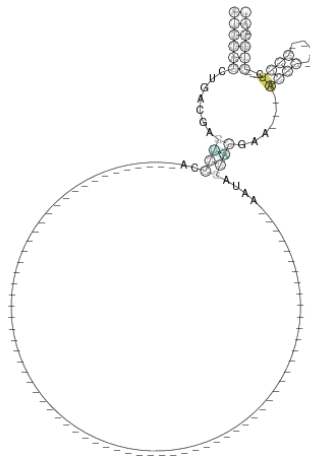


Hammerhead 1 Ribozyme

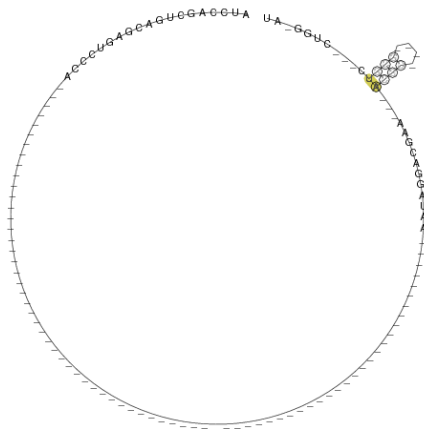
Comparison of the reference Rfam structure of the Hammerhead1 Ribozyme and predicted structures. Two of the stems can not be predicted using the original RNAalifold. Better treatment of gaps is enough to predict all stems, but only using the RIBOSUM scoring scheme predicts all base pairs correctly.

Reference structure

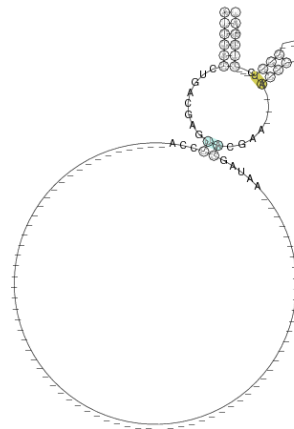
Identical to RIBOSUM structure



Structure using the original
RNAalifold



Structure when using the new gap
treatment



When looking at the structure annotated alignment, one can see that the blue hairpin loop is much too long if the old *RNAalifold* is used, and therefore will not be formed. This in turn leads to a very long, energetically highly unfavorable interior loop between the green and the red stem. Thus, the red stem can also only be correctly predicted if gaps are not used to evaluate loop energies.

The two outer blue base pairs have so many counter examples that only the RIBOSUM way of giving a small bonus to identical base pairs also leads to their inclusion into the structure.

Z69690.1/342-390	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69700.1/341-389	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69693.1/343-393	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69694.1/342-390	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69701.1/341-389	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69688.1/265-313	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69695.1/341-389	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69689.1/341-389	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69697.1/341-389	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Z69696.1/342-390	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
M19148.1/160-204	ACGAGCCAGGCGA.....	GAAGAGCCGAA..AGUUCGACUUA..	
AF036745.1/119-163	ACGAGCCAGGCGA.....	GAAGAGCCGAA..AGUUCGACUUA..	
L07513.1/84-40	ACGAGCCAGGCGA.....	GAAGAGCCGAA..AGUUCGACUUA..	
AF036398.1/98-102	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036755.1/118-162	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
X15621.1/76-34	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AY020787.1/23621-23665	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
U23117.1/1024-1031	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036743.1/118-165	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF109181.1/634-589	ACGAGAGGUCAC.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036390.1/118-165	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
X15620.1/19-62	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036741.1/118-165	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036749.1/121-167	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
X15619.1/121-168	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036394.1/118-165	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036756.1/118-162	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036393.1/119-166	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036396.1/121-168	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036397.1/119-166	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
X15621.1/101-144	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF213693.1/184-228	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036389.1/120-167	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
DB7492.1/743-788	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036746.1/113-157	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
DB7492.1/2147-2192	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036750.1/119-165	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036748.1/120-164	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
L07513.1/246-290	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036740.1/117-159	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036752.1/118-162	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036395.1/119-163	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036747.1/117-160	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036392.1/121-168	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
DB7493.1/3564-3609	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036751.1/118-163	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF213692.1/353-397	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036391.1/121-168	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
DB7492.1/1478-1524	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036754.1/91-138	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036404.1/122-166	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036401.1/123-167	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036400.1/123-167	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF036402.1/123-167	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040091.1/70-187	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040093.1/70-186	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF229821.1/380-64	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040071.1/70-162	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
X52044.1/178-64	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040031.1/70-184	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040029.1/178-64	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040055.1/70-187	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040068.1/70-185	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040052.1/70-187	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040062.1/178-64	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040061.1/70-185	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040040.1/70-186	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
X52041.1/178-64	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040051.1/70-186	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040061.1/176-63	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040041.1/70-183	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
974687.1/181-64	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040054.1/70-188	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040067.1/70-184	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
AF040046.1/177-64	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	
Consensus structure	CGAAGAGGUCAG.....	GGAGAGCCGAA..AGUUCGACUUA..	