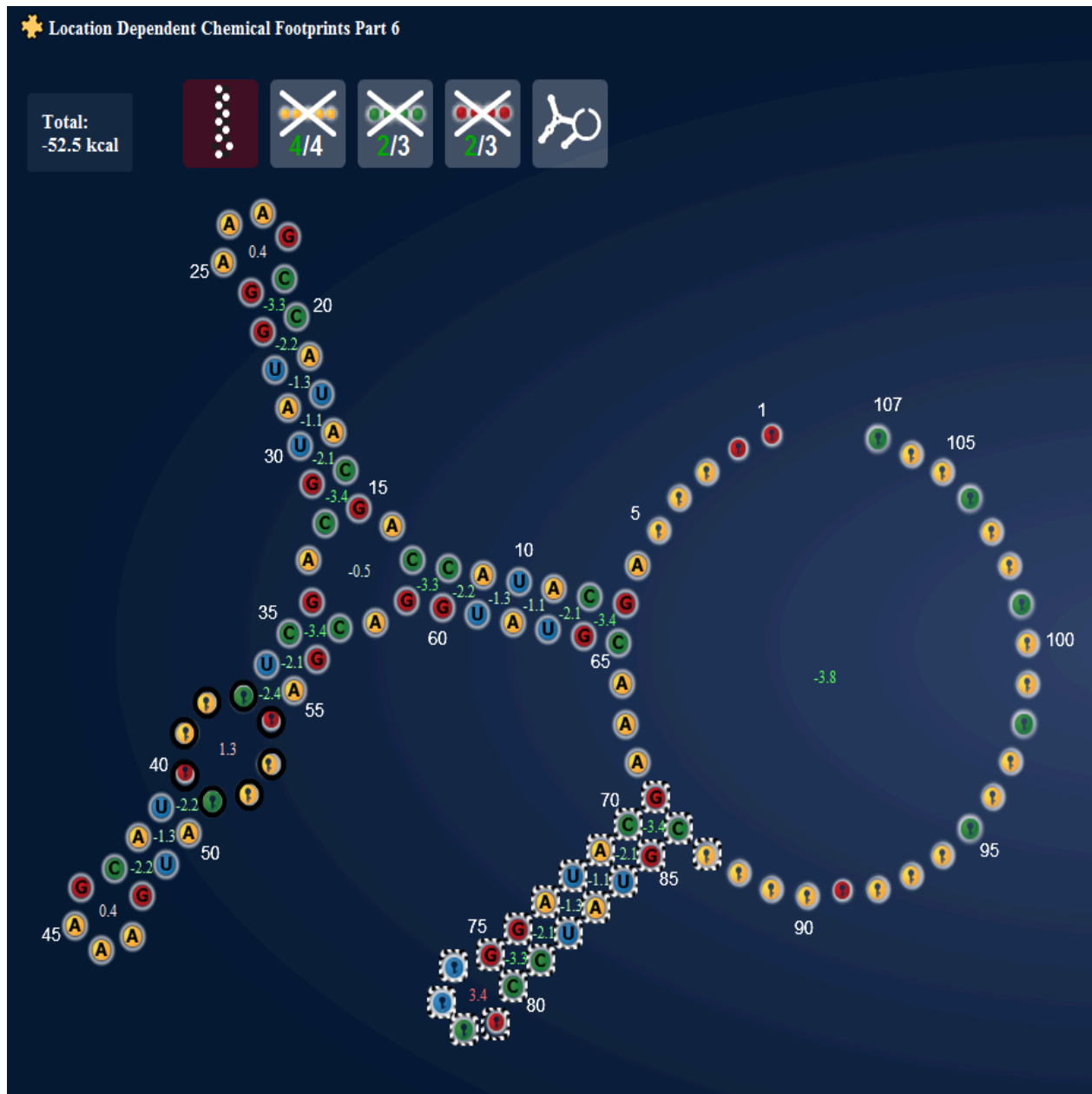
I think this pattern in a 4 nt stem, opens up to misfolding. I saw it misfold in other designs too.



Estimate

Location dependant chemical Footprints Part 6

I also find the results of this experiment interesting. Notice the marked/locked bases area.



Now look at the SHAPE data for this area (marked with orange) It is different for these locked area though they are identical. Backing basepairs do have effect.

Location Dependent Chemical Footprints Part 6			
Title	Synthesis score ▼		Sequence
search	min	max	search
FP Perfection	96 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Bigfootprints 1...	94 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Fiskers RNA foo...	94 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Chemical footprints	94 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Diri	93 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Mat - Location ...	93 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
JR_LocDep_06_Rn...	93 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
LDCF6-C - Brou...	93 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Mod of Broud	92 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Broud's Footpr...	90 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
LDCF6-B - Brou...	90 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Eli mod	89 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Bigfootprints 1...	89 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
loca-6	89 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
LDCF #2	89 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Footprints II	89 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Mod of Zanna's ...	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Chemical Depend...	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Mod of Zanna's ...	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
crystal clear f...	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Solaerin	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Gelearaqu	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Leinquus	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
JR_LocDep_06_Rn...	88 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
LDCF #1	86 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Qubereanis	86 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Setting Q(Pl. 6)	86 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Setting A(Pl. 6)	86 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
LDCF6-2	86 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
stable solution...	85 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
crystal beach w...	85 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
LDCF6-A - Brou...	85 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Bigfootprints 1...	84 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Fiskers RNA foo...	82 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Ortece	82 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Chemfoot	82 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
Alpha B	82 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
JR_LocDep_06_Rn...	81 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
LDCF6	80 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA
ChemFipmtPrt6d...	80 / 100		GGAAAA GCAUAGCAGGUAUCGAAAA GGUUAGCAGC CAAAGUACGAAA GUA CAAAGCAGGUA

It is the same for the others in the same series.

However there is a problem with the lab data in general. Broud noticed:

Chatlog 25 Aug 2013

Broud: <http://prntscr.com/1nevq9> - Unlucky, as per usual [0:42 AM]

Broud: weird, the barcode in that lab was exposed for many designs, hmm [0:44 AM]

Eli Fisker: And it looks like it is not just that one lab you mentioned that got troubles with the barcodes. Those I checked, look more shaky than usual [2:01 AM]

Broud: @ Eli - exposed barcodes were common in this round, not sure why though. Nando probably still has his theories [2:05 AM]

Eli Fisker: Hi Mat, checking [2:06 AM]

Brouard: I'm slightly more interested in the CGGAAACG tetraloop now though [2:06 AM]

Nando: nope, I'm completely baffled actually [2:07 AM]

Nando: hi guys [2:07 AM]

Brouard: Could be experimental noise in the barcode, but at this level and number of designs? [2:08 AM]

Nando: very strange, yes [2:08 AM]

Eli Fisker: I don't know what is causing it either [2:09 AM]

Nando: I observed a case that just doesn't make any sense [2:09 AM]

Eli Fisker: Mat, mail back [2:09 AM]

Eli Fisker: Let us see, Nando [2:09 AM]

Nando: and I'm pretty sure that's not the only one [2:09 AM]

ElNando888: http://eterna.cmu.edu/sites/default/files/chat_screens/49507_1377475834.png [2:10 AM]

Nando: the Us pair, but not the CGs?? [2:11 AM]

Brouard: indeed [2:12 AM]

Eli Fisker: Ah, in the barcode [2:12 AM]

Nando: yes [2:12 AM]

Eli Fisker: I have noticed for this batch that it is often at the bottom and top of the barcode the split happens [2:12 AM]

Eli Fisker: This is a more extreme case of that, I'm guessing [2:12 AM]

Nando: wow, it's global in that lab it seems [2:14 AM]

Brouard: hmmm [2:14 AM]

Nando: many similar cases [2:14 AM]

Brouard: according to the rmdb, the reactivity error is only around .15 [2:15 AM]

Eli Fisker: <http://prntscr.com/1nffsi> [2:15 AM]

Eli Fisker: also many of the GC's in trouble [2:15 AM]

Brouard: could be a temperature spike [2:16 AM]

Eli Fisker: From what I see so far it is the whole batch that has some trouble in the barcode [2:16 AM]

Eli Fisker: That could explain why it happened at the same spot in all designs [2:17 AM]

Eli Fisker: Lucky that it wasn't in the main design then [2:17 AM]

Brouard: Well, I have no clue :) [2:17 AM]

Eli Fisker: But nice guess [2:18 AM]

Nando: melting points all very high in that lab, incomplete denaturation? [2:19 AM]

Brouard: hmmm [2:20 AM]

Eli Fisker: It is typical with high melt [2:20 AM]

Eli Fisker: for long stems [2:20 AM]

Eli Fisker: So labs with long stems have a higher frequency of the 107 melt ones [2:20 AM]

Eli Fisker: than average [2:20 AM]

Nando: longer stacks are more stable, usually [2:21 AM]

Eli Fisker: And that doesn't explain why the barcodes also looks shaky in the other labs. (Though this lab is real bad) [2:21 AM]

Eli Fisker: Yes [2:21 AM]

Brouard: I'm slightly more interested in this though <http://prntscr.com/1nfh06> [2:21 AM]

Eli Fisker: I'm interested in this: [2:22 AM]

Eli Fisker: <http://prntscr.com/1nfh94> [2:22 AM]

Brouard: The barcode overall is a rather nasty score changer, one of you should send Rhiju an email, since this is more in their realm of investigation [2:22 AM]

Nando: mysterious as well [2:22 AM]

Eli Fisker: The further to the right, the more shaky the data becomes [2:23 AM]

Eli Fisker: I will send him our chatlog discussion [2:23 AM]

Brouard: Even better Nando - <http://prntscr.com/1nfhe0> - happened twice :) [2:23 AM]

I looked through the labs again, in order, when I found this oddity. It almost looks like they grow worse and worse. But not quite. However It do looks like that each series of lab has its own error pattern in the barcode. I marked the visible stretch of the barcode hairpin with orange. Teeny tRNA is the only lab with normal looking barcode.

Teeny tRNA				Me	Roadmap
Title	Synthesis score ▾		Sequence		
search	min	max	search		
teeny trouble	100 / 100		GGAAA GCAUGCAA GCAUGGAA GGCAGCUC GACCUAA GA 40 AA GAGGUUCAAUU UCUGGCAUG ACCA CGAGAUC JUCG		
Mod of Teeny tR...	98 / 100		GGAAA GGAGUCAAG GCAUGGUA GGCAGUCC GACCUAA GGACAA CGUCUUCAAAUG ACGGGACUCC ACCA CGUGUCC JUCG		
Mat - Teeny tRN...	98 / 100		GGAAA GCAUGCAA GAGAUUGAA CUCAGAUCAA CCUAA GAUCAAG GCACUUCAAAUG UUGCGACUCC ACCA GACGAUG JUCG		
Teeny rRNA V2	96 / 100		GGAAA GAGAGCAA GUCAUUGAA GACAGCUC AACCUAA GACAA GCAUUCAAAUG UCUGCGUCUCC ACCA CUAGUAU JUCG		
Teeny t V3	96 / 100		G AAAA GGAUCCAA GGC AUGGAC GGCAGUGG GACCUAA GCACAA GUCCUUCAAA GGCACGGAUCC ACCA CCACACG JUCG		
spider	96 / 100		GGAAA GUAGACAA GAGAUUGAC CUCAGUGG GACCUAA GCACAA GACCUUCAAAUG UUGUGUCUAC ACCA CAUCUGA JUCG		
Turtle	96 / 100		GGAAA CAUAGCAA GUC AUGGUAG ACAGCAC GUCCUAA GUGCAA CGGCUUCAAAUG GCGGCUAUC ACCA CCUCAAC JUCG		
Mini tRNA - Bro...	96 / 100		GGAAA GUCGACAA GCAUGGUA AGCAGCGAAC CUAA GCGCAA GCGCUUCAAAUG GCGGCUCCAC ACCA CCGCAUC JUCG		
Modification 2	94 / 100		GGAAA GCAUGCAA GAGAUUGAA CUCAGUCC AACCUAA GAUCAAG GCACUUCAAAUG UUGCGACUCC ACCA CCGCAUC JUCG		
Mote	94 / 100		GGAAA GUGCUCAA GUCAUGGAA GACAGUGG GACCUAA GCACAA UUGGUUCAAUU CCACGACCA ACCA GACUCCG JUCG		
Christmas tRNA	94 / 100		G AAAA GCUCACAA ACC AUGGUU GGGAGCGG AACCUAA CGGCAA GAGCUUCAAA GCGUCUGAC ACCA CUGCGUG JUCG		
Itsy Bitsy Teen...	93 / 100		GGAAA CCAUGCAA GCC AUGGUAG GCGAGUGG AACCUAA GCGCAA GCGCUUCUUU CCGCGCUAC ACCA CCGCAAG JUCG		
teeniest amount...	92 / 100		GGAAA CCAUGCAA GCC AUGGAA GGCAGCGAAC CUAA GCGCAA GCGCUUCAAAUG CCGCGCUAG ACCA CCGCAAG JUCG		
Told U So	92 / 100		GGAAA CCUGACAA GCAUGGUA AGCAGGAC ACCCUAA CUCCAA GUCCUUCAAAUG GAGCGUCCAC ACCA CCGUACG JUCG		
Fiskers Teeny tRNA	90 / 100		G AAAA GCAGACAA GGC AUGGAA GGCAGCG AACCUAA CCUCAA CUGUUCAAAUG CACGGACUCC ACCA CACUACG JUCG		
Bite Sized RNA ...	90 / 100		GGAAA GACUACAA GGC AUGGAA GGCAGG AACCUAA CCUCAA CUGGUUCAAAUG GAGGGUAGUAC ACCA CACGUAG JUCG		
Pygmy tRNA - Br...	89 / 100		GGAAA GUAAUCAA GAC AUGGUA AGCAUA GACCUAA GUACAA CAUCUUCAAAUG GAUGGAUAC ACCA CUUGAUC JUCG		
Not Pretty	88 / 100		GA AAA GCUUACAA GCAUGGAA GGCAGG AACCUAA GCGCAA GCGCUUCAAAUG UCCGCUUAC ACCA CUUAGUC JUCG		
Crossroads III	86 / 100		GGAAA CUGGCAAG GGAUGUA CCGAGCG AACCUAA GCGCAA GCGCUUCAAAUG GCGGCGAGC ACCA GUUACAC JUCG		
Teeny 13-19	85 / 100		G AAAA GCAUGCAA GGC AUGGAA GGCAGG AACCUAA CU GCAA CACCUUCAAC GUGGCGAUGCA ACCA CGUUGGC JUCG		

Location Dependent Chemical Footprints Part 6				Me	Roadmap
Title	Synthesis score ▾		Sequence		
search	min	max	search		
FP Perfection	96 / 100		GGAAA GCAUACCA GCAUAC 20 GAAA GCUAUGCA GCUAA 40 GAAAGUAACA GAGCAG GCUAUGC 60 AAA GCAUACG JUCG		
Bigfootprints 1...	94 / 100		GGAAA GCAUACCA GCAUAC GCGAAA GCUAUGCA GCUAA GAGCGUAACA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Fiskers RNA foo...	94 / 100		GGAAA GCAUACCA GCAUAC GCGAAA GCUAUGCA GCUAA GAGCGUAACA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Chemical footprints	94 / 100		GGAAA GCAUACCA GCAUAC GCGAAA GCUAUGCA GCUAA GAGCGUAACA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Dini	93 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Mat - Location ...	93 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
JR_LocDep_06_Rn...	93 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
LDCF6-C - Brour...	93 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Mod of Brourd	92 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Brourd's Footpr...	90 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
LDCF6-B - Brour...	90 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Eli mod	89 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Bigfootprints 1...	89 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
loca-6	89 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
LDCF #2	89 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Footprints II	89 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Mod of Zanna's ...	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Chemical Depend...	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Mod of Zanna's ...	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
crystal clear f...	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Solaerin	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Gelearaq	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Leinquus	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
JR_LocDep_06_Rn...	88 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
LDCF #1	86 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Qubereanis	86 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Settling Q(Pt. 6)	86 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Settling A(Pt. 6)	86 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
LDCF6-2	86 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
stable solution...	85 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
crystal beach w...	85 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
LDCF6-A - Brour...	85 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Bigfootprints 1...	84 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Fiskers RNA foo...	82 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Ortece	82 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Chemfoot	82 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
Alpha B	82 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
JR_LocDep_06_Rn...	81 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
LDCF6	80 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		
ChemFtpmtPrt6d...	80 / 100		GGAAA GCGGAAU GUGUAAG GAAA CUUAACCA GUACAA GAGCAAG GCUAUGC AAA GCAUACG JUCG		

94

Free Energy		Title	Synthesis score ▾		Sequence
min	max		min	max	
		search			search
29.2 kcal		Design III	94 / 100		G G A A A A G U A C A A G A U G A G A U A C A A A G U A U A U C A G U A U A U C A A A A G A U A U A A C A U C A A A G U A C A A A G A A U U U G U U
54.4 kcal		Zanna's Footprint I	94 / 100		G G A A A A G U G C A A G C A C A G U U G U G G C A A A C C A U A G C A C G U G U G G A A A C A U A U C A G U G C A A G C A C A A A C G U G U A C U U
47.1 kcal		Mat - Location ...	93 / 100		G G A A A A C U C A A A G U A C A G U A U A C G G A A A C G U A U A U C A G U A G U C G A A A G A U G U A C A G U A C A A G A G C A A A C G A C U U U U
42.9 kcal		Footprints by Z	93 / 100		G G A A A A G U G C A A G C G C A G A U G U A G U U C G C U A U A U C A C A U G U A C U U C G U A U A U A G C C C A A G C A C A A A C G U G U A C U U
52.7 kcal		LDCF 4-C - Brou...	93 / 100		G G A A A A G A G C A A G G A C A G C A G A C G U C U A C G U C U G C A G A C C U G U C U A A C A G C G U C A G U C C A G C U C A A A A G C U C A A A A G C A C A C U U
48.3 kcal		chemical footpr...	92 / 100		G G A A A A G A G C A A G A U C A C U A U A U C G A A A G A U A U A G A G A U A A U G A A A C A U U A U C A G A U C A A G C U C A A A G C A C A G C U U
53.3 kcal		LDCF 4-B - Brou...	92 / 100		G G A A A A G A G C A A G G A C A G C A G A C C U C U A G G U C U G C A G A C C U G C U C U A G C A C G U C A G U C C A A G U C G A A A G U C G A U C U U
61.3 kcal		mod of Janet 'w...	90 / 100		G G A A A A G C A C A A G C U C A G C U G U G C A A A G C A C A C A C A G G U G U G G A A A C A C A C C A G A G C A A G U G C A A A G U G A A A A G U C G A U C U U
57.1 kcal		Fiskers RNA foo...	90 / 100		G G A A A A G C A C A A G U C C A G U A G U A C A A A G U A C U A C A G A C A U G C G A A A C A U G U C A G G A C A A G U G C A A A C C A G G U C U U
54.1 kcal		LD - #2	90 / 100		G G A A A A G A G C A A G G A C G C A G A U C G U A A G G U C U G C A G A C C U G C G U A A G A U G U C A G U C C A A G C U C A A A C A G A A C U U
50.5 kcal		Mat - Location ...	90 / 100		G G A A A A G C U C A A G U A C A G U G U A U G A A A C A U A C A C A G U A G A U C G A A A G A U C U A C A G U A C A A G A C A A A G C U G G A C U U
49.54 kcal		Remaceon	90 / 100		G G A A A A U A U C A A G U C A A C C C G U G C A U C A G C A C G G G A G U A U C G C A A U A G C G A U C A U G A C A A G A U A A A C A G U G U C U U
40.24 kcal		Dilegeenti	90 / 100		G G A A A A C U A C A A G C U U A U U A U C A C A A C A G U C A U A A C U U U A U C A U C A G A U A A G A A A G C A A G U A G A A A G U U G C G C U U
57.2 kcal		Settling Q(Pl. 4)	90 / 100		G G A A A A G C A C A A G U G C A C C A U A G G G A A A C C U A U G A C C C A U A G G G A A A C C U A U G G A C C A A G U G C A A A G G G U G U C U U
28.8 kcal		Rinbeon	90 / 100		G G A A A A C U U C A A G U U C A G U U A U U G A A A C A A U A A C A C U U U A U C A A A A G A U A A G A G A A C A A G A A G A A A C U G G U U C U U
29.2 kcal		Rebibi	90 / 100		G G A A A A C U U C A A G U U C A G U U A U U G A A A C A A U A A C A C U U U A U C A A A A G A U A A G A G A C A A G A A G A A A C U U A U U C U U
55.2 kcal		Chem FlpmtPr4...	90 / 100		G G A A A A G U A C A A G U A C A G A C U C A C G A A A G U G A G U C A G A G U C A C G A A A G U G A C U C A G U A C A A G U A C A A A G G C G G C U U
60.1 kcal		LDCF 4-A - Brou...	90 / 100		G G A A A A G A G C A A G G A C A G C A G A C C A A A G G U C U G C A G A C G U G C G A A A G C A C G U C A G U C C A A G C U C A A A G A C G U A C U U
60 kcal		ldcf 4	89 / 100		G G A A A A G C A C A A G C A C A G C U C U G C G A A A G C A G A G C G C C A C A G C G A A A C U G U G G A G U G C A A G U G C A A A C C A G A A C U U
58.2 kcal		Four Footprints	89 / 100		G G A A A A G C A C A A G C A C A G C U C U G C U A C G G C A G A G C G C C A C A G C U A C G G C U G U G G A G U G C A A G U G C A A A C C U C A U C U U
35.9 kcal		Meechi LDCFP 4	89 / 100		G G A A A A G U A C A A G U U C A G U U A U U C A A A A G A A U A A C A G A U U A C A A A A G U U A A U C A G A A C A A G U A C A A A G U G A A C C U U
55.4 kcal		Settling A(Pl. 4)	89 / 100		G G A A A A G C A C A A G A C C A G G U A U C G G A A A C G A U A C A C A G G U A U C G G A A A C G A U A C C A G G U C A A G U C G A A A G G C U A U C U U
60.9 kcal		Who left that f...	88 / 100		G G A A A A G C A C A A G C A C A G C U G U G C G A A A G C A C A G C A G G U G U G C G A A A G C A C A C C A G U G C A A G U G C A A A G G A C A U C U U
53.9 kcal		Fiskers RNA foo...	88 / 100		G G A A A A G C A C A A G U A C A G U A G U A C U A A A G U A C U A C A G A C G A U C G A A A G A U C G U C A G U A C A A G U G C A A A G A C C G A C U U
52.7 kcal		footprint Part 4	88 / 100		G G A A A A C U G C A A G C U C A G A U C U A C G A A A G U A G A U C A G A U C U A C G A A A G U A G A U C A G A G C A A G C A G A A A G G U C A A C U U
56.3 kcal		LD - #1	88 / 100		G G A A A A G A G C A A G G A C A G C A G A U C G A A A G G U C U G C A G A C C U G C G A A A G C A U G U C A G U C C A A G C U C A A A G A C U U C U U
48.6 kcal		chemical footpr...	88 / 100		G G A A A A G A G C A A G A U C A C U A U A U C G A A A G A U G U A G A G A U G A U G A A A C A U U A U C A G A U C A A G C U C A A A G G A G U G C U U
52.9 kcal		Mat - Location ...	88 / 100		G G A A A A G C U C A A G U A C A G U G U A U G G A A A C A U A C A C A G C A U A G C G A A A G C U A U G C A G U A C A A G A G C A A A G C U G U A C U U
57.2 kcal		Settling F(Pl. 4)	88 / 100		G G A A A A G G U C A A G A G C A G C U A A C C G A A A G G U U A G C A G C U A A C C G A A A G G U U A G C A G C U C A A G A C A A A G G G U A U C U U
47.4 kcal		Beautiful Footprint	88 / 100		G G A A A A G A G C A A G U G C A G G U G U G C G A A A C G A U A C A C A U G C G U G A G A G G G U A U G G C A A A G G C A A A G C U A U G C U U
64.3 kcal		Bigfootprints 1...	86 / 100		G G A A A A G G U C A A G A C C A G G A G A G G G A A A C C U C U C C A G C U C U G G A A A C C A G A G C A G G U C A A G A C C A A A G C C U C U C U U
62.8 kcal		Lay down Sally	86 / 100		G G A A A A G A C A A G G A C A G U G G U C C G A A A G G A C C A C A G G A C A C G G A A A C G U G U C A G U C C A A G U C C A A A G U G C A G C U U
60.4 kcal		Bigfootprints 1...	85 / 100		G G A A A A G A G C A A G A C A G G A G A G G U A A A C C U C U C C A G C U C U G G A A A C C A G A G C A G U G C A A G C U C A A A G U G U G A G U U
53.7 kcal		Brouard's Footpr...	85 / 100		G G A A A A G C U C A A G A G C A G U A U G U C U A A A G A C A U A C A G A G U A U C G A G A G A U A C U C G C U C A A G A G A A A G U G A C G C U U
57 kcal		FP-4	85 / 100		G G A A A A G C U C A A G A U C A G G U A U C G G A A A C G A U A C C A G C U A U G C G A A A G C A U A C A G A U C A A G A G C A A A G C U G G U C U U
49.11 kcal		Inondidi	85 / 100		G G A A A A U G G C A A G A A U A G A A U A G G A C A C C U A U U C G A G G G A C A A C A G U C C C U C A U U C A A G C C A A A C G A G U C G C U U
47.6 kcal		Location Depend...	82 / 100		G G A A A A U G C A A G U G C A G A U G C A G G A A A C U G C G U C A G C A G U A C A A A G U G C U U C A G U A C A A G C C G A A A G C U U G G C U U
50.2 kcal		Parts are Parts 4	81 / 100		G G A A A A G A C A A G U A C A G C U A U G C G A A A G C A U A G C A G C A U A G C G A A A G C U A U G C G A U A C A A G U C G A A A G C U C G U A U U
59.1 kcal		JR_LocDep_04_Rn...	81 / 100		G G A A A A G C A C A A G C A C A G U G C U G U A C G G C A G C A C A G C A C A G C U A G C G C U G U G C A G U G C A A G U G C A A A G C U C A C U U
31.1 kcal		Dierite	78 / 100		G G A A A A G C U C A A G U U C A G U U A U U G A A A A C A G U G A C C U U U A U C A A A A G A U G A A G A A C A A G A U G A A A C U G U U C U U

Title	Synthesis score ▾	Sequence
search	min max	search
Mat - Location ...	94 / 100	GGAAAA G C A G A G U A C A A G U A G G A A A C U A C A A G U A C A G A U C A A G U G C G A A A G C A C A A G A U C A C U G C A A A G C G A U C G U U C G
chemical footpr...	93 / 100	GGAAAA G U C G A G U G C A A G C A G G U G A C U G C A A G C A C A G A G C A A G G U G G U G A C A C C A A G C U C A C G A C A A A G C A A G U C
Starry's Footprints	92 / 100	GGAAAA G A U C A G A U C A A G A A C A A A A G U U C A A G A U C A G A A C A A G U A C A A A A G U A C A A G U U C A G A U C A A A G A U U A G C U U C G
Meechl LDCF P3	92 / 100	GGAAAA G C U C A G U A C A A G U U C G A A A G A A C A A G U A C A G A U C A A G U A C U A A A G U A C A A G A U C A G A G C A A A C A U U G A C U U C G
LDCF 3A - Brour...	92 / 100	GGAAAA G C U C A G U A C A A G U A G G A A A C U A C A A G A U C A G U A C A A G A U C G A A A G A U C A A G U A C A G A G C A A A C A G C A U G U U C G
722 5	92 / 100	GGAAAA G A C A G U A C A A G U A G G A A A C U A C A A G U A C A G A U C A A G U A G G A A A C U A C A A G A U C A G U U C A A A G A A U U A U U U C G
Bear footprint	90 / 100	GGAAAA G C U C A G A U C A A G U A C G A A A G U A C A A G A U C A G U U C A A G U A C G A A A G U A C A A G A A C A G A G C A A A G U C A A C U U C G
Barefoot footprint	90 / 100	GGAAAA G C U C A G A U C A A G U A C G A A A G U A C A A G A U C A G U A C A A G U A C G A A A G U A C A A G A C A G A G C A A A G A C C U A G U U C G
chemical footpr...	90 / 100	GGAAAA G U C G A G U G C A A G C A G G A A C U G C A A C C A C A G C C A G G U G A A A C A C C A A G C C A C C A G C A C A A G C A U C A C U U C G
Design V	90 / 100	GGAAAA G U A C A G U A C A A G U A C A A A A G U A C A A G U A C A G U A C A A G U A C A A A A G U A C A A G U A C A G U A C A A A C U A U U U G U U C G
One Small Step 3.1	90 / 100	GGAAAA G A G C A G U A C A A G A U C G A A A G A U C A A G U A C A G G U C A A G A G C A A A G C U C A A G A C C A G C U C A A A C C C U A G U U C G
Location Depend...	89 / 100	GGAAAA G A C U A A G U C A A G A U G G A A A C G U C A A G G C U A A G A C A A A G A G G A A A C C U C A A G U C U A A G U C A A A C U G A G U C U U C G
LDCF P3 V2	89 / 100	GGAAAA G A U C A G A U C A A G A U C G A A A G A U C A A G A U C A A G A U C A A G A U C G A A A G A U C A A G A U C A A G A U C A A A G U C A A G C U C A G U U C G
Mat - Location ...	89 / 100	GGAAAA G C A G A G U A C A A G A A A A C U A C A A G U A C A G A U C A A G A U C A A G A U C G A A A G A U C A A G A U C A C U G C A A A G C C U A G U U C G
ChemFIPrtPrt3de...	89 / 100	GGAAAA G C C A G C A C A A G A G C G A A A G C U C A A G U G U A G G A A A G U A C G A A A G U A C A A G U C U A G G C A A A G U G G G C G U U C G
Gemini Three	89 / 100	GGAAAA G U A C A G A U C A A G U G U A A C A U C A A G A U C A G A U C A A G U A C G A A A G U A C A A G A U C A G U A C U A A G A G U U G C U U C G
Chemical depend...	88 / 100	GGAAAA G C G C A G C G C A A G C G C A A A A G C G C A A G C G C A A G C G C A A G C G C A A G C G C A A G C G C A A A C C G G G U C U U C G
Anveshna's LDC 3	88 / 100	GGAAAA G C C G A G A C C A A G C U C A A A A G C A A G G U C A G A C C A A G G A C A A A A G U C C A A G C U C A G G G C A A A G G U C U G G U U C G
LD - #3	88 / 100	GGAAAA G C U C G A C C A A G U A G G A U C C U A C A A G G U C A G U A C A A G A G C G A U C G G U C A A G U A C A G A G C G A A C C C A A G G U U C G
Three Footprints	88 / 100	GGAAAA G C A C A G A G C A A G U C C U A C G G A C A A G C U C G C C U C A A G C U C U A C G A G C A A G A G G A G U G C A A A C C U C U A C U U C G
Setting Q(Pt. 3)	88 / 100	GGAAAA G C G G A G C C A C A A G A G G G A A A C C U C A A G U G A C C C A C A A G A G G G A A A G C U C A A G U G G A C C G C A A A G C G C A G C U U C G
Raoredbid	88 / 100	GGAAAA G G G C G G A C A A G A U A G G A A U A U C A A G U C C A U U C A A G A G G A A G A C C U C A A G U A A A G C C A A A A U G G A U C U U C G
LDCF 3C - Brour...	88 / 100	GGAAAA G C U C A G U C A A G U A C G U A A G U A C A A G G A C A G A U C A A G A C G G U A A C G U C A A G A U C A G A G C A A A G A C G U A G U U C G
summerwave 3	86 / 100	GGAAAA G C A G A C A C C A A G U C G G A G A C G A C A A G G U G A G C U C A A G C U G G A G A C A G C A A G A G C A C U G C A A A C A U G G A G U U C G
Location Depend...	86 / 100	GGAAAA G A C U A G G U C A A G G U G G A A A C A C C A A G A C U A G G A C A A G C A G G A A A C U G C A A G U C U A G G U C A A A C U G A G U C U U C G
Dieresusge	86 / 100	GGAAAA C A U C A C A A C A A G A A G A A A C U U C A A G U U G A C U U C A A G U U C A A A A G A A C A A G A A G A G A U G A A A C U U C U C U U C G
Codependent	86 / 100	GGAAAA G C C C A C U U C A A G G C G A A A A G C C C A A G A A G A G G U C A A G C U G A A A A C A G C A A A G A C C A G G G C A A A G C C U C A C U U C G
LDCF P3 V3	86 / 100	GGAAAA G A U C A G U G C A A G U A C G A A A G U G C A A G U A C A G A U C A A G U A C G A A A G U G C A A G G U C A G A U C A A A G C U G A G G U C G
chemical footpr...	86 / 100	GGAAAA G U C G A G U G C A A G C A G G A G A C U G C A A G C A C A G A G C A A G G U G G A G A C A C C A A G C U C A C G A C A A A G C U A C U C U U C G
One Small Step 3.2	86 / 100	GGAAAA G C U C A G G U C A A G A G C A A A G C U C A A G A C C A G G U C A A G A G C G A A A G C U C A A G A C C A G A G C A A A G C U G U A G U U C G
ChemFIPrtPrt3de...	86 / 100	GGAAAA G C C C A G C G C A A G U U U A A A G A A C A A G C G C A C G G C A G U U U A A A G A A A C A G C C G A G G G C A A A G C G C G G U U C G
Default title	86 / 100	GGAAAA G G G U A G U A C A A G U A C A A A G U A C A G U A C A G G C C A G G C C G A A A G G C C A A G G C C A A C C C A A A C G C A U A U U C G
JR_LocDep_03_Rn...	86 / 100	GGAAAA G C U C A G U G C A A G U A C U U A G G U A C A A G C A C A G A U C A A G A G C U U A G G C U C A A G A U C A G A G C A A A G C A U A G U U C G
JR_LocDep_03_Rn...	86 / 100	GGAAAA C U G C A G C A C A A G A U C U U C G G A U C A A G U G C A C G A C A A G U A C U U C G G U A C A A G U C A G A G C A G A A A C A C U A A C U U C G
Speedy01	85 / 100	GGAAAA G C G C A C U A C A A G C A C G A A A G U G C A A G U A G A G A U C A A G A U C G A A A G A U C A A G A U C A G C G C A A A G A U G C C U U C G
Mat - Location ...	85 / 100	GGAAAA G C A G A G U A C A A G U C G A A A C G A C A A G U A C A G A U C A A G U A C G A A A G U A C A A G A U C A C U G C A A A G C G G A U C U U C G
LDCF 3B - Brour...	85 / 100	GGAAAA G G A C A G A C A A G U C G A A A C G A C A A G U A C A G U C A G G U C A A G C U C G A A A G A G C A A G A C C A G U C C A A A G A C C U A C U U C G
Bearen	84 / 100	GGAAAA C A U C A C A A C A A G A A G A A A C U U C A A G U U G A C U U C A A G U U C A A A A G A A C A A G A G A G A G A U G A A A C U U C U U C U U C G
Parts are Parts 3	84 / 100	GGAAAA C U A G A C A G C A A G A U C G A A A G U A C A A G C U G A G C U C A A G C A C G A A A G U G C A A G A G C A C U A G A A A G C A G C U G U U C G
LDCF P3-2	84 / 100	GGAAAA G C U C A G U A C A A G A C C A A A G G U C A A G U A C A G U U C A A G A U C G A A A G A U C A A G A A C A G A G C A A A G U A U U C U U C G

97

Title	Synthesis score ▾		Sequence
search	min	max	search
SemiCir-5bendsd...	90 / 100		GGAAAA GCAA CUUGAGCGA GAGAGCG CGUC AAGUAG GAAA GCUA UUGAG CGGC CGGCUAGAGU GCA GCGCGUGG UUCG
semicircle boos...	90 / 100		GGAAAA GUCCUAGCUAGCG GAGGAGG GUAGCGUGUGG GAAA GCAC GAGCUACGCC CGCUAGCUAGGAC CAGAUGUUCG
Mat - Semicirc...	90 / 100		GGAAAA CGGAUACUAGCG GAGAGCG CGUUCUACUUG GAAA GCAAUGUAGA GGC CGGAUAGUAGU GCA CAGAUCUCG
U-Turn III	90 / 100		GGAAAA GCAUUAUAGCA GUGAUAGCA GCAGCGGUUG GAAA GCAUUGUGUGGCA CGCUUAUUAUUG CGGGAUAC
Semicircle - R...	89 / 100		GGAAAA GUUUCUAGCGA GAGAGCA CAUUGUACAUU GAAA GUAUUGUAGCAAG GGAUGCGUAUAUC CUGAGAC
Rapids around t...	89 / 100		GGAAAA GAUUUAUUUA CAGAGC GCUUAUUUAUAC GAAA GUUUUUUAUAGGC CGUUAUUUAUAC CAGAUGC
Mostly InSane ~...	89 / 100		GGAAAA GGAUCUACAGCA CAGAGCAG CUCUACUACAG GUUAU CGUUAUUAGAG CCGCGUUAUUCAG CAGUUCUC
U tube	88 / 100		GGAAAA GAGCACA CACUCUGA GAGAGAGA CUACGUAGC UUAUC GAGCGUACG UAGCC CGAGUGUGUGUC CUAUCUCG
mod of janet 5 ...	88 / 100		GGAAAA GACACACACCG GAGAGAGA GUACGUAUCUG GAGAGACGUAUCGUAACCCC CGGUGUGUGUC GGCUGUC
Total green vio...	88 / 100		GGAAAA GUCAUUGACAG CCGCGCG CGGCGUACAUU GAAA GUUAGUACGAGCC CCGUGUACAUGAC CAGCAGC
U-Turn I	88 / 100		GGAAAA GUGUACUAGCG GAGAGAGA GCACGGCGUG GCAA GCGAUGUGUGGCC CGGUGUGUAUAC CCGUGUAC
Wicked U-Turn S...	86 / 100		GGAAAA GCUUAUCUAG CUGAGAGAG CUCUUAUAACA UAGAAA UAUUGUUUAUGGGC CGUAGUAUAUAG CAGUCGUC
Constrained	86 / 100		GGAAAA UUAUCUGUAU GAGAGAGC GUAAUUAUAU GAAA GAUUAUUUAUAGC CCAUUAU CUGAAC CUUUAAC
JR_SemiCircle_5...	86 / 100		GGAAAA GACAGAGUCA GGUACUUCG CAUCUGUAGCA GGUUA CUGCUACGUA GGUAGUGUGAGUCUGUC CAGUCGUC
SeminSane - Bro...	86 / 100		GGAAAA GACUCAGUCA GUGUGUGUG GAUCGUGA GCGA GUUA CUGCUACGUA GGC CGGUAUCUGAGUC CAGUCGUC
Extra Cheese	85 / 100		GGAAAA GUGCGAGCUCU GAGAGAGCA CUAGCGCUGA GAAA CGUCGAGCUGAGGC CACAGCUAGGCAG GAAGCAG
Green violation	85 / 100		GGAAAA GUCGUAUGCAG CAGAGAGAG CUCGACAGUA GAAA GUACUGUGCAGGCCC CGGAUAGCUAGCAG CAGCGUGC
Thales' Theorem 3	85 / 100		GGAAAA GCAUCUGUAG CAGAGAGCA CUCUACAUCU GAAA GAUCAGUAGAGGG GCGCUACGAGUGGC CAUCAUC
Esraareses	85 / 100		GGAAAA UUAUUAUUC GAGAGAGCA UCUGCUAGAG GCUAA CUCUAGCAGAGC CGGCAUUAUAGUA CUGGGCG
Semicircle3	85 / 100		GGAAAA CAUGUGUGUCU GAGAGAGC GCACACAGAG GAAA CCGCUGUGUGGCC CACGCGCGCAUC CUUUAUG
JR_SemiCircle_5...	85 / 100		GGAAAA GUUAGUACA UAGCGAGCGA GAUAUCAAUU CUCUGGAA UGUUAUAGCCC CCUAUUGUACA UAGAGUAUC
Meechl 5 bends	85 / 100		GGAAAA GUAUUAUUAUU GAGAGAGCA UUUUAUGUAU GAAA CAUUUAUUAACCC CAAUAUUAUAC CAGAUUGC
Amperсанд	85 / 100		GGAAAA GCAAAGUAUAG GAGAGUCA CGUGUCAUG AUGAGA GUACAGCAGGGC CGCUAACUGUUGCA CUAUUC
Semi Sane - Bro...	85 / 100		GGAAAA CUGACGCA CUGAGAGAGCA CUAGCCCCAG UGUUA GAUCUGGGCUAGCG CGCAGUCAGUCAG CUAACGAC
Semi-2	84 / 100		GGAAAA GUCGUAUGCA UAGAGAGAG CCGGACAGUA GAAA GUACUGUGCGGCC CGAUGCAGUCGAG GUGGUCC
5 Bends	84 / 100		GGAAAA GACACGAC CUGAGAGAGCA GUACGUACGUG GAGACAGCGUACGUA CCCC CGCAGUGUGUCAG CUCUUC
Bendy Bits	84 / 100		GGAAAA GACUCGUAGCGAGAGAGCA GCUAUCGUA GAAA GAUCGUAUACCCC CCGCUAGCAUUC CAGUAGC
TEST 2	84 / 100		GGAAAA GAAACAAACAG GAGAGAGAG CUACGUAUGUG GAAA CACA UUCGUAAGCC CGGUGUUGGUUCAGAUAC
semicircle boos...	84 / 100		GGAAAA GCUUAGCGUA GAGGAGCG GUAGCGUGUG GAAA GCACGAGCUACCCC CGCUAGCUAGGAC CAGUAUC
Semi Solution	84 / 100		GGAAAA GUUAACAUGA CAGAGAGCG CCAAGACUA GCUAAA GGAUAGUCUUGGC CGGUACUAGUAG CAGUGAAC
Spring of Fox	84 / 100		GGAAAA GCGCGCGCGC GAGAGAGAG CCGCGCGCGCG GAAA GCGCGCGCGCGGCC CGCGCGCGCGCC CAGCGCG
C string with q...	82 / 100		GGAAAA GCUUACGUUAG GAGAGAGAG GAUAGCUUA GCUAAA GCUAUGCUUAACCCC CUAACGUAAG CAGAUUGC
Voting Magnet	82 / 100		GGAAAA CCGCGGGCC GAGAGAGCG CCGCGCGCG GCGAAA GCGCGGGCGCGGCC CGCGCGCGCGCG CAGCAGU
Good kcal	82 / 100		GGAAAA CGCGCGCGCC CAGAGAGAG CAGCGCGCG GCGAAA GCGCGCGCGCGUUC CGUGGGCGCGCG GCGCGCG
SemiCir-5bendsd...	82 / 100		GGAAAA GCGACUGAGCGA GAGAGAGCG CGUACGAA GCUAAA CCUUCGUGAGCGGCC CGCUAGGUGCG CCGCGGG
U-Turn II	82 / 100		GGAAAA GCAUUAUAGCA CAGAGAGCA CGACGCGUUG GCUAAA GCAAUGUGUGGCC CGGUUAUUAUAG CAGUAUC
Arc de Cytomphe...	81 / 100		GGAAAA GCUACUGU UCAGAGAGAG CUAUCUUAAG GCUAAA CCUUAGUAUGGCC CGCUAGUACA UAGCAGUAGC
Hairpin in a ha...	81 / 100		GGAAAA GUCCUAGCGU GAGAGAGAG CAUAGUCGAG CAAAAC CGUGGAGCUAGGCC CACAGCUAGGAC CAGUCCAC
Break Spine	81 / 100		GGAAAA CUAAUUAU GCGAGAGAGCG CGGCUAAUUA UGAGA GUUAUUAGCGCGCC CGGGAAUUAUAG CCGCUUC
S5 - 1	72 / 100		GGAAAC GUGCGUUUUUAAG GAGAGAGC CUAUAUUAU GCUAAA GAUUAUUUAAGC CUAAGAGAUUAC CUAUAUUG

Semicircle - 2 bends				Me Roadmap	
Title	Synthesis score ▼		Sequence		
	min	max	search		
search					
sfltmtpit	90 / 100		GGAAAA	GCUCGAGCGUGCU	20
SC 2B V1	90 / 100		GGAAAA	GGUACUGUGUGCG	20
Two Bulge semi ...	90 / 100		GGAAAA	GCGGAUUGAUUC	20
I've got the da...	89 / 100		GGAAAA	GAGAGUAUGAUCC	20
Circle Sane - B...	89 / 100		GGAAAA	GUCAUACUUAUC	20
AU Zebra Bending 2	88 / 100		GGAAAA	GGAGUGACUGAGA	20
Semicircle - 2 ...	88 / 100		GGAAAA	BUGACGUGCUGUGA	20
Two Bulge semi ...	88 / 100		GGAAAA	GCGGAUUGAUUGA	20
Quasispecies style	88 / 100		GGAAAA	GCGAUUCUAGCAGC	20
Theory	86 / 100		GGAAAC	ACUUGACCUUAUA	20
Mat - Semicirc...	86 / 100		GGAAAA	GCGUAUAGCUAGC	20
I'm Bent III	86 / 100		GGAAAA	GAUGUGGCGUGCGA	20
Klaustro(G-C Ve...	86 / 100		GGAAAA	CAUUAACAUAUU	20
2 bends in the road	85 / 100		GGAAAA	GCUAUGAUUACGA	20
Semi Freddi UACG	85 / 100		GGAAAA	CACUCCCUAUCGA	20
Boomarang	85 / 100		GGAAAA	GCGUAUAGGUUAUG	20
Gnaramoob	85 / 100		GGAAAA	GCGUAUAGGUUAUG	20
Two Bulge semi ...	85 / 100		GGAAAA	GCGGAUUGAUUAC	20
Based on 2XZN	85 / 100		GGAAAA	GAAUUAUGGGAAG	20
Esmaus	85 / 100		GGAAAA	GAUUAUAGGAUAG	20
I'm Bent Two	85 / 100		GGAAAA	GACGUGGCAUGCGA	20
Circle Saneix - ...	85 / 100		GGAAAA	GUCUUAUCUACUG	20
IT	84 / 100		GGAAAA	GUGUAUGGUGAG	20
Leesarve	84 / 100		GGAAAA	CUUUGUUUGUUUC	20
Meechi Semicirc...	84 / 100		GGAAAA	GUUAUGUUUAUUG	20
TEST 2	84 / 100		GGAAAA	GAUGGUGAUCUUC	20
Variation on Qu...	84 / 100		GGAAAA	GCAUUCUAGCAUG	20
Simply Semi	84 / 100		GGAAAA	GCUACUACUACUA	20
AU Zebra Bending 3	82 / 100		GGAAAA	GGAGUGACUGACA	20
bent with blueb...	82 / 100		GGAAAA	GCUACUAGAUACG	20
dntdrstdtn	82 / 100		GGAAAA	GCUCGAGCAUGCU	20
Semi Freddi GAAA	82 / 100		GGAAAA	CGCAUCGCUAUCGA	20
tired of choosing	82 / 100		GGAAAA	GAUAAAUUAUUA	20
Peppermint	82 / 100		GGAAAA	GGAUGCAUGGUGG	20
Semi test Circ...	82 / 100		GGAAAA	CUGACUGGCUAUG	20
bent	81 / 100		GGAAAA	GCUCUUGUUAAGA	20
Thales' Theorem 2.1	81 / 100		GGAAAA	GAUGACUAGAUCA	20
Mat - Semicirc...	81 / 100		GGAAAA	GCGUAUAGGUUAUC	20
I'm Bent	81 / 100		GGAAAA	GACGUGGCAUGCGA	20
GC	73 / 100		GGAAAA	GCGGCGGCGCGC	20

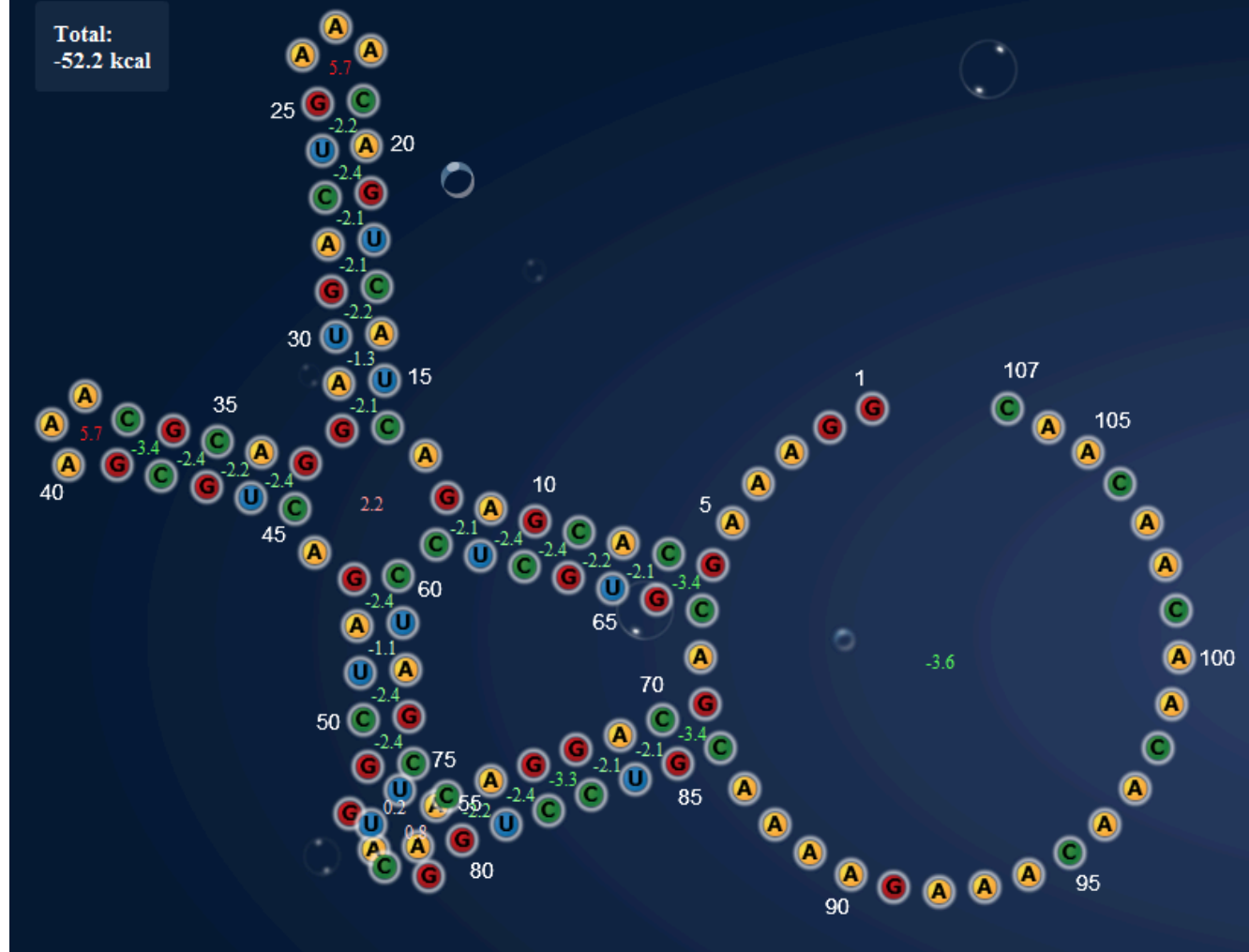
28 Aug 2013

Intersecting stacks 2

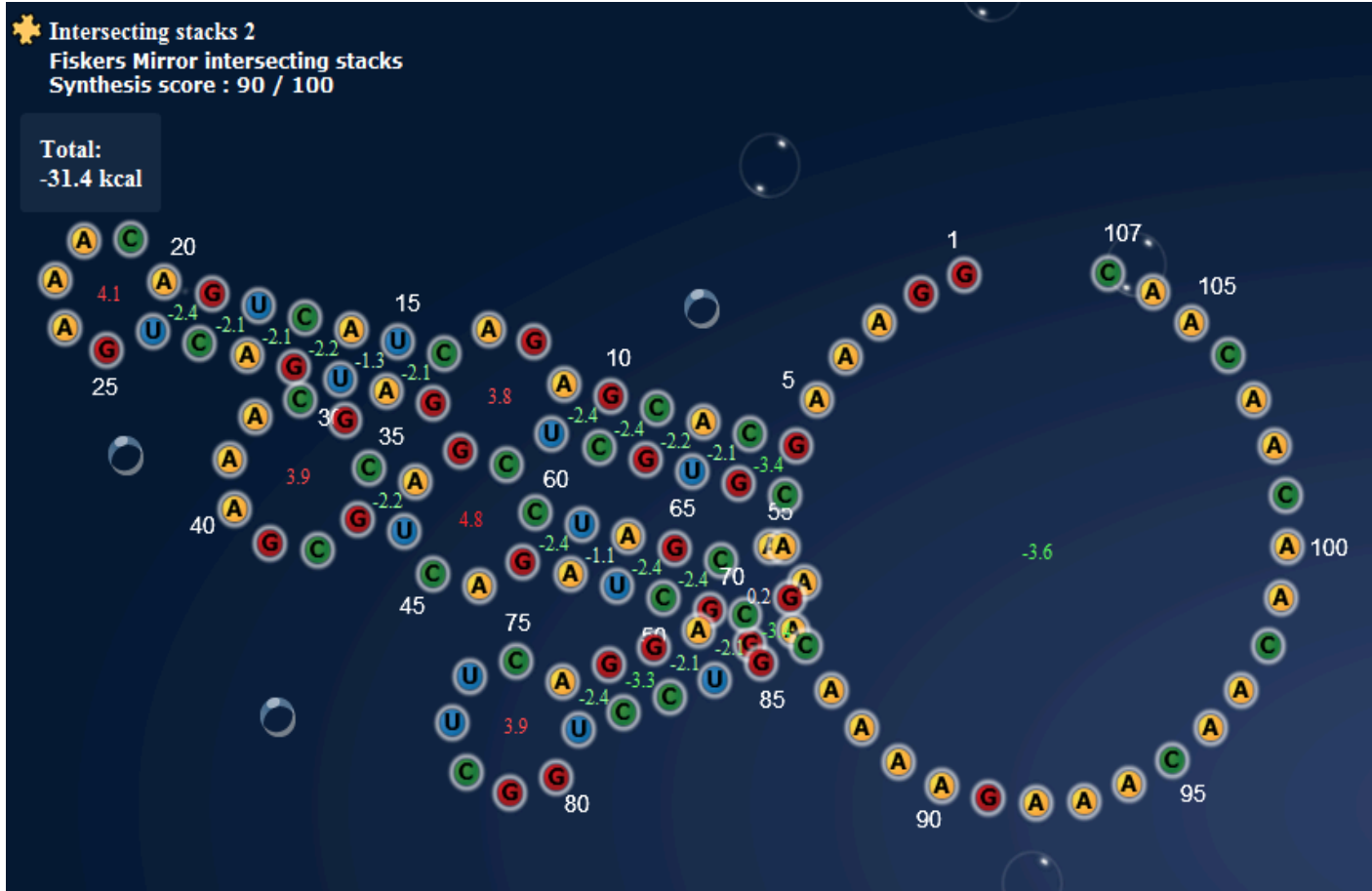
Looks like I found a quite certain way to create a double multiloop.

✦ Intersecting stacks 2
 Fiskers Mirror intersecting stacks
 Synthesis score : 90 / 100

Total:
 -52.2 kcal



Estimate

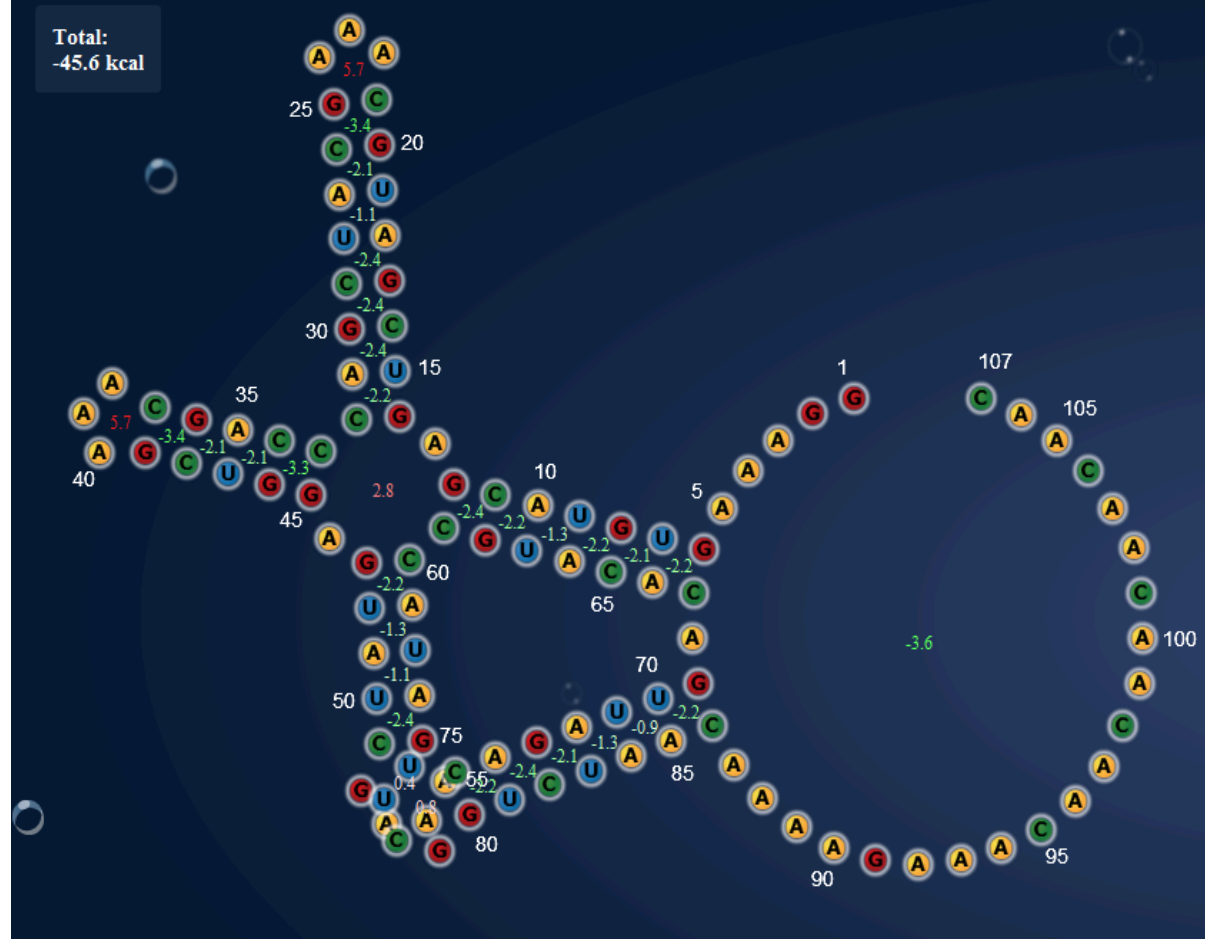


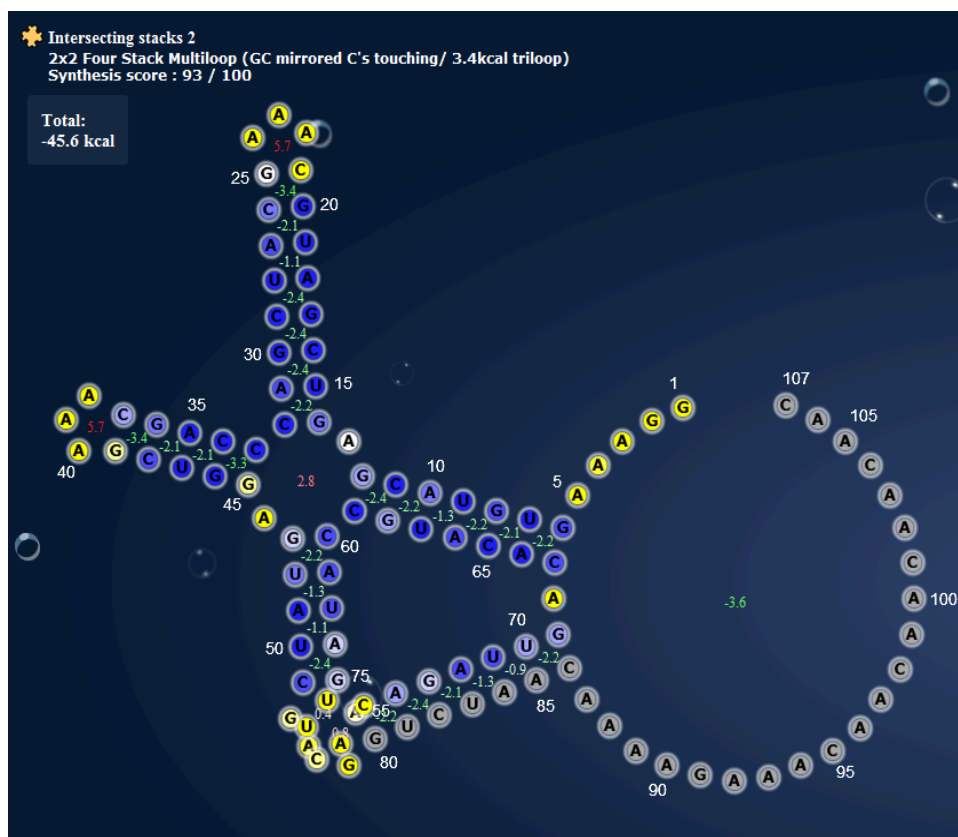
So not one of each of those.

As expected, red facing red in the adjacent spots, did do rather well. Even a pure green facing green did quite well. (only one yellow base in the SHAPE colors)

✦ **Intersecting stacks 2**
2x2 Four Stack Multiloop (GC mirrored C's touching/ 3.4kcal triloop)
Synthesis score : 93 / 100

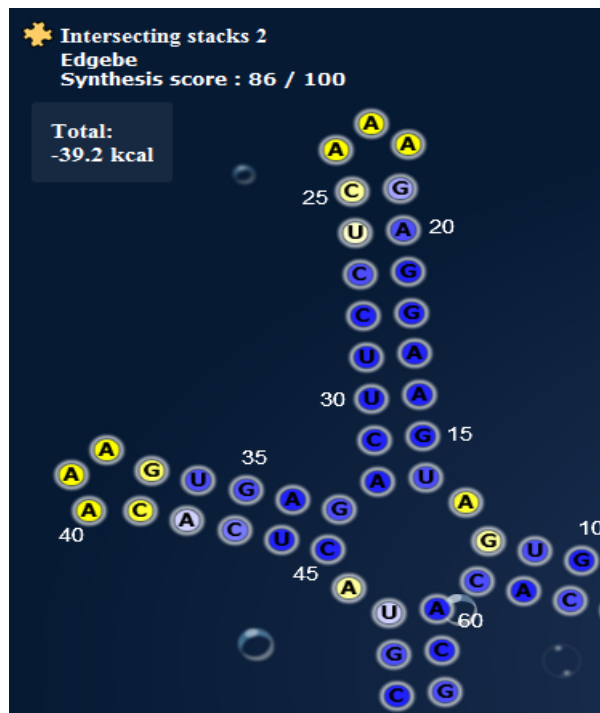
Total:
-45.6 kcal



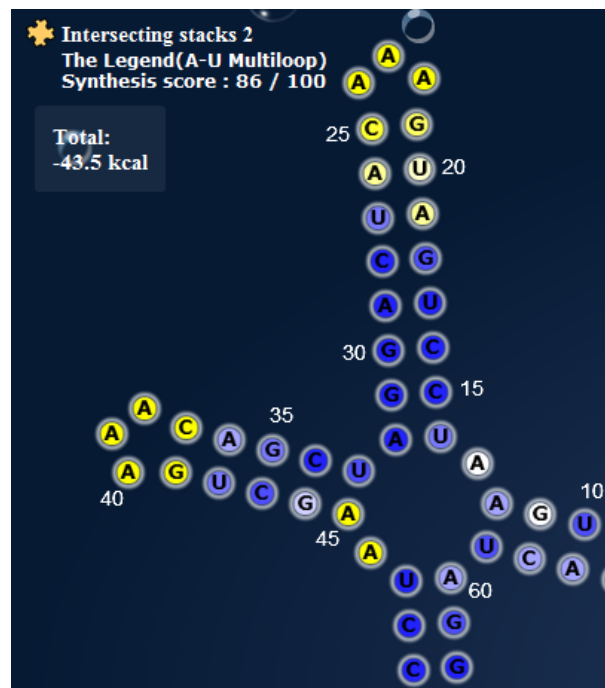
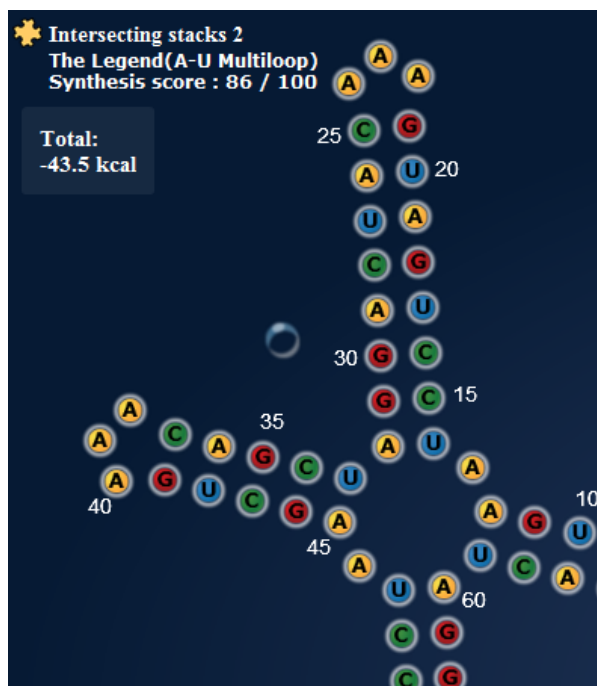


Else usual orientation was also quite regular.

Vinnie made it quite well with a mixture of GC's and AU's.



Redspah almost made it with all AU's



One base (45) is often in trouble in the SHAPE colors. It looks like it demands to have C. However it won't be a guarantee. So can it be that it is more important to have these red facing red, in the first part of the RNA? I see several designs do fine with just one of these formations. Two can sometimes be overkill.

Intersecting stacks 2			
Title	Synthesis score ▾		Sequence
search	min	max	search
iStack	94 / 100		GGAAA GCGUA GCA GCGUAUG ²⁰ CAAA GCAUAC GCGGAG CAAA ⁴⁰ GCGU
2x2 Four Stack ...	93 / 100		GGAAA GUGUA GCA GUGUAUG CAAA GCAUCG ACCCAG CAAA GCGU
In the Intersection	93 / 100		GGAAA GCUCU ACAG CAGUA G CAAA GCUCAUG CGCUC CAAA CCGA
crossroads 1	92 / 100		GGAAA GUAUAG CAGCUAUAUC AAA GAUAUA GCGGUAC AAA GUUA
Scissors 1	92 / 100		GGAAA GGAUCA GACAUGCUA GAAAC UAGCAUG GUCA GAAACU C
Crossroads I	92 / 100		GGAAA GGUGUA CAGCACAUG CAAA GCAUGU GCGCAC CAAA CCGU
Intersection	90 / 100		GGAAA GCUAUG CAGCUAUA G CAAA GCUAUA GCGCU CAAA CCGA
Interesting sticks	90 / 100		GGAAA GGUUAUG CAGCAUAUA CAAA GUUAUA GCGGUAC AAA GUUA
AD impluvium	90 / 100		GGAAA GGAUUG CAGUUCUAUG CAAA GCAUAG CCGAGA CAAA GUUA
Fiskers Mirror ...	90 / 100		GGAAA GCAUGA GACUAUCUGA CAAA GUCAGUA GGCAG CAAA GCGU
The Stack Worsh...	90 / 100		GGAAA GUCGUA CACUGCUAUC UAA GAUAGCA GGGAC CUAAGGU
Some mirroring	90 / 100		GGAAA GUUCAUC ACUAUCUG CAAA GGCAGUA GGUAC CAAA GGUU
2x2 Four Stack ...	89 / 100		GGAAA GUGUAG CAGUCGAUG CAAA GCAUCG ACCCAG CAAA GCGU
Mat - Intersect...	89 / 100		GGAAA GCGUAUC ACACU GUUA GAAAC UAAACA UGGUA GCAAA GCGU
X 2-1	88 / 100		GGAAA GUAUGUC AGGCUAGUC AAA GACUA GCGGCAU CAAA GAGU
Fiskers Interse...	88 / 100		GGAAA GCACCU GACAUCUGA CAAA GUCAGA UGGUUG CAAA GCGU
InterstgStacks...	86 / 100		GGAAA GGUGCC CACCGGUA UAA GAUUCG GCGCCU GAAA UAGU
Fiskers Adjacen...	86 / 100		GGAAA GCACGUC ACAUCUGA CAAA GUCAGA UGGCGU CAAA GAGU
Edgebe	86 / 100		GGAAA UAAUGUGAUGAAGGAG AAA CUCUUA CAGAGU GAAACA C
Crossroads III	86 / 100		GGAAA GGUUAUG CAGCAUAUG CAAUG CAUAUG CCGCAC CAAUGGU
The Legend(A-U ...	86 / 100		GGAAA GUCAUGA AUCCUGAUG AAA CAUCAG GAUCGAC AAA GUUA
Terinsecting Ta...	85 / 100		GGAAA GCUAUG CAGCUGUA G CAAA GCAUCG CCGGUG CAAA GCGA
Lowest Free Energy	85 / 100		GGAAA GCGGGGCC AGGCGCGC CAAA GCGCGG CCGCGG GAAA CCGU
2x2 Four Stack ...	85 / 100		GGAAA GCGUA GCAUCACAUG CAAA GCAUGUA GGGAG CAAA GCGU
Surprise AU	85 / 100		GGAAA GAGCUA CAGCGUUC GAAAC GAA CAGUA GUAUC CAAUGGA
Crossroads II	85 / 100		GGAAA GGUUA GAGCGUAUG CAAUG CAUAUG GGCACC AUA GGUU
Stacktresting - ...	85 / 100		GGAAA GUCAUA CACUAUAUC UAA GAUA GUA GGGAU CUAAGAU
Sectresting - B...	82 / 100		GGAAA GUUAUA CACUAUAUC UAA GAUAUA GGAUA CUAAGAU
Maoninti	78 / 100		GGAAA UAAUAAG AGCGAGAC CAAAG GGUUUC GCGGCAG AACCUU
Arinvedi	70 / 100		GGAAA UUAUAUA UAUAAC GCGC GAA GCGCUA UAGGCAC CAAAGU

31 Aug 2013

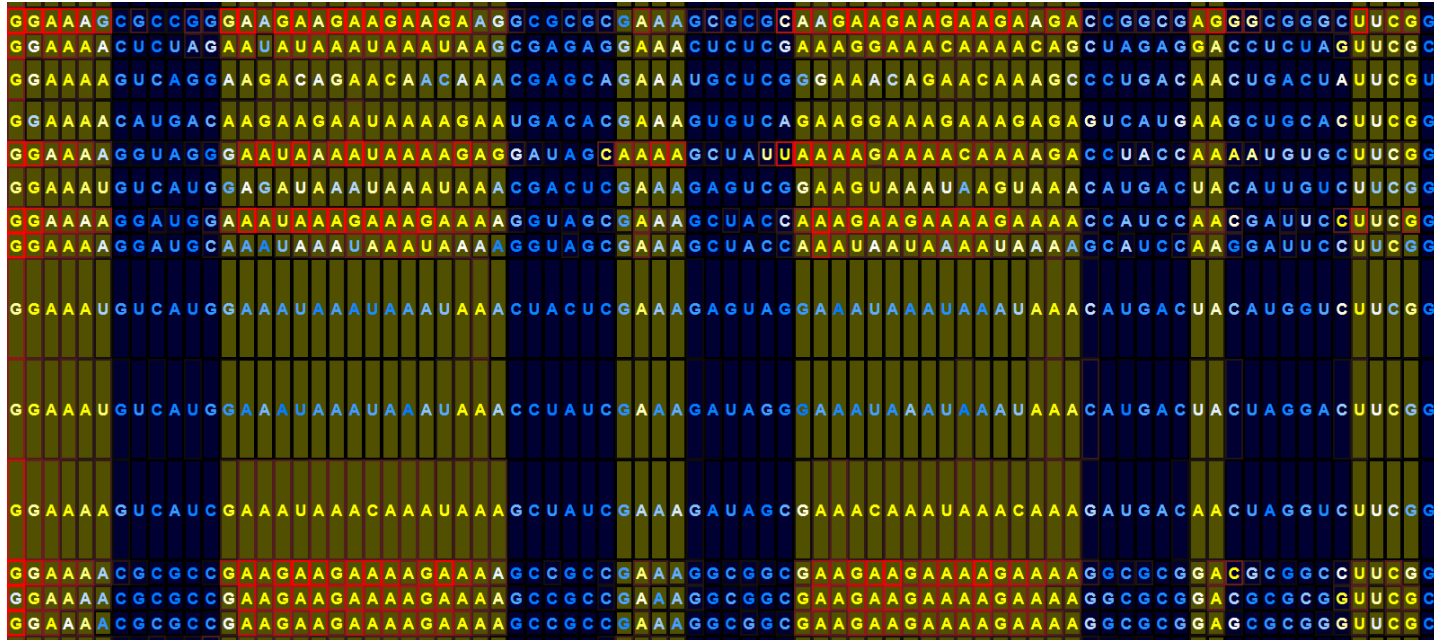
Things that trigger the error values

This is a few things that I stumbled on while playing with [Omei's tool](#). It is funny seeing these patterns trigger error values. Many of them I already knew was bad, but seeing that they actively triggers error values, is something different.

Frog leg - Electric

Billy Reuben's design Rana 3

Totally GC-pair and them shifting among each other, also send the error rate high
GCGCGC



I wonder if that is the same in the big end loops too. That it is the error values that

Here are some examples of A and U overuse from the (Reversed G-C Multibranch Loop Closing Base Pairs Lab. With many of the same color in line.



G-U Closing Base Pairs 2

AUAU and lots of it also seems to trigger the error values

76 [steven123505](#) [spanda](#)



Hmm, there is high error values in the bigger end loop in the two bulge zigzag labs. I wonder if that continues.

11 Sep 2013

More thoughts about the barcode hairpin problem.

I wonder if the length of the cloud lab designs on 63 nucleotides had something to do with where the strain appeared. I mean that the problem mainly turned up in the barcode in certain labs.

Will this pattern with bad barcodes move elsewhere or get weaker in the RNA design if the design sequence gets longer. I think it might.

Which reminds me that the SHAPE data overall did look different in the player projects where the designs were often shorter in sequence length. Many of the labs had more shaky overall lighter blue color for the whole of the stems - compared to pre-cloud and cloud labs. It happened in particular with the labs with shorter stems. I can't see what the barcodes look like for the player projects. But I'm guessing that they will be more overall dark blue, and thus pushing the backbone strain back into the main design. Because the barcode has a better shot at getting stable, due to it being relatively long compared to the few other stems. Like Nando's idea.

Another thing that might have added to the difference in player project SHAPE data is that many of the designs are blunt ended in the neck. I think I see a tendency for labs with blunt end doing worse than designs that have 1 or 2 single bases between the barcode and the main design.

26 Sep 2013

[Relaxed multiloops 2](#)

27 Sep 2013

Semicircle - 3 Bends

Again I see this funny pattern with this rather long stemmed design and the winners in particular having most of the blue on the 5' end of the two long strands. Actually here the red is also clearly distributed on the 5' side, and the yellow and green, mostly distributed on the 3' side. I usually see this reversal with blue on the 5' side in long stemmed designs, but here the

★ Semicircle - 3 bends
 Enintean
 Synthesis score : 96 / 100

Total:
 -49.2 kcal

[illegible]

109

It was similar with the two other semicircle labs before that. One showed excess U's on 5 prime side and the the other not. Since they have different number of bulges/semicircle building parts, can this be the explanation?

11 bp in stems

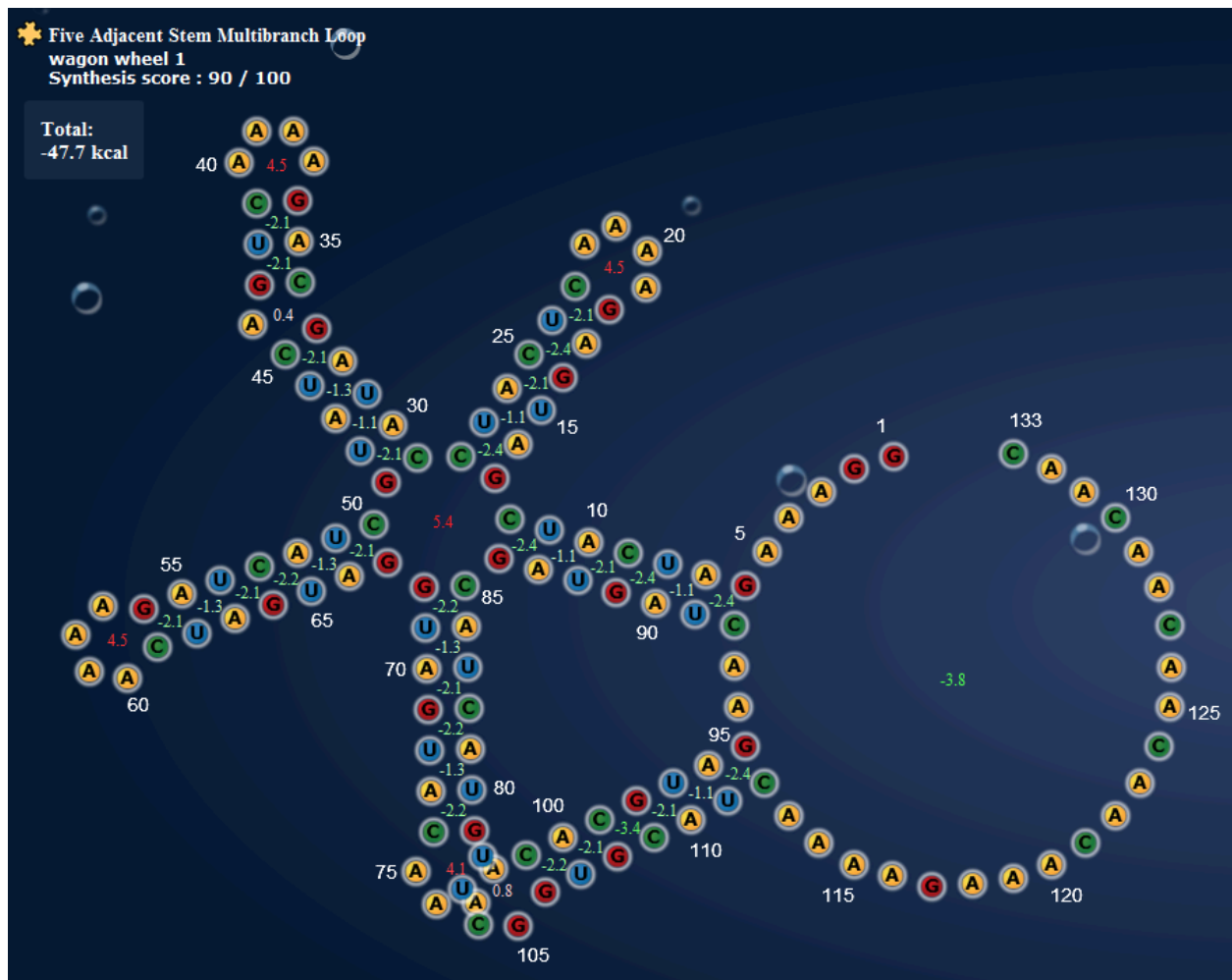
Semicircle - 5 bends		
Title	Synthesis score ▼	Sequence
search	min max	search
SemiCir-5bendsd...	90 / 100	GGAAAA GCAAGUUGA GCGAGAGAGCGGUCAAGUAGCAAAGCUUUUAGCGGCCGCGUCAAAGUUG
semicircle boos...	90 / 100	GGAAAA GUCCUAGCUAGCGAGCGAGCGGUACUCUGGAAAGCAAAGAGCGUACGCCCGCUAGCUAGGAC
Mat - Semicirc...	90 / 100	GGAAAA GCGAUAGUUGCGAGAGCGCGGUACUUGCAAAGCAAAGUAGAGCGCGCUAGCUAGUUGCG
U-Turn III	90 / 100	GGAAAA GCAUUAUAGCGAGAGCGAGCGCGUUGCGCAAAGCAAAGUUGCGCGAGCGCGUUAUUAUG
Semicircle - R...	89 / 100	GGAAAA GUUUGUAGCAUACACACAUUGCUACAUACGAAAGCGUAGUACAAAGGCGAGUUCUAGAUAG
Rapids around L...	89 / 100	GGAAAA GAUUUAUUUACAGAGAGAGCGCUUAUUUAACGAAAGUUUAUUAAGCGCGCGUAAUUAUAGU
Mostly inSane -...	89 / 100	GGAAAA GAGAUUACAGAGAGAGAGCGUACUACUACGUAACUUGUAUUAAGCGCGCGUUAUUAUUGU
U tube	88 / 100	GGAAAA GACACACACUGAGAGAGAGAGCGUACGUGUACGGAGCGUACGUAACGCCCGAGUGUGUGU
mod of janet 5 ...	88 / 100	GGAAAA GACACACACCGAGAGAGAGAGUACGUGUACGUGAGACAGCGUACGUAACGCCCGCGUGUGUGU
Total green vio...	88 / 100	GGAAAA GUCAUUGACAGCGCGCGCGCGUACAUACGAAAGUUAUGUACGACCGCGCGUGUCAAUGAG
U-Turn I	88 / 100	GGAAAA GUGUACAUACGAGAGAGAGAGCGCGUUGCGAAAGCGAUUGUGCGCGCGCGUGUGUUAUAG
Wicked U-Turn S...	86 / 100	GGAAAA CUAAUCUAGGUGAGAGAGGUCUAUACAUAGAAAUAGUUAUAGGCCCGUGUACAUUAGCG
Constrained	86 / 100	GGAAAA GUUCAUGUAUUAAGAGAGGUAAAUUAUGCAAAGUUAUUAAGGCCCGAUUACUAGAG
JR Semicircle_5...	86 / 100	GGAAAA GACAGAGUACGCGUACUUGCGAUUGUAGCGUACGUAACUUGUACGAUUGGAUUGCGUAGUUG
SeminSane - Bro...	86 / 100	GGAAAA GACUAGUACGUGUGUGUGAUUGUACGUAACGUAACUUGUACGAUUGCGCGUACUAGUUG

I thought the bulge length was involved and now I think it was only indirectly. Rather it is the effect of different stem length. So I think what I see is an effect of stem length and fascinating enough I can see the U and G on the 5' strand getting more clear in the designs that has longest stems. (See [Orientation bias](#)). I find it fascinating that I can see a beginning shift with such a small stem prolongation.

12 Oct 2013

Five adjacent stem multibranch loop

Interesting that three each follow same orientation, after each other and two goes in the opposite direction, for the multiloop. The same happens in several of the other top scorers that follows that pattern. Having all follow same orientation as usual won't do as well. The ones with 3 one way and 2 the other looked much better in the shape data.



I'm not too surprised. 4 ways usually like a 2 / 2 each way, though the do allow same orientation. However this one can't do coaxial stacking for all the stems and thus is harder to make happy. Probably same reason why the 3 ways are also hard to make happy. Also see what I wrote on the results on the [Relaxed multiloop lab](#).

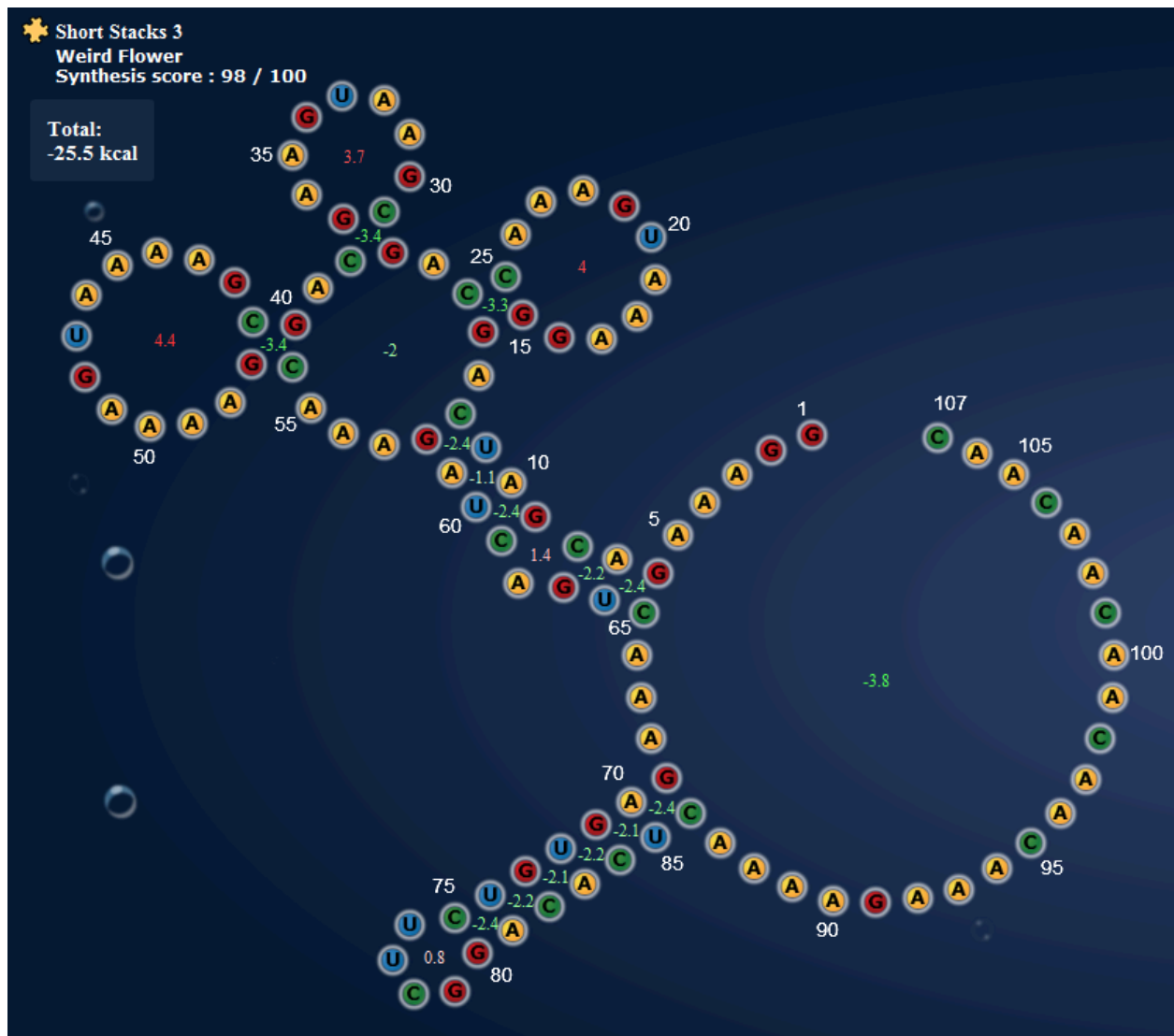
Short stacks 3

In this lab we got the task of placing one base in one color in 3 different end loops. What characterizes the top scorers to a higher degree than the lower scoring designs, is that the base placement isn't at the same spot in each loop, but rather has variation to them. This is just as I expected. Generally variation helps.

Title	Synthesis score ▾		Sequence
	min	max	
search			search
Weird Flower	98 / 100		G G A A A G A C G A U C A G G G A A A U G A A A C C A G C G A A U G A A G C A G C G A A A A U G A A A A S C A A A G A U C A G U C
Short stack blues	98 / 100		G G A A A G U C C G U C A G G G A A A U A A A A C C A G C G A A U A A A G C A G C G A A A A U A A A A A C C A A A G A C G A G A C
Pilas Cortas - Tres	98 / 100		G G A A A G U C C U C A G G G A A A U A A A A C C A G C G A A U A A A G C A G C G A A A A U A A A A A C C A A A G A U C G U G A C
Meechi SS3 - AAC	97 / 100		G G A A A G C C C A U C A G G G A A A A A A A A C A G C G A A G A A A G C A G C G A A A A A A A A A C C A A A G A U C A G U C
Short Stacks wi...	97 / 100		G G A A A G C C C A U C A G G G A A A A A A A A C A G C G A A G A A A G C A G C G A A A A A A A A A C C A A A G A U C A G U C
Short stacks Red	97 / 100		G G A A A G U C C G U C A G G G A A A A A A A A C C A G C G A A A A A A G C A G C G A A A A A A A A A C C A A A G A C G A G A G
Mat - Short sta...	97 / 100		G G A A A G A C C G U C A G G G A A A U A A A A C C A G C G A A A U A A G C A G C G A A A A A U A A A A C C A A A G U A G A G U C
Double S,B - Br...	97 / 100		G G A A A G U C C G A C A G G G A A A U A A A A C C A G C G A A U A A A G C A G C G A A A A A U A A A A C C A A A G U C G A G A C
Short #2	96 / 100		G G A A A G U C C G A C A G G G A A A A A A A A C C A G C G A A G G A A G C A G C G A A A A A G A A A A C C A A A G U C G A G A C
Short Stacks wi...	96 / 100		G G A A A G C G C A U C A G G G A A A A A A A A C C A G C G A A A G A A C C A G C G A A A A A G A A A A C C A A A G A U G A C C G
Short Stacks wi...	96 / 100		G G A A A G C G C A U C A G G G A A A A A A A A C C A G C G A A G A A A C C A G C G A A A A A G A A A A C C A A A G A U G A C C G
Pilas Cortas - Uno	96 / 100		G G A A A G U C C U C A G G G A A A A U A A A A C C A G C G A A A U A A G C A G C G A A A A A U A A A A C C A A A G U A G U G A C
Mat - Short sta...	96 / 100		G G A A A G C C C U C A G G G A A A U A A A A C C A G C G A A A U A A G C A G C G A A A A A U A A A A C C A A A G U A G A C C G
Short Stacks ZII	96 / 100		G G A A A G C C C G C G A G G G A A A A A A A A C C A G C G A A A A A A G C A G C G A A A A A G A A A A C C A A A C C G A G G C
AUA	96 / 100		G G A A A G C A A G A G A G G G A A A U A A A A C C A G C G A A U A A A G C A G C G A A A A A U A A A A C C A A A C U C U A U G G
U Moves 2 - Jie...	94 / 100		G G A A A G U C C U C A C A G G G A A A U A A A A C C A G C G A A U A A A C C A G C G A A A A A U A A A A C C A A A G U C G A G G
Short #1	94 / 100		G G A A A G U C C G A C A G G G A A A A A A A A C C A G C G A A G G A A G C A G C G A A A A A G A A A A C C A A A G U C G A G A C
Meechi SS3 - ACA	94 / 100		G G A A A G A C C A U C A C G G A A A A A A A A C C A G C G A A C A A A G G A G C G A A A A A C A A A A C C A A A G A U G A G U C
Meechi SS3 - CAA	94 / 100		G G A A A G A C C A U C A C G G A A A A A A A A C C A G C G A A C A A A G G A G C G A A A A A C A A A A C C A A A G U C G A G U C
SS3 - 1	94 / 100		G G A A A G U C C G A C A G G G A A A A C A A A C C A G C G A A A C A A G G A G C G A A A A A C A A A A C C A A A G U C G A G A C
SS 3 V1	94 / 100		G G A A A G U C C U C A C A G G G A A A A A A A A C C A G C G A A A C A A G G A G C G A A A A A G A A A A C C A A A G U A C A G A C
JR_Short3_Rnd1_Sub2	94 / 100		G G A A A G U C C U C A C A G G G A A A C A A A A C C A G C G A A C A A A G C A G C G A A A A A C A A A A C C A A A G U A C A G A C
Double S,A - Br...	94 / 100		G G A A A G U C C G A C A G G G A A A A U A A A C C A G C G A A A U A A G C A G C G A A A A A U A A A A C C A A A G U C G A G A C
JR_Short3_Rnd1_Sub1	94 / 100		G G A A A G U C G U C A C A G G G A A A A A A A A C C A G C G A A A C A A G G A G C G A A A A A C A A A A C C A A A G U A C A G A C
UAA	94 / 100		G G A A A G C A A G A G A G G G A A A A U A A A C C A G C G A A A U A A G C A G C G A A A A A U A A A A C C A A A C U C U A U G C
Heretic (U-A-G...	94 / 100		G G A A A G C G G G C A G C A A A G A U A A A C C A G C A A G A U A A G C A G G A A A A G A U A A A C C A A A C G C G A G G C
U Moves 3 - Jie...	93 / 100		G G A A A G U C C U C A C A G G G A A A A U A A A C C A G C G A A A U A A G C A G C G A A A A A U A A A A C C A A A G U A G G C A G
SS - C1	93 / 100		G G A A A G C A A G C A G G G A A A A A A A A C C A G C G A A A C A A G C A G C G A A A A A G A A A A C C A A A C G C U A G G C
Short #3	93 / 100		G G A A A G U C G C A C A G G G A A A A A A A A C C G G C G A A G G A A G C A G C G A A A A A G A A A A C C G A A C U C A C A C
Shorty 1	93 / 100		G G A A A G U A C U A C A G G G A A U A A A A A C C A G C G A C U A A A G C A G C G A A A A A U U A A A A C C A A A C U A C A U A C
SS 3 V2	93 / 100		G G A A A G U G G U C A C A G G G A A C A A A A A C C A G C G A C A A A A C C A G C G A A A A A C A A A A A C C A A A G U A C A C A C
Double S,C - Br...	93 / 100		G G A A A G U C C G A C A G G G A A U A A A A A C C A G C G A U A A A A G C A G C G A A A A U A A A A A C C A A A G U C G A G A C
Shorty 3	92 / 100		G G A A A G A A C U U G A G G G A A U U A A A A C C A G C G A C U A A A G C A G C G A A A A U U A A A A C C A A A C A A G A U U C
Short Stacks-A...	92 / 100		G G A A A G U G C A A C A G G G A A A U A A A A C C A G C G A A U A A A G C A G C G A A A A U A A A A A C C A A A C U U G A C A C
AAUJ	92 / 100		G G A A A G A A G A G A G G G A A U A A A A A C C A G C G A U A A A A G C A G C G A A A A U A A A A A C C A A A C U C U A U G C
U Moves 1 - Jie...	90 / 100		G G A A A G U C C U C A C A G G G A A U A A A A A C C A G C G A U A A A A G C A G C G A A A A U A A A A A C C A A A G U A G G A G C

A pattern that to a higher frequency characterizes the loop patterns for the absolute top scorers, compared to the lower scoring designs

It is also noticeable that the among the highest scoring is one that has two different bases other than yellow. A mixture of bases helps in bigger loops.



Another interesting pattern for that lab was the presence of 3 G's in a row (like base 14-16 above) for one of the short stems. I know that some of it comes from the presence of 3 very short stems and that variation is needed. But there seems to be a need for this pattern. In particular for the first stem (14-15).

20 Oct 2013

Don quixote

When I was looking at this lab while voting, one thing stood out. I was expecting most designs to have a melt temp around 107 as this design have real long stems. However that was not the

case.

This is similar to what I mention under [Melt plot](#).

“If I add just two GU-pairs – even at places where they would be best tolerated, the curve rises quicker at the middle.”

Now the difference is that the design I play with in my melt plot investigation (The branches lab) has relatively short stems. GU's seems to have a rather destabilizing and thus melt temp lowering nature.

Then I thought about another feature that is important for stems as long in this Don Quixote design. And that is GU. However in long stem designs GU's seem to have a relaxing effect. ([Lab designs that crave GU...](#))

The designs that has a high melting point, has a low amount of GU's.

GU Pairs ▼		Melting Point ▼		Free Energy		Title
min	max	min	max	min	max	search
		107	107			
10 (24%)		107 °C		-65.2 kcal		Zanna's 100% de...
8 (20%)		107 °C		-70.8 kcal		Quixote #3
8 (20%)		107 °C		-66.7 kcal		Quixote Spice
7 (17%)		107 °C		-72.59 kcal		Quixote #2
5 (12%)		107 °C		-76 kcal		Quixote #1
4 (10%)		107 °C		-75.3 kcal		Mat - Mod of Starry
4 (10%)		107 °C		-77.09 kcal		Nascar's 100% d...
3 (7%)		107 °C		-67.3 kcal		JR_DonQuixote_R...
1 (2%)		107 °C		-80.09 kcal		Mod of Windmill
1 (2%)		107 °C		-83.2 kcal		Don #1
0 (0%)		107 °C		-82.8 kcal		Mat - Mod of Nando
0 (0%)		107 °C		-106 kcal		Man of La Manch...
0 (0%)		107 °C		-107.3 kcal		Man of La Manch...
0 (0%)		107 °C		-107.3 kcal		Man of La Mancha
0 (0%)		107 °C		-75.7 kcal		Variation on Qu...
0 (0%)		107 °C		-74.09 kcal		Quasispecies style
0 (0%)		107 °C		-70.3 kcal		DQ - 1
0 (0%)		107 °C		-78 kcal		Nando Quixote 2...
0 (0%)		107 °C		-83.6 kcal		Nando Quixote 2...
0 (0%)		107 °C		-83.1 kcal		Nando Quixote 1...
0 (0%)		107 °C		-73.59 kcal		Chivalry - Brou...
0 (0%)		107 °C		-70.7 kcal		The Impossible ...
0 (0%)		107 °C		-75.09 kcal		Pseudoknottin' ...
0 (0%)		107 °C		-83.5 kcal		Nando mod with ...
0 (0%)		107 °C		-71.8 kcal		Full Tilt 2
0 (0%)		107 °C		-65.59 kcal		Full Tilt
0 (0%)		107 °C		-71.09 kcal		Third Tilt
0 (0%)		107 °C		-71.3 kcal		Second Tilt
0 (0%)		107 °C		-70.3 kcal		First Tilt
0 (0%)		107 °C		-68.7 kcal		QuixoteZ
0 (0%)		107 °C		-75.2 kcal		DQ Delight 3
0 (0%)		107 °C		-73.2 kcal		DQ Delight 2
0 (0%)		107 °C		-70.4 kcal		DQ Delight 1
0 (0%)		107 °C		-79.09 kcal		Windmill 2
0 (0%)		107 °C		-76.5 kcal		Sancho Panza
0 (0%)		107 °C		-83.1 kcal		Try 1: Bracing

While the designs with a lower melt temp, has a higher amount of GU.

Don Quixote

GU Pairs ▼		Melting Point ▼		Free Energy		Title
min	max	min	max	min	max	search
			97			
23 (56%)		77 °C		-21.5 kcal		DQf2
14 (34%)		87 °C		-41.9 kcal		DQf3
11 (27%)		87 °C		-45.5 kcal		Don
8 (20%)		97 °C		-49.5 kcal		JR_DonQuixote_R...
8 (20%)		97 °C		-51.1 kcal		smattering
7 (17%)		97 °C		-54.9 kcal		dq 1
6 (15%)		97 °C		-54.7 kcal		dq 3
6 (15%)		97 °C		-54.9 kcal		dq 2
6 (15%)		77 °C		-38.6 kcal		Lyra Eternal
5 (12%)		97 °C		-59.1 kcal		Mat - Mod of Hy...
4 (10%)		97 °C		-67.5 kcal		Don-Key-Hotay 3...
4 (10%)		97 °C		-64.3 kcal		Don-Key-Hotay 2...
4 (10%)		97 °C		-60.6 kcal		Don-Key-Hotay (...)
4 (10%)		97 °C		-67.4 kcal		Quixote II
3 (7%)		96 °C		-64.5 kcal		Maxerete
2 (5%)		87 °C		-36.1 kcal		JR_DonQuixote_R...
1 (2%)		87 °C		-41.2 kcal		Don Quixote Try 2
1 (2%)		77 °C		-28.7 kcal		131020iii
0 (0%)		97 °C		-37.9 kcal		Don Quixote Try 1
0 (0%)		97 °C		-68.59 kcal		Lyra Eternal II
0 (0%)		97 °C		-51 kcal		Meechi Don Quixote
0 (0%)		97 °C		-53.4 kcal		crongnivourious
0 (0%)		97 °C		-53.8 kcal		awesomeiliola
0 (0%)		87 °C		-47.5 kcal		Quixotic
0 (0%)		87 °C		-46 kcal		Don Quixote Try 3
0 (0%)		87 °C		-42.3 kcal		ipodiddleydoo
0 (0%)		77 °C		-28.4 kcal		Keeping it simple
0 (0%)		77 °C		-24 kcal		DQf1
0 (0%)		77 °C		-25.3 kcal		QuixoteQ
0 (0%)		77 °C		-32 kcal		alex's Don Quixote

It is a general tendency, but not totally overlapping.

25-10-2013

Robot serial killer 2

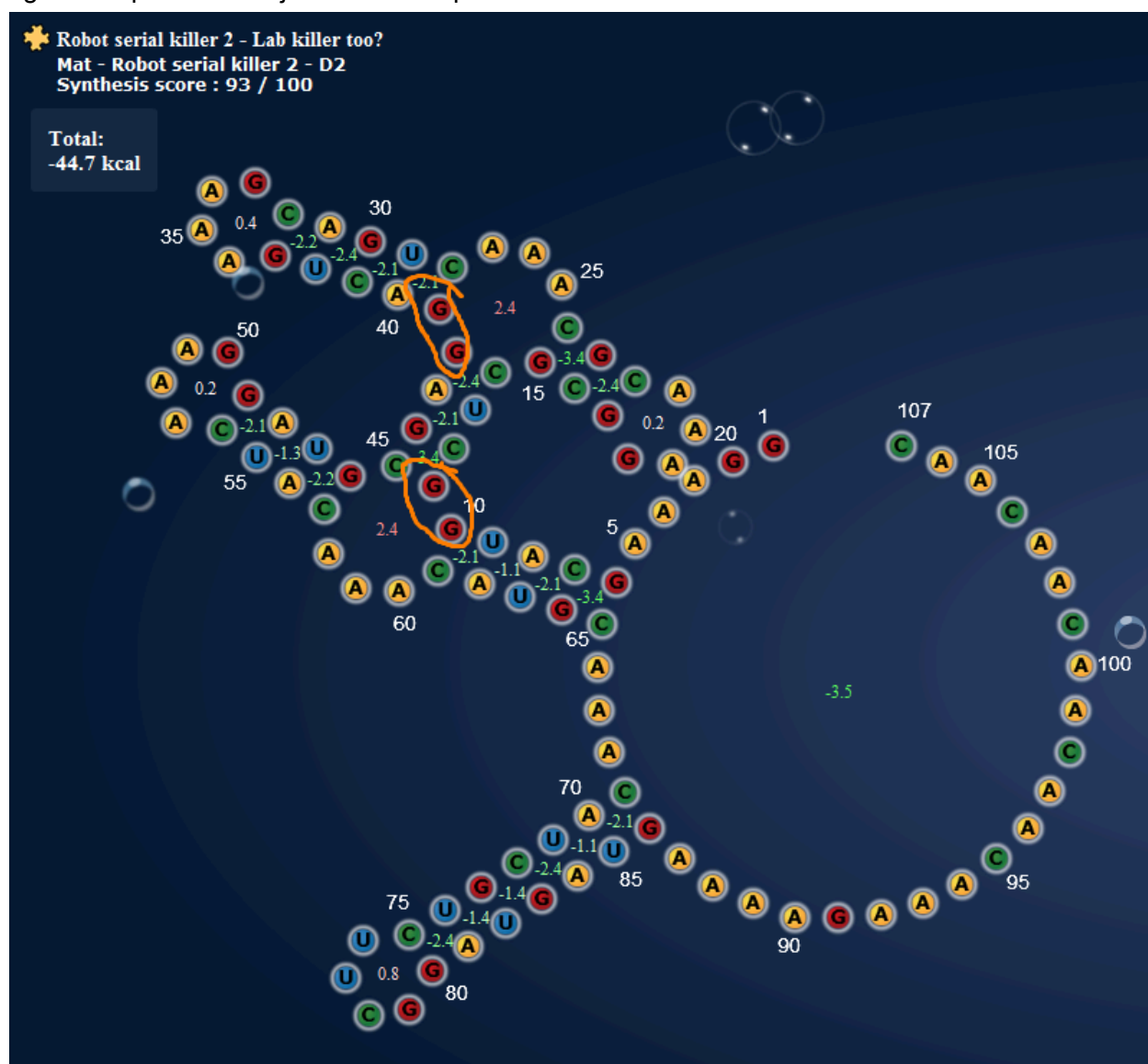
This is a lab that has generally few GU pairs. There are a few high scorers with a couple. But I generally think that designs with an on average shorter stems will have fewer GU-pairs, whereas GU will be more needed in long stem designs.

Now this lab doesn't have totally short stems. However it is pressured due to two closely placed adjacent multiloop. Also worth noting is the general high GC-content.

Robot serial killer 2 - Lab killer too?												
GC Pairs		UA Pairs		GU Pairs		Melting Point		Free Energy		Title	Synthesis score ▼	
min	max	min	max	min	max	min	max	min	max	search	min	max
20 (71%)		8 (29%)		0 (0%)		107 °C		-46.4 kcal		Terminator 2.3	94 / 100	
17 (61%)		10 (36%)		1 (4%)		107 °C		-44.7 kcal		Mat - Robot ser...	93 / 100	
22 (79%)		4 (14%)		2 (7%)		107 °C		-55.4 kcal		Power of Two	93 / 100	
20 (71%)		8 (29%)		0 (0%)		107 °C		-48.1 kcal		Murder 6 - Jieu...	92 / 100	
21 (75%)		7 (25%)		0 (0%)		107 °C		-53 kcal		Murder 5 - Jieu...	92 / 100	
17 (61%)		10 (36%)		1 (4%)		87 °C		-30.2 kcal		Robotikon 2	92 / 100	
14 (50%)		14 (50%)		0 (0%)		97 °C		-39.2 kcal		RSK2 - 1	90 / 100	
20 (71%)		7 (25%)		1 (4%)		107 °C		-50.1 kcal		Gunness (G's to...	90 / 100	
15 (54%)		12 (43%)		1 (4%)		80 °C		-37.69 kcal		Aedator	90 / 100	
17 (61%)		10 (36%)		1 (4%)		107 °C		-43 kcal		JR_Robot2_Rnd1_Sub2	90 / 100	
16 (57%)		12 (43%)		0 (0%)		67 °C		-38.83 kcal		Engerbi	89 / 100	
17 (61%)		11 (39%)		0 (0%)		97 °C		-45.9 kcal		The Clean-cut K...	89 / 100	
21 (75%)		7 (25%)		0 (0%)		107 °C		-52.7 kcal		Lethal Computer...	89 / 100	
21 (75%)		5 (18%)		2 (7%)		97 °C		-46 kcal		Power of One	89 / 100	
22 (79%)		6 (21%)		0 (0%)		107 °C		-52.4 kcal		Murder 4 - Jieu...	88 / 100	
15 (54%)		13 (46%)		0 (0%)		107 °C		-40.2 kcal		Meechl RSK2	88 / 100	
18 (64%)		10 (36%)		0 (0%)		107 °C		-47.6 kcal		Manson (G's tow...	88 / 100	
21 (75%)		7 (25%)		0 (0%)		107 °C		-50.9 kcal		Robot Killer Take 2	88 / 100	
22 (79%)		6 (21%)		0 (0%)		107 °C		-54.4 kcal		The Lamb	88 / 100	
18 (64%)		8 (29%)		2 (7%)		107 °C		-48.9 kcal		Stable, with GU	86 / 100	
19 (68%)		9 (32%)		0 (0%)		107 °C		-49.6 kcal		Fiskers Robot S...	86 / 100	
19 (68%)		9 (32%)		0 (0%)		107 °C		-48.8 kcal		JR mod	86 / 100	
19 (68%)		9 (32%)		0 (0%)		107 °C		-48.6 kcal		Fatal Automaton...	86 / 100	
12 (43%)		12 (43%)		0 (0%)		97 °C		-40.29 kcal		Deadly Metal - ...	86 / 100	
20 (71%)		8 (29%)		0 (0%)		107 °C		-47.7 kcal		Robby the Robot	86 / 100	
19 (68%)		9 (32%)		0 (0%)		107 °C		-50.3 kcal		Fiskers Robokil...	85 / 100	
7 (25%)		21 (75%)		0 (0%)		77 °C		-15.6 kcal		7 GC	85 / 100	
17 (61%)		11 (39%)		0 (0%)		80 °C		-41.24 kcal		Isonbi	85 / 100	
19 (68%)		9 (32%)		0 (0%)		107 °C		-49.7 kcal		Berkowitz (G's ...	84 / 100	
17 (61%)		11 (39%)		0 (0%)		97 °C		-46.2 kcal		Lady Killer Too	84 / 100	
23 (82%)		4 (14%)		1 (4%)		107 °C		-53.4 kcal		King Carrion	84 / 100	
22 (79%)		6 (21%)		0 (0%)		107 °C		-52.5 kcal		Bot Killer App	82 / 100	
19 (68%)		9 (32%)		0 (0%)		97 °C		-38.9 kcal		killer 1	81 / 100	
7 (25%)		21 (75%)		0 (0%)		77 °C		-15.3 kcal		7 GC	80 / 100	
23 (82%)		4 (14%)		1 (4%)		107 °C		-56.5 kcal		Power of Two	80 / 100	
19 (68%)		9 (32%)		0 (0%)		107 °C		-50.5 kcal		RSK 2 V1	77 / 100	
12 (43%)		16 (57%)		0 (0%)		87 °C		-29.2 kcal		Robot serial ki...	76 / 100	
7 (25%)		21 (75%)		0 (0%)		77 °C		-15.4 kcal		Die Robots!	73 / 100	

Another thing I found interesting is that the melt point is this high. That is more usually the case in the long stem designs. However it is most likely partly due to the high GC content.

Again this pattern in adjacent multiloops.



The winner had this pattern and 1 multi loop with usual multi loop pattern

Robot serial killer 1 - Lab killer too?

Roomba

Synthesis score : 97 / 100

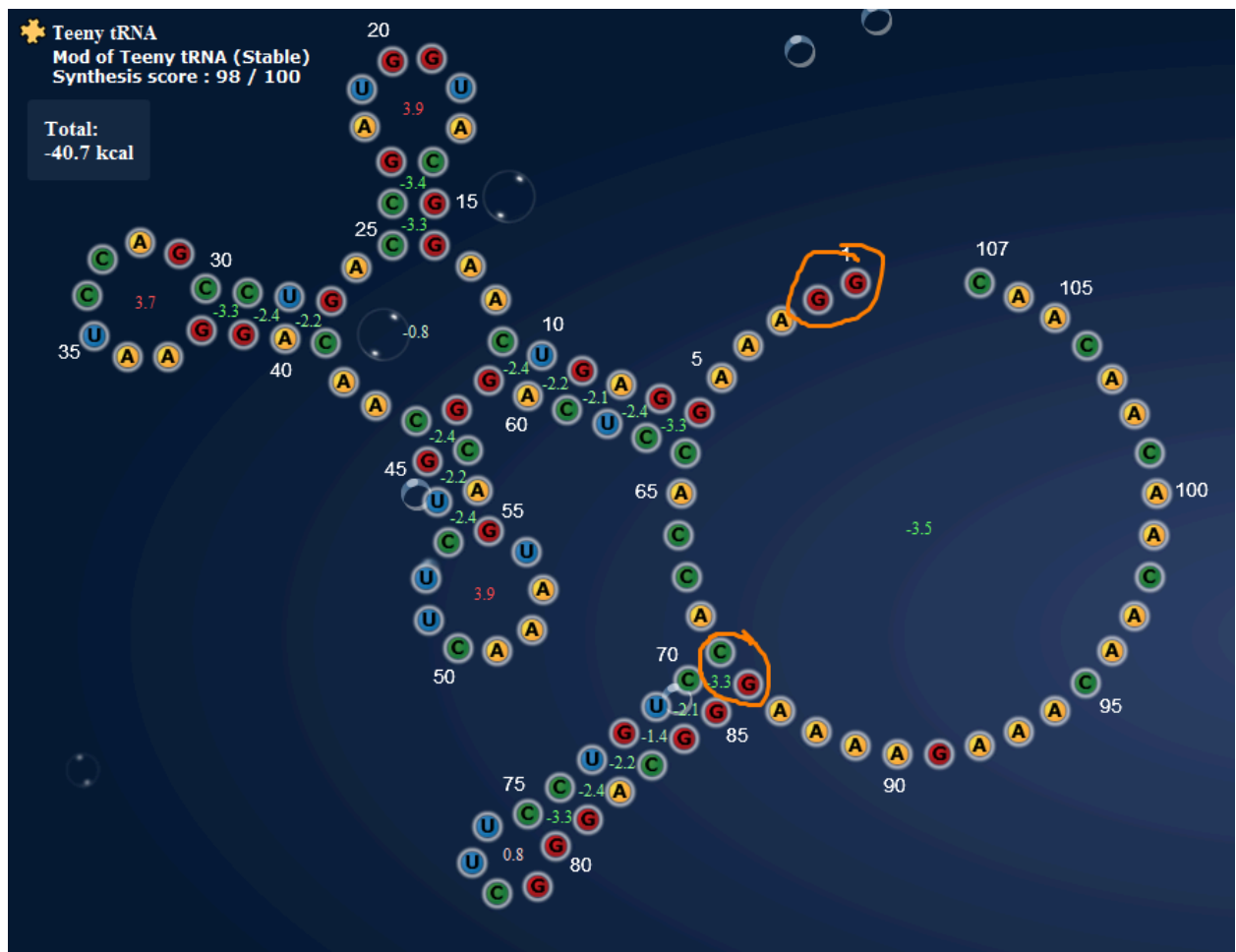
Total:
-45.7 kcal

The diagram shows the secondary structure of the Roomba RNA sequence, which is 107 nucleotides long. The sequence is represented by colored circles containing the base letter (A, G, C, U). The structure features several stems and loops. A specific stem between positions 68 and 70 is highlighted with an orange circle. Nucleotide numbers are placed near their corresponding bases. Energy values in kcal/mol are shown next to some bases, such as 0.4 at position 35, -2.2 at position 45, and -3.2 at position 107. The total free energy of folding is indicated as -45.7 kcal.

Dimer B also has a high tendency of C's there. This lab has more winners and is less pressured. It do has an adjacent multiloop.

Dimer B			Me	Roadmap
Title	Synthesis score	Sequence		
search	min max	search		
icab - Dimer B1	98 / 100	G C A A A A C A G U A U U A G C A G A A U A A G G U A G C G U G C G A A A G C A C A A U A A G A U G G A A A C A U C A G C U A C G A A A G A G C A U U U C		
Fiskers Dimer B2	98 / 100	G C A A A A C A G U A U U A G C A G A A U A A G G U A G C G U G C G A A A G C A C A A U A A G A U G G A A A C A U C A G C U A C G A A A G A G C A U U U C		
icab - Dimer B2	97 / 100	G C A A A A C A G U A U U A G C A G A A U A A G G U A G C G U G C G A A A G C A C A A U A A G A U G G A A A C A U C A G C U A C G A A A G A G C A U U U C		
2nd Dimer B	97 / 100	G C A A A A C A G U A U U A G C A G A A U A A G G U A G C G U G C G A A A G C A C A A U A A G A U G G A A A C A U C A G C U A C G A A A G A G C A U U U C		
BD - #3	96 / 100	G C A A A A C A G U A U U A G C A G A A U A A G G U A G C G U G C G A A A G C A C A A U A A G A U G G A A A C A U C A G C U A C G A A A G A G C A U U U C		
Dimer B2II	96 / 100	G C A A A A C A G U A U U A G C A G A A U A A G G U G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
Loomer	96 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
3	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
MIRED B	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
Dimer Bee	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
DB - 1	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
3rd Dimer B	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
Hyphens Dimer B...	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
Dimer B V3	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
Lumch	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		
Dimer B2I	94 / 100	G C A A A A C A G U A U U A G C A G A A A G A G U G C G C G A A A G G C G A A U A A G G C G A A A G G C G A C C A C A A A G U A C U G G U U C		

In teeny trna most of the 69 bases are C's as the general locking of bases in the rest of the puzzles will make the red bases at position 1 and 2 pair up with



28-10-2013

Even energy + CSE style

(From discussion between Mat and I yesterday.)

mat

one day i would like to see a CSE style script used a starting point for solving player puzzles

Eli

Ah, that is a fine idea

Sort of an elements catalog

mat

a very old idea

Eli

It won't work for everything

as there is interaction between elements, but

it could still be a help

To locate successful patterns

mat

yes that is the same for the lab too

Eli

yes

getting access to all solves, will be the first step for the programmers

I think it was Dennis that showed interest for this kind of a catalog in the forum recently

mat

but remember CSE is a tool used to help design, but not make the design. a design is more than just a bunch of parts

Eli

true

mat

that where the lab or puzzle strategies are used to solve/design

Eli

Yes, there will be needed strategies for choosing what to sew together

mat

yep

Eli

I still see even energy very much in play. Necks still can go different. And small stems have higher energy concentration than longer ones. But still

If not this is taken into account, it doesn't matter if the separate parts are the best

mat

what would you define as short/small stems

Eli

3 nt stems

and below

I see those get maxed out GC wise more often than the 4 nts

Though they often do like something like 75% GC, if there are many short stems

For stems longer than 4 nt, I see a more 50% distribution of GC and AU. And real long stems gets grumpy if they have a high GC content, whereas they better tolerate an excess of AU

And for 2 nt stems I almost always see 100% GC.

mat

as you know i would see 3 nt as a shared element

Eli

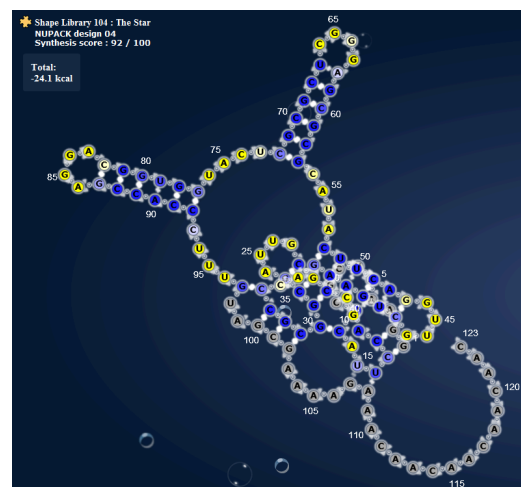
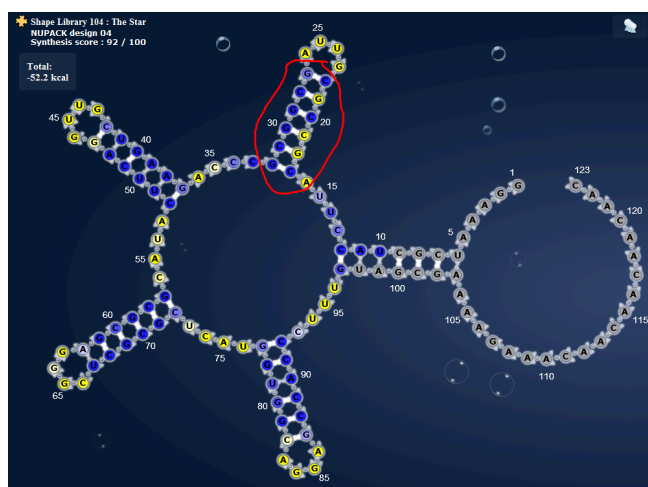
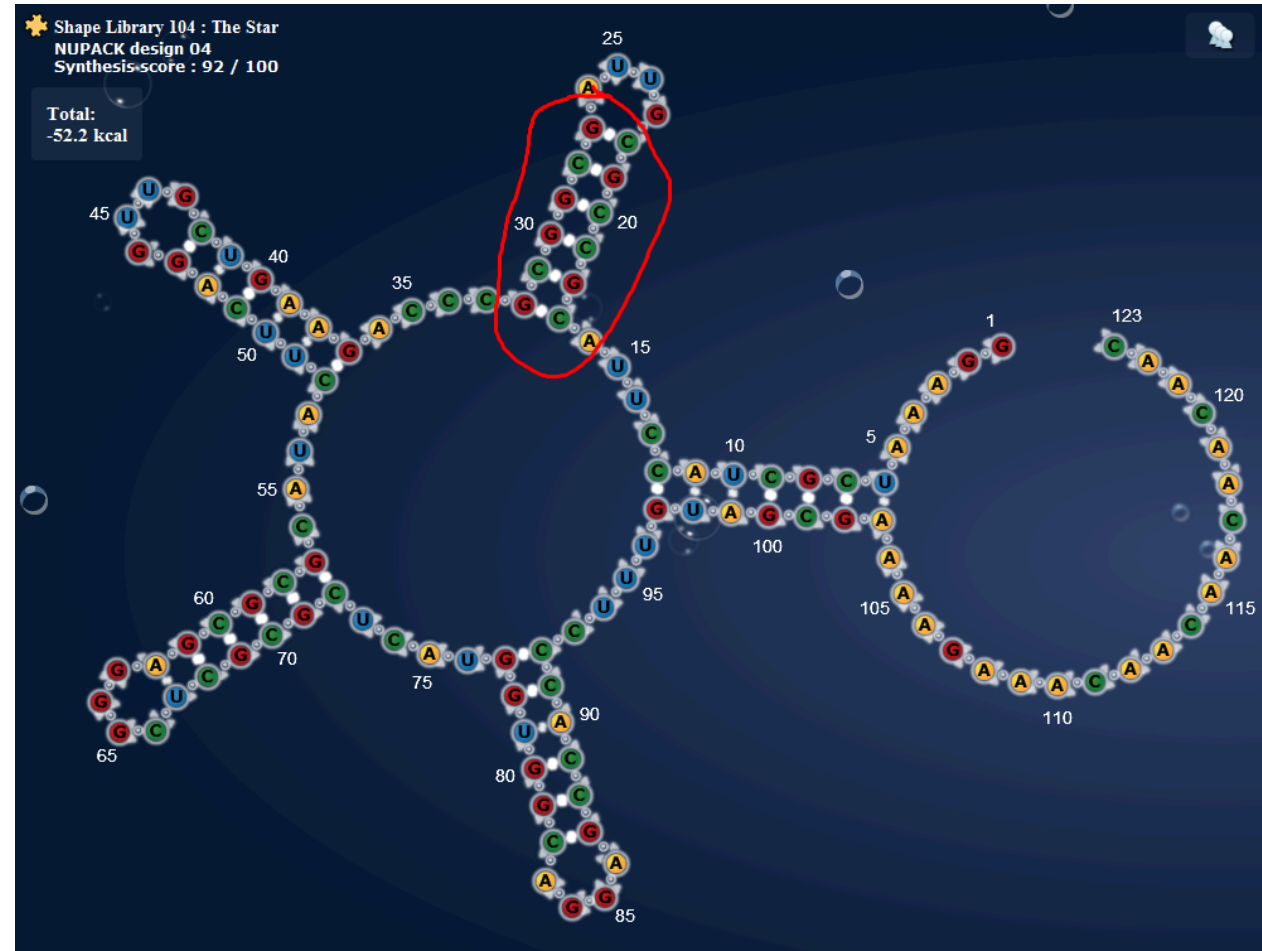
ah, I forgot, but I like that perspective a lot

Mat added: And last night were talking about CSE and the design side of CSE and i was thinking of other ways to explain.

Its like ego blocks. Just because those pieces fit together didn't mean they go together.

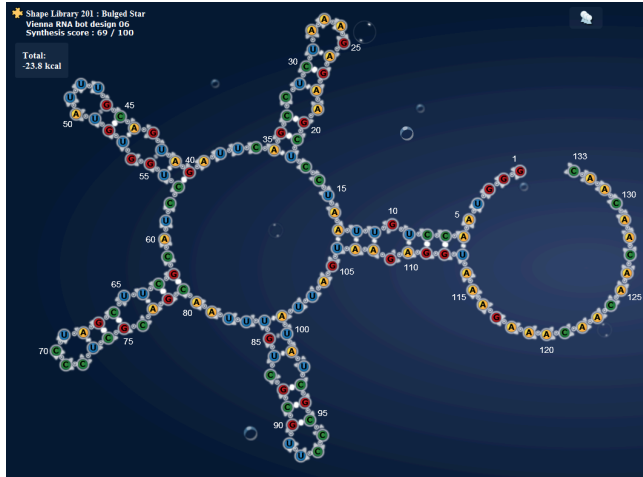
29 Oct 2013

I was looking at some old designs. I find it interesting that exactly this stem that is all GC'd out

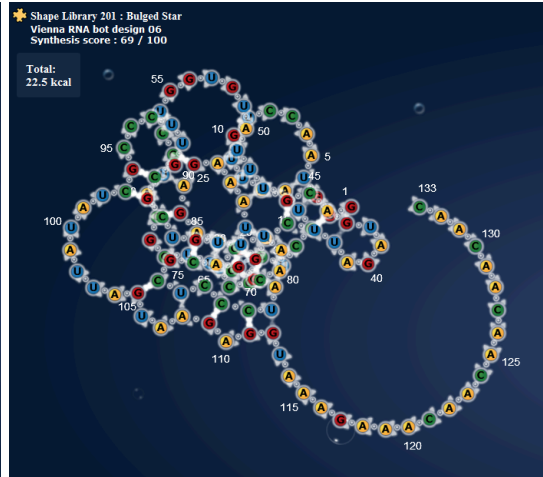


And though I know that I can't read too much into the estimate fold, I still find it interesting that so big amount of the repeat bases, end up in the loop (or otherwise single base) area in the estimate.

Target



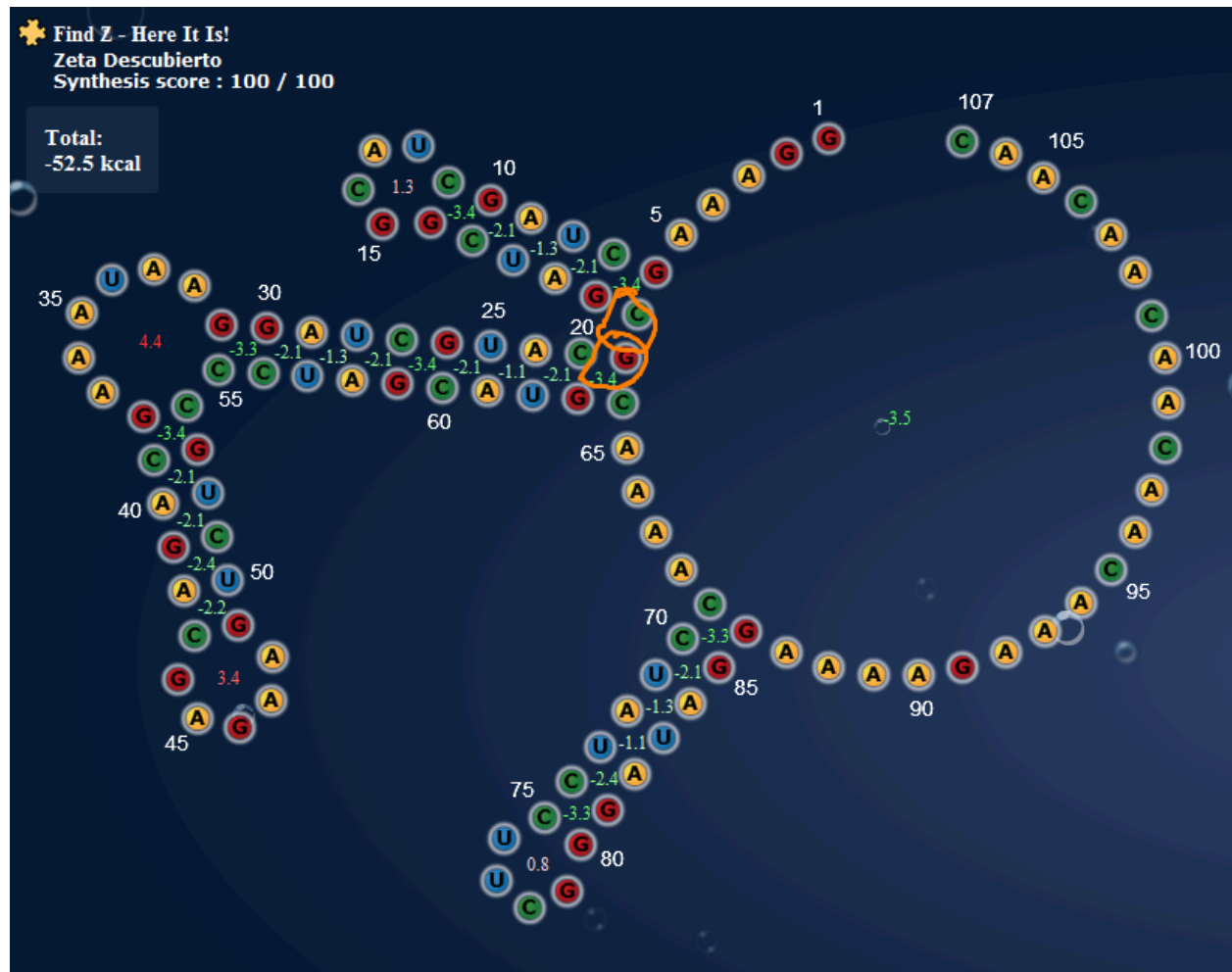
Estimate



And that is not a single case.

Adjacent stems attached to the hook

Still the overall pattern for hook nucleotides is red first and then green for closing base pair attached to the hook. And green facing green is also still doing well for these adjacent stacks. They are very calm blue in the shape data.



Find Z - Here It Is!

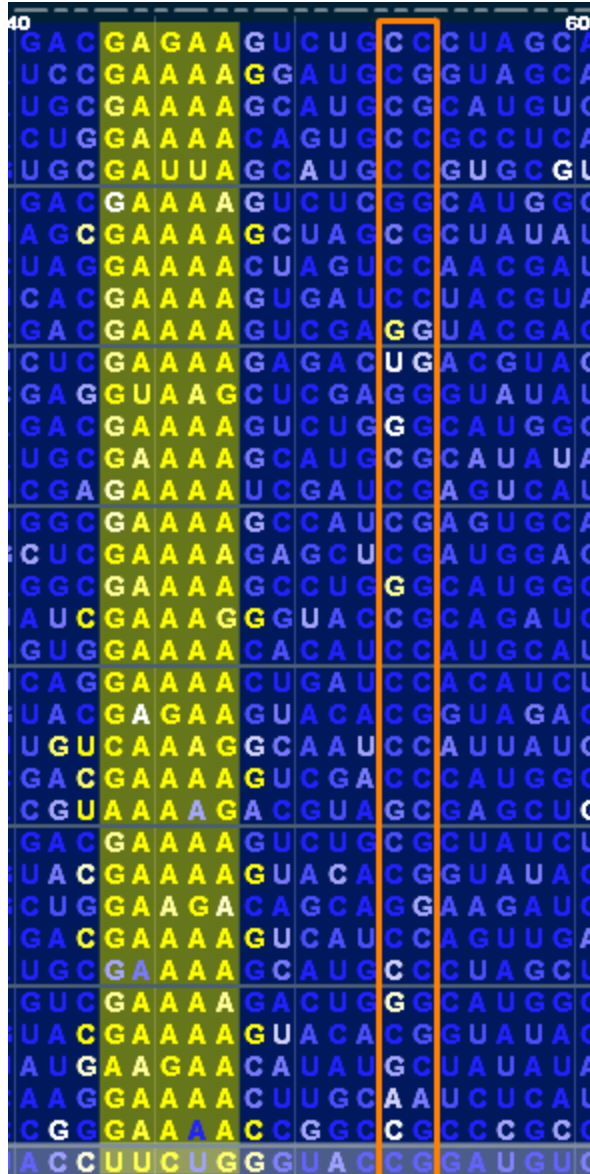
Title	Synthesis score ▼		Sequence
	min	max	
search			search
Zeta Descubierto	100 / 100		G G A A A G C U A G C U A C G G C U A G C G C A
Z Best Mod	98 / 100		G G A A A G C U A G C G A A A G C U A G C G C A
Now you Zee it,...	98 / 100		G G A A A G C A U G C G A A A G C A U G C G C A
Bone Yard	98 / 100		G G A A A G C G U G G G A A A C C A C G C C A G
Z is for amaZing!	98 / 100		G G A A A G C U A G C U U C G G C U G G C G C U
Fiskers Z-aires 2	98 / 100		G G A A A G A U G A C G A A A G U C A U C G U A
FlipZee	97 / 100		G G A A A G C U A G C G A A A G C U A G C G C U
TEST 2	97 / 100		G G A A A G U U G U G G A A A C A C A A C G A C
Mat - Find Z - D3	97 / 100		G G A A A G C U A U C G A A A G A U A C C G G A
DYE 3 - Broud ...	97 / 100		G G A A A G A G A U C G A A A G U C U C G C A U
DYE 2 - Broud ...	97 / 100		G G A A A G A G U A C G A A A G U A C U C G A U
Loopy bulge 1	97 / 100		G G A A A C G G U G U G U A A C A C C C G C A U
Fiskers Z-Rando...	97 / 100		G G A A A G A U G A C G A A A G U C A U C G U A
Z is for Zebra	96 / 100		G G A A A G C A U G C G A A A G C A U G C G C A
finding nemo sub 3	96 / 100		G G A A A G U C A A C G A A A G U U G A C C G U
XYZ sub2	96 / 100		G G A A A G A U A C G G A A A G C U A U C C G A
Mod of Broud's...	96 / 100		G G A A A G A G U A G G A A A C U A C U C G U A
Z - #2	96 / 100		G G A A A G A U G A G G A A C C U C A U C G U A
Find Z - #1	96 / 100		G G A A A G C A U U C G A A A G G A U G C G C A
TEST 3	96 / 100		G G A A A G A G U U G G A A A C A A C U C G A C
TEST 1	96 / 100		G G A A A G A C A A G G A A A C U U G U C G A C
Zeta 3	96 / 100		G G A A A G U A C A C G A A A G U G U A C C A A
It's a Z? (CG b...	96 / 100		G G A A A G C U G C A G A A A U G C A G C G A U
Fiskers Z-aires	96 / 100		G G A A A G A U G A C G A A A G U C A U C G U A
manyclr	96 / 100		G G A A A U C A G C A G A A A U G C U A C G C A
Mod of Garydfisher	94 / 100		G G A A A G C U A G U G A G A G C U A G C G C U
Zeta 1	94 / 100		G G A A A G U A U G C G A A A G C A U A C C A A
Starry's Z	94 / 100		G G A A A C U G U A G G A G A C U A C A G G U C
there it goes	93 / 100		G G A A A G A U G U C G A A A G A C A U C G U A
Z best	93 / 100		G G A A A C G U A G C G A A A G C U A C G G C U
Z - #1	93 / 100		G G A A A G A U G A G G A A C C U C A U C G U A
Zeta 2	93 / 100		G G A A A G U A U G C G A A A G C A U A C C A A
Design XVII	93 / 100		G G A A A G U A U A C A A A A G U A U A C C U A
it is	93 / 100		G G A A A G U A G U U G A G A G A C U A C G U A
BEST FREE ENERGY	92 / 100		G G A A A G G C G G C G A A G G C C G C C G G C
Z V1	92 / 100		G G A A A G G A U C C G A A A G G A U C C G G U

Find Z - 6 nt bulge

I was also in particular interested in the bulge area. I focused on the inside bend of the bulge, for GC-orientation. CC are there in a high rate, followed by regular orientation (G-pattern) and then GG pattern.

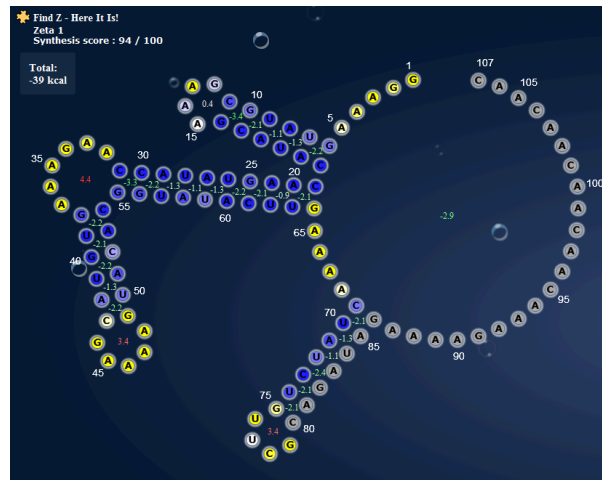
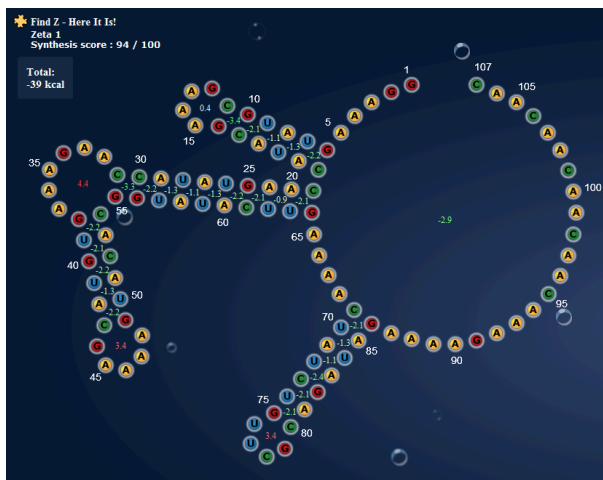
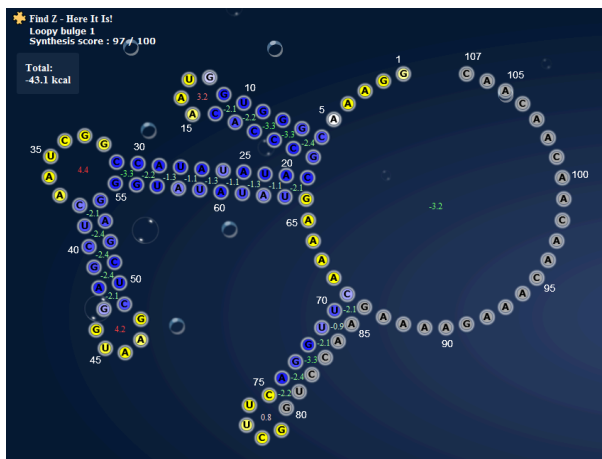
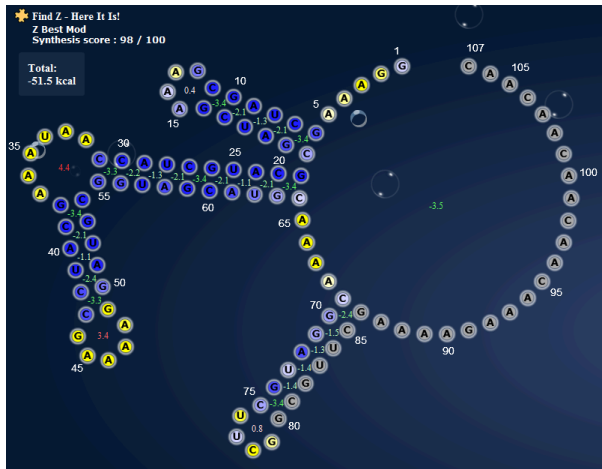
Find Z - Here It Is!			
Title	Synthesis score ▾		Sequence
	min	max	
search			search
Zeta Descubierto	100 / 100		GGAAAGGUAAGCUAGGCUAGGCAUGGUAAGGAUAAAGCAAGAGAAAGUUGCGUAGGCA
Z Best Mod	98 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Now you Zee it...	98 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Bone Yard	98 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Z is for amaZing!	98 / 100		GGAAAGGUAAGCUUGCGGCGUAGGCUAGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Fiskers Z-aires 2	98 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
FlipZee	97 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
TEST 2	97 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Mat - Find Z - D3	97 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
DYE 3 - Broud...	97 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
DYE 2 - Broud...	97 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Loopy bulge 1	97 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Fiskers Z-Rando...	97 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Z is for Zebra	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
finding nemo sub 3	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
XYZ sub2	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Mod of Broud's...	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Z - #2	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Find Z - #1	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
TEST 3	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
TEST 1	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Zeta 3	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
It's a Z? (CG b...	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Fiskers Z-aires	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
manyclr	96 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Mod of Garyfisher	94 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Zeta 1	94 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Starry's Z	94 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
there it goes	93 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Z best	93 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Z - #1	93 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Zeta 2	93 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Design XVII	93 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
it is	93 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
BEST FREE ENERGY	92 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA
Z V1	92 / 100		GGAAAGGUAAGGCAAGCUAGGCAUGGUAAGGAUAAAGCAUGCGAAAGGAUGCGUAGGCA

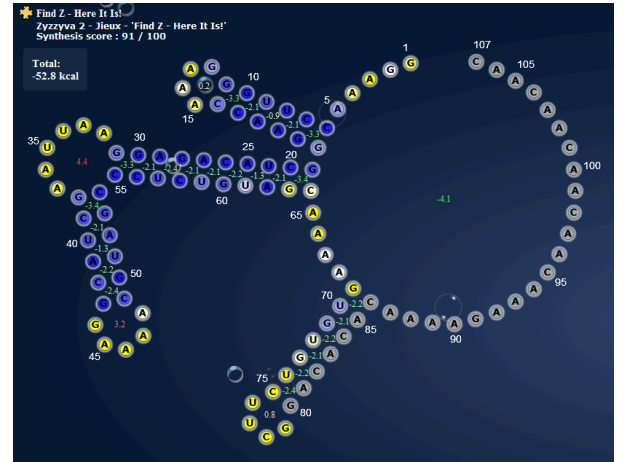
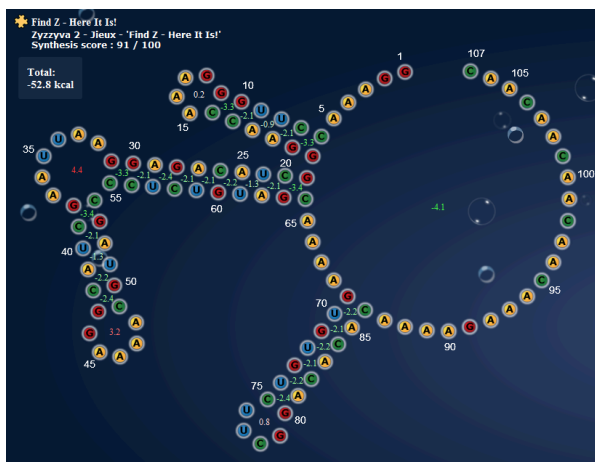
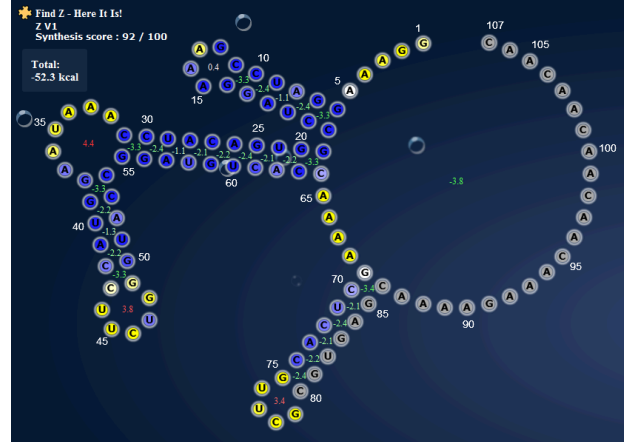
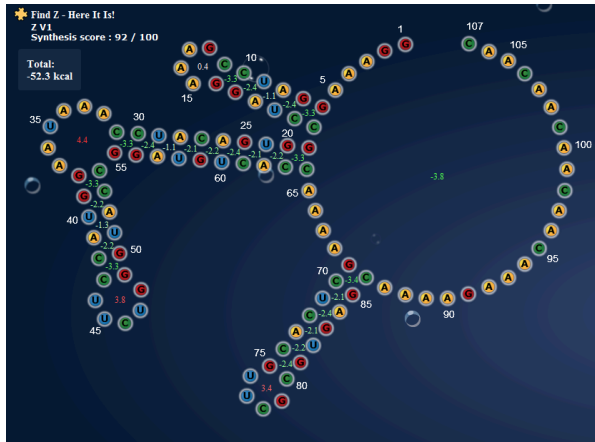
It does look like CC's are particularly calm. The GG's doesn't always go well, actually one of them very often is non binding. So CC at the inside of a bulge this size seems to be best or have it follow G-pattern.



However there seem to be a reverse relationship between the inside bases of the bulge being stable compared to the outside bases (closing base pair) and opposite.

This one has stable both places.



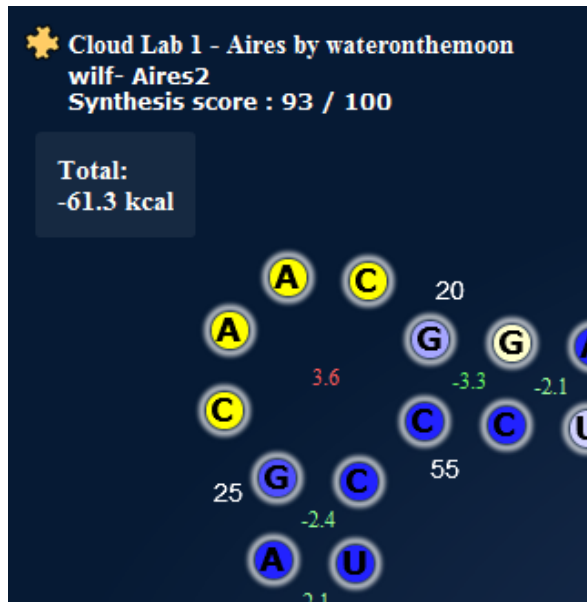


What these designs particular has in common is the double GC block at the I wonder if this is common for bigger bulges.

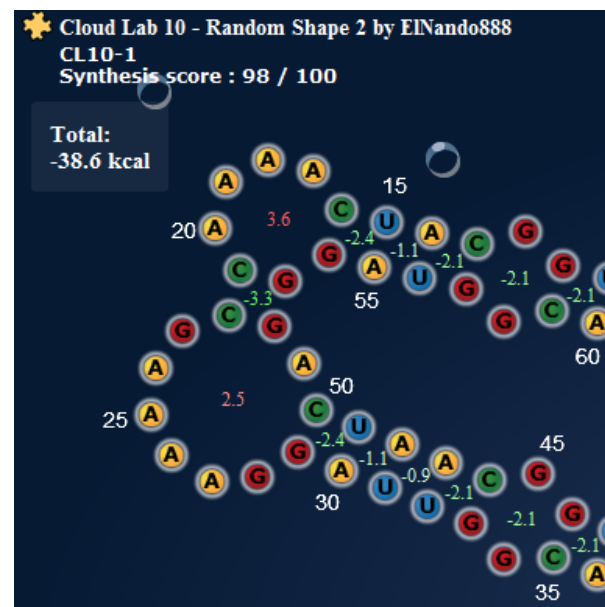
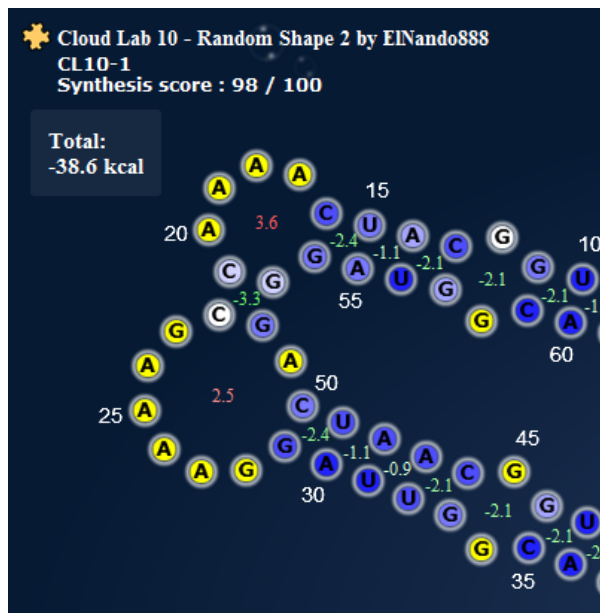


So according to these, G-pattern orientation is best in bulges. Or is it perhaps the double GC-block at the start of the bulge?

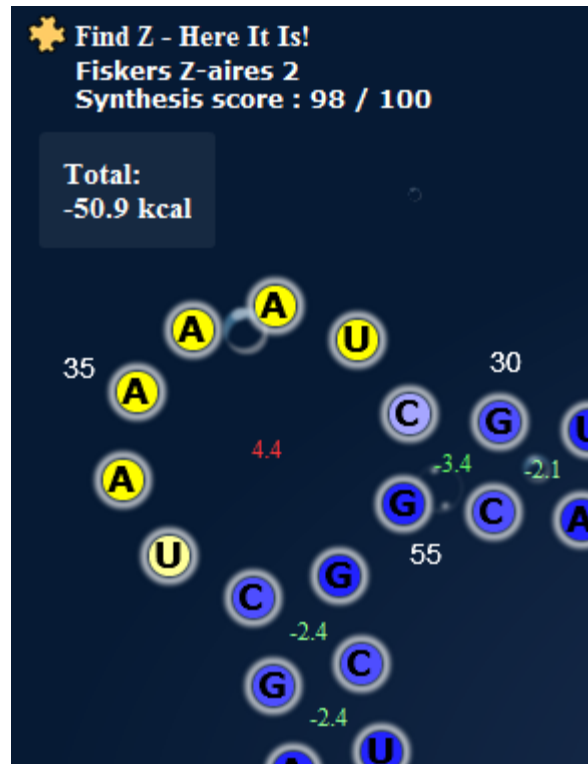
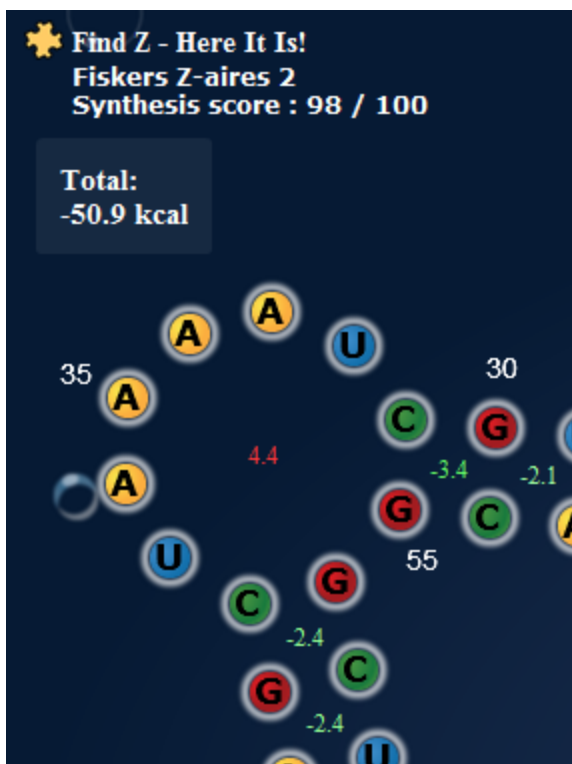
These didn't all go well in the Aires lab. Here is one of the best of this type. Actually it was this lab's all time best bulge. So some merit goes to this same turning GC quad pattern.



The best and stablest bulge in this lab had the double GC-pair after the bulge. Note this was also the case in the 2 bottom examples from Find the Z! lab.



Though this one isn't darkest blue shape data, it isn't doing bad. And it is stable.



So crossed GC's at both sides of the bulge is doing surprisingly well.

For the bigger bulges (4 nt+) it seems to be the fewest that are totally stable, however a certain pattern do seem to have merit.

31 Oct 2013

The making of a triloop

Jieux made some lab designs with a GU as closing base pair end and GC's in the loop. He pointed my attention to them, before the lab was synthesized. It looks like he found a way to cause a triloop to form. As half the G's and C's snap together and form stem.

Target



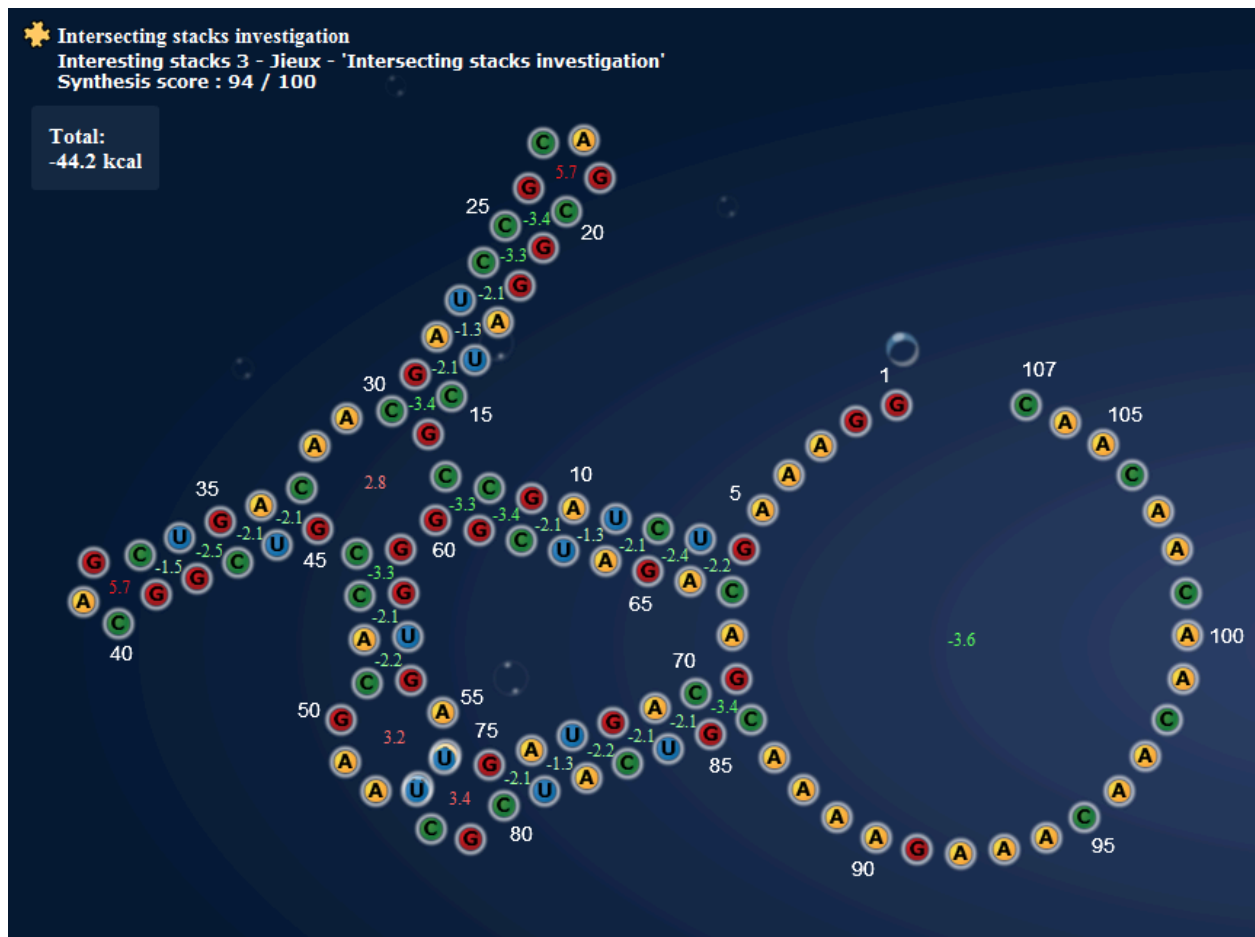
Intersecting stacks investigation
 Interesting stacks 3 - Jieus - 'Intersecting stacks investigation'
 Synthesis score : 94 / 100

Total:
 -44.2 kcal

The diagram shows an RNA secondary structure with the following features:

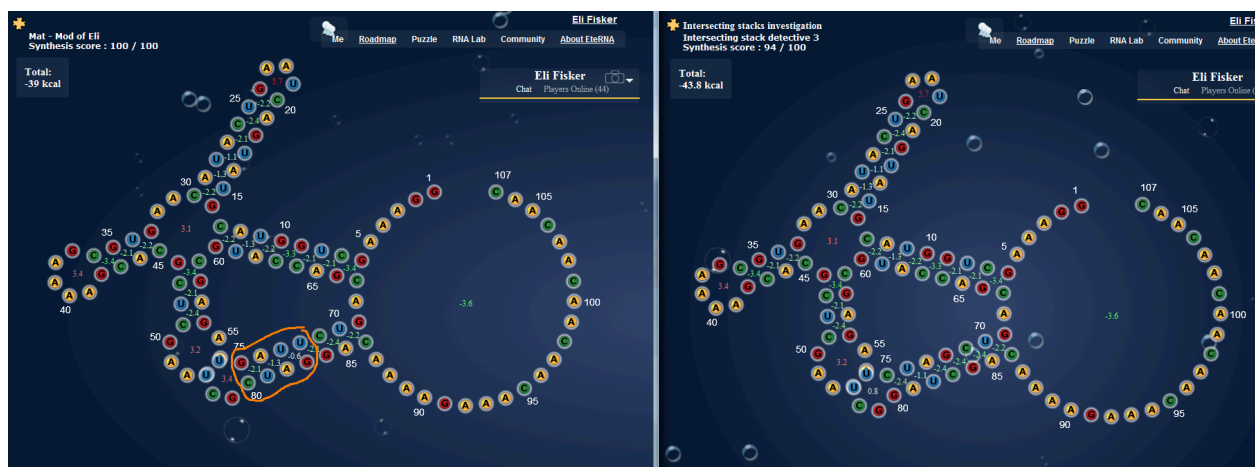
- Sequence:** A 100-nucleotide RNA sequence (positions 1 to 100 are labeled).
- Base Pairs and Energy:**
 - 1-2 (A-G): -5.7
 - 3-4 (C-G): -3.4
 - 5-6 (G-C): -3.3
 - 7-8 (U-G): -2.1
 - 9-10 (A-A): -1.3
 - 11-12 (U-U): -2.1
 - 13-14 (G-C): -3.4
 - 15-16 (G-C): -3.3
 - 17-18 (A-G): -2.1
 - 19-20 (U-G): -2.1
 - 21-22 (G-C): -3.4
 - 23-24 (G-C): -3.3
 - 25-26 (A-G): -2.1
 - 27-28 (U-G): -2.1
 - 29-30 (G-C): -3.4
 - 31-32 (G-C): -3.3
 - 33-34 (A-G): -2.1
 - 35-36 (U-G): -2.1
 - 37-38 (G-C): -3.4
 - 39-40 (G-C): -3.3
 - 41-42 (A-G): -2.1
 - 43-44 (U-G): -2.1
 - 45-46 (G-C): -3.4
 - 47-48 (G-C): -3.3
 - 49-50 (A-G): -2.1
 - 51-52 (U-G): -2.1
 - 53-54 (G-C): -3.4
 - 55-56 (G-C): -3.3
 - 57-58 (A-G): -2.1
 - 59-60 (U-G): -2.1
 - 61-62 (G-C): -3.4
 - 63-64 (G-C): -3.3
 - 65-66 (A-G): -2.1
 - 67-68 (U-G): -2.1
 - 69-70 (G-C): -3.4
 - 71-72 (G-C): -3.3
 - 73-74 (A-G): -2.1
 - 75-76 (U-G): -2.1
 - 77-78 (G-C): -3.4
 - 79-80 (G-C): -3.3
 - 81-82 (A-G): -2.1
 - 83-84 (U-G): -2.1
 - 85-86 (G-C): -3.4
 - 87-88 (G-C): -3.3
 - 89-90 (A-G): -2.1
 - 91-92 (U-G): -2.1
 - 93-94 (G-C): -3.4
 - 95-96 (G-C): -3.3
 - 97-98 (A-G): -2.1
 - 99-100 (U-G): -2.1
- Highlighted Region:** Nucleotides 1, 2, 3, and 4 are circled in orange.

In particular these crossed GC-s at closing base pair and triloop tip seems to be happy to create triloops. Watch the top loop, which is folding as it should. Where as the bottom pentaloop becomes a triloop with the same pattern. And I seen this triloop pattern work elsewhere in this lab.

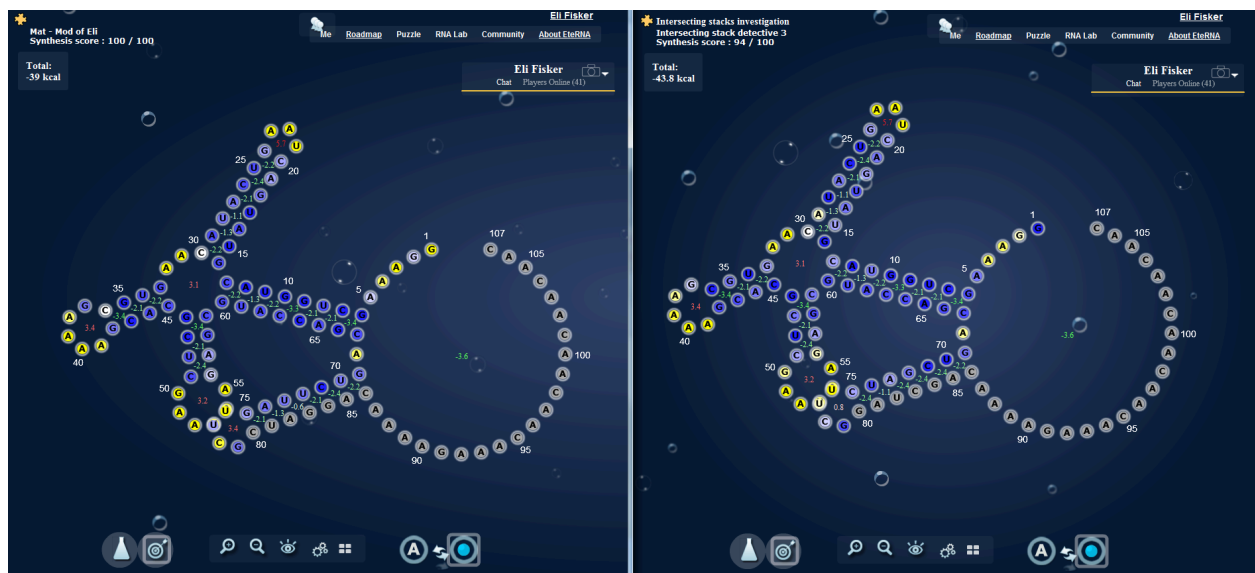


Barcode differences causing scores and SHAPE data differences

I found another thing I find interesting. Mat made a mod of one of my designs. Only difference is in the barcode (the section marked orange in Mat's design). Mine scores 94, Mat's scores 100. What is most different is that his has less negative energy and contains a GU - the later is something that have proved to relax a design and improve the shape data. Especially if it has longer stems. And there are two longer in here. One more time pointing out that GU's has a special potential. See [Lab designs that crave GU's](#) and [A backbone strain hypothesis for interpreting SHAPE data](#).



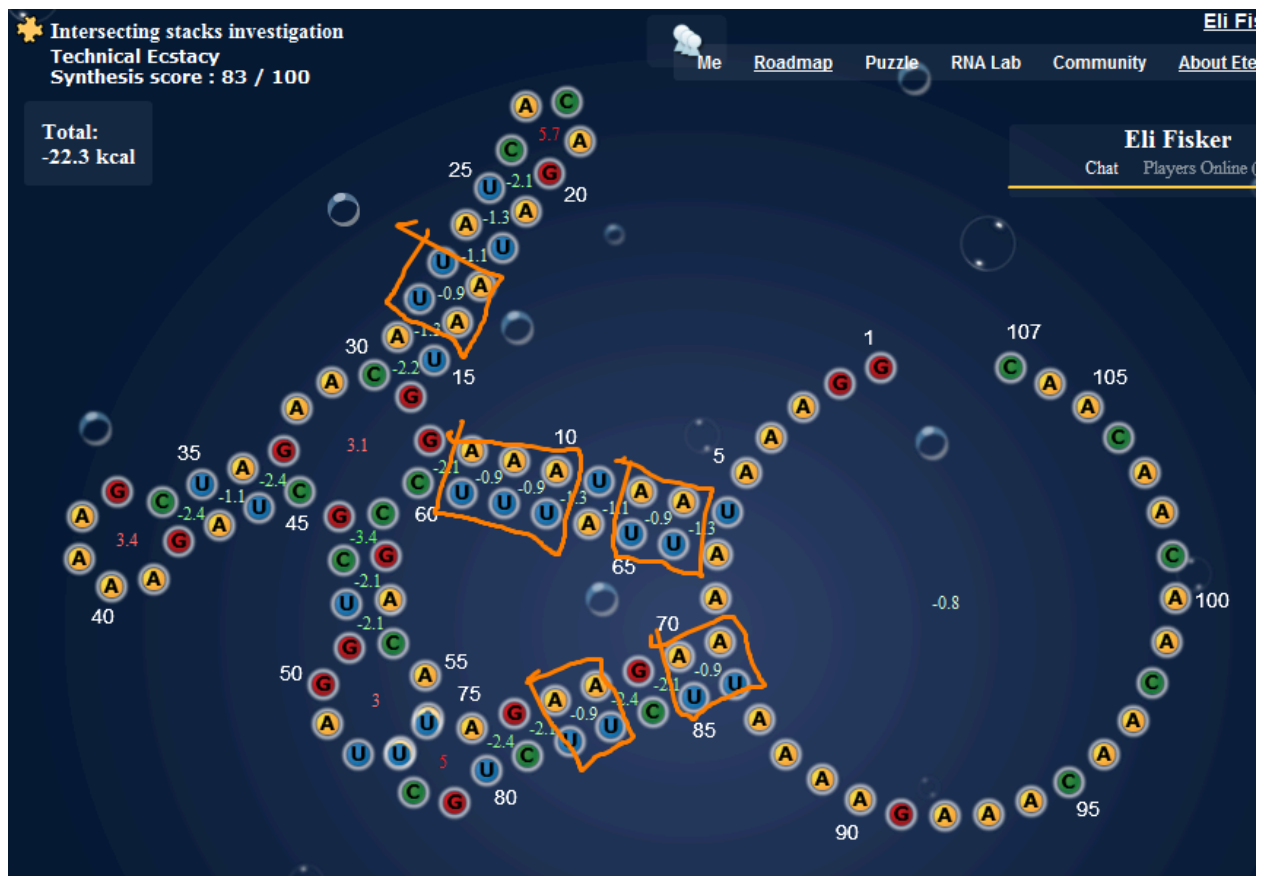
Also these designs have difference in their SHAPE colors in the main design, as I have earlier pointed out [here](#).



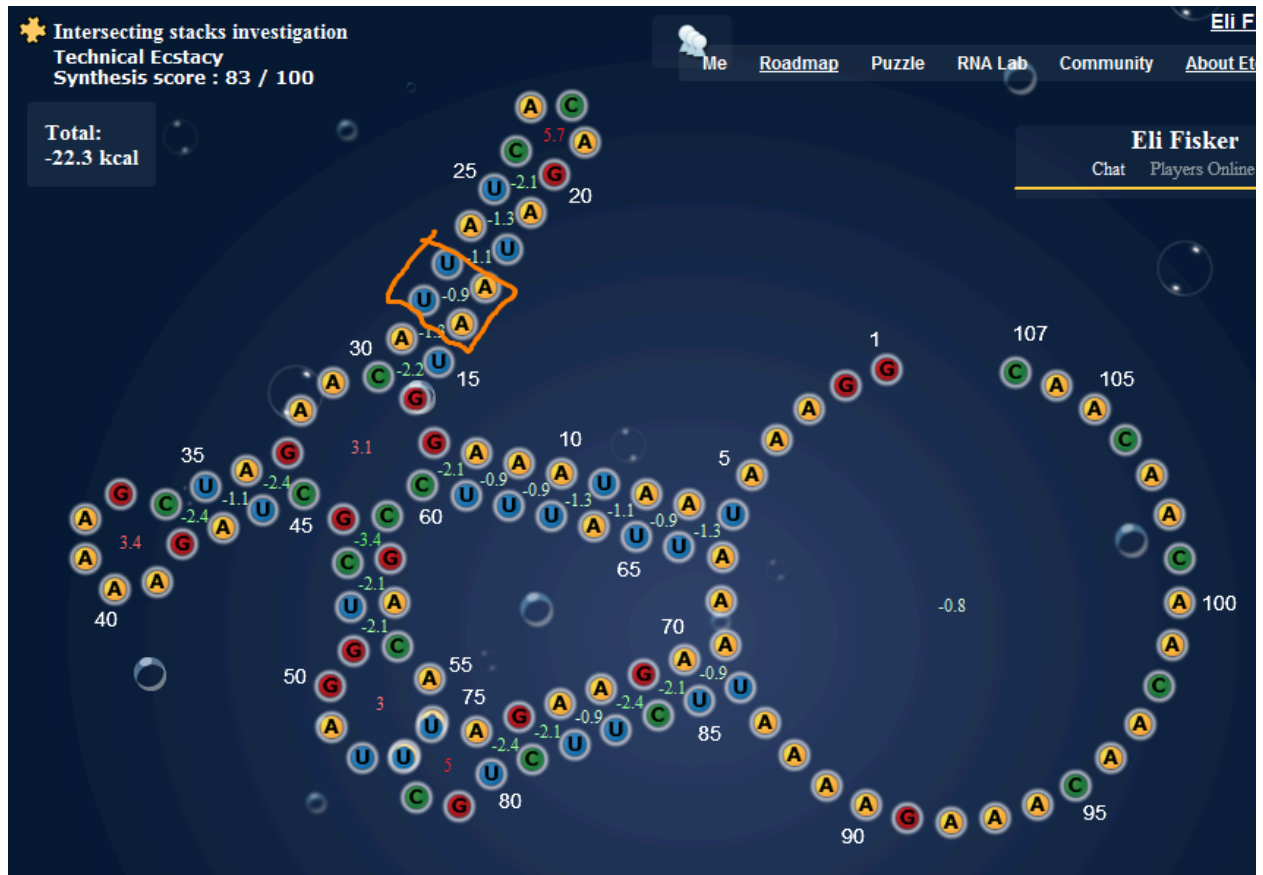
On repeat bases in line

By the way, the discussion about if mRNA folds stronger than our kind of RNA, caused me to rethink something I have been saying earlier. I sort of have been split about, seeing double same turning pairs as sort of both weak and strong. Weak, because I often saw them split in our lab designs, where we wanted to have them binding but also strong because I saw them at a higher rate in short stemmed and strongly pressured designs and involved in the switching area in switches. Since the discussion and the paper Omei dug up, it is clear that repeat bases do necessarily give a weaker overall fold. Rather I think I will have to shift perspective from what I think of as weak to what is actually forming and strong. I think I might be able to give an early example here.

Here is a typical example of what I will think as weak.



Now lets focus on one of them (Only two of them split)



A new double block (a quad of two same turning basepairs) is created.



But what I think is the main cause of all this happening, besides the weakness of the AU's is this new double block forming:



So to sum up, I sort of still think AU's in line are weak, and they are the ones making way for other misfolds to happen. But it is because the GC-blocks are stronger. Here it seems, even strong enough to make this mostly AU neck happen.

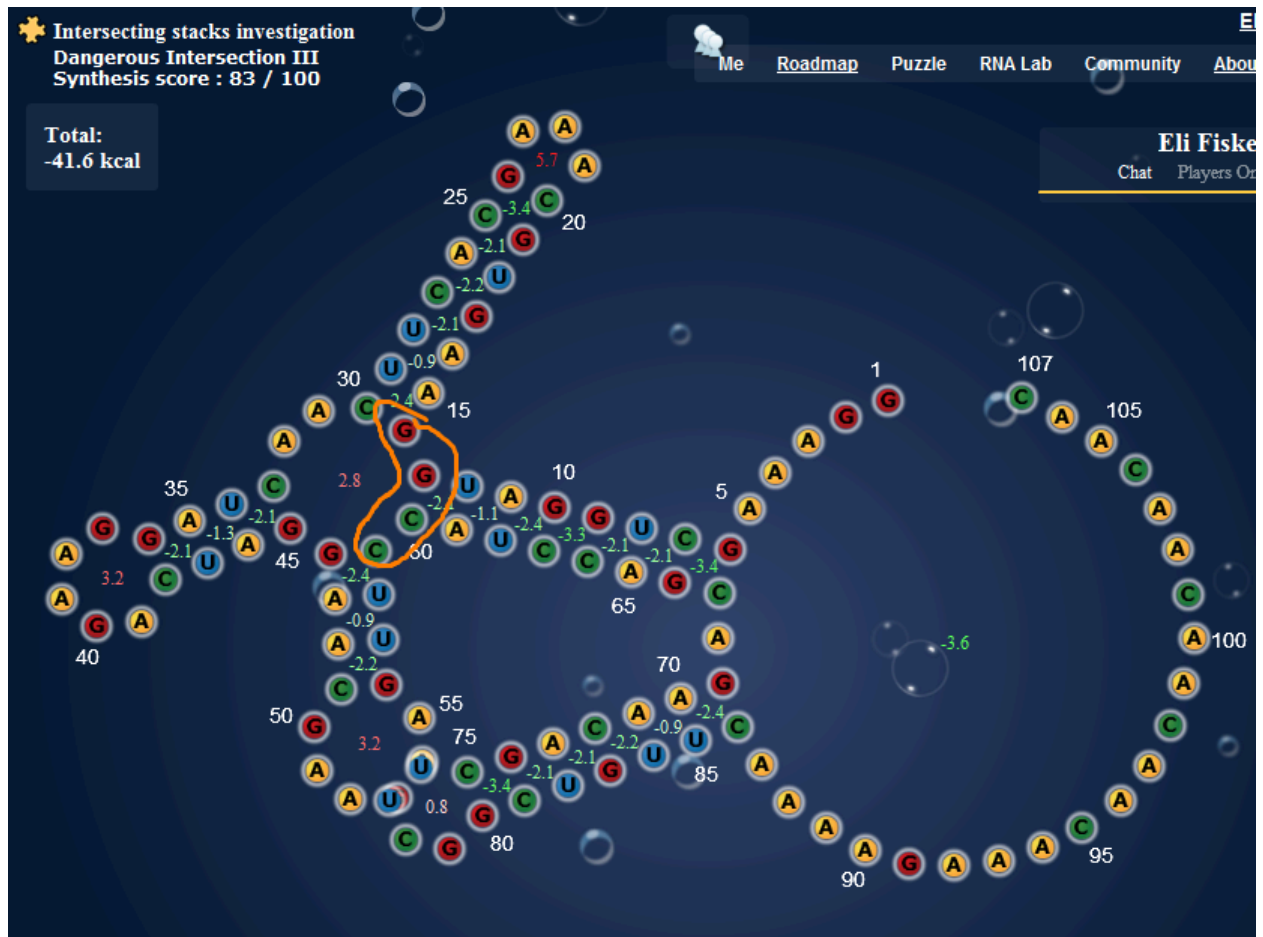
So this new way of seeing things might also explain something that I had a real hard time understand. Why ribosomal RNA and really huge RNA's had so many repeat basepairs compared to ours. Now it kind of makes sense. So repeat lines of bases, can be quite strong, but somehow they have a tendency to want to fold alternatively to seek out alternative partners, in a way that I don't understand. So they are not being weak, because they are breaking, they are being strong because they fold somewhere else. And there must be some rules about why they prefer elsewhere, that we just don't understand.

And somehow twisting basepairs so there is less repeat, seems to diminish that problem. Reducing the amount of potential elsewhere.

I have most likely not finished thinking this through.

Again this double GC-pair block forming, seems to have a very strong influence of the wanted structure not forming:

Target



Estimate

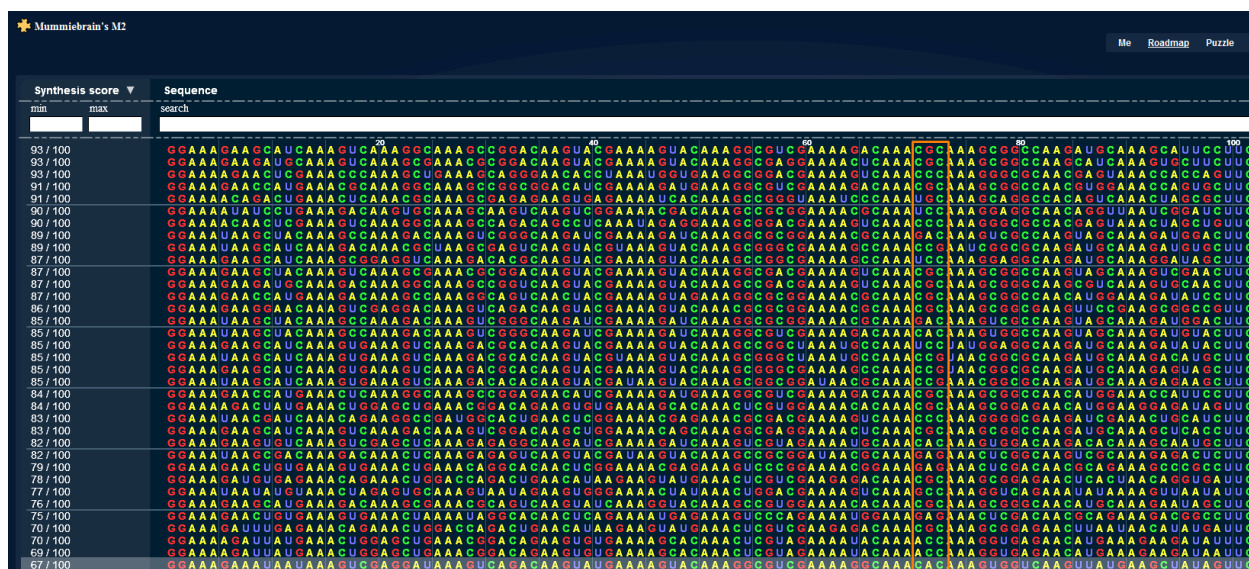
10 Nov 2013

AU's in adjacent multiloops

For the high scoring designs there was a tendency of having C's in particular on each end of a stem. However there also was a few U's at the one side.

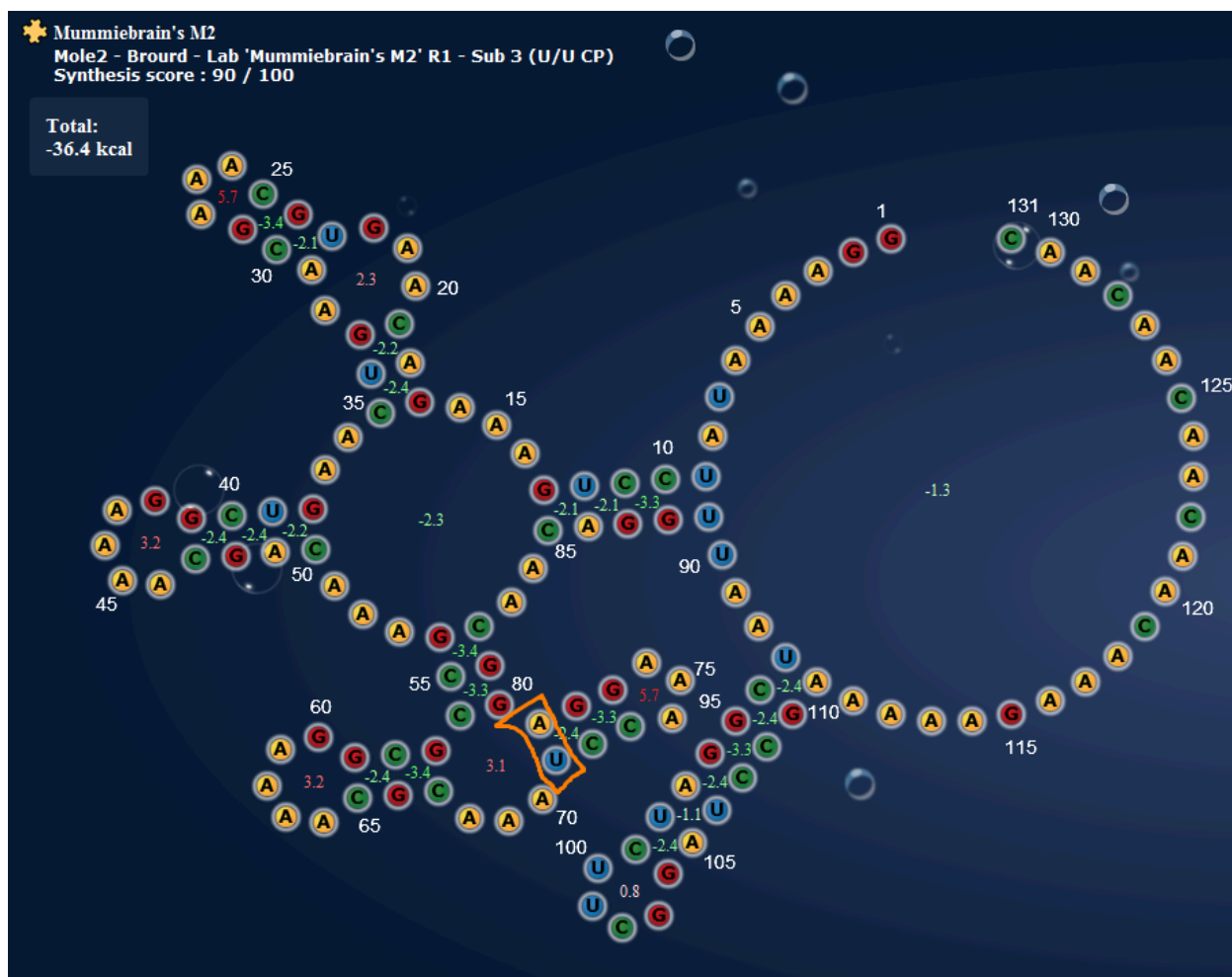
When I looked at the sequences something stood out. I was already expecting a high amount of GC-pairs in the short 3 nt stacks in general. I wasn't either surprised seeing them in particular in the 3 nt stack adjacently attached to a multiloop.

I have earlier seen short 3 nt stacks with a tri loop end having a higher tendency of same turning pairs.



However I in particular find it interesting that there is a high presence of designs which has AU at a particular spot in the adjacent multiloop. It seems like an AU here is a legal way of letting steam out and take off some of the pressure that the adjacency causes. It could look like this AU favors a particular spot and orientation too. Is this so?

Ok, only the two of Bround's designs were actually holding. The others didn't hold. So I will have to check some other labs.



I also have an idea that this only works in these “T” types of multiloops.

✦ Robot serial killer 2 - Lab killer too?
Stable, with GU
Synthesis score : 96 / 100

Total:
-48.9 kcal

107
105
100
95
90
85
80
75
70
65
60
55
50
45
40
35
30
25
20
15
10
5
1

Same orientation of AU's

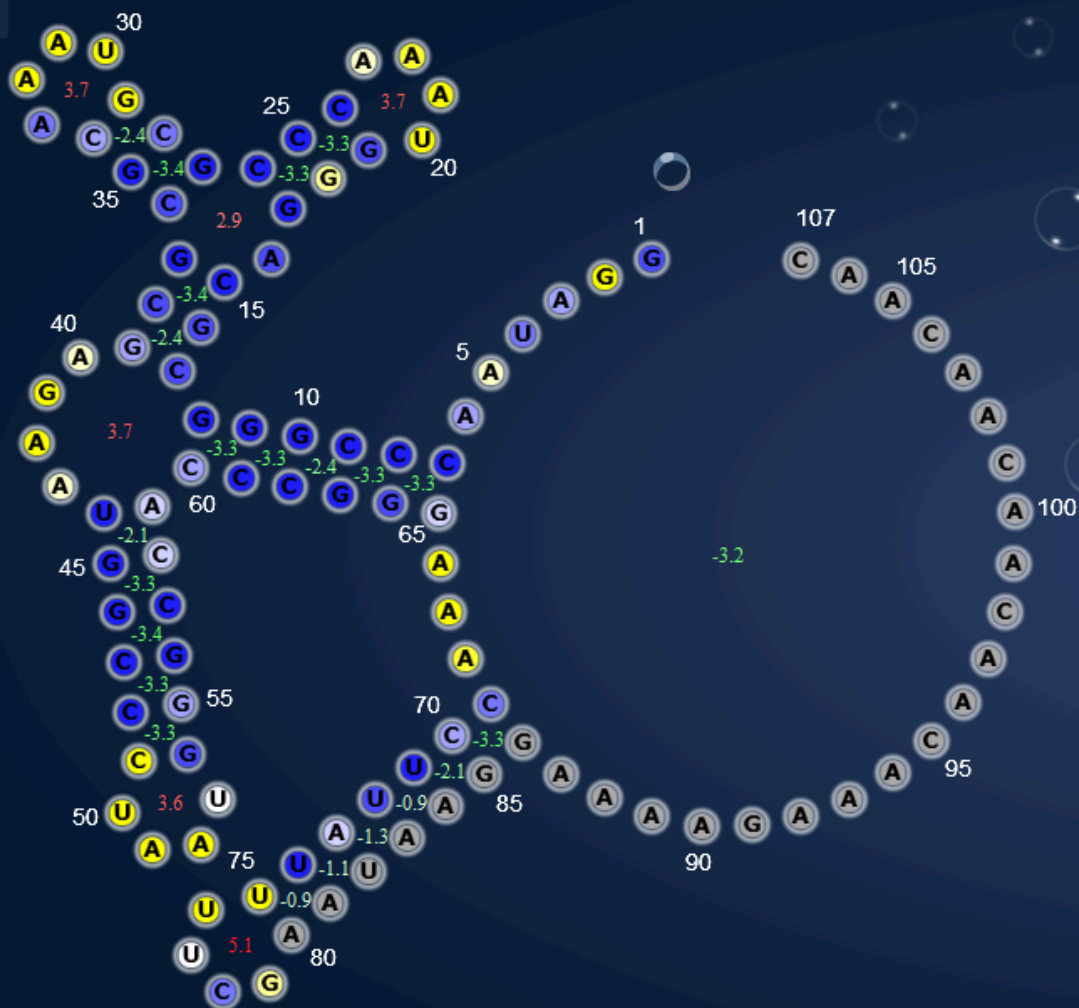


Mod 1

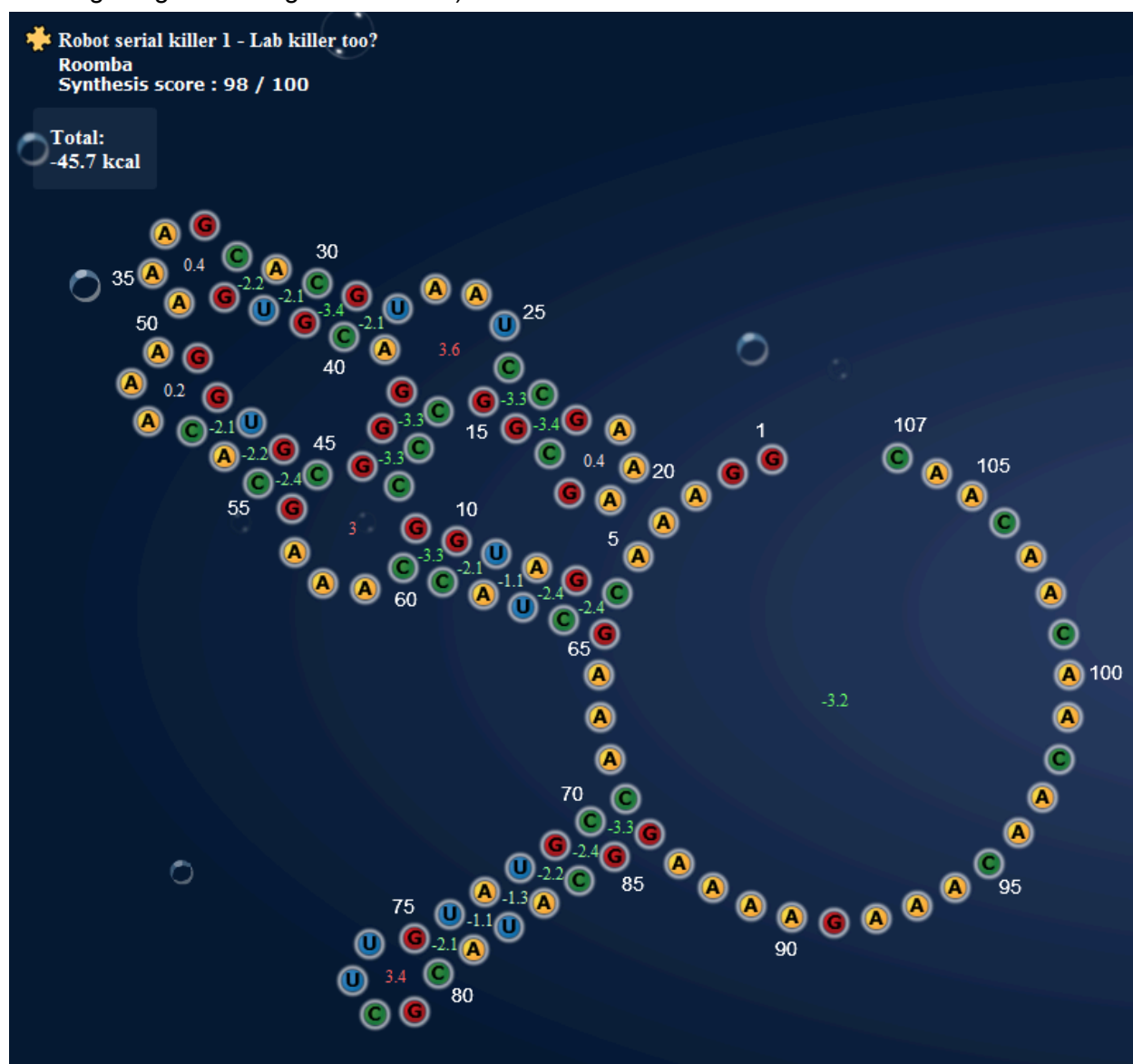
Synthesis score : 94 / 100

Total:

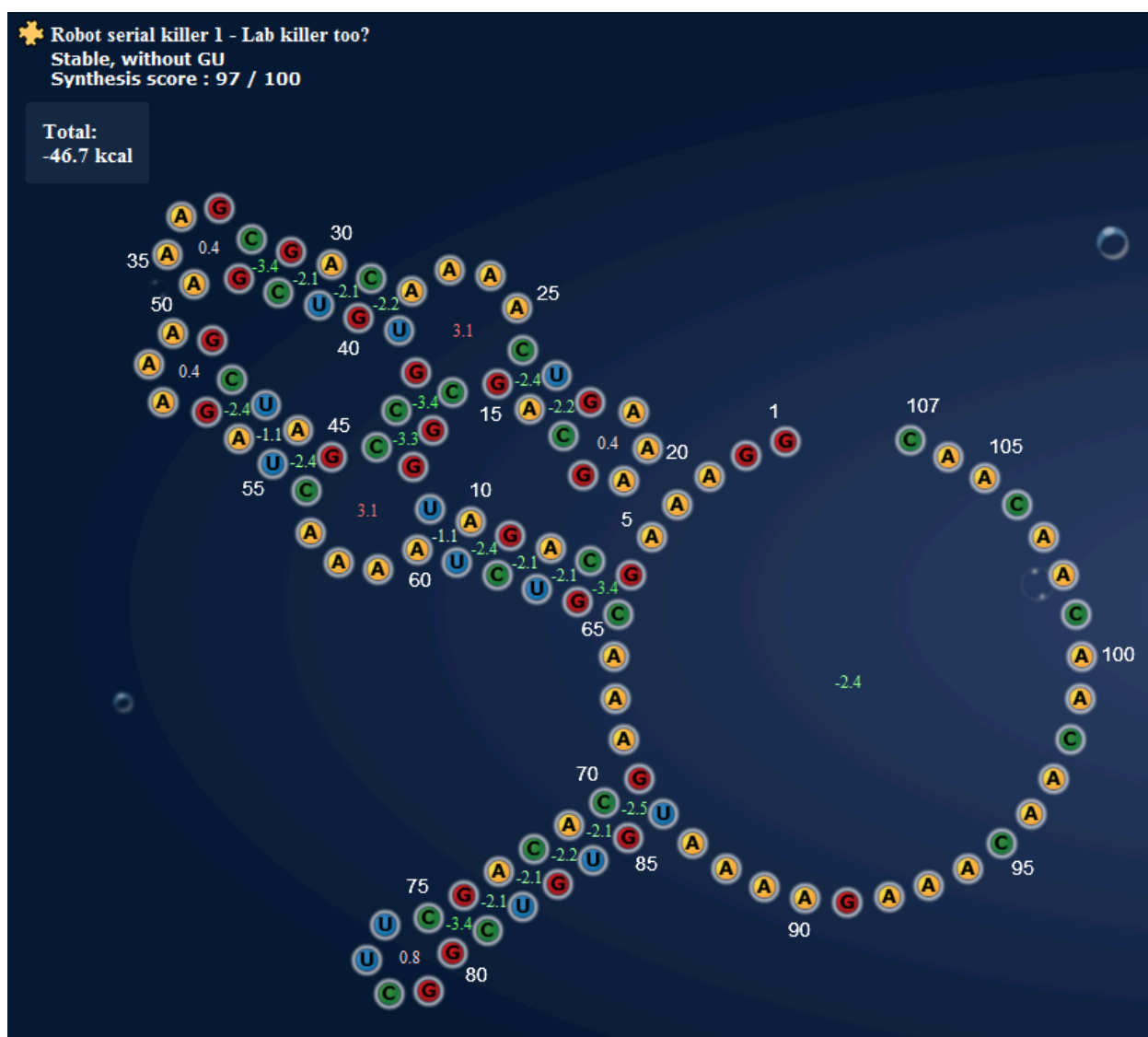
-39.3 kcal



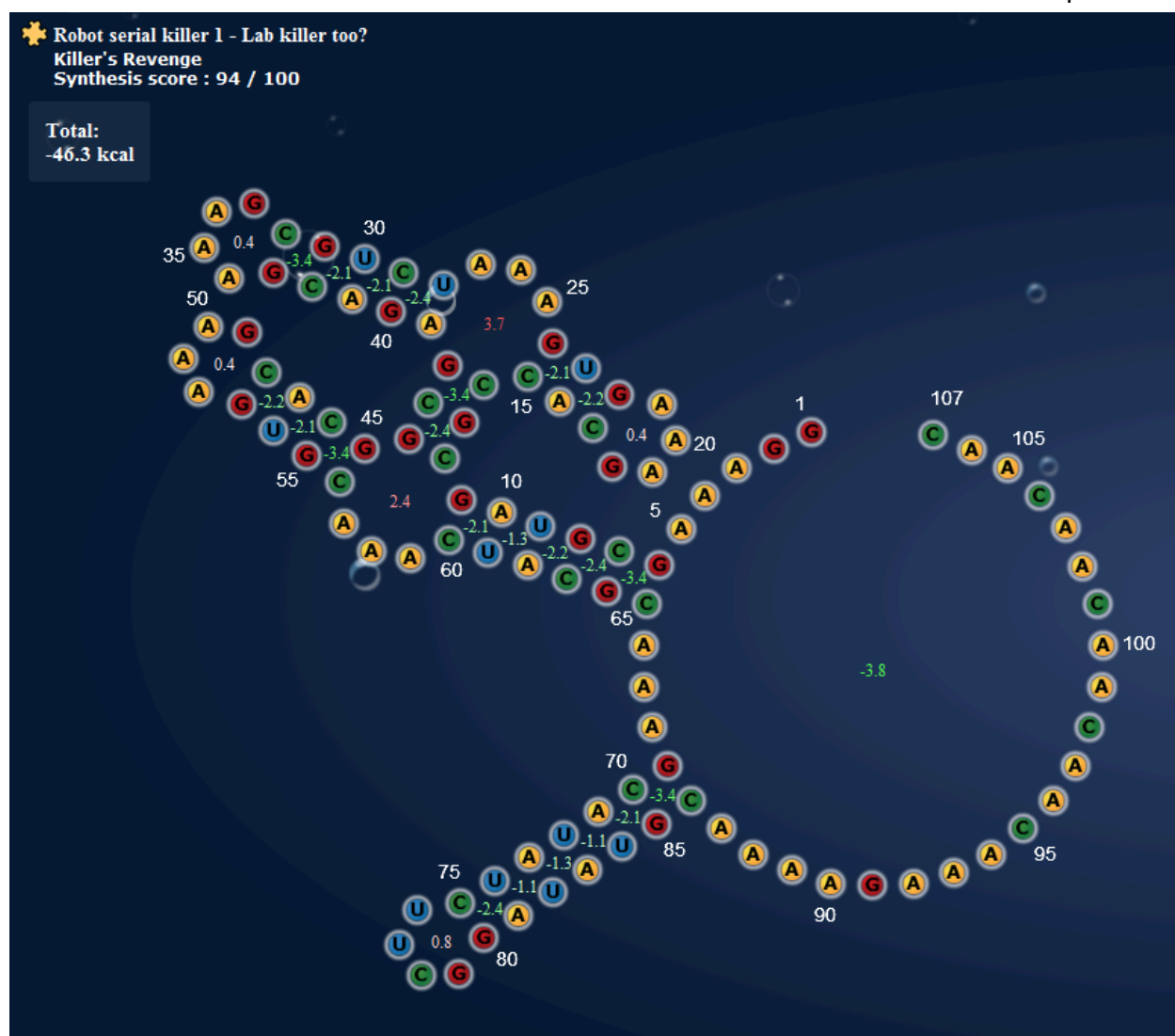
This is getting interesting. One more. :)



Yet another



And even one more. This one does not hold in the middle stem. But is stable in the AU part.



Intersecting stacks investigation

Xeorat
Synthesis score : 88 / 100

Total:
-37.6 kcal

The diagram illustrates the secondary structure of an RNA molecule, represented by a circular path of nucleotides numbered from 1 to 107. Each nucleotide is shown as a colored circle containing its base letter (A, U, G, C). Base pairs are indicated by lines connecting complementary bases across the structure. Stacking interactions are labeled with numerical values (e.g., -2.1, -2.4, -3.4) between adjacent base pairs. A specific region of the structure, involving nucleotides 30 through 60, is highlighted with an orange box, indicating an area of interest for intersecting stacks.

Note that most of the designs in these above labs, do have GC-pairs for all basepairs in the multiloops. I just find it very interesting that it goes well and is stable. They are a rarity, but still ends up among the highest scoring. And I find it particularly interesting that there seems to be a pattern in where the AU's like to turn up, and there might be a favored orientation.

Motor protein labs

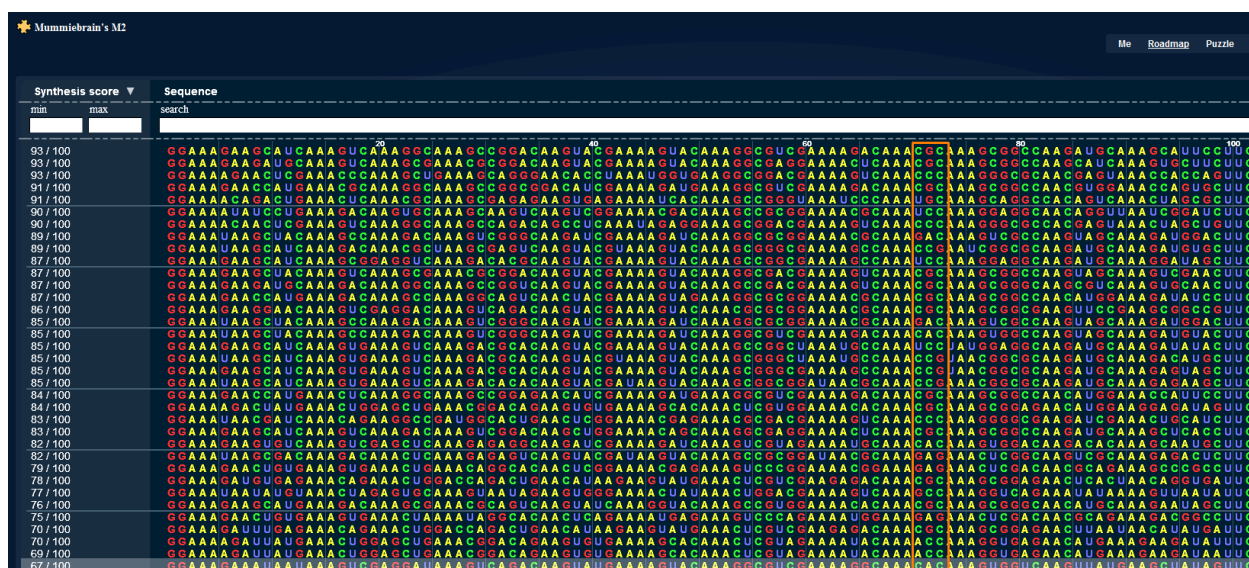
It seems that length of stem had everything to do with adjacent multiloops being hard. :) Real nice to know.

There was a fine amount of winners in all the labs with different kind of adjacent multiloops, as soon as I prolonged the stacks.

For the high scoring designs there was a tendency of having C's in particular on each end of a stem. However there also was a few U's at the one side.

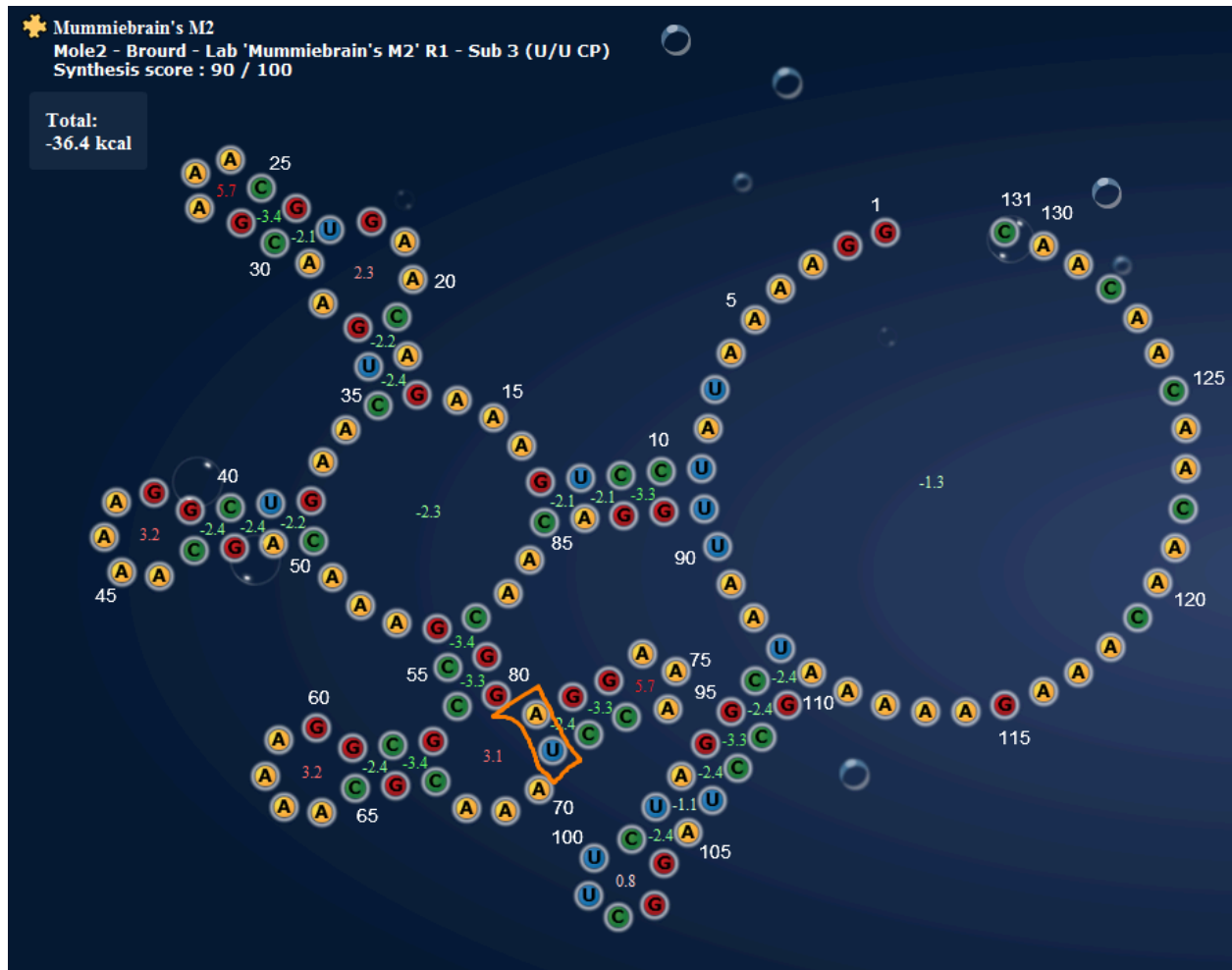
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I have earlier seen short 3 nt stacks with a tri loop end having a higher tendency of same turning pairs.



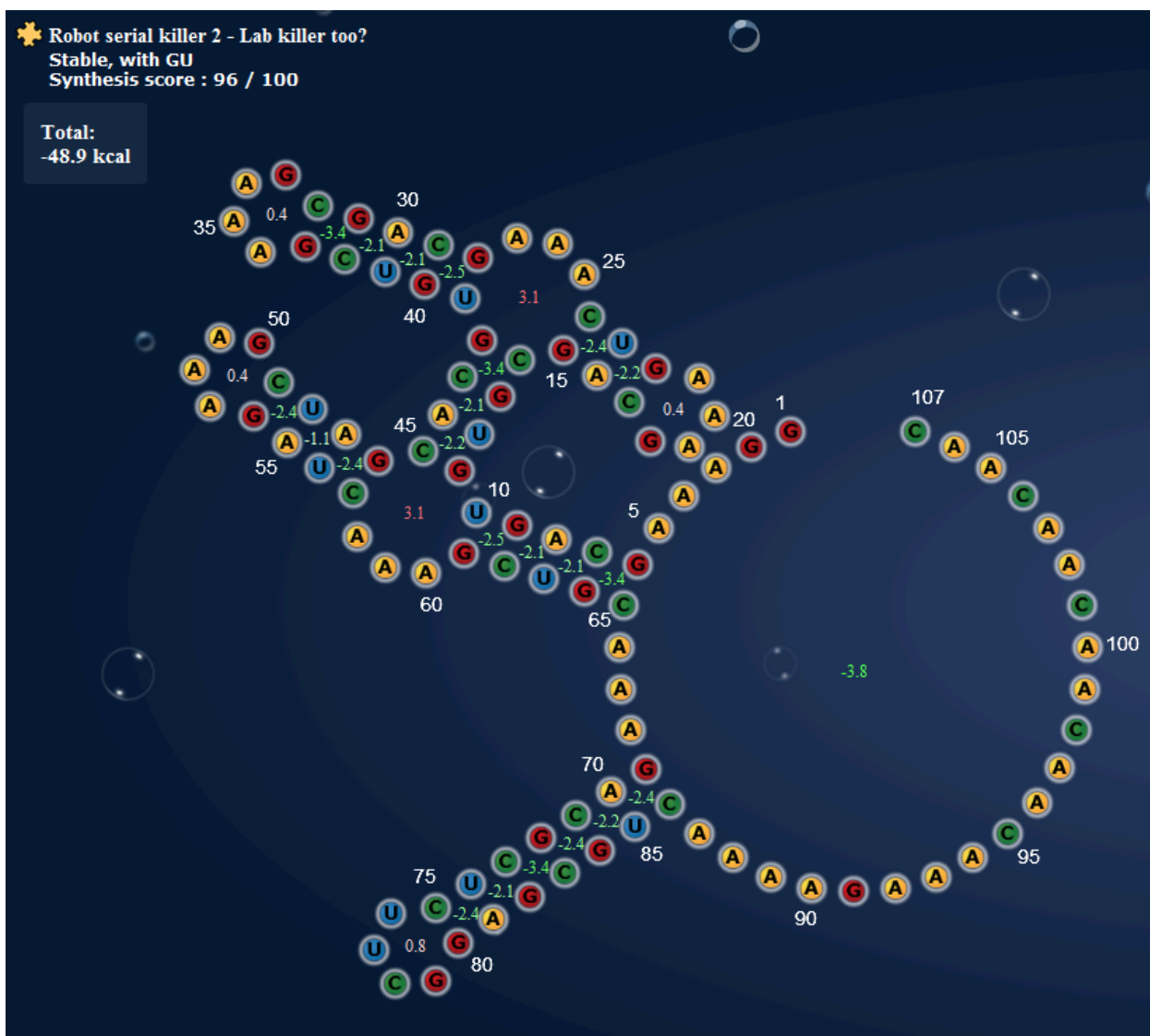
However I in particular find it interesting that there is a high presence of designs which has AU at a particular spot in the adjacent multiloop. It seems like an AU here is a legal way of letting steam out and take off some of the pressure that the adjacency causes. It could look like this AU favors a particular spot and orientation too. Is this so?

Ok, only the two of Brouard's designs were actually holding. The others didn't hold. So I will have to check some other labs.



I also have an idea that this only works in these “T” types of multiloops.

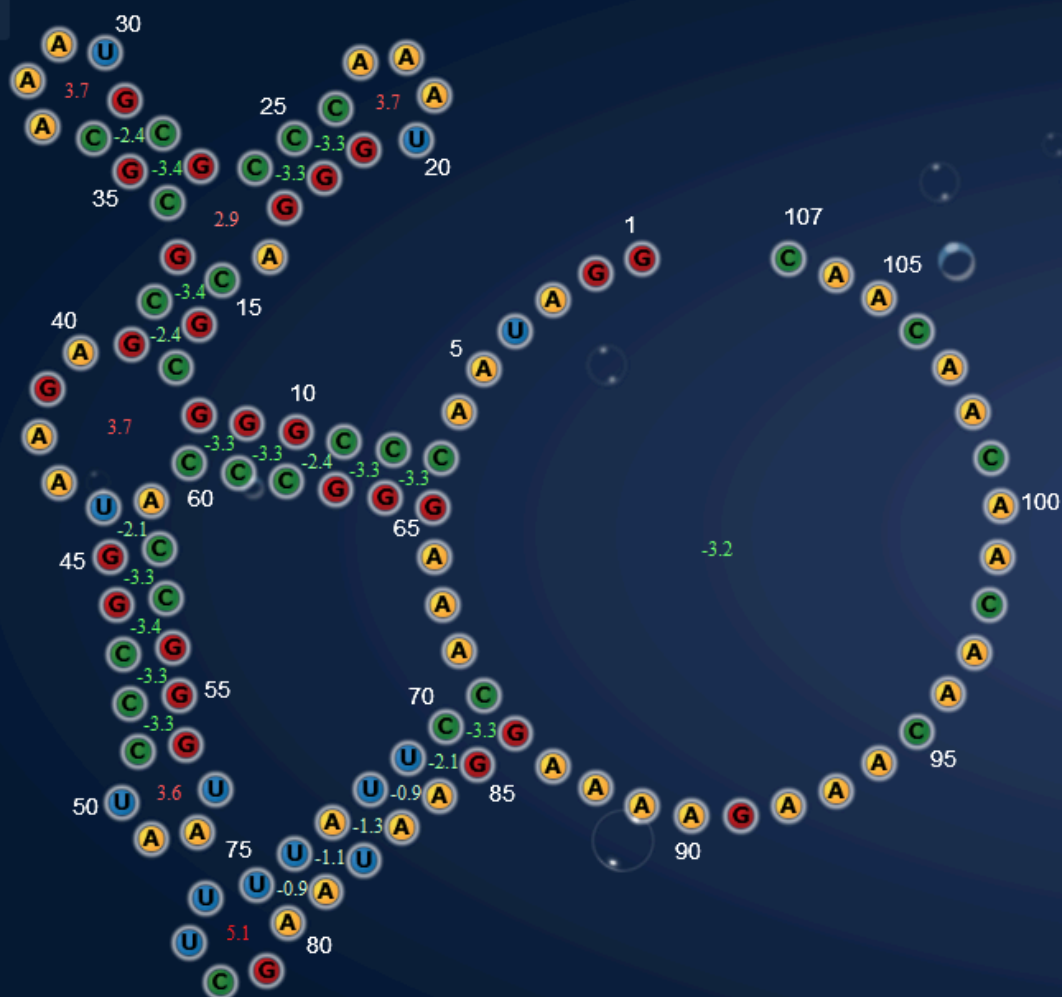
Starry made one too. The alternative pair ended up in same position (interesting!), however with different orientation and it was a GU instead of an AU.

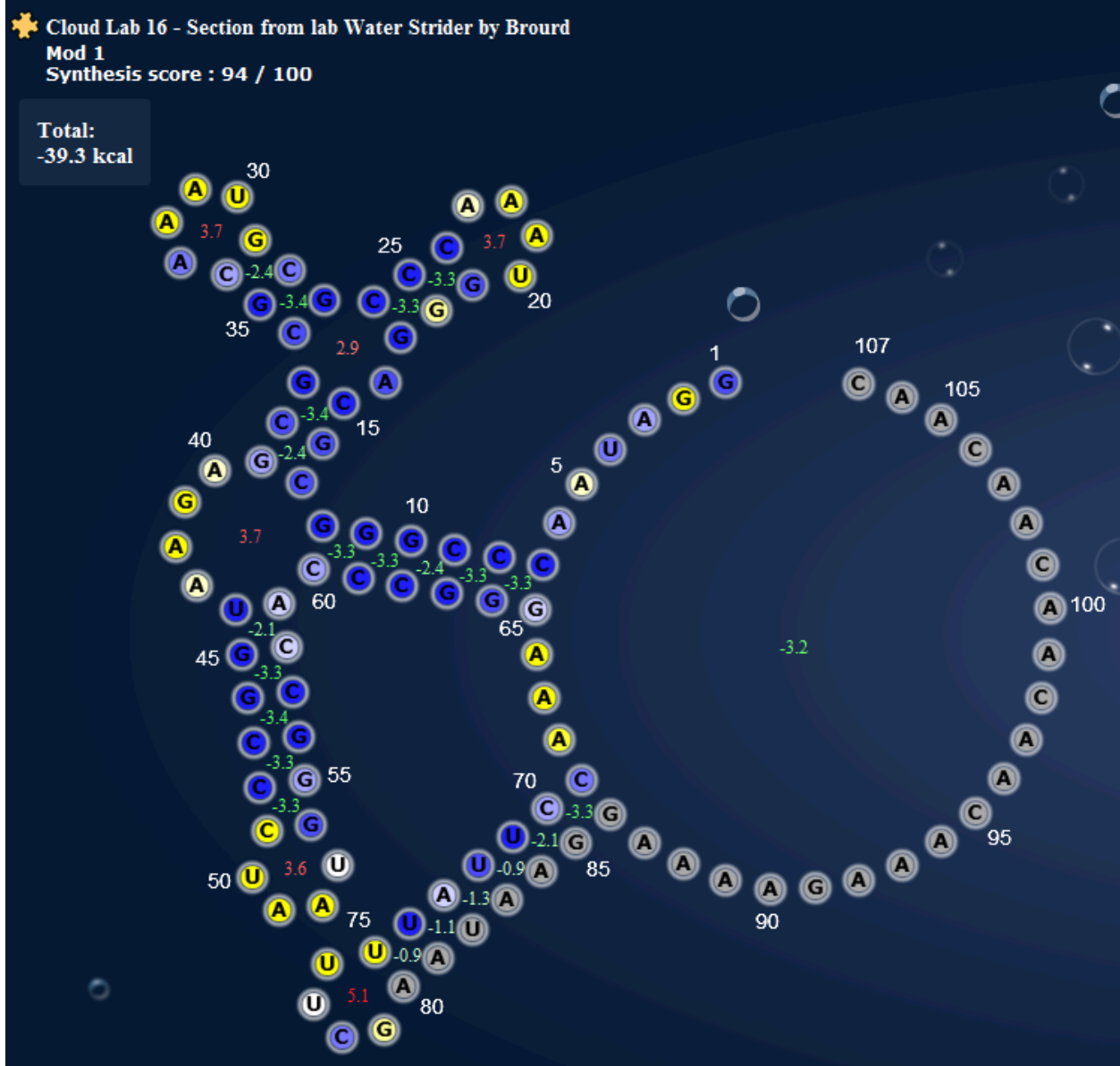


Same orientation of AU's

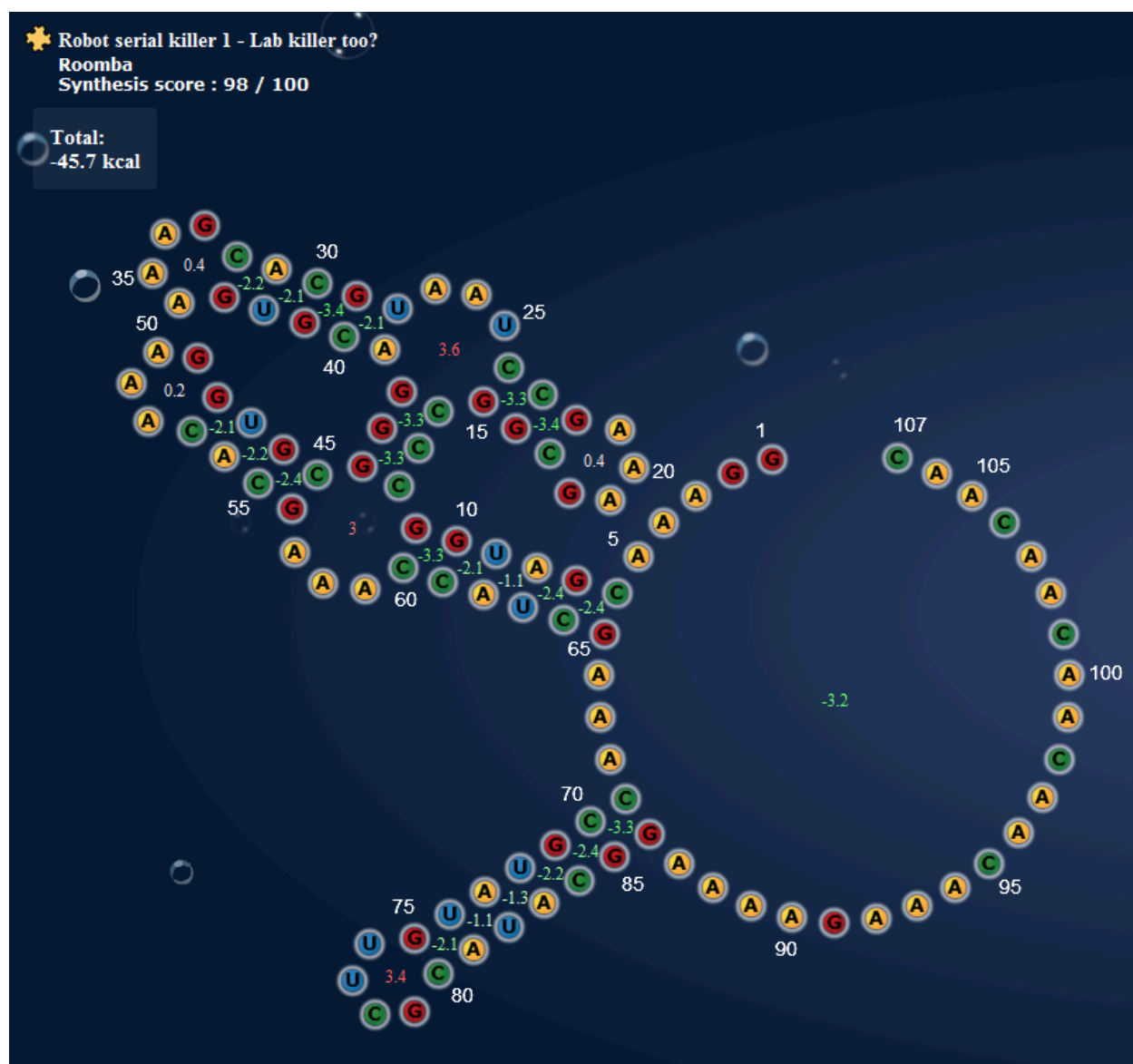
Cloud Lab 16 - Section from lab Water Strider by Bround
 Mod 1
 Synthesis score : 94 / 100

Total:
 -39.3 kcal

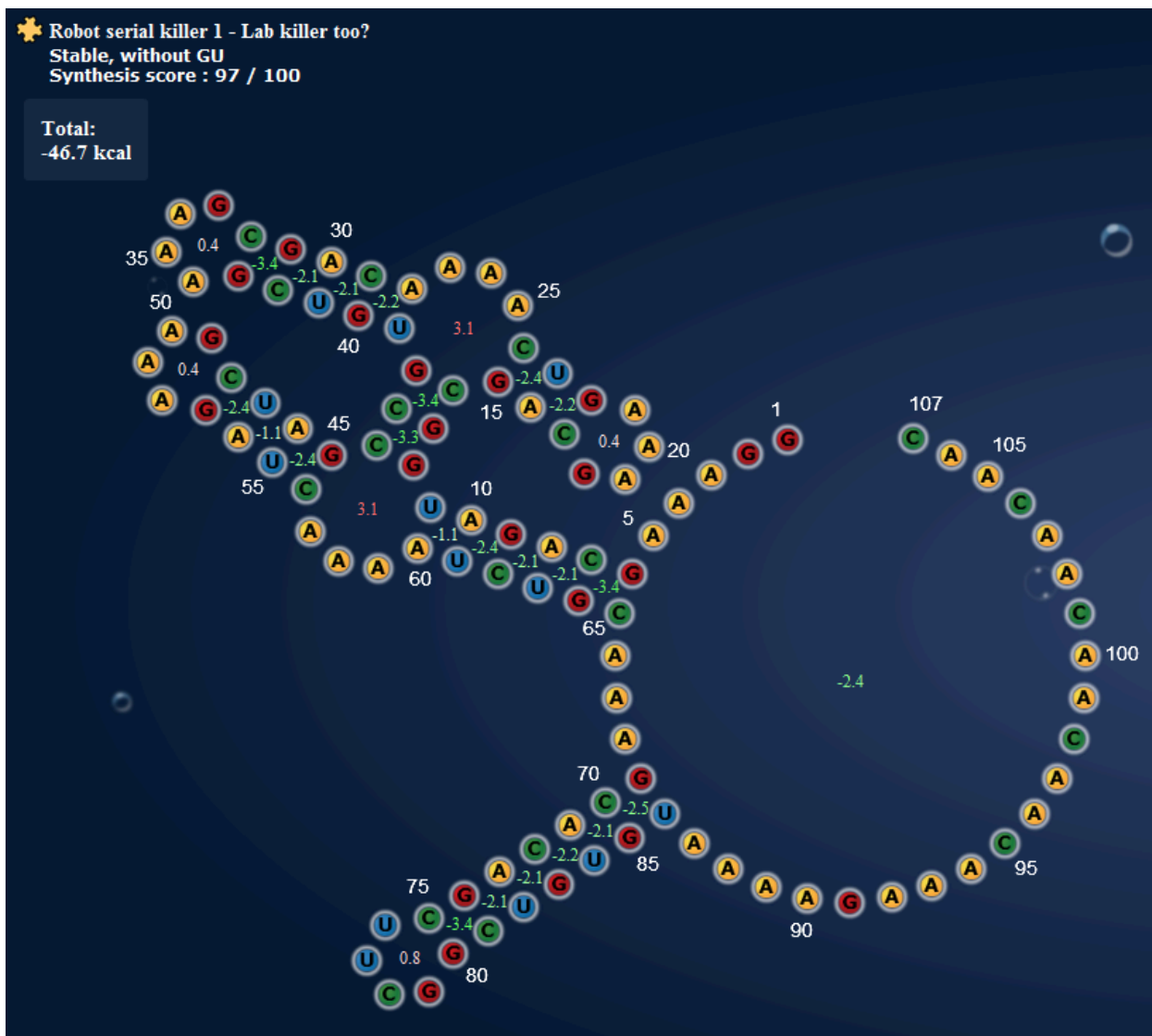




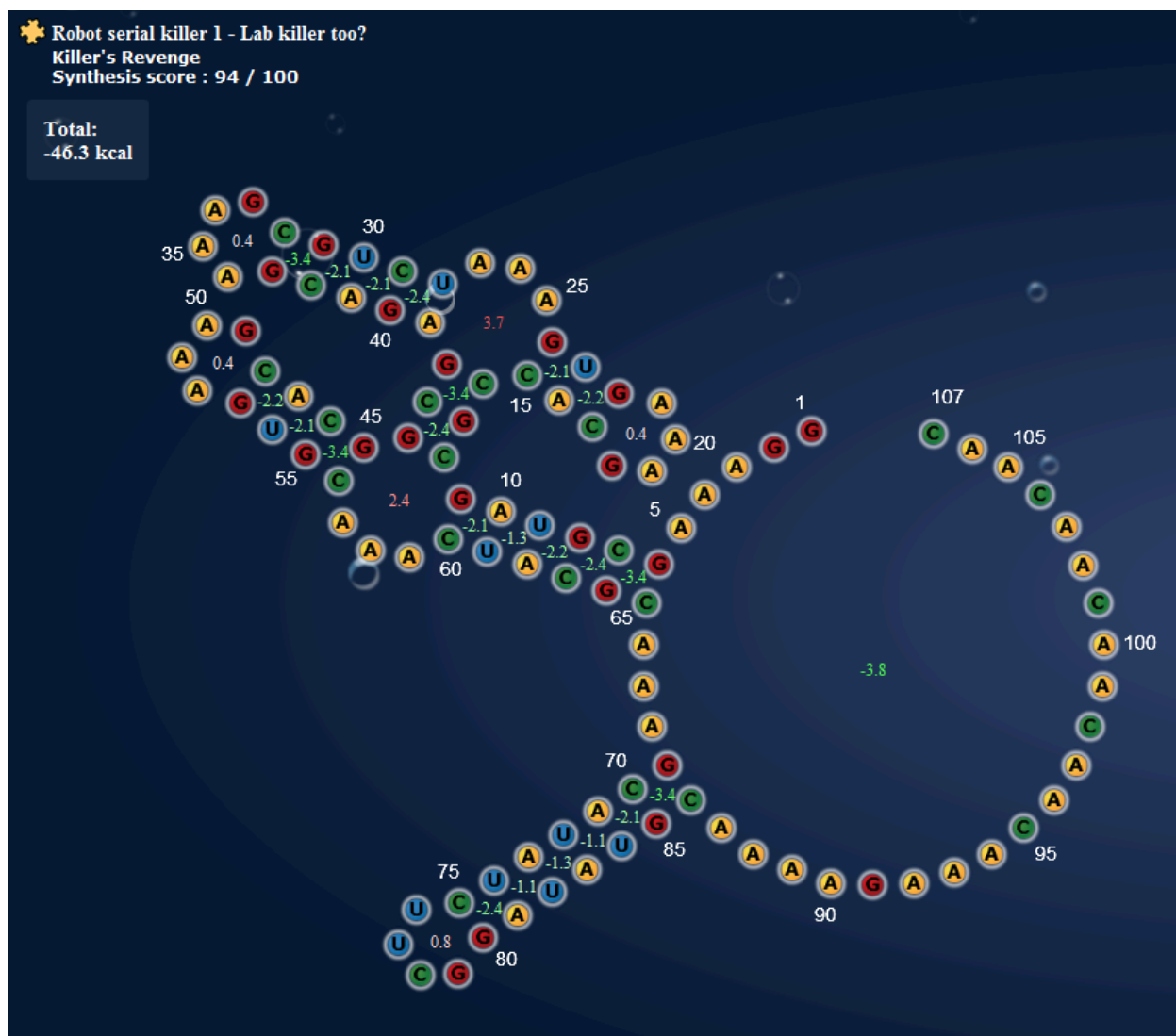
This is getting interesting. One more. :)



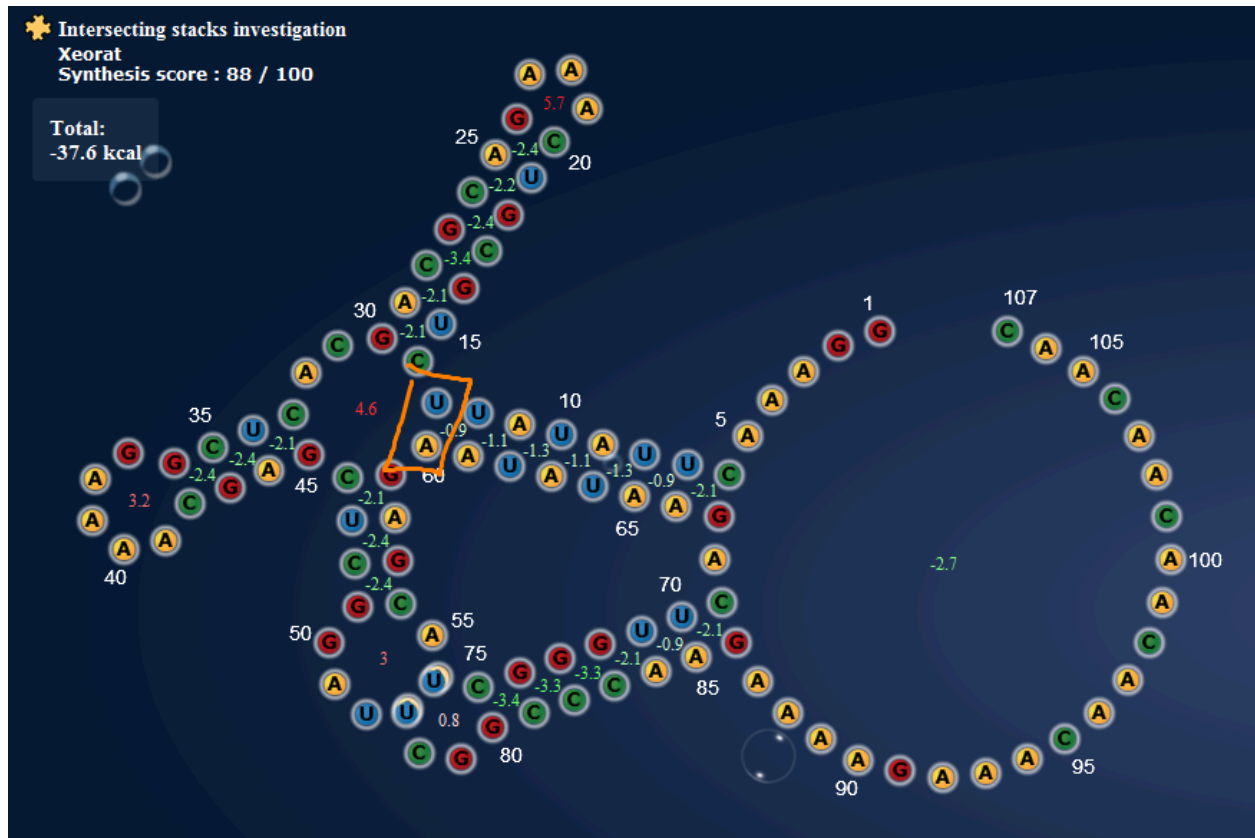
Yet another



And even one more. This one does not hold in the middle stem. But is stable in the AU part.



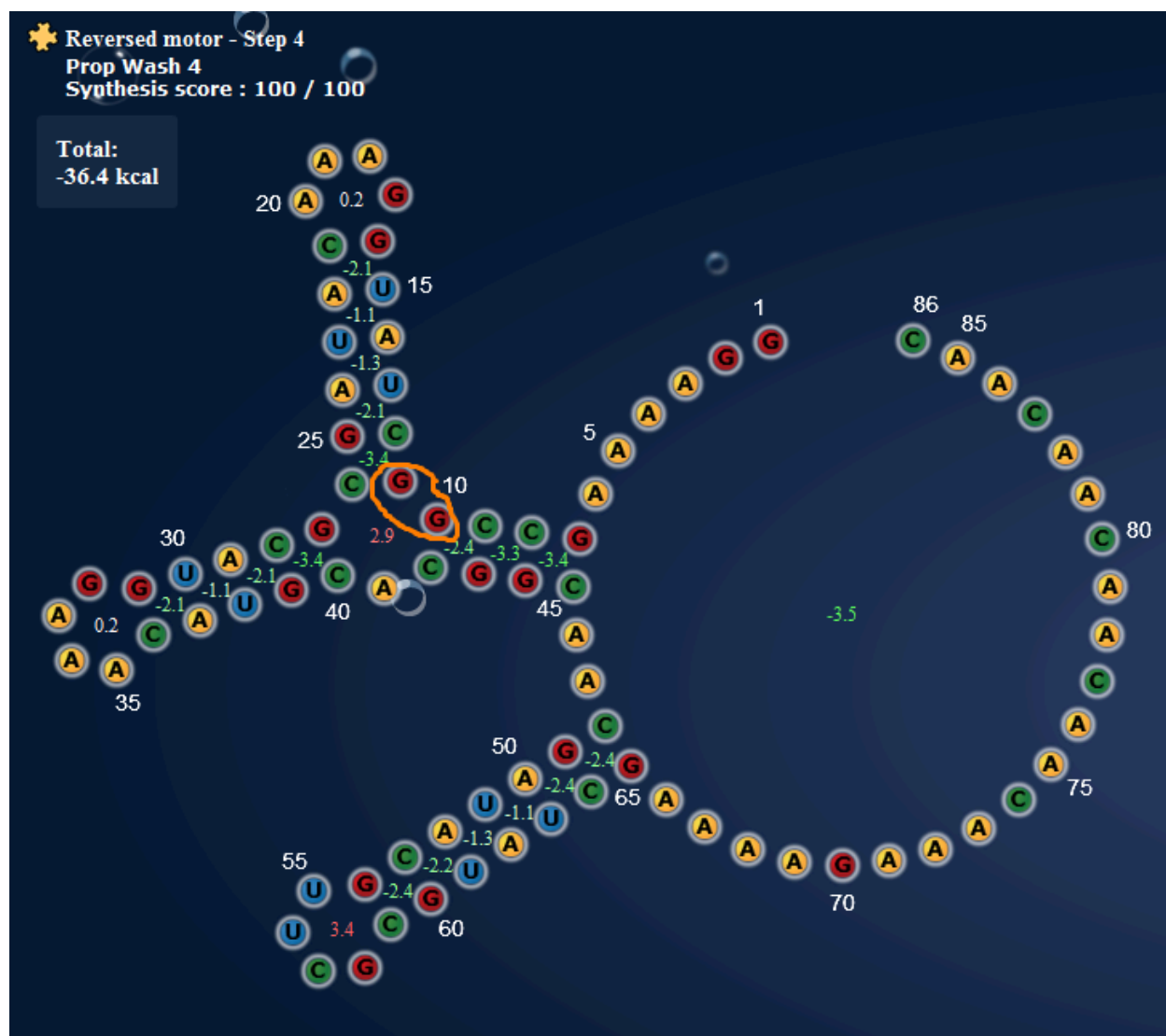
A related one here, and a very strange neck. :) But true to the weird nature of necks.



So this thing with AU's seem to particular to turn up when designs has 3 or more adjacent stems. I think JL mentioned something about it being less penalized, when he reverse engineered Vienna's energy model.

Note that most of the designs in these above labs, do have GC-pairs for all basepairs in the multiloops. I just find it very interesting that it goes well and is stable. They are a rarity, but still ends up among the highest scoring. And I find it particularly interesting that there seems to be a pattern in where the AU's like to turn up.

Reverse motor 4 (24 af 40 winners)



And again I see that the facing bases in the adjacent multi loop likes to turn up in a specific spot.
(Base 10-11 rather than 26-27) Usual orientation also do well.

Title	Synthesis score ▾	Sequence
search	min max	search
Prop Wash 4	100 / 100	GGAAAGCGCGCUAU ²⁰ GAAACAUA ⁴⁰ CGGCAACGAUAGCUUC
Bebiorbe	100 / 100	GGAAAGCGCGCUUCCAUACGGGAA ²⁰ CGCUCAAUAGAGGACGACGUAUGGCUUC
JR_Reversed4_Rn...	100 / 100	GGAAAGCGCGCAUAAGAAAUUAUUG ²⁰ CAUGAAAUAGUCACAGCAAGAGUAGCUUC
Testing 'barcod...	98 / 100	GGAAAGCGCGCAUAAGAAAUUAUUG ²⁰ CAUGAAAUAGUCACAGCAAGAGUAGCUUC
RM4 - #1	98 / 100	GGAAAGAGCGGACGACUUCGGUUCG ²⁰ CAUUCUGGAUGGACGUCAAAGAGUAGCUUC
rotom 4 revival	98 / 100	GGAAAGCGCGCUUCCAUACGGGAA ²⁰ CGCUCAAUAGAGGACGACGUAUGGCUUC
JR_Reversed3_Rn...	98 / 100	GGAAAGCGCGCAUUCGAAACGAUG ²⁰ CGCUCGAAACGAGCAGCAGCAAGGCUUC
RSM4 1	98 / 100	GGAAAGCGCGCUUCCAUACGGGAA ²⁰ CGCUCAAUAGAGGACGACGUAUGGCUUC
Mageonre	98 / 100	GGAAAGCGCGUCCACUACAGUGGAG ²⁰ CGCAGUAGCAGACAGUGGAAAGUAGGCUUC
Dinner is reSer...	96 / 100	GGAAAGCGCGGUCAGGAAACUGAG ²⁰ CGAUGGAAAGCAUCAGCGGAAAGUAGCUUC
Dinner is Serve...	96 / 100	GGAAAGCGCGGUCAGGAAAGUACG ²⁰ CGAUGGAAAGCAUCAGCGGAAAGUAGCUUC
RM4 - #2	96 / 100	GGAAAGAGCGGACGACUUCGGUUCG ²⁰ CAUUCUGGAUGGACGUCAAAGAGCUCUUC
RSM4 3	96 / 100	GGAAAGAGCGGACUAGGAAAGUAUUG ²⁰ CAUGAAAGCAUCAGCAGCAAGGCUUC
RSM4 2	96 / 100	GGAAAGAGCGGAUUAACGAAAGUUAUG ²⁰ CAUGAAAGCAUCAGCAGCAAGGCUUC
Aazage	96 / 100	GGAGGAGCGGUCUGGAAAGCAAG ²⁰ CGUUGGAAAGCAUCAGCAGCAAGGCUUC
Fiskers reverse...	94 / 100	GGAAAGAGCGGACGACGAAAGUGCG ²⁰ CAUGGAAAGCAUCAGCAGCAAGGCUUC
Fiskers reverse...	94 / 100	GGAAAGAGCGGACGACUUCGAAACGCU ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
wsr 3	94 / 100	GGAAAGAGCGGACUUCGAAACGAAUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
20/20 v.3 (0-0...	94 / 100	GGAAAGAGCGGCAUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
20/20 v.2 (0-0...	94 / 100	GGAAAGAGCGGCAUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
Mat - Reversed ...	94 / 100	GGAAAGAGCGGAUAAGGAAAGCUAUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
October	94 / 100	GGAAAGAGCGGACUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
17 something	94 / 100	GGAAAGAGCGGCGCAUCGAAAGUAGG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Spic N Span	94 / 100	GGAAAGAGCGGACUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
Dinner is Deer ...	93 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
RM S4 V1	93 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
RM4 - #3	93 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
a step in the r...	93 / 100	GGAAAGAGCGGCAUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Rotom 4	93 / 100	GGAAAGAGCGGCAUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Mat - Mod of Eli	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Fiskers reverse...	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
wsr 2	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
mod 17	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
October II	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Step four	89 / 100	GGAAAGAGCGGCAUACGAAAGUUAUG ²⁰ CGAAGCAAGUUGAGGCGCAAGGCUUC

There are much more instabilities for the the latter than the first orange box, though and growing instability in the design. I'm thinking on strain on the backbone. Like Omei mentioned earlier.

Title	Synthesis score ▾	Sequence
search	min max	search
Prop Wash 4	100 / 100	GGAAAGCGCGCUAU ²⁰ GAAACAUA ⁴⁰ CGGCAACGAUAGCUUC
Bebiorbe	100 / 100	GGAAAGCGCGCUUCCAUACGGGAA ²⁰ CGCUCAAUAGAGGACGACGUAUGGCUUC
JR_Reversed4_Rn...	100 / 100	GGAAAGCGCGCAUAAGAAAUUAUUG ²⁰ CAUGAAAUAGUCACAGCAAGAGUAGCUUC
Testing 'barcod...	98 / 100	GGAAAGCGCGCAUAAGAAAUUAUUG ²⁰ CAUGAAAUAGUCACAGCAAGAGUAGCUUC
RM4 - #1	98 / 100	GGAAAGAGCGGACGACUUCGGUUCG ²⁰ CAUUCUGGAUGGACGUCAAAGAGUAGCUUC
rotom 4 revival	98 / 100	GGAAAGCGCGCUUCCAUACGGGAA ²⁰ CGCUCAAUAGAGGACGACGUAUGGCUUC
JR_Reversed3_Rn...	98 / 100	GGAAAGCGCGCAUUCGAAACGAUG ²⁰ CGCUCGAAACGAGCAGCAGCAAGGCUUC
RSM4 1	98 / 100	GGAAAGCGCGCUUCCAUACGGGAA ²⁰ CGCUCAAUAGAGGACGACGUAUGGCUUC
Mageonre	98 / 100	GGAAAGCGCGUCCACUACAGUGGAG ²⁰ CGCAGUAGCAGACAGUGGAAAGUAGGCUUC
Dinner is reSer...	96 / 100	GGAAAGCGCGGUCAGGAAACUGAG ²⁰ CGAUGGAAAGCAUCAGCGGAAAGUAGCUUC
Dinner is Serve...	96 / 100	GGAAAGCGCGGUCAGGAAAGUACG ²⁰ CGAUGGAAAGCAUCAGCGGAAAGUAGCUUC
RM4 - #2	96 / 100	GGAAAGAGCGGACGACUUCGGUUCG ²⁰ CAUUCUGGAUGGACGUCAAAGAGCUCUUC
RSM4 3	96 / 100	GGAAAGAGCGGACUAGGAAAGUAUUG ²⁰ CAUGAAAGCAUCAGCAGCAAGGCUUC
RSM4 2	96 / 100	GGAAAGAGCGGAUUAACGAAAGUUAUG ²⁰ CAUGAAAGCAUCAGCAGCAAGGCUUC
Aazage	96 / 100	GGAGGAGCGGUCUGGAAAGCAAG ²⁰ CGUUGGAAAGCAUCAGCAGCAAGGCUUC
Fiskers reverse...	94 / 100	GGAAAGAGCGGACGACGAAAGUGCG ²⁰ CAUGGAAAGCAUCAGCAGCAAGGCUUC
Fiskers reverse...	94 / 100	GGAAAGAGCGGACGACUUCGAAACGCU ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
wsr 3	94 / 100	GGAAAGAGCGGACUUCGAAACGAAUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
20/20 v.3 (0-0...	94 / 100	GGAAAGAGCGGCAUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
20/20 v.2 (0-0...	94 / 100	GGAAAGAGCGGCAUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
Mat - Reversed ...	94 / 100	GGAAAGAGCGGAUAAGGAAAGCUAUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
October	94 / 100	GGAAAGAGCGGACUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
17 something	94 / 100	GGAAAGAGCGGCGCAUCGAAAGUAGG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Spic N Span	94 / 100	GGAAAGAGCGGACUACGAAAGUAUUG ²⁰ CGAUGGAAAGCAUCAGCAGCAAGGCUUC
Dinner is Deer ...	93 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
RM S4 V1	93 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
RM4 - #3	93 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
a step in the r...	93 / 100	GGAAAGAGCGGCAUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Rotom 4	93 / 100	GGAAAGAGCGGCAUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Mat - Mod of Eli	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Fiskers reverse...	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
wsr 2	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
mod 17	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
October II	91 / 100	GGAAAGAGCGGCGUUCGAAAGCAAG ²⁰ CGUUCGAAAGCAUCAGCAGCAAGGCUUC
Step four	89 / 100	GGAAAGAGCGGCAUACGAAAGUUAUG ²⁰ CGAAGCAAGUUGAGGCGCAAGGCUUC

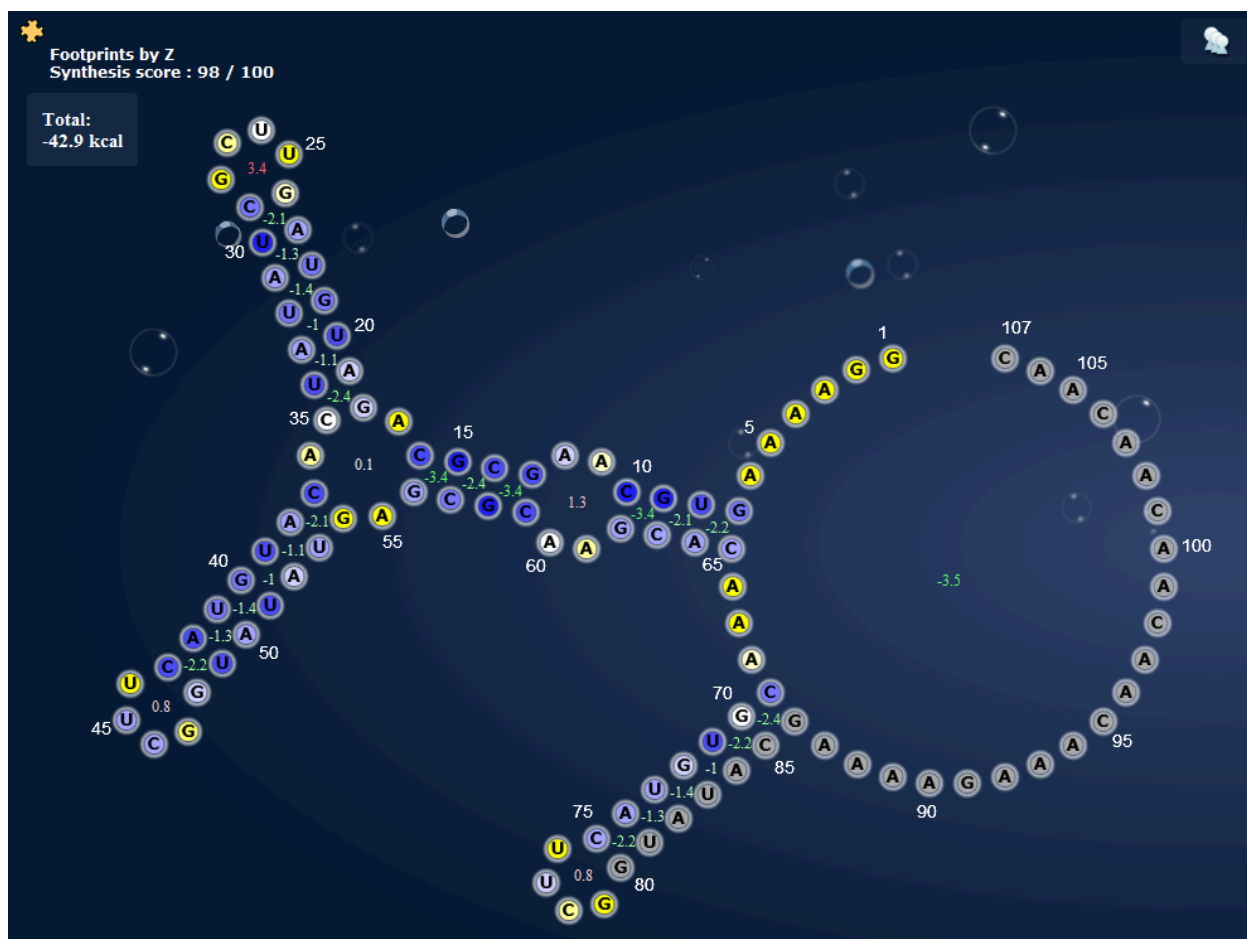
Reverse motor 3 (27 winners of 40)

This one seemed to like facing pairs between the adjacent multi loop stem, much less. Is it so that this is most useful in designs where the non hairpin stem is adjacently attached?

Reverse motor 2 (29 af 40)

There wasn't nearly as big a difference in the amount of winners as I suspected would be the case in relation to adjacent multiloops and the adjacent spots positioning in relation to the neck as I expected. I expected reverse motor 2 and 4 to do worse than 3.

Here is a design of a similar nature to the reversed motor ones, except isn't adjacent. Stems are a bit longer and there is a 2-2 loop in the neck. Still I think the fate of the multiloop could be useful for comparison. This lab has a slightly lower number of winners, if compared the ones with adjacent multiloops,. 20 out of 40. Actually it could seem that this one fare worse than the ones with adjacent stem. So can adjacent stems actually be an advantage sometimes?



This one also goes even more unstable, the longer in the sequence it comes.

Location Dependent Chemical Footprints Part 4

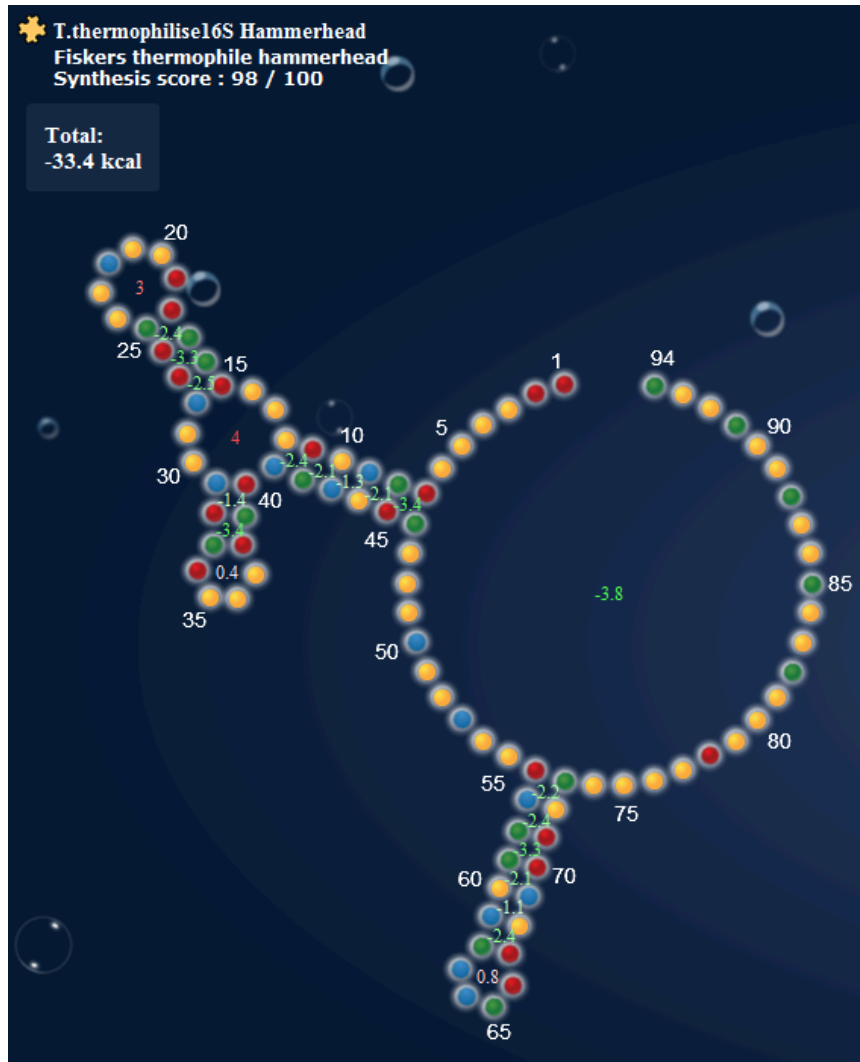
Me

Roadmap

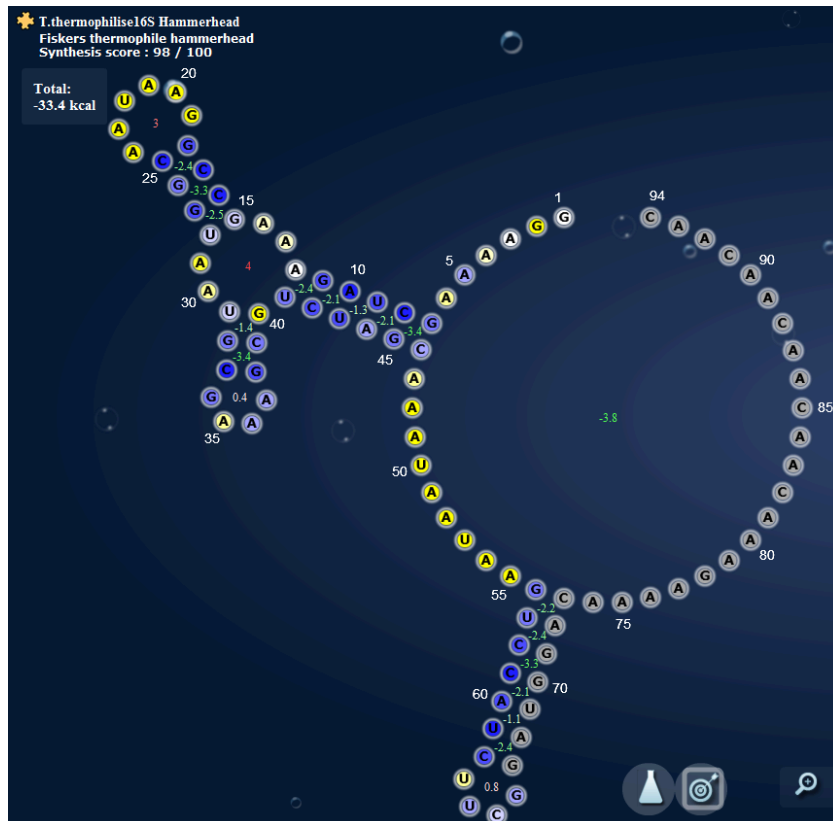
Title	Synthesis score ▾	Sequence
search	minmax	search
Who left that f...	98 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
chemical footpr...	98 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Mat - Location ...	98 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Mat - Location ...	98 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Footprints by Z	98 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Fiskers RNA foo...	97 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
LD - #2	97 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
LD - #1	97 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
JR LocDep_O4_Rn...	97 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Zanna's Footprint I	97 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
LD#100 - Brou...	96 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
rod of janet w...	96 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Four Footprints	96 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Setting Q(Pl. 4)	96 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Setting A(Pl. 4)	96 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Beautiful Footprint	96 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
LDGF A-B - Brou...	96 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
FP-4	94 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Mat - Location ...	94 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
LDGF A-C - Brou...	94 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
rodmap Part 4	93 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
chemical footpr...	93 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Remaneon	93 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Setting F(Pl. 4)	93 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
BigFootprints 1...	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
BigFootprints 1...	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
ldcf 4	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Parts are Parts 4	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Dilegent	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Dimbeon	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Rebbi	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Chem FlpmfPr4...	92 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Fiskers RNA foo...	91 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC
Mesochi LDGFP 4	88 / 100	GGAAAAAGCAGAGGCAAGCGUCGCGAAAGCGACAGCGGUGCGCGAAAGCGACAGCGAGCAGCGGAAAGGGAAGCUCUUC

T.thermophilise

This one has the AU's/GU's built into the multi loop by default



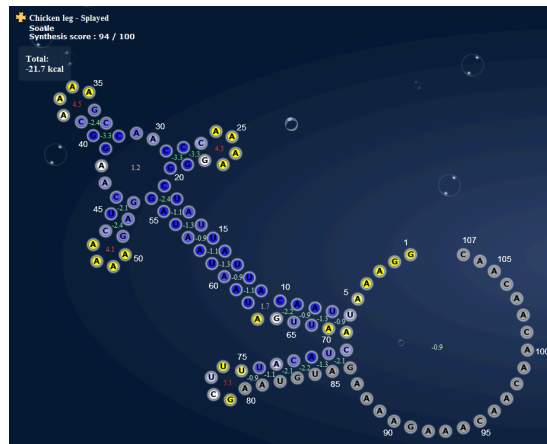
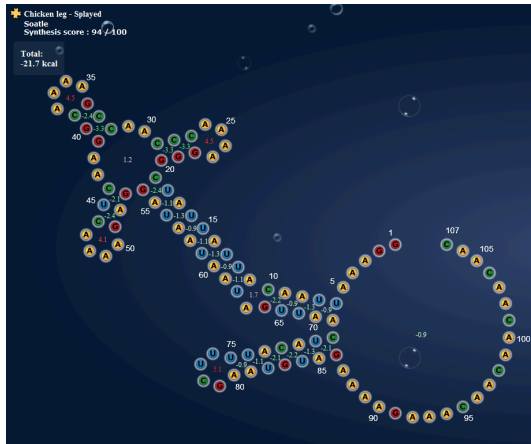
Again the first closing base pair in the multi loop is generally more stable than the last.



Similar in this one

Loose note

Here is one more of the designs with a real low amount of GC-s in the long stem. And this one I can't totally call this the neck. So real long stems are surprisingly tolerant to AU's

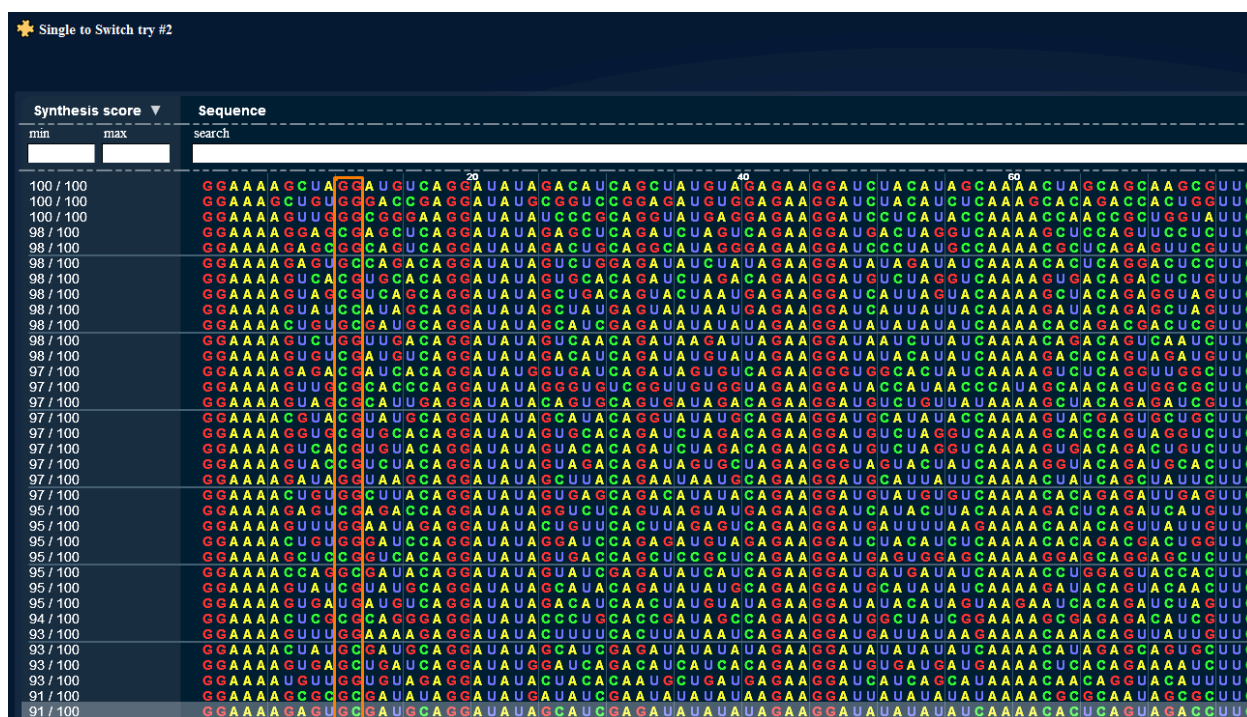


13 Nov 2013

Single switch to try - Mirror version

I refound found a tendency I noticed have earlier. It might matter to which side an adjacent stem is to on the neck, for what bases like to face each other most. Though usual multi loop orientation works too.

Green facing green if adjacent to the left and red facing red if adjacent to the right.

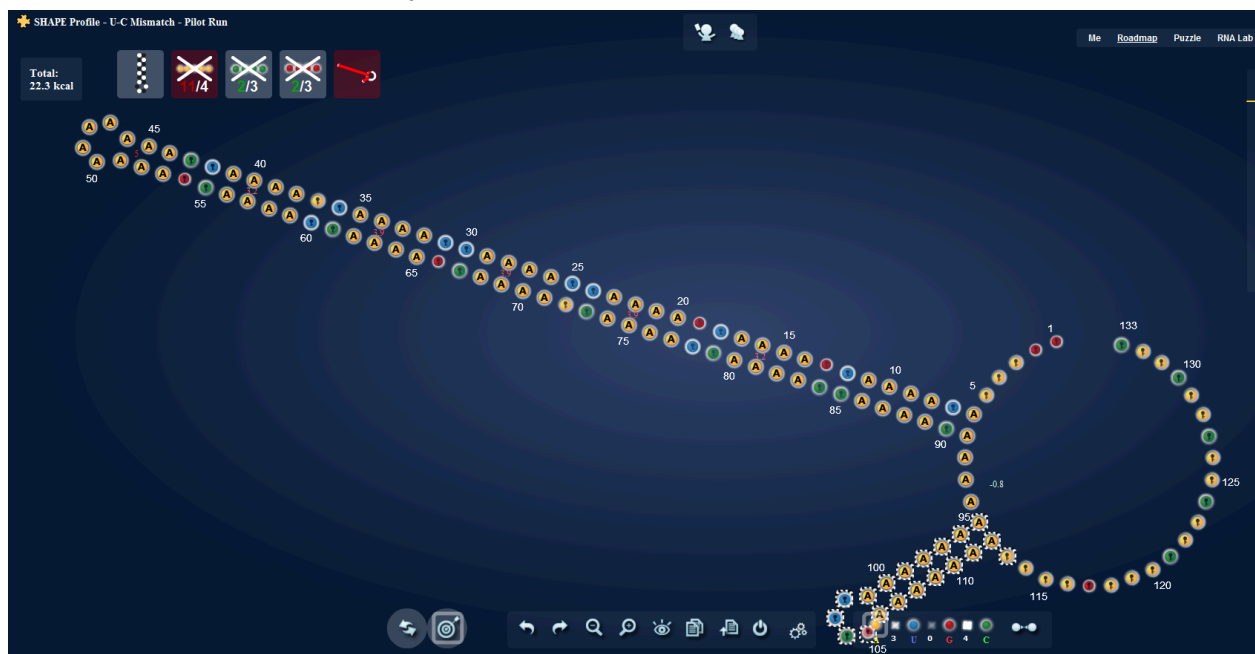


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GC Pairs		UA Pairs		GU Pairs		Melting Point		Free Energy		Title	Synthesis score		Sequence
min	max	min	max	min	max	min	max	min	max	search	min	max	search
19 (40%)		20 (42%)		2 (4%)		107 °C		-55.6 kcal		UC	99 / 100		GGAAAGUCUAUAUCGUAUCUGCAUUCUUAUCUUUUAUG
19 (40%)		20 (42%)		2 (4%)		107 °C		-58.9 kcal		You Can See (UC...	99 / 100		GGAAAGUCUAUCUGUAUCUGCAACUUUCGUUUUGUAC
20 (42%)		19 (40%)		2 (4%)		84 °C		-67.89 kcal		Inbielari	99 / 100		GGAAAGUCGUGUUGUUGUUGUAUGUAUGUUUAUGU
19 (40%)		20 (42%)		2 (4%)		107 °C		-55.6 kcal		In the mU-Ck- B...	98 / 100		GGAAAGUCAGUGUGGUAUGUGUAAGUUUGUUGUAG
23 (48%)		16 (33%)		2 (4%)		107 °C		-66.9 kcal		bUCdic	98 / 100		GGAAAGUCAGUGGUAUGUGUAAGUUUGUUGUAG
17 (35%)		22 (46%)		2 (4%)		97 °C		-52.1 kcal		You see?	98 / 100		GGAAAGUCUACUGUAUAUGUGUAACUUUAUUGUUAUG
19 (40%)		20 (42%)		1 (2%)		107 °C		-57.5 kcal		I Can See (UC...	98 / 100		GGAAAGUCUAUCUGUAUGUGCAAGUUUCGUUUUGUAG
17 (35%)		22 (46%)		2 (4%)		89 °C		-62.9 kcal		Tileoren	98 / 100		GGAAAGUCGAUUUGGUGUAUGUAUUUUUGAUUUUAUGA
23 (48%)		16 (33%)		2 (4%)		107 °C		-67.8 kcal		Nels Box	98 / 100		GGAAAGUCUGUGUGUAUUUGGUAUUUGCAAGUUUAUG
20 (42%)		19 (40%)		2 (4%)		107 °C		-62.1 kcal		do you see?	97 / 100		GGAAAGUCUACUGUAUGUGUAAGUUUGUUGUUGUAG
15 (31%)		24 (50%)		1 (2%)		97 °C		-51.5 kcal		U-C My Design?	97 / 100		GGAAAGUCUACUGUAUGUGUAUUCUUUAACUUUAUG
21 (44%)		18 (38%)		1 (2%)		107 °C		-60.2 kcal		Mat - Shape Pro...	97 / 100		GGAAAGUCUACUGUAUGUGUAUUCUUUAACUUUAUG
20 (42%)		19 (40%)		1 (2%)		107 °C		-58.3 kcal		Mat - Shape Pro...	97 / 100		GGAAAGUCUACUGUAUGUGUAUUCUUUAACUUUAUG
16 (33%)		23 (48%)		2 (4%)		97 °C		-54.5 kcal		We Can See (UC...	97 / 100		GGAAAGUCUGUGUAUUUGGUAUUUGCAUUUGUGUGU
12 (25%)		27 (56%)		1 (2%)		97 °C		-43.9 kcal		walk and whine 2	97 / 100		GGAAAGUUUUGUGUAUUUGUGUAUUCUUUAUGUUUAUG
30 (63%)		8 (17%)		2 (4%)		107 °C		-79.09 kcal		I'm Your Huckle...	96 / 100		GGAAAGUCUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG
4 (8%)		35 (73%)		2 (4%)		77 °C		-24.1 kcal		SHAPEUCPR2	95 / 100		GGAAAGUUUUAUUUGUUUAUUUGUAUUUUUAUUUUUAU
25 (52%)		14 (29%)		1 (2%)		107 °C		-69 kcal		How Does It	95 / 100		GGAAAGUACGAUGUGUGUGUGUGUGUGUGUGUGUGUG
27 (56%)		12 (25%)		2 (4%)		107 °C		-74.3 kcal		you see 2	94 / 100		GGAAAGUCAGUGUGUAUGUGUGUGUGUGUGUGUGUGUG
19 (40%)		19 (40%)		2 (4%)		107 °C		-61.3 kcal		JR ShapeUC Rad1...	94 / 100		GGAAAGUUUGCAUGUGCAUGUGCAUUAUGCAUUAUGCA
32 (67%)		8 (17%)		2 (4%)		107 °C		-79.5 kcal		I'm Your Huckle...	92 / 100		GGAAAGUCUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG
36 (75%)		3 (6%)		1 (2%)		107 °C		-79.2 kcal		Jelly - U-C Mis...	89 / 100		GGAAAGUCGUGUGUGUGUGUGUGUGUGUGUGUGUGUG
30 (63%)		8 (17%)		2 (4%)		107 °C		-79.3 kcal		I'm Your Huckle...	88 / 100		GGAAAGUCUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG
9 (19%)		1 (2%)		1 (2%)		107 °C		-77.4 kcal		Mat - Shape Pro...	86 / 100		GGAAAGUCUGUGUGUGUGUGUGUGUGUGUGUGUGUGUG
2 (4%)		22 (46%)		16 (33%)		77 °C		-18.7 kcal		SPUCMPR2	53 / 100		GGAAAUUUUAUACAUUUUAUAUUUAUUUAUUUAUUU

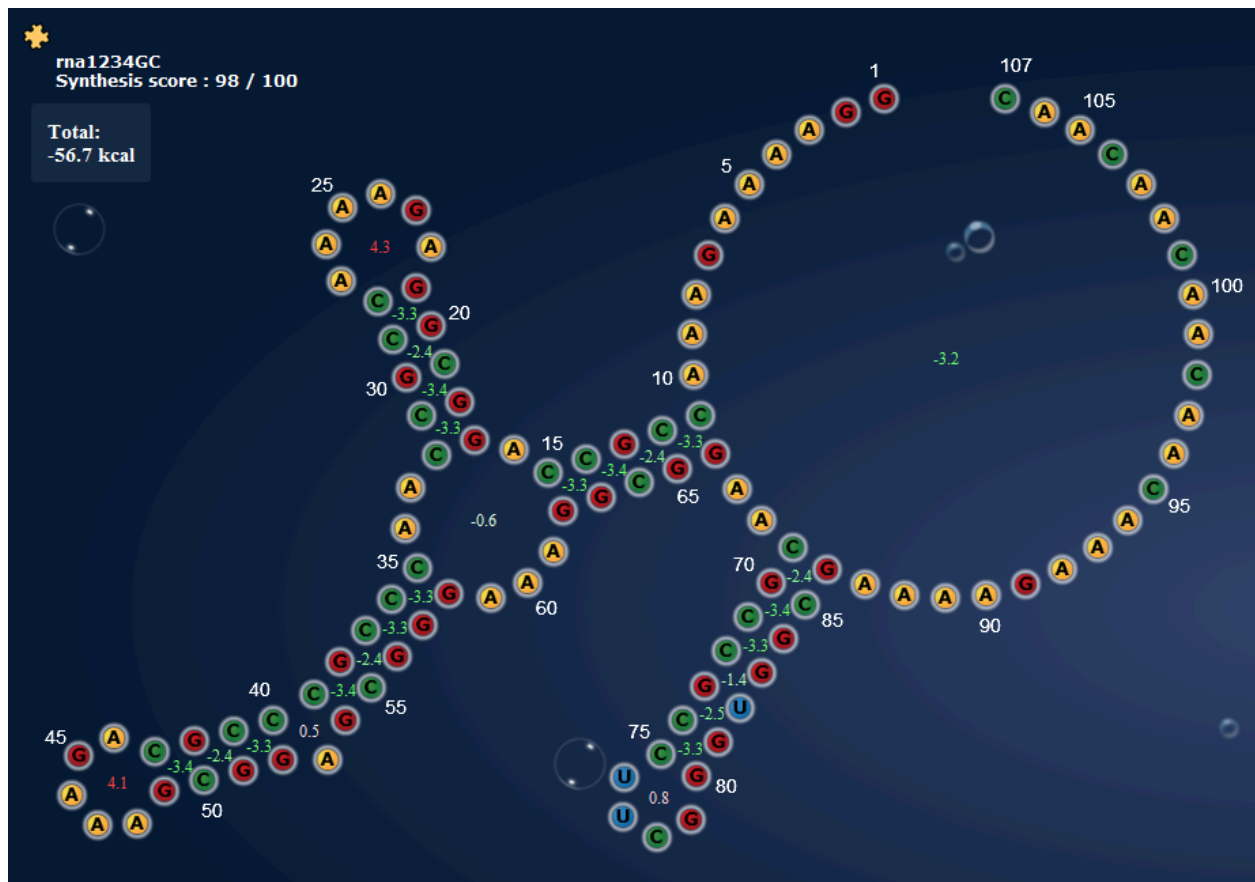
I wonder how much the locked nucleotides has got to do with this?

Ok, they do have a lot to do with it. They are the first starting the pattern. However Vinnie's pattern enhances it and don't try break it.



25 Nov 2013 Christmas three

I found this beauty. I'm fascinated it passed. I know this lab isn't very hard (had a high winning percentage) and what I will call unpressured. But still almost GC, except from a GU and fine SHAPE data. I notice that there are at least one, often two same turning GC-pair blocks pr. stem. Is this similar for other successful almost totally christmas tree designs? I know it turned up more often for the designs, that was pressured and had a generally high GC ratio.



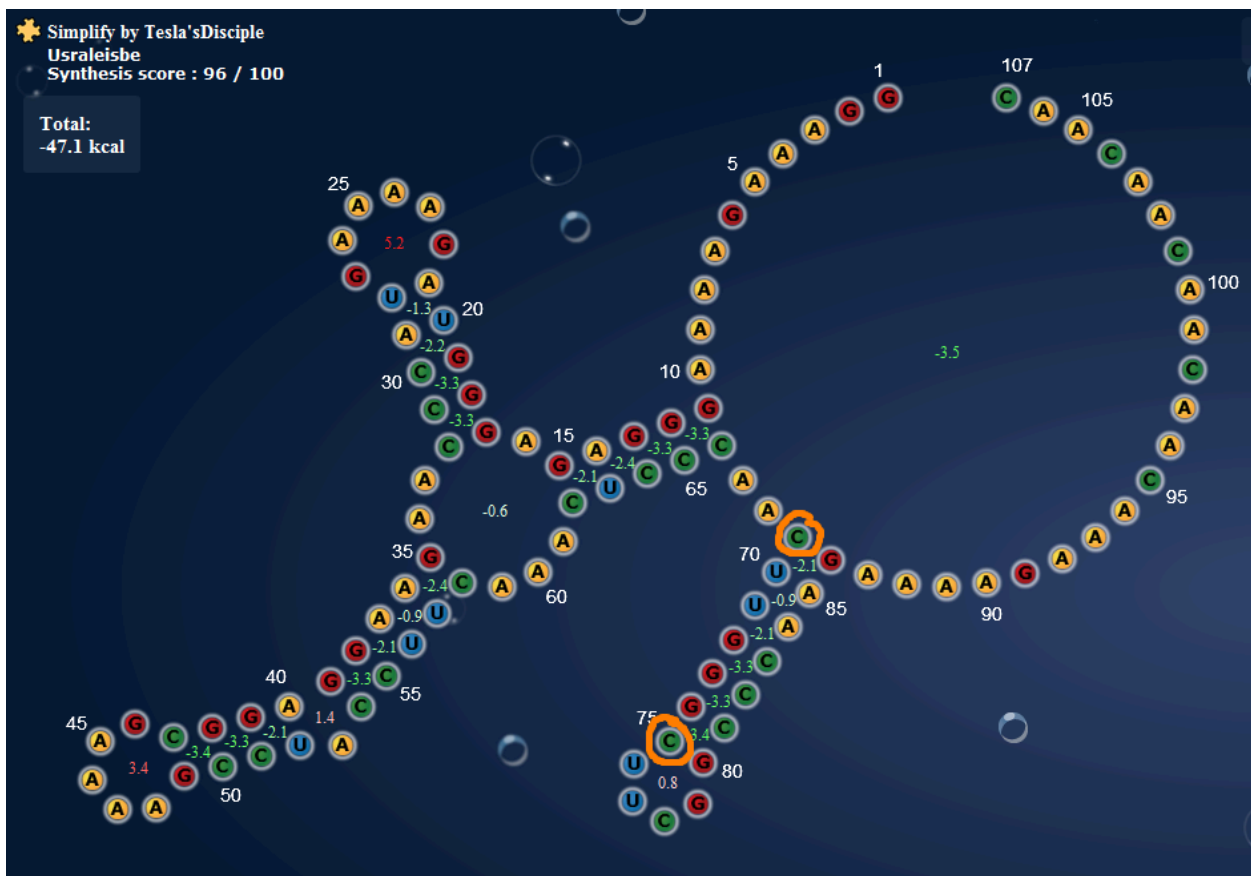
2 Dec 2013

Happy barcodes

I noticed that some of the happiest barcodes actually didn't follow the more usual crossed GC-pairs at opposite ends of the stem. But actually have G at one end and G at the other end of

the strand or similar but with C. Interesting.

Synthesis score ▾			Sequence
min	max	search	
100 / 100		GGAAAAUAAA GCAUC A GACGG GAAAUAA CCGUCAA GUACCCUGG GAAAA CAGC GUGACAAA GAUC A GGGACUG UUGG	
100 / 100		GGAAAAUAAA GCGAC GAUAG GAUAAA CUUCAA GUUCCGUAC GAAAA GUACAGAUACAAA GUCGCA AGCAUCAG UUGG	
100 / 100		GGAAAAUAAA GAGAC GAUAG GAGAAA GCUCAA GCUACCCUGG GAGAA GCAGAGUAGCAA GUCUCA AGCGUGUC UUGG	
100 / 100		GGAAAAUAAA CCUGG CCUAC GAAUUA GUAGGAG GCAUCCUAC GAAAA GAUGUGAUGCAA CCAGGAA CCUAUGC UUGG	
100 / 100		GGAAAAUAAA GUCUA GUCUG GAAUUA CAGACAA GCAUGGUAC GAAAA GUACA CAUGCAA GAGACA GCGUACG UUGG	
100 / 100		GGAAAAUAAA GAUAC GAUAC GAAGAA GUUCAA GCAUGCUAC GAAAA GUAGA CAUGCAA GUUCAA GUGGUAG UUGG	
100 / 100		GGAAAAUAAA GCUAC GUCUC GAAGAA GAGACAA GUGACCAUC GAAUA GAUGUGUCGCAA GUAGCA ACUCUGUC UUGG	
100 / 100		GGAAAAUAAA GCUAC GACUC GAAUUA GAGUCAA GUGACCAUC GAAUA GAUGUGUCACAAA GUAGCA AGUCUGAC UUGG	
98 / 100		GGAAAAUAAA GUGUA GCGAG GAAUUA CCGUCAA GCGCCGUGG GAAAA CUAGA CGAGCAA GACACA GCGAGUA UUGG	
98 / 100		GGAAAAUAAA GUCUG A GACAG GAUAAA CCGUCAA A CAGCCGUGG GAAAA CUAGA CGAGCAA GACACA GCGAGUA UUGG	
98 / 100		GGAAAAUAAA CCGCG A GCGCG GAAAA CCGCG CCGCG GAAAA GCGGA GCGGCAA GCGGCA CCGCGCC UUGG	
98 / 100		GGAAAAUAAA GAUAC GAUAC CAA GAA GUUCAA CCAUGCUAC GAAAA GUACA CAUGCAA GUUCAA GUAAUA UUGG	
98 / 100		GGAAAAUAAA GAUAC CCGUG CAGAAA GCUCAA CCGUCCUAC GAAAA CGAGA GUAGCAA GCAUCAA GJAGAAC UUGG	
98 / 100		GGAAA ACAAAC GAUAC GAUAC GUAAA CUUCAA CCGUCCUAC GAAAA CGAGA GUAGCAA GUUCAA GAUGUAC UUGG	
98 / 100		GGAAAAUAAA GUGAC A GUCUG GAAUUA CAGACAA GUCAGGUAG GAAUA CUACA CUGACAAA GUCAGA AGGUCUG UUGG	
98 / 100		GGAAAAUAAA GUGUA GUCUG GAAUUA CAGACAA GUGUCCUAG GAAAA CUAGA CACACAAA GACACA GUACAUA UUGG	
97 / 100		GGAAAAUAAA GCUAC GUCCU GAUUAU GGGACAA GGAUCCGCG GAUUA GCUA GAUCCGAA GUAGCA AGAUUUC UUGG	
97 / 100		GGAAAAUAAA GCAAC GCAUG GAAUUA CGUGCAA GACUGGCAU GAUUA AUGCA CAGUCAA GGUGCA GUGUUAU UUGG	
97 / 100		GGAAAAUAAA GAGAC GAUAG GAGAAA GCUCAA GCUACCUAC GAGAA GUAGA GUAGCAA GUCUCAA GAGUGUC UUGG	
97 / 100		GGAAAAUAAA GAUGA GACUC GAAUUA GAGUC A GUA GCGUAG GAAAA CUAGA GCUACAAA GCAUCAA GCGAUC UUGG	
97 / 100		GGAAAAUAAA GCUAC GAUAG GAUAAA CUUCAA GUUCCGUAC GAAAA GUACA GAUACAAA GUACCA AGCAUAG UUGG	
96 / 100		GGAAA GGGAG CUGAG GCGUCUGACAAA AGAGGAA CUGUCCUUG GACAAA CAGAGACAGAAA CUACAG AGCAGUCU UUGG	
96 / 100		GGAAAAUAAA GCUA GUCAC GAAUUA GAGUUA GUGCCUUGG GAAAA GCAAG GCGAUAAA GUGGCA AGCUGGAC UUGG	
96 / 100		GGAAAAUAAA GUGA GACUC GAAUUA GAGUCAA GUGACGUGG GAGAG CAGAG GUCACAAA GUCACA GGAUAUC UUGG	
96 / 100		GGAAAAUAAA GAUAC GAUAG GAAUUA GCUCAA GAUACGUGG GAAAA GGAUA GUUACAAA GUUCAA GCGUGAC UUGG	
96 / 100		GGAAAAUAAA GUCUC GUCUG UAAAUA CAGACAA GCAUGGUAC UAAAUGUACA CAUGCAA GAGACA GCGGACG UUGG	
96 / 100		GGAAAAUAAA GAUAC GACUC GAAUUA GAGUCAA GUAGCCUAG GAAAA GUAGA GCUACAAA GUUCAA GUCGUAC UUGG	
96 / 100		GGAAAAUAAA CUUGA CUUC CAAAAA GAGAGAA CACUCCUUC GAAAA GAAGA GUGUAAA CAGAGA ACACAUC UUGG	
96 / 100		GGAAA GAAAA GGGAG GGGUA GAAAA GUACCAA GAAGGAGGG GAAAA GCUA CCUUCAA CUCGCA CUUGGGG UUGG	
96 / 100		GGAAA GAAAA CUUGA GCUAC GAAAG GUACCAA CAUGCCGUGG GAAAA GCAAG CCAUAAA CAUAGAA GCACACG UUGG	
96 / 100		GGAAA GAAAA CAAUG AGAUC GAAAG GUUCAA CAUGCCGUGG GAAAA GUAGA GCUACAAA GUUCAA GCUAAG CCAACG UUGG	
94 / 100		GGAAA GAGAA CUGAG GCAUCAA AGAUCAA CUGUCCUAG GAC AAGACA CAGACAAA CUCAGAA GCAUCU UUGG	
94 / 100		GGAAAAUAAA GAGAC GAUAG CUAUUA GCUCAA CUA CCGUAC GUGUA CUAGA GUAGCAA GUCUCAA GAUGGUC UUGG	
94 / 100		GGAAAAUAAA GUGUG CCGUG GAAUUA CCGCGAA GCAAGGAGG GAAAA GUCAGUAUCAA CCACCG GCGGCGC UUGG	
94 / 100		GGAAAAUAAA GUAAC GACUG GAAUUA CAGUCAA GUCACGAGG GAUA GUCU GUGACAAA GCUACA GUCUCU UUGG	
94 / 100		GGAAAAUAAA CAAUGA GUUUA CACACAC GUAACAA CUUGACUAGACACA CUAGA UCAAGAAA CAUUGAA CAUUAUC UUGG	



Barcode next right to design

Lab Data Miner v0.17

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or ((.(((.))).)

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

omit sequences:

omit structs:

mode: ☐ summary ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv

flags: ☐ just labs ☒ group by lab id (nid)

lab type: ☒ Early Lab ☒ Cloud Lab

	nid	count	score	rank	
(ALL)	1319	91.01	43.37	details	

Lab Data Miner v0.17

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or ((.((.)).))

substructure:	(((((((.....)))))))).
filterBy:	GNNNNNGUUCGNNNNNNN
groupBy:	
lab ids:	
min score:	80
max score:	
subsequence:	
omit sequences:	
omit structs:	
mode:	☐ summary ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv
flags:	☐ just labs ☒ group by lab id (nid)
lab type:	☒ Early Lab ☒ Cloud Lab
Submit	

	nid	count	score	rank	
(ALL)		1430	91.42	44.86	details

Lab Data Miner v0.17

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. `(((...)))` or `((.((.)).))`

substructure:	(((((((....)))))))).
filterBy:	GNNNNNCUUCGNNNNNNN
groupBy:	
lab ids:	
min score:	80
max score:	
subsequence:	
omit sequences:	
omit structs:	
mode:	☐ summary ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv
flags:	☐ just labs ☒ group by lab id (nid)
lab type:	☒ Early Lab ☒ Cloud Lab
Submit	

nid	count	score	rank	
(ALL)	3585	91.25	42.64	details

Lab Data Miner v0.17

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. `((...)))` or `((.((.)).))`

substructure:	(((((((.....)))))))).
filterBy:	C N N N N N G U U C G N N N N N N N
groupBy:	
lab ids:	
min score:	80
max score:	
subsequence:	
omit sequences:	
omit structs:	
mode:	☐ summary ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv
flags:	☐ just labs ☒ group by lab id (nid)
lab type:	☒ Early Lab ☒ Cloud Lab
Submit	

nid	count	score	rank	
(ALL)	603	90.68	45.55	details

I wanted an idea about which bases that would be best to have at these two spots I'm looking at as I like Mat consider closing basepairs extra important to stability, compared to basepairs in the middle of a stem.

substructure: |(((((((.....)))))))).

filterBy: |NNNNNNNUUCGNNNNNNNN

groupBy: |XNNNNNXNNNNNNNNNNNN

lab ids:

min score: 85

max score:

subsequence:

omit sequences:

omit structs:

mode: ☐ summary ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☒ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	6754	92.25	43.92	details
CG	504	92.3	46.32	details
CA	55	90.93	46.13	details
GG	1264	92.6	45.48	details
GA	116	91.14	44.51	details
GU	115	90.4	44.5	details
CC	1145	92.3	43.89	details
UU	20	91.3	43.61	details
CU	45	91.78	43.28	details
AC	126	91.75	43.17	details
AG	36	91.94	43.15	details
AU	34	90.53	43.11	details
GC	3189	92.34	43.06	details
UC	44	90.27	40.3	details
UG	6	89.83	39.59	details
AA	41	90.46	38.66	details
UA	14	90.07	38.52	details

One base between main design and stem

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

omit sequences:

omit structs:

mode: ☒ summary ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☒ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	1484	91.72	48.9	details
CA	13	92.31	54.81	details
CG	105	91.13	50.82	details
GG	274	92.05	50.78	details
GA	31	91.45	50.76	details
CU	7	90.29	50.04	details
GU	27	91	49.7	details
GC	698	91.9	48.81	details
AG	13	90.92	48.17	details
CC	231	91.57	47.2	details
AC	38	91	47.09	details
AU	8	92	44.77	details
UC	5	91.6	42.51	details
AA	20	90.45	42.07	details
UA	10	90.2	39.75	details
UU	4	87.5	37.42	details

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

omit sequences:

omit structs:

mode: ☐ summary ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☒ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	920	94.01	48.8	details
CU	6	92	53.77	details
GG	193	94.13	50.93	details
AG	6	96	50.83	details
CA	7	88.71	49.94	details
CG	69	94.14	49.91	details
GA	10	94.4	49.64	details
AC	20	95.65	49.12	details
GC	418	93.83	48.13	details
CC	163	94.64	48.12	details
UG	1	98	47.7	details
UC	10	91.8	45.43	details
UU	2	92.5	44.7	details
UA	1	92	44.52	details
GU	6	92	41.63	details
AU	6	91.17	41.59	details
AA	2	88.5	34.78	details

Ok, it doesn't look like my CC or GG pattern is overall favorite. But it does well and that is nice to remember when one wants alternative good barcodes.

11 Dec 2013

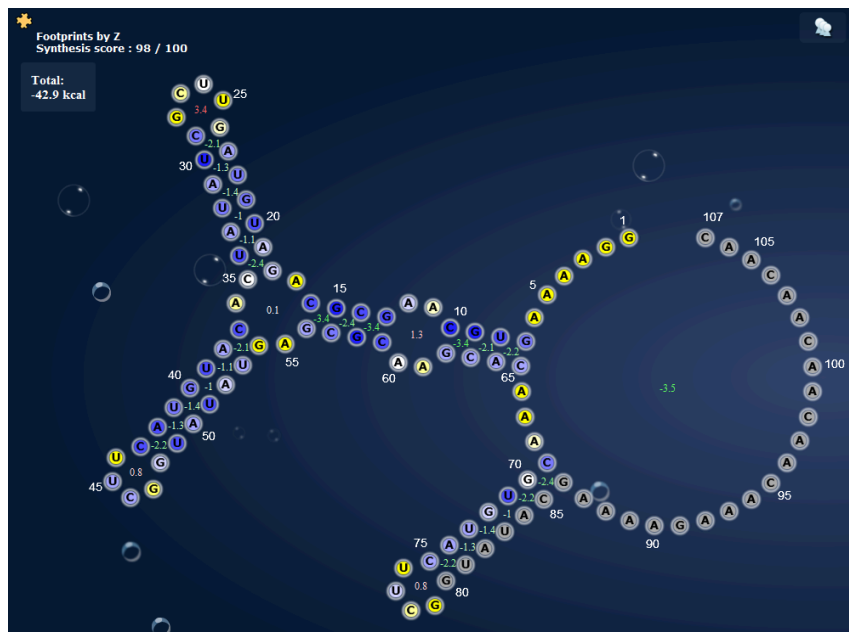
Improving the Nearest Neighbor Energy Model Using Eterna

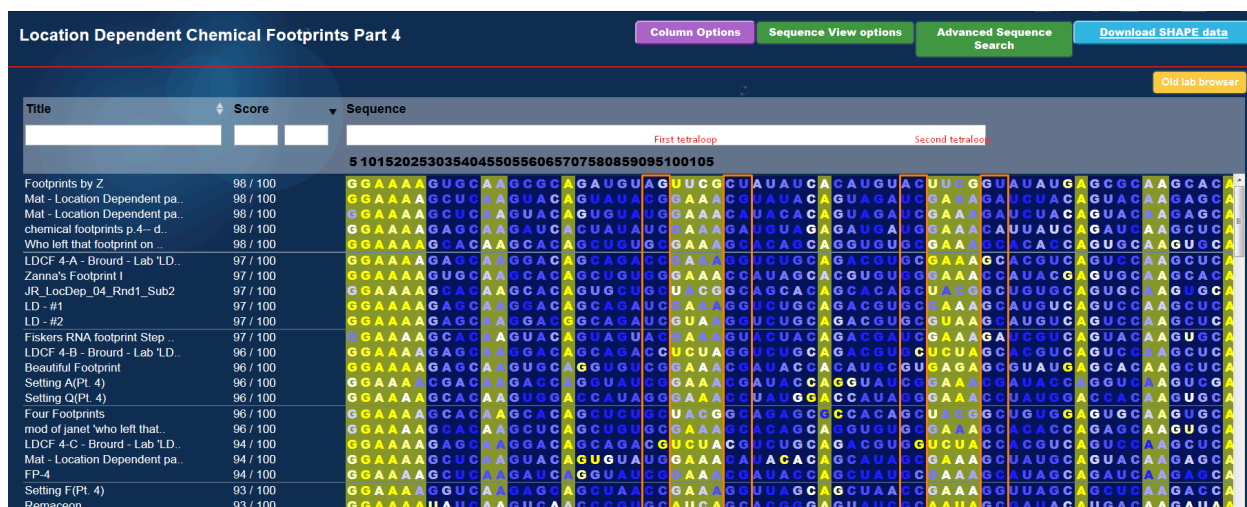
See start of discussion [here](#).

Location Dependent Chemical Footprints Part 4

This lab has two equal length stems and some of them have same tetraloop and closing base pair + next pair. For the designs that has same base sequence in the tetraloop and two bases to each side, there is a tendency for that the stem around the second tetraloop is more unstable. It isn't huge, but it is there.

<http://eterna.cmu.edu/web/browse/3105062/>

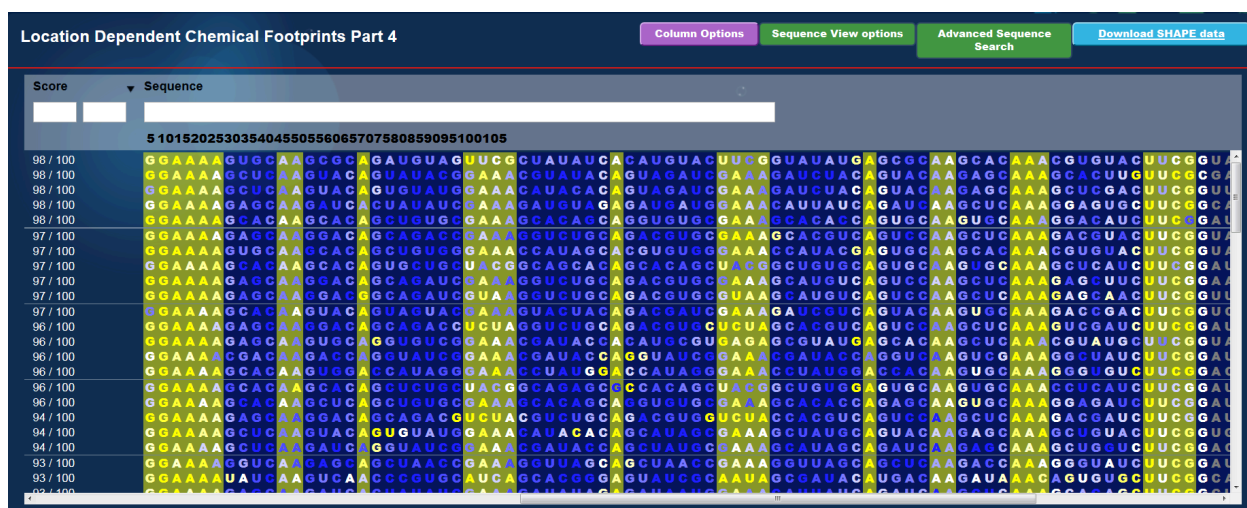




Also here is a link to some of my earlier thoughts on stability of multi loop closing basepair.

Reversed Motor 4

I am wondering about the SHAPE data bias I see in our Cloud labs, with the data grow more unstable over the middle and towards the end of the sequence. Typical example:



I have been looking at the Eterna Classic data. And I am not sure it there to the same degree, though I can find it in some labs. A few labs do even show a different pattern. More instability at first

about proposing some labs with the same shapes of some of the Classic Eterna labs + added current barcode. I will like to compare the SHAPE data picture between Classic and Cloud and if bias is extra strong in Cloud, for the long stem designs in particular. As I suspect it is. However that is of cause not helping on getting enough data in the old labs for comparison. So I'm thinking about picking the labs there that has most data.

14 Dec 2013

I can even show with the new version of JL's tool that the closing basepairs of this multiloops of this design go more unstable later in the sequence.

Lab Data Miner v0.19

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or ((.((!)).))

substructure:	(((.(((!))).(((!))).))
filterBy:	
groupBy:	NNXNXNN!NNXNXNN!NNXNXNN
lab ids:	
min score:	
max score:	
subsequence:	
omit sequences:	
omit structs:	
mode:	☐ summary ☐ base ☒ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv
flags:	☐ just labs ☐ group by lab id (nid)
lab type:	☐ Early Lab ☒ Cloud Lab
Submit	

For search

(((.(((!))).(((!))).))

NNXNXNN!NNXNXNN!NNXNXNN

Notice how right side generally becomes a little more unstable than the left

subseq	count	score	rank	
AGCAGCC GGCAGCU AGCAGCU	1	89	94.05	details
AGGAGGU ACCAGCA UGCACCU	1	94	92.86	details
GGCAGCC GGCAGAC GUCAGCC	1	87	92.24	details
GACAGUG CACAGGA UCCAGUC	1	87	91.57	details
CAGAGUA UACACAG CUGACUG	1	94	90.81	details
GUCAGGA UCCAGCA UGCAGAC	1	93	90.52	details
AGCAGUC GACAGAG CUCAGCU	2	89	90.43	details
CGCAGCC GGCAGAG CUCAGCG	1	98	90.38	details
GUCAGCA UGCAGCU GGCAGAC	1	96	90.29	details
GCCAGCA UGCAGAG CUCAGGU	1	100	90.1	details
ACGGGCU GGCGCCG CGGCGU	1	89	90.05	details
AGCAGGG CCCAGAC GUCAGCU	1	93	90	details
GACAGUG CACAGUU AACAGUC	1	86	90	details
AGCAGCC GGCAGGU ACCAGCU	1	93	89.76	details
GUCAGUC GACAGCA UGCAGAC	1	94	89.43	details
GUCAGUA UACAGCU AGCAGAC	1	92	89.38	details
AUCAGAC GUCAGCU AGCAGAU	1	92	89.1	details
GACAGCA UGCAGAC GUCAGUC	4	96	89.09	details
UGCAGUA UACAGCA UGCAGCA	1	89	88.81	details
UGGACCG CGGACCA UGGACCA	1	93	88.52	details
ACCAGGA UCCAGCU AGCAGGU	1	92	88.38	details
AGCAGUA UACAGAC GUCAGCU	3	95.67	88.22	details
CGCAGCG CGCACGC GCGAGCG	1	98	88.14	details
CUCGGUA UACAGAU AUCAGAG	1	96	88.1	details
CUCAGCU AGCAGGU ACCAGAG	1	96	88	details
ACCACUC GAGAGGU ACCAGGU	1	87	87.76	details
CGCACAG CUGAGCU AGCAGCG	1	93	87.67	details
GUCAGUA UACAGAG CUCAGAU	1	98	87.38	details
ACCAGCA UGCAGCU AGCAGGU	1	98	87.38	details

GUGAGGC GCCAGGA UCCACAC 1	91	87.24	details
AGCAGUA UACAGCA UGCAGCU 1	94	87.24	details
GACAGGU ACCAGUC GACAGUC 1	98	87.24	details
UCCACAU AUGAGGU ACCAGGA 1	93	87.19	details
GUCAGUG CACAGCA UGCAGAC 1	88	87.14	details
CCCAGCG CGCAGUA UACAGGG 1	97	87.1	details
AGGAGCU AGCAACU AGUACCU 1	93	87.1	details
UGCAGAC GUCAGAG CUCAGCA 1	96	86.95	details
AGGACAG CUGAGCA UGCACCU 1	94	86.81	details
CCCAGAC GUCAGAG CUCAGGG 1	93	86.81	details
UUCAGUU AACAGAU AUCAGAA 1	88	86.81	details
CCAAGUG CACAGAG CUCAUGG 1	91	86.29	details
CACAGCA UGCAGCU AGCAGUG 1	96	86.24	details
AGCAGCU AGCAGAC GUCAGCU 1	88	86.19	details
UACAGUA UACAGAC GUCAGUA 1	97	86.19	details
CUCAGUC GACAGAU AUCAGAG 4	94.5	86.1	details
GUCGGUC GACAGCA UGCAGAC 1	98	86	details
AUCAGUA UACAGAG CUCAGAU 1	92	86	details
UUCAGUU AACACUU AAGAGAA 2	92	85.91	details
ACCACCU AGGAGAA UUCAGGU 1	91	85.71	details
ACCAGUG CACAGCU AGCAGGU 1	96	85.48	details
CACAGUG CACAGGU ACCAGUG 1	94	85.43	details
CGCAGGC GCCAGCC GGCAGCG 1	82	85.38	details
AGGAUCU GGAAGCU AGCACCU 1	93	85.24	details
ACGACAG CUGAGCA UGCACGU 1	98	85.19	details
GUCAGUA UACAGAU AUCAGAC 2	91	85.15	details
GCCACGU ACGAGCA UGCAGGC 1	94	85.1	details
UCAACCC GGGAGUA UACAUGA 1	93	85.05	details
UACAGAC GUCAGAG CUCAGUA 7	93.86	85	details

14 Dec 2013

Relaxed multiloops

I decided to take a look at bigger multiloops with 3 stacks with [JandersonLee's tool](#).

5-5-5

In this loop usual orientation ranks highest, but reverse orientation doesn't do much worse. Aloop with a non GC closings as AU and GU does nearly as well as the highest ranking.

Lab Data Miner v0.19

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or (((()))).

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

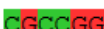
omit sequences:

omit structs:

mode: ☐ summary ☒ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☐ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	40	97.05	81.92	details
	16	97.56	83.87	details
	1	92	83.52	details
	6	96.67	82.24	details
	3	96	82.02	details
	9	96.89	79.79	details
	1	96	79.61	details
	3	98.33	78.98	details
	1	98	77.24	details

6-6-6

The 6-6-6 multiloop shows a changed pattern. Solely GC-s as closing basepair for the top ranked. But a changed pattern of orientation. Usual orientation as we know it from many multiloops isn't the top ranked.

cluster	count	score	rank	
(ALL)	40	93.23	85.97	details
GGCGCC	1	97	91	details
CCGGCG	2	96.5	89.54	details
CGCCGG	2	97	87.39	details
CGCGCG	23	94.39	87.27	details
GCGCGC	7	96.86	87.25	details
AUAUAU	1	93	87.25	details
GGCCGC	1	96	86.83	details
AUAAUU	1	79	75.47	details
UGUGUG	1	70	69.61	details
UUAGUG	1	58	56.58	details

7-7-7

cluster	count	score	rank	
(ALL)	40	96.23	81.6	details
CGCCGG	5	97.4	84.98	details
CCGGCG	3	94.67	83.66	details
CGCGCG	12	96.83	83.53	details
GGCCGC	2	97.5	83.38	details
GGCGCC	5	93.6	83.27	details
CCGCGG	2	96.5	78.41	details
GCGCGC	8	96.88	77.74	details
GUAGCC	1	90	75.95	details
GCGGCC	2	97.5	74.09	details

Closing GC-basepairs seems to become more and more crucial. Usual orientation is ranked third highest

Interesting enough it is opposite of what I thought. The bigger the loop the more crucial

GC-closing basepairs seem. I do see a lot of GC-closing basepairs in the huge ribosomal RNA. However it seems like orientation change much more. Usual orientation often isn't followed. And some of the multiloops are really huge.

I also checked a few smaller multiloops to compare to the bigger multiloops.

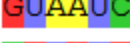
3-3-3

Here I see Brouard's labs with locked GU and AU's at closing basepairs in multiloops, hit through. Some of them did very well. Another thing I find interesting, is first and last position. in the colored sequence. Those bases are for the neck area. These shows a particular tolerance for AU and GU basepairs. Where as the stem bases is generally, but not always, more conservative GC-basepairs. The 3-3-3 loop seem to be the multiloop size, that is the one most large with alternative closing basepairs, than GC.

cluster	count	score	rank	
(ALL)	579	91.68	84.62	details
UGCGUG	1	92	92.37	details
UCGGCG	6	92	91.82	details
GGCUAU	1	90	90.44	details
UGCGCA	46	93.78	90.16	details
UGCGCG	37	90.7	90.02	details
GCGCGC	82	94.98	89.87	details
UUAUAA	1	94	89.63	details
UCGGCA	7	92.14	88.5	details
AGCGCU	89	93.63	87.78	details
GGCGCU	49	92.06	87.31	details
AGCCGU	14	93.64	86.33	details
ACGGCU	18	94.39	86.12	details
AUAGCU	4	92.5	85.82	details
UUAGCG	1	88	85.52	details
ACCGGU	13	94.62	85.47	details
UGUAUA	2	91.5	85.22	details
UGCCGA	5	93	85.16	details
GCGCGU	8	91.5	85.08	details
UGCCGG	11	89.27	84.83	details
CGCGCG	27	96.15	84.45	details
UUAUA	1	90	83.59	details
GGCCGU	8	90.38	83.26	details
GCGGCC	5	94	83.01	details
UGCAUG	1	93	82.74	details
UCGCGA	4	89.5	81.87	details
CGCCGG	14	95	81.84	details
UUGUGG	1	84	81.3	details
CCGGCG	10	94.2	80.87	details

2-2-2 loop

Here most of the top ranked closing basepairs are GC-pairs. with one single exception.

cluster	count	score	rank	
(ALL)	184	87.06	73.51	details
	1	93	84.92	details
	1	89	80.88	details
	34	88.62	76.3	details
	3	87	75.76	details
	19	90.58	75.22	details
	97	87.48	74.14	details
	3	84.67	73.65	details
	1	78	71.88	details
	5	87	70.03	details
	7	84.86	69.79	details
	1	79	69.5	details
	2	79	63.27	details
	4	80.25	62.54	details
	1	77	61.38	details
	2	75.5	61.17	details
	1	79	58.96	details
	1	68	54.88	details
	1	62	42.63	details

1-1-1 loops

cluster	count	score	rank	
(ALL)	360	89.93	76.95	details
CGCGCG	202	91.5	79.44	details
CGCCGG	26	91.65	74.45	details
CCGGCG	22	88.09	77.26	details
GGCGCC	22	92.18	79.36	details
GCGGCC	13	93.77	81.18	details
GCGCGC	9	91.22	78.46	details
CCGCGG	9	84.22	68.39	details
UGUGUG	6	83.83	59.46	details
AAUUAU	6	71	54.08	details
AGCGCU	5	88.2	77.93	details
ACGGCU	4	87.5	76.73	details
GGCCGC	3	90.67	83.81	details
UCGCGA	3	87	81.29	details
UAUCGA	3	81.33	72.52	details
GUAGCC	2	93	78.6	details
CGCAUG	2	67	48.05	details
AUAAUU	2	83.5	54.29	details
UGCGCA	2	89	80.46	details
UAUUAA	1	68	58	details
UCGAGA	1	79	72.48	details
AAUGCU	1	87	74.19	details
AGCUAU	1	69	53.14	details
AUAUAU	1	60	42.19	details
AUAGCU	1	70	42.62	details
CUACGG	1	96	81.76	details
AGCAUU	1	79	63.9	details
ACGCGU	1	84	59.57	details
CGUGCG	1	83	52.14	details
UAUAUA	1	93	65.33	details

4 way

Here is a shot of one of my absolute favorite 4 way multi loop patterns. It scores high. Here is [my forum post](#) on it.

Best

Lab Data Miner v0.19

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or ((.([])).)

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

omit sequences:

omit structs:

mode: ☐ summary ☒ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☐ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	110	91.99	96.1	details
	1	84	100	details
	1	96	97.06	details
	10	92.3	96.95	details
	97	92.06	95.97	details
	1	86	94.63	details

Now I will try out the same pattern but in different orientation. It's siblings were popular, now I might be able to find out which is best.

Second best

Lab Data Miner v0.19

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or ((.((.)).))

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

omit sequences:

omit structs:

mode: ☐ summary ☒ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☐ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	177	93.1	94.81	details
AGCCGCGU	3	92.67	97.71	details
CGCCGUAG	3	91.67	96.02	details
UGCCGUAA	1	93	95.94	details
CGCCGCGG	167	93.19	94.77	details
CGCCGGCG	2	87	92.51	details
CACCGCGG	1	97	92.25	details

Third best

Lab Data Miner v0.19

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or ((.((()))).)

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

omit sequences:

omit struts:

mode: ☐ summary ☒ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☐ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	57	91	93.76	details
	1	96	98.75	details
	1	94	98.06	details
	54	90.8	93.6	details
	1	94	93.06	details

Fourth best

Lab Data Miner v0.19

Link to [Prior Quasi-Stable Version](#)

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or (((()))-))

substructure:

filterBy:

groupBy:

lab ids:

min score:

max score:

subsequence:

omit sequences:

omit structs:

mode: ☐ summary ☒ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv

flags: ☐ just labs ☐ group by lab id (nid)

lab type: ☐ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	199	91.2	92.09	details
GGCGCCGC	188	91.59	92.38	details
CGCGCCGC	5	84.2	90.19	details
AGCGCCGU	2	79	73.63	details
GUAGCCGC	2	91	95.72	details
AUAGCCGU	2	85	84.63	details

Ok no big surprise here. The highest ranked is my favorite and the second highest is the 180 degree version.

However with Janderson's tool it will now be much easier to dig up all the alternative ways of solving that is also there.

15 Dec 2013

Continuation...

I have earlier been discussing Multiloops with Mat.

Mat. We were talking/kicking a few idea around like the idea of the size of the multiloop have an effect.

Eli: I expected the bigger multiloops to be more forgiving. But it seems like they really like their GC-pairs.

Mat: I think the bigger size the less the same turned GC's has

Eli: I thought that they would be more tolerant of other closings than GC-pairs but that was not what happened. The most forgiving seems to be the 3-3-3 multiloop

Thats exactly what happened.

16 Dec 2013

Continuation...

This also fits well with what I see in big multiloops in ribosomal RNA. ([Huge RNA](#)) I also found an article, [Choreographed origami – Folding ribosomal RNA requires paired tagging sequence](#), that I found interesting in relation to the folding of the ribosome.

“An important step in building ribosomes – the cell’s protein factories – is like a strictly choreographed dance, scientists at the European Molecular Biology Laboratory (EMBL) in Heidelberg, Germany, have discovered. To build these factories, other ‘machines’ inside the cell have to produce specific RNA molecules and fold them into the right shape, then combine the folded RNA with proteins to form a working ribosome. Like a budding origami artist pencilling in the folds, the cell uses tags called methyl groups to help mark where and how an RNA molecule should be folded.”

19 Dec 2013

I have been playing with JandersonLee's LabDataMiner and its new function RankBy.

[Update on multiloops](#)

I have added the main conclusions in this [forumpost](#)

22 Dec 2013

I have earlier mentioned that it seems to be that G's did better in the multi loop ring, that blue that usually does quite well in end loops.

I think I can better show that this is happening now. I took a look at a 7-7-7 multiloop. Here I rank the single bases highest and only watches for +90% scoring designs and watch which designs that has highest ranking multiloop ring. Result is that Red makes for the most calm multiloop ring content. Followed by Green and at bottom Blue.

Lab Data Miner v0.21

Link to [Prior Quasi-Stable Version](#)

NEW: min count and rankBy

Enter a substructure shape pattern to search past lab results for sequences that have been tried, e.g. (((...))) or ((.((.)).))

substructure:	((.....(!)).....(!)).....)
filterBy:	
groupBy:	NNXXXXXXXXNN!NNXXXXXXXXNN!NNXXXXXXXXNN
rankBy:	00111111100!00111111100!00111111100
lab ids:	
min score:	90
max score:	
min count:	
subsequence:	
omit sequences:	
omit structs:	
mode:	☐ summary ☒ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv
flags:	☐ just labs ☐ group by lab id (nid) ☐ full SHAPE data
lab type:	☒ Early Lab ☒ Cloud Lab
Submit	

cluster	count	score	rank	
(ALL)	40	96.23	74.31	details
AAAAGAAAAAGAAAAAGAA	1	96	92.38	details
AAAAGAAAAAGAAAAAGAA	1	98	91.1	details
AAAGAAAAAGAAAAAGAA	2	97.5	86.67	details
AAAAGAAAAAGAAAAAGAA	1	100	85.9	details
AAAGAAAAAGAAAAAGAA	7	95.86	85.82	details
AAAGAAAAAGAAAAAGAA	2	97.5	83.1	details
GGAAAGAAAGAAAGAAUA	1	98	82.67	details
AAAGAAACAAAGAAACAA	1	97	82.67	details
AGAAAGAAAGAAAGAAAG	1	91	82.43	details
AAAGAAAAAGAAAAAGAA	1	98	81.24	details
AAAAUAAACAGAAACAAAC	1	96	80.33	details
GGAAAGAAAGAAAGAAAG	2	97.5	75.24	details
AAACAAAAACAAAAACAAA	10	96	71.37	details
AAAAAAAAAAAAAAAAAAAA	2	91.5	70.17	details
AAAAGAAACACAAACAAAG	1	97	66.9	details
AAACAAAGAAAAUACAAAG	1	90	63.29	details
AAUAAAAAAAAUAAAAAAAA	1	100	63.14	details
AAAUAAAAAAAAUAAAAA	4	97.25	38.92	details

It could even look like there is some frequency preference,. Too close “dirty bases” lower overall ranking. Well except for the Uracils. Mixed colors don’t seem to doo as well either.

Looking at the 6-6-6 loop in the same manner, something similar happens. And it seems like that “dirty bases” too close, isn’t popular. Not even if red.

cluster	count	score	rank	
(ALL)	35	96.11	91.39	details
AAGGAAAAAGAAAAAGAA	1	96	98.44	details
AAAGAAAAAGAAAAAGAA	3	97.33	96.7	details
AAAGAAAAAGAAAAAGAA	5	93.4	96.43	details
AAACAAAAACAAAAACAA	1	93	95.61	details
AAAAAGAAAGAAAAAGAA	1	97	95	details
AAAGAAAAAGAAAAAGAA	2	96.5	94.56	details
AAGGAAAAAGAAAAAGAA	3	98	93.52	details
AAACAAAAACAAAAACAA	1	98	92.78	details
AAGGAAAAAGAAAAAGAA	3	97	90.61	details
AAUAAAAAUAAAAAGAA	3	98	90.39	details
AAUAAAAAUAAAAAUAAA	1	93	90.06	details
AAUAAAAAAACAAAAACA	1	97	90	details
AAAAAAAAAAAAAAAAAAAA	1	96	89.89	details
AAGAGAGAGAGAAAGAGAGAA	1	98	89.83	details
AAAAAGAAAAAGAAAAAGAA	2	93.5	88.14	details
AAUAAAAAUAAAAAUAAA	2	95	87.84	details
AAACAAAAAUAAAAACAA	2	96	82.37	details
AACAAACAAACAAACAAAC	1	98	77.78	details
GAAAGAGAGAGAGAGAGAA	1	98	77.67	details

5-5-5 multiloop

In this slightly smaller multiloop U's seem to do better. I wouldn't be surprised if optimal filling pattern will change with size of multiloop.

cluster	count	score	rank	
(ALL)	40	97.05	75.95	details
AAAGAAAAGAAAAGAA	4	95	90.37	details
AAUAAAAUAAAAUAA	4	97.25	89.94	details
AGUAAAUAAGAAUAA	1	94	83.6	details
AAAAAGGAAAAAAAG	2	97	80.07	details
GAAAAAGAAAAAAGA	3	98	79.6	details
AAGAAAAAGAAAAGAA	1	98	79	details
AAAAGAAAAAGAAAAG	1	96	78.33	details
AAAACAAAACAAAAC	5	97.4	76.08	details
AAAACAAAACAAAACA	1	100	75.13	details
AAACAAAACAAAAACC	1	96	74.6	details
AACAAAACAAAACAA	2	98	73.37	details
GAAAAGAAAAGAAAA	4	96.5	71.47	details
AAUAAAUAAAAAUAA	2	98.5	67.87	details
AAAAAAAAAAAAAAAAA	7	97.29	66.2	details
AAAAAGAAAAGAAAAG	1	97	62.27	details
AAACACAAAACAAAA	1	97	52.8	details

27 Dec 2013

[How RNA folds](#)

I am reading a paper on RNA folding. It said that RNA folded up in the secondary structure first. And then it made tertiary interactions afterwards.

The folding of RNA is hierarchical in that secondary structure is much more stable than tertiary folding.

Metal ion concentration is important for how much tertiary structure there was made. And the bases in the loops too as those primarily were the ones ending up making tertiary interactions with other areas, like other loops, bulges and in the case of making pseudoknots, also with stem area.

But most of the secondary structure did not change, when the tertiary level formed. I mean base pairing in secondary structure didn't change much. Most changes occurred with high concentration of metal ions.

But sometimes tertiary interactions did change the base pairing of the secondary structure. But as I understand it, mostly in loop and bulge area.

If the scientists are right, it makes solving the folding problem easier. They think that the secondary folding problem was already mostly solved. (Paper is from 1999) I don't agree on that. Neither did Mat. I have had many a structure prediction tool at hand and most often they did not fully predict the shape of the harder of the RNA design structures we have been playing with in lab and have had SHAPE data for that can give us an idea about their structure.

However I like their line of thought here:

Here we will try to systematize and generalize some of what is known about how RNA folds, and to suggest an algorithm to predict the three-dimensional structure of RNA from a knowledge of its sequence. For a review that describes the earlier work in this field, see Brion & Westhof (1997). Our goal is to encourage others to enter this relatively unpopulated field. If 10 % of protein fold researcher switched to RNA, the problem could be solved in one or two years. If the lack of competition in the field is not sufficiently enticing, we hope that by making sweeping statements about RNA folding we can at least goad people into proving us wrong.

Seems to work. :)

30 Dec 2013

I'm interested in comparing designs with identical shapes, made with the classic and current labs method with with barcodes. For more about why, see intro [here](#).

I have compared two player projects that were close matches to two of our Eterna classic shapes. Bround mentioned two eterna labs that was made with the new method. I had forgot about those. I earlier checked them but dumped them as the data didn't matched up with the originals. I decided to take a deeper look into things this time.

[The backwards C](#)

Classic

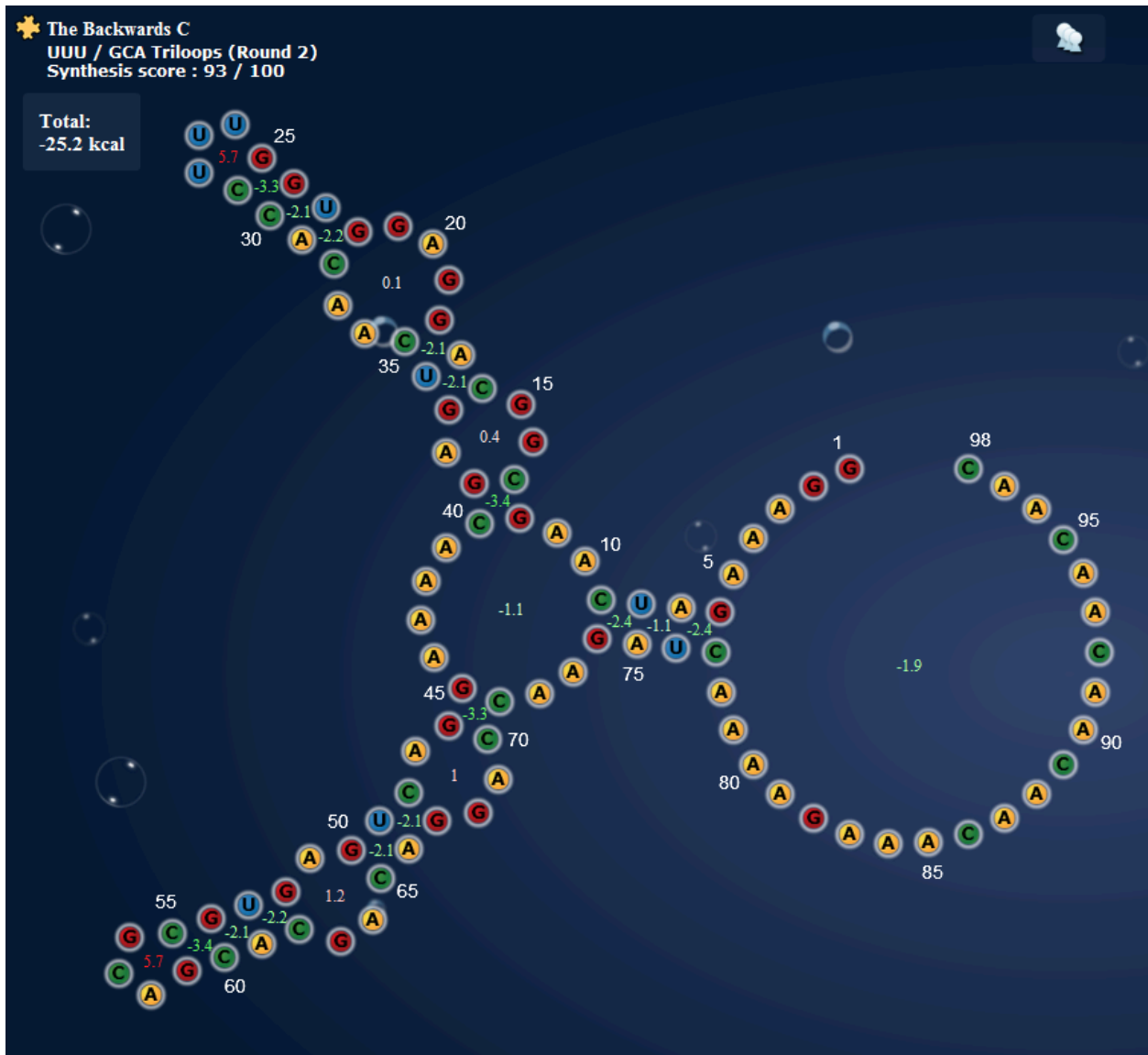
UUU / GCA Tril... GGAAA GAUCAA GCGGCAG GAGGUGUUUCCACAACUGAGCAAAA GGACUGAGUGCG AGCACGACAGGACCAAC

'UUU / GCA Tril... GGAAA GGAAAGAUCAA GCGGCAG GAGGUGUUUCCACAAC CAGCAAAA AGGACUGAGUGCG CCGACGACAGCAAGA

Redone

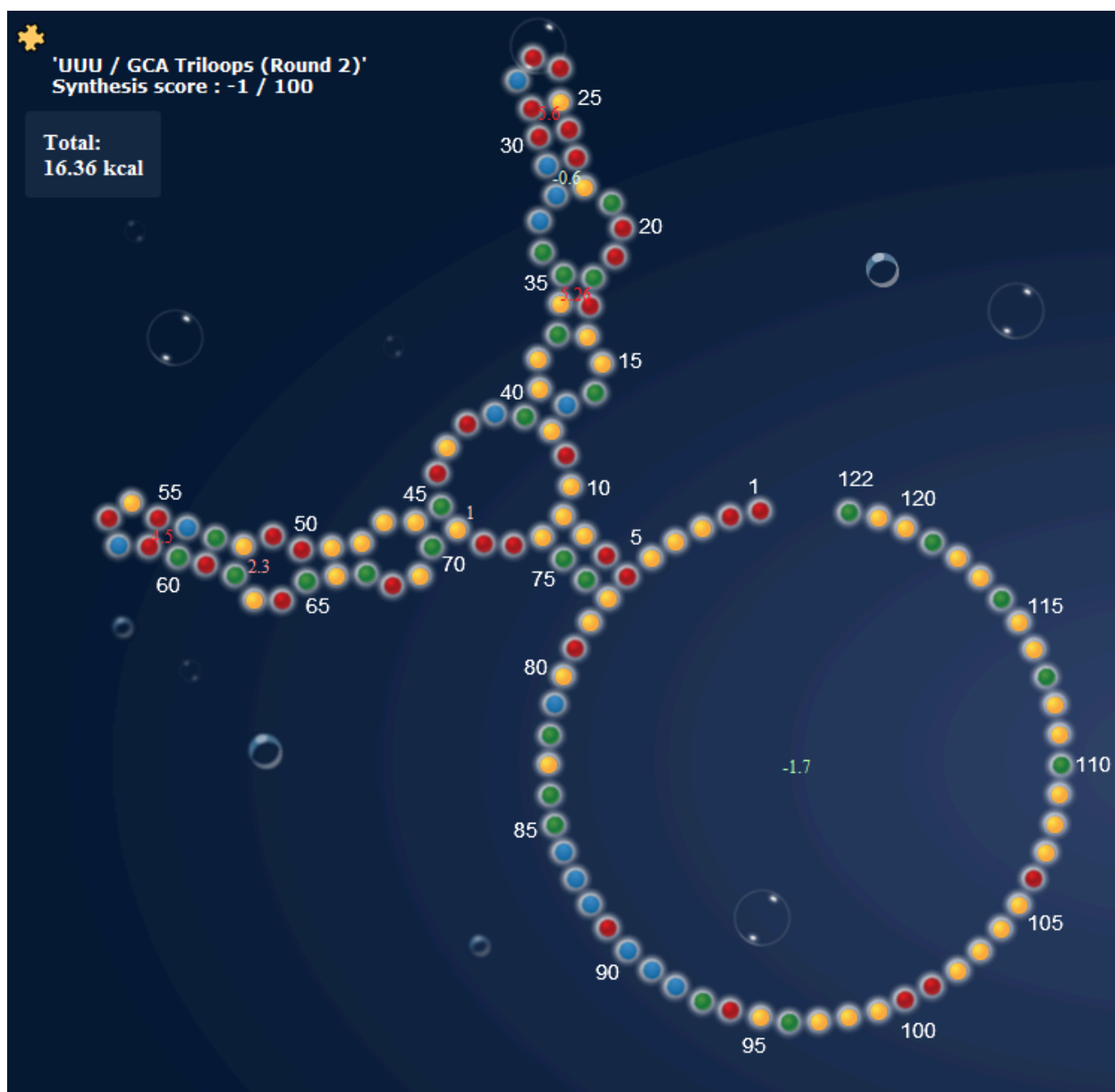
The results don't line up. It is not the same sequence, though the title claims it to be.

Original



<http://eterna.cmu.edu/game/puzzle/535658/>

Redone



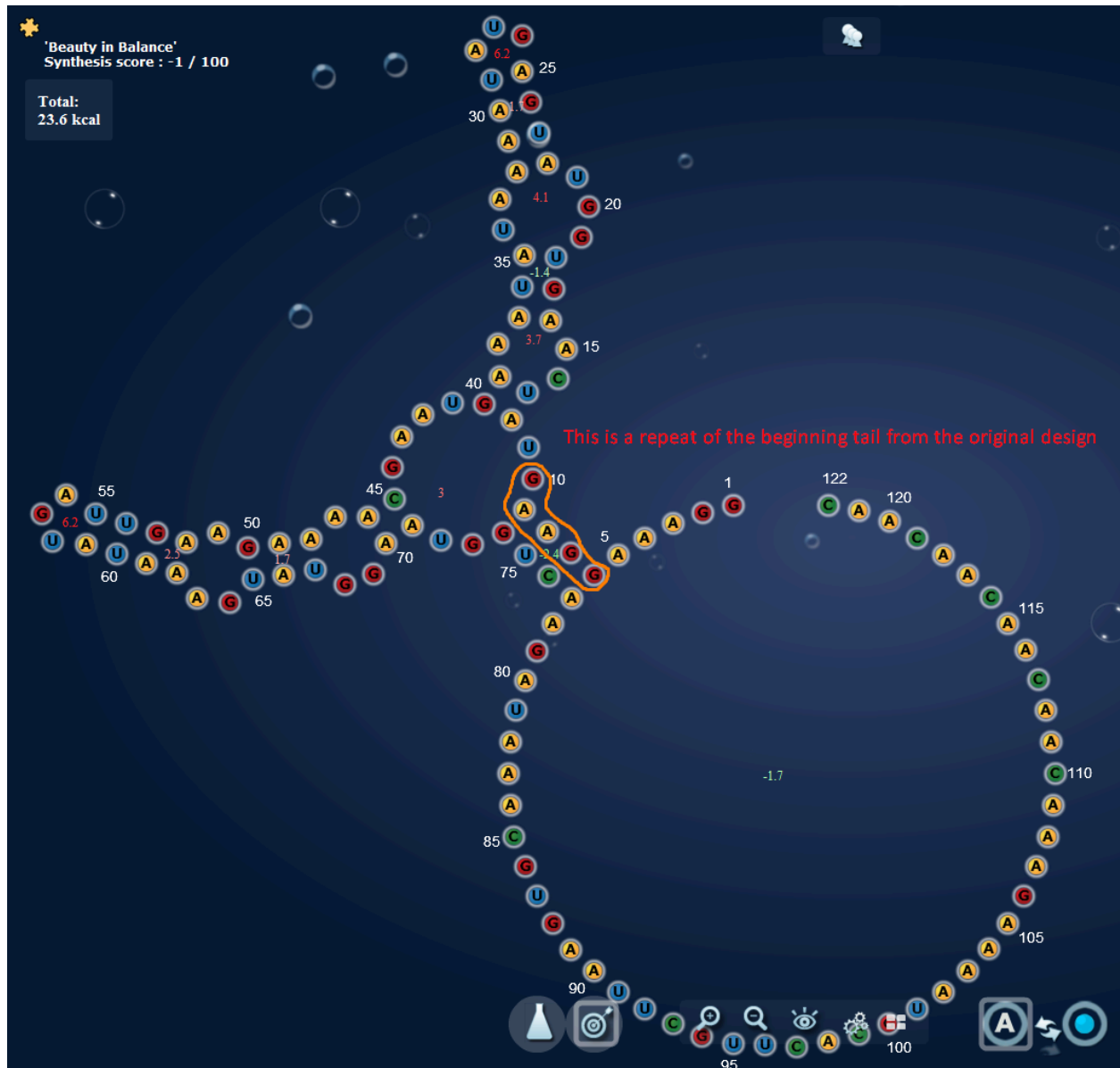
<http://eterna.cmu.edu/game/solution/3281145/3281146/seeresult/>

Notice the many discrepancies. My question is why.

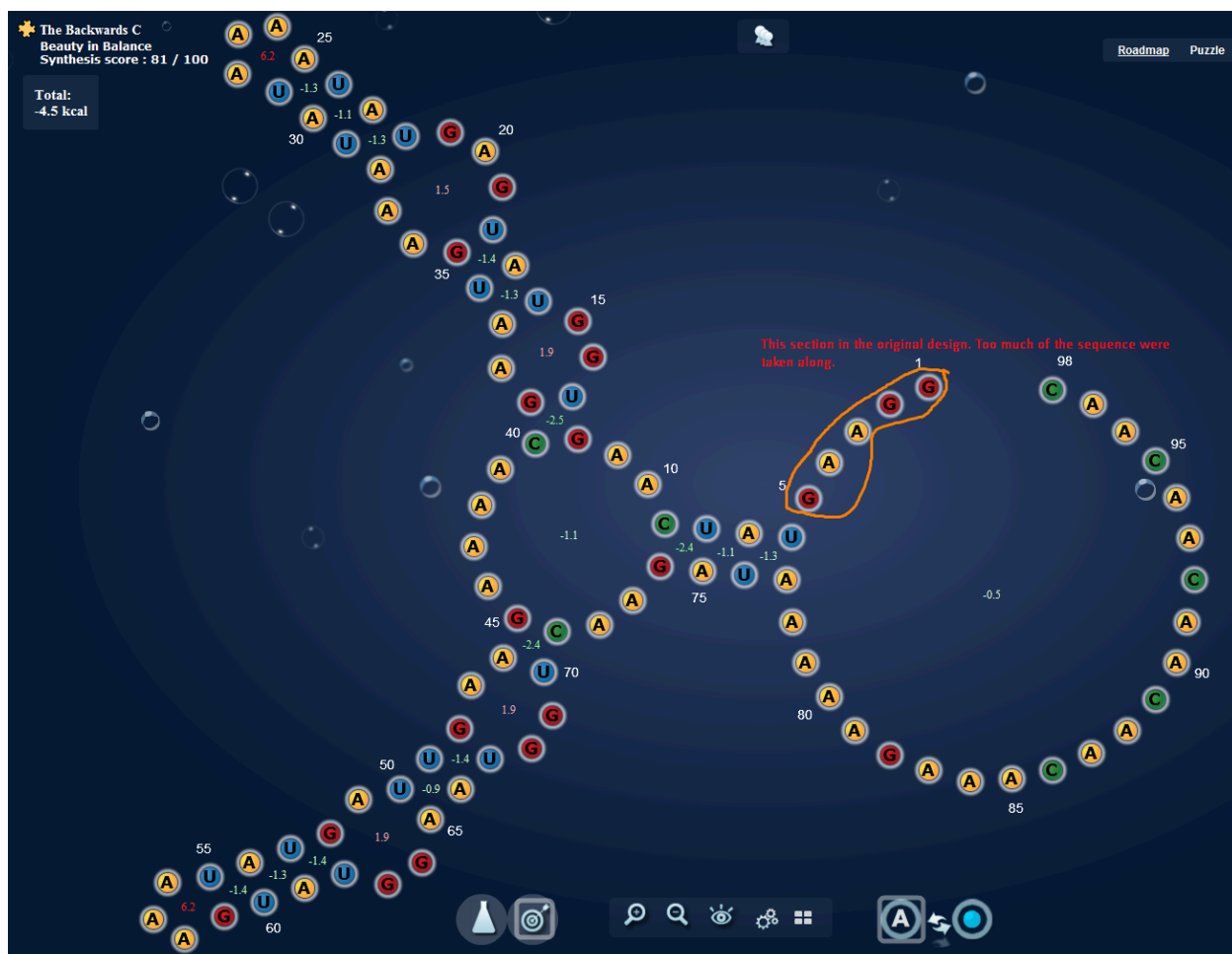
This is the main reason I have been ignoring a lot of the results from the scientist labs. They simply don't make sense. Even though I wanted to compare classic Eterna designs to remakes with the new method. So what I compared was player projects since they don't have this problem.

I decided to look through the results of this lab anyway and I think I discovered the reason for the problem. The tail, beginning sequence from the original, were taken along and making the tail sequence become double in the new redone version. No wonder things doesn't make sense.

Remake



Original



Now it also makes sense why the designs score negative and we can't get all the normal data on them. (I still haven't figured out why we can't get melt, etc data, as other labs that doesn't have this particular problem, also lacks data too) One more thing that makes a lot of sense, is that the estimate mode looks more like the intended shape than the target. Of course the RNA prefers to form more like it already showed it did in our old results, than a not very favorable mainly non complementary version.

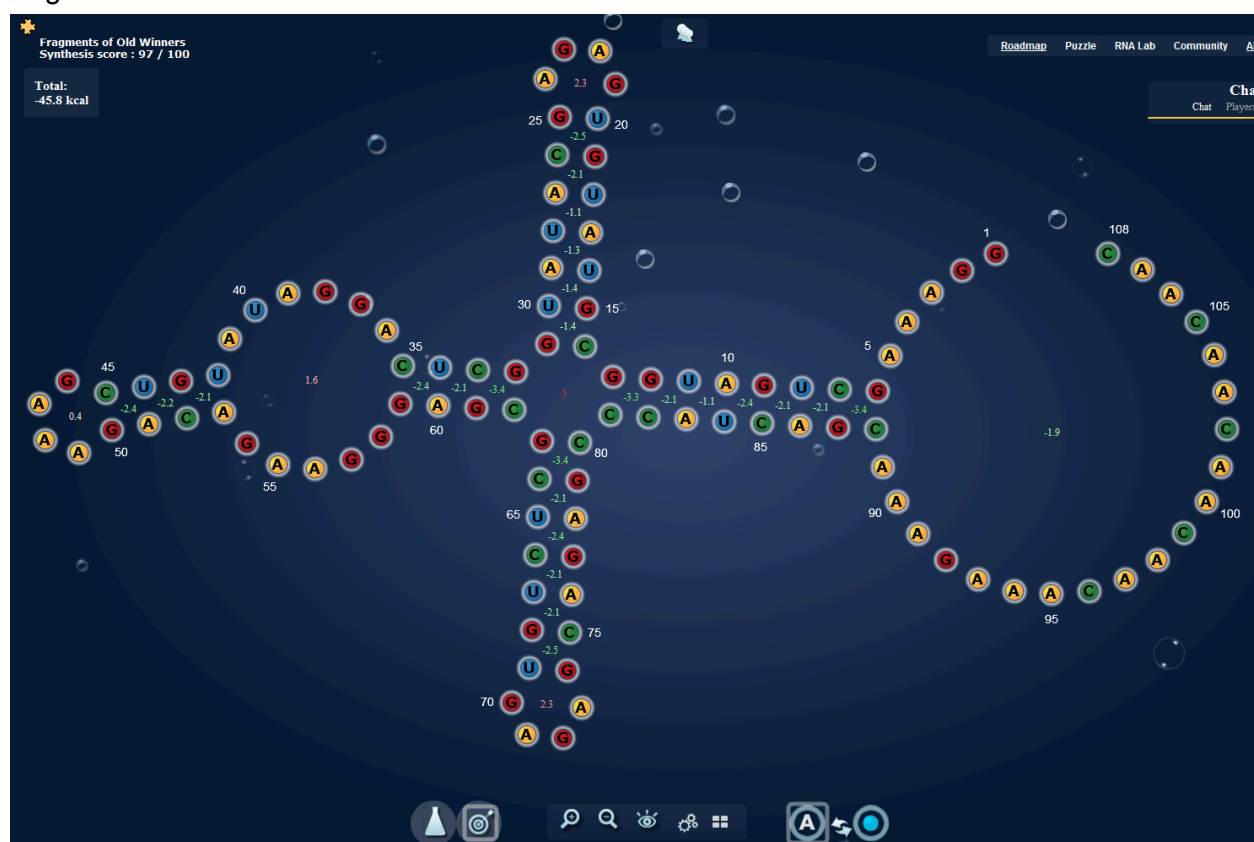
The other Eterna Classic lab redone

This one got old beginning tail + new beginning tail included. Also notice how the yellow SHAPE data for single bases is pushed into the stem area, continuously.

EteRNA R45-46 FMN Aptamer with Single Binding Site			Advanced Sequence Search	Download SHAPE data
Column Options		Sequence View options		
Designer	Title	Sequence		
		I lost this is the new tail I think this is the old beginning tail - taken along from the original design		
		5 101520253035404550556065707580859095100105110115120		
Hanjoo Kim	'Fragments of Old Winners'	G G G A A C C U G A U G C G U A U G U G A G A G C A U A U		
Hanjoo Kim	'FNM Apatamet 1st try'	G G G G A A A G C U A U A C C G A A G A U C G A A A G A U C U U		
Hanjoo Kim	'Freywa - Cross FMN - Reshi..	G G G G A A A G A G C A G A G G A G A C U C G A A A G A G U C U		
Hanjoo Kim	'wisdave"s apatamer #1'	G G G G A A A G U C A G A C C G A C A G U C G A A A G A C U G U		
Hanjoo Kim	'Fiskers single aptamer 2'	G G G G A A A G C U C C U G C G A C U G U C G A A A G A U A G U		
Hanjoo Kim	'Starry"s Single III'	G G G G A A A G G A G U A C C G C U A U A G G A A A C U A U A G		
Hanjoo Kim	'fold vs shapes'	G G G G A A A G A U A G A U G C U G A U C G A A A G A U U A G		
Hanjoo Kim	'ViennaRNA design 01'	G G G G A G G A G C U C U U G C U C A U U U U G C A A A U G A		
Hanjoo Kim	'ViennaRNA design 03'	G G G G C U A G A C A G C A C C A G A U G G U U G C C G U U U		
Hanjoo Kim	'ViennaRNA design 04'	G G G G A G A G A C G A U G U G C U A U G A A U G U A U A G U		
Hanjoo Kim	'NUPACK design 02'	G G G G C A C C G G G U A G C C C U C C U G C A U G C A G G A G		
Hanjoo Kim	'NUPACK design 04'	G G G G A A A C G G G C A G G C A C C C G C G U G A G C G G G U		
Hanjoo Kim	'Freywa - Cross FMN R2 - Ze..	G G G G A A A G C U G C U G C G G A G U U C G A A A G A G C U C		
Hanjoo Kim	'Tadpole 2.0'	G G G G A A A G C U A C U G G C G U G A C U G C G U A C G U A C U		
Hanjoo Kim	'Kiwi'	G G G G A A A G G U G U G C C G G U C U C C G A A G G G A G A C		
Hanjoo Kim	'LROppy 93.4% FMN'	G G G G A A A G U A U A U A G G U A U A U C G A A A C A U A U A		
Hanjoo Kim	'EteRNA ensemble design 01 ..	G G G G A A A C U U A G A G C G G C G U C A A A A G A C G G C		
Hanjoo Kim	'EteRNA ensemble design 02 ..	G G G G A A A G U A U G G A G C U A A U G G A A A C U A U U A		
Hanjoo Kim	'EteRNA ensemble design 03 ..	G G G G A A A G U A C A A G G C G C A G U C A A A A G A C U G C		
Hanjoo Kim	'EteRNA ensemble design 04 ..	G G G G A A A C C U C G A A C C U U U A C C A A A A G G U A A		

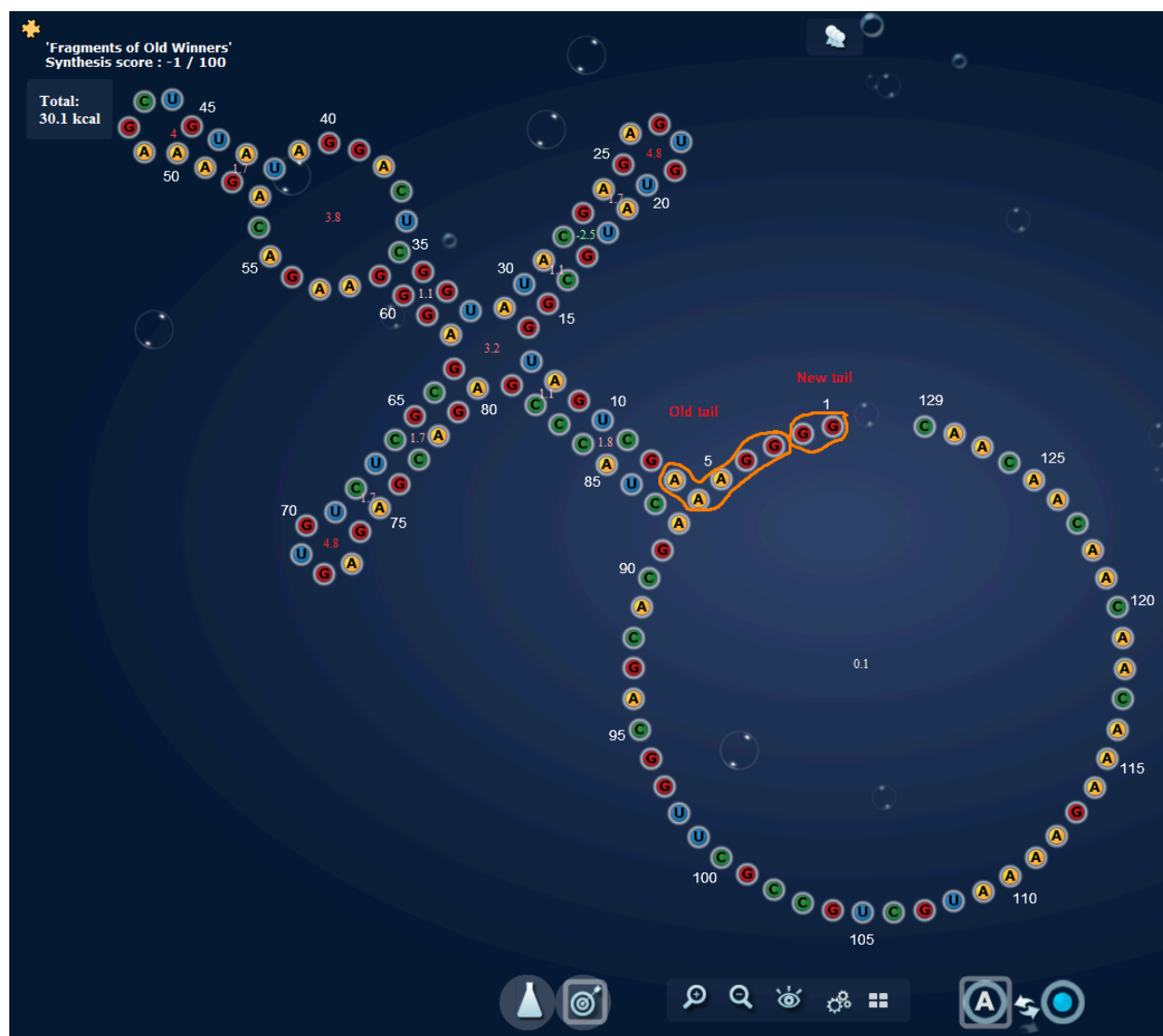
<http://eterna.cmu.edu/web/browse/3376322/>

Original



<http://eterna.cmu.edu/game/solution/669347/669610/seeresult/>

Remake



2 Jan, 2014

Ensemble diversity

Mat mentioned a joint post by him and Dimension9. I looked at the numbers again and commented below.

https://getsatisfaction.com/eternagame/topics/labs101_to_104_base_pair_percentages_and_rnafold_results

High ensemble diversity - like real high. That happens for the designs that has real many GU's and one of the 100% GC. Half of the winning designs have GU'pairs.

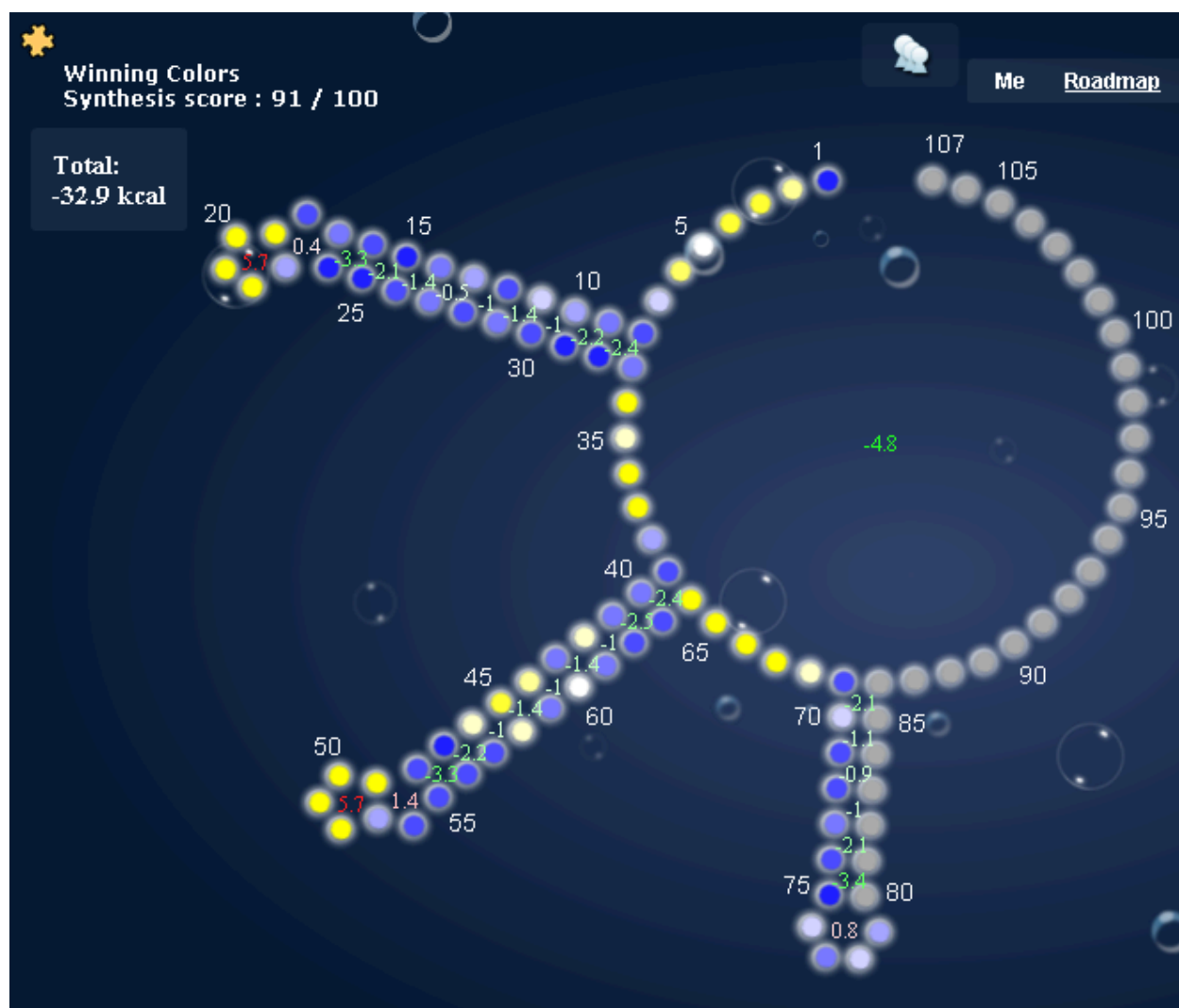
What if the GU's are partly helping raising the ensemble diversity out of that thought of sweet spot of 0.05?

It isn't a clear cut case but I think it is a tendency. That presence of GU's might raise ensemble diversity but yet GU's have a stabilizing effect if placed right

28 Jan, 2014

I was watching some designs in this lab : [Modeled Impossible: 1 Nucleotide Bulge/Triloop Lonely base pair V2](#), when I got a thought about my [old idea on GU placement](#). Now I have through the time learned that GU's can be placed any place imaginable. But I still think it has favorite positions. Below the design has two almost mirroring stems. The top one folds fine while the bottom one doesn't. The GU's are orientated different, the Guanine is up on the 5' side of the first stem and down on the 3' side of the last stem.





Now most of the bottom stem actually sticks together and it is not like no GU's will ever be found turning different. For really long stems there are other patterns occurring, like GU's turning one way in start of stem, opposite in middle and again reverse at last. And more patterns. But there variations seems more needed.



Now the basepair from the hook in the second stem, could be what cause the second stem to break. But notice that the GU's with the G on 5'prime does well, while the ones on second stem 3'prime doesn't.



Modeled Impossible: 1 Nucleotide Bulge/Triloop Lonely base pair V2

Winning Colors II

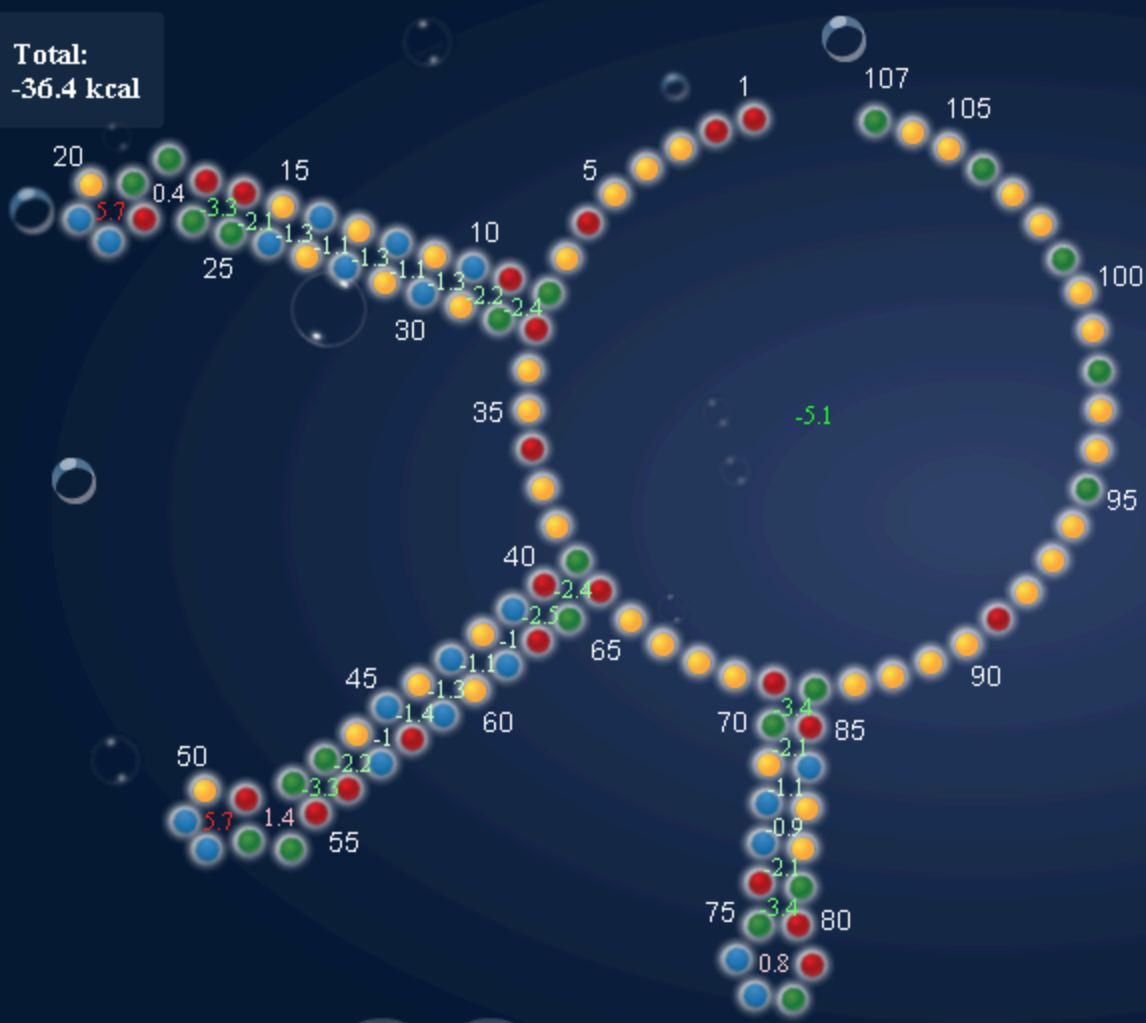
Synthesis score : 91 / 100

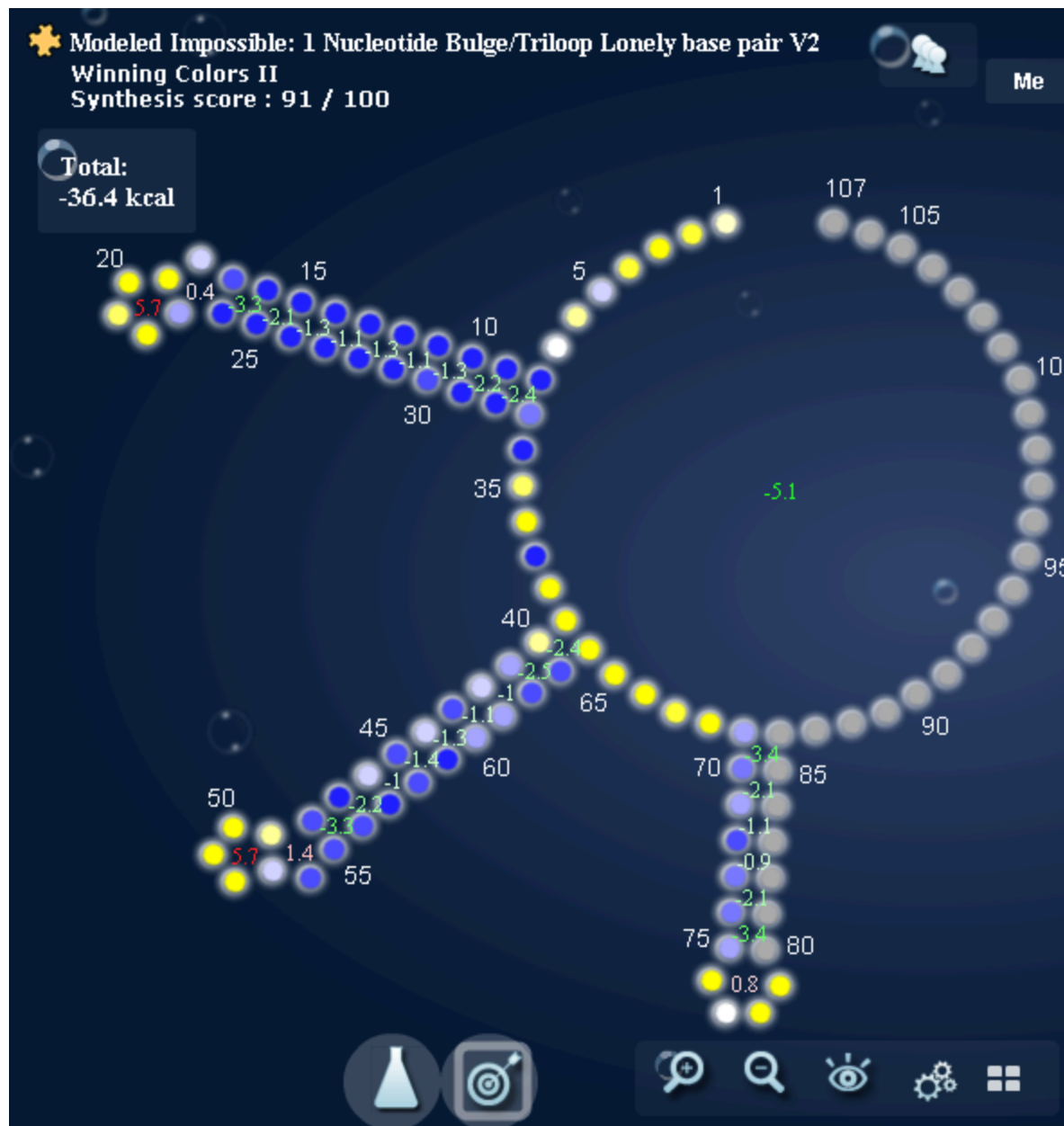


Me

R

Total:
-36.4 kcal



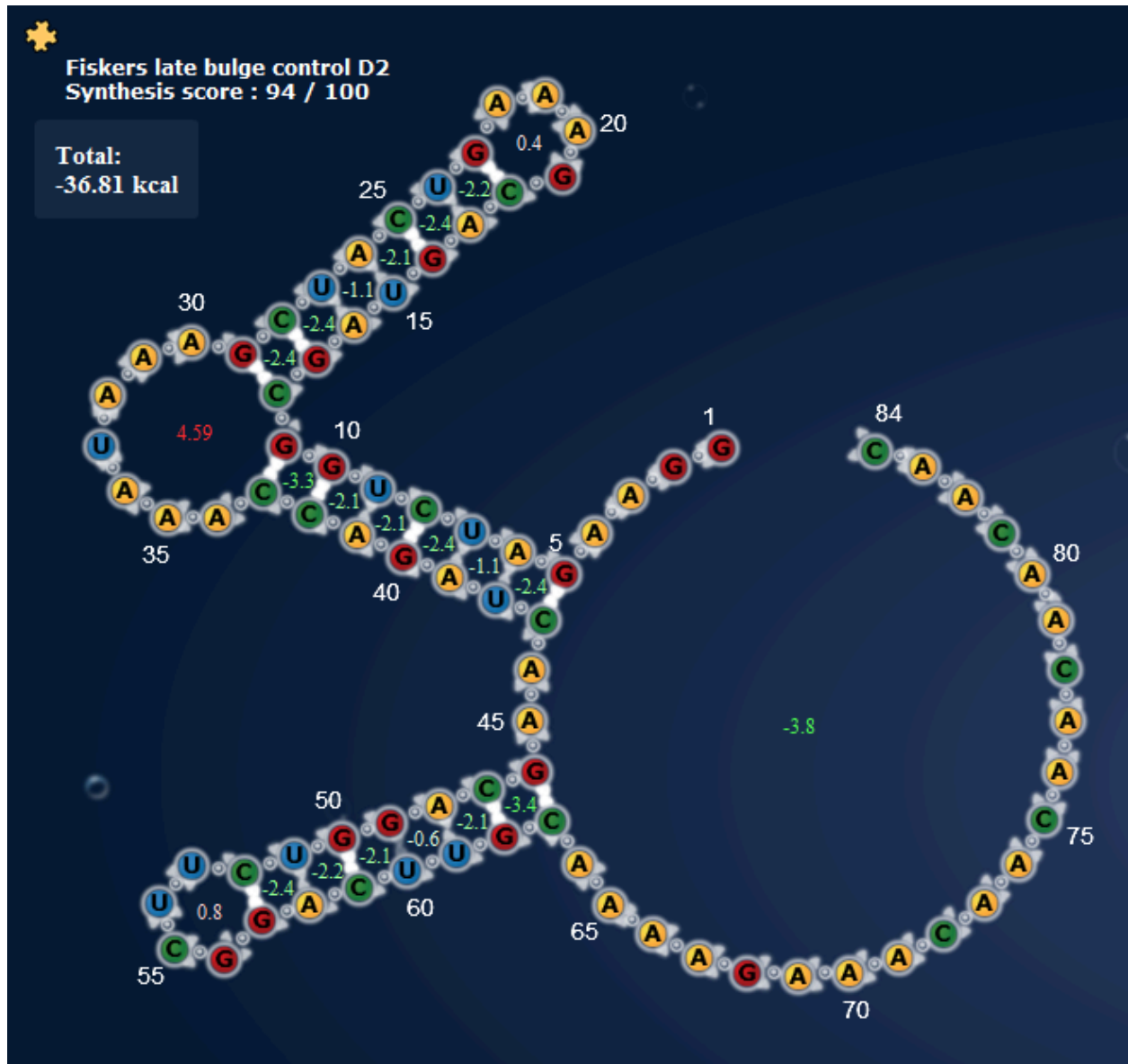


Yes, it is really this GU (marked that makes this stretch unstable.

However the other GU's that are orientated like in the top stem do seem happier than the opposite orientated one in the bottom stem.

19 Feb 2014 - Bulges

I find it fascinating how badly this bulge want green in particular for the beginning of the bulge. As earlier big bulges, it took a liking to double same turning basepairs at bulge start. Be they green (in particular) but red also.



Late bulge control			
Title	Synthesis score ▾		Sequence
search	min	max	search
LBCf3	94 / 100		GGAAGGCACACGGGCUUGGAAACACACCCAGAAAGAUUGGCAAGGAUACUUC
Clipp III [C at 33]	94 / 100		GGAAACAGGGGGCGGCUAGGAAACUACGGCAAAAGAAAGCGGCGUAAAGGACUUCUUC
Cobalaminated	94 / 100		GGAAAGGGGCGUCUGAGUACACACUACGAAAGCAUUGGCGCAAGGUUCUUCUUC
Fiskers late bu...	94 / 100		GGAAAGAUUGGCGGAUAGGAAAGUACUAGAAAUAAAGCAGAUCAAGGAGGUUCUUC
LBC - 1	92 / 100		GGAAAGAUUGCGCGAUUAGGAAAGUACUAGCAACAAAGGAUUAUCAAUGAGAUCUUC
Coba III	91 / 100		GGAAAGGGGAUUGGGAUACGGGUACUUCGAAAGCAUAGUUGCGCAAGUGGGAUUCUUC
Edgelaatar	91 / 100		GGAAAGGGAGGAUUGGUGAGUAAUACUAGAAAGAAUCCUCCCAAGUAUGGGUUCUUC
Coba II	89 / 100		GGAAAGGGGAUUGGGAUAAUUAUACUUCGAAAGCAUAGUUGCGCAAGUUAGGGUUCUUC
A-U Bulge - Bro...	89 / 100		GGAAAGGAGUAGAGCUAGUGAUAGAUAGUAAAUAAAUCAUUGCAAUGCGUAGUUCUUC
Clipp II [U at 33]	87 / 100		GGAAACAGGGCGCGCCUAGGAAACUACGGCAAAUAAAGCGGCGUAAAGCGUUCUUCUUC
Mat - Late Bulg...	87 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Fiskers late bu...	87 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Flipped pattern...	85 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Magnifying Glasses	85 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Blaireri	85 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
MatMod 5 - Jieu...	83 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Hippie Beads III	82 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
JR_LateBulgeCon...	81 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Battle of the B...	80 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Battle of the B...	80 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Bulge Control 1	80 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
JR_LateBulgeCon...	80 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
MatMod 6 - Jieu...	78 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Mat - Mod of Eli	78 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Simple Perfection	78 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Battle of the B...	76 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
too late? 2	75 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
LateBulgeCtrl#1	75 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
walnut	73 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
LBC1	73 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Mat - Late Bulg...	73 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Bulge Control 2	73 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Hippie Beads I	73 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
LBC2	71 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
U-A Bulge Contr...	71 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
U-A Bulge - Bro...	71 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
G32	69 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC
Hippie Beads II	66 / 100		GGAAAGGUGACGGGAUACGGAAACGUUAGCAAUAAAGUGAGCGCAAGAGCUAGUUCUUC

However C's are the most liked at this position. And there werent many fully stable closing quads for the bulge.

Late bulge control			
Title	Synthesis score ▾		Sequence
search	min	max	search
LBCf3	94 / 100		GGG GGCACCA CCGGUGUG GAA ²⁰ CACACCC A GAAAGA GUGG ⁴⁰ UGCA A GBAUC CUUCG
Clipp III [C at 33]	94 / 100		GGAA CAGGC GCGCUGAG GAA CUCAGC A AAGCAA CGCCUGAA CCGACUCU CG
Cobalaminated	94 / 100		GGAA GCGGAG CUCUGAGUACAC AUCAG A AAGCAU GCUCCCAA GGUUCUCUUCG
Fiskers late bu...	94 / 100		GGAA GAUCUG GGAUGA GAA AUCU C A AUA A A CCA GAUC A GCA GGUU CG
LBC - 1	92 / 100		GGAA GAUGUC CCGAUUA GAA CUGAU C C AACA A GGAUUA C A GUA GAUCUUCG
Coba III	91 / 100		GGAA GCGGAU CUGGAGUA C GGGU ACUCCA A AAG AU GAUCGCCA GUGGGAGUUCG
Edgelaatar	91 / 100		GGAA CCGAGG A AUCGUGAGUAA UCACCAU A AAGAA UCCUCCCA GUAUGGGUUCG
Coba II	89 / 100		GGAA GCGGAU CUGGAGUA UUAU ACUC C A AAGCAU GAUCGCCA GUUAGGGUUCG
A-U Bulge - Bro...	89 / 100		GG A CCAUGA AGCUAUC GAU GAUAGGU A AAAAAA UCAUGUCA CUCGUA GU CG
Clipp II [U at 33]	87 / 100		GG A CAGGC CCGCUGAG T AA CUCAGGC A A AAAAA GCGCUGAA CCGUCUCUUCG
Mat - Late Bulg...	87 / 100		GGAA CGUCA CCGAUACG T AA CGUAUCC A AAAAA GTGACGC A GAGCUAGUUCG
Fiskers late bu...	87 / 100		GGAA GCUCAG CCGAUACG T AA CGUAUCC A AAAAA GGUGAGCA GCAUGUUCUUCG
Flipped pattern...	85 / 100		GGAA CGUAG CCGUAGUC T A GACUACC A AAAAA GCUACGCA GUAUGUUCUUCG
Magnifying Glasses	85 / 100		GGAA GUGU CCGAUUA AAG A UAAUUC A AAGAAA CAACUAGA GGAUGUUCUUCG
Barrieri	85 / 100		GGAA GCGA UGGUGGAGGAG TUCAC C A AACA A CAUCGCC A GCGUGACUUCG
MatMod 5 - Jieu...	83 / 100		GGAA CCGAG CCGUAACG T AA GGUUA C A AAAAA GUCUGGGA GUGGAAGUUCG
Hippie Beads III	82 / 100		GA CGAUAG CCGACAC T AA CGUGU GG UUUUUU GCUAUCS A GCAUACUUCG
JR_LateBulgeCon...	81 / 100		GAAGUAU CCGUUAACG T AA CGUUAU GAACCCAA GUAUACGA CAGUAGCUUCG
Battle of the B...	80 / 100		GGAA GAUCG CCGUUAAC T A GAUAUCG A AAAAA GCUAUCGA GUGCUUCUUCG
Battle of the B...	80 / 100		GG A GAUUC CCGUUAAC T A GAUAUCG A AAG T A GCGAUAC A GUGCUACUUCG
Bulge Control 1	80 / 100		GAAGCAU AGGCGCAUAG GAA CUAU GCA AAAAA GCUAUCG A GCUAGACU CG
JR_LateBulgeCon...	80 / 100		GAAGUGA UACCAUAUG T AA CAUUAU GAACCAU GUAUACCA CAGUAUCUUCG
MatMod 6 - Jieu...	78 / 100		GAAGAGAG UCCUGUGCG T AA CACAGCA A AAAAA GACUCUCAA GCGUUCUUCG
Mat - Mod of Eli	78 / 100		GAAGCAUUGCGCAUGAG GAA GUCAUCCA A AAAAA CCA GAUC CCGAGAUU CG
Simple Perfection	78 / 100		GGAA CUAUGCGCAUAGC T A GCAUAGCA A AAAAA GCAUAGCA CCGUGACUUCG
Battle of the B...	76 / 100		GAAGUAU CCGCAUAG T A GUAUAGCA A AAAAA GCGAUAC GCGCAUGUUCG
too late? 2	75 / 100		GAAGCAUAGCGCAUAG GCA GCUAUC C A AAAAA GCUAUCG GCGUGGCUUCG
LateBulgeCtrl#1	75 / 100		GGAAUAUAGCGCAUAG T AA UAUAU GCA AAAAA CUUAUA A GAGUAAGUUCG
walnut	73 / 100		GG A GAUAC GGUUCU CAAAAGAGACUCA AAAAA CUGAGUCA CCGUGCCUUCG
LBC1	73 / 100		GG A GUGACUGGAUGGUG T A GAGCAUCA T A A CUGACCA GACCGUCUUCG
Mat - Late Bulg...	73 / 100		GAAGCAU CCGAUAG GAA GAUAUC A AAAAA GCUAUGCA GAGCAUGUUCG
Bulge Control 2	73 / 100		GG A GCAUAG CCGAUAG GCAUA GCA A AAAAA GCUAUGCA GCUUUGUUCG
Hippie Beads I	73 / 100		GAAGCAUAGCGCGUACG T AA GGUAGCG A AAAAA GCUAUGCA GCGACUUCG
LBC2	71 / 100		GAAGUGAUCGCAUGUG T AA GACCAUG A AAAAA GCUAUGCA GAGGCUUCUUCG
U-A Bulge Contr...	71 / 100		GG A CAGUAUCUGAGUG T AU GACUCG A AAAAA AGUACUGA AGUGGCUUCG
U-A Bulge - Bro...	71 / 100		GAAGCAUAGCGCUAUGG T AU GACUCG A AAAAA AGUACUGA AGUGGCUUCG
G32	69 / 100		GAAGCAUAGCGCUAUGG T AU GCAUAGC A AAAAA GCUAUGCA GACUGGCUUCG
Hippie Beads II	66 / 100		GAAGCAUAGCGCGUACG T AA GGUAGCG A AAAAA GCUAUGCA GACUGGCUUCG

In the other one the C's at closing basepair rules

Late bulge			
Title	Synthesis score ▾		Sequence
search	min	max	search
Clementine 2	94 / 100		GAG CCGGGCC CCGUGAGCGA ²⁰ AUUCACCC A AAAAAA GGC ⁴⁰ CCGCA A GAUCG UGUUCG
Battle of the B...	92 / 100		GGAA GAUAGCGCGAGU GCUUUGG UUCAG C A AAAAAA GCUUAC AAGUGUGUUCG
LB - 1	91 / 100		GGACUGAUGCGGUAUC GUGACA GAUUGUA AAAAAA GGAUUA CAGGUGUACUUCG
Fiskers late bu...	89 / 100		GGAA GAUUGCGGUAUC GACA GAUUGUA AAAAAA GCUUAC AAGGUGUACUUCG
Battle of the B...	87 / 100		G A GAUAAG CCGCUUAG GTTAA CUAAGCG A AAAAAA GCUUAC AAGGUGUACUUCG
Sleeping Beauty II	85 / 100		GG A GCACA CCGGUGUGG T AA GCACA CCA AAAAAA CUGUGG AAGGUA CCUUCG
Fiskers late bu...	83 / 100		GGAA GCAUAC CCGAUAG C GAAAGU C AUCGA A AAAAA GCUUAC AAGGUGUACUUCG
Eninxteen	82 / 100		GAAGCGGAG GGAUGAG GAAAGU C AUCGA A AAAAA CUGUGG AAGGUGUACUUCG
Mat - Late Bulg...	80 / 100		GG A CCGACAG CGAUAGCG T AA CUAAGCG A AAAAAA GCUUAC AAGGUGUACUUCG
lb-2	76 / 100		GGAA GCGUAG CCGGAGAGGG T AA CUCUUC C AAAAAA GCUAGCA AAGGUGUACUUCG
Fiskers late bu...	75 / 100		G A GCUAUGCGCAUGACG T AA GCUAUGCA AAAAAA GCUAUGCA AAGGUGUACUUCG
JR_LateBulge_Rn...	74 / 100		GAAGCAUUGA CCAUAUG CUAAGCAU A AAAAAA AGUACAG A GCAAUUUCG
Clementine 1	73 / 100		GGAA CCGGGCC GCAACG CUAAGGUGG T AA AAAAAA GGCCCG AAGGUGUACUUCG
Fashionably Lat...	71 / 100		G AAGCAGAGGGCAUGCG T AA GAGUAG C AAAAAA GGCGUG AAGGUGUACUUCG
Erincexe	71 / 100		GAAGGAGGGA GGAAGGGCG T AA GCGCUC C AAAAAA GGCCUG AAGGUGUACUUCG
nakedly late 2	66 / 100		G AAGCAU AUCGGGAUAGCG T AA GCUAUC C AAAAAA GCUAUGCA AAGGUGUACUUCG
nakedly late	64 / 100		GAAGCAUUGGGCUAUGG T AA GCUAUGCA AAAAAA ACCAUGC AAGGUGGCUUCG
Algeribe	64 / 100		G AAGCUGUCUGAAUA GAAAGCUA A AAAAAA CAGACGA AAGGUGGCUUCG
U G and U G, bu...	62 / 100		G AAGCUGAUCUGCUACUC T AA CAGAGUA GUA AAAAAA GCUAUGCA AAGGUGUACUUCG
Sleeping Beauty III	60 / 100		GAAGUA CAGCGGUGUA C T AA GUAAC CCA AAAAAA GUGUAC AAGGUGUACUUCG

I wonder why there was so high error rate in this data. It wasn't the same for the controlled one.
Is it the locked A's provoking this?

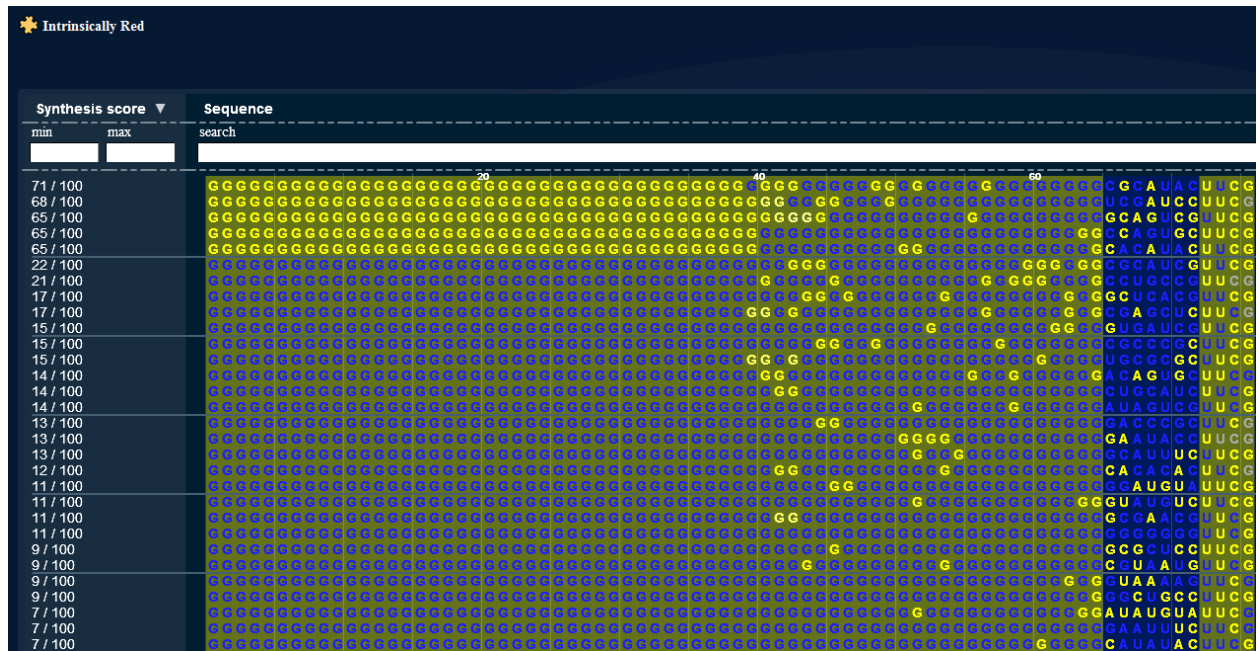
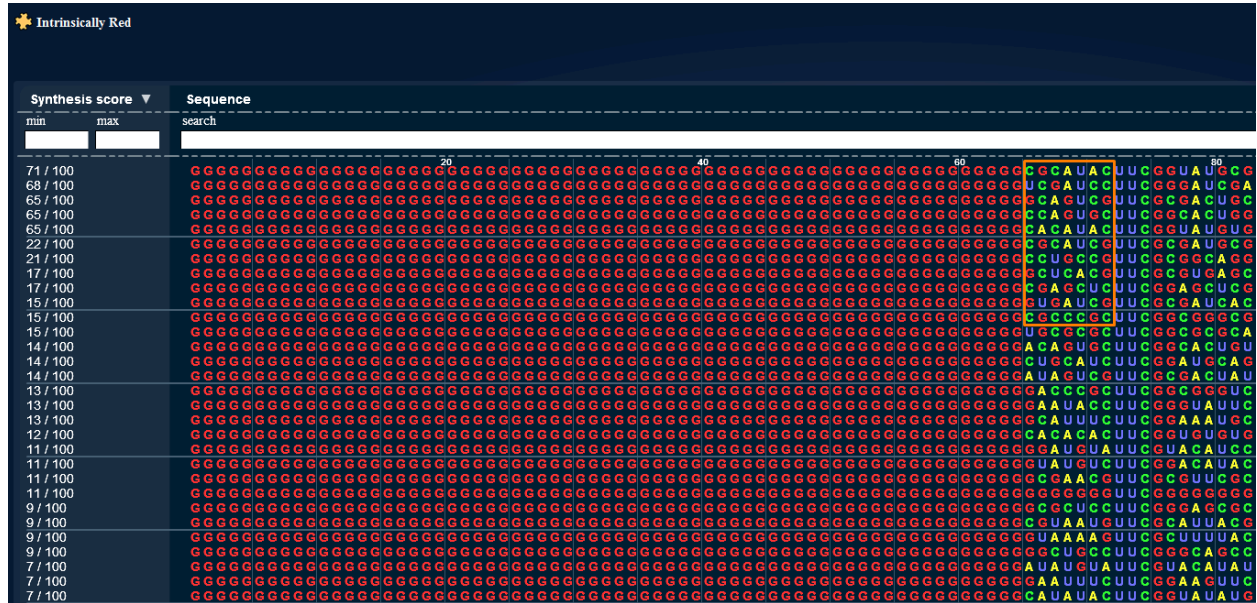
Late bulge control			
Title	Synthesis score ▾		Sequence
search	min	max	search
LBC3	94 / 100		GGAGGCACCCAGGGUGUGGAAACACACCCAGAAAGAAGGUGCAAAGGAUCACUUCG
Clipp III [C at 33]	94 / 100		GGAGGCAGCCGCGCCUGAGGAAACUCAGGCAGAAACAAACGCGUGAAACCGACUCUUCG
Cobalaminated	94 / 100		GGAGGGCGAGCCUCUGAGUACACACUCAGAGAAAGCAUGCUCGCCAAAGGUUCUUCG
Fiskers late bu...	94 / 100		GGAGGAUCUGGCGGAUGAGCAAGAGUCUAGCAAAUAAACAGAUCAAAGCAGGUCUUCG
LBC - 1	92 / 100		GGAGGAUGUGCCGAUUAAGAAACUGAUGCCAAACAAAGGAUAUCAAAGUAGAUCUUCG
Coba III	91 / 100		GGAGGGCGAUCUGGAGUACGGGUACUCCAAGAGTAUGAUCGCCAAAGUGGAGUUCG
Edgelaatar	91 / 100		GGAGGGGAGCAUUGGUGAGUUAUCACCAUAAAGAAUCCUCCCAAGUAGGGUUCG
Coba II	89 / 100		GGAGGGCGAUCUGGAGUUAUUAUCUCCAAGAGCAUGAUCGCCAAAGUAGGGUUCG
A-U Bulge - Bro...	89 / 100		GGAGACAUAGAGCUAUGCAUAGAUAGCUAAAAAAAUCAUGUCAAUCUGUAGUUCG
Clipp II [U at 33]	87 / 100		GGAGCAGGCCCGCCUGAGGAAACUCAGGCAAAUAAACGCGUGAAACGUCUUCG
Mat - Late Bulg...	87 / 100		GGAGCGGUACGGGAUACGAAACGUAUCCAAUAAAAAGUACGCAAGAGCUAGUUCG
Fiskers late bu...	87 / 100		GGAGGCUACGCCGAUAGCAAAACGUAUCCAAUAAAAAGUGAGCAAGCAUGUUCG
Flipped pattern...	85 / 100		GGAGGCGUAGGGGUAUCAAAGAGUACCAAAUAAACCUACGCCAAGUCAUGUUCG
Magnifying Glasses	85 / 100		GGAGCUAGUUGGAUUAUAAAGAUAAUUAUAGAAAGAAACCAUAGAAAGGAGUUCG
Biarreri	85 / 100		GGAGGCGAUGGGUGGAGGAGAUUACCAAAACAAACCAUGGCCAAGCUGAUCUUCG
MatMod 5 - Jieu...	83 / 100		GGAGCCAGAGCGGUACGAAAGGUAUCCAAUAAAAUUCUGGGAAACUGGAUUCG
Hippie Beads III	82 / 100		GGAGCGAUAGCCACACCAGAAAGGUGUGUUUUUUUGCUAUGCAAAGCACUUCG
JR_LateBulgeCon...	81 / 100		GGAGCGUAUACCGUAUACGAAAGCUUAGAACCCAAUUAUACGACAGUAGUUCG
Battle of the B...	80 / 100		GGAGGAUUCGCCCUAUACAAAGUAUAGGAAAGAAACCGAUACAAAGUCUACUUCG
Battle of the B...	80 / 100		GGAGCAUAGCGCAUUAAGAAACUAUUGCAAAUAAAGCUAUGCAAAGCUAGACUUCG
Bulge Control 1	80 / 100		GGAGGUGAUACCAUAUAGAAACAUUAUAGAACAAUGUAUCACAAAGUAUCUUCG
JR_LateBulgeCon...	80 / 100		GGAGGAGAGUCCUGUGCCAAAGCAAGCAAAUAAACACUUCAAAGACCUUUCG
MatMod 6 - Jieu...	78 / 100		GGAGGAUCUGGCGUAUGCAAAAGUCUAGCAAAUAAACAGAUCAAAGCGAGUUCG
Mat - Mod of Eli	78 / 100		GGAGGCUAUGCGCUAUGCAAAAGCAUAGCAAAUAAACCGAUACCAAGGUGACUUCG
Simple Perfection	78 / 100		GGAGGAUUCGCCCUAUACCAAAAGUAUAGGAAALAAACCGAUACAGUCCAUUCG
Battle of the B...	76 / 100		GGAGCAUAGCGCCUAUAGCAAAAGCUUAGGAAALAAACCGAUACAGUCCAUUCG
too late? 2	75 / 100		GGAGCAUAGCGCAUAGCAAAAGCUUAGGCAAAUAAACCGAUACAGUCCAUUCG
LateBulgeCtrl#1	75 / 100		GGAGGAUUAUAGCGUAUUAUAAAUUAUAGCAAAALAAACCUAUAAGAGUAUUCG
walnut	73 / 100		GGAGCAUAGCAAGAGUUCGAAAGAGACUCAAALAAACCUAGUCAAAGGUGCCUUCG
LBC1	73 / 100		GGAGGUGACUGGAUUGGCAAAAGACCAUCAAALAAACAGUCACAAGGCCUUCUUCG
Mat - Late Bulg...	73 / 100		GAAGCGUAGCGGAUAGCAAAACAUUAGCAAAUAAAGCUAUGCAAAGGCAUUCG
Bulge Control 2	73 / 100		GGAGCAUAGCCGCUAUGCAAAAGCAUAGCAAAALAAAGCUAUGCAAAGCUUUCG
Hippie Beads I	73 / 100		GAAGCAUAGCCGCUAUGCAAAAGCAUAGCAAAALAAAGCUAUGCAAAGCUUUCG
LBC2	71 / 100		GAAGGUAUGCAUAGGUGCAAAAGACCAUCAAALAAACAGUCACAAGAGGCUUCG
U-A Bulge Contr...	71 / 100		GGAGCAGUACUUCGAGUCGAUAGACUCCAAALAAAGUAUCGAAGUCUUCG
U-A Bulge - Bro...	71 / 100		GAAGCAGUACUUCGAGUCGAUAGACUCCAAALAAAGUAUCGAAGUCUUCG
G32	69 / 100		GATCGAUAGCGCUAUGGCAAAAGCAUAGCAAGAAAAAGUAUCGAAGUCGUCG
Hippie Beads II	66 / 100		GATCGAUAGCGCGUACCGAAAGUAGCGCAAUAAAGUAUCGAAGUCUUCG

Early bulge lab had U's and C's at best for closing base pair and not many. Apparently it is the first stretch on a bulge that is hardest solving, for all of the labs. On the other side G is a clear winner for closing base.

Early bulge			
Title	Synthesis score ▾		Sequence
search	min	max	search
Early Bird III	98 / 100		GGAAACUACGCCAAALAAAGGUGUGGAAAGCACACCGCGUAGCAAGUGUGUUCG
Late & Great 2 ...	96 / 100		GGAAACCCAGCAALAAAGGUGUGGAAAGCUGAGCCCGUGGCCAAAGUGUGUUCG
Early Bulge 2	96 / 100		GGAAAGCUAUUGCAALAAAGGUAUUGCAAAAGCAUAGCCGUAAGCAAGUGAGUUCG
Vemaxege	96 / 100		GGAAAGAGGGUAAALAAAGGUGUGGAAAGCUCGCCAACCCUCCAAAGUGUAGUUCG
Golden Arch I	94 / 100		GGAAAGGAGUGAAALAAAGGUGUGGAAAGCUCGCCAACCCUCCAAAGUGUAGUUCG
C-GAUA-G 2 - Br...	94 / 100		GGAAAGCUUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Mat - Early bul...	94 / 100		GGAAAGCUUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Fiskers early b...	94 / 100		GGAAAGCUUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
JR_EarlyBulge_R...	94 / 100		GGAAAGCUUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Early Bird	94 / 100		GGAAAGCUUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
C-GAUA-G 1 - Br...	92 / 100		GGAAAGCAUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
9am	92 / 100		GGAAAGCAUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
4/3 Ratio GC/AU	92 / 100		GGAAAGCAUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Early Bird... n...	89 / 100		GGAAAGCUUACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Late & Great 3 ...	89 / 100		GGAAAGGCGACAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
7am	89 / 100		GGAAAGCAGCAAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Lucky 7's v.3 ...	87 / 100		GGAAAGUAUUGCAAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Lucky 7's v.2 ...	83 / 100		GGAAAGUAUUGCAAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
EBrow 1	80 / 100		GGAAAGUAUUGCAAAALAAAGGUAUUGCAUAGUACCGUGUAGCAAGUAGUUCG
Gravity I	78 / 100		GTAAAGGUGGAAALAAAGGUGGAGCAAGUCCGCGACGCAAGUCCUUCG

Intrinsically

Those that did best particularly had more C's than G's on the 5' end of the barcode.



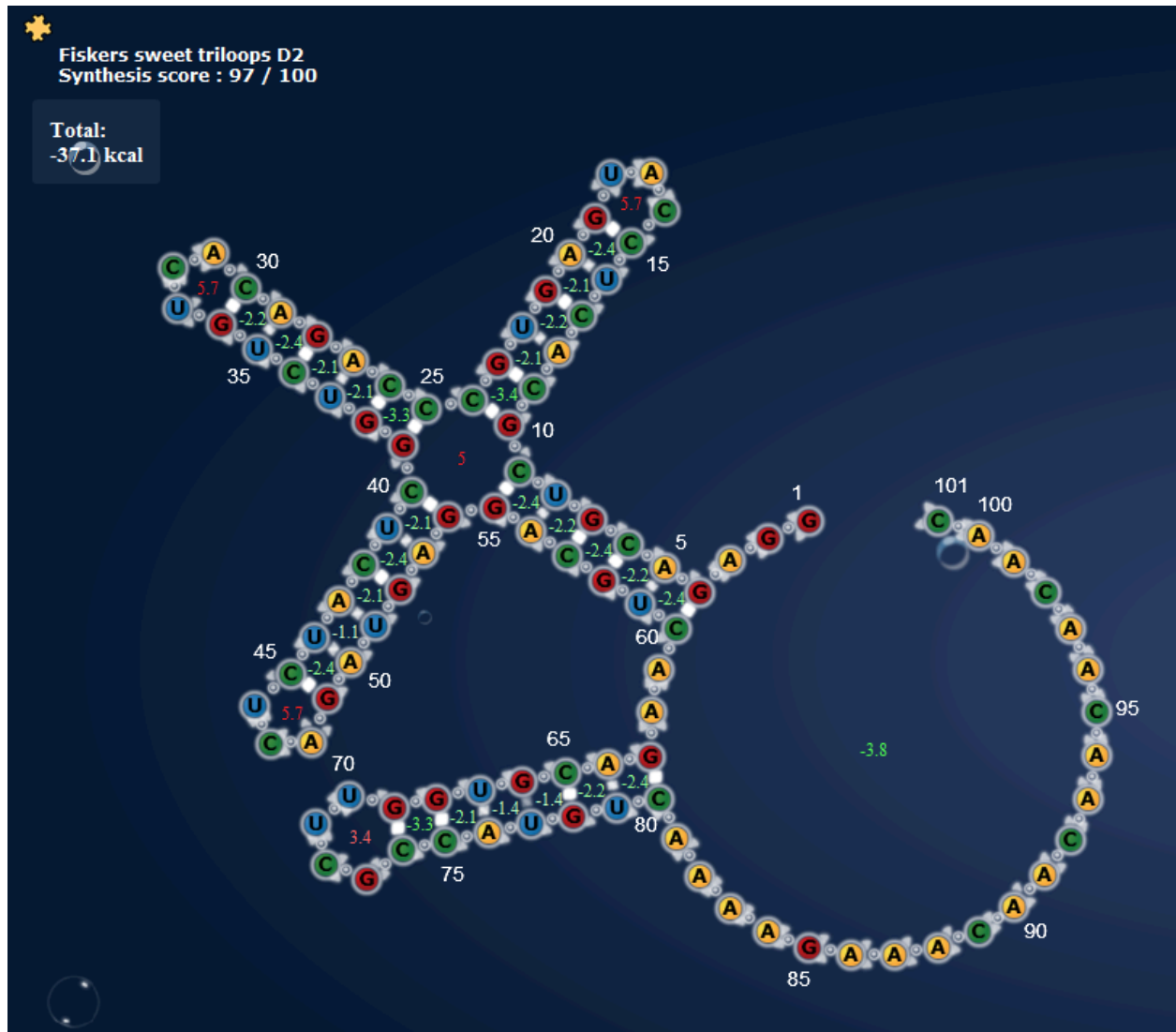
Frequency 8. Here green C dominates for making the A's accessible to the SHAPE probe.

Intrinsical - Frequency 8									
Synthesis score ▾		Sequence							
min	max	search							
79 / 100		G	A	A	A	A	A	A	A
78 / 100		G	G	A	A	A	A	A	A
69 / 100		G	A	A	A	A	A	A	A
69 / 100		G	A	A	A	A	A	A	A
68 / 100		G	A	A	A	A	A	A	A
62 / 100		G	A	A	A	A	A	A	A
60 / 100		G	A	A	A	A	A	A	A
56 / 100		G	A	A	A	A	A	A	A
54 / 100		G	A	A	A	A	A	A	A
53 / 100		G	A	A	A	A	A	A	A
51 / 100		G	A	A	A	A	A	A	A
50 / 100		G	A	A	A	A	A	A	A
49 / 100		G	A	A	A	A	A	A	A
46 / 100		G	A	A	A	A	A	A	A
46 / 100		G	A	A	A	A	A	A	A
45 / 100		G	A	A	A	A	A	A	A
44 / 100		G	A	A	A	A	A	A	A
40 / 100		G	A	A	A	A	A	A	A
37 / 100		G	A	A	A	A	A	A	A
37 / 100		G	A	A	A	A	A	A	A
35 / 100		G	A	A	A	A	A	A	A
35 / 100		G	A	A	A	A	A	A	A
35 / 100		G	A	A	A	A	A	A	A
31 / 100		G	A	A	A	A	A	A	A
31 / 100		G	A	A	A	A	A	A	A
30 / 100		G	A	A	A	A	A	A	A
30 / 100		G	A	A	A	A	A	A	A
29 / 100		G	A	A	A	A	A	A	A
29 / 100		G	A	A	A	A	A	A	A
29 / 100		G	A	A	A	A	A	A	A
27 / 100		G	A	A	A	A	A	A	A
27 / 100		G	A	A	A	A	A	A	A
27 / 100		G	A	A	A	A	A	A	A
26 / 100		G	A	A	A	A	A	A	A
26 / 100		G	A	A	A	A	A	A	A
26 / 100		G	A	A	A	A	A	A	A

A mixture is not working as in my Big hairpin loop lab and in Leontis Intrinsical lab. I simply think the bases are too far apart for them to be able to work their trick in making the bases accessible.

Intrinsical frequency 7

Actually the C's tendency only grow stronger here. And as can be seen from the better score, the C's have much better luck, making the single bases accessible to the SHAPE probe.



But to sum up the new overall pattern for this lab is that Pyrimidines (C and U are high at the 5' side of the triloop. And in the loop as well

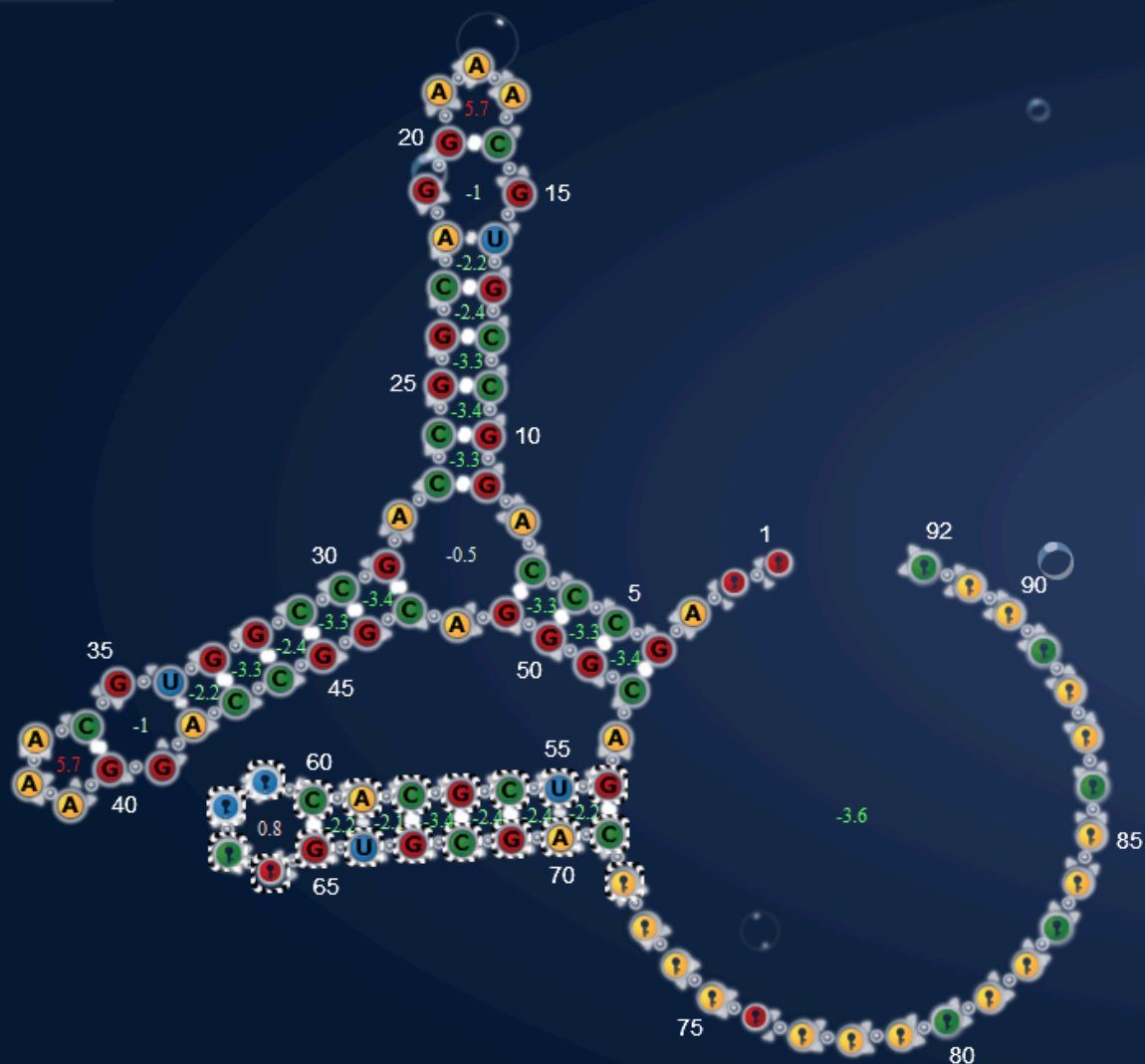
Also take note of the high prevalence of U's in the triloop among the highest scoring.

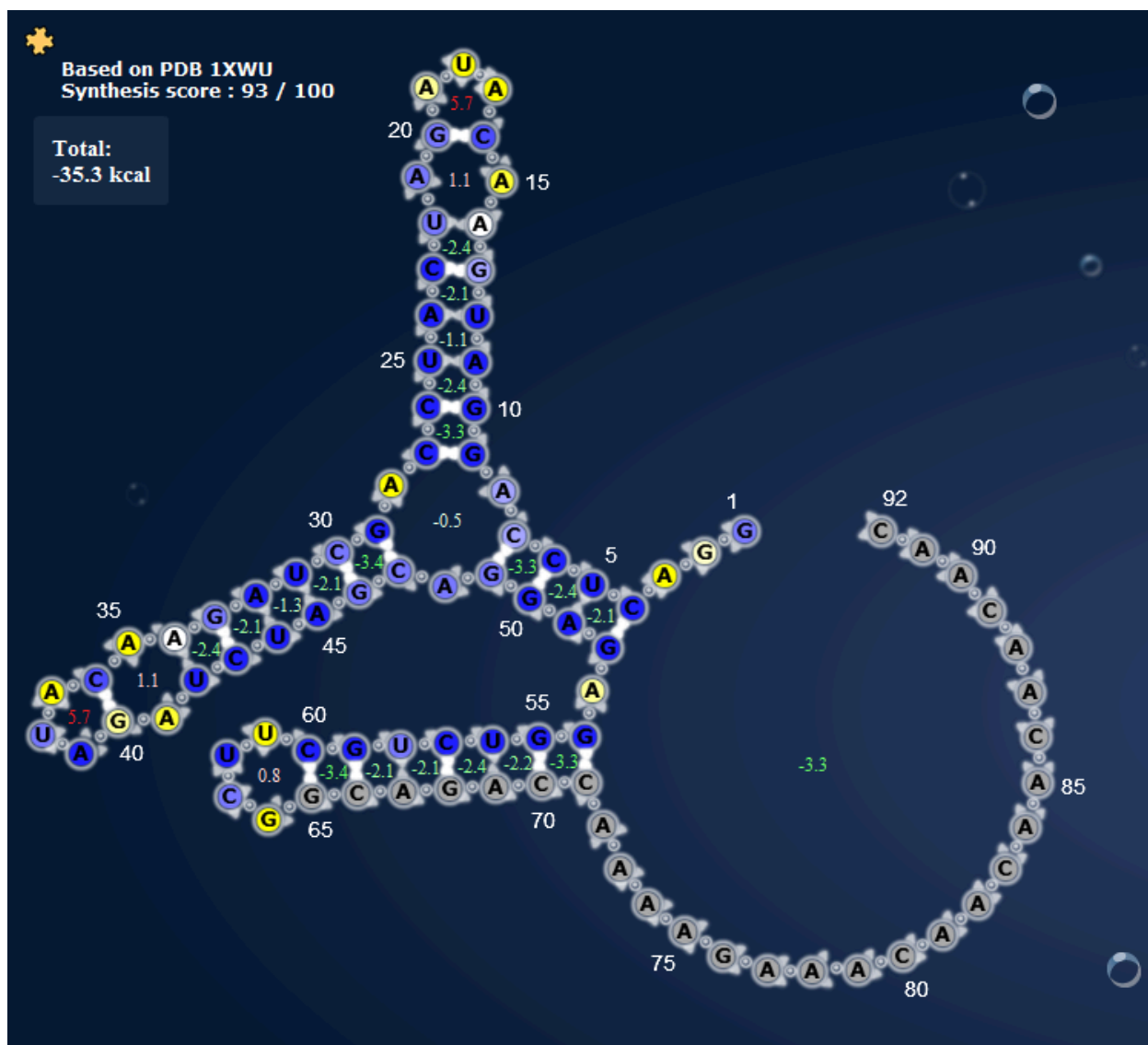
What I see for his loops is a phenomenon I have seen before for loops attached to multiloops. By turning down the energy in the 1-1 loop (Opposite having full power by using two GC closing basepairs for the 1-1 loop) it seems to bring relief to the small triloop. This compares to having closing base pair energy turned down for Multi Loop with an internal loop attached. Mainly it was the multi loop closing base pair that was adjusted on. But it generally seem to help to not go full power in these attached loops.

So these holding tips have the rather low energy -1 for a 1-1 loop. Mine had an energy of -1,7. Not as high as could be. I will go through them to see if this pattern continue. That very high negative energy = breaking, middle holding and really low breaking too.

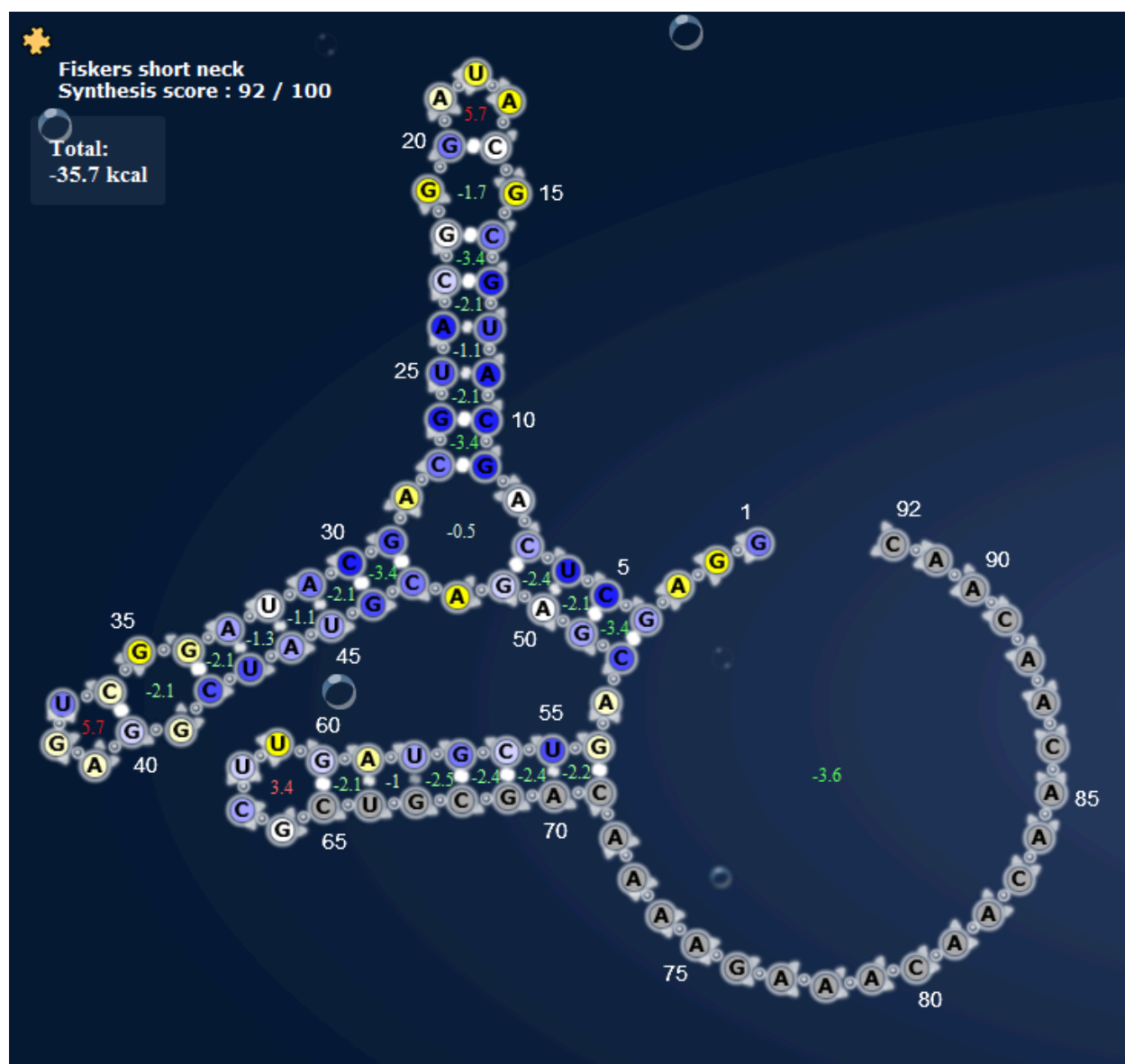
Short Neck and Split Ends

Total:
-47.8 kcal



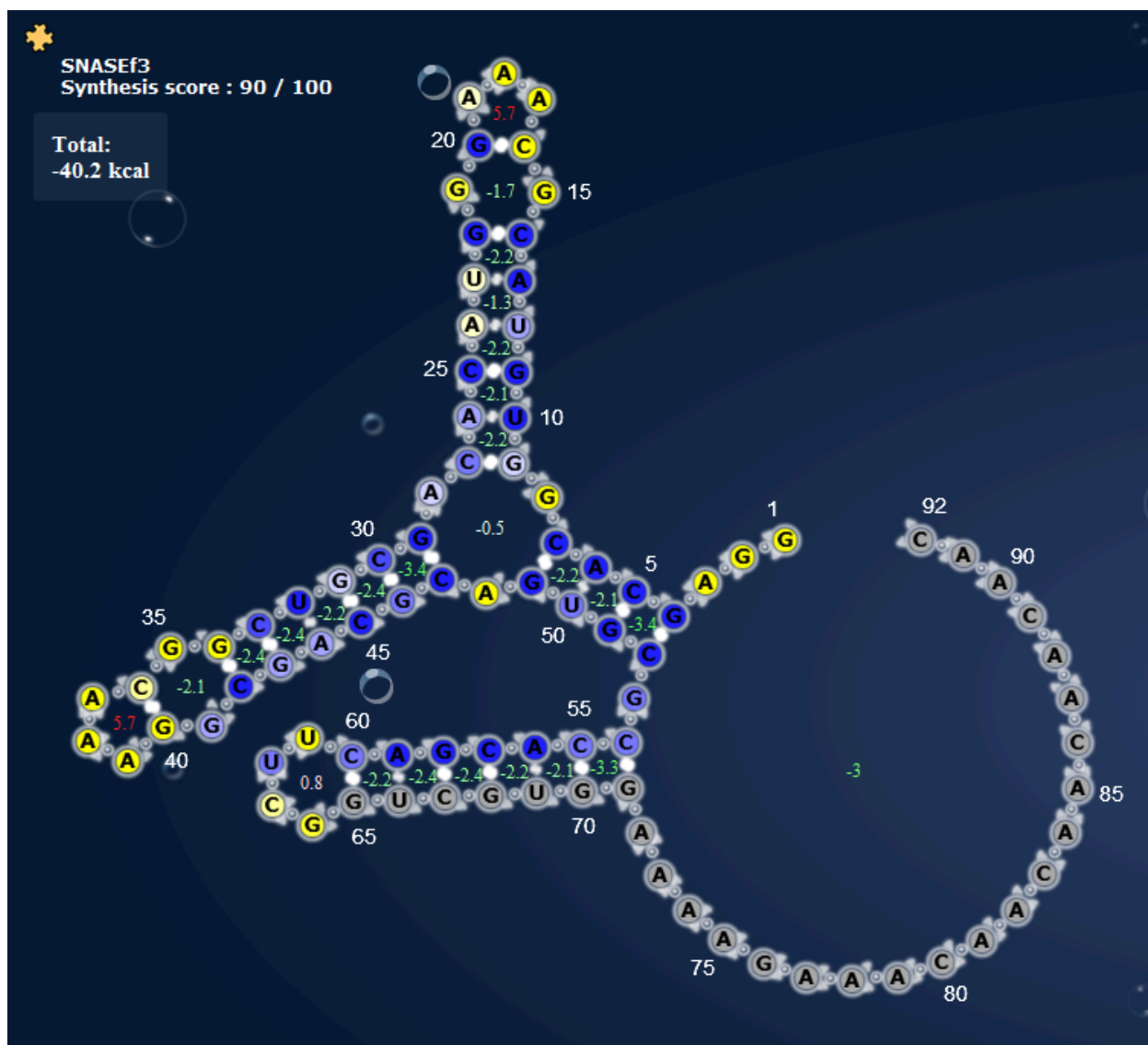


Actually one of my tips holds. The top one holds in estimate, though not looking too stabile. So -1,7 flies in some cases. However the bottom one with more negative energy breaks. As did the ones with very low negative energy or positive energy in the 1-1 loop, in an earlier design.

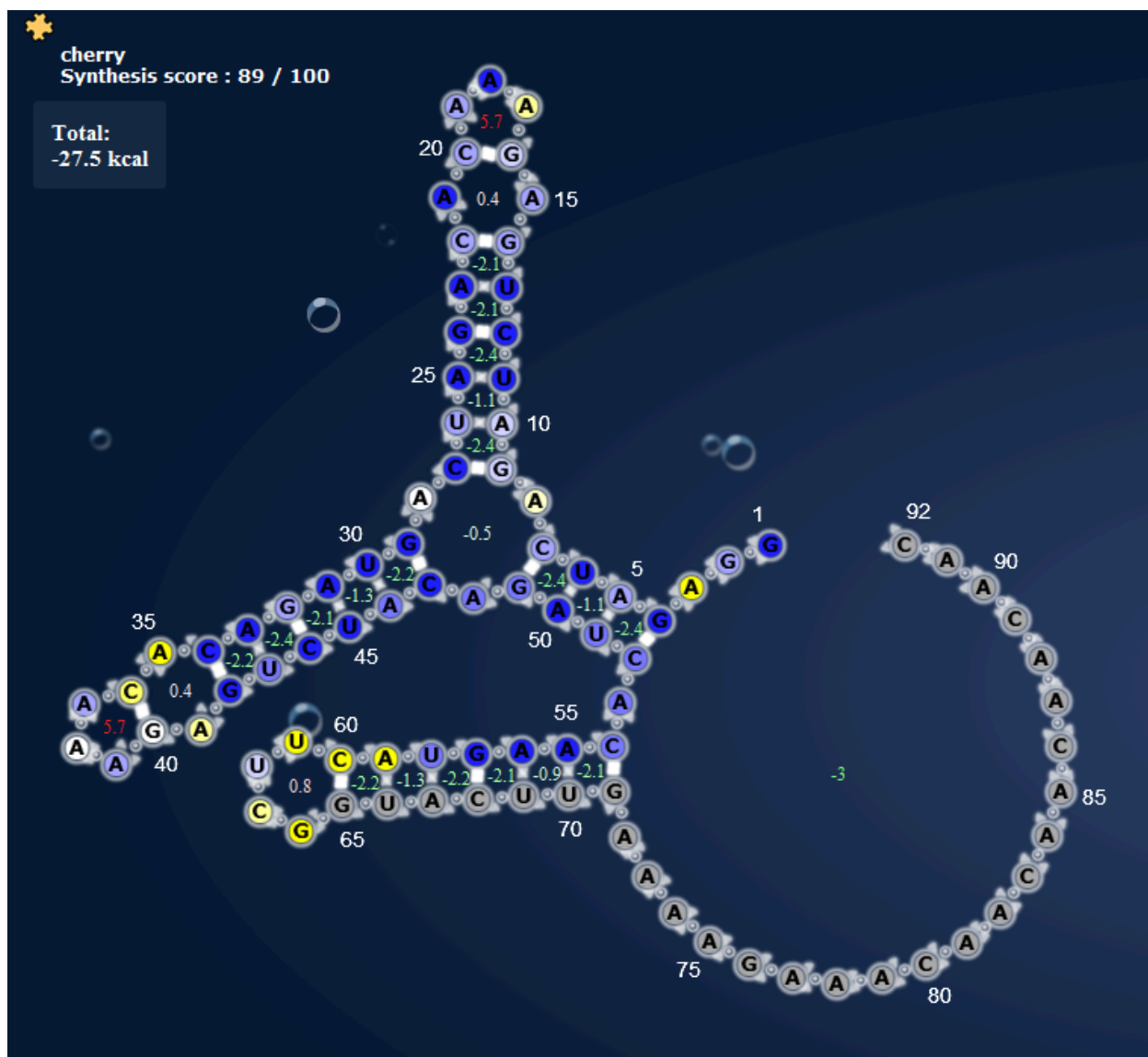


It is the same in this one. Top one holds, bottom one breaks. It looks like my U in the triloop tip made it more unstable than the all A's in this one.

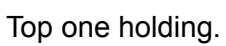
Top one is holding

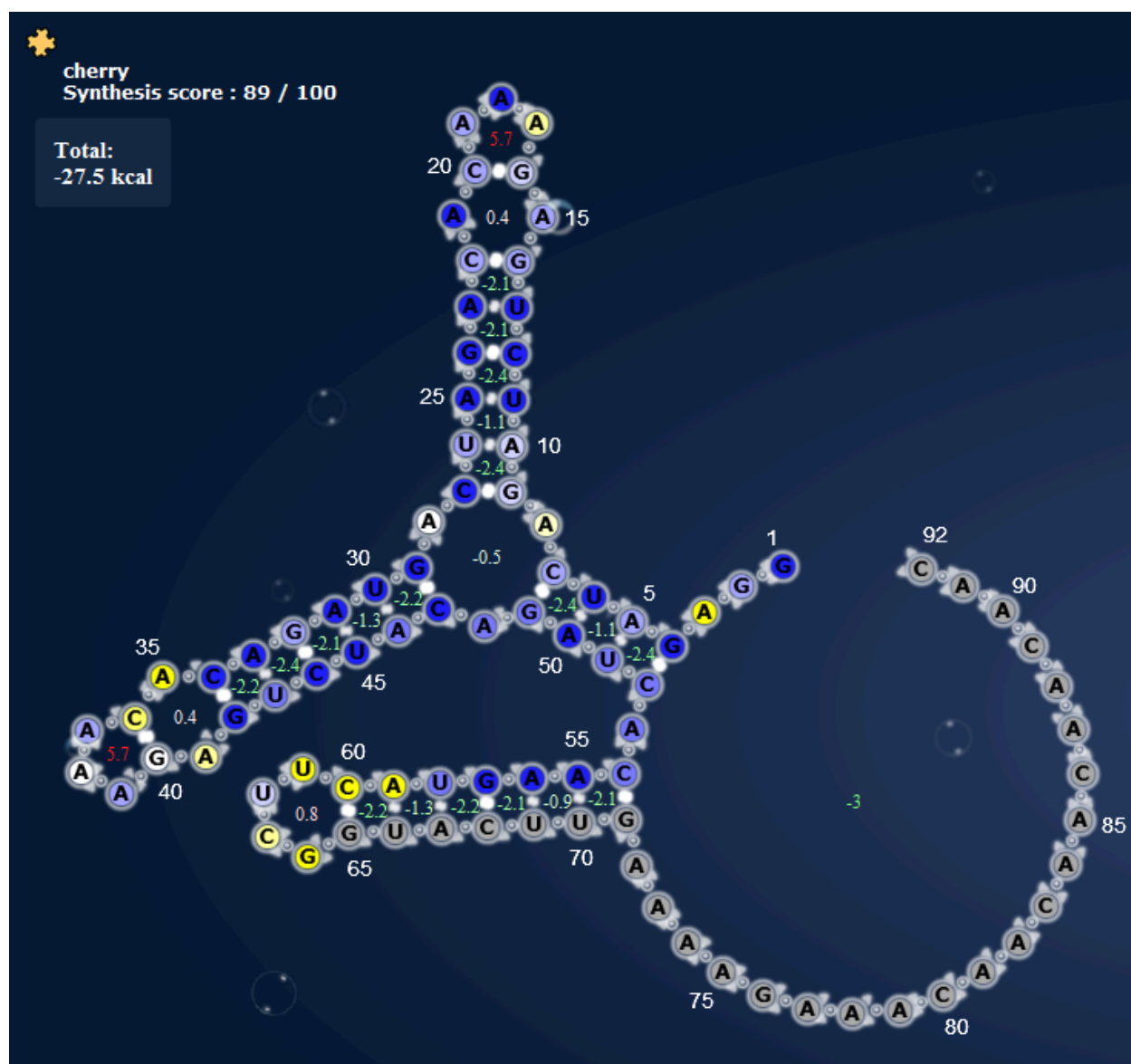


However here is one low energy one. Top one is holding. That was rather a surprise.

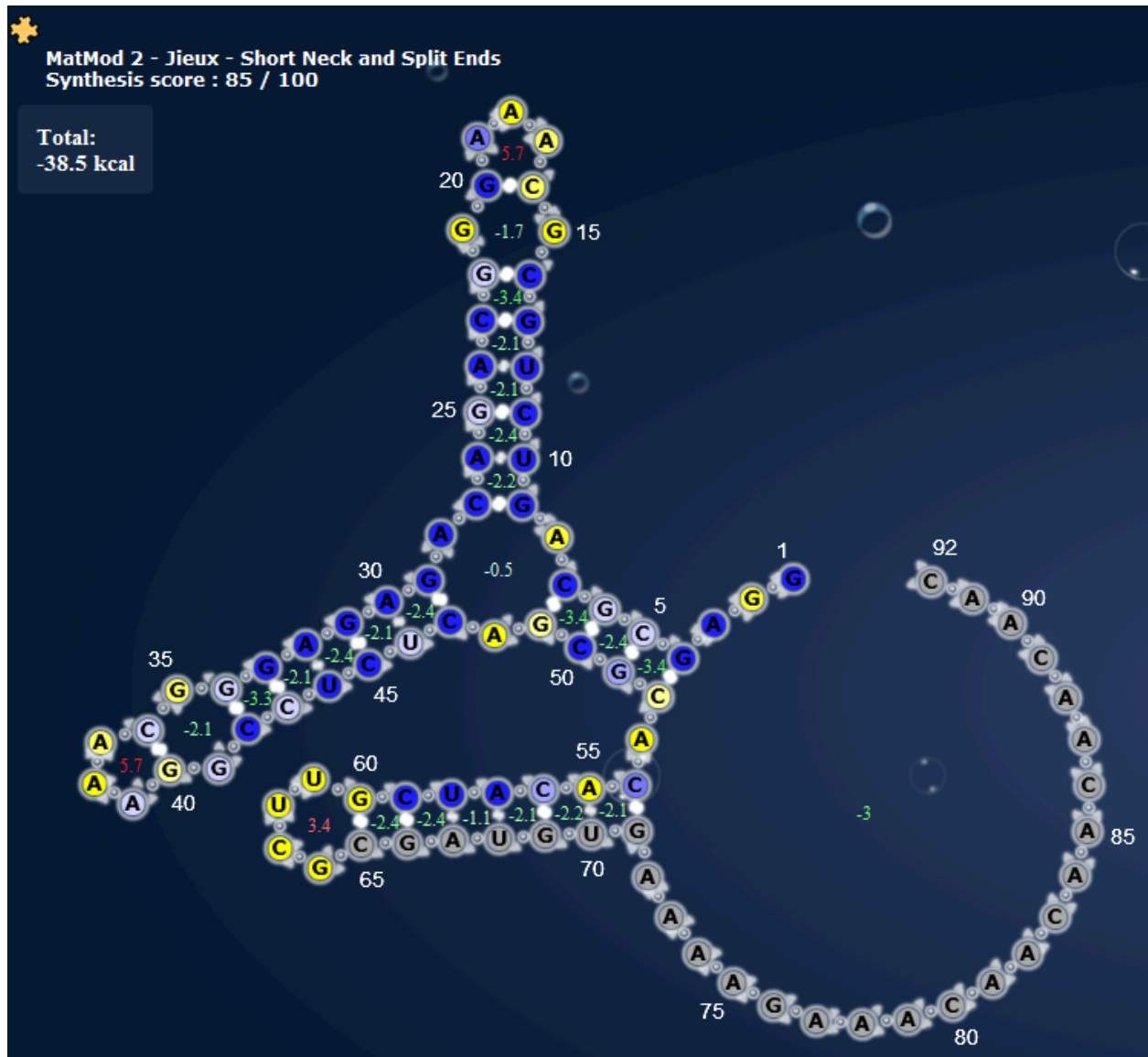


Top one is holding. Actually it is mainly the top one that is holding. Only RedSpah's winner has both tips holding.

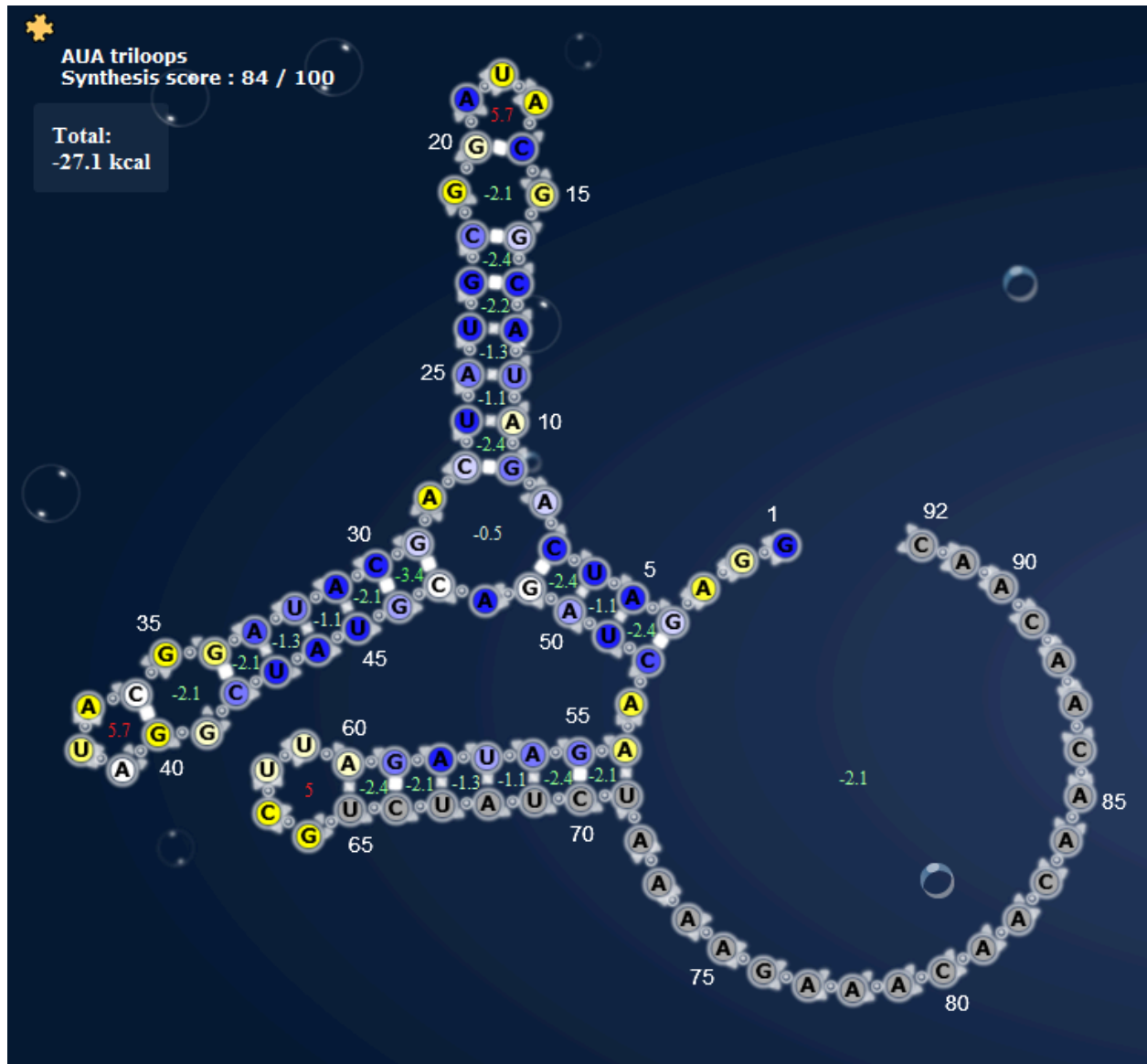




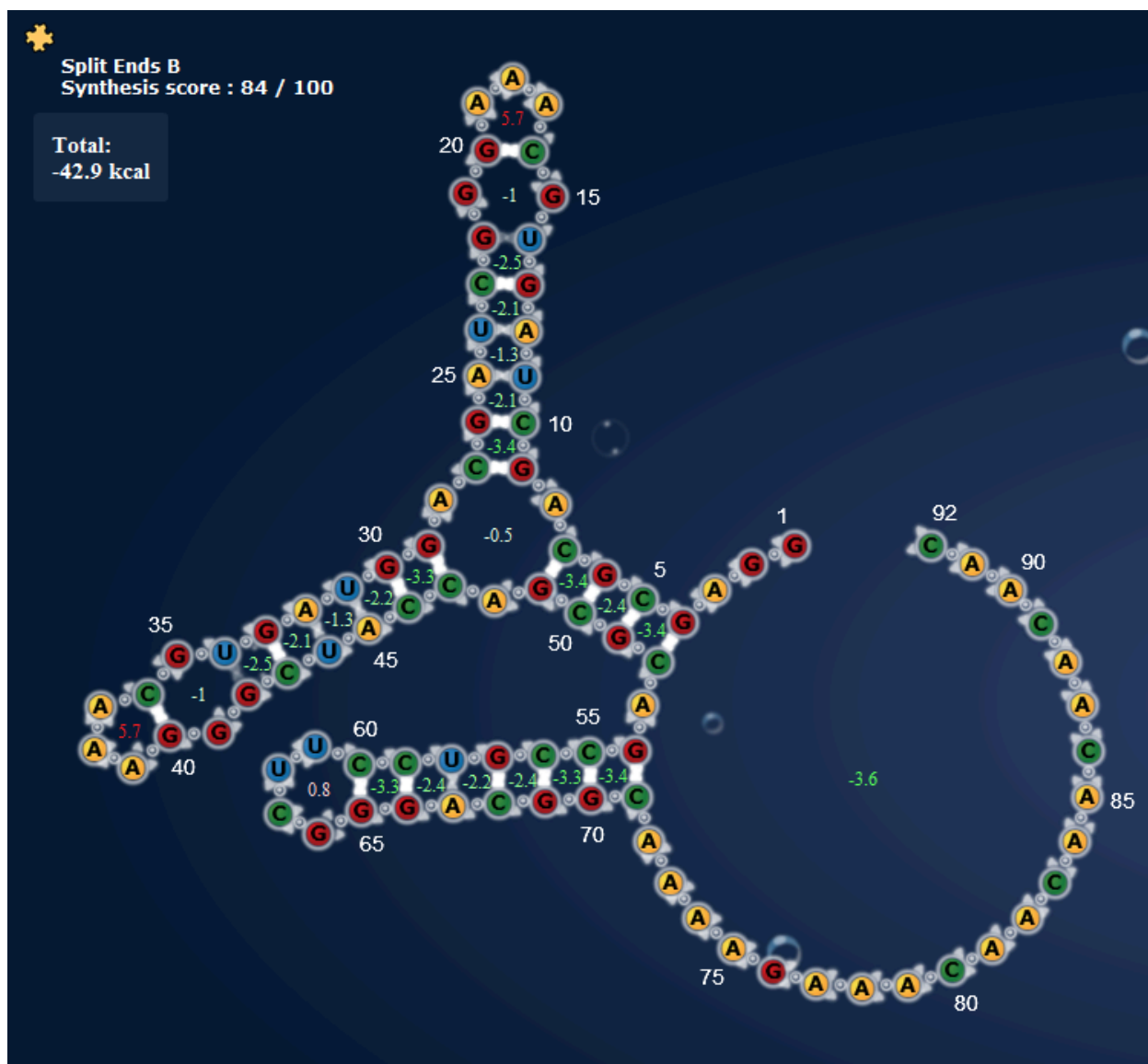
Top one folds



Hmm, this high negative top one is holding too. There went my theory. Still the ones around -1 and -1,1, seems to be safest. And to some degree -1,7



These has a good energy range, but the GU spit things.



I noticed that the designs that had rather stable SHAPE data around the notorious hard to make all blue 1-1-1 multiloop, had a rather high GC content. Usually multiloops prefer not having too heavy GC-pairing around them at next pair also. Meaning that having two GC-pairs at each closing quad in a multiloop most times will be unnecessary most of the time. (one is often fine)

Title	Synthesis score	Sequence
search	min max	search
Mythed III	98 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Fiskers short n...	95 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Based on PDB 1XWU	93 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Conditioner (4 ...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
mod of Eli's st...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Mildly Sane (Sh...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
GUG triloops	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
sn&se-3	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Fiskers short neck	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Banana Split En...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
SNASER3	90 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
UUU triloops	90 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Blue Splits - B...	90 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Mid-air splits	89 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
cherry	89 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
neCk and Umbrel...	89 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Conditioner (4 ...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
SN - 1	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Mat - Short Nec...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
JR_ShortSplit_R...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
sn&se-2	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Turtleneck and ...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
JR_ShortSplit_R...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Banana Split En...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Banana Split Ends I	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
MatMod 2 - Jieu...	85 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Arrasobi	85 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Enre	85 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Split Ends B	84 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Mat - Short Nec...	84 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
AUA triloops	84 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
U Splitter - Br...	84 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
SN-SE V2	82 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Short & Split 3	82 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Shortneck-split...	82 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Split Ends 3	81 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Split Ends 2	81 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Split Ends 1	81 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC

Here it stands much more out, that the ones that are most stable (dark blue) around the multiloop (marked in orange boxes) are the ones that are having G and C's there. This is an unusual pattern for a multiloop as the multiloops most often does best without this extra GC backup behind the closing base pair and to sometimes go wrong if that is added.

Title	Synthesis score	Sequence
search	min max	search
Mythed III	98 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Fiskers short n...	95 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Based on PDB 1XWU	93 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Conditioner (4 ...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
mod of Eli's st...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Mildly Sane (Sh...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
GUG triloops	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
sn&se-3	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
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Banana Split En...	92 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
SNASER3	90 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
UUU triloops	90 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Blue Splits - B...	90 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Mid-air splits	89 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
cherry	89 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
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Mat - Short Nec...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
JR_ShortSplit_R...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
sn&se-2	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Turtleneck and ...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
JR_ShortSplit_R...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Banana Split En...	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Banana Split Ends I	87 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
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Arrasobi	85 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Enre	85 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Split Ends B	84 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Mat - Short Nec...	84 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
AUA triloops	84 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
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Split Ends 3	81 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Split Ends 2	81 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC
Split Ends 1	81 / 100	GGAGCCGAAAGCGGUGGAAAGGACGGCAGCGGUGGAAAGGACCGGAGGCGAGUGCGACGACUUC

So this stubborn multiloop seem to wanting them is sort of poetic justice. Checking old labs to

see if this is also the case there.

And the answer is yes. :)

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groupBy:	XXNXX!XXNXX!XXNXX
rankBy:	
lab ids:	
min score:	90
max score:	
min count:	
subsequence:	
omit sequences:	
omit structs:	
require structs:	
mode:	☐ summary ☒ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv
flags:	☐ just labs ☐ group by lab id (nid) ☐ full SHAPE data
lab type:	☐ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	214	94.23	78.23	details
GGGGCCGCGCCC	1	94	90.93	details
AGGUACCAUGCU	1	94	88.47	details
UCGAUCGCGCGA	1	92	87.13	details
GCGCGCGGCGCG	1	93	87.07	details
GCGAUCGAUCGC	1	96	86.4	details
GCGUACGCGCGC	1	94	86.07	details
UCGUACGCGCGA	4	94.25	85.73	details
CCGGCCGCGCGG	1	92	85.6	details
GCGAUCGUACGC	2	92.5	85.6	details
CCCAUGGGCCGG	1	93	85.2	details
ACGGCCGUACGU	1	98	85	details
UCGCGCGCGCGA	2	94.5	84.73	details
ACGCGCGAUCGU	6	96.33	84.7	details
CCGAUCGAUCGG	1	93	84.67	details
UGGGCCGGCCCA	1	91	84.53	details
GCGGCCGAUCGC	2	93	84.4	details
CCGCGCGAUCGG	2	96	84.37	details
CAGUACGAUCUG	1	91	83.93	details
GGCAUGGCGCCC	1	94	83.87	details
UCGCGCGGCCGA	2	94	83.37	details
GCCAUGGCGCGC	1	93	83.27	details
GCGUACGGCCGC	1	98	83.2	details
CCGUACGCGCGG	1	96	83.07	details
CCCCGGGAUCGG	1	91	82.6	details
GGGCGCACGUCC	1	93	82.53	details
ACGCGCGGCCGU	1	98	82.27	details
ACGGCCGCGCGU	2	96	82.14	details
GGUCGAGCGCCC	1	93	81.87	details
GGCCGGCCGGCC	5	92.4	81.61	details
CCGCGCGUACGG	2	95	81.57	details

substructure:	((. (!)) . (!)) .)
filterBy:	
groupBy:	
rankBy:	
lab ids:	
min score:	90
max score:	
min count:	
subsequence:	
omit sequences:	
omit structs:	
require structs:	
mode:	☐ summary ☐ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☒ CFTB ☐ json ☐ csv
flags:	☐ just labs ☐ group by lab id (nid) ☐ full SHAPE data
lab type:	☐ Early Lab ☒ Cloud Lab

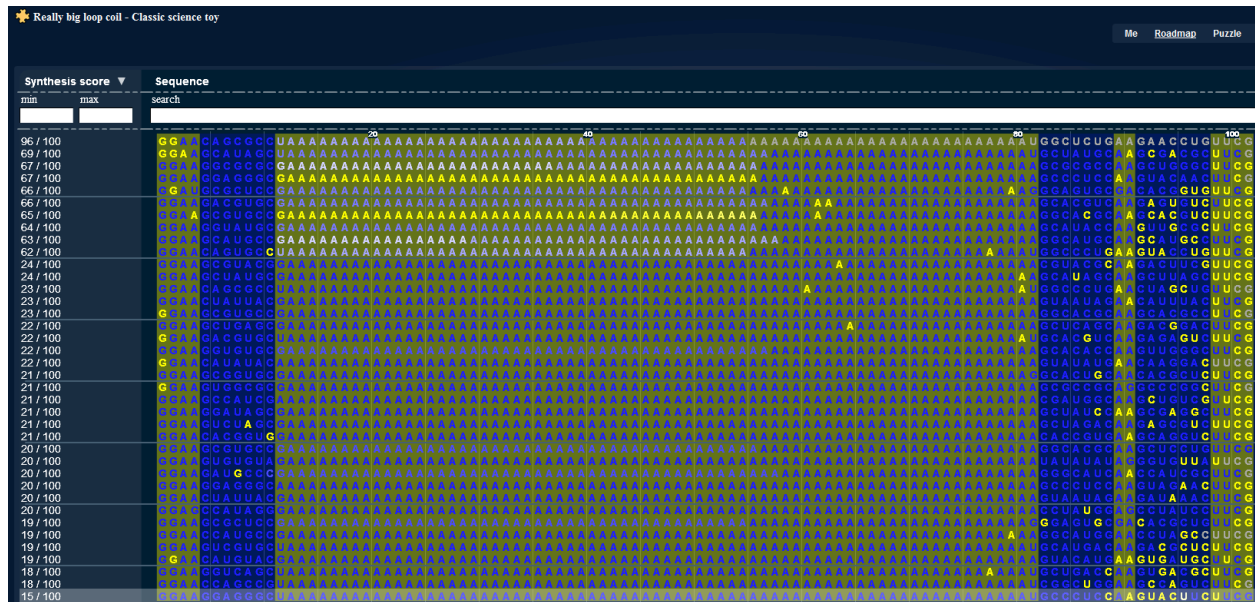
cluster	count	score	rank	
(ALL)	214	94.23	78.23	details

subseq	count	score	rank	
GGAGG CCAGC GCACC	1	94	90.93	details
AGAGU ACACA UGACU	1	94	88.47	details
UCAGA UCAGC GCAGA	1	92	87.13	details
GCAGC GCAGG CCAGC	1	93	87.07	details
GCAGA UCAGA UCAGC	1	96	86.4	details
UCGGU ACAGC GCAGA	1	98	86.27	details
GCAGU ACAGC GCAGC	1	94	86.07	details
UCGGU ACAGA UCAGA	1	96	85.73	details
CCAGG CCAGC GCAGG	1	92	85.6	details
GCAGA UCAGU ACAGC	2	92.5	85.6	details
UCAGU ACAGC GCAGA	3	93	85.55	details
ACAGC GCAGA UCAGU	5	96.2	85.24	details
CCACA UGAGG CCAGG	1	93	85.2	details
ACAGG CCAGU ACAGU	1	98	85	details
UCAGC GCAGC GCAGA	2	94.5	84.73	details
CCAGA UCAGA UCAGG	1	93	84.67	details
UGAGG CCAGG CCACA	1	91	84.53	details
GCAGG CCAGA UCAGC	2	93	84.4	details
CCAGC GCAGA UCAGG	2	96	84.37	details
CAAGU ACAGA UCAUG	1	91	83.93	details
GGACA UGAGC GCACC	1	94	83.87	details
UCAGC GCAGG CCAGA	2	94	83.37	details
GCACA UGAGC GCAGC	1	93	83.27	details
GCAGU ACAGG CCAGC	1	98	83.2	details
CCAGU ACAGC GCAGG	1	96	83.07	details
UCAGU ACACU AGAGA	2	92	82.87	details
CCACC GGAGA UCAGG	1	91	82.6	details
GGAGC GCAAC GUACC	1	93	82.53	details

There is a very high degree of GC's also for next pair after the multi loop closing base pair, in the highest ranked 1-1-1 multiloops. Not always, but a rather high tendency still.

They also seem to have a certain like for double same turning basepairs.

GGAGG CCAGC GCACC	1	94	90.93	details
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Hyphema: hows perusing your lab results going? [2:32 PM]

Hyphema: sounds like the error rate is too high [2:32 PM]

Nando: err, is it? :P [2:32 PM]

Hyphema: :) [2:32 PM]

Nando: I didn't have that many projects in the runs, so it's kinda ok, but still annoying [2:35 PM]

Eli Fisker: morning Hyph hi Nando [2:36 PM]

Eli Fisker: Yes, error rate is high for most labs I have looked at this far [2:36 PM]

Eli Fisker: So I'm not sure how much the results are to be trusted [2:37 PM]

Nando: I would say, they are on the bad-smelling side of the untrustworthiness [2:39 PM]

Eli Fisker: Yes, I'm leaning to that side too [2:39 PM]

Eli Fisker: I can even see it in the SHAPE colors [2:40 PM]

Eli Fisker: I mean I noticed some time back that some designs looked special [2:40 PM]

Eli Fisker: and those happened to be those with high error rate [2:40 PM]

Eli Fisker: They gets squeamish yellow and strong blue [2:40 PM]

Eli Fisker: not much in between [2:40 PM]

Eli Fisker: so they sort of look like SHAPE data with advanced mode turned of [2:40 PM]

Nando: yes [2:40 PM]

Eli Fisker: And I see this a lot [2:41 PM]

Eli Fisker: In particular for my intrinsical frequency [2:41 PM]

Eli Fisker: Plus the pattern that turns up in my Big loop coil lab, is actually reversed, compared to what I expect [2:41 PM]

Eli Fisker: I mean, the pattern turns up where I do expect it, but the shape colors are reversed between blue and yellow [2:45 PM]

26 Feb 2014

Note on the high error rate in the lab data or Perfect recipe for Bad RNA

On Feb 25, 2014, Eli Fisker wrote

Quest for RNA resonance contamination

Hi Rhiju!

Nando and I have started wondering if it was my intrinsical frequency labs with the long stretches of single A's + frequencies, that made the error rate for the latest lab batches explode?

(Chatlog from 23 Feb 2014)

Hyphema: hows perusing your lab results going? [2:32 PM]

Hyphema: sounds like the error rate is too high [2:32 PM]

Nando: err, is it? :P [2:32 PM]

Hyphema: :) [2:32 PM]

Nando: I didn't have that many projects in the runs, so it's kinda ok, but still annoying [2:35 PM]

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Eli Fisker: I mean, the pattern turns up where I do expect it, but the shape colors are reversed between blue and yellow [2:45 PM]

Nando: @Eli: maybe this all simply means that the current technology in our pipeline just cannot deal with poly(N) [2:48 PM]

Eli Fisker: Nando, yes, that could very well be [2:48 PM]

Nando: and maybe we should just leave that topic aside, until it does handle it properly [2:48 PM]

Eli Fisker: So the longer they get, they might actually cause trouble to the other labs too? [2:49 PM]

Eli Fisker: This is what I guess [2:49 PM]

Nando: not sure Eli, but it could be I think [2:50 PM]

Eli Fisker: RNAions [2:50 PM]

Eli Fisker: like Prions [2:50 PM]

Nando:

the one thing I got back from the Dimers labs is that there are interactions between separate and unrelated sequences [2:50 PM]

Eli Fisker: RNA that makes other RNA turn bad :) [2:50 PM]

Nando: but then, it's all a matter of concentration, how strong the effect will be [2:51 PM]

Eli Fisker: I wish there was an easy way to see which lab was in which batch [2:51 PM]

Eli Fisker: Because then it would be easier to come with a qualified guess on what may have caused the trouble [2:51 PM]

Nando: that should be priority number 1, yes, totally agree [2:51 PM]

All my intrinsic frequency labs had relatively crappy barcodes and low scores. Well except for one (Intrinsic Frequency). This lab let people pick frequency and colors themselves. While the others had locked frequencies. This one does not either have crazy high error rates. (It is the first of them I suggested. Only there is some error on the lower scoring designs. But I'm thinking what could be the cause of the trouble in the other labs and explain why this one is rather untouched, is not just the length of A's, but also the repeat frequencies could interfere.

Another loose thought, if my labs are interfering with the other labs, perhaps part of the barcode issues may come from this. Both Mat and I have from the start suspect that the barcode would cause trouble. So I still very much thinking the barcode itself is causing trouble, but perhaps there is an additional reason.

I have some proof of that growing length of single bases/single A's is causing increasing amount of barcode distress:

I made 3 "relaxed multiloops with 5, 6 and 7 single bases between the stems. They scored fine results in lab, as folks were able to break the A's pattern in the multiloop ring, however there still was a growing barcode distress with increase in multiloop ring size. My latest lab Very relaxed Multiloop, had 9 single locked A bases between the stems. Result, not a single winner and crappy scores and real crappy barcodes. And what is interesting for all of these labs, is that they do not have long stems, like the usual labs with crappy barcodes.

I posted a report on my Very Relaxed Multiloop lab the other day.

https://docs.google.com/document/d/1M1og8eWGlnMNvumXYNpd9W5P_s9PJTJhvFSf6xMp3Oc/edit#

Eli

To Eli, 25 Feb 2014

Yes, we noticed this independently. In our current order we have filtered out any sequences with polyC or polyG, and will impose a hard constraint on future labs.

By the way, we are also retaking all the data from the last 3 rounds to get lower error rates. However that will not correct for any sequences whose RNA folds are disrupted by other sequences!

Rhiju

To Rhiju, 25 Feb 2014

Ah, that makes totally sense. These Poly C and G beasts are anxious to bind anywhere. I see them as likely prion suspects.

I'm happy the data gets retaken. Ok. So most of my intrinsically labs are still in there. If it is only the Poly C and G's causing trouble, then we should get much better data. However if it is also the frequency of my other labs that also causes trouble as I suspect it might too, then there will still be a rather high error rate. Since the Intrinsical lab with mixed frequency went fine. No matter what it should makes us wiser on what really happened.

Eli

9 Mar 2014

[JR's Lets Break the barcode - Adjacent barcode version](#)

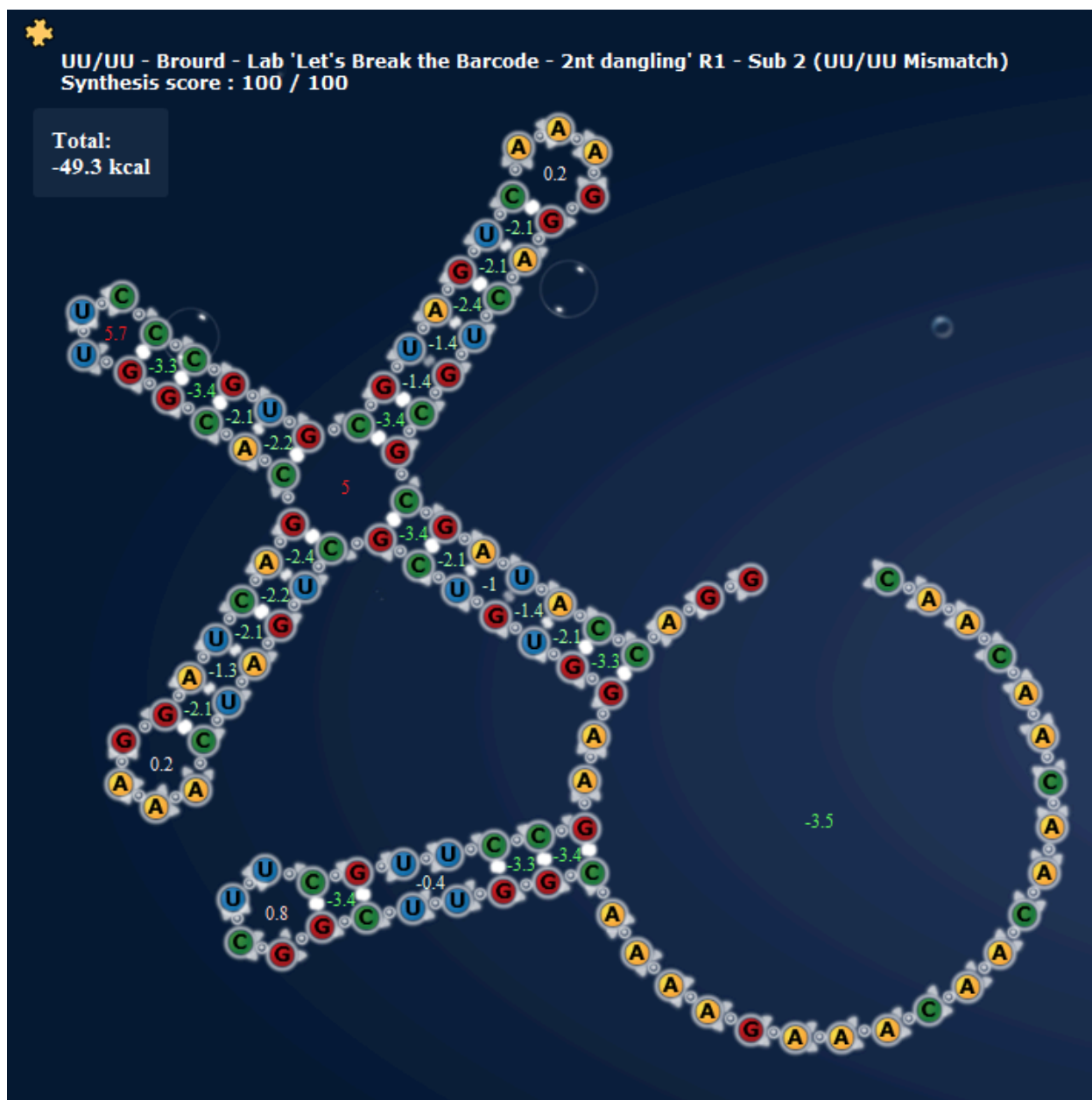
I think that each nucleotide difference between barcode and main design, makes the design take a slightly different barcode.

[illegible]

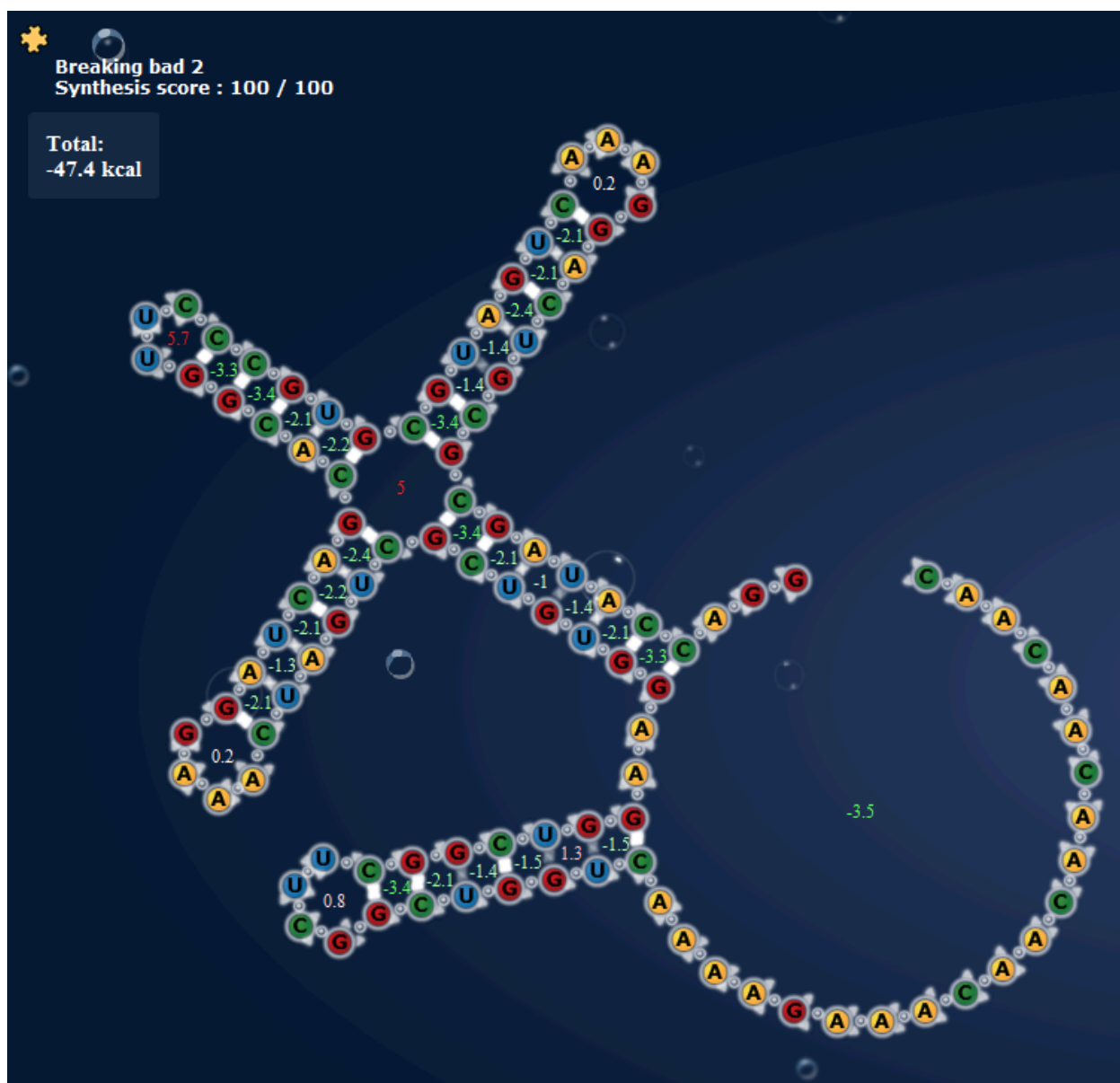


If you notice closely there is a difference between 2 and 3 nt dangling ends. Notice that the C's comes earlier in the barcode in the 2 nt dangling lab than in the 3 nt dangling lab. And there is more of them in the first than the latter. So for the lab with 0 distance between barcode and main design, I predict even more green and earlier. [[Looks like my prediction held.](#)]

And just like GU's helps barcodes relax in designs with long stems, Brouds experiments with non canonical pairs the same places, did real well too.



Even Watermoon's crossed GU's fly:



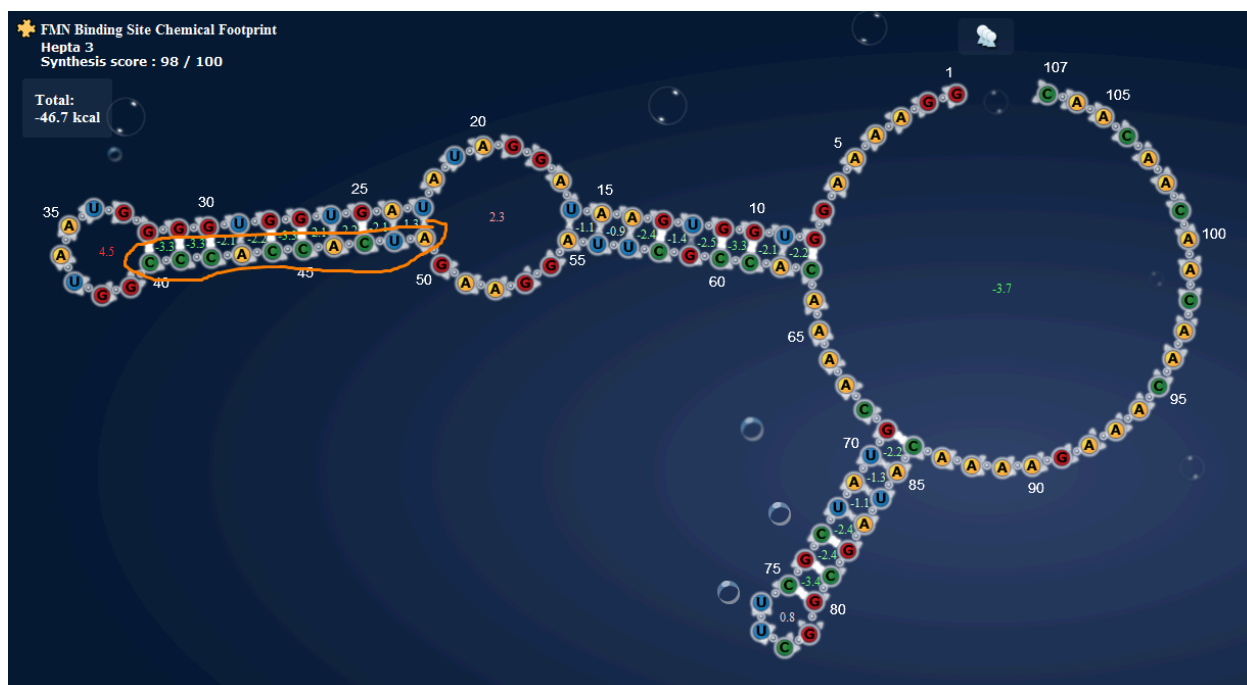
For my lab experiments for the barcode and main design adjacent in this lab series, I reused a stable barcode from high scoring designs in one of the sibling labs. The intention is that I will like to know how the same design will do with the same barcode, so the only variance between them is the size of the dangling end. That should give me a good shot at getting data on that the the distance means something. If these experiment goes as I expect, this designs will score lower than the one I borrowed from, as I think that barcodes next to the main design can have a negative effect, causing more misfolds than if design and barcode is distanced a bit. This time I picked from the 2 nt distanced lab, over the 3 nt lab, as I think the closer in shape the design is, the more likely the transfer is to work. However I think that each of these labs will have a difference in preference of barcode, just based on the distance the barcode has to the main design. I think the closer they are, the more likely to interfere with each other they is, and thus they call for different solutions to avoid that.

FMN Binding Site Chemical Footprint - Round 2

Another thing I found curious when looking at the lab in this round where the aptamer is reversed, is the clear bias for C's in particular or U's on the one side of the stem. And as a natural consequence, red on the other side of the stem.



Here is Nando's winner with an unusual biased distribution of GC-s.



It might make sense that the Gs are the longest away from the part of the aptamer that has most G's. However I'm surprised about how much this is actually biased. I wonder if the same bias will occur with the reversed aptamer or it will be reversed also.

The other thing I also found striking was the high prevalence of U's on the other side of the aptamer as for using a (base 16) With a preference for this being either a U if a AU pair was used or a or a C, if a GC pair was used. I would have expected a GC-pair to be first pick as closing basepair as the other one was an AU. Interesting.



29 Apr 2014

[Return of the boost](#)

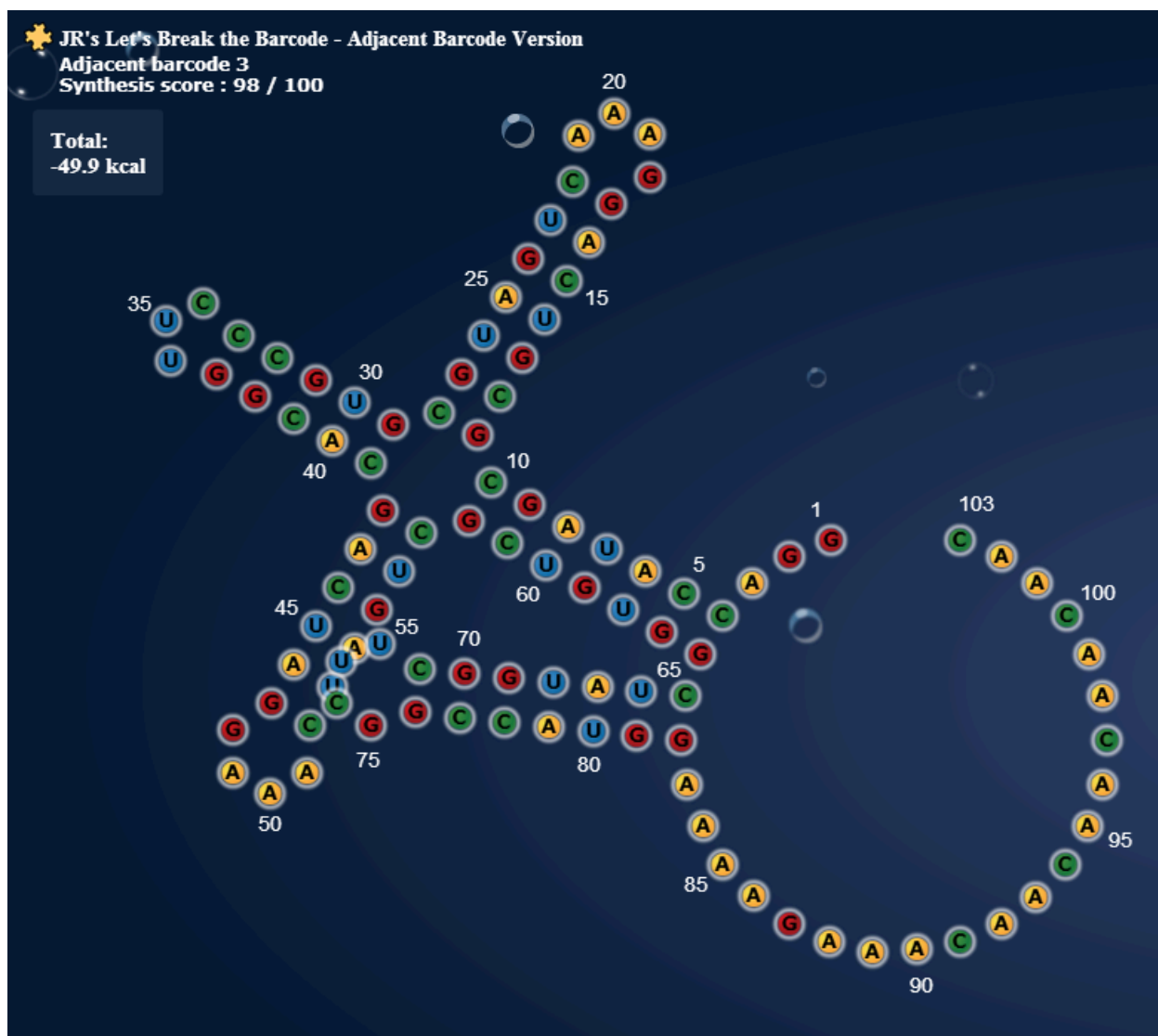
8 May 2014

I put up my lab notes for the one paper lab [Unconventional RNA Structure and Sequence Design](#):

[Analysis for mismatch lab](#)

13 May 2014

JR's Let's Break the Barcode



Actually here is rather an interesting result. I have earlier predicted that designs would do worse with a barcode adjacent to the main design than if they kept a distance. Because I saw barcodes do bad and sometimes fold up with the design itself. (Particular if the neck was short) Something which I disliked. Now this lab has overall long stems and the design was already a winner. So I suspect that we might not see the worst case scenarios for barcodes gone bad when close to a short neck in a design of a winner, and the same lab setting.

Think this is an idea for a pilot project. That could be a way of showing that barcodes actually affects designs differently depending on the main design. So take a 100 % design with generally short stems and neck. Freeze it, make lab versions with different gaps and just add different barcodes. I think it will look worse for the lab with least distance between barcode and design.

But the lab with adjacent barcode has 18 winners, against 18 winners in the one with two base distance and 14 for the 3 base distance. And actually the SHAPE data is much more calmer for the main design in the ones with zero or small distance. Well, thats except for the barcode.

Earlier I have said that designs with generally long stems often has a crappy barcode. This is the case here too, even if the starter design was originally scoring 100%.

The overall picture for these labs is the following. The closer the barcode is to the main design, the worse it fares. (Barcode gets yellow, right side in the pictures) So perhaps the bad barcode is a price worth paying for nicer data in the main design?

✦ JR's Let's Break the Barcode - Adjacent Barcode Version

Title	Synthesis score		Sequence
	min	max	
search			search
Adjacent barcode 3	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Adjacent barcode	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Mutalating good...	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Recycled barcod...	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
JR's Let's Brea...	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
JR's Let's Brea...	97 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
JR's Let's Brea...	97 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Karate Chop! (B...	97 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
UUU know nothin...	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Recycled barcod...	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BC - 1	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Directin in	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Adjacent barcode	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
LBTB-ABV V2	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
GU Closing Pair...	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Karate Chop! 2 ...	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Barcode	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
UUC nothing - B...	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Breakadjacent - ...	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BTB-1	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Broken BC	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Ceoninat	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Break it	92 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Meschl LBIB ABV	92 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Bigiditl	92 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
JR AdjBarcode_Sub2	90 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BIB Crossed + 2	90 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BarBreak#3	89 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG

✦ JR's Let's Break the Barcode - 2 nt Dangling End Gap

Title	Synthesis score		Sequence
	min	max	
search			search
Breaking bad 2	100 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
UUUUU - Bround ...	100 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Barcode Goes By ...	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Omei JRLBB2 - 3	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BIB Crossed GU	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
To Stabiliz! ...	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
JR_BB2_2ntDangl...	98 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Break dance 2nt 1	97 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Omei JRLBB2 - 2	97 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Broken Code II	97 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Quartz III	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Omei JRLBB2 - 1	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Neck Echo	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
UUU + UUC - Bro...	96 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Implosion (Brea...	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
JRLBTEC-2ntIDEG3	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BTB 2NT V3	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Radioactive	94 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
pine	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BIB GU	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Breaking in and...	93 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Fisker testing ...	92 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
I fixed it 6 - ...	90 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Mat - JR's Brea...	90 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Bad Barcode v1	90 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
BTB 2NT V1	88 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Broken Code III	88 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Zaat	87 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
Best Worst Case	85 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG
JRSB-the-B2ntdes2	74 / 100		GGACCAUAGCGCGGUCAGGAAACUGAUUGCGUGCCUUGGCACGACUAGGAAACUAGUCCGUGUGGUAUGGCUUCG

JR's Let's Break the Barcode - 3 nt Dangling End Gap				Me	Roadmap
Title	Synthesis score		Sequence		
search	min	max	search		
Esrrer	98 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
BTB V3	98 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Omei JRLBB3 - 3	98 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Fisker breaking ...	98 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
All aboard the ...	98 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
JR_BBC_3ntDangl...	98 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Reversal of For ...	97 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Omei JRLBB3 - 2	97 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
UUUUU - Broud ...	97 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Double U/U - Br ...	97 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Peanut Butter I ...	96 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Break dance-3 nt 1	94 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
It's broken for ...	94 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Class Presentat...	94 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Jam it Up!! (Br...	93 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Mat - JR's Brea...	93 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Break a Leg I	93 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
cedar	92 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Mat - JR's Brea...	92 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Coffee Break	92 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
End Cap 1	92 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Break a Leg II	92 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Massively Disru...	91 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Break a Leg III	91 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Sparkling III	89 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Omei JRLBB3 - 1	89 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Sparkling I	85 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Solution 2	95 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Class Presentation	78 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	
Class Presentat...	75 / 100		GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC	CCUGUGGAAAAGCGGUCUUCG	

<http://eterna.cmu.edu/web/lab/3534130/>

<http://eterna.cmu.edu/web/lab/3534128/>

<http://eterna.cmu.edu/web/lab/3534058/>

There are growing error rates on the lab with a bigger gap.

JR's Let's Break the Barcode - Adjacent Barcode Version			Column Options	Sequence View options	Advanced Sequence Search													
Designer	Title	Sequence																
			5	10	15	20	25	30	35	40	45	50	55	60	65	70	75	
IconMaster	JR's Let's Break the Barcode.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
IconMaster	JR's Let's Break the Barcode.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Eli Fisker	Recycled barcode from sibli.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Eli Fisker	Mutalating good barcode fro.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
wateronthemoon	Adjacent barcode	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
wateronthemoon	Adjacent barcode 3	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Hypheia	Karate Chop! (Break the Bar.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
IconMaster	JR's Let's Break the Barcode.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
mat747	Mat - JR Adjacent Barcode V.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
ViennaUCT	Direatinin	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
aknyatt	BC - 1	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Eli Fisker	Recycled barcode from sibli.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Broud	UUU know nothing - Broud -	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
nogiahoo	Barcode	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Hypheia	Karate Chop! 2 (Break the B.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
starmjess	GU Closing Pair Barcode	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
nascarnut	LBTB-ABV V2	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
wateronthemoon	Adjacent barcode	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
ViennaUCT	Ceoninat	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
salish99	Broken BC	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
wiambeth	BTB-1	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Broud	BreakAdjacent - Broud - La.	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Broud	U/C nothing - Broud - Lab ..	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
ViennaUCT	Bigediti	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Meechi	Meechi LBIB ABV	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
DHammond	Break it	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Testa'sDisciple	BTB Crossed + 2	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
JR	JR_AdjBarcode_Sub2	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																
Malcolm	BarBreak#3	GGAACCAUAGCGCGCUCAGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUC																

JR's Let's Break the Barcode - 2 nt Dangling End Gap			Column Options	Sequence View options	Advanced Sequence Search	Download											
Designer	Title	Sequence															
			5	10	15	20	25	30	35	40	45	50	55	60	65	70	75
Bround	UUUU - Bround - Lab 'Let's...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUUGCGUUCG															
wateronthemoon	Breaking bad 2	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
JR	JR_BBC_2ntDangle_Rnd1_Sub3	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGAUCUUCG															
Bround	To Stabilia! - Bround - Lab...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUCGUAAGUUCG															
Tesla'sDisciple	BBB Crossed GU	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUGGCGUUCG															
Omei	Omei JRLBB2 - 3	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
Hyphema	Barcode Goes Bye Bye! (Brea...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUGUGACUUCG															
Zanna	Broken Code II	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
Omei	Omei JRLBB2 - 2	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
wateronthemoon	Break dance 2nt 1	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAAGCGUUCG															
Bround	UUU + UUC - Bround - Lab 'L...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
jandersonee	Neck Echo	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
Omei	Omei JRLBB2 - 1	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
RedSpah	Quartz II	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
TomoeUzumaki	Radioactive	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCGUUCG															
nascarnut	BTB 2NT V3	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCAGACUUCG															
fat13	JRLBTBC-2NTDEG3	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCAGACUUCG															
Hyphema	Implosion (break the barcod...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGCCUAGCAGACUUCG															
TomoeUzumaki	Breaking in and shaping up	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAAGAGUUCG															
Tesla'sDisciple	BBB GU	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAUUGUUCG															
hoglahoo	pine	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGAAACCGUUCG															
Eli Fisker	Fisker testing the Barcode ...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGAAACCGUUCG															
naprat	Bad Barcode v1	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGAAACCGUUCG															
mat747	Mat - JR's Break the Barcod...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAUUGUUCG															
Jleux	I fixed it 6 - Jleux - JR's...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGAAACCGUUCG															
Zanna	Broken Code III	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAUUGUUCG															
nascarnut	BTB 2NT V1	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAUUGUUCG															
ViennaUCT	Zaaf	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAUUGUUCG															
rnjensen45	Best Worst Case	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAUUGUUCG															
cataway	JRSB-the-B2Ndes2	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGUUAUUGUUCG															

JR's Let's Break the Barcode - 3 nt Dangling End Gap Version										Column Options	Sequence View options	Advanced Sequence Search	Download				
Designer	Title	Sequence															
			5	10	15	20	25	30	35	40	45	50	55	60	65	70	75
JR	JR_BBC_3ntDangle_Rnd1_Sub3	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Bround	All aboard the Stability Tr...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Eli Fisker	Fisker breaking the Barcode...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Omei	Omei JRLBB3 - 3	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
nascarnut	BTB V3	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
ViennaUCT	Esere	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Bround	Double U/U - Bround - Lab '...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Bround	UUUU - Bround - Lab 'Let's...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Omei	Omei JRLBB3 - 2	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Troppy	Reversal of Fortune03	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Hyphema	Peanut Butter it Up! (Just ...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
TomoeUzumaki	Class Presentation III	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
jarelmason	It's broken for sure	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
wateronthemoon	Break dance - 3 nt 1	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Zanna	Break a Leg I	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
mat747	Mat - JR's Break the Barcod...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Hyphema	Jam it Up! (Break the Barc...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Zanna	Break a Leg II	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
garydfisher	End Gap 1	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Tesla'sDisciple	Coffee Break	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
mat747	Mat - JR's Break the Barcod...	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
hogihoo	cedar	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Zanna	Break a Leg III	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
rnjensen45	Massively Disruptive	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
Omei	Omei JRLBB3 - 1	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
RedSpah	Sparkling III	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
rckt_scnst	Solution 2	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
RedSpah	Sparkling I	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
TomoeUzumaki	Class Presentation	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															
TomoeUzumaki	Class Presentation II	GGACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUCGCGUGGAAAGGUGCGCGUUCG															

I know these labs are just a mood of one single design which gets varied its barcode. My question is which set of the data can we best trust. The ones with the stabler barcode, high error rates and the more messier main design or the ones with crappy barcodes, calm main design and lower error rates.

As I have noted, the distance between barcode and design has an effect on what color mode the barcode is in. It looks like my [prediction](#) from earlier held. I was predicting that the adjacent version of the lab would have more of its green move to the first strand of the barcode.

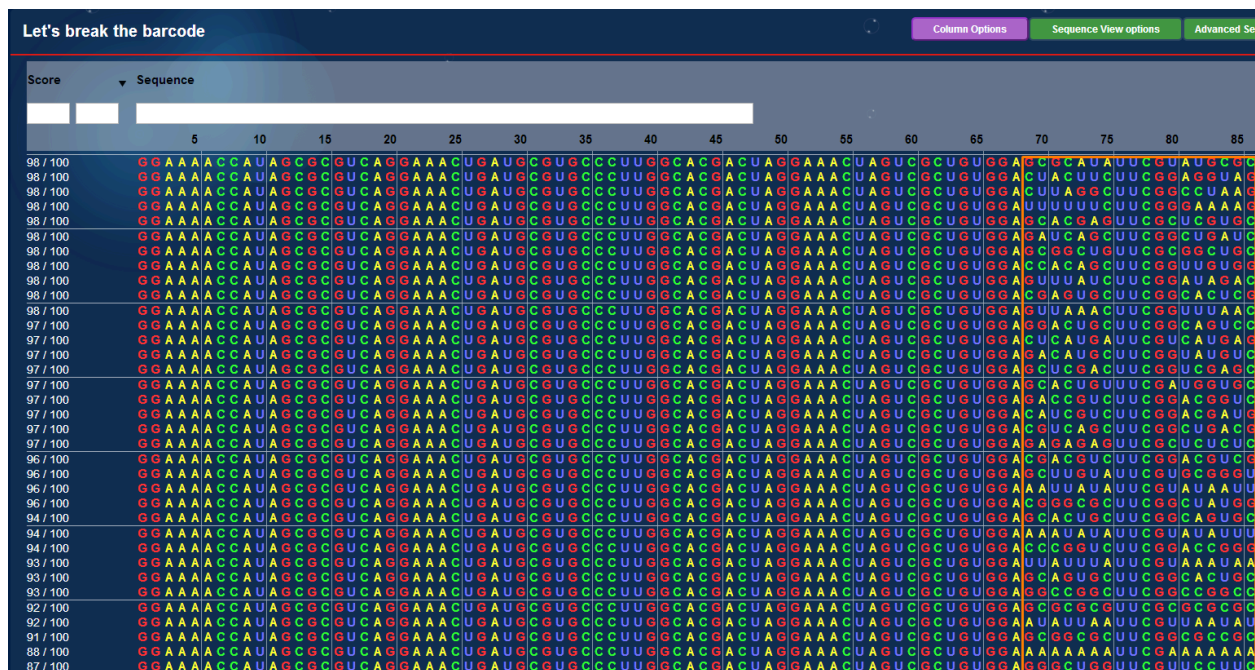
JR's Let's Break the Barcode - Adjacent Barcode Version			
			Me Roadmap Puzzle
Title	Synthesis score ▾	Sequence	
search	min max	search	
Adjacent barcode 3	98 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Adjacent barcode	98 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Mutafating good...	98 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Recycled barcod...	98 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
JR's Let's Brea...	98 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
JR's Let's Brea...	98 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Mat - JR Adjace...	97 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
JR's Let's Brea...	97 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Karate Chop! (B...	97 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
UUU know nothin...	96 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Recycled barcod...	96 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
BC - 1	96 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Direatinn	96 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Adjacent barcode	94 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
LBTB-ABV V2	94 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
GU Closing Pair...	94 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Karate Chop! 2 ...	94 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Barcode	94 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
UCG nothing - B...	93 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Breakadacent ...	93 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
BTB-1	93 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Broken BC	93 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Cosmonat	93 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Break II	92 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Meechl LBIB ABV	92 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
Bigediti	92 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
JR AdjBarcode_Sub2	90 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
BIB Gressed + 2	90 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	
BarBreak#3	89 / 100	G G A C C A U A G C G C U C A G G A A A C U G A U G C G U C C C U U G G C A C G A C U A G G A A A C U A G U C G C U U G G C U A U G G C U U C G G C C A U G G	

So the gap will affect which barcode a certain design needs. This is just one design, but I imagine that the sequence of another design, will crave a slightly different type of barcode. As what really is needed for the barcode to do is to not be complementary with the main design to avoid binding up. But rather it is to be the lightning conductor, taking all the stress from the main design away.

14 May 2014

The attempt to break the barcode in JR's lab on a 100% design. Generally the barcodes that looks most unstable in the SHAPE data, are the ones with most repeat bases or mainly AU basepairs for the whole barcode. One barcode with almost only UU's do end up high on the scoring total. But doesn't look too stable itself.

<http://eterna.cmu.edu/web/browse/3376325/>



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I suspect that the old lab UI runs on legacy scaling and the new on absolute scaling. Same lab and very different. [Rhiju says that it is most certainly a case of legacy scaling versus absolute scaling]

JR's Let's Break the Barcode - Adjacent Barcode Version			
Title		Synthesis score	Sequence
search	min	max	search
Adjacent barcode 3	98 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Adjacent barcode	98 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Mutating good...	98 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Recycled barcod...	98 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
JR's Let's Brea...	98 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
JR's Let's Brea...	98 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Mat - JR Adjace...	97 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
JR's Let's Brea...	97 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Karate Chop1 (B...	97 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
U/U know nothin...	96 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Recycled barcod...	96 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
BC - 1	96 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Directlinin	96 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Adjacent barcode	94 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
LBTB-ABV V2	94 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
GU Closing Pair...	94 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Karate Chop1 2 ...	94 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Bearcode	94 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
U/C nothing - B...	93 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Breakadjacent - ...	93 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
BTB-1	93 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Broken BC	93 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Ceoinnat	93 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Break it	92 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Meechl LBIB ABV	92 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Bigeditl	92 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
JR AdjBarcode_Sub2	90 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
BTB Crossed + 2	90 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
BarBreak#3	89 / 100		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG

JR's Let's Break the Barcode - Adjacent Barcode Version			
Designer		Title	Sequence
IconMaster	JR's Let's Break the Barcode...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
IconMaster	JR's Let's Break the Barcode...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Eli Fisker	Mutating good barcode fro...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Eli Fisker	Adjacent barcode		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
wateronthemoon	Adjacent barcode 3		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
wateronthemoon	Karate Chop1 (Break the Bar...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Hyphema	JR's Let's Break the Barcode...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
IconMaster	Mat - JR Adjacent Barcode V...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
mat747	Directlinin		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
ViennaUCT	BC - 1		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
akhyatl	Recycled barcode from sibil...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Eli Fisker	U/U know nothing - Bround - ...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Bround	Bearcode		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
hoglahoo	Karate Chop1 2 (Break the B...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Hyphema	GU Closing Pair Barcode		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
starryess	LBTB-ABV V2		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
nascamut	Adjacent barcode		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
wateronthemoon	Ceoinnat		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
ViennaUCT	Broken BC		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
salish99	BTB-1		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
wlambeth	Breakadjacent - Bround - La...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Bround	U/C nothing - Bround - Lab ...		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
ViennaUCT	Bigeditl		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Meechl	Meechl LBIB ABV		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
DHammond	Break it		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Tesla'sDisciple	BTB Crossed + 2		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
JR	JR AdjBarcode_Sub2		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG
Malcolm	BarBreak#3		GAACCAUAGCGCGUCAGGAAACUGAUGCGUGCCUUGGCACGACUAGGAAACUAGUGCGUGGCAUUGCGUUCG

I think the closer the barcode is to the main design, the more it needs to be a negative mirror. So the locked G in the closest stem is turning their backs on the C's in the barcode.

JR's Let's Break the Barcode - Adjacent Barcode Version

Column Options Sequence View options Advanced Sequence Search Download SHAPE

Old lab

Designer	Title	Score	Sequence
IconMaster	JR's Let's Break the Barcod	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
IconMaster	JR's Let's Break the Barcod	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Eli Fisker	Recycled barcode from sibil	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Eli Fisker	Mutating good barcode fro..	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
wateronthemoon	Adjacent barcode	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
wateronthemoon	Adjacent barcode 3	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Hyphema	Karate Chop! (Break the Bar..	97 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
IconMaster	JR's Let's Break the Barcod	97 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
mat747	Mat - JR Adjacent Barcode V..	97 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
ViennaUCT	Dreadlin	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
akhyatt	BC - 1	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Eli Fisker	Recycled barcode from sibil	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Bround	UUU know nothing - Bround -	96 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
hoglahoo	Bearcode	94 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Hyphema	Karate Chop! 2 (Break the B..	94 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
starryess	GU Closing Pair Barcode	94 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
nasarnut	LBTB-ABV V2	94 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
wateronthemoon	Adjacent barcode	94 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
ViennaUCT	Ceoinat	93 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Satish99	Broken BC	93 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
wimbeth	LTB-1	93 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Bround	Breakadjacent - Bround - La..	93 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Bround	UUC nothing - Bround - Lab	93 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
ViennaUCT	Bigidli	92 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Meechil	Meechil LBIB ABV	92 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Diamond	Break 1	92 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Tesla'sDisciple	BIB Crossed + 2	90 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
JR	JR_AdjBarcode_Sub2	90 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Malcolm	BarBreak#3	89 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Malcolm	BarBreak#1	0 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
Malcolm	BarBreak#2	0 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
TheRealDrako	RealDrak	0 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
TheRealDrako	RealDrak	0 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
TheRealDrako	RealDrak	0 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC
JR	JR AdjBarcode_Sub1	0 / 100	GGACCAUAGCGGCUAGGAAACUGAUCCUUGGCAAGACUAGGAAACUAGUCGUGGCAAGCAUUC

18 May, 2014

Thoughts on Huge RNA

(From discussion with Mat 18 May, 2014)

Eli: I think what RNA designing is really about is frequencies. Patterns change with frequencies, in relation to design size, design structure

So like the double sameturning GC's and AU's are most often bad in small designs, but needed in bigger designs. The bigger designs, the more weird patterns will be allowed. Also I believe that RNA designs are split into sections, so one section is locked of, like a smaller puzzle. And sealed with a rather strong pattern, so it has peace to find itself and not misfold with all the rest of the coming design

Mat: yes size does make a different

Eli: So the bigger design, the longer sameturning sections we will see and I think also a little less even energy distribution

Mat: more chance of interaction i guess too

Eli: Yes, that too.

Mat: About the "The bigger designs, the more weird patterns will be allowed". I have thought about that sometimes, a big guess about that, that weird patterns may help with making sequence less complimentary, there would be another reason as well i guess.

Eli: I agree, with you on weird patterns making things less complementary. Lets say you have 4 U's in line and only one sections of them and have no stretches of 4 A's. Then they are more likely to stay unpaired

What matters is how many stretches are potentially complementary to each other

Mat: yep

Eli: The higher frequency of the same complementary fragments, the higher chance of an accident

Mat: the lengths of sections/fragment could get bigger too, as a ratio to the overall design/lab size too

Eli: Yes, thats what I think will happen

5 June, 2014

I was looking at some of my old lab data from the first cloud lab. I made changes in winners from first round to see what would happen if I tested out different things.

Mod of Mod. of Starry's design 2 by [Eli Fisker](#)

prevnext

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[SYNTHESIZED!]

This design was synthesized with score 81/ 100

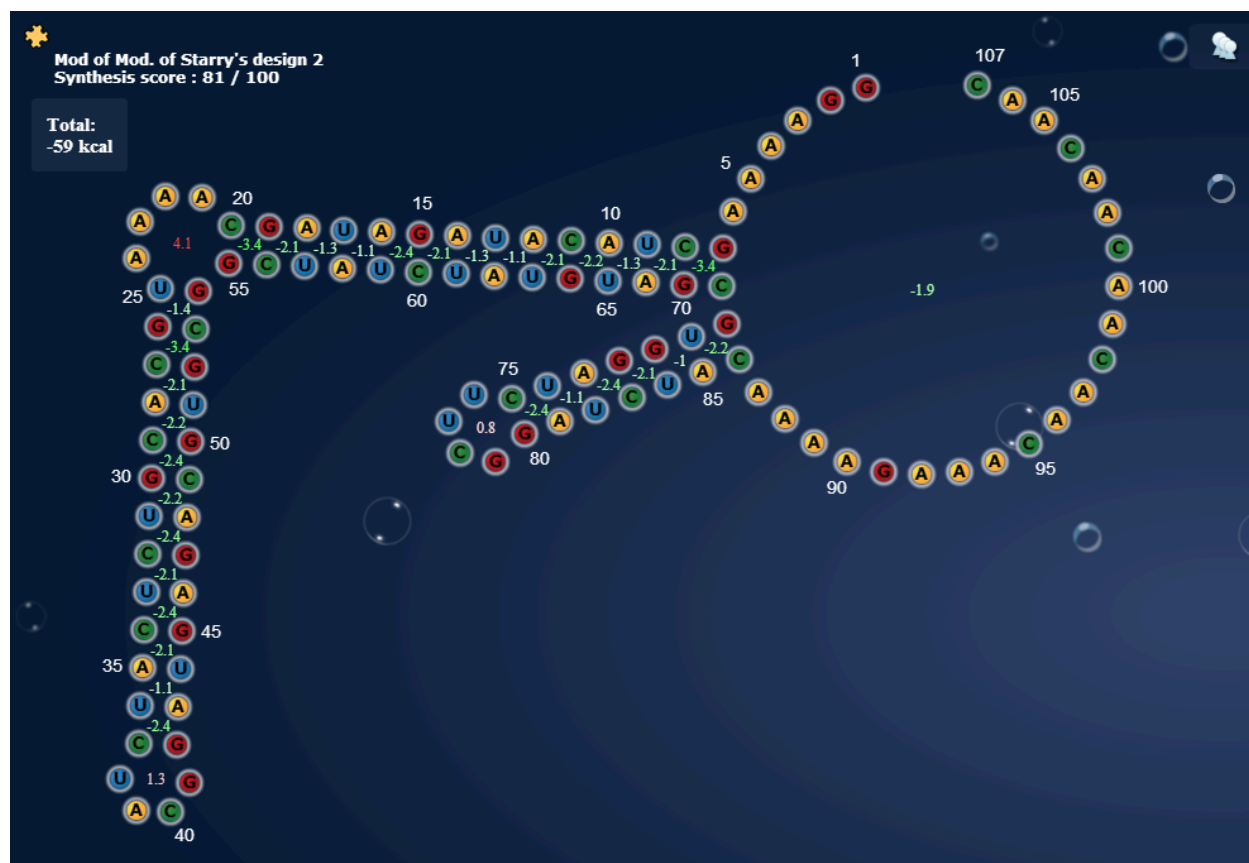
Design Description

I made a mod of Janelle's 97% scoring design. I took a look at the lab results and since the only design that had a stable nucleotide at base 20 was Spacefolder's design Default title, I added in a GU-pair, I let the bulge closing follow the pattern from it. I added in a GC-pair behind the GU-pair that closes the bulge, in the hope that it will hold. For the sake of the purity of the experiment, I will change nothing else and not add new constraints.

[illegible]

<http://eterna.cmu.edu/game/solution/2333227/2389657/seeresult/>

Mod



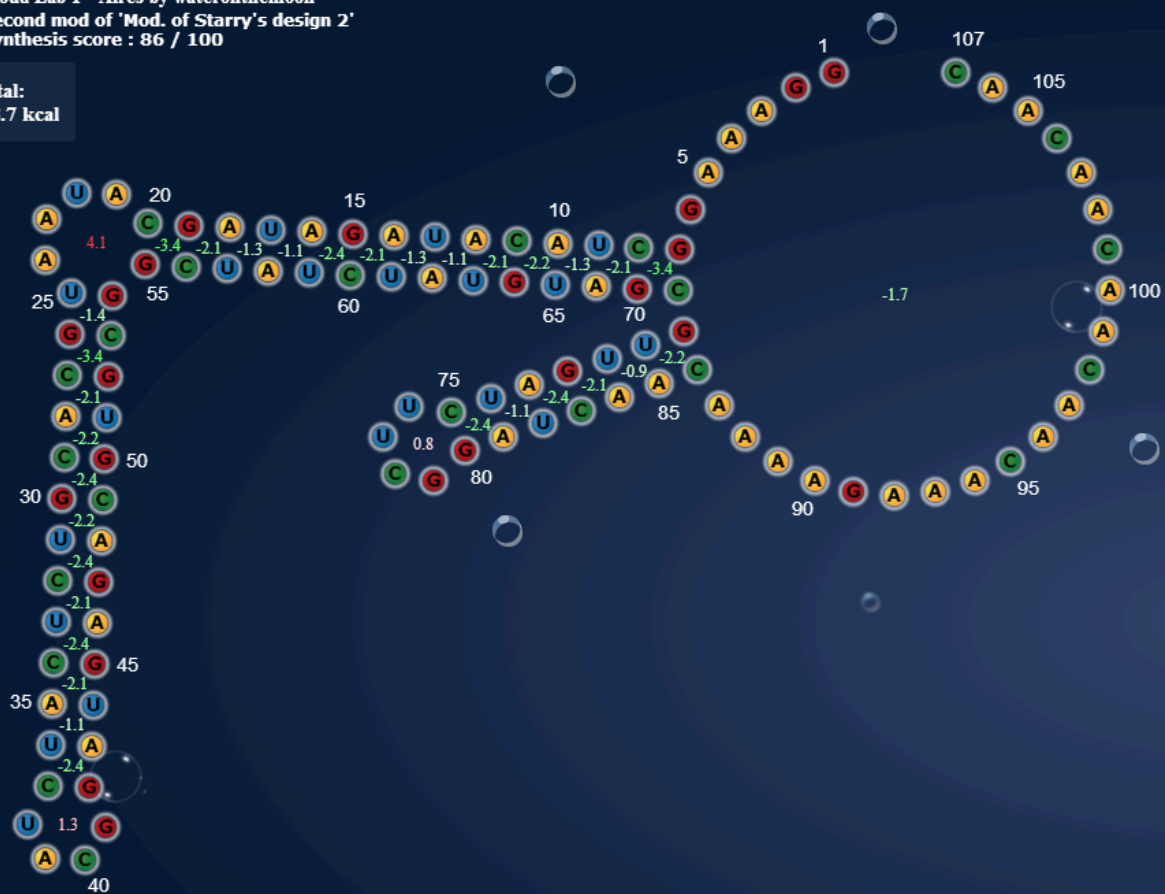
<http://eterna.cmu.edu/game/solution/2333227/2600643/seeresult/>

I even managed to snatch the same barcode. Only difference is this area.



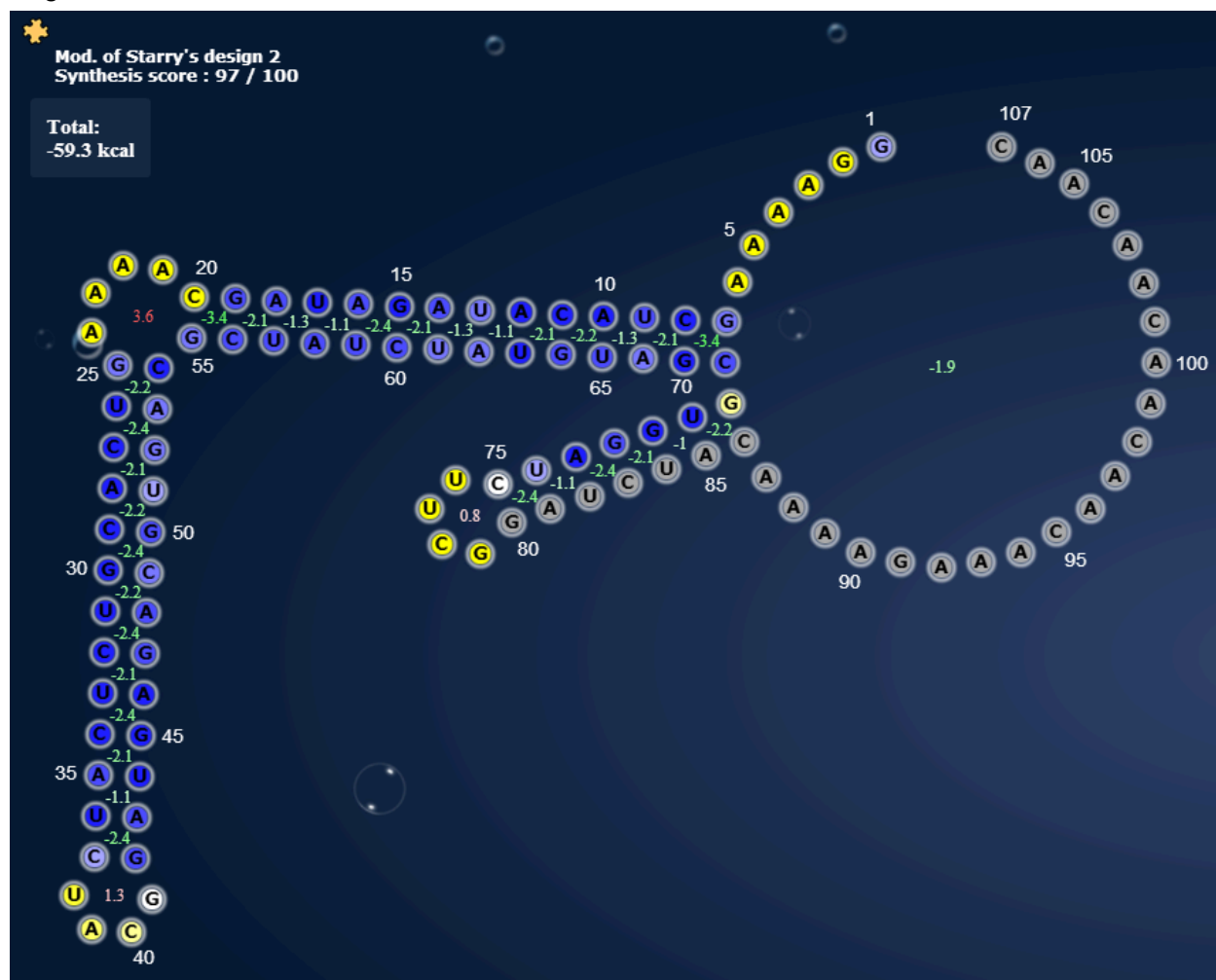
★ Cloud Lab 1 - Aires by wateronthemoon
Second mod of 'Mod. of Starry's design 2'
Synthesis score : 86 / 100

Total:
-58.7 kcal



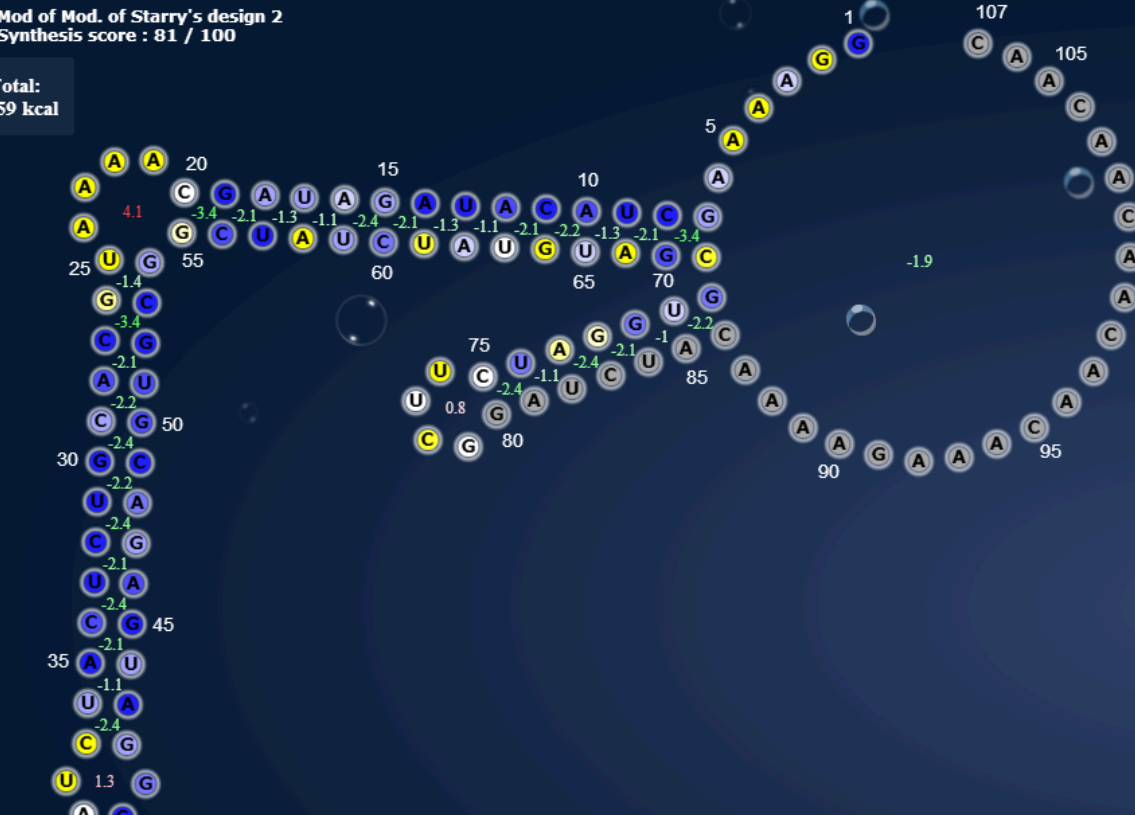
However their SHAPE data are strikingly different with instabilities spreading far from the area of change.

Original




Mod of Mod. of Starry's design 2
 Synthesis score : 81 / 100

Total:
 -59 kcal



The diagram illustrates the secondary structure of an RNA sequence, showing base pairing and energy values. The sequence is 107 nucleotides long. The structure is composed of several stems and loops. Nucleotides are represented by circles with their base letter (A, U, G, C) and a number. Some circles are highlighted in yellow or blue. Energy values are shown between some bases, indicating base pairing strength. The sequence starts with 1, 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 105, 107.

I also did a second mod of Janelle's design, this time following the new constraints and putting in a U in the bulge ring. This showed to have a relaxing effect and the design scored a bit better. However I had to change the barcode. But the SHAPE data shows a lot less instability.

prev next

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This design was synthesized with score 86/ 100

I made a mod of Janelle's 97% scoring design. I took a look at the lab results and since the only design that had a stable nucleotide at base 20 was Spacefolder's design Default title, I added in a GU-pair, I let the bulge closing follow the pattern from it. I added in a GC-pair behind the GU-pair that closes the bulge, in the hope that it will hold. This time with new constraints.

🌟 **Cloud Lab 1 - Aires by wateronthemoon**
Second mod of 'Mod. of Starry's design 2'
Synthesis score : 86 / 100

Total:
-58.7 kcal



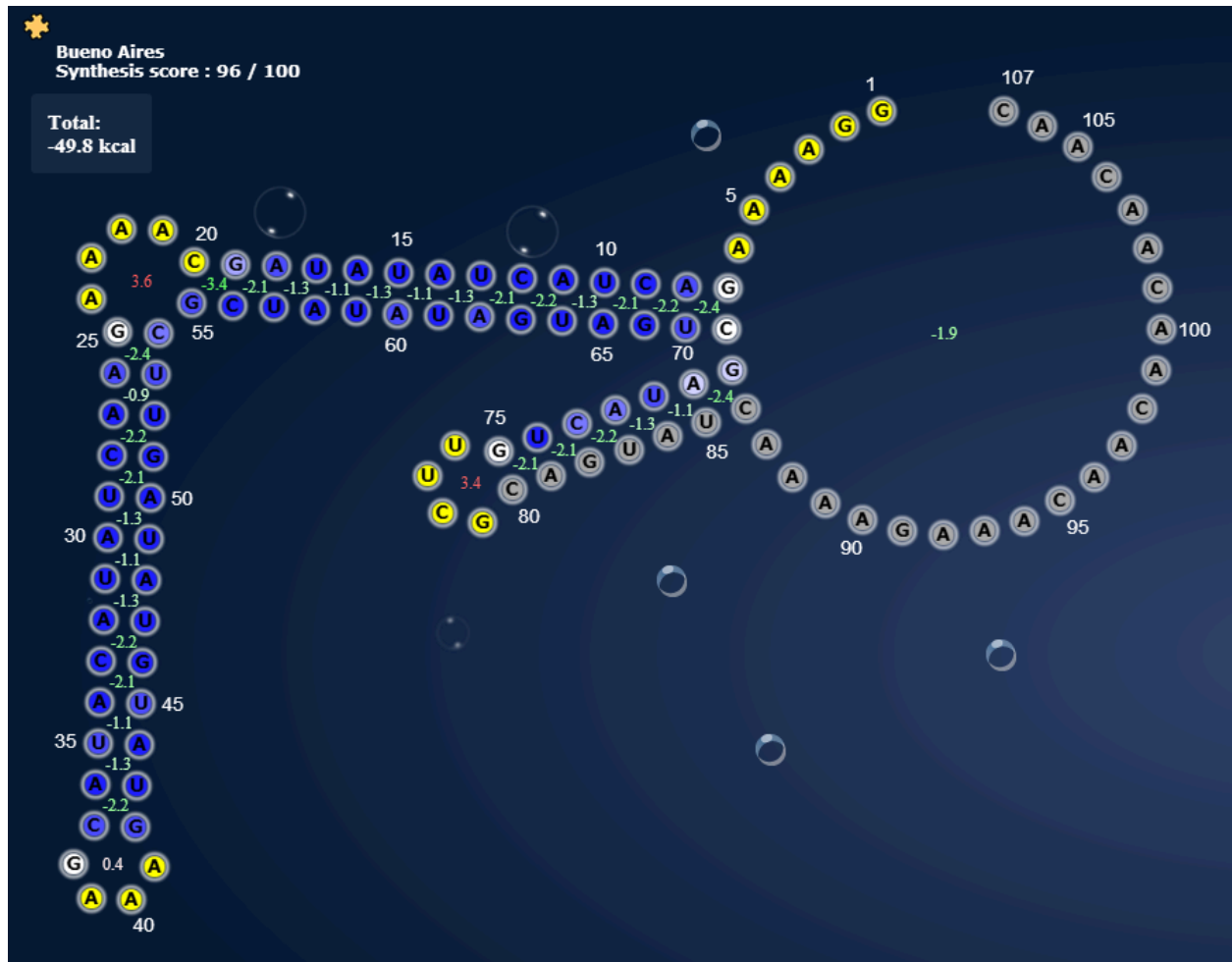
283

I successfully interchanged the exact GU and GC bulge closing in another design. Also here I managed to snatch the original barcode, only difference this section:



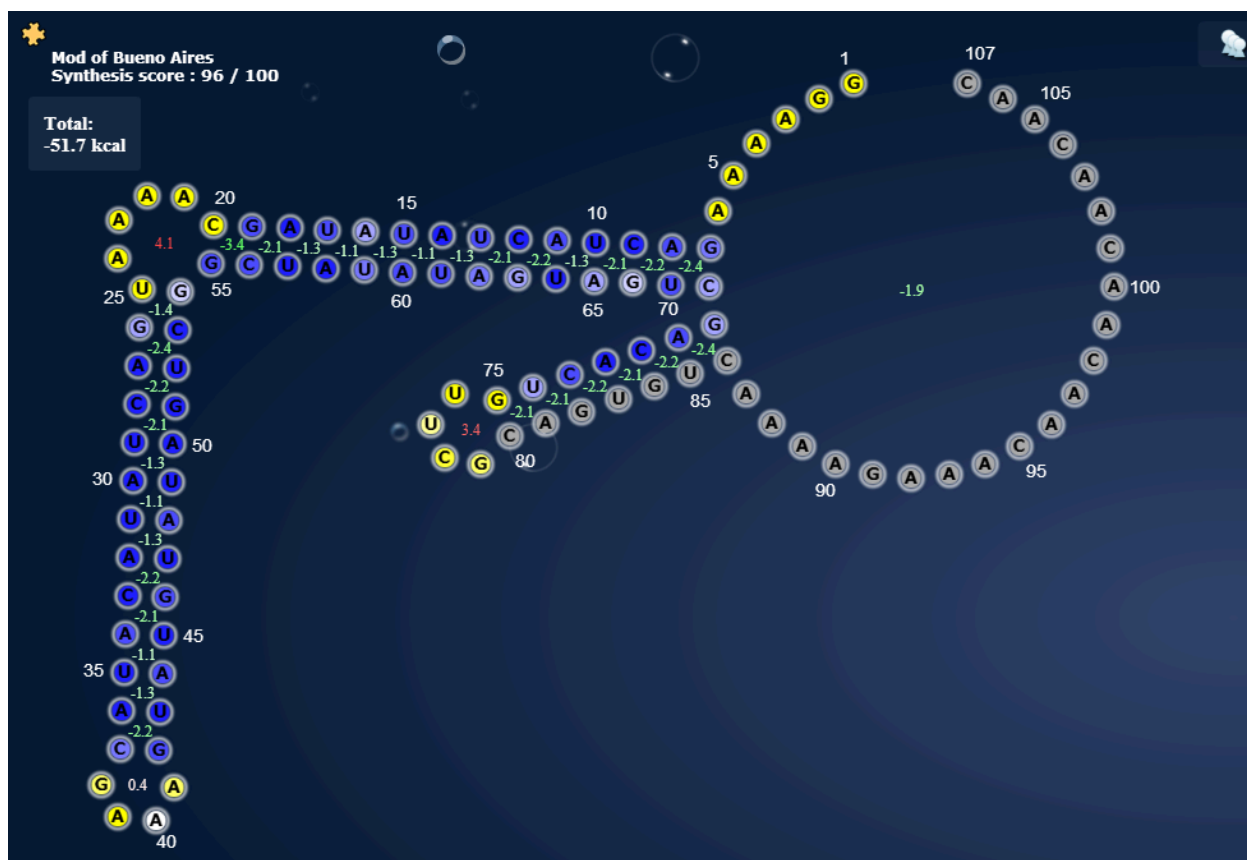
Original



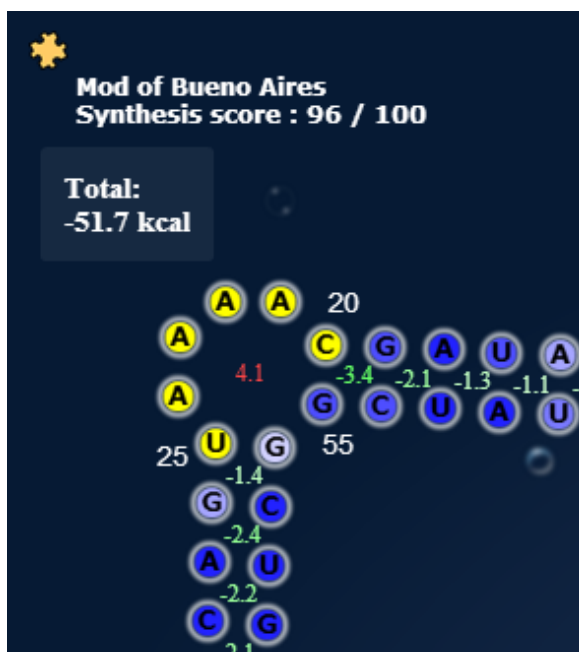


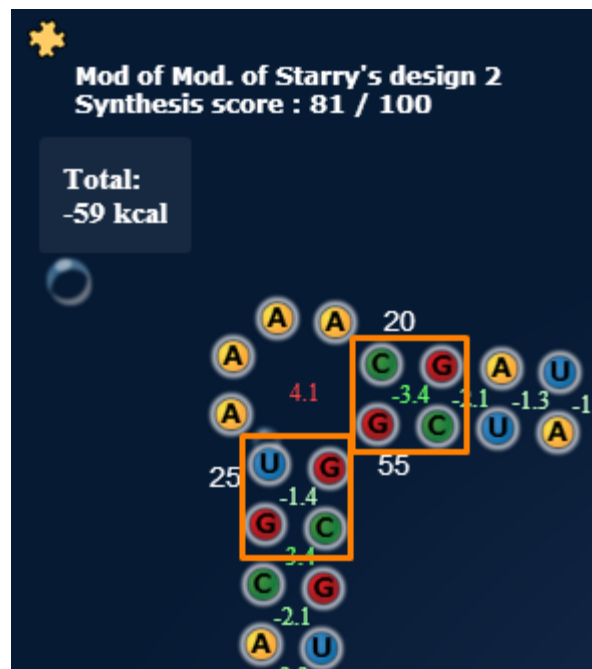
<http://eterna.cmu.edu/game/solution/2333227/2333463/seeresult/>

Mod



Identical structure element from bulge:





Exact same bulge closing for both design and this is the only difference. So the stability of the rest of the design will also decide if a certain bulge closing will work. And instabilities can be induced far away from the zone of change.

Mat also made a near mod of jandersonlee's winner



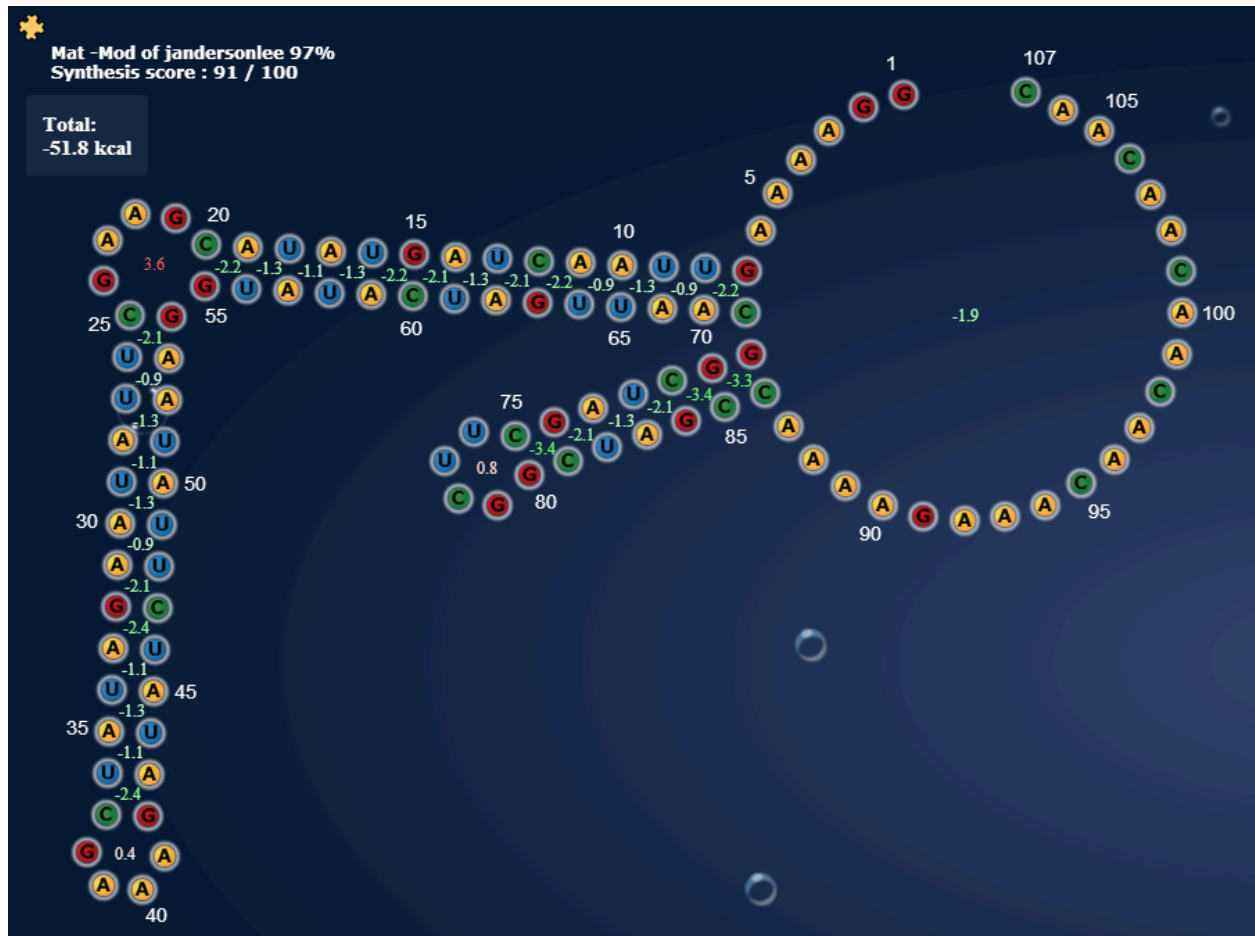
Aires Reflections

Synthesis score : 97 / 100

Total:

-51.8 kcal



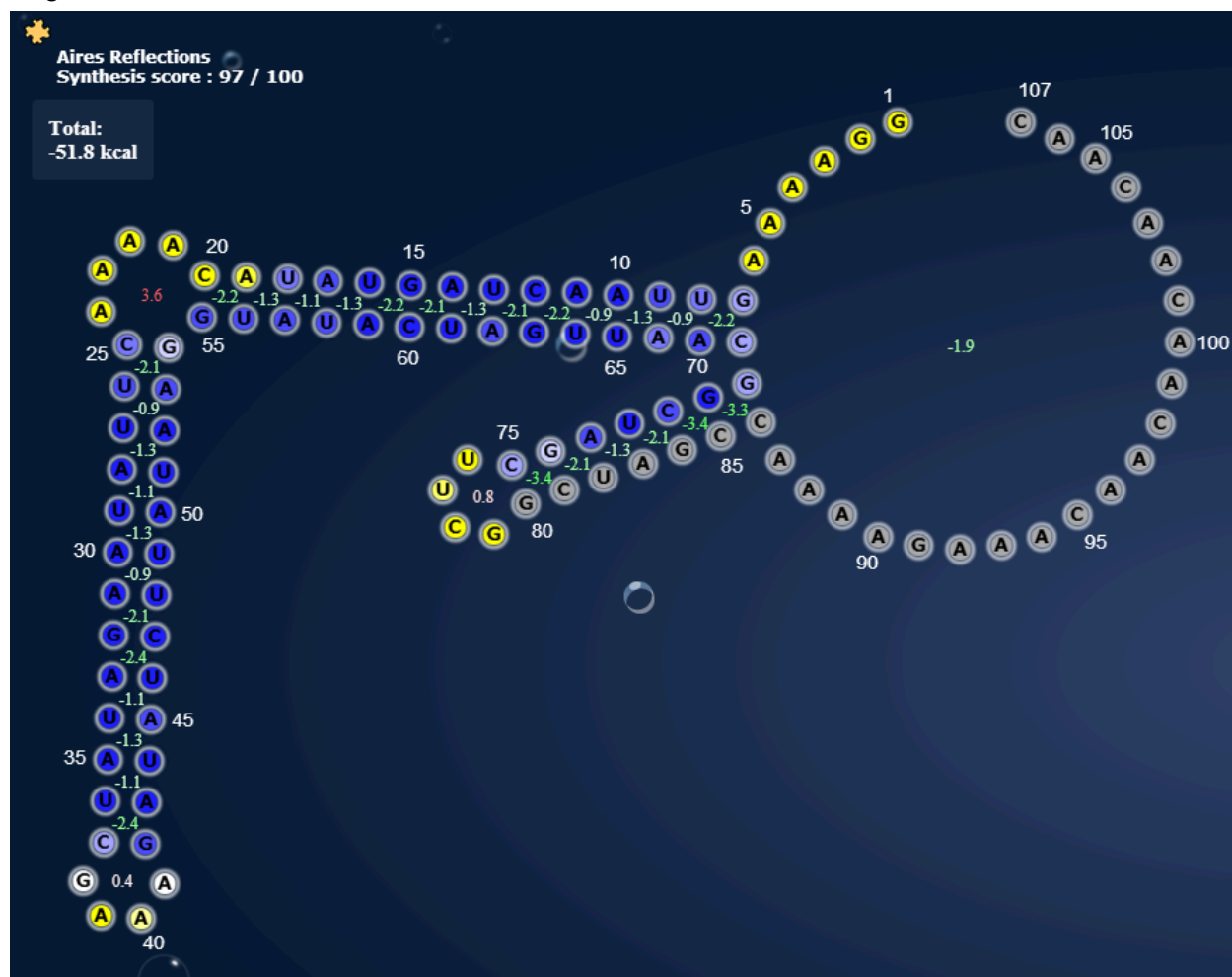


Only difference.

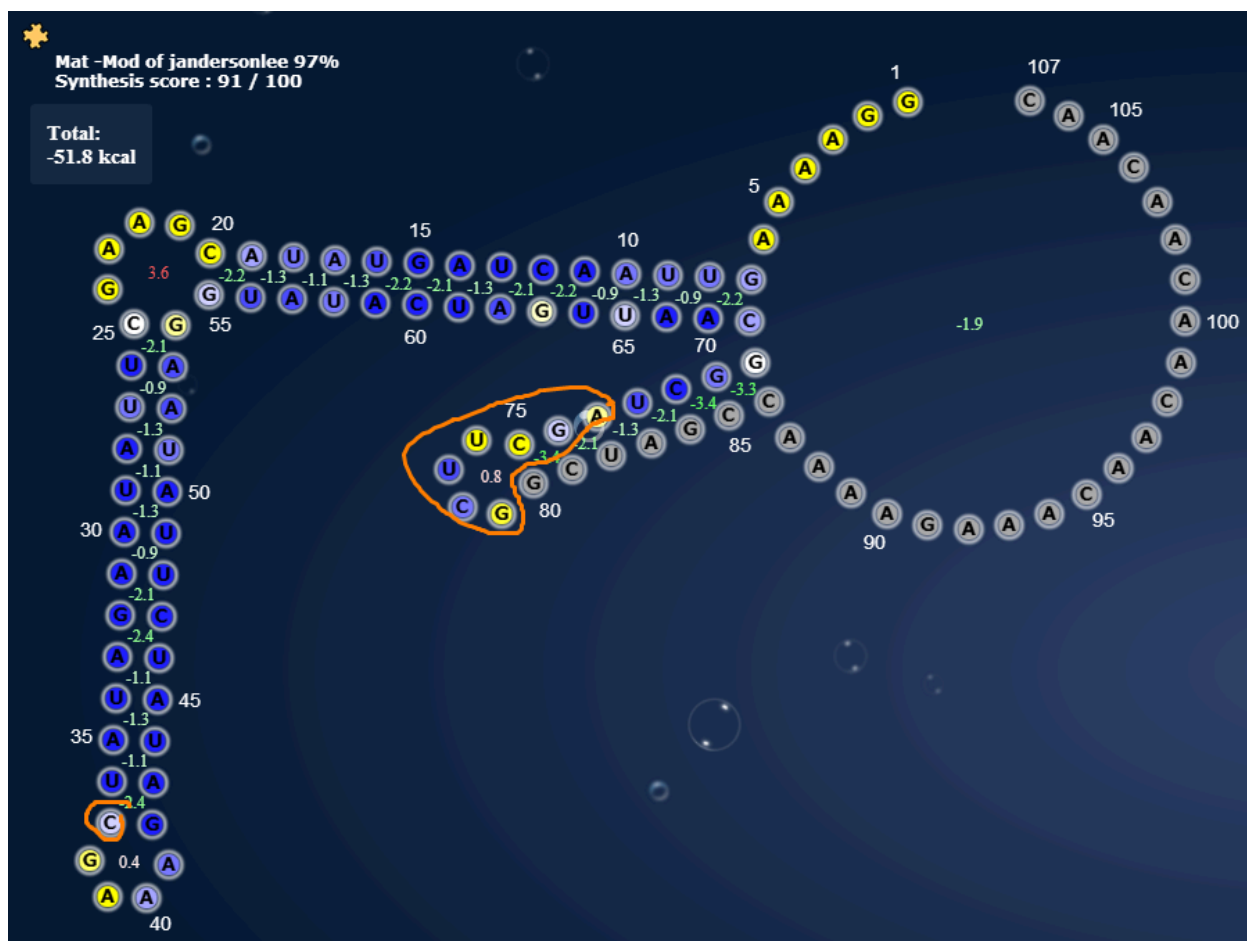


Yet there are several differences in SHAPE data, not just on changing side, but at opposite end of stem and even further away.

Original



Mod

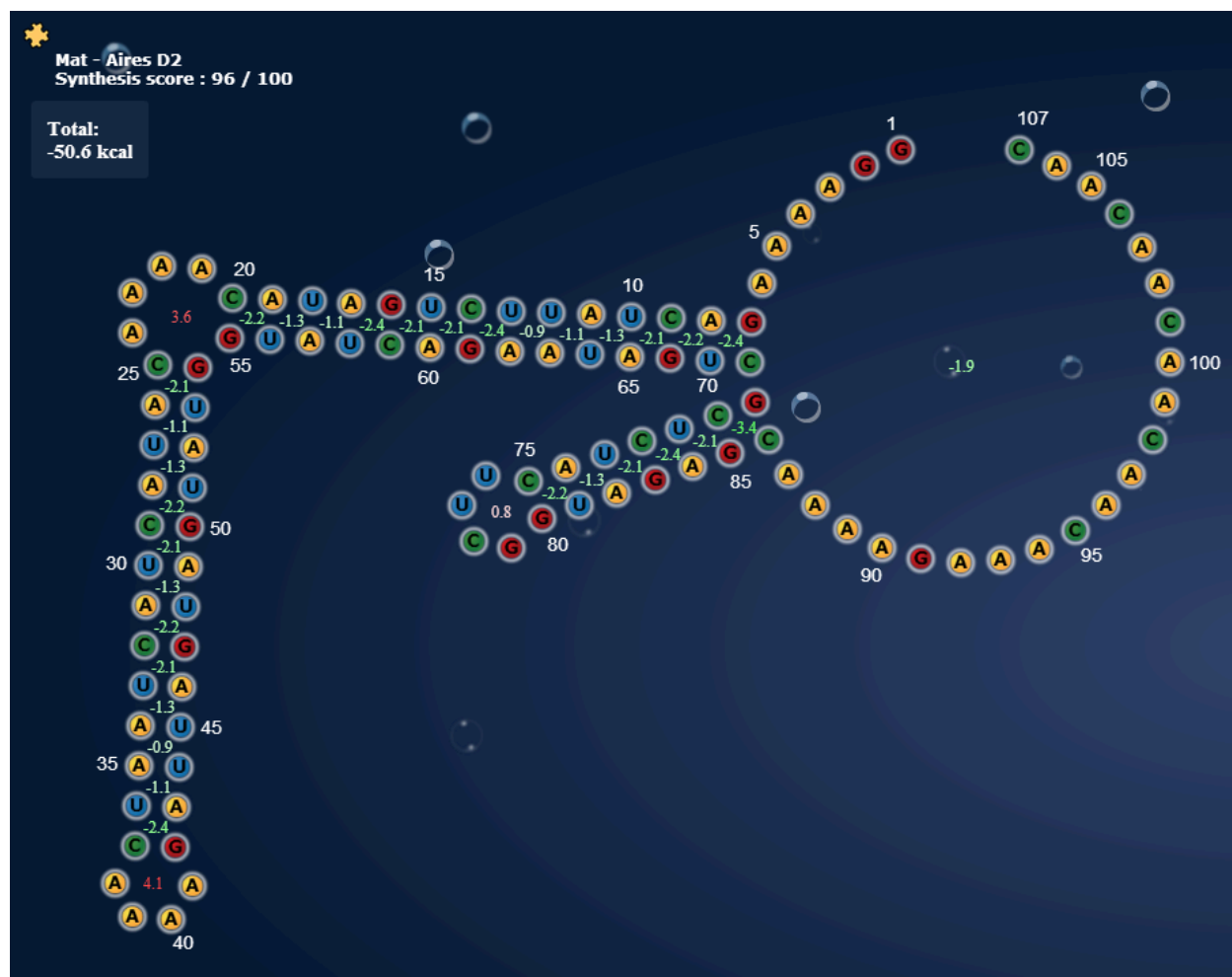


Stevetclark did a similar mod of his round 1 winner. Added two red “boosts” for the bulge, with dramatic decrease in score. 96 against 87%. His barcode was different though.



Generally the bulges that did best didn't have other than A at first or last base of the bulge ring.

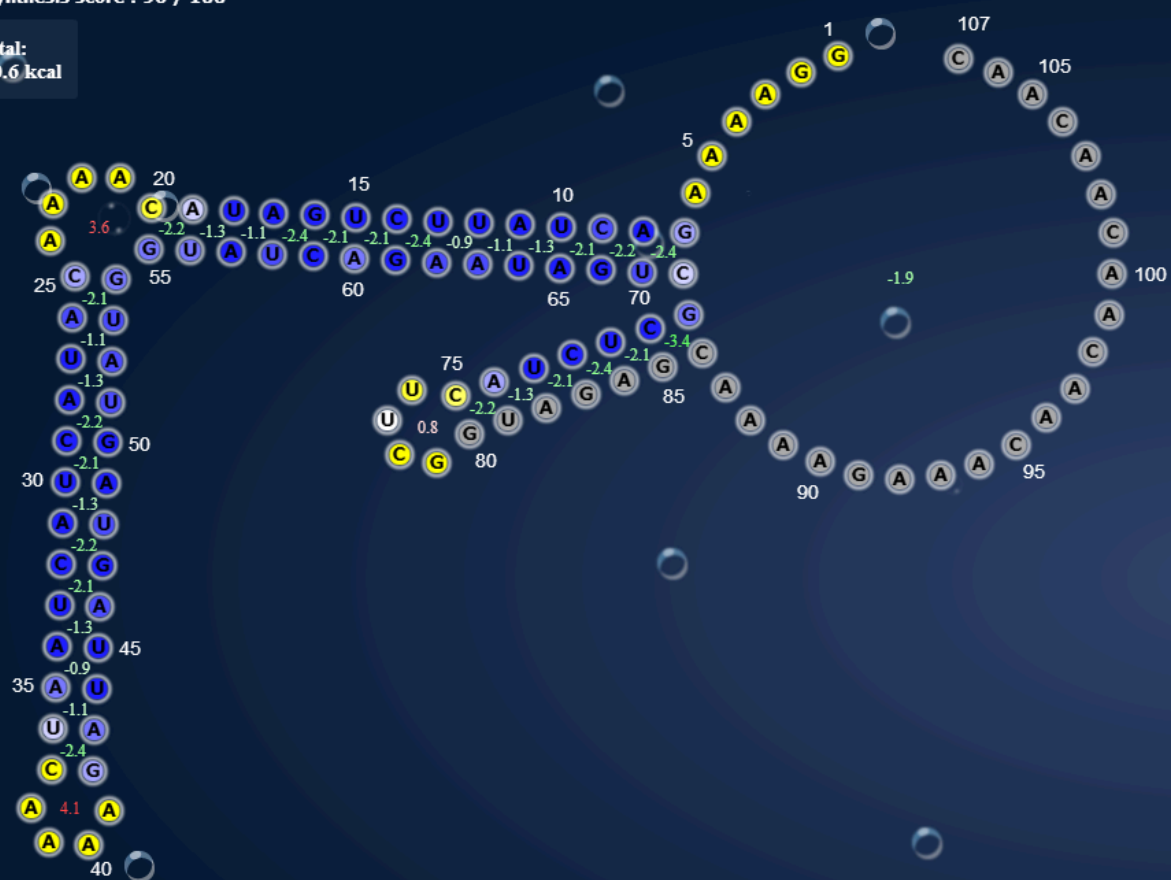
Mat did another experiment where he just added one single G boost at the tetraloop.





Mat - Aires D2
Synthesis score : 96 / 100

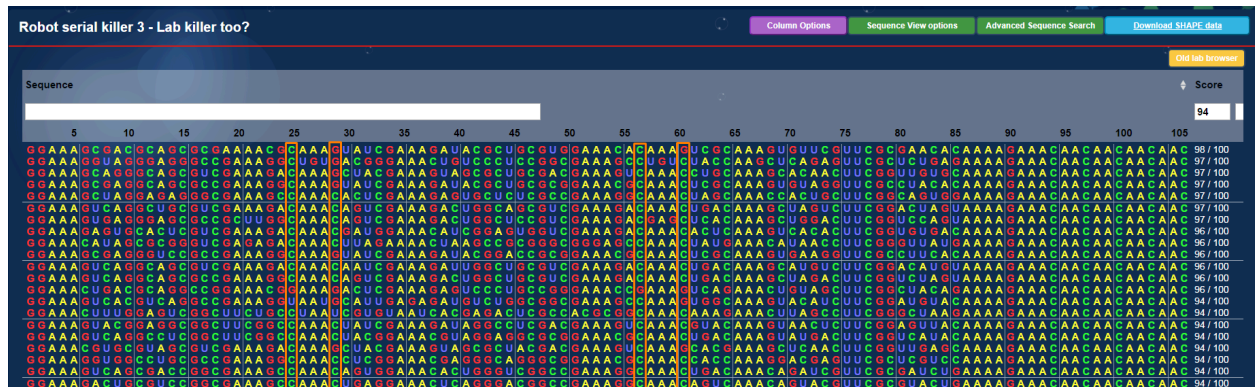
Total:
-50.6 kcal





Motor Protein - Step 1

Title	GU	Score
Myosin 3	2 (6%)	94 / 100
This is a Perfect Title	8 (24%)	94 / 100
This is an Epic Title	6 (18%)	94 / 100
Motoring with GC	3 (9%)	93 / 100
Beinusus	0 (0%)	93 / 100
MP-Step1-Z1	10 (30%)	92 / 100
....	9 (27%)	92 / 100
Fiskers Motor Protein Step ..	2 (6%)	92 / 100
Fiskers Motor Protein Step ..	2 (6%)	92 / 100
Mat - Motor Protein - Step ..	1 (3%)	92 / 100
stray cat strut	2 (6%)	92 / 100
Myosin 2	2 (6%)	92 / 100
Mod of Eli's first submissi..	2 (6%)	92 / 100
MP Step1 Zanna3	4 (12%)	90 / 100
motor1b	4 (12%)	90 / 100
MP1 - 1	6 (18%)	90 / 100
Mat - Motor Protein - Step ..	1 (3%)	90 / 100
Motor Protein Step 1	7 (21%)	90 / 100
Step up	0 (0%)	90 / 100
Myosin 1	2 (6%)	90 / 100
Motoring with GC/ one AU cl..	3 (9%)	90 / 100
Motoring with GC (inline GC..	3 (9%)	90 / 100
Motopro1	1 (3%)	90 / 100
try 1	0 (0%)	89 / 100
motor1c	4 (12%)	89 / 100
relaxed walking	0 (0%)	89 / 100
Mat - Motor Protein - Step ..	0 (0%)	89 / 100
second 19.4 @ 77	0 (0%)	89 / 100
Propellor Beanie and Antenn..	0 (0%)	89 / 100
TEST 2	1 (3%)	89 / 100
TEST 3	1 (3%)	89 / 100
MotorProtStp1design1	2 (6%)	89 / 100
Riquelque	1 (3%)	89 / 100
Tin Gear (G-U Multiloop)	3 (9%)	88 / 100
JR_Motor1_Rnd1_Sub1	0 (0%)	88 / 100



24 Oct 2014

I was looking at one of the old switch labs while preparing for the current round of mimics. I mentioned the following in the forum post [Switch Types](#).

- If a whole hairpin in the unbound state is involved in the switching area, it is a bad idea of boosting the end loop too effective. Making it less negative however, can help the switch on the way. It has to break so it can get moving.

Since there is a small hairpin involved in the switching area I was thinking about what would be the best closing base pair for the hairpin loop, if I made it a GC.

My first thought was to use the opposite pattern to what I think is really the most effective (if not overused) for stabilizing a hairpin loop. (Besides the G boost) As to not make it too stable, so it can break for a switch.

My favorite

My second favorite



Also notice that there is a lower energy in the loop to the left.

I did a query in the LabDataMiner. I kicked classic eterna results out as I knew that all A's tetraloops were favored way too much in that dataset.

Favorite

substructure:
 filterBy:
 groupBy:
 rankBy:
 lab ids:
 min score:
 max score:
 min count:
 subsequence:
 omit sequences:
 omit structs:
 require structs:
 mode: ☒ summary ☐ base ☐ RedGreen ☐ CBNF ☐ CBTF ☐ CFNB ☐ CFTB ☐ json ☐ csv
 flags: ☐ just labs ☐ group by lab id (nid) ☐ full SHAPE data
 lab type: ☐ Early Lab ☒ Cloud Lab

cluster	count	score	rank	
(ALL)	106	96.12	87.18	details
CG	106	96.12	87.18	details

Second favorite

substructure:

filterBy:

groupBy:

rankBy:

lab ids:

min score:

max score:

min count:

subsequence:

omit sequences:

omit structs:

require structs:

mode:
☒ summary
 ☐ base
 ☐ RedGreen
 ☐ CBNF
 ☐ CBTF
 ☐ CFNB
 ☐ CFTB
 ☐ json
 ☐ csv

flags:
☐ just labs
 ☐ group by lab id (nid)
 ☐ full SHAPE data

lab type:
☐ Early Lab
 ☒ Cloud Lab

(ALL)	136	95.89	85.51	details
GC	136	95.89	85.51	details

My favorite pattern did best

Then I decided to look up the past switch lab, which I knew had a breaking hairpin.

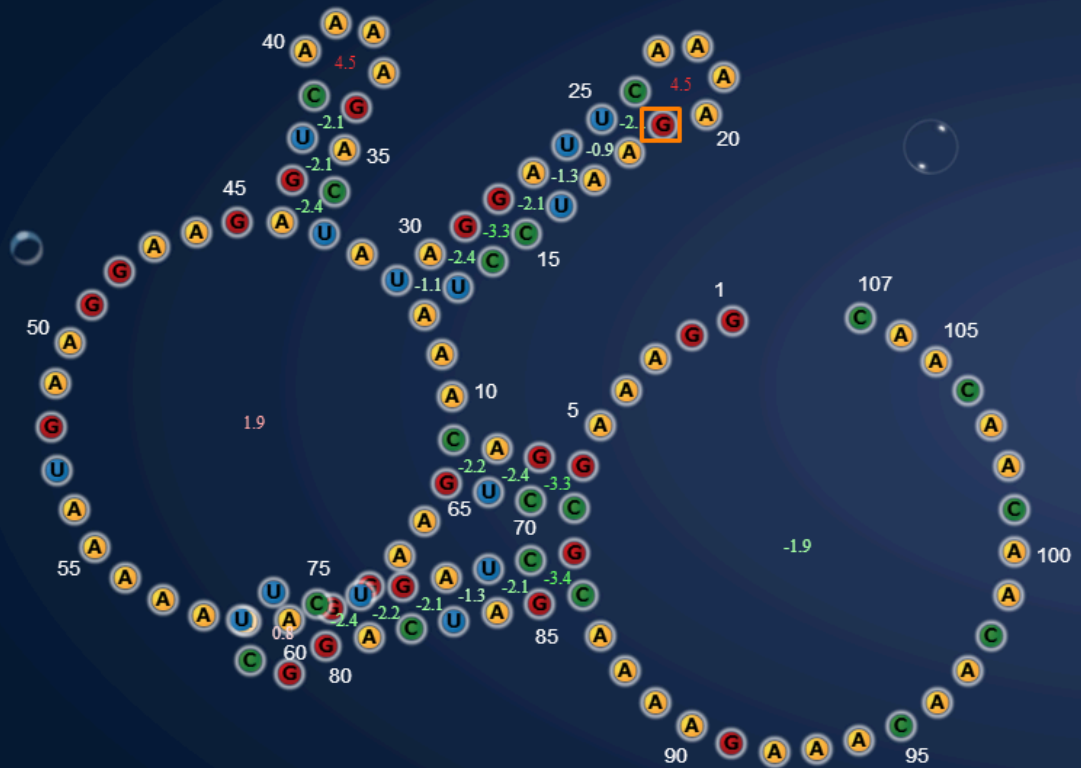


And interestingly enough the switch designs which score highest seems in favor of the slightly less stable closing.



Bround - Hair Trigger - Sub 2 (Stable)
Synthesis score : 95 / 100
(state 1 : 92 / 100, state 2 : 89 / 100)

Total:
-31.4 kcal



Highest scoring designs have a higher prevalence of G's of this closing base spot and the reverse pattern get more prevalent for the lower scoring designs. And that is despite that most haven't even boosted the tetraloop.

Hair Trigger by space_miser				Me	Roadmap
Title	Synthesis score ▾		Sequence		
search	min	max	search		
Brouard - Hair T...	95 / 100		GGAAAAGACAAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Hair Trigger #1	87 / 100		GGAAAAGAUCAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Eronon	77 / 100		GGAAAAGACAAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Sudden Death	75 / 100		GGAAAAGCCCGAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
JR space sw d1	74 / 100		GGAAAAGUACAAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Where Trigger? mod	73 / 100		GGAAAAGUACAAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Hair Trigger #3	73 / 100		GGAAAAGUACAAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
JR space sw_e1	72 / 100		GGAAAAGUACAAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Brouard - Hair T...	71 / 100		GGAAAAGGACAAAUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Fiskers Hair Tr...	70 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
HairTriggerSoft1	70 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Mat - Mod of Jieux	66 / 100		GGAAAAGGACAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Hair Apparent	66 / 100		GGAAAAGGACAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Mat - Mod of Eli	66 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Trigger Finger	66 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
LiOppy's Hairly ...	63 / 100		GGAAAAGGACAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Hair Trigger #2	62 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Itchy Trigger F...	62 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Tigeonquis	61 / 100		GGAAAAGGACAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Dennis Hair Trigger	60 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Teleken	60 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Mod of Jieux's	58 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Shot in the Dark 3	58 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Brouard - Hair T...	57 / 100		GGAAAAGGACAAAUUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Best Shot	56 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Less xmas Jieux	55 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
constraints mod	54 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Mod of Jieux Tr...	54 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Cleaneest Possib...	52 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Trigger Finger +	51 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Hair Trigger by ...	50 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Where Trigger?	50 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
2nd mod of Jieux	49 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Hyphema's HT2	49 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Trigger Happy	46 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Ela Carinae	46 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
mod Mike Reynolds	45 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Shot in the Dark 2	44 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Rapunzel	44 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		
Mod of Jieux	32 / 100		GGAAAAGUCCAAAGUCCUAAAGAAACUUUAGGAUUAUCAGAAAAGUCAAAGGAAAGUAAAAAAAGAAAGUCCGCUAGUUCUUC		

20 Dec 2014

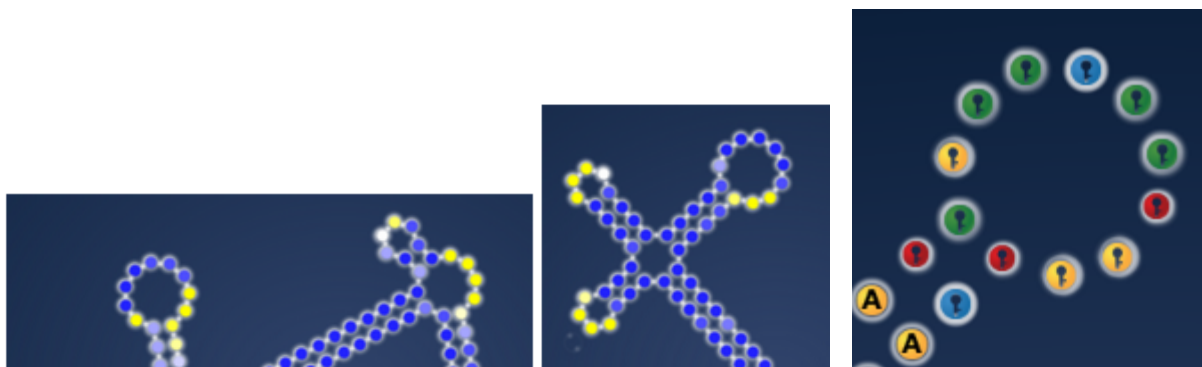
I noticed something while designing for Cody's [second round of Kissing Hairpin Loops](#).

I copy pasted the first kissing hairpin from each of Cody's labs and pasted the sequence beside the results.

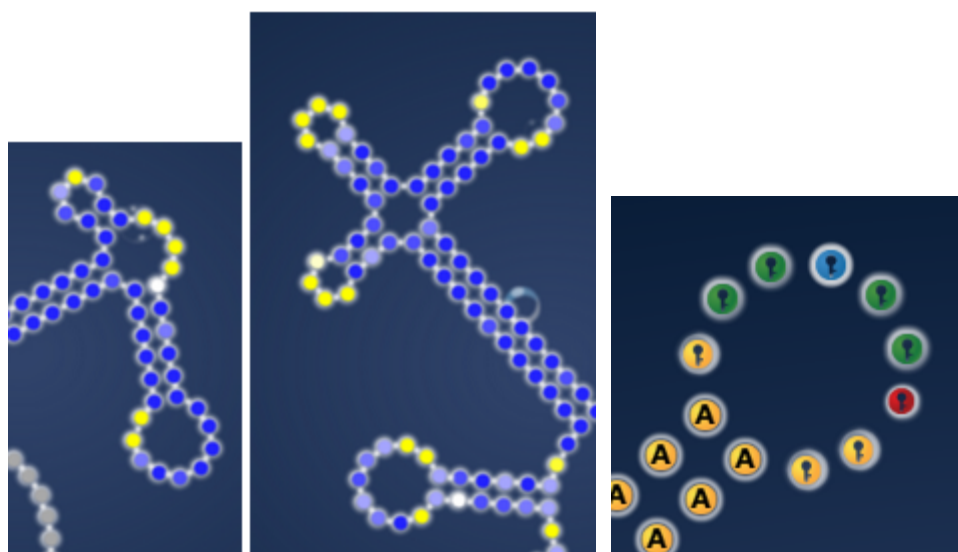
This time I sorted them after amount of C's in the first kissing hairpin loop, from highest to lowest.

From what I see to now, it seems like C's help best if placed mainly at the first kissing hairpin, whereas red helps best in the second. I wonder if the trend continues like this for kissing hairpins.

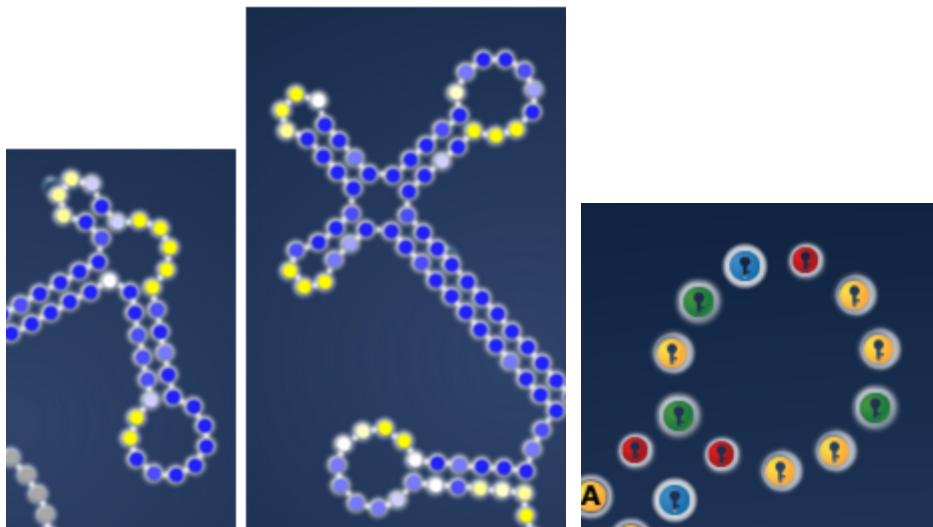
S1-KL1 / S2-KL1



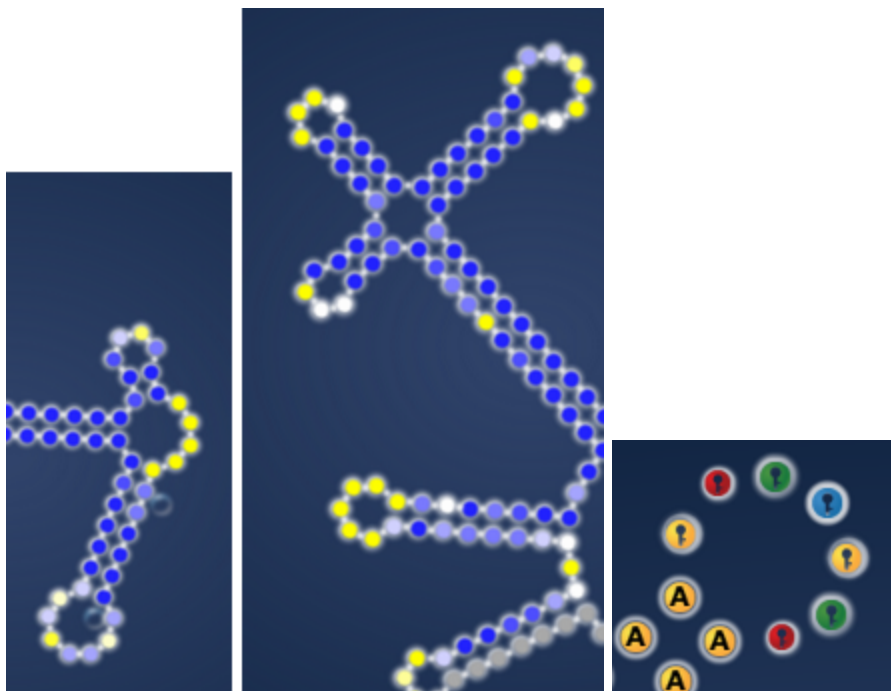
S1-KL1_noGU / S2-KL1_noGU



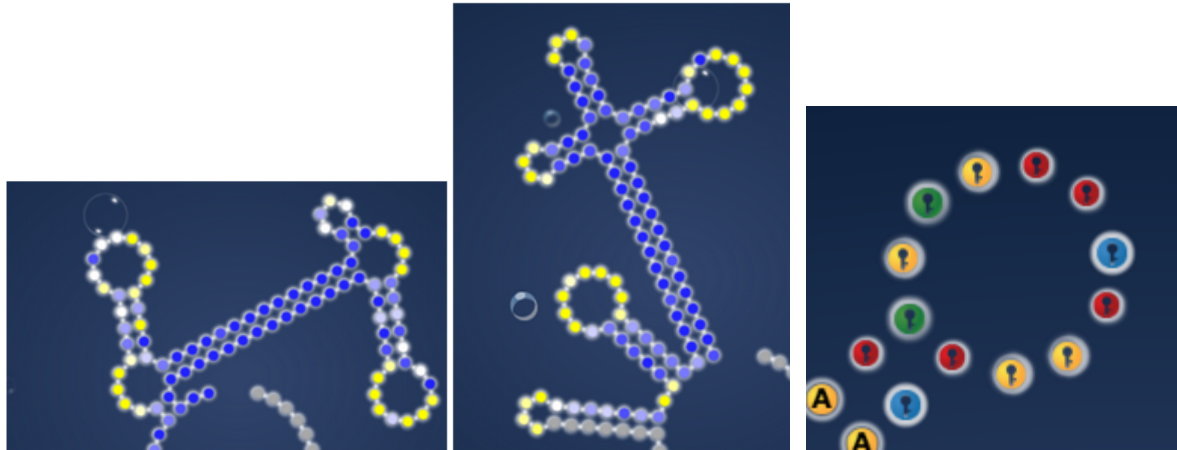
S1-KL_newA / S2-KL_newA



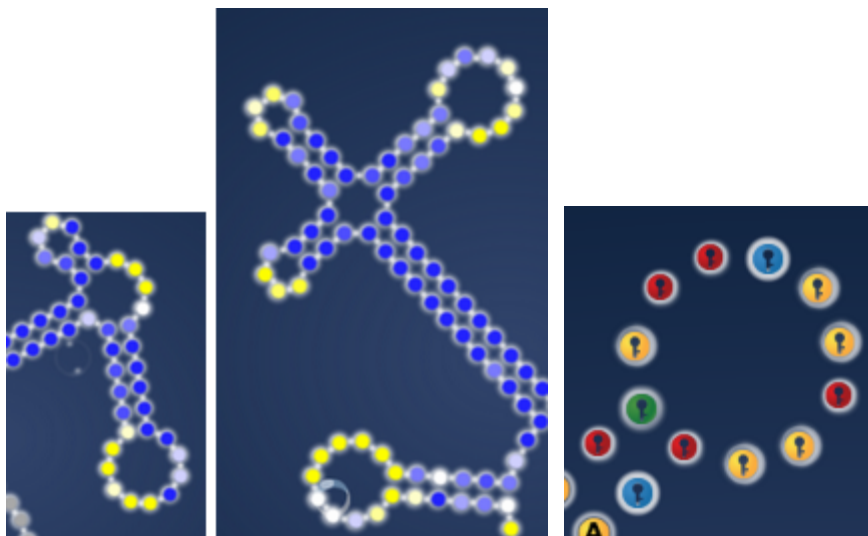
S1-KL_1S72 / S2-KL_1S72



S1-KL1_negative / S2-KL1_negative



S1-KL_newB / S2-KL_newB



This one actually did a little better than the S1-KL1_negative / S2-KL1_negative, that did not have a single C.

New b with 3 G's reds and 0 C in first hairpin loop, actually did a little better than the **negative** one with 3 G and one 1 C. I think C's at both ends of the kissing loop sequence is helping make the kiss happen, even if there are fewer strong bases like G and C in the kissing loop sequence. If a kiss could be made this way, I see it as preferable, as it would help insure that there are fewer potential complementary kissing loop sequences in the stems.

[More notes on my lab designs](#)

