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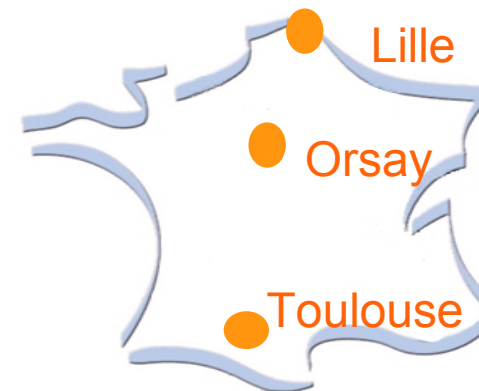
RNAspace

plateforme d'annotation d'ARN non-codant

**Projet RNG/ReNaBi
2007-2009**

Contexte du projet

- Besoin fort des biologistes
- Outils nombreux, dispersés, non intégrés
- Compétences présentes au niveau national
- Volonté de travailler ensemble



Objectif

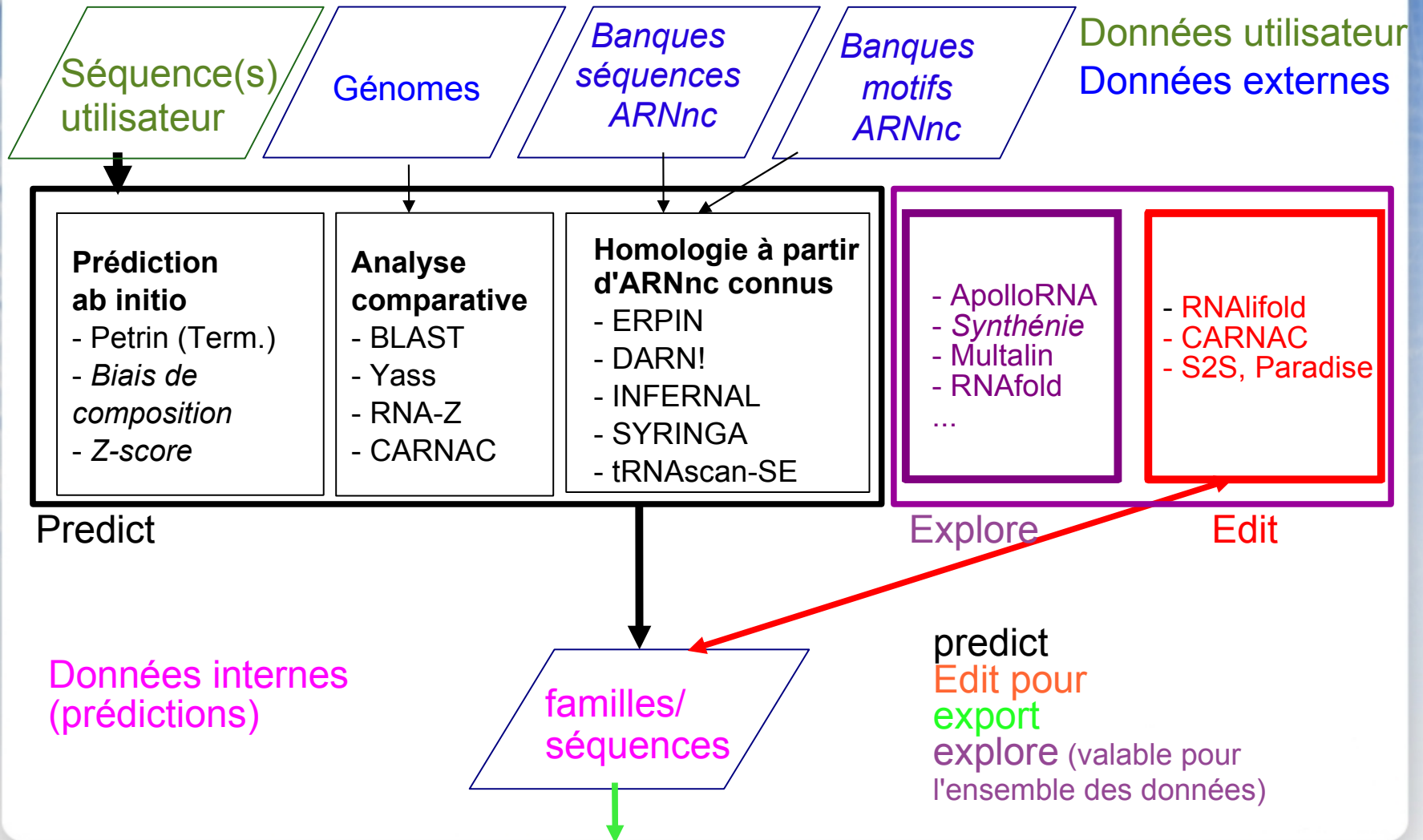
Proposer un environnement intégré permettant, à partir d'une (plusieurs) séquence(s) d'ADN :

- de réaliser des prédictions de gènes d'ARN
- d'analyser les prédictions obtenues au regard de :
 - * la séquence
 - * la structure
 - * la famille
 - * le contexte sur le génome
 - * propriétés
- d'annoter, d'ordonner les prédictions au regard des analyses réalisées,
- d'exporter les résultats

Moyens & organisation

- **Soutien du RNG/ReNaBi**
 - 18 mois de CDD
 - Animation : 6000 euros
- **Participation active de 5 équipes avec l'aide de 2 CDD**
 - 6 mois CDD (Lille)
 - 12 mois CDD (Toulouse)
- **Réunions**
 - Visios/audios (>1/mois) depuis octobre 2007
 - JOBIM 2008
 - Journées ARENA/ReNaBi (février 2008, avril 2009)
- **Outils mis en place**
 - Ouverture d'un projet sur SourceForge : <http://sourceforge.net/projects/maspace/>
 - Installation d'un wiki
<http://intron.toulouse.inra.fr/maspace/>

Vue générale

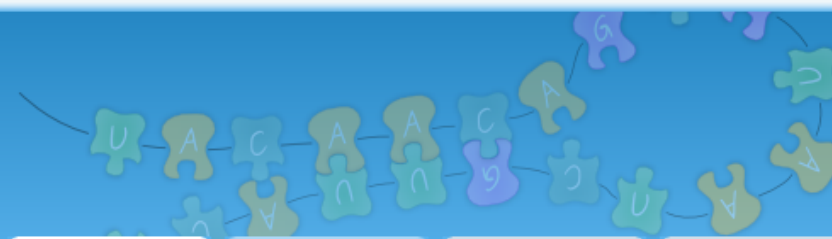


Cahier des charges informel

- Permettre d'intégrer les outils développés dans les équipes au plan national
- Prise en compte des organismes de type procaryote et eucaryote
- Deux niveaux de service:
 - plateforme avec identification, espace de travail personnel, traçabilité
 - **formulaire web pour un site bridé**
- Architecture ouverte (modulaire, extensible)

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The non-coding RNA annotation platform

[Home](#)[1. Load data](#)[2. Predict](#)[3. Explore](#)

Welcome to RNAspace

RNAspace is a platform which aims at providing an integrated environment for non-coding RNA annotation.

The increasing number of ncRNA discovered since 2000 and the lack of user friendly tools for finding and annotating them, have made necessary to propose to biologists an in silico environment allowing structural and functional annotations of these molecules with regard to available protein genes annotation environments.

RNAspace makes available a variety of [ncRNA gene finders](#) and [ncRNA databases](#) as well as user-friendly tools to explore computed results including comparison, visualization and edition of putative RNAs. RNAspace also allows to export putative RNAs in various [formats](#).

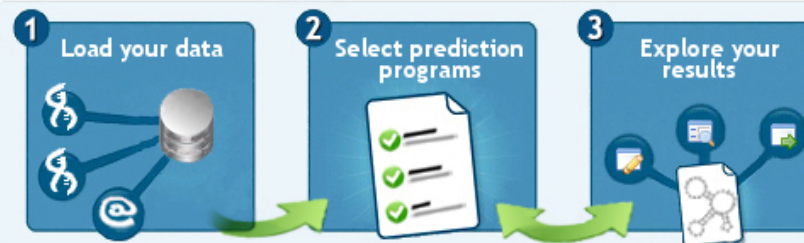
[Partners](#)[FAQ](#)[Contact](#)

Beware

This site is not yet fully operational.
Last update April 3, 2009. 14h20.

Availability

RNAspace is an open source project. It is developed in Python. It is copyrighted with the GNU General Public License, and is free (in the GNU sense) for all to use, and is in constant development. RNAspace is hosted at [Sourceforge](#). It is also available as a web server at [rnaspac.org](#).

[Get Started](#)

Comments and remarks: contact@rnaspac.org.

You can enter as many sequences as you want by repeating this process.

Once all sequences are loaded, you should enter your Email address, in order to be alerted when job will be finished. You can then access the Predict page by clicking on the **Submit button**, at the bottom of the page.

4. Predict page: choose gene finders

RNAspace offers you a collection of complementary gene finders to help identify noncoding RNAs.

Select one or several programs by selecting the corresponding check box. For each program, help can be accessed by clicking on the associated hyperlinked question mark. A synthetic description of the software is displayed on the Predict page. The 'More' hyperlink, at the end of the description, opens (if not yet done) this general Help page and displays the related section.

Optionally modify parameters value. Each gene finder is proposed with default parameter values. There are two kinds of parameters: visible ones, displayed on the Predict page (in drop down lists), and advanced ones reachable clicking on the 'parameters' button located on the gene finder line. All gene finders do not have visible and/or advanced parameters.

For the sake of clarity, available programs are organized in three sections:

- Known RNAs based gene finders
- Comparative analysis based gene finders
- *ab initio* gene finders

Time limitation on www.rnaspacespace.org For the web site rnaspacespace.org, maximum allowed running time for a gene finder is 8 hours. If exceeding this duration, the process is stopped.

4.1. Known RNAs based gene finders

4.1.1. Sequence homology search tools

RNAspace first proposes sequence search against noncoding RNA databases. The following databases are available.

- **RFAM** is a collection of multiple sequence alignments and covariance models covering many common noncoding RNA families. We use RFAM 9.1 (Dec. 2008), which contains more than 192445 sequences gathered in 1471 families. [[more information on RFAM](#)]

Table of contents

1. Introduction
2. Navigation on rnaspacespace.org
3. Load data page: load genomic sequences
- + 4. Predict page: choose gene finders
- + 5. Explore page: visualize, explore and export results
6. Frequently Asked Questions

Gene finders list

BLAST
YASS
darn
erpin
RNAmmer
tRNAscan-SE
CARNAC
RNAz
atypicalGC

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[Home](#)[1.Load data](#)[2.Predict](#)[3.Explore](#) ?

Describe genomic sequence(s) to upload with their attached characteristics. For a same organism and replicon, a multifasta file can be uploaded. For different organisms, it is necessary to upload each sequence with its characteristics, one after the other.
Remark: There is a global limitation of **5.0 Mo** for the uploaded sequences.

Upload sequence(s) Example: Load **example** of sequence.

Sequence name:

Domain:

Optional information:

Species:

Strain:

Replicon:

Upload sequence(s) FASTA format from a file:

Or paste it here:

Comments and remarks: contact@rnaspacespace.org.

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[Home](#)[1.Load data](#)[2.Predict](#)[3.Explore](#)

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[Home](#)[1.Load data](#)[2.Predict](#)[3.Explore](#)

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[Home](#)
[1.Load data](#)
[2.Predict](#)
[3.Explore](#)


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Optional information:

Species:

Strain:

Replicon:

Upload sequence(s) in FASTA format from a file:

Or paste it here:

Sequence name	Size	Domain	Species	Strain	Replicon	Header
seq_000001	2814816	bacteria	Saureus	N315	chromosome	47118324 Staphylococcus aureus subsp. aureus N315 genomic DNA, complete genome d

Email address (multiple addresses splited by a coma):

Comments and remarks: contact@rnaspacespace.org.

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[Home](#)
[1.Load data](#)
[2.Predict](#)
[3.Explore](#)


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The non-coding RNA annotation platform

[Home](#)
[1.Load data](#)
[2.Predict](#)
[3.Explore](#)


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The non-coding RNA annotation platform

Home

1.Load data

2.Predict

3.Explore



Known RNAs

- | | | | | |
|-------------------------------------|--|---------------|--------------|----------------------------|
| <input checked="" type="checkbox"/> | BLAST (<i>sequence homology</i>) [?] | Database: | Rfam_9.1 | parameters |
| <input type="checkbox"/> | darn (<i>RNA motif search</i>) [?] | Descriptor: | All [domain] | |
| <input checked="" type="checkbox"/> | erpin (<i>RNA motif search</i>) [?] | Training set: | All [domain] | |
| <input checked="" type="checkbox"/> | RNAmer (<i>specialized</i>) [?] | | | parameters |
| <input checked="" type="checkbox"/> | tRNAscan-SE (<i>specialized</i>) [?] | | | parameters |
| <input checked="" type="checkbox"/> | YASS (<i>sequence homology</i>) [?] | Database: | Rfam_9.1 | parameters |

Comparative Analysis

1. Select a set of organisms (at most four)

2. Define your comparative analysis method

Sequence alignment

- blast [?] [parameters](#)
- yass [?] [parameters](#)

Sequence aggregation

- matt-ygraph [?] [parameters](#)

Structure inference

- CARNAC [?] [parameters](#)
- RNAz [?] [parameters](#)

Ab initio prediction

- atypicalGC [?] [parameters](#)

Run

The non-coding RNA annotation platform

Home

1.Load data

2.Predict

3.Explore

Known RNAs

- | | | | | |
|-------------------------------------|--|---------------|--------------|------------|
| <input checked="" type="checkbox"/> | BLAST (<i>sequence homology</i>) [?] | Database: | Rfam_9.1 | parameters |
| <input type="checkbox"/> | darn (<i>RNA motif search</i>) [?] | Descriptor: | All [domain] | |
| <input checked="" type="checkbox"/> | erpin (<i>RNA motif search</i>) [?] | Training set: | All [domain] | |
| <input checked="" type="checkbox"/> | RNAmmr (<i>specialized</i>) [?] | | | parameters |
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Comparative Analysis

1. Select a set of organisms (at most four)

Select an organism

2. Define your comparative analysis method

Sequence alignment

- blast [?] parameters
- yass [?] parameters

Sequence aggregation

- matt-ygraph [?] parameters

Structure inference

- CARNAC [?] parameters
- RNAz [?] parameters

Ab initio prediction

- atypicalGC [?] parameters

Run

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Results for job 0000290522b816b: **678 RNAs found** (run r01: 678 RNAs)

Gene finder(s)		
62 RNAs	tRNAscan-SE	r01
9 RNAs	BLAST	r01
591 RNAs	atypicalGC	r01
16 RNAs	RNAmmer	r01

Query sequence(s)					
seq_000001	2814816 nt	bacteria	unknown	unknown	unknown

RNA predictions may be explored using the below dynamic filtering capabilities to update the following table... [click for +/- ...](#)

Field	Operator	Value	
Criterium	Comparison	Give value	<input type="button" value="Add/Update"/>

Predictions 1 - 20 of 678 Display Show Page 1 of 34

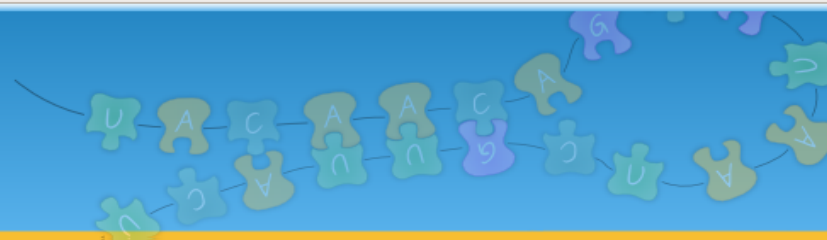
All	ID	Seq name	Family	Begin	End	Size	Strand	Species	Domain	Replicon	Predictor	Align.	Run
<input type="checkbox"/>	000001	seq_000001	unknown	6196	6254	59	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000002	seq_000001	unknown	10623	10683	61	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000003	seq_000001	unknown	24151	24318	168	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000231	seq_000001	tRNA-Glu	24160	24234	75	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000232	seq_000001	tRNA-Asp	24242	24314	73	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000004	seq_000001	unknown	30900	30952	53	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000005	seq_000001	unknown	33967	34045	79	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000006	seq_000001	unknown	35962	36099	138	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000007	seq_000001	unknown	40381	40459	79	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000008	seq_000001	unknown	41010	41098	89	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000009	seq_000001	unknown	41391	41443	53	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000010	seq_000001	unknown	63307	63379	73	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000011	seq_000001	unknown	64091	64148	58	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000012	seq_000001	unknown	71705	71845	141	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000013	seq_000001	unknown	72862	73001	140	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000014	seq_000001	unknown	80338	80391	54	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000015	seq_000001	unknown	87672	87746	75	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000016	seq_000001	unknown	98594	98692	99	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000017	seq_000001	unknown	102523	102649	127	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000018	seq_000001	unknown	103658	103833	176	.	unknown	bacteria	unknown	atypicalGC	0	r01

With **selected** predictions:

With **all** predictions:

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ID: 000889
 Family: Purine
 Sequence name: seq_000001 (*unknown unknown - bacteria - unknown*)

Predicted by: YASS 1.14 with a 0.0 score on 14-4-2009

Start: 430796

Stop: 430899

Strand: .

Genome context: CAGTTATTGAAAAAATGCCGAAAATTTGCTATTAT ... [000889] ... GGAGTAGCTTCAGCCATTAATTGTAACCATGGTG

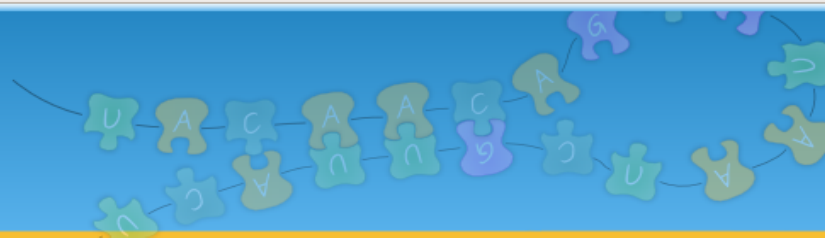
000889	1	GTTAAATAATTTACATAAACTCATATAATCTAAAGAATATGGCTTTAGAAGTTTCTACCATGTTGCCTTGAACGACATGACTATGAGTAACAACAATA
	101	CTA

Edit 

Comments and remarks: contact@rnaspace.org.

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ID:
 Family:
 Sequence name: seq_000001 (*unknown unknown - bacteria - unknown*)

Predicted by: YASS 1.14 with a 0.0 score on 14-4-2009

Start:
 Stop:
 Strand:

Genome context: CAGTTATTGAAAAAATGCCGAAAATTTGCTATTAT ... [000889] ... GGAGTAGCTTCAGCCATTAATTGTAACCATGGTG

[Update preview](#)

000889 **1** 1 CGTTAAATAATTTACATAAACTCATATAATCTAAAGAATATGGCTTTAGAAGTTTCTACCATGTTGCCTTGAACGACATGACTATGAGTAACAACAAT
 101 ACTA

To add another secondary structure, chose a secondary structure predictor in the list below or type directly the structure. Finally ask to add the structure to the description by clicking the above link.

See [RNAfold](#) secondary structure prediction:

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

[Add this structure in the preview page](#) **2**

[Reset initial values](#)

[Save](#)

[Cancel](#)

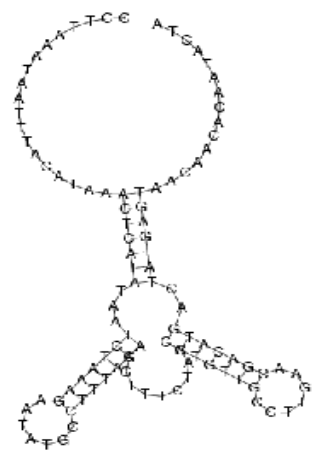
Comments and remarks: contact@rnaspace.org.

ID:
 Family:
 Sequence name: seq_000001 (*unknown unknown* - bacteria - unknown) Predicted by: YASS 1.14 with a 0.0 score on 14-4-2009

Start:
 Stop:
 Strand:
 Genome context: CAGTTATTGAAAAAATGCCGAAAATTTGCTATTAT ... [000889] ... GGAGTAGCTTCAGCCATTAATTGTAACCATGGTG Update preview

```
000889      1  CGTTAAATAATTTACATAAACTCATATAATCTAAAGAATATGGCTTTAGAAGTTTCTACCATGTTGCCTTGAACGACATGACTATGAGTAAACAACAAT
RNAfold    .....(((.....(((.....)))))).....(((.....)))).....

101  ACTA
RNAfold    ....
```



Predicted by RNAfold Remove in preview

To add another secondary structure, chose a secondary structure predictor in the list below or type directly the structure. Finally ask to add the structure to the description by clicking the above link.

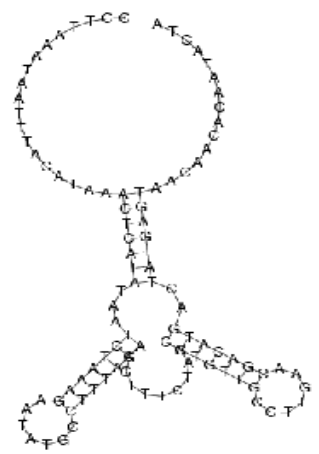
See [RNAfold](#) secondary structure prediction:
 Add this structure in the preview page

ID:
 Family:
 Sequence name: seq_000001 (*unknown unknown - bacteria - unknown*)
 Predicted by: YASS 1.14 with a 0.0 score on 14-4-2009

Start:
 Stop:
 Strand:
 Genome context: CAGTTATTGAAAAAATGCCGAAAATTTGCTATTAT ... [000889] ... GGAGTAGCTTCAGCCATTAATTGTAACCATGGTG

000889 RNAfold 1 CGTTAAATAATTTACATAAACTCATATAATCTAAAGAATATGGCTTTAGAAGTTTCTACCATGTTGCCTTGAACGACATGACTATGAGTAACAACACAAT

 RNAfold 101 ACTA



Predicted by RNAfold

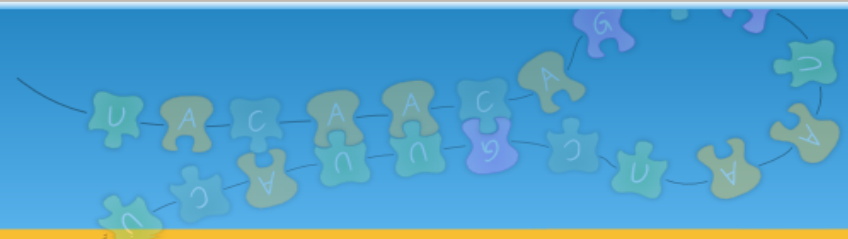
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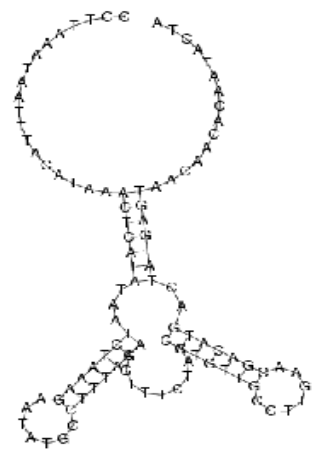
ID: 000889
Family: Purine
Sequence name: seq_000001 (*unknown unknown - bacteria - unknown*)

Predicted by: YASS 1.14 with a 0.0 score on 14-4-2009

Start: 430796
Stop: 430899
Strand: .
Genome context: CAGTTATTGAAAAAATGCCGAAAATTTGCTATTAT ... [000889] ... GGAGTAGCTTCAGCCATTAATTGTAACCATGGTG

```
000889      1  CGTTAAATAATTTACATAAACTCATATAATCTAAAGAATATGGCTTTAGAAGTTTCTACCATGTTGCCTTGAACGACATGACTATGAGTAACAACAAT
RNAfold    .....(((((((.....(((((((.....))))))))).....(((((((.....))))))))).....

101  ACTA
RNAfold    ....
```

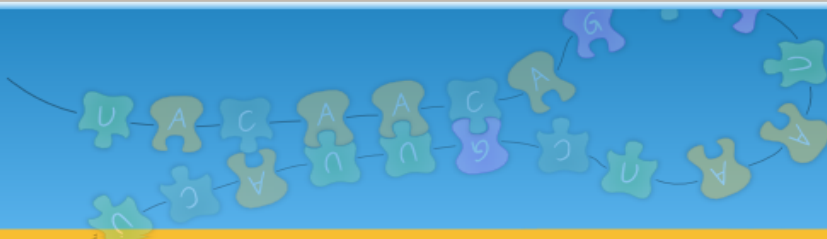


Predicted by RNAfold

[Edit](#)

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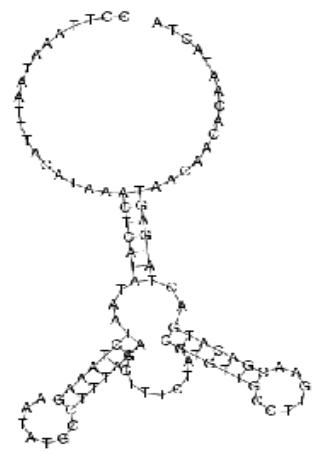


ID: 000889
Family: Purine
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.....(((((((.....(((((((.....))))))))).....(((((((.....))))))))).....
101 ACTA
RNAfold



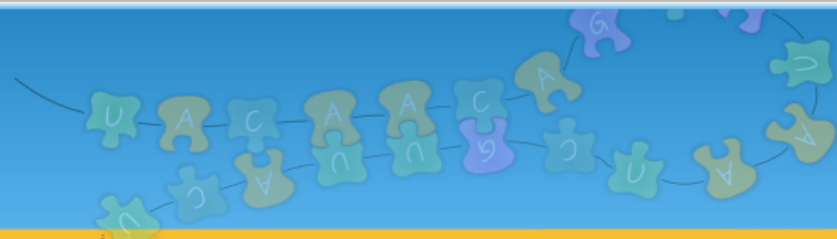
Predicted by RNAfold



Edit

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ID:

Family:

Sequence name: seq_000001 (unknown unknown - bacteria - unknown)

Predicted by: YASS 1.14 with a 0.0 score on 14-4-2009

Start:

Stop:

Strand:

Genome context: CAGTTATTGAAAAAATGCCGAAAATTTGCTATTAT ... [000889] ... GGAGTAGCTTCAGCCATTAATTGTAACCATGGTG

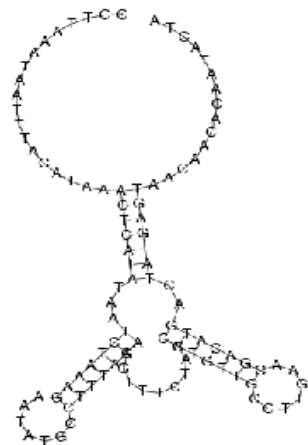
[Update preview](#)

```

000889      1  CGTTAAATAATTTACATAAACTCATATAATCTAAGAATATGGCTTTAGAAGTTTCTACCATGTTGCCTTGAACGACATGACTATGAGTAACAACAAT
RNAfold    .....(((((((.....(((((((.....)))))).....(((((((.....)))))).....)))))).....

RNAfold    101 ACTA
          ....

```



Predicted by RNAfold [Remove in preview](#)

ID: 000889

Family: Purine

Sequence name: seq_000001 (unknown unknown - bacteria - unknown)

Predicted by: YASS 1.14 with a 0.0 score on 14-4-2009

Start: 430810

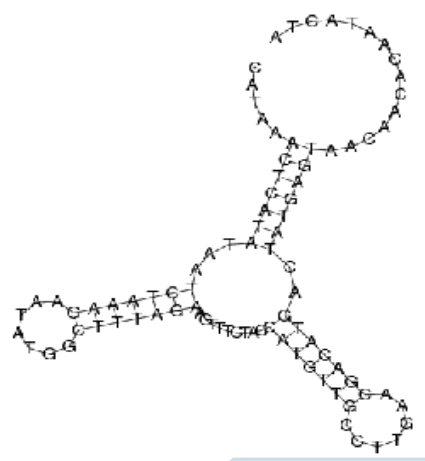
Stop: 430899

Strand: .

Genome context: ATGCCGAAAATTTGCTATTATCGTTAAATAATTTA ... [000889] ... GGAGTAGCTTCAGCCATTAATTGTAACCATGGTG

Update preview

000889 RNAfold 1 CATAAACTCATATAATCTAAAGAATATGGCTTTAGAAGTTTCTACCATGTTGCCTTGAACGACATGACTATGAGTAACAACACAATACTA(((((((.....(((((((.....)))))))).)))))).....(((((((.....)))))))).)))))).....



Predicted by RNAfold Remove in preview

To add another secondary structure, chose a secondary structure predictor in the list below or type directly the structure. Finally ask to add the structure to the description by clicking the above link.

See RNAfold secondary structure prediction:

Add this structure in the preview page

Reset initial values Save Cancel

<input type="checkbox"/>	000084	seq_000001	unknown	387348	387424	77	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000085	seq_000001	unknown	405360	405417	58	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000670	seq_000001	T-box	407534	407903	370	.	unknown	bacteria	unknown	BLAST	0	r01
<input type="checkbox"/>	000086	seq_000001	unknown	417846	417901	56	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000087	seq_000001	unknown	418518	418579	62	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000088	seq_000001	unknown	424080	424131	52	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000089	seq_000001	unknown	424596	424679	84	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000090	seq_000001	unknown	424783	424833	51	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000091	seq_000001	unknown	444568	444724	157	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000092	seq_000001	unknown	453695	453814	120	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000093	seq_000001	unknown	456943	457070	128	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000094	seq_000001	unknown	463292	463384	93	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000095	seq_000001	unknown	464523	464643	121	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000096	seq_000001	unknown	474540	474622	83	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000097	seq_000001	unknown	480246	480347	102	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000098	seq_000001	unknown	484734	484798	65	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000099	seq_000001	unknown	490548	490616	69	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000100	seq_000001	unknown	490783	490869	87	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000101	seq_000001	unknown	495612	495670	59	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000233	seq_000001	tRNA-Ser	496913	497005	93	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input checked="" type="checkbox"/>	000102	seq_000001	unknown	496927	496983	57	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000103	seq_000001	unknown	499900	499949	50	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000104	seq_000001	unknown	501447	501498	52	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000105	seq_000001	unknown	501577	501641	65	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000665	seq_000001	16s_rRNA	506169	507708	1540	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input checked="" type="checkbox"/>	000106	seq_000001	unknown	506186	506315	130	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000672	seq_000001	SSU_rRNA_5	506187	506781	595	.	unknown	bacteria	unknown	BLAST	0	r01
<input checked="" type="checkbox"/>	000107	seq_000001	unknown	506394	506609	216	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000108	seq_000001	unknown	506645	507164	520	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000109	seq_000001	unknown	507169	507413	245	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000110	seq_000001	unknown	507506	507717	212	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000234	seq_000001	tRNA-Ile	507805	507881	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input checked="" type="checkbox"/>	000111	seq_000001	unknown	507817	507967	151	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000235	seq_000001	tRNA-Ala	507900	507975	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
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<input checked="" type="checkbox"/>	000114	seq_000001	unknown	508595	508842	248	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000115	seq_000001	unknown	508849	509182	334	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000116	seq_000001	unknown	509213	509267	55	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000117	seq_000001	unknown	509363	509774	412	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000118	seq_000001	unknown	509776	510984	1209	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000660	seq_000001	5s_rRNA	511186	511299	114	+	unknown	bacteria	unknown	RNAmmer	0	r01
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<input type="checkbox"/>	000084	seq_000001	unknown	387348	387424	77	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000085	seq_000001	unknown	405360	405417	58	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000670	seq_000001	T-box	407534	407903	370	.	unknown	bacteria	unknown	BLAST	0	r01
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<input type="checkbox"/>	000089	seq_000001	unknown	424596	424679	84	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000090	seq_000001	unknown	424783	424833	51	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000091	seq_000001	unknown	444568	444724	157	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>						120	.	unknown	bacteria	unknown	atypicalGC	0	r01
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<input type="checkbox"/>						93	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>						57	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000103	seq_000001	unknown	499900	499949	50	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000104	seq_000001	unknown	501447	501498	52	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000105	seq_000001	unknown	501577	501641	65	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000665	seq_000001	16s_rRNA	506169	507708	1540	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input checked="" type="checkbox"/>	000106	seq_000001	unknown	506186	506315	130	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000672	seq_000001	SSU_rRNA_5	506187	506781	595	.	unknown	bacteria	unknown	BLAST	0	r01
<input checked="" type="checkbox"/>	000107	seq_000001	unknown	506394	506609	216	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000108	seq_000001	unknown	506645	507164	520	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000109	seq_000001	unknown	507169	507413	245	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000110	seq_000001	unknown	507506	507717	212	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000234	seq_000001	tRNA-Ile	507805	507881	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input checked="" type="checkbox"/>	000111	seq_000001	unknown	507817	507967	151	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000235	seq_000001	tRNA-Ala	507900	507975	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000654	seq_000001	23s_rRNA	508191	511111	2921	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input checked="" type="checkbox"/>	000112	seq_000001	unknown	508221	508285	65	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000113	seq_000001	unknown	508394	508501	108	.	unknown	bacteria	unknown	atypicalGC	0	r01
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<input checked="" type="checkbox"/>	000115	seq_000001	unknown	508849	509182	334	.	unknown	bacteria	unknown	atypicalGC	0	r01
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<input checked="" type="checkbox"/>	000117	seq_000001	unknown	509363	509774	412	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000118	seq_000001	unknown	509776	510984	1209	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input type="checkbox"/>	000660	seq_000001	5s_rRNA	511186	511299	114	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input type="checkbox"/>	000119	seq_000001	unknown	511316	511396	81	.	unknown	bacteria	unknown	atypicalGC	0	r01

atypicalGC :

- beaucoup de trop de candidats
- découpage de l'ARNr

A supprimer !!!

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The non-coding RNA annotation platform

Home

1.Load data

2.Predict

3.Explore



Results for job 0000290522b816b: **1056 RNAs found** (run r01: 678 RNAs, run r02: 9 RNAs, run r03: 202 RNAs, run r04: 237 RNAs)

Gene finder(s)		
62 RNAs	tRNAscan-SE	r01
9 RNAs	BLAST	r01
591 RNAs	atypicalGC	r01
16 RNAs	RNAmmer	r01
9 RNAs	BLAST	r02
80 RNAs	YASS	r03
122 RNAs	erpin	r03
237 RNAs	atypicalGC	r04

Query sequence(s)					
seq_000001	2814816 nt	bacteria	unknown	unknown	unknown

RNA predictions may be explored using the below dynamic filtering capabilities to update the following table... [click for +/-](#) ...

Field	Operator	Value		
Predictor	=	atypicalGC	Upd	Del
Run	=	r01	Upd	Del
Criterion	Comparison	Give value	Add/Update	

Predictions 1 - 535 of 535

Display Terse set Show 1000

Page 1 of 1

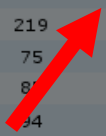
None	ID	Seq name	Family	Begin	End	Size	Strand	Species	Domain	Replicon	Predictor	Align.	Run
<input checked="" type="checkbox"/>	000001	seq_000001	unknown	6196	6254	59	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000002	seq_000001	unknown	10623	10683	61	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000004	seq_000001	unknown	30900	30952	53	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000005	seq_000001	unknown	33967	34045	79	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000006	seq_000001	unknown	35962	36099	138	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000007	seq_000001	unknown	40381	40459	79	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000008	seq_000001	unknown	41010	41098	89	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000009	seq_000001	unknown	41391	41443	53	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000010	seq_000001	unknown	63307	63379	73	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000011	seq_000001	unknown	64091	64148	58	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000012	seq_000001	unknown	71705	71845	141	.	unknown	bacteria	unknown	atypicalGC	0	r01
<input checked="" type="checkbox"/>	000013	seq_000001	unknown	72862	73001	140	.	unknown	bacteria	unknown	atypicalGC	0	r01

✓	000617	seq_000001	unknown	2617382	2617433	52	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000618	seq_000001	unknown	2617603	2617672	70	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000619	seq_000001	unknown	2619199	2619249	51	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000620	seq_000001	unknown	2620813	2620902	90	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000621	seq_000001	unknown	2631193	2631283	91	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000622	seq_000001	unknown	2634639	2634698	60	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000623	seq_000001	unknown	2644710	2644787	78	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000624	seq_000001	unknown	2646913	2646968	56	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000625	seq_000001	unknown	2657153	2657211	59	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000626	seq_000001	unknown	2662680	2662790	111	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000627	seq_000001	unknown	2677744	2677802	59	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000628	seq_000001	unknown	2678293	2678402	110	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000629	seq_000001	unknown	2684495	2684574	80	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000630	seq_000001	unknown	2690779	2690835	57	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000631	seq_000001	unknown	2697866	2697933	68	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000632	seq_000001	unknown	2700402	2700494	93	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000633	seq_000001	unknown	2704839	2704924	86	.	unknown	bacteria	unknown	atypicalGC	0	r01
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✓	000635	seq_000001	unknown	2709964	2709964	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000636	seq_000001	unknown	2718539	2718539	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000637	seq_000001	unknown	2719099	2719099	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000638	seq_000001	unknown	2720939	2720939	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000639	seq_000001	unknown	2720989	2720989	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000640	seq_000001	unknown	2727699	2727699	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000641	seq_000001	unknown	2729559	2729777	219	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000642	seq_000001	unknown	2730514	2730588	75	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000643	seq_000001	unknown	2730591	2730675	85	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000644	seq_000001	unknown	2733971	2734064	94	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000645	seq_000001	unknown	2734585	2734676	92	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000646	seq_000001	unknown	2755051	2755108	58	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000647	seq_000001	unknown	2762253	2762472	220	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000648	seq_000001	unknown	2763460	2763524	65	.	unknown	bacteria	unknown	atypicalGC	0	r01
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✓	000650	seq_000001	unknown	2771247	2771303	57	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000651	seq_000001	unknown	2773269	2773325	57	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000652	seq_000001	unknown	2776465	2776560	96	.	unknown	bacteria	unknown	atypicalGC	0	r01
✓	000653	seq_000001	unknown	2796419	2796469	51	.	unknown	bacteria	unknown	atypicalGC	0	r01

Confirm

Are you sure you want to delete the 535 RNA(s) selected ?

OK Cancel



With selected predictions: Edit... Analyse... Export...

With all predictions: EXPORT...

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The non-coding RNA annotation platform



Results for job 0000290522b816b: **521 RNAs found** (run r01: 678 RNAs, run r02: 9 RNAs, run r03: 202 RNAs, run r04: 237 RNAs)

Gene finder(s)		
62 RNAs	tRNAscan-SE	r01
9 RNAs	BLAST	r01
591 RNAs	atypicalGC	r01
16 RNAs	RNAMmer	r01
9 RNAs	BLAST	r02
80 RNAs	YASS	r03
122 RNAs	erpin	r03
237 RNAs	atypicalGC	r04

Query sequence(s)					
seq_000001	2814816 nt	bacteria	unknown	unknown	unknown

RNA predictions may be explored using the below dynamic filtering capabilities to update the following table... [click for +/- ...](#)

Field Operator Value Add/Update

Criterion Comparison Give value

Predictions 1 - 521 of 521 Display Terse set Show 1000 Page 1 of 1

All	ID	Seq name	Family	Begin	End	Size	Strand	Species	Domain	Replicon	Predictor	Align.	Run
<input type="checkbox"/>	000890	seq_000001	unknown	6196	6254	59	.	unknown	bacteria	unknown	atypicalGC	0	r04
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<input type="checkbox"/>	000705	seq_000001	Bacterial_T-box	12663	12724	62	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000815	seq_000001	SAM	15956	16054	99	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000891	seq_000001	unknown	24151	24318	168	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000231	seq_000001	tRNA-Glu	24160	24234	75	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000716	seq_000001	Type_I_tRNA	24160	24230	71	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000848	seq_000001	tRNA	24160	24314	155	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000232	seq_000001	tRNA-Asp	24242	24314	73	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
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<input type="checkbox"/>	000790	seq_000001	RprA_RNA	24322	24351	30	+	unknown	bacteria	unknown	erpin	0	r03
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<input type="checkbox"/>	000895	seq_000001	unknown	41391	41443	53	.	unknown	bacteria	unknown	atypicalGC	0	r04

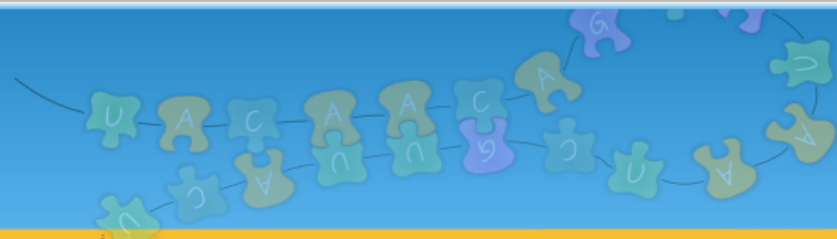
<input type="checkbox"/>	000935	seq_000001	unknown	499900	499949	50	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000936	seq_000001	unknown	501447	501498	52	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000813	seq_000001	SRP_bact	501537	501639	103	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000799	seq_000001	[Bacterial_signal_rec...]	501563	501602	40	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000937	seq_000001	unknown	501577	501641	65	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000879	seq_000001	SSU_rRNA_5	506165	507683	1519	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000665	seq_000001	16s_rRNA	506169	507708	1540	+	unknown	bacteria	unknown	RNAmmer	0	r01
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<input type="checkbox"/>	000941	seq_000001	unknown	507169	507413	245	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000942	seq_000001	unknown	507506	507717	212	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input checked="" type="checkbox"/>	000234	seq_000001	tRNA-Ile	507805	507881	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input checked="" type="checkbox"/>	000718	seq_000001	Type_I_tRNA	507805	507877	73	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000770	seq_000001	Type_II_tRNA	507805	507877	73	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000850	seq_000001	tRNA	507805	507972	168	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000943	seq_000001	unknown	507817	507967	151	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000235	seq_000001	tRNA-Ala	507900	507975	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000719	seq_000001	Type_I_tRNA	507900	507971	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000654	seq_000001	23s_rRNA	508191	511111	2921	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input type="checkbox"/>	000819	seq_000001	5_8S_rRNA	508201	508357	157	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000944	seq_000001	unknown	508221	508285	65	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000945	seq_000001	unknown	508394	508501	108	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000946	seq_000001	unknown	508595	508842	248	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000947	seq_000001	unknown	508849	509182	334	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000948	seq_000001	unknown	509213	509267	55	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000949	seq_000001	unknown	509363	509774	412	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000950	seq_000001	unknown	509776	510984	1209	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000838	seq_000001	PK-G12rRNA	510497	510605	109	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000880	seq_000001	SSU_rRNA_5	510647	510824	178	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000700	seq_000001	[23S/28S_rRNA_sarcin_...]	510862	510889	28	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000873	seq_000001	5S_rRNA	511184	511298	115	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000660	seq_000001	5s_rRNA	511186	511299	114	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input type="checkbox"/>	000688	seq_000001	Bacterial_5S_rRNA	511200	511245	46	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000951	seq_000001	unknown	511216	511306	91	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000952	seq_000001	unknown	511499	511591	93	.	unknown	bacteria	unknown	atypicalGC	0	r04



With selected predictions: Edit... Analyse... alignment Export... With all predictions: EXPORT...

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Page 1 of 1

ID	name	begin	end	size	family	strand	domain	species	strain	replicon
User sequence(s)										
000237	seq_000001	549835	549910	76	tRNA-Thr	+	bacteria	unknown	unknown	unknown
000721	seq_000001	549835	549906	72	Type_I_tRNA	+	bacteria	unknown	unknown	unknown

Alignment produced by clustalw + RNAz

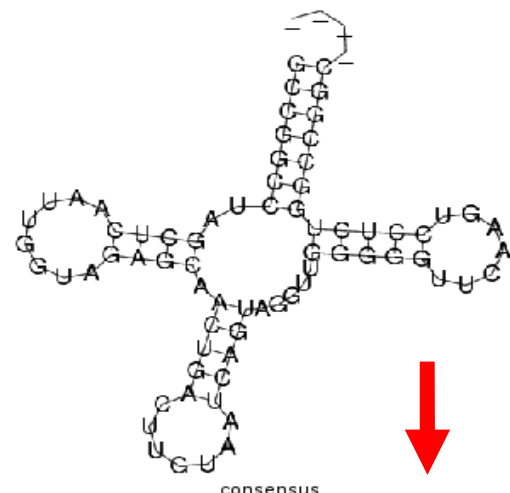
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000237      GCCGGCCUAGCUCAAUUGGUAGAGCAACUGACUUGUAAUCAGUAGGUUGGGGGUUCAAGUCCUCU
000721      GCCGGCCUAGCUCAAUUGGUAGAGCAACUGACUUGUAAUCAGUAGGUUGGGGGUUCAAGUCCUCU
consensus  *****
```

```
000237      GGCCGGCACCA
000721      GGCCGGC----
consensus  GGCCGGC
*****
```

```
000237      ((((((.....))))).(((.....)))).....(((.....)))
000721      ((((((.....))))).(((.....)))).....(((.....)))
consensus  ((((((.....))))).(((.....)))).....(((.....)))
GCCGGCCUAGCUCAAUUGGUAGAGCAACUGACUUGUAAUCAGUAGGUUGGGGGUUCAAGUCCUCU
```

```
000237      )))))))....
000721      )))))))....
consensus )))))))....
GGCCGGC
```

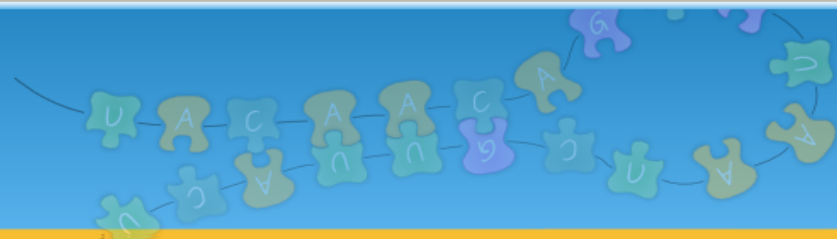


Save

Explore page

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Page 1 of 1

ID	name	begin	end	size	family	strand	domain	species	strain	replicon
User sequence(s)										
000237	seq_000001	549835	549910	76	tRNA-Thr	+	bacteria	unknown	unknown	unknown
000721	seq_000001	549835	549906	72	Type_I_tRNA	+	bacteria	unknown	unknown	unknown

Alignment produced by clustalw + RNAz

tmp_0000290522b816b_alignment000005

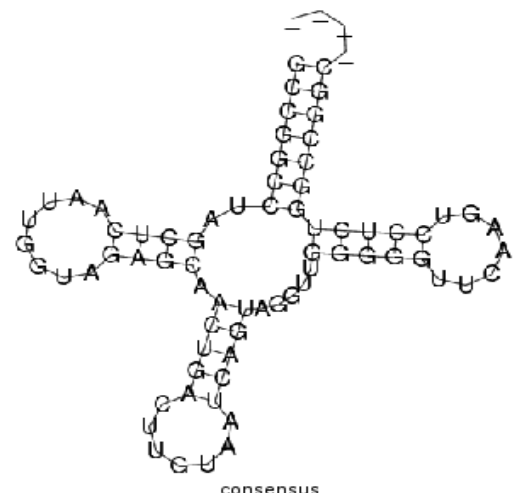
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000237      GCGGCCUAGCUCAAUUGGUAGAGCAACUGACUUGUAAUCAGUAGGUUGGGGGUUCAAGUCCUCU
000721      GCGGCCUAGCUCAAUUGGUAGAGCAACUGACUUGUAAUCAGUAGGUUGGGGGUUCAAGUCCUCU
consensus  *****

000237      GGCCGGCACCA
000721      GGCCGGC----
consensus  GGCCGGC
*****

000237      ((((((.....))))).(((.....)))).....(((.....)))
000721      ((((((.....))))).(((.....)))).....(((.....)))
consensus  GCGGCCUAGCUCAAUUGGUAGAGCAACUGACUUGUAAUCAGUAGGUUGGGGGUUCAAGUCCUCU

000237      )))))))....
000721      )))))))....
consensus  )))))))....
GGCCGGC
    
```



Save

[Explore page](#)

80 RNAs	YASS	r03
122 RNAs	erpin	r03
237 RNAs	atypicalGC	r04

RNA predictions may be explored using the below dynamic filtering capabilities to update the following table... [click for +/-](#) ...

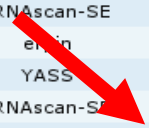
Field	Operator	Value	
Critereum	Comparison	Give value	Add/Update

Predictions 101 - 150 of 521

Display Terse set Show 50

Page 3 of 11

All	ID	Seq name	Family	Begin	End	Size	Strand	Species	Domain	Replicon	Predictor	Align.	Run
<input type="checkbox"/>	000953	seq_000001	unknown	521786	521839	54	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input checked="" type="checkbox"/>	000874	seq_000001	5S_rRNA	549616	549730	115	.	unknown	bacteria	unknown	YASS	0	r03
<input checked="" type="checkbox"/>	000663	seq_000001	5s_rRNA	549618	549731	114	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input checked="" type="checkbox"/>	000689	seq_000001	Bacterial_5S_rRNA	549632	549677	46	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000954	seq_000001	unknown	549648	549951	304	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000236	seq_000001	tRNA-Val	549743	549818	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000720	seq_000001	Type_I_tRNA	549743	549814	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000851	seq_000001	tRNA	549743	549907	165	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000237	seq_000001	tRNA-Thr	549835	549910	76	+	unknown	bacteria	unknown	tRNAscan-SE	1	r01
<input type="checkbox"/>	000721	seq_000001	Type_I_tRNA	549835	549906	72	+	unknown	bacteria	unknown	erpin	1	r03
<input type="checkbox"/>	000238	seq_000001	tRNA-Lys	549917	549989	73	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000722	seq_000001	Type_I_tRNA	549917	549988	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000239	seq_000001	tRNA-Gly	550023	550097	75	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000723	seq_000001	Type_I_tRNA	550023	550093	71	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000955	seq_000001	unknown	550057	550241	185	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000240	seq_000001	tRNA-Leu	550105	550193	89	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000771	seq_000001	Type_II_tRNA	550105	550189	85	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000852	seq_000001	tRNA	550105	550465	361	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000241	seq_000001	tRNA-Arg	550199	550275	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000724	seq_000001	Type_I_tRNA	550199	550271	73	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000242	seq_000001	tRNA-Pro	550296	550369	74	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000725	seq_000001	Type_I_tRNA	550296	550368	73	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000956	seq_000001	unknown	550343	550468	126	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000243	seq_000001	tRNA-Ala	550393	550468	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000726	seq_000001	Type_I_tRNA	550393	550464	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000881	seq_000001	SSU_rRNA_5	550593	552111	1519	.	unknown	bacteria	unknown	YASS	0	r03
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<input type="checkbox"/>	000957	seq_000001	unknown	550615	550743	129	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000958	seq_000001	unknown	550822	551037	216	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000959	seq_000001	unknown	551073	551858	786	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000695	seq_000001	16S_rRNA_helix_18	551101	551136	36	+	unknown	bacteria	unknown	erpin	0	r03



80 RNAs	YASS	r03
122 RNAs	erpin	r03
237 RNAs	atypicalGC	r04

RNA predictions may be explored using the below dynamic filtering capabilities to update the following table... [click for +/- ...](#)

Field	Operator	Value	
Criterion	Comparison	Give value	Add/Update

Predictions 101 - 150 of 521

Display Terse set Show 50

Page 3 of 11

All	ID	Seq name	Family	Begin	End	Size	Strand	Species	Domain	Replicon	Predictor	Align.	Run
<input type="checkbox"/>	000953	seq_000001	unknown	521786	521839	54	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input checked="" type="checkbox"/>	000874	seq_000001	5S_rRNA	549616	549730	115	.	unknown	bacteria	unknown	YASS	0	r03
<input checked="" type="checkbox"/>	000663	seq_000001	5s_rRNA	549618	549731	114	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input checked="" type="checkbox"/>	000689	seq_000001	Bacterial_5S_rRNA	549632	549677	46	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000954	seq_000001	unknown	549648	549951	304	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000236	seq_000001	tRNA-Val	549743	549818	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000720	seq_000001	Type_I_tRNA	549743	549814	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000851	seq_000001	tRNA	549743	549907	165	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000237	seq_000001	tRNA-Thr	549835	549910	76	+	unknown	bacteria	unknown	tRNAscan-SE	1	r01
<input type="checkbox"/>	000721	seq_000001	Type_I_tRNA	549835	549906	72	+	unknown	bacteria	unknown	erpin	1	r03
<input type="checkbox"/>	000238	seq_000001	tRNA-Lys	549917	549989	73	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000722	seq_000001	Type_I_tRNA	549917	549988	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000239	seq_000001	tRNA-Gly	550023	550097	75	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000723	seq_000001	Type_I_tRNA	550023	550093	71	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000955	seq_000001	unknown	550057	550241	185	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000240	seq_000001	tRNA-Leu	550105	550193	89	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000771	seq_000001	Type_II_tRNA	550105	550189	85	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000852	seq_000001	tRNA	550105	550465	361	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000241	seq_000001	tRNA-Arg	550199	550275	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000724	seq_000001	Type_I_tRNA	550199	550271	73	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000242	seq_000001	tRNA-Pro	550296	550369	74	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
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<input type="checkbox"/>	000243	seq_000001	tRNA-Ala	550393	550468	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000726	seq_000001	Type_I_tRNA	550393	550464	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000881	seq_000001	SSU_rRNA_5	550593	552111	1519	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000668	seq_000001	16s_rRNA	550597	552136	1540	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input type="checkbox"/>	000957	seq_000001	unknown	550615	550743	129	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000958	seq_000001	unknown	550822	551037	216	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000959	seq_000001	unknown	551073	551858	786	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000695	seq_000001	16S_rRNA_helix_18	551101	551136	36	+	unknown	bacteria	unknown	erpin	0	r03



000723	seq_000001	Type_I_tRNA	550023	550093	71	+	unknown	bacteria	unknown	erpin	0	r03
000955	seq_000001	unknown	550057	550241	185	.	unknown	bacteria	unknown	atypicalGC	0	r04
000240	seq_000001	tRNA-Leu	550105	550193	89	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000771	seq_000001	Type_II_tRNA	550105	550189	85	+	unknown	bacteria	unknown	erpin	0	r03
000852	seq_000001	tRNA	550105	550465	361	.	unknown	bacteria	unknown	YASS	0	r03
000241	seq_000001	tRNA-Arg	550199	550275	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000724	seq_000001	Type_I_tRNA	550199	550271	73	+	unknown	bacteria	unknown	erpin	0	r03
000242	seq_000001	tRNA-Pro	550296	550369	74	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000725	seq_000001	Type_I_tRNA	550296	550368	73	+	unknown	bacteria	unknown	erpin	0	r03
000956	seq_000001	unknown	550343	550468	126	.	unknown	bacteria	unknown	atypicalGC	0	r04
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000726	seq_000001	Type_I_tRNA	550393	550464	72	+	unknown	bacteria	unknown	erpin	0	r03
000881	seq_000001	SSU_rRNA_5	550593	552111	1519	.	unknown	bacteria	unknown	YASS	0	r03
000668	seq_000001	16s_rRNA	550597	552136	1540	+	unknown	bacteria	unknown	RNAmmer	0	r01
000957	seq_000001	unknown	550615	550743	129	.	unknown	bacteria	unknown	atypicalGC	0	r04
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000959	seq_000001	unknown	551073	551858	786	.	unknown	bacteria	unknown	atypicalGC	0	r04
000695	seq_000001	16S_rRNA_helix_18	551101	551136	36	+	unknown	bacteria	unknown	erpin	0	r03
000960	seq_000001	unknown	551934	552145	212	.	unknown	bacteria	unknown	atypicalGC	0	r04
000244	seq_000001	tRNA-Ile	552236	552312	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
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000853	seq_000001	tRNA	552236	552309	74	.	unknown	bacteria	unknown	YASS	0	r03
000657	seq_000001	23s_rRNA	552482	555402	2921	+	unknown	bacteria	unknown	RNAmmer	0	r01
000820	seq_000001	5_8S_rRNA	552492	552648	157	.	unknown	bacteria	unknown	YASS	0	r03
000961	seq_000001	unknown	552509	552576	68	.	unknown	bacteria	unknown	atypicalGC	0	r04
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000963	seq_000001	unknown	552886	553133	248	.	unknown	bacteria	unknown	atypicalGC	0	r04
000964	seq_000001	unknown	553140	553473	334	.	unknown	bacteria	unknown	atypicalGC	0	r04
000965	seq_000001	unknown	553504	553558	55	.	unknown	bacteria	unknown	atypicalGC	0	r04
000966	seq_000001	unknown	553654	554065	412	.	unknown	bacteria	unknown	atypicalGC	0	r04
000967	seq_000001	unknown	554067	555275	1209	.	unknown	bacteria	unknown	atypicalGC	0	r04
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000882	seq_000001	SSU_rRNA_5	554938	555115	178	.	unknown	bacteria	unknown	YASS	0	r03
000701	seq_000001	[23S/28S_rRNA_sarcin_...]	555153	555180	28	+	unknown	bacteria	unknown	erpin	0	r03
000875	seq_000001	5S_rRNA	555475	555589	115	.	unknown	bacteria	unknown	YASS	0	r03
000662	seq_000001	5s_rRNA	555477	555590	114	+	unknown	bacteria	unknown	RNAmmer	0	r01

With selected predictions:

Edit...

Analyse...

Export...

With all predictions:

EXPORT...

Edit...

- put in same family
- split into 2 families
- add a new prediction
- delete

Comments and remarks: contact@rnaspace.org.

000723	seq_000001	Type_I_tRNA	550023	550093	71	+	unknown	bacteria	unknown	erpin	0	r03
000955	seq_000001	unknown	550057	550241	185	.	unknown	bacteria	unknown	atypicalGC	0	r04
000240	seq_000001	tRNA-Leu	550105	550193	89	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000771	seq_000001	Type_II_tRNA	550105	550189	85	+	unknown	bacteria	unknown	erpin	0	r03
000852	seq_000001	tRNA	550105	550465	361	.	unknown	bacteria	unknown	YASS	0	r03
000241	seq_000001	tRNA-Arg	550199	550275	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000724	seq_000001	Type_I_tRNA	550199	550271	73	+	unknown	bacteria	unknown	erpin	0	r03
000242	seq_000001	tRNA-Pro	550296	550369	74	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000725	seq_000001	Type_I_tRNA	550296	550368	73	+	unknown	bacteria	unknown	erpin	0	r03
000956	seq_000001	unknown	550343	550468	126	.	unknown	bacteria	unknown	atypicalGC	0	r04
000243	seq_000001	tRNA-Ala	550393	550468	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000726	seq_000001	Type_I_tRNA	550393	550464	72	+	unknown	bacteria	unknown	erpin	0	r03
000881	seq_000001	SSU_rRNA_5	550593	552111	1519	.	unknown	bacteria	unknown	YASS	0	r03
000668	seq_000001	16s_rRNA	550597	552136	1540	+	unknown	bacteria	unknown	RNAmmmer	0	r01
000957	seq_000001	unknown	550615	550743	129	.	unknown	bacteria	unknown	atypicalGC	0	r04
000958	seq_000001	unknown	550822	551037	216	.	unknown	bacteria	unknown	atypicalGC	0	r04
000959	seq_000001	unknown	551073	551858	786	.	unknown	bacteria	unknown	atypicalGC	0	r04
000695	seq_000001	16S_rRNA_helix	551073	551858	786	.	unknown	bacteria	unknown	erpin	0	r03
000960	seq_000001	unknown	551073	551858	786	.	unknown	bacteria	unknown	atypicalGC	0	r04
000244	seq_000001	tRNA-Ile	551073	551858	786	.	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000727	seq_000001	Type_I_tRNA	551073	551858	786	.	unknown	bacteria	unknown	erpin	0	r03
000772	seq_000001	Type_II_tRNA	551073	551858	786	.	unknown	bacteria	unknown	erpin	0	r03
000853	seq_000001	tRNA	551073	551858	786	.	unknown	bacteria	unknown	YASS	0	r03
000657	seq_000001	23s_rRNA	551073	551858	786	.	unknown	bacteria	unknown	RNAmmmer	0	r01
000820	seq_000001	5_8S_rRNA	551073	551858	786	.	unknown	bacteria	unknown	YASS	0	r03
000961	seq_000001	unknown	552509	552576	68	.	unknown	bacteria	unknown	atypicalGC	0	r04
000962	seq_000001	unknown	552685	552785	101	.	unknown	bacteria	unknown	atypicalGC	0	r04
000963	seq_000001	unknown	552886	553133	248	.	unknown	bacteria	unknown	atypicalGC	0	r04
000964	seq_000001	unknown	553140	553473	334	.	unknown	bacteria	unknown	atypicalGC	0	r04
000965	seq_000001	unknown	553504	553558	55	.	unknown	bacteria	unknown	atypicalGC	0	r04
000966	seq_000001	unknown	553654	554065	412	.	unknown	bacteria	unknown	atypicalGC	0	r04
000967	seq_000001	unknown	554067	555275	1209	.	unknown	bacteria	unknown	atypicalGC	0	r04
000839	seq_000001	PK-G12rRNA	554788	554896	109	.	unknown	bacteria	unknown	YASS	0	r03
000882	seq_000001	SSU_rRNA_5	554938	555115	178	.	unknown	bacteria	unknown	YASS	0	r03
000701	seq_000001	[23S/28S_rRNA_sarcin_...]	555153	555180	28	+	unknown	bacteria	unknown	erpin	0	r03
000875	seq_000001	5S_rRNA	555475	555589	115	.	unknown	bacteria	unknown	YASS	0	r03
000662	seq_000001	5s_rRNA	555477	555590	114	+	unknown	bacteria	unknown	RNAmmmer	0	r01


Put In Same Family

Family:

Save Cancel

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Home 1.Load data 2.Predict 3.Explore ?

Results for job 0000290522b816b: **521 RNAs found** (run r01: 678 RNAs, run r02: 9 RNAs, run r03: 202 RNAs, run r04: 237 RNAs)

Gene finder(s)		
62 RNAs	tRNAscan-SE	r01
9 RNAs	BLAST	r01
591 RNAs	atypicalGC	r01
16 RNAs	RNAmmer	r01
9 RNAs	BLAST	r02
80 RNAs	YASS	r03
122 RNAs	erpin	r03
237 RNAs	atypicalGC	r04

Query sequence(s)					
seq_000001	2814816 nt	bacteria	unknown	unknown	unknown

RNA predictions may be explored using the below dynamic filtering capabilities to update the following table... [click for +/- ...](#)

Field	Operator	Value	
Criterion	Comparison	Give value	Add/Update

Predictions 101 - 150 of 521

Display Terse set Show 50

Page 3 of 11

All	ID	Seq name	Family	Begin	End	Size	Strand	Species	Domain	Replicon	Predictor	Align.	Run
<input type="checkbox"/>	000953	seq_000001	unknown	521786	521839	54	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000874	seq_000001	5S	549616	549730	115	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000663	seq_000001	5S	549618	549731	114	+	unknown	bacteria	unknown	RNAmmer	0	r01
<input type="checkbox"/>	000689	seq_000001	5S	549632	549677	46	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000954	seq_000001	unknown	549648	549951	304	.	unknown	bacteria	unknown	atypicalGC	0	r04
<input type="checkbox"/>	000236	seq_000001	tRNA-Val	549743	549818	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000720	seq_000001	Type_I_tRNA	549743	549814	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000851	seq_000001	tRNA	549743	549907	165	.	unknown	bacteria	unknown	YASS	0	r03
<input type="checkbox"/>	000237	seq_000001	tRNA-Thr	549835	549910	76	+	unknown	bacteria	unknown	tRNAscan-SE	1	r01
<input type="checkbox"/>	000721	seq_000001	Type_I_tRNA	549835	549906	72	+	unknown	bacteria	unknown	erpin	1	r03
<input type="checkbox"/>	000238	seq_000001	tRNA-Lys	549917	549989	73	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000722	seq_000001	Type_I_tRNA	549917	549988	72	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000239	seq_000001	tRNA-Gly	550023	550097	75	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
<input type="checkbox"/>	000723	seq_000001	Type_I_tRNA	550023	550093	71	+	unknown	bacteria	unknown	erpin	0	r03
<input type="checkbox"/>	000955	seq_000001	unknown	550057	550211	155	.	unknown	bacteria	unknown	atypicalGC	0	r04



000723	seq_000001	Type_I_tRNA	550023	550093	71	+	unknown	bacteria	unknown	erpin	0	r03
000955	seq_000001	unknown	550057	550241	185	.	unknown	bacteria	unknown	atypicalGC	0	r04
000240	seq_000001	tRNA-Leu	550105	550193	89	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000771	seq_000001	Type_II_tRNA	550105	550189	85	+	unknown	bacteria	unknown	erpin	0	r03
000852	seq_000001	tRNA	550105	550465	361	.	unknown	bacteria	unknown	YASS	0	r03
000241	seq_000001	tRNA-Arg	550199	550275	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000724	seq_000001	Type_I_tRNA	550199	550271	73	+	unknown	bacteria	unknown	erpin	0	r03
000242	seq_000001	tRNA-Pro	550296	550369	74	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000725	seq_000001	Type_I_tRNA	550296	550368	73	+	unknown	bacteria	unknown	erpin	0	r03
000956	seq_000001	unknown	550343	550468	126	.	unknown	bacteria	unknown	atypicalGC	0	r04
000243	seq_000001	tRNA-Ala	550393	550468	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000726	seq_000001	Type_I_tRNA	550393	550464	72	+	unknown	bacteria	unknown	erpin	0	r03
000881	seq_000001	SSU_rRNA_5	550593	552111	1519	.	unknown	bacteria	unknown	YASS	0	r03
000668	seq_000001	16s_rRNA	550597	552136	1540	+	unknown	bacteria	unknown	RNAmmer	0	r01
000957	seq_000001	unknown	550615	550743	129	.	unknown	bacteria	unknown	atypicalGC	0	r04
000958	seq_000001	unknown	550822	551037	216	.	unknown	bacteria	unknown	atypicalGC	0	r04
000959	seq_000001	unknown	551073	551858	786	.	unknown	bacteria	unknown	atypicalGC	0	r04
000695	seq_000001	16S_rRNA_helix_18	551101	551136	36	+	unknown	bacteria	unknown	erpin	0	r03
000960	seq_000001	unknown	551934	552145	212	.	unknown	bacteria	unknown	atypicalGC	0	r04
000244	seq_000001	tRNA-Ile	552236	552312	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
000727	seq_000001	Type_I_tRNA	552236	552308	73	+	unknown	bacteria	unknown	erpin	0	r03
000772	seq_000001	Type_II_tRNA	552236	552308	73	+	unknown	bacteria	unknown	erpin	0	r03
000853	seq_000001	tRNA	552236	552309	74	.	unknown	bacteria	unknown	YASS	0	r03
000657	seq_000001	23s_rRNA	552482	555402	2921	+	unknown	bacteria	unknown	RNAmmer	0	r01
000820	seq_000001	5_8S_rRNA	552492	552648	157	.	unknown	bacteria	unknown	YASS	0	r03
000961	seq_000001	unknown	552509	552576	68	.	unknown	bacteria	unknown	atypicalGC	0	r04
000962	seq_000001	unknown	552685	552785	101	.	unknown	bacteria	unknown	atypicalGC	0	r04
000963	seq_000001	unknown	552886	553133	248	.	unknown	bacteria	unknown	atypicalGC	0	r04
000964	seq_000001	unknown	553140	553473	334	.	unknown	bacteria	unknown	atypicalGC	0	r04
000965	seq_000001	unknown	553504	553558	55	.	unknown	bacteria	unknown	atypicalGC	0	r04
000966	seq_000001	unknown	553654	554065	412	.	unknown	bacteria	unknown	atypicalGC	0	r04
000967	seq_000001	unknown	554067	555275	1209	.	unknown	bacteria	unknown	atypicalGC	0	r04
000839	seq_000001	PK-G12rRNA	554788	554896	109	.	unknown	bacteria	unknown	YASS	0	r03
000882	seq_000001	SSU_rRNA_5	554938	555115	178	.	unknown	bacteria	unknown	YASS	0	r03
000701	seq_000001	[23S/28S_rRNA_sarcin_...]	555153	555180	28	+	unknown	bacteria	unknown	erpin	0	r03
000875	seq_000001	5S_rRNA	555475	555589	115	.	unknown	bacteria	unknown	YASS	0	r03
000662	seq_000001	5s_rRNA	555477	555590	114	+	unknown	bacteria	unknown	RNAmmer	0	r01

With selected predictions:

Edit...

Analyse...

Export...

With all predictions:

EXPORT...

Edit...

put in same family

split into 2 families

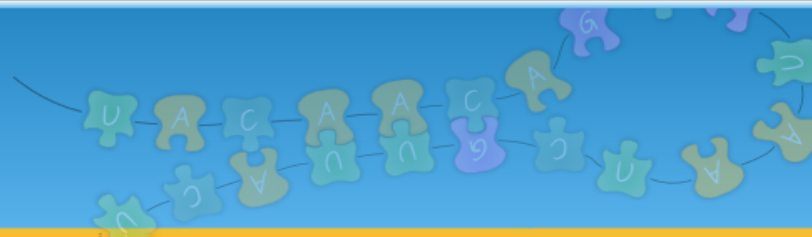
add a new prediction

delete

Comments and remarks: contact@rnaspace.org.

RNAspace.org

The non-coding RNA annotation platform



ID:
Family:
Sequence name: seq_000001 (*unknown unknown - bacteria - unknown*)

Start:
Stop:
Strand:
Genome context: ... [001127] ... GATTAAAGATAGAAATACACGATGCGAGCAATCAA

[Update preview](#)

001127 1 C

To add another secondary structure, chose a secondary structure predictor in the list below or type directly the structure. Finally ask to add the structure to the description by clicking the above link.

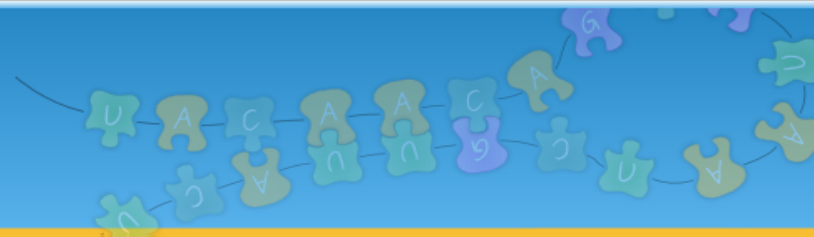
See [RNAfold](#) secondary structure prediction:

[Add this structure in the preview page](#)[Save](#)

Comments and remarks: contact@rnaspace.org.


RNAspace.org

The non-coding RNA annotation platform



ID:
Family:
Sequence name: seq_000001 (*unknown unknown - bacteria - unknown*)

Start:
Stop:
Strand:
Genome context: ... [001127] ... GATTAAAGATAGAAATACACGATGCGAGCAATCAA



001127 1 C

To add another secondary structure, chose a secondary structure predictor in the list below or type directly the structure. Finally ask to add the structure to the description by clicking the above link.

See [RNAfold](#) secondary structure prediction:

Comments and remarks: contact@rnaspace.org.

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The non-coding RNA annotation platform



ID:
Family:
Sequence name: seq_000001 (*unknown unknown - bacteria - unknown*)

Start:
Stop:
Strand:
Genome context: ... [001127] ... ACAGTTCTTATACATACTTTATAAATTATTTCCCA [Update preview](#)

001127 1 CGATTAAGATAGAAAATACACGATGCGAGCAATCAAATTCATAACATCACCATGAGTTTGGTCCGAAGCATGAGTGTTTACAATGTTTGAATACCTTAT

To add another secondary structure, chose a secondary structure predictor in the list below or type directly the structure. Finally ask to add the structure to the description by clicking the above link.

See [RNAfold](#) secondary structure prediction:

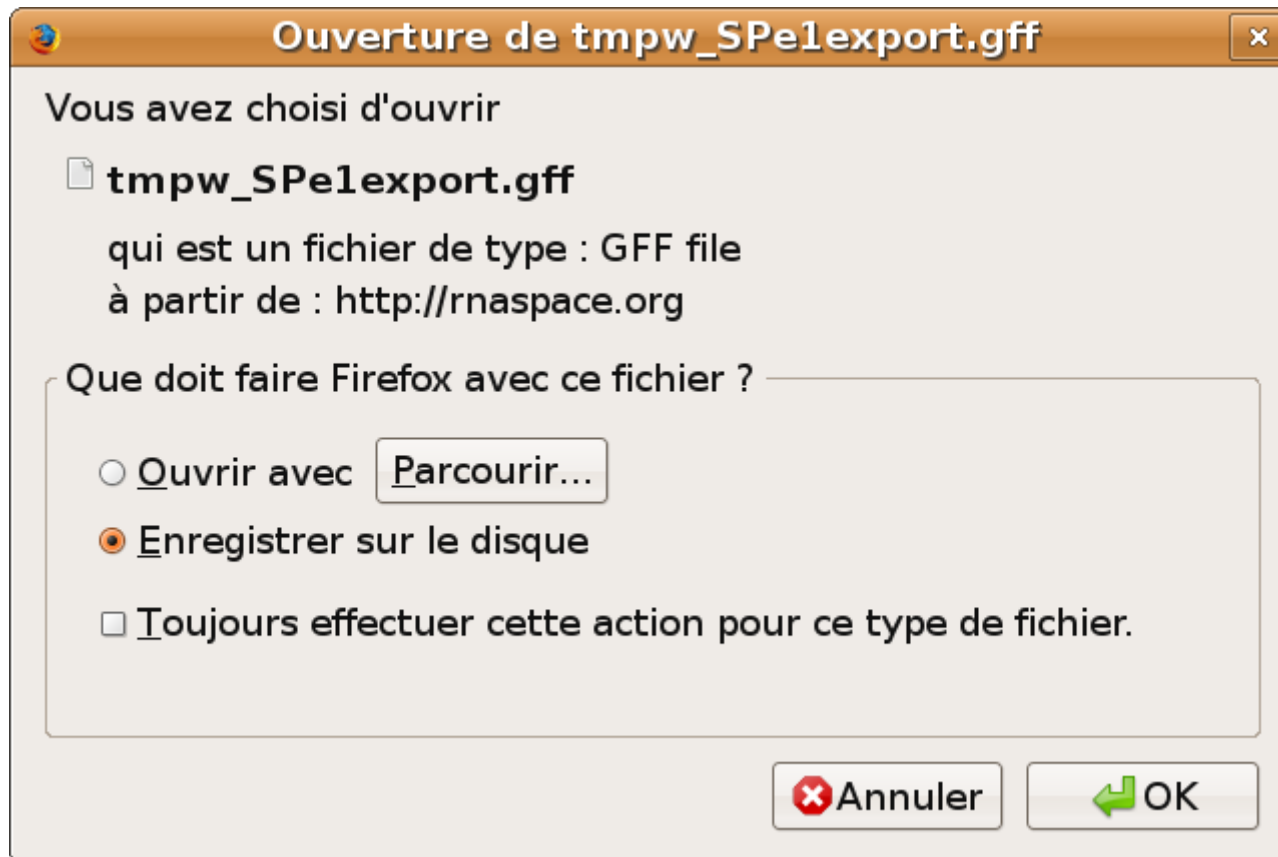
[Add this structure in the preview page](#)

[Save](#)

Comments and remarks: contact@rnaspace.org.

00723	seq_000001	Type_I_tRNA	550023	550093	71	+	unknown	bacteria	unknown	erpin	0	r03
00955	seq_000001	unknown	550057	550241	185	.	unknown	bacteria	unknown	atypicalGC	0	r04
00240	seq_000001	tRNA-Leu	550105	550193	89	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
00771	seq_000001	Type_II_tRNA	550105	550189	85	+	unknown	bacteria	unknown	erpin	0	r03
00852	seq_000001	tRNA	550105	550465	361	.	unknown	bacteria	unknown	YASS	0	r03
00241	seq_000001	tRNA-Arg	550199	550275	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
00724	seq_000001	Type_I_tRNA	550199	550271	73	+	unknown	bacteria	unknown	erpin	0	r03
00242	seq_000001	tRNA-Pro	550296	550369	74	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
00725	seq_000001	Type_I_tRNA	550296	550368	73	+	unknown	bacteria	unknown	erpin	0	r03
00956	seq_000001	unknown	550343	550468	126	.	unknown	bacteria	unknown	atypicalGC	0	r04
00243	seq_000001	tRNA-Ala	550393	550468	76	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
00726	seq_000001	Type_I_tRNA	550393	550464	72	+	unknown	bacteria	unknown	erpin	0	r03
00881	seq_000001	SSU_rRNA_5	550593	552111	1519	.	unknown	bacteria	unknown	YASS	0	r03
00668	seq_000001	16s_rRNA	550597	552136	1540	+	unknown	bacteria	unknown	RNAmmer	0	r01
00957	seq_000001	unknown	550615	550743	129	.	unknown	bacteria	unknown	atypicalGC	0	r04
00958	seq_000001	unknown	550822	551037	216	.	unknown	bacteria	unknown	atypicalGC	0	r04
00959	seq_000001	unknown	551073	551858	786	.	unknown	bacteria	unknown	atypicalGC	0	r04
00695	seq_000001	16S_rRNA_helix_18	551101	551136	36	+	unknown	bacteria	unknown	erpin	0	r03
00960	seq_000001	unknown	551934	552145	212	.	unknown	bacteria	unknown	atypicalGC	0	r04
00244	seq_000001	tRNA-Ile	552236	552312	77	+	unknown	bacteria	unknown	tRNAscan-SE	0	r01
00727	seq_000001	Type_I_tRNA	552236	552308	73	+	unknown	bacteria	unknown	erpin	0	r03
00772	seq_000001	Type_II_tRNA	552236	552308	73	+	unknown	bacteria	unknown	erpin	0	r03
00853	seq_000001	tRNA	552236	552309	74	.	unknown	bacteria	unknown	YASS	0	r03
00657	seq_000001	23s_rRNA	552482	555402	2921	+	unknown	bacteria	unknown	RNAmmer	0	r01
00820	seq_000001	5_8S_rRNA	552492	552648	157	.	unknown	bacteria	unknown	YASS	0	r03
00961	seq_000001	unknown	552509	552576	68	.	unknown	bacteria	unknown	atypicalGC	0	r04
00962	seq_000001	unknown	552685	552785	101	.	unknown	bacteria	unknown	atypicalGC	0	r04
00963	seq_000001	unknown	552886	553133	248	.	unknown	bacteria	unknown	atypicalGC	0	r04
00964	seq_000001	unknown	553140	553473	334	.	unknown	bacteria	unknown	atypicalGC	0	r04
00965	seq_000001	unknown	553504	553558	55	.	unknown	bacteria	unknown	atypicalGC	0	r04
00966	seq_000001	unknown	553654	554065	412	.	unknown	bacteria	unknown	atypicalGC	0	r04
00967	seq_000001	unknown	554067	555275	1209	.	unknown	bacteria	unknown	atypicalGC	0	r04
00839	seq_000001	PK-G12rRNA	554788	554896	109	.	unknown	bacteria	unknown	YASS	0	r03
00882	seq_000001	SSU_rRNA_5	554938	555115	178	.	unknown	bacteria	unknown	YASS	0	r03
00701	seq_000001	[23S/28S_rRNA_sarcin_...]	555153	555180	28	+	unknown	bacteria	unknown	erpin	0	r03
00875	seq_000001	5S_rRNA	555475	555589	115	.	unknown	bacteria	unknown	YASS	0	r03
00662	seq_000001	5s_rRNA	555477	555590	114	+	unknown	bacteria	unknown	RNAmmer	0	r01

selected predictions:



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Results for job 0000290522b816b: **0 RNAs found** (run r01: 678 RNAs, run r02: 9 RNAs, run r03: 202 RNAs, run r04: 237 RNAs)

Gene finder(s)		
62 RNAs	tRNAscan-SE	r01
9 RNAs	BLAST	r01
591 RNAs	atypicalGC	r01
16 RNAs	RNAmmer	r01
9 RNAs	BLAST	r02
80 RNAs	YASS	r03
122 RNAs	erpin	r03
237 RNAs	atypicalGC	r04

Query sequence(s)					
seq_000001	2814816 nt	bacteria	unknown	unknown	unknown

RNA predictions may be explored using the below dynamic filtering capabilities to update the following table... [click for +/-](#) ...

Field	Operator	Value	
Criterion	Comparison	Give value	<input type="button" value="Add/Update"/>

Predictions 0 - 0 of 0 Display **Terse set** Show **1000** Page 0 of 0

All	ID	Seq name	Family	Begin	End	Size	Strand	Species	Domain	Replicon	Predictor	Align.	Run
-----	----	----------	--------	-------	-----	------	--------	---------	--------	----------	-----------	--------	-----

With selected predictions:	<input type="button" value="Edit..."/>	<input type="button" value="Analyse..."/>	<input type="button" value="Export..."/>
With all predictions:	<input type="button" value="EXPORT..."/>		

Comments and remarks: contact@rnaspace.org.

Côté technique

Language de développement : Python

Framework WEB : Cherrypy

-> simplicité d'utilisation

Système de template: Cheetah

-> syntaxe proche du python

Architecture 3tiers :

- couche interface utilisateur
- couche métier
- couche accès au données

Modèle de conception MVC

- Model
- Vue
- Controleur

Perspectives

... à court terme

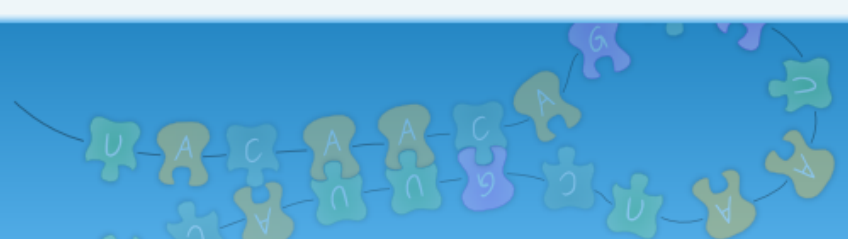
- Finaliser les tests, ouvrir le site et le publier

... à plus long terme

- Site authentifié
- Ajout de fonctionnalités
 - * accéder au génome,
 - * combiner de manière pertinente les prédictions
 - * ajouter des outils de prédiction et d'exploration
- Etre plus efficace pour relever le défi du haut débit

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Home

1. Load data

2. Predict

3. Explore



Funding

RNASpace is funded since 2007 by the RNG (french National Network of Genomic Centers) for two years.

Partners

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Marie-Josée Cros
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PF Bioinformatique, INRA Toulouse

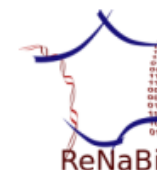
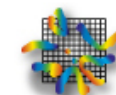
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