CMV - Supplement and User Guide

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Table of Contents

CN	/IV - 3	Supplement and User Guide	1
	Flore	ian Eggenhofer, Ivo L. Hofacker, Rolf Backofen, Christian Höner zu	Siederdissen
Α	Intro	oduction	3
В	Insta	llation	3
	B.1	Source availability	3
	B.2	Usage via biocontainer - macOS	4
	B.3	Installation via bioconda - <i>Linux</i>	4
	B.4	Installation via cabal-install	4
	B.5	Precompiled Executables	4
\mathbf{C}	HMN	M-Tools	4
	C.1	Program flowcharts	5
	C.2	Input	5
	C.3	Commandline usage	8
	C.4	Output	8
		HMMV output	8
		HMMCV output	8
	C.5	Examples	9
D	CM-	Tools	9
	D.1	Program flowcharts	10
	D.2	Input	10
	D.3	Commandline usage	12
	D.4	Output	12
		CMV output	12
		Secondary structure visualisation	12
		CMCV output	13
		Secondary structure visualisation	13
	D.5	Examples	13
	D.6	Benchmark	13
Е	Auxi	iliary tools	16
	E.1	CMCtoHMMC	16
	E.2	HMMCtoCMC	16

3

A Introduction

CMV offers tools for the visualisation of RNA family models, also known as covariance models (CM) and Hidden Markov Models (HMM). Moreover, comparisons between models, the multiple sequence alignments they were constructed from and, in the case of RNA families, the consensus secondary structure can be visualised. The aim is to simplify model construction and evaluation by providing visualisations with different levels of detail. Minimal and simple detail representations give a overview over the size of the model by showing all nodes and in case of covariance models depict the guide tree, meaning nestedness of the secondary structure elements, of the model. Detailed views show nodes, states, emission as well as transition probabilities. Comparison results are highlighted by color labels which are consistently applied to model, alignment and secondary structure visualisation, allowing to inspect found similarities between models in their context. The tools can be applied to already existing HMMs (in HMMER [1] format) and CMs (in Infernal [2,3] format) from the Pfam [4,5] and Rfam database [6], as well as newly constructed models from RNAlien [7]. Comparisons between covariance models can be computed via CMCompare [8] and its webservice [9]. The first section describes installation and how to obtain the source code, see also the Tool subpage of the webservice. The second part of the guide explains the application of the tools for hidden markov models HMMV (Hidden markov model visualisation tool) and their comparisons HMMCV (Hidden markov model comparison visualisation tool) on the command line, as well as on the web service. The third part addresses the usage of the tools for covariance models CMV (Covariance model visualisation) and their comparisons CMCV (Covariance model comparison visualisation). For each of these for tools an example is depicted in this guide, which is also available as single click-example submission on the webservice, complete with input files. The fourth part introduces the two auxiliary tools, CMCtoHMMC mapping CMCompare output on HMMs and HMMCtoCMC mapping HMMCompare output on CMs. This document is included with the tool as manual.pdf and as a variant serves as Help section of the webservice.

B Installation

The visualisation tools are available as a commandline tool and as a webservice. For *Linux* we recommend installation via bioconda, for *macOS* usage of the docker container. The example input files used in the webservice (EGF, Piwi, Hammerhead Clan, tRNA Clan) can be retrieved here: Example input

B.1 Source availability

The source code is open source and available via GitHub and Hackage both licenced with GPL-3.

B.2 Usage via biocontainer - macOS

CMV can be retrieved and used as docker container with all dependencies via docker. Once you have docker installed simply type: docker run -i -t quay.io/biocontainers/cmv:1.0.7-0 /bin/bash

B.3 Installation via bioconda - Linux

The package can be installed via conda. Once you have conda installed simply type: conda install -c bioconda -c conda-forge cmv

B.4 Installation via cabal-install

The package is implemented in Haskell and can be installed via the Haskell package distribution system cabal. Once you have cabal installed simply type: $cabal \ install \ CMV$

B.5 Precompiled Executables

Linux x86_64: HMMV Linux x86_64: HMMCV Linux x86_64: CMV Linux x86_64: CMCV

Auxiliary tools: Linux x86_64: CMCtoHMMC Linux x86_64: HMMCtoCMC

C HMM-Tools

Hidden Markov models are used to represent the sequence information of biopolymers. Nodes of the model represent columns of a multiple sequence alignment. The guide first describes the program flow and then the required input and parameters for the commandline and webserver instances of both tools. A visualisation for the EGF-protein Pfam [4,5] family and a comparison visualisation for the hammerhead-RNA Rfam clan [6] with corresponding command line calls are used as output examples. Detailed model view has been inspired by visualisation provided by SAM (drawmodel) [10].



Fig. 1. Detailed flowchart representation of HMMV, showing options on the left, processing in the center and output on the right.

C.1 Program flowcharts

Flowchart representation of HMMV (see Figure 1) showing the possible options for the commandline tool and the processing of input models via HMMDraw. Optional input alignments trigger the output of alignment visualisation via StockholmDraw. Both modules are based on the diagrams library and a cairo backend. Flowchart representation of HMMCV (see Figure 2) showing possible options for the commandline tool and the processing of input models and input comparisons via HMMDraw. Linked nodes are highlighted in both alignment and model visualisation. Both modules are based on the diagrams library and a cairo backend.

C.2 Input

Example inputs can be found in the Help section of the webservice and on the webserver submission (HMMV, HMMCV) pages for each tool.



Fig. 2. Flowchart representation of HMMCV, showing options on the left, processing in the center and output on the right.

HMMM (-m) Input models are supported in HMMER3 [11] (see HMMER User-guide) format, as used by Pfam [4,5] and as part of Rfam [12] Infernal [2] models. Multiple input models can be provided by concatenating them in one file, see *hammerhead-RNA* family clan sample file. The webservice accepts a file upload, the commandline tool a absolute filepath.

Alignment (-s) Optionally the multiple sequence alignment used to construct the input model can be provided in Stockholm format, e.g. *EGF* alignment. For multiple input models the same number of alignments must be provided. The alignments must be concatenated into one file, in the same order as the models (e.g. *hammerhead-RNA*). Provide a file upload for the webservice or a absolute filepath for the commandline tool.

6

CMV - User Guide and Supplement 7

Comparison (-r) HMMCV requires a comparison file, detailing the relationship between the input models. The commandline tool requires an absolute filepath. This format is derived from the CMCompare output format and contains on each line following white space separated fields: model1Name model2Name linkscore1 linkscore2 linksequence model1matchednodes model2matchednodes

Here is a example line from a hammerhead clan comparison, the whole file can be found here: hammerheadClan-comparison.

Hammerhead_1 Hammerhead_3 6.168 5.244 GUCCCAGUAAUAGGAC [17,18,19,20,21,22,23,23,24,25,26,27,28] [36,37,38,39,40,41,42,43,44,45,46,47,48]

Detail level (-d) Three detail level for each node are available:

- minimal showing the node number.
- simple showing emission probabilites
- detailed showing emission and transition probabilities

Emission layout (-e) Controls display of emission probabilities for detail levels simple and detailed. The selected variant is shown next to the emitted symbol.

- box fill state of a box
- score bit score, as a floating pint number
- probability as a floating point number

Output format (-f) Available output formats are pdf, png, svg and ps. The webservice always generates svg by default for rendering of the preview.

Max. number of alignment entries (-n) This controls how many entries are displayed for optionally uploaded alignments.

Image size scaling factor (-c) Scales the result image by set factor. Please consider that resulting .svg output can be easily rescaled.

Transition probability cutoff (-t) Minimum necessary cutoff for a transition probability to be displayed.

Output directory path (only cmdline, -o) Absolute path to output directory

Help (only cmdline, -help) Prints help with all default options and commandline parameters

C.3 Commandline usage

HMMV visualisation for the Piwi protein family, as used for the webservice, can be obtained with the following commandline call: HMMV -d detailed -m Piwi.hmm -s /home/user/PF02171_seed.txt

HMMCV comparison visualisation for the hammer head-RNA clan can be computed like this:

HMMCV -d detailed -m /home/user/hammerhead.hmm -s /home/user/hammerhead.stockholm.txt -r /home/user/hammerhead.hmmc -f pdf

C.4 Output

HMMV **output** For each input model a outputfile in the requested format is generated. Als filename the modelname encoded in the file is used and as file extension the request output format (.png,.svg,.ps,.pdf). If stockholm alignments have been provided, then for each model a alignment visualisation with index colums is created. The alignment file name is the model name, followed by ".aln" and then the requested file format extension. The webservice gzips all results and provides a download link. Following are minimal (see Figure 3), simple (see Figure 4) and detailed (see Figure 5 6) visualisations for the *EGF* protein Pfam family. The results for this and the other models can be viewed by clicking the sample button of the HMMV webservice. The webservice also creates a zoom- and panable preview, that can be expanded by clicking.

, showing nodes with their index and emission probabilities.

HMMCV output While also providing visualisation output for each model and corresponding alignment, HMMCV additionally annotates regions found to be linked by model comparison via color tags. Each provided model is associated with a color that is depicted in the legend table. The nodes of each model visualisation are then tagged with the color of the linked model. The coloring is also applied to the running index of the alignment visualisation. This allows to study in detail which parts of models are connected, or shared in e.g. clans and which not. The file naming scheme is similar to HMMV. The following example comparison was computed for the whole Hammerhead clan from Rfam, pairwisely comparing Hammerhead_HH9, Hammerhead_3, Hammerhead_1, Hammerhead_II and Hammerhead_HH10 with the CMCompare webserver. The comparison results from the covariance models were mapped on the prefilter HMMs supplied with each covariance model with the included auxiliary CMCtoHMMC tool. The result for the Hammerhead_HH9 RNA with the linked regions of the other models is shown in minimal (see Figure 8), simple (see Figures 9, 10) and detailed (see Figures 11, 12, 13) visualisations and in the alignment visualisation (see Figure 14). The results for this and the other models can be viewed by clicking the sample button of the HMMCV webservice.



Fig. 3. Minimal detail *EGF* Pfam family visualisation, just showing model nodes with their index.

C.5 Examples

Additional examples for the first 1600 models from **Pfam** in 3 detail labels can be found here: Link.

D CM-Tools

Covariance, also called RNA family, models are used to represent the sequence and structure information of RNA molecules. The guide first describes the program flow and then the required input and parameters for the commandline and webserver instances of both tools. Parameters that only work for the command line tool and not on the webserver are annotated with "cmdline-only". This guide uses the tRNA family for a demonstration of CMV (Covariance model visualisation) in minimal the hammerhead-RNA clan for demonstration of CMCV (Covariance model comparison visualisation) also in three levels of detail. Layout of the detailed output has been inspired by depections used in the Infernal user guide and the book 'Biological sequence analysis' [13]. For both tools a webserver corresponding command line calls are use

D.1 Program flowcharts

The flowchart representation of CMV (see Figure 15) shows that the tool accepts multiple covariance models and optionally the corresponding Stockholm alignments as input. After parsing and validating the input, for each provided model a visualisation output is created via the CMDraw module, which is based on the diagrams library and a cairo backend. The optional input alignments are used for creating a visualisation of the input alignment via StockholmDraw module.

Flowchart representation of CMCV (see Figure 16) showing possible options for the commandline tool and the processing of input models and input comparisons via CMDraw. Optional input alignments trigger the output of alignment visualisation via StockholmDraw. Linked nodes are highlighted in both alignment and model visualisation. Both modules are based on the diagrams library and a cairo backend.

D.2 Input

Example inputs can be found in the Help section of the webservice and on the webserver submission (CMV, CMCV) pages for each tool.

CM (-m) Input models are supported in Infernal (see Infernal User-guide) format, as used by Rfam or constructed by RNAlien [7] or the RNA workbench [14,15]. Here is the tRNA family as example. Multiple input models can be provided by concatenating them in one file, see hammerhead-RNA family clan sample file. The webservice accepts a file upload, the commandline tool a absolute filepath.

Alignment (-s) Optionally the multiple sequence alignment used to construct the input model can be provided in Stockholm format, e.g. tRNA alignment. For multiple input models the same number of alignments must be provided. The alignments must be concatenated into one file, in the same order as the models (e.g. hammerhead-RNA). Provide a file upload for the webservice or a absolute filepath for the commandline tool.

Comparison (-r) CMCV requires a comparison file, detailing the relationship between the input models. The commandline tool requires an absolute filepath. The used CMCompare output format contains on each line following white space separated fields:

model1Name model2Name linkscore1 linkscore2 linksequence model1matchednodes model2matchednodes Here is a example line from a hammerhead clan comparison, the whole file can be found here: hammerheadClan-comparison.

Hammerhead_1 Hammerhead_3 6.168 5.244 GUCCCAGUAAUAGGAC ((((...,...)))) (((((.....)))) [17,18,19,20,21,22,23,23,24,25,26,27,28] [36,37,38,39,40,41,42,43,44,45,46,47,48] The CMCompare Webserver [9] offers cmcv.result files that can be directly used as input for (-r) Link. **Detail level** (-d) Three detail level for each node are available:

- minimal showing the node number.
- simple showing node number and node type
- detailed showing node number, type, emission and transition probabilities

Emission layout (-e) Controls display of emission probabilities for detail levels simple and detailed. The selected variant is shown next to the emitted symbol.

- box fill state of a box
- score bit score, as a floating point number
- probability as a floating point number

Model layout (-l)

- tree model is branched at each bifurcation according to guide tree
- flat nodes are all arranged on a line

Secondary structure visualisation tool (only commandline, -x) CMV and CMCV can create input files for the secondary structure visualisation tools forma [16] and R2R [17]. This input file containes the consenus secondary structure of the input alignment. Moreover CMCV labels nucleotides that are annotated to be similar with compared models in the input files and in case of R2R color encodes them according to the color scheme used for the model comparison visualisation. In case of the webservice both visualisations are triggered on providing a input alignment.

- forna for each model a input structure file and a color scheme is generated for upload to forna
- R2R for each model a input file for R2R is generated

Output format (-f) Available output formats are pdf, png, svg and ps. The webservice always generates svg by default for rendering of the preview.

Max. number of alignment entries (-n) This controls how many entries are displayed for optionally uploaded alignments.

Image size scaling factor (-c) Scales the result image by set factor. Please consider that resulting .svg output can be easily rescaled.

Transition probability cutoff (-t) Minimum necessary cutoff for a transition probability to be displayed.

Output directory path (only cmdline, -o) Absolute path to output directory

Help (only cmdline, -help) Prints help with all default options and commandline parameters

D.3 Commandline usage

 $\tt CMCV$ comparison visualisation for the hammerhead RNA clan can be computed like this:

CMCV -d simple -m /home/user/hammerheadClan.cm -s /home/user/hammerheadClan.sto -r /home/user/hammerheadClan.cmcompare -f pdf -l tree

D.4 Output

CMV output For each input model a outputfile in the requested format is generated. Also filename the modelname encoded in the file is used and as file extension the request output format (.png,.svg,.ps,.pdf). If stockholm alignments have been provided, then for each model a alignment visualisation with index colums is created. The alignment file name is the model name, followed by ".aln" and then the requested file format extension. The webservice compresses all results and provides a download link. Extensive information about the node types (with abbreviations MATP, MATL, MATR, BIF, ROOT, BEGL, BEGR, END) and state types (with abbreviations P, L, T, B, D, S, E) used by covariance models can be found in the **Infernal** user guide, specifically pages 52 and 53. The webservice also creates a zoom- and panable preview, that can be expanded by clicking. Following is the minimal (see Figure 17), simple (see Figure 18) and detailed (see Figures 19, 20, 21, 22, 23, 24, 28) *tRNA* **Rfam** family model visualisation. For the corresponding alignment visualisation see Figure 26.

Secondary structure visualisation Table provides the consensus secondary structure visualisation of the structural alignment for each model by R2R as well as forna.

CMCV output CMCV also provides visualisation output for each model and corresponding alignment. The naming scheme is similar to CMV. However it annotates regions found to be linked by model comparison via color tags. Each provided model is associated with a color that is depicted in the legend table. The nodes of each model visualisation are then tagged with the color of the linked model. The coloring is also applied to the running index of the alignment visualisation. This allows to study in detail which parts of models are connected, or shared in e.g. clans and which not. Extensive information about the node types (with abbreviations MATP, MATL, MATR, BIF, ROOT, BEGL, BEGR, END) and state types (with abbreviations P, L, T, B, D, S, E) used by covariance models can be found in the Infernal user guide, specifically pages 52 and 53. The following example shows the result for the *Hammerhead_HH9 RNA* CMCV output as minimal (see Figure 29), simple (see Figures 30, 31) and detailed (see Figures 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42) visualisation. The alignment is shown in Figure 43.

The webservice also creates a zoom- and panable preview, that can be expanded by clicking.

Secondary structure visualisation Moreover linked nodes are also annotated in the consensus secondary structure of the provided models, if a stockholm alignment with consensus structure has been provided. This allows to identify specific secondary structure elements that are linked between families. This is done for pairs of models with R2R as well as forna.

D.5 Examples

Additional examples for all models from Rfam in three detail labels can be found here: Link. Examples for comparisons of Rfam clans can be found here: Link.

D.6 Benchmark

Runtime and memory consumption for the first 100 Rfam families are shown in Table 1 and were computed on a Intel(R) Xeon(R) CPU E5-2630 v4 @ 2.20GHz cpu with a single thread.

Rfam family name	Elapsed real time [seconds]	Maximum resident set size
		[kbytes]
5S_rRNA	12.79	715140
5_8S_rRNA	13.36	784956
U1	16.41	867316
U2	17.77	1071648
tRNA	06.61	444100
Vault	08.85	550828

U12	15.04	850800
Hammerhead_3	06.40	389308
RNaseP_nuc	24.38	1391292
RNaseP_bact_a	39.83	1953500
RNaseP_bact_b	34.91	1963264
U3	23.86	1220600
6S	19.19	1063516
DsrA	09.75	558360
U4	12.97	765668
SNORD14	09.33	565648
Metazoa_SRP	31.33	1810600
CsrB	29.43	1770356
Y_RNA	10.02	555420
U5	12.99	698060
Spot_42	10.88	729424
GcvB	18.18	1115148
tmRNA	34.49	1799168
Telomerase-vert	42.88	2172452
Telomerase-cil	16.64	895780
U6	06.99	527964
let-7	08.84	555552
Intron_gpI	24.16	1257588
Intron_gpII	08.05	539248
RNase_MRP	23.07	1353624
SECIS_1	05.71	409756
Histone3	03.95	302612
MicF	08.60	543284
RprA	10.39	574844
OxyS	12.28	683444
RRE	35.82	1939584
IRE_I	03.95	302136
PrfA	12.39	702136
DicF	05.22	363060
rne5	30.26	1812964
Entero_OriR	09.44	717796
CopA	08.12	561304
Plasmid_R1162	06.33	513064
Phage_pRNA	20.36	1241372
SNORA73	19.07	1180256
snoR30	07.31	513408
mir-2	06.97	443128
Entero_CRE	06.05	385656
SNORD36	06.58	399556
FMN	10.97	744152
mir-17	08.44	536708
lin-4	06.78	443840
mir-7	08.95	557020

SNOPD25	06.24	493344
SNORD25	05.24	425544
SNORD30	12.44	410272
DruhD	05.67	405002
LucaE	17.56	405092
TDD	00.58	502776
IFF UmF	19.38	095770
IDEC HOV	12.04	(14410
ILES_ICV	24.20	13/62/0
HgcC	11.01	138/10
SSCA	08.23	545260
HgcG	25.36	1362644
snoR9	12.48	706812
U7	06.34	386840
SNORD15	10.51	607972
SNORD21	06.94	452528
SNORD24	06.20	397048
SNORD29	05.18	366832
SNORD73	05.72	389652
SNORA75	11.00	747536
mir-156	08.46	541540
mir-29	06.40	440452
mir-166	11.40	690084
mir-181	07.29	520416
SraB	14.83	880924
MicA	06.16	434544
OmrA-B	08.18	538008
yybP-ykoY	13.90	816788
ArcZ	10.06	566836
SraG	16.49	872468
GlmZ_SraJ	19.11	1173580
CsrC	22.38	1325628
SNORD28	05.76	397704
SNORD27	05.78	384396
SNORD26	06.35	397440
SNORD30	05.43	395044
SNORD31	05.16	374096
SNORA74	20.63	1195224
SNORA62	12.20	798120
SNORA63	10.27	723496
SNORD18	05.42	390436
HDV_ribozvme	07.85	551132
snoPyro CD	04.42	315896
U8	10.19	728664
snoB71	09.31	539732
SNORD22	09.48	570696
7SK	30.55	1778300
SraC ByeA	12.30	768748
~~~~ <u>~</u>	1-2.00	100110

Table 1: Benchmark table showing the runtimes and memory consumption for computing a detailed covariance model visualisation with CMV on a Intel(R) Xeon(R) CPU E5-2630 v4 @ 2.20GHz cpu with a single thread.

#### E Auxiliary tools

We created two auxiliary tools to simplify the handling of comparison results.

#### E.1 CMCtoHMMC

CMCompare results contain the node intervals of linked models. Since both the Infernal covariance models and the HMMER hidden markov models have the alignment columns the were derived from annotated, it is possible to map these intervals from a CM to a HMM of the same family. This tool was used to create the HMMCompare files used for the HMMCV. Here is a example call:

CMCtoHMMC -c /home/user/models.cm -h /home/user/models.hmm -r /home/user/model.cmcwsresult

#### E.2 HMMCtoCMC

HMMCompare results contain the node intervals of linked models. Since both the Infernal covariance models and the HMMER hidden markov models have the alignment columns the were derived from annotated, it is possible to map these intervals from a HMM to a CM of the same family. Here is a example call:

HMMCtoCMC -c /home/user/models.cm -h /home/user/models.hmm -r /home/user/model.cmcwsresult

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EGF



Fig. 4. Simple detail EGF Pfam family visualisation, showing nodes with their index and emission probabilities.

19



Fig. 5. Detailed EGF Pfam family visualisation, showing nodes with insertion, deletion and match states and emission and transition probabilities. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part¹

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CMV - User Guide and Supplement 21

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Fig. 6. Detailed EGF Pfam family visualisation, showing nodes with insertion, deletion and match states and emission and transition probabilities. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 2

	1 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2 3 4 5 6 7 8 9 0 1 2
BM86 RHIMP/209-245	CKTKEAGFVCKHGCRSTGKAYECTCP.SGSTVAEDGIT
AGRIN CHICK/1351-1381	CDS HP CLHGGT C EDDG REFTCRCP. AG KGGAV
- A 4 V 3 4 6 DROME / 2 6 0 - 2 8 7	CVL EPN. CI HGT C
PROS BOVI N/ 121-153	CNP LP CNEDGFMTC KDGQ ATFTCICK. SG WQGEK
CRB DROME / 1209 - 1239	CKP NP CHSNGE C TDL W HTFACHCP. RP FFGHT
CRB DROME / 1483 - 1513	CRK. NP. CLHNAE. C. RNTW NDYTCKCP. NG YKGKN
SLIT DROME / 1052 - 1084	CSPEFNP. CANGAK. C. MDHF THYSCDCO. AG FHGTN
O01768_CAEEL/4584-4614	CDD YCTNNSK C TI TNG THFECDCK. PG FKGLR
CRB_DROME / 982 - 1017	CDQ NP CLNGGA C LPYLI NEVTHLYNCTCE. NG FQGDK
	CSP NP CYNDAK CLVTLDTORGDI FTEYI COCP. VG YSGI H
	CAS. NR. CKNEAK. C. TPSS. NFLDFSCTCK. LG YTGRY
NOT C 1 _ X E NL A/ 6 2 - 9 7	CTI K. NQ CMNFGT C EPVLQGNAI DFI CHCP. VG FTDKV
URT2 DESRO/ 87 - 119	CSE LR CFNGGT C WQAA SFSDFVCOCP. KG YTGKO
	CNS MR CONGGT COVTFRNG RPGI SCKCP. LG FDESL
CRB_DROME / 547-577	CNA TNGKCLNGGT C SMNGTHCYCA. VG YSGDR
NOTC1_XENLA/260-290	CPSNNCRNGGTCVDGVNTYNCQCP.PDWTGQY
CRB DROME / 390 - 421	CAS OP CONNGS C I DRI NGFSCDCSGTG YTGAF
PROC BOVI N/ 98 - 127	CD LP CCGRGK C I DGL GGFRCDCA. EG WEGRF
LYAM1 HUMAN/160-190	C OP WS CS GHGE C VEI I NNYTCNCD. VG YY GP O
NOTC1 XENLA/ 1270-1302	~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~ ~
NOTC1 XENLA/ 22-55	CTO TAE MCLNGGR C EMTP GGTGVCLCG. NL YFGER
O01768 CAEEL/4544-4577	~ COK OPNWCHNGGR C LDTP GYPGKCKCL. PR FAGPR
CRB DROME / 308 - 339	CAK NP CENGGS C LENS RGDYQCFCD. PN HSGQH
CRB_DROME / 1993 - 2025	CNM EGDYCGGLGR C FNKP GSFQCI CQ. KP YCGAY
L T B P 1 _ HUMAN/ 8 7 7 - 9 0 8	CTV NPDI C. GAGH C I NLP VRYTCI CY. EG YRFSE
L T B P 1 _ HUMAN/ 1 6 2 5 - 1 6 5 5	CGI L. NG CE. NGR C VRVQ EGYTCDCF. DG YHLDT
M9 NE 6 7 _ DR OME / 4 1 3 - 4 4 5	CTS NP CHADAI C DTSP I NGSYACSCA. TG YKGVD
C R B _ D R O M E / 2 6 9 - 2 9 9	CLN DP CMGHGT C SSSP EGYECRCT. AR YSGKN
F B P 2 _ S T R P U / 1 1 1 - 1 4 7	CLS DTSNCDGHGI C QLSTFGRNERYICFCA. LG FRNNN
C R B _ D R O M E / 1 7 6 0 - 1 7 9 0	CFQ SD CKNDGF C QSPS DEYACTCQ. PG FEGDD
T R B M_ B O VI N/ 1 4 3 - 1 7 2	CF D NN CE Y Q C QP V G R S E H K C I C A. E G F A P V P
SLIT_DROME / 935-966	CFE QP CQNQAQ C VALP QREYQCLCQ. PG YHGKH
C R B _ D R O ME / 2 0 3 2 - 2 0 6 6	CNA TD. LCSNGGR C VESC GAKPDYYCECP. EG FAGKN
TSP1_HUMAN/650-686	CTD GTHDCNKNAK C NYL GHYS DP MYRCECK. PG YAGNG
NI D1 _ HUMAN/ 672 - 705	CYIGTHGCDTNAACRPGPRTQFTCECS.IGFRGDG
NI D1 _ HUMAN/ 3 9 0 - 4 2 2	CAN NR HQCS VHAE C RDYA TGF CCS CV. AG YTGNG
EGF_HUMAN/ 835-865	CAP VG CS MYAR C I SEG EDATCQCL. KG FAGDG
O 0 1 7 6 8 _ C A E E L / 4 6 2 1 - 4 6 5 0	CSE CSNEAKCIKKPSGTVICQCP.QGLGGEY
AGRI N_CHI CK/ 1607 - 1638	CDP TP CHISAT C LVLP EGGAMCACP. MG REGEF
EGF_HUMAN/318-353	CKLRKGNCSSTVCGQDLQSHLCMCA.EGYALSRDRKY
EGF_HUMAN/401-435	CPR NVSECSHD C VLTS EGPLCFCP. EGSVLERDGKT
L R P 5 _ MOUS E / 2 9 8 - 3 3 4	CEE DNGGCSHL C LLSP REPFYSCACP. TGVQLQDNGKT
LRP5_MOUSE/1216-1247	CAR DNGGCSHI C I AKG DGTPRCSCP. VH LVLLQ
L R P 5 _ MOUS E / 6 0 4 - 6 3 8	CAD GNGGCSHL C FFTP RATKCGCP. I GLELLSDMKT
A0 A0 2 4 R7 D5 _ HUMAN/ 3 1 8 - 3 5 1	CLD NNGGCSHV C NDLK I GYECLCP. DGFQL. VAQRR
O 0 1 7 6 8 _ C A E E L / 3 1 2 2 - 3 1 5 5	CPK AN CSHF C I DRR DVGHQCFCA. PGYILSENQKD
F B P 2 _ S T R P U / 2 5 6 - 2 8 8	CSQ GTNDCNENGE C VEED GKYWCECG. EG YEENE
FBP2_STRPU/52-89	CES DTNKCNNHGT C I EGR WGTYYCKCE. MPFRVGI PDSS
L T B P 1 _ R A T / 1 4 6 2 - 1 4 9 6	CQ DPNSCIDGQ C VNTE GSYNCFCT. HPMVLDASEKR
C R B _ D R O ME / 1 9 1 6 - 1 9 4 6	CEI TP CDNGGL C LTTG AVP MCKCS.LG YTGRL
SS_cons	GCST. TTTSSTTT-EEEETTTTEEEEEECTTTEESTT

Fig. 7. EGF Pfam family alignment visualisation, the number of alignment entries can be set via option. The displayed column indices allow association with the corresponding nodes in the model.

Legend: Hammerhead_1 Hammerhead_3 Hammerhead_HH10 Hammerhead_II



Fig. 8. Minimal detail HMMCV visualisation of *Hammerhead_HH9* with linked nodes highlighted by color. Families corresponding to the color can be looked up in the legend.

Legend: Hammerhead_1 Hammerhead_3 Hammerhead_HH10 Hammerhead_II



**Fig. 9.** Simple detail HMMCV visualisation of *Hammerhead_HH9* family, showing nodes with their index and emission probabilities. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part 1.



**Fig. 10.** Simple detail HMMCV visualisation of *Hammerhead_HH9* family, showing nodes with their index and emission probabilities. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part 2.





**Fig. 11.** Detailed HMMCV visualisation of *Hammerhead_HH9* family visualisation, showing nodes with insertion, deletion and match states and emission and transition probabilities. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part1.



**Fig. 12.** Detailed HMMCV visualisation of *Hammerhead_HH9* family visualisation, showing nodes with insertion, deletion and match states and emission and transition probabilities. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part2.









**Fig. 13.** Detailed HMMCV visualisation of *Hammerhead_HH9* family visualisation, showing nodes with insertion, deletion and match states and emission and transition probabilities. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part3.

	111111111111111122222222222 12345678901234567890123456 <mark>7890123456<mark>789012545678901</mark>2345678901234567890123456789012345678901234567890123456789012345</mark>
ABQF01059171.1/305-384	UUGGGCCG- UUACCUACAGCUGAUGAGCUCCAAGAAGAGCGAAACCUGCU- AAGCAAGGUCCUGUAGUAUUGGCCUGAACCC
AADN03003451.1/4511-4593	CUGGGCCG- UUACCUACAGCUGAUGAGCUCCAAGAAGAGGGGAAACCUUGU- AAAAUAGGUCCUGUAGUAUUGGCCUGAUGAGCUC
AAWZ02032198.1/15823-15741	UGAGGCCG- UUACCUACAGCUGAUGAGCUCCAAAAAGAGCGAAACCUGUU- AAAAUAGGUCCUGUAGUAUUGGCCGACUGAGCCG
AGAI 0 1 0 5 5 0 1 6 . 1 / 6 3 2 8 7 - 6 3 2 0 5	UUAGGCCG- UUACCUACAGCUGAUGAGCUCCAAGAAGAGGGAAACCUUUU- AAGAUAGGUCCUGUAGUAUUGGCCUGAAAACCAU
AANN0 1 0 6 6 0 0 7 . 1 / 5 8 8 - 5 1 1	CUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GCUAGGUCCUGCAGUACUGGCUUAAGAGGCUA
AAQR03161315.1/4048-3972	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U AUUAGGUCCUGCAGUACUGGCUUAAGAGAAU-
A B R N 0 1 3 7 5 6 7 0 . 1 / 2 1 7 0 3 - 2 1 7 7 7	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U AUUAGGUCCUGCAGUACUGGCUUGAGAUA
A B R P 0 1 2 7 0 9 0 6 . 1 / 1 9 6 6 - 2 0 4 3	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U AUUAGGUCCUGCAGUACUGGCUUAAGAUAAUA
ACTA01058962.1/24761-24837	AUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCU- AUUAGGUCCUGCAGUACUGGCUUAAGAUAUA-
AAKN02030441.1/10428-10505	UUGGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U ACUAGGUCCUGCAGUACUGGCUUAAGAUAAUG
AEYP01022184.1/5895-5972	GUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U AUUAGGUCCUGCAGUACUGGCUUAAGAUGGAA
AFTD01093388.1/13316-13239	CUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GUUAGGUCCUGCAGUACUGGCUUAUGACAGUA
A A P N 0 1 2 3 1 0 7 7 . 1 / 1 5 1 9 8 - 1 5 1 2 1	UCCUGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A ACCAGGUCCUGCAGUACUGGCGAAAGGAGCUU
A A G U 0 3 0 1 8 5 3 2 . 1 / 5 7 5 7 1 - 5 7 4 9 7	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC G AAUAGGUCCUGCAGUACUGGCUUAAGACA
A A F R 0 3 0 2 7 1 9 7 . 1 / 9 9 7 4 2 - 9 9 8 1 6	UUAGGCCG-UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCAAUUAGGUCCUGCAGUACUGGCUUUAGCAU
AAQQ01544543.1/2644-2721	UAGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC 6 AUAAGGUCCUGCAGUACUGGCUUAAGACGGUA
A B R Q 0 1 0 5 6 5 3 2 . 1 / 2 0 1 9 - 2 0 9 6	CUGAGEEG- UUACEUGEAGEUGAUGAGEUCEAAAAAGAGEGAAAEE G AAEAGGUEEUGEAGUAEUGGEUUAAGAUAGUG
ADDD01012933.1/19585-19662	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A GUUAGGUCCUGCAGUACUGGCUGAAAUCUUUC
AAWR02025218.1/31065-31139	CCGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC G GUUAGGUCCUGCAGUACUGGCUUAAGAUA
AEKR01154328.1/10424-10501	UCUGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GUUGGGUCCUGCAGUACUGGCUUACCAUAGUA
AALT01643156.1/444-367	UCCAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U ACGAGGUCCUGCAGUACGGGCUUAGGGGAGCA
AFYH01089550.1/2099-2023	- CAAGCAAGUUACCUACAGCUGAUGAGGUCCAAGAAGAGGGAAACC U UAUAGGUCCUGUAGUACUGGCUUGUUACCAU-
A A I Y 0 1 4 9 8 6 9 3 . 1 / 2 0 1 4 - 1 9 3 7	CCGAGCCG-UUGCCUGCAGCUGAUGAGCUCCAACAAGAGCGAAACCGAACAGGUCCUGCAGUACGGGUGGGGUCAGCAG
AADN03002802.1/91438-91372	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A GUUAGGUCCUGCAGUACUGGCUG
AGCE01141575.1/4443-4377	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U AUUAGGUCCUGCAGUACUGGCUU
ACI V010818800.1/185-250	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAG- GCGAAACC U AUUAGGUCCUGCAGUACUGGCUU
A B Q O 0 1 0 1 2 9 8 2 2 . 1 / 1 1 8 7 - 1 2 5 3	AGGCCG- UUACCUGCAGCUGAUGAGCUCCAAUAAGAGCGAAACC A AUUAGGUCCUGCAGUACUGGCUU
A B Q F 0 1 0 2 3 9 0 0 . 1 / 7 3 4 8 - 7 4 1 4	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A GUUAGGUCCUGCAGUACUGGCUA
AAHX01036414.1/22499-22433	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GUUAGGUCCUGCAGUACUGGCUU
A G A I 0 1 0 6 1 3 0 9 . 1 / 2 4 3 9 4 - 2 4 4 6 0	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A GUUAGGUCCUGCAGUACUGGCUA
AFEY01454121.1/10166-10232	AGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A AUUAGGUCCUGCAGUACUGGCUU
AGTP01043633.1/33547-33613	··· GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC····G··AUAAGGUCCUGCAGUACUGGCUU·····
AL773539.18/161561-161627	UGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GUUGGGUCCUGCAGUACUGGCUU
SS_cons	:::(((((((,,,((((((,,,((,,((((,,,((((,,,(((,,((,,((,,((,,(),((,,((,

Fig. 14. *Hammerhead_HH9* Rfam family alignment visualisation, the number of alignment entries can be set via option. The displayed column indices allow association with the corresponding nodes in the model. The consensus secondary structure is shown in the last line.



Fig. 15. Detailed flowchart representation of CMV, showing options on the left, processing in the center and output on the right.



Fig. 16. Detailed flowchart representation of CMCV, showing options on the left, processing in the center and output on the right.

# tRNA



Fig. 17. Minimal tRNA Rfam family visualisation, showing model nodes with their index arranged according to guide tree.

# tRNA

0 ROOT					
1 MATR					
2 MATP					
3 MATP					
4 MATP					
5 MATP					
6 MATP					
7 MATP					
8 MATP					
9 MATL					
10 MATL					
11 BIF					
	1				
12 BEGL	1				
13 BIF					
42 BEGR	27	BEGR		14	BEGL
43 MATL	28	MATL		15	MATP
44 MATL	29	MATP		16	MATP
45 MATL	30	MATP		17	MATP
46 MATL	31	MATP		18	MATP
47 MATP	32	MATP		19	MATL
48 MATP	33	MATP		20	MATL
49 MATP	34	MATL		21	MATL
50 MATP	35	MATL		22	MATL
51 MATP	36	MATL		23	MATL
52 MATL	37	MATL		24	MATL
53 MATL	38	MATL		25	MATL
54 MATL	39	MATL		26	END
55 MATL	40	MATL		_	
56 MATL	41	END			
57 MATL			-		
58 MATL					
59 END					

Fig. 18. Simple tRNA Rfam family visualisation, showing model nodes, labeled with node type and index, arranged according to guide tree.



Fig. 19. Detailed tRNA Rfam family visualisation, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 1



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Fig. 20. Detailed tRNA Rfam family visualisation, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 2

x x



Fig. 21. Detailed tRNA Rfam family visualisation, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 3



Fig. 22. Detailed tRNA Rfam family visualisation, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 4

#### CMV - User Guide and Supplement

37





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LIR20

Fig. 23. Detailed tRNA Rfam family visualisation, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 5

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#### CMV - User Guide and Supplement

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Fig. 24. Detailed tRNA Rfam family visualisation, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 6

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Fig. 25. Detailed tRNA Rfam family visualisation, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability - Part 7

#### CMV - User Guide and Supplement 41

		9990
AB003409.1/96-167	UEFFDFUFPPUFFPDFUFPDUFFPDUFFPDUFFPDUFFPD	- AA-
AB009835.1/1-71	CAUUAGAU- G- ACUGAA- · · · AG- · · · CAAGUA- C- UGGUC- UCUUAAACCA- UUU- · · · · · · · · · · · · · · · · ·	- C A -
AB013372.1/8-81 AB013373.1/3754-3825	GCGCCCGU- A- GCUCAAUU GGAU AGAGCG- U- UUGAC- UACGGAUCAA- AAG	- AC-
AB017063.1/58819-58900	GUGGACGU- G- CCGGAGU GGUU AUCGGG- C- AUGAC- UAGAAAUCAU- GU GGG- C UUU	- AA-
AB027572.1/4261-4342	GGGUUCGAU- G- CCCGAGU GGUUA- AUGGGG- A- CGGAC- UGUAAAUUCG- UU- · GAC- · · · · AAU- · · · · · · · · GUCUA- · CGCU- GGU- UCA	- AA-
AB031211.1/7799-7884 AB031211.1/8065-8137	GCCGGGGU- G- GUGGAAUU GGCA GACACA- C- AGGAC- UUAAAAUCCU- GC GGU- AG GUG A CUACCG UGCC- GGU- UCA GGGGCCUU- A- GCUCAGCU GGG AGAGCG- C- CUGCU- UUGCACGCAG- GAG	- AG-
AB031213.1/2203-2276	GGUCCGGU- A- GUUCAGUU GGUU AGAAUG- C- CUGCC- UGUCACGCAG- GAG	- AG-
AB031213.1/2678-2748	GCGGGUGU- A- GUUUAGU GGU AAAACC- U- CAGCC- UUCCAAGCUG- AUG	- AU -
AB031214.1/4204-4277 AB031215.1/9125-9195	GGGCCUGU- A- GCUCAGCU GGUU AGAGCG- C- ACGCC- UGAUAAGCGU- GAG	- AG-
AB035922.1/6128-6200	AGGGGGGGU- A- GUUCAAUU GGU AGAGCA- C- CGGUC- UCCAAAACCG- GGU	- AG-
AB035923.1/6106-6178	GCUGAUAU- G- GCUCAGUU GGU AGAGCG- C- ACCCU- UGGUAAGGGU- GAG	- AC-
AB042240.3/6758-6687 AB042240.3/15036-15107	UGGGGGGU- G- GCCAAGU GGU AAGGCA- G- CGGGU- UUUGGUCCCG- UUA	- AA-
AB042240.3/36390-36319	GCGUCCAU- U- GUCUAAU GGAU AGGACA- G- AGGUC- UUCUAAACCU- UUG	- AA-
AB042240.3/82974-82901	GCAUCCAU- 6- GCUGAAU GGUU AAAGCG- C- CCAAC- UCAUAAUUGG- UAA AUU- UGCG- GGU- UCA	- AU -
AB042240.3/84552-84472 AB042432.1/3845-3913	GCCUUGAU- G- GUGAAAU GGU- A- GACACG- C- GAGAC- UCAAAAUCUC- GU GCU	- AG-
A B 0 4 2 4 3 2 . 1 / 6 9 4 2 - 7 0 1 1	AAGAUAUU- A- GUAAAAU CA AUUACA- U- AACUU- UGUCAAAGUU- AAA	- U A -
AB042432.1/14140-14072	GUUUCUGU- A- GUUGAA UU ACAACG- A- UGAUU- UUUCAUGUCA- UUG	- AU -
AB042524.1/5257-5192 AB042524.1/9391-9458	ACUCCCUU- A- GUAUAA UU AAUAUA- A- CUGAC- UUCCAAUUAG- UAG	- AC-
AB042809.1/5159-5089	UAGAUUGA- A- GCCAGUA AU AGGGUA- U- UUAGC- UGUUAACUAA- AUU	- AU-
AB042809.1/7700-7764	CACUAUGA- A- GCUA AGAGCG- U- UAACC- UUUUAAGUUA- AAG	- AA-
AB049357.1/1-68 AB049357.1/11673-11743	ACUUUUUU- A- GCUUAAUAU AGU AAUCCA- U-UGGUC-UUAGGAACCA- AAA	- AA-
AB066098.1/1687-1760	GGGCCUAU- A- GCUCAGCU GGUU AGAGUG- C- ACCCC- UGAUAAGGGU- GAG	- AG-
AB067577.1/1615-1688	GGGCUAUU- A- GCUCAGGU GGUU AGAGCG- C- ACCCC- UGAUAAGGGU- GAG	- AG-
AC004941.2/32735-32806	GGGGGUAU- A- GCUCAGGG GUA GAGCA- U- UUGAC- UGCAGAUCAA- GAG	- 44-
AC005329.1/7043-6971	GCCGAAAU- A- GCUCAGUU GGG AGAGCG- U- UAGAC- UGAAGAUCUA- AAG	- AU-
AC005783.1/27398-27326	GUUUCCGU- A- GUGUAGC GGUU AUCACA- U- UCGCC- UCACACGCGA- AAG	- AU-
AC007298.17/145366-145295	UCCUCGUU- A- GUAUAGU GGUG AGUAUC- C- CCGCC- UGUCACGCGG- GAG A CCGG- GGU- UCC	- AU -
AC008345.4/147881-147810	AGCAGAGU- 6- GCGCAGU GGA AGCGUG- C- UGGGC- CCAUAACCCA- GAG	- AA-
AC008443.10/8240-8321	GGUAGCGU- G- GCCGAGC GGUCU- AAGGCG- C- UGGAU- UAAGGCUCCA- GU CUC UUC GG	- AA-
AC008443.10/42590-42518	GCCCGGCU- A- GCUCAGUC GGU AGAGCA- U- GAGAC- UCUUAAUCUC- AGG GU CGUG- GGU- UCC	- AG-
AC008443.10/43006-42934	GUUUCCGU- A- GUGUAGU GGUU AUCACG- U- UCGCC- UCACACGCGA- AAG	- AA-
AC008670.6/83597-83665 AC008670.6/83725-83795	GUAAAUAU- A- GUUUAA CC AAAACA- U- CAGAU- UGUGAAUCUG- ACA	- CG-
AC009323.4/12825-12742	GUGGACAU- G- CCGGAGU GGUGUUAUCGGG- C - AUAAC- UAGAAAUCAU GU- GGG- C UUU	- AA-
AC009323.4/14362-14281	GUGGACGU- G- CCGGAGU GGUU AUCGGG- A- AUGAC- UAGAAAUCAU- GGA- GGC UUU	- AA-
AC009395.7/99012-98941 AC009461.5/128651-128579	GGCUCAAU- G- GUCUAGG GGU AUGAUU- C- UCGCU- UUGGGUGCGA- GAG	- AA-
AC009742.4/51767-51839	GUUUUCGU- A- GUGUAGU GGUU AUCACG- U- GUGCU- UCACACGCAC- AAG	- AA-
AC018638.5/4694-4623	GGCUCGUU- G- GUCUAGG GGU AUGAUU- C- UCGCU- UAGGUGCGA- GAG	- AA-
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$\begin{array}{c} AB003409,\ 1/96-167\\ AB009835,\ 1/1-71\\ AB009835,\ 1/1-71\\ AB013372,\ 1/3831\\ AB013372,\ 1/38319-58900\\ AB013321,\ 1/38319-58900\\ AB031213,\ 1/3263-8137\\ AB031211,\ 1/7203-2276\\ AB031213,\ 1/2203-276\\ AB031213,\ 1/2203-276\\ AB031213,\ 1/2203-276\\ AB031213,\ 1/4204-427\\ AB031213,\ 1/4204-427\\ AB031213,\ 1/4204-427\\ AB033213,\ 1/4204-427\\ AB033213,\ 1/4204-427\\ AB033213,\ 1/4204-427\\ AB033213,\ 1/4204-427\\ AB033223,\ 1/4128-6200\\ AB033223,\ 1/4128-6200\\ AB033223,\ 1/6138-687\\ AB042240,\ 3/15036-15107\\ \end{array}$	UCCCA. 0: UGGGUCC- A           : UUCCA. 0: UUGGGUCC- A           : UUCCA. 0: UUGGUCC- A           : UUCCA. 0: UUGGUCC- A           : UUCCA. 0: UUCGGUCC- A           : UUCCA. 0: UUCGGUCC- A           : UUCCA. 0: UUCGGUCC- A           : UUCCA. 0: UCGGUCC- A           : UUCUL 0: CUGCUCU- G           : UUCUL 0: CUUCCA. 0: UCGGUCU- G           : UUCUL 0: CUUCCA. 0: UCCA. 0           : UUCUL 0: CUUCCA. 0: UCCA. 0           : UUCUL 0: CUUCCA. 0: UCCA. 0	
$\begin{array}{c} AB 00 34 09 ,\ 1/ 96 -1 67\\ AB 00 98 35 ,\ 1/ 1-7 1\\ AB 01 33 72 ,\ 1/ 38 1\\ AB 01 33 72 ,\ 1/ 37 54 -3 82 5\\ AB 01 70 63 ,\ 1/ 38 31 9- 58 90 0\\ AB 01 32 11 ,\ 1/ 38 63 -3 84 2\\ AB 03 12 11 ,\ 1/ 70 96 -7 88 4\\ AB 03 12 11 ,\ 1/ 70 96 -7 88 4\\ AB 03 12 11 ,\ 1/ 70 96 -8 13 3\\ AB 03 12 13 ,\ 1/ 22 05 -2 27 6\\ AB 03 12 13 ,\ 1/ 22 05 -2 27 6\\ AB 03 12 13 ,\ 1/ 24 26 -4 42 77\\ AB 03 12 15 ,\ 1/ 91 25 -9 19 5\\ AB 03 32 11 ,\ 1/ 42 04 -4 42 77\\ AB 03 12 15 ,\ 1/ 91 25 -9 19 5\\ AB 03 32 11 ,\ 1/ 42 04 -4 42 77\\ AB 03 32 15 ,\ 1/ 91 25 -9 19 5\\ AB 03 59 92 ,\ 1/ 61 26 -6 17 8\\ AB 03 59 22 ,\ 1/ 61 26 -6 17 8\\ AB 04 22 46 ,\ 3/ 6 57 8 -6 68 7\\ AB 04 22 46 ,\ 3/ 6 57 8 -6 85 19 7\\ \end{array}$	E UCCA U CACCCCA G UCCCA U CACCCCA G UCCCA U CACCCCA G UCCCA U CACCCCA A UCCCA U CAUCACCA A UCCCA U CAUCACCA A UCCCA U CAUCACCA A	
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$\begin{array}{c} A B & 0 & 0 & 3 & 4 & 0 & 0 & 1 & 1 & 0 & 6 & 1 \\ A B & 0 & 0 & 3 & 3 & 5 & 1 & 1 & 1 & - 1 \\ A B & 0 & 0 & 3 & 3 & 7 & 2 & 1 & 1 & - 8 & 1 \\ A B & 0 & 1 & 3 & 3 & 7 & 2 & 1 & 1 & - 8 & 1 \\ A B & 0 & 1 & 3 & 3 & 7 & 1 & 7 & 8 & 1 & - 8 & 8 & 0 \\ B & 0 & 1 & 1 & 0 & 5 & 1 & 1 & 7 & 1 & 0 & - 8 & 4 \\ A B & 0 & 3 & 1 & 2 & 1 & 1 & 7 & 4 & 0 & 1 & - 4 & 2 & 2 \\ A B & 0 & 3 & 1 & 2 & 1 & 1 & 7 & 4 & 0 & 1 & - 4 & 2 & 2 \\ A B & 0 & 3 & 1 & 2 & 1 & 1 & 7 & 4 & 0 & 1 & - 4 & 2 & 7 \\ A B & 0 & 3 & 1 & 2 & 1 & 1 & 7 & 4 & 0 & 4 & - 4 & 2 & 7 \\ A B & 0 & 3 & 1 & 2 & 1 & 7 & 4 & 0 & 4 & - 4 & 2 & 7 \\ A B & 0 & 3 & 1 & 2 & 1 & 7 & 4 & 0 & 4 & - 4 & 2 & 7 \\ A B & 0 & 3 & 2 & 2 & 1 & 7 & 1 & 0 & -6 & 1 & 7 \\ A B & 0 & 3 & 2 & 2 & 1 & 7 & 1 & 0 & -6 & 1 & 7 \\ A B & 0 & 4 & 2 & 4 & 0 & 3 & 7 & 5 & 8 & -6 & 8 & 7 \\ A B & 0 & 4 & 2 & 4 & 0 & 3 & 7 & 5 & 8 & -6 & 8 & 7 \\ A B & 0 & 4 & 2 & 4 & 0 & 3 & 7 & 5 & 8 & -6 & 8 & 7 \\ A B & 0 & 4 & 2 & 4 & 0 & 3 & 7 & 5 & 8 & -6 & 8 & 7 \\ A B & 0 & 4 & 2 & 4 & 0 & 3 & 7 & 5 & 8 & -6 & 8 & 7 \\ A B & 0 & 4 & 2 & 4 & 0 & 3 & 7 & 5 & 1 & 7 & 6 \\ A B & 0 & 4 & 2 & 4 & 0 & 3 & 7 & 1 & 7 & 6 & 7 & 6 \\ A B & 0 & 4 & 2 & 3 & 1 & 1 & 7 & 7 & 0 & 7 & 7 & 6 \\ A B & 0 & 4 & 3 & 3 & 1 & 1 & 7 & 7 & 0 & 7 & 7 & 6 \\ A B & 0 & 4 & 3 & 5 & 1 & 1 & 7 & 7 & 0 & 7 & 7 & 6 \\ A B & 0 & 4 & 3 & 5 & 1 & 1 & 1 & 6 & 7 & 7 & 6 \\ A B & 0 & 4 & 3 & 5 & 7 & 1 & 1 & 1 & 6 & 7 & 7 & 6 \\ A B & 0 & 6 & 0 & 8 & 5 & 7 & 1 & 1 & 1 & 6 & 7 & 7 & 6 \\ A B & 0 & 0 & 5 & 7 & 7 & 1 & 1 & 1 & 6 & 7 & 7 & 7 & 7 & 7 & 7 & 7 & 7 & 7$	• UCCCA. 60. UGGGUCC- A         • UUCCA. 60. UGGGUCC- A         • UUCCA. 60. UGGGUCC- A         • UUCCG. 0. CUUCAGC- U         • UUCCG. 0. CUUCACC- G         • UUCCG. 0. CUUCACC- A         • UUCCG. 0. CUUCACC- G         • UUCCG. 0. CUUCACC- A         • UUCCG. 0. CCGGACC- A         • UUCCG. 0. CCGGACC- A         • UUCCG. 0. CCGGACC- A         • UUCCG. 0. CACCCGAC- A         • UUCCG. 0. CACCCGAC- A         • UUCCG. 0. CACCCGAC- A         • UUCCG. 0. CACCCCAC- A         • UUCCG. 0. CACCCCAC- A         • UUCCGA. 0. ACACCCAC- A         • UUCCAL. 0. UGCACCC- A         • UUCCAL. 0. UACAGCC- A         • UUCCAL. 0. UACAGCCA. A	
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Fig. 26. tRNA Rfam family alignment visualisation, the number of alignment entries can be set via option. The displayed column indices allow association with the corresponding nodes in the model. The consensus secondary structure is shown in the last line.



Fig. 27. Consensus secondary structure visualisation for tRNA with forma



Fig. 28. Consensus secondary structure visualisation for tRNA with  $\tt R2R$ 





Fig. 29. Minimal detail CMCV visualisation of Hammerhead_HH9, showing model nodes with their index arranged according to guide tree.

Legend: Hammerhead_1 Hammerhead_3 Hammerhead_HH10 Hammerhead_II



**Fig. 30.** Simple detail CMCV visualisation of *Hammerhead_HH9*, showing model nodes, labeled with node type and index, arranged according to guide tree - Part 1



Fig. 31. Simple detail CMCV visualisation of Hammerhead_HH9, showing model nodes, labeled with node type and index, arranged according to guide tree - Part 2

Legend: Hammerhead_1 Hammerhead_3 Hammerhead_HH10 Hammerhead_II



**Fig. 32.** Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part1.



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Fig. 33. Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part2.



**Fig. 34.** Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part3.

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Fig. 35. Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part4.

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**Fig. 36.** Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part5.



Fig. 37. Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part6.

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**Fig. 38.** Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part7.



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Fig. 39. Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part8.

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Fig. 40. Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part9.



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Fig. 41. Detailed CMCV visualisation of *Hammerhead_HH9*, showing nodes with states, emission and transition probabilities, arranged according to guide tree. Transitions below threshold that can be set via option are not shown and line strength corresponds to probability. Linked are nodes highlighted by color which correspond to the clan families in the automatically created legend - Part10.





ML185D186 48 MATL 11187 49 MATL ML188D189 11190 50 MATL ML1910192 A U G C 1283 ft193 E194 END 51

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BQF01059171.1/305-384	UUGGGCCG- UUACCUACAGCUGAUGAGCUCCAAGAAGAGCGAAACCUGCU- AAGCAAGGUCCUGUAGUAUUGGCCUGAACCC
ADN03003451.1/4511-4593	CUGGGCCG- UUACCUACAGCUGAUGAGCUCCAAGAAGAGCGAAACCUUGU- AAAAUAGGUCCUGUAGUAUUGGCCUGAUGAGCUC
AWZ02032198.1/15823-15741	UGAGGCCG- UUACCUACAGCUGAUGAGCUCCAAAAAGAGCGGAAACCUGUU- AAAAUAGGUCCUGUAGUAUUGGCCGACUGAGCCG
GAI01055016.1/63287-63205	UUAGGCCG- UUACCUACAGCUGAUGAGCUCCAAGAAGAGCGAAACCUUUU- AAGAUAGGUCCUGUAGUAUUGGCCUGAAAACCAU
ANN01066007.1/588-511	CUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GCUAGGUCCUGCAGUACUGGCUUAAGAGGCUA
AQR03161315.1/4048-3972	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCUAUUAGGUCCUGCAGUACUGGCUUAAGAGAAU-
BRN01375670.1/21703-21777	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGGAAACC U AUUAGGUCCUGCAGUACUGGCUUGAGAUA
BRP01270906.1/1966-2043	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGGAAACC U AUUAGGUCCUGCAGUACUGGCUUAAGAUAAUA
CTA01058962.1/24761-24837	AUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCUAUUAGGUCCUGCAGUACUGGCUUAAGAUAUA-
AKN02030441.1/10428-10505	UUGGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U ACUAGGUCCUGCAGUACUGGCUUAAGAUAAUG
EYP01022184.1/5895-5972	GUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCUAUUAGGUCCUGCAGUACUGGCUUAAGAUGGAA
FTD01093388.1/13316-13239	CUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GUUAGGUCCUGCAGUACUGGCUUAUGACAGUA
APN01231077.1/15198-15121	UCCUGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A ACCAGGUCCUGCAGUACUGGCGAAAGGAGCUU
AGU03018532.1/57571-57497	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCGAAUAGGUCCUGCAGUACUGGCUUAAGACA
AFR03027197.1/99742-99816	UUAGGCCG-UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCAAUUAGGUCCUGCAGUACUGGCUUUAGCAU
AQQ01544543.1/2644-2721	UAGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC G AUAAGGUCCUGCAGUACUGGCUUAAGACGGUA
BRQ01056532.1/2019-2096	CUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC G AACAGGUCCUGCAGUACUGGCUUAAGAUAGUG
DDD01012933.1/19585-19662	UUGAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACCA GUUAGGUCCUGCAGUACUGGCUGAAAUCUUUC
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EKR01154328.1/10424-10501	UCUGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GUUGGGUCCUGCAGUACUGGCUUACCAUAGUA
ALT01643156.1/444-367	UCCAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U ACGAGGUCCUGCAGUACGGGGCUUAGGGGAGCA
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AIY01498693.1/2014-1937	CCGAGCCG-UUGCCUGCAGCUGAUGAGCUCCAACAAGAGCGAAACCGAACAGGUCCUGCAGUACGGGUGGGGUCAGCAG
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GCE01141575.1/4443-4377	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U AUUAGGUCCUGCAGUACUGGCUU
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BQF01023900.1/7348-7414	- GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A GUUAGGUCCUGCAGUACUGGCUA
AHX01036414.1/22499-22433	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAAACC U GUUAGGUCCUGCAGUACUGGCUU
GAI 0 1 0 6 1 3 0 9 . 1 / 2 4 3 9 4 - 2 4 4 6 0	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A GUUAGGUCCUGCAGUACUGGCUA
FEY01454121.1/10166-10232	- AGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC A AUUAGGUCCUGCAGUACUGGCUU
GTP01043633.1/33547-33613	GAGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC G AUAAGGUCCUGCAGUACUGGCUU
L 7 7 3 5 3 9 . 1 8 / 1 6 1 5 6 1 - 1 6 1 6 2 7	- · UGGCCG- UUACCUGCAGCUGAUGAGCUCCAAAAAGAGCGAAACC U GUUGGGUCCUGCAGUACUGGCUU
S cons	:::((((((

Fig. 43. *Hammerhead_HH9* Rfam family alignment visualisation, the number of alignment entries can be set via option. The displayed column indices allow association with the corresponding nodes in the model. The consensus secondary structure is shown in the last line.



Fig. 44. Consensus secondary structure visualisation for Hammerhead HH9 with forna. Nucleotides linked to Hammerhead_1 family are highlighted by color.



Fig. 45. Consensus secondary structure visualisation for Hammerhead HH9 with R2R. Nucleotides linked to Hammerhead_1 family are highlighted by color.



Fig. 46. Consensus secondary structure visualisation for Hammerhead HH9 with forna. Nucleotides linked to Hammerhead_3 family are highlighted by color.



Fig. 47. Consensus secondary structure visualisation for Hammerhead HH9 with R2R. Nucleotides linked to Hammerhead_3 family are highlighted by color.

58



**Fig. 48.** Consensus secondary structure visualisation for Hammerhead HH9 with forna. Nucleotides linked to Hammerhead HH10 family are highlighted by color.



Fig. 49. Consensus secondary structure visualisation for Hammerhead HH9 with R2R. Nucleotides linked to Hammerhead HH10 family are highlighted by color.