RP-001
Prova Prática

Tarcísio Fontenele de Brito

Rio de Janeiro, 31.01.2025

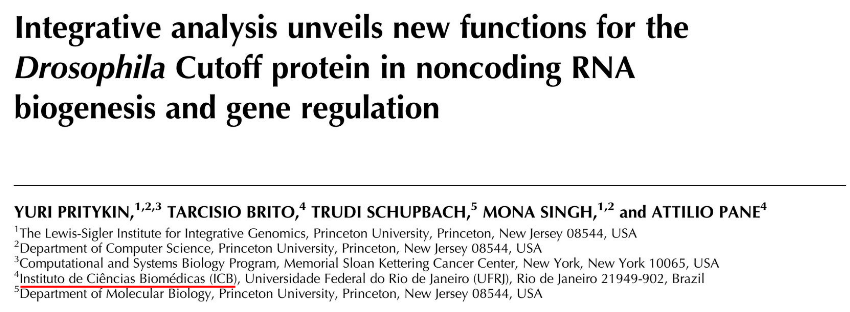
Histórico

Histórico

- Graduação
    - Orientador: Prof. Attilio Pane

instituto de biologia
UNIVERSIDADE FEDERAL DO RIO DE JANEIRO

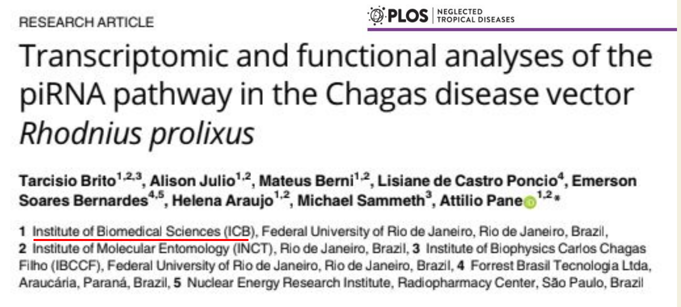
ICB INSTITUTO DE CIÊNCIAS BIOMÉDICAS



Integrative analysis unveils new functions for the *Drosophila* Cutoff protein in noncoding RNA biogenesis and gene regulation

YURI PRITYKIN,[1,2,3] TARCISIO BRITO,[4] TRUDI SCHUPBACH,[5] MONA SINGH,[1,2] and ATTILIO PANE[4]

[1]The Lewis-Sigler Institute for Integrative Genomics, Princeton University, Princeton, New Jersey 08544, USA
[2]Department of Computer Science, Princeton University, Princeton, New Jersey 08544, USA
[3]Computational and Systems Biology Program, Memorial Sloan Kettering Cancer Center, New York, New York 10065, USA
[4]Instituto de Ciências Biomédicas (ICB), Universidade Federal do Rio de Janeiro (UFRJ), Rio de Janeiro 21949-902, Brazil
[5]Department of Molecular Biology, Princeton University, Princeton, New Jersey 08544, USA



RESEARCH ARTICLE

PLOS NEGLECTED TROPICAL DISEASES

Transcriptomic and functional analyses of the piRNA pathway in the Chagas disease vector *Rhodnius prolixus*

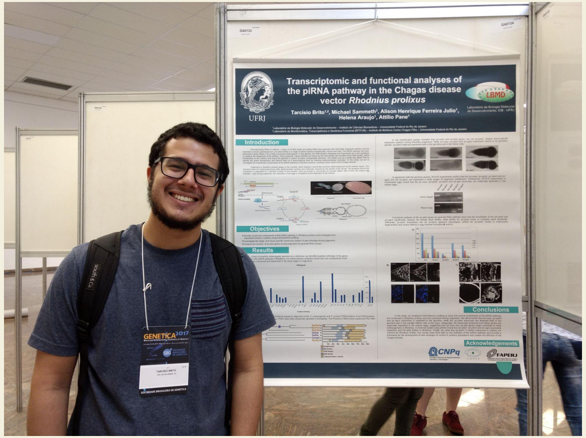
Tarcisio Brito[1,2,3], Alison Julio[1,2], Mateus Berni[1,2], Lisiane de Castro Poncio[4], Emerson Soares Bernardes[4,5], Helena Araujo[1,2], Michael Sammeth[3], Attilio Pane[1,2]*

1 Institute of Biomedical Sciences (ICB), Federal University of Rio de Janeiro, Rio de Janeiro, Brazil, 2 Institute of Molecular Entomology (INCT), Rio de Janeiro, Brazil, 3 Institute of Biophysics Carlos Chagas Filho (IBCCF), Federal University of Rio de Janeiro, Rio de Janeiro, Brazil, 4 Forrest Brasil Tecnologia Ltda, Araucária, Paraná, Brazil, 5 Nuclear Energy Research Institute, Radiopharmacy Center, São Paulo, Brazil

Histórico

- Graduação
  - Orientador: Prof. Attilio Pane
  - Coorientador: Prof. Michael Sammeth

BITFUN



GENETICA 2017
BRAZILIAN-INTERNATIONAL CONGRESS OF GENETICS

SEPTEMBER 12-15, 2017
MONTE REAL RESORT - ÁGUAS DE LINDÓIA/SP - BRAZIL

Certificado

A Sociedade Brasileira de Genética concede a *TARCÍSIO FONTENELE DE BRITO* o Prêmio Painel Graduação de melhor trabalho na área de GENÉTICA ANIMAL, intitulado "TRANSCRIPTOMIC AND FUNCTIONAL ANALYSES OF THE PIRNA PATHWAY IN THE CHAGAS DISEASE VECTOR RHODNIUS PROLIXUS" autoria de BRITO, T.F.; SAMMETH, M.; JULIO, A.H.; ARAUJO, H.M.; PANE, A. apresentado durante o *GENÉTICA 2017 - Brazilian-International Congress of Genetics* , em Águas de Lindóia, SP, período de 12 a 15 de Setembro de 2017.

Patrocinador: Myleus Biotecnologia GA0134

Márcia Maria A N P Margis
Presidente da SBG

SBG SOCIEDADE BRASILEIRA DE GENÉTICA

Nilce Maria Martinez Rossi
Primeira Secretária da SBG

Histórico

PCM UFRJ

ICB INSTITUTO DE CIÊNCIAS BIOMÉDICAS

- Graduação
- Doutorado direto
  - Orientação: Prof. Attilio Pane
  - Projeto: Caracterizar perfil de pequenos RNAs não-codificantes no vetor da doença de Chagas *Rhodnius prolixus*
  - Análise de dados de RNA-Seq e smallRNA-seq (PVS e Ovo maduro)

Laboratório de Genômica Funcional

Histórico

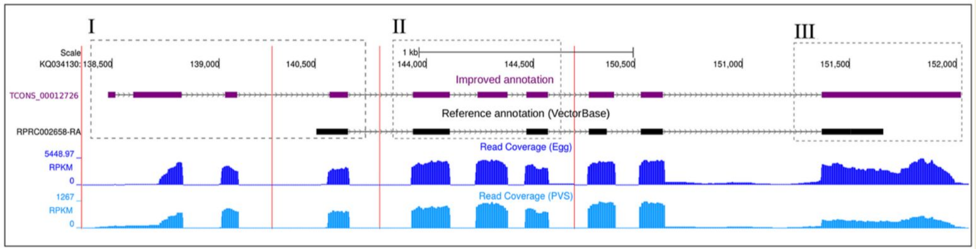
- Graduação
- Doutorado

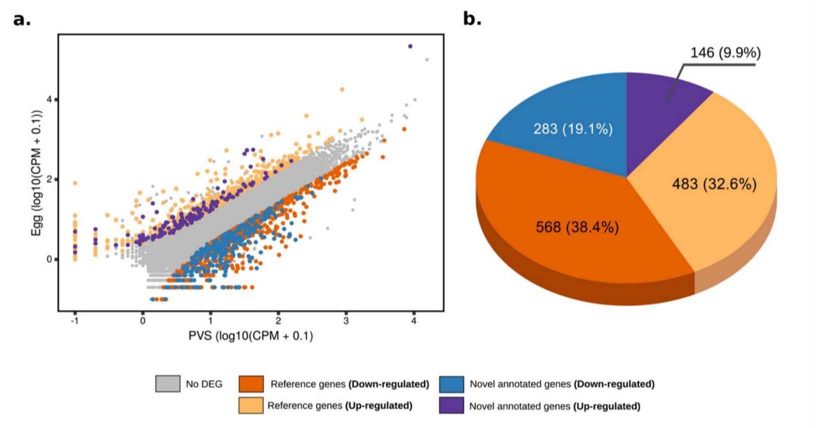
www.nature.com/scientificreports

scientific reports

Analysis of ovarian transcriptomes reveals thousands of novel genes in the insect vector *Rhodnius prolixus*

Vitor Lima Coelho[1], Tarcísio Fontenele de Brito[1], Ingrid Alexandre de Abreu Brito[1], Maira Arruda Cardoso[1], Mateus Antonio Berni[1], Helena Maria Marcolla Araujo[1,3], Michael Sammeth[2,4] & Attilio Pane[1]✉





Histórico

- Graduação
- Doutorado

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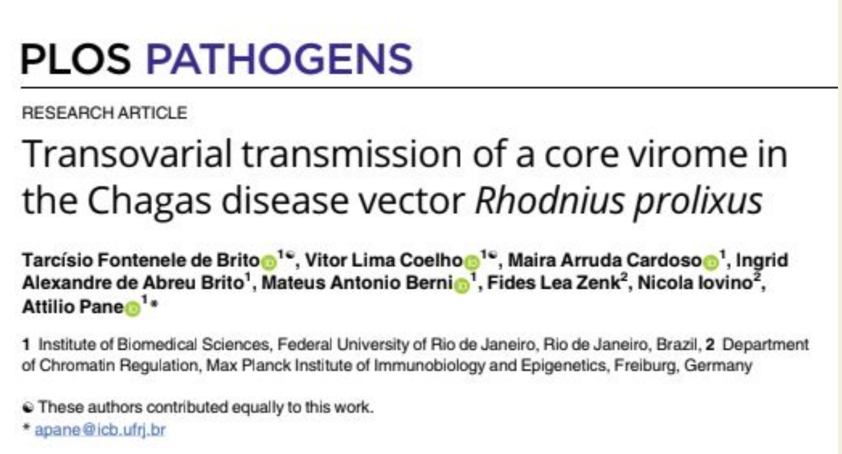


PLOS PATHOGENS

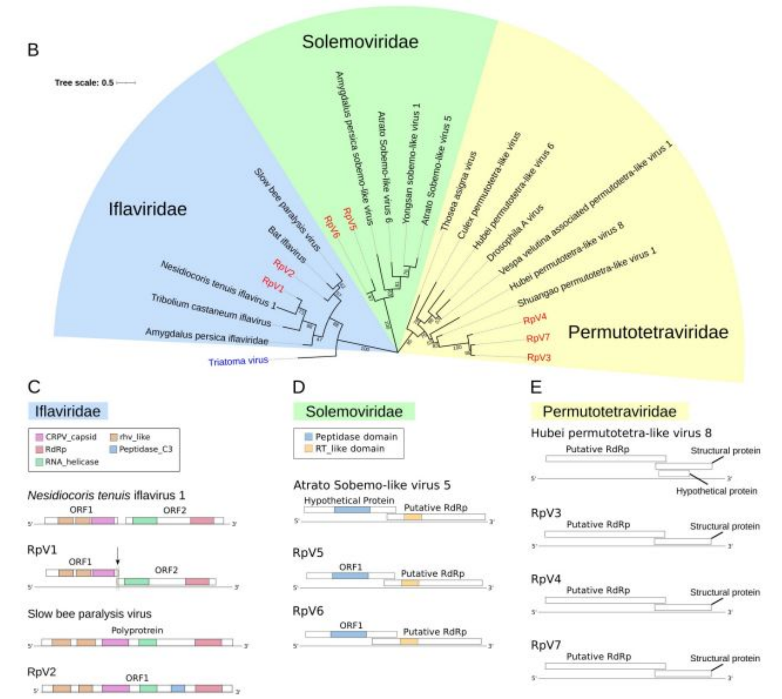
RESEARCH ARTICLE

Transovarial transmission of a core virome in the Chagas disease vector *Rhodnius prolixus*

Tarcísio Fontenele de Brito[1☯], **Vitor Lima Coelho**[1☯], **Maira Arruda Cardoso**[1], **Ingrid Alexandre de Abreu Brito**[1], **Mateus Antonio Berni**[1], **Fides Lea Zenk**[2], **Nicola Iovino**[2], **Attilio Pane**[1*]

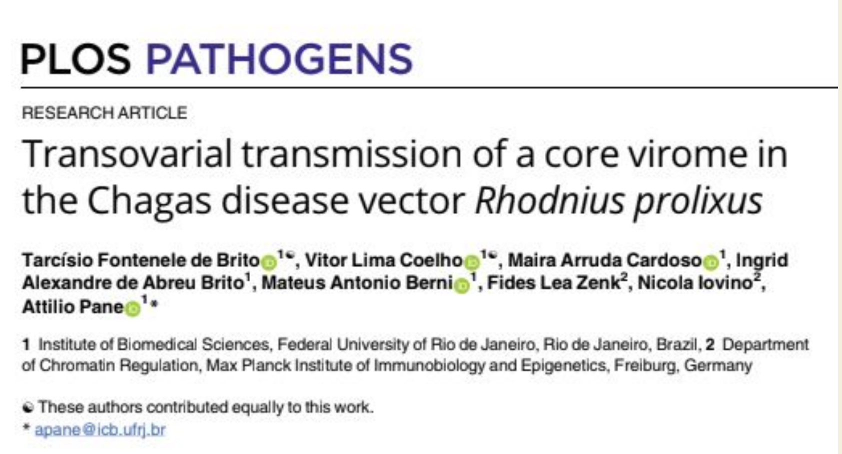
1 Institute of Biomedical Sciences, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil, **2** Department of Chromatin Regulation, Max Planck Institute of Immunobiology and Epigenetics, Freiburg, Germany

☯ These authors contributed equally to this work.
* apane@icb.ufrj.br



Histórico

- Graduação
- Doutorado



PLOS PATHOGENS

RESEARCH ARTICLE

Transovarial transmission of a core virome in the Chagas disease vector *Rhodnius prolixus*

Tarcísio Fontenele de Brito[1◐], Vitor Lima Coelho[1◐], Maira Arruda Cardoso[1], Ingrid Alexandre de Abreu Brito[1], Mateus Antonio Berni[1], Fides Lea Zenk[2], Nicola Iovino[2], Attilio Pane[1]*

1 Institute of Biomedical Sciences, Federal University of Rio de Janeiro, Rio de Janeiro, Brazil, 2 Department of Chromatin Regulation, Max Planck Institute of Immunobiology and Epigenetics, Freiburg, Germany

◐ These authors contributed equally to this work.
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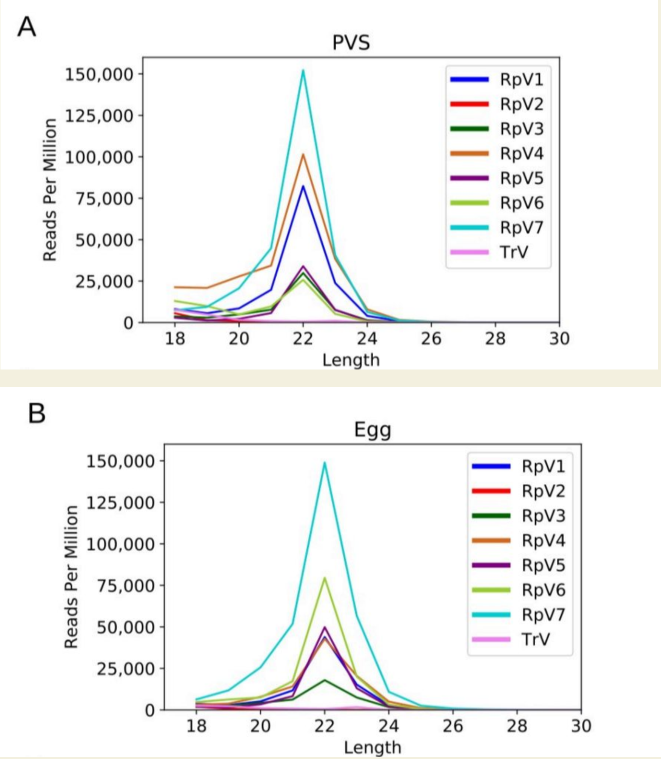

Histórico

- Graduação
- Doutorado
    - 1 ano Max Planck Institute
    - Dr. Nicola Iovino
    - RNA-Seq, ChIP-Seq, CUT&Tag, ATAC-Seq
    - Snakemake, HPC, Linux Avançado

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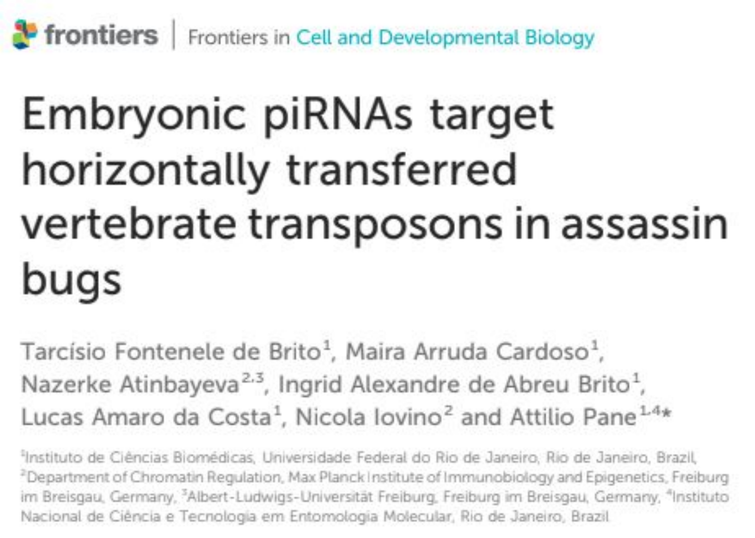
MAX PLANCK INSTITUTE
OF IMMUNOBIOLOGY AND EPIGENETICS

Histórico

UFRJ

INSTITUTO DE CIÊNCIAS BIOMÉDICAS

- Graduação
- Doutorado

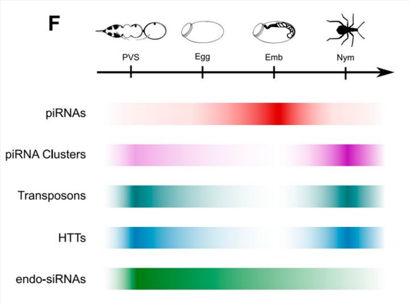


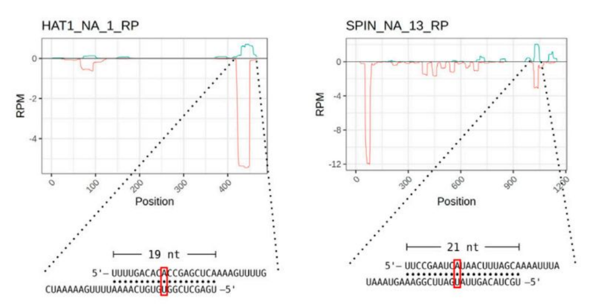
frontiers | Frontiers in Cell and Developmental Biology

Embryonic piRNAs target horizontally transferred vertebrate transposons in assassin bugs

Tarcísio Fontenele de Brito[1], Maira Arruda Cardoso[1], Nazerke Atinbayeva[2,3], Ingrid Alexandre de Abreu Brito[1], Lucas Amaro da Costa[1], Nicola Iovino[2] and Attilio Pane[1,4]*

[1]Instituto de Ciências Biomédicas, Universidade Federal do Rio de Janeiro, Rio de Janeiro, Brazil, [2]Department of Chromatin Regulation, Max Planck Institute of Immunobiology and Epigenetics, Freiburg im Breisgau, Germany, [3]Albert-Ludwigs-Universität Freiburg, Freiburg im Breisgau, Germany, [4]Instituto Nacional de Ciência e Tecnologia em Entomologia Molecular, Rio de Janeiro, Brazil





Histórico

- Graduação
- Doutorado
- Pós-doutorado:
    - PPG Anatomia Patológica (ICB-UFRJ)
        - Coord.: Prof. Kátia Carneiro
        - WES, DNAme, RNA-Seq, smallRNA-Seq
    - Programa de Carcinogênese Molecular
        - Prof. Luís Felipe Ribeiro Pinto
        - DNAme, ATAC-Seq, RNA-Seq

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- Start up em Bioinformática
- Prof. Attilio Pane
- Desafios
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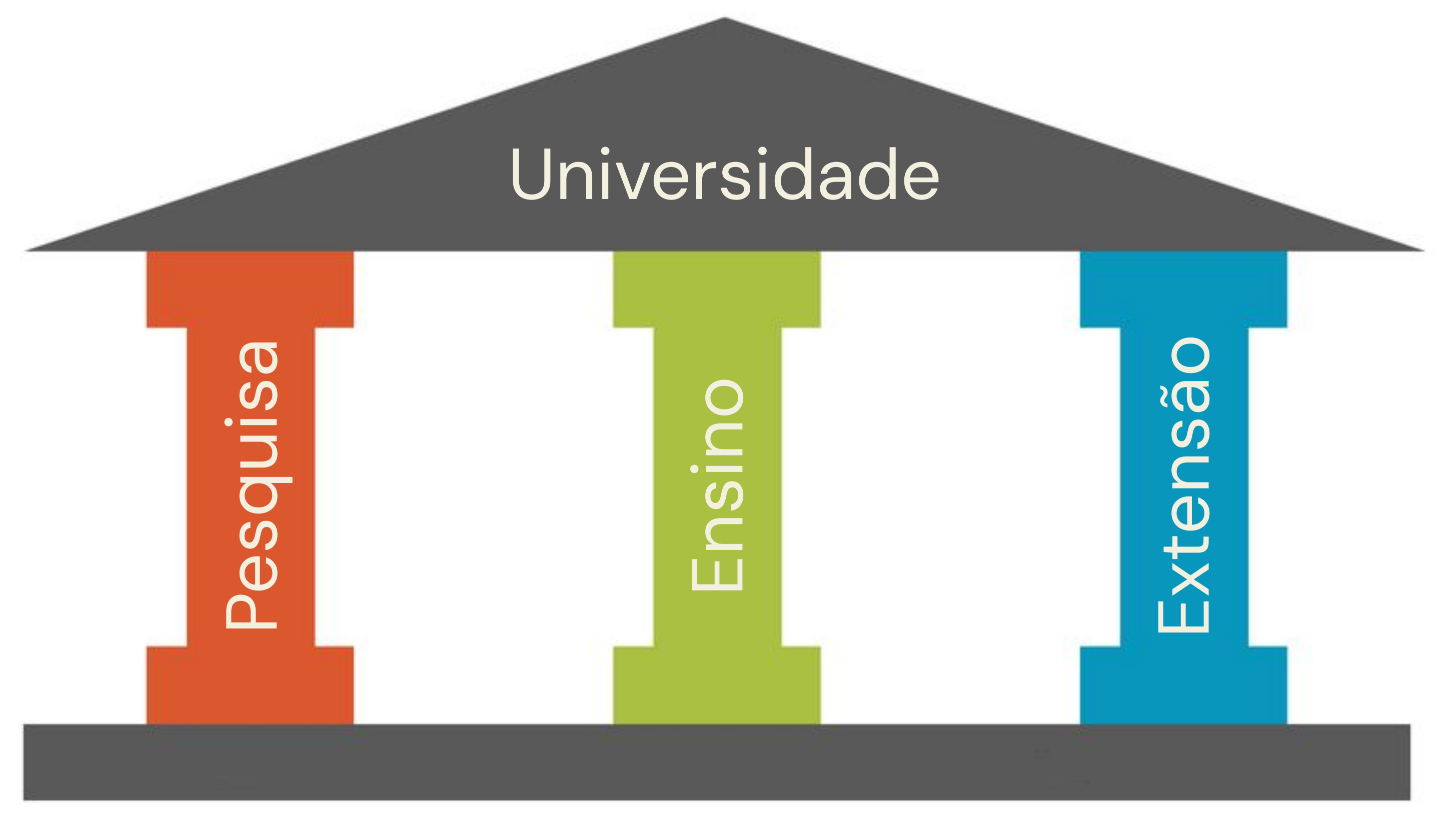
Projeto

Art. 207 - princípio da indissociabilidade



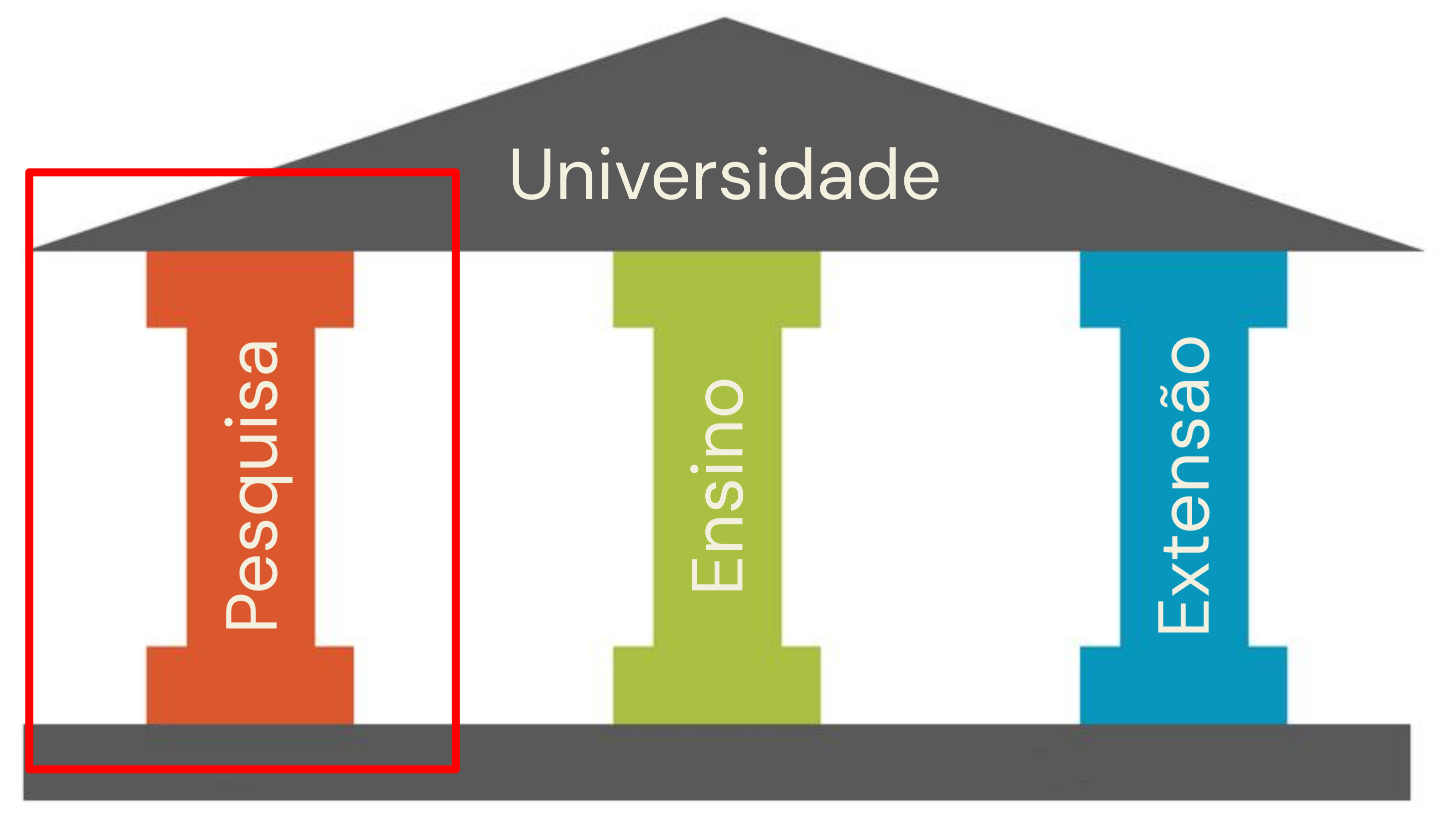
Universidade

Pesquisa

Ensino

Extensão

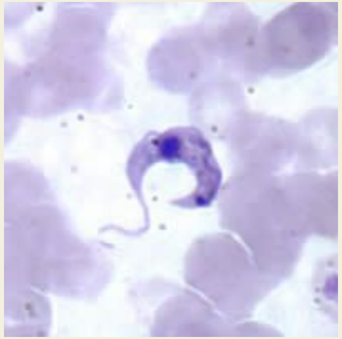
Art. 207 - princípio da indissociabilidade



Rhodnius prolixus

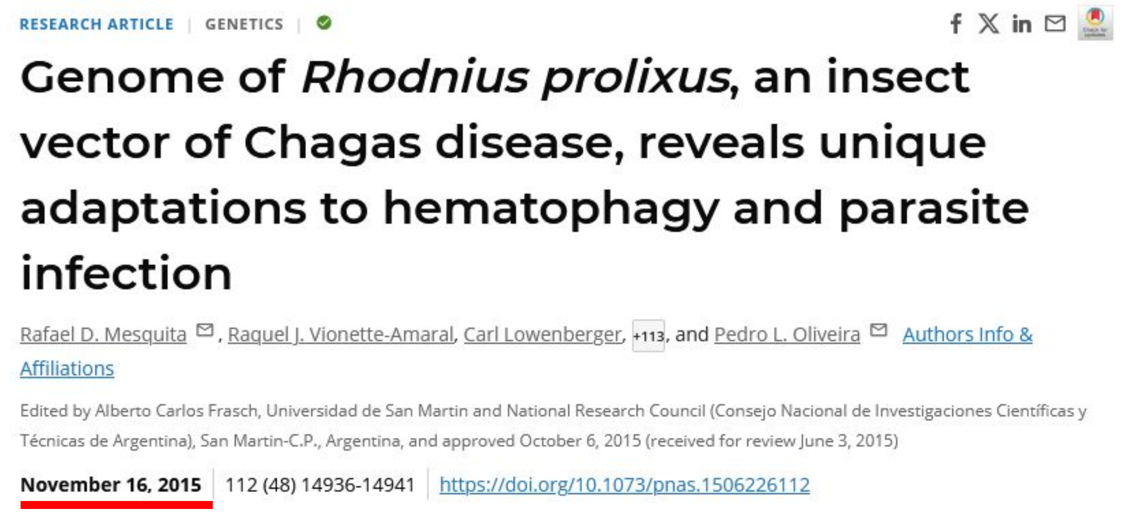
- Triatomíneo da ordem Hemiptera
- Hematófago
- Um dos principais vetores da doença de Chagas
- Agente etiológico: *Trypanosoma cruzi*
- doença de Chagas:
    - Parasitose endêmica em 21 países da América Latina
    - ~ 6 a 7 milhões de pessoas no mundo acometidas pela doença
    - Atinge principalmente populações mais pobres
    - Não existem vacinas ou cura

Rhodnius prolixus



Trypanosoma cruzi

Genoma de *Rhodnius prolixus*



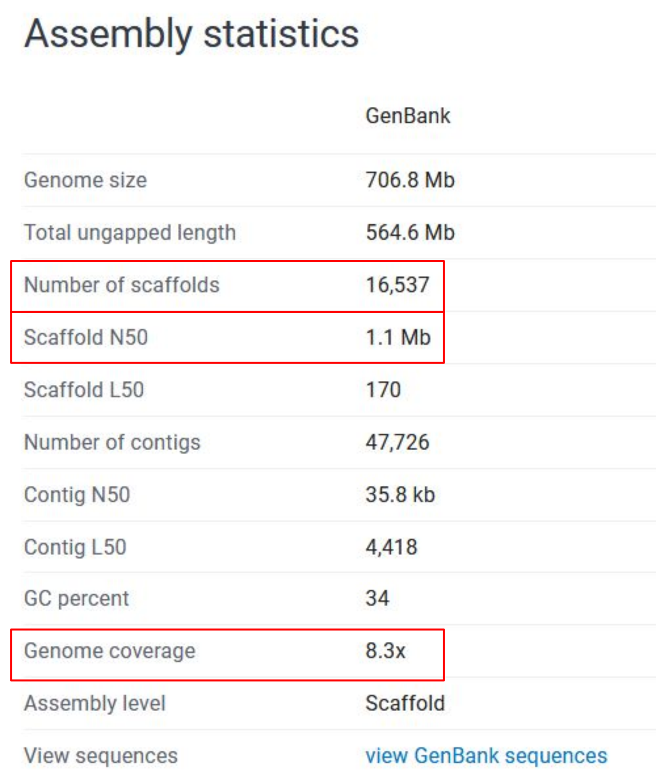
RESEARCH ARTICLE | GENETICS |

Genome of *Rhodnius prolixus*, an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection

Rafael D. Mesquita, Raquel J. Vionette-Amaral, Carl Lowenberger, +113, and Pedro L. Oliveira Authors Info & Affiliations

Edited by Alberto Carlos Frasch, Universidad de San Martin and National Research Council (Consejo Nacional de Investigaciones Científicas y Técnicas de Argentina), San Martin-C.P., Argentina, and approved October 6, 2015 (received for review June 3, 2015)

November 16, 2015 | 112 (48) 14936-14941 | https://doi.org/10.1073/pnas.1506226112



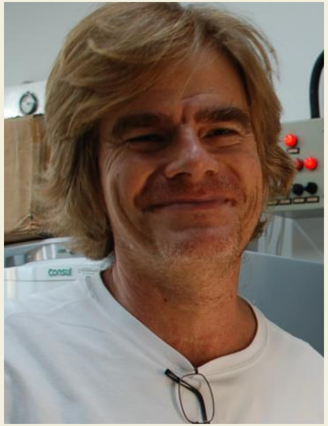
Assembly statistics

	GenBank
Genome size	706.8 Mb
Total ungapped length	564.6 Mb
Number of scaffolds	16,537
Scaffold N50	1.1 Mb
Scaffold L50	170
Number of contigs	47,726
Contig N50	35.8 kb
Contig L50	4,418
GC percent	34
Genome coverage	8.3x
Assembly level	Scaffold
View sequences	view GenBank sequences

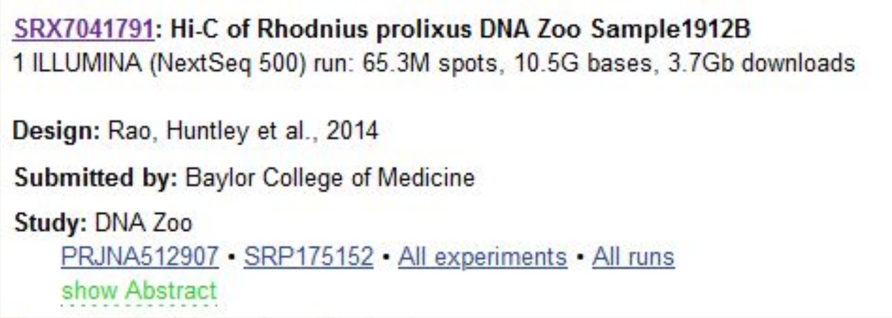
Nova montagem do genoma de *Rhodnius prolixus*

- Sequenciamento Oxford Nanopore
- Sequenciamento Illumina
- Incorporação de dados de Hi-C

Professor Attilio Pane
(ICB-UFRJ)



Professor Bernardo de Carvalho
(IB-UFRJ)



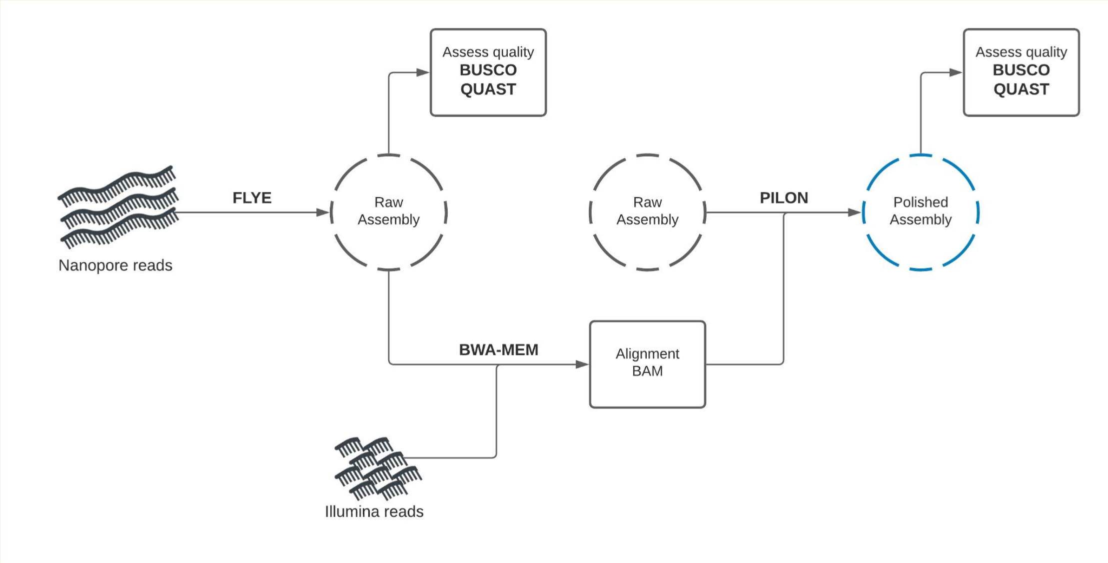
SRX7041791: Hi-C of Rhodnius prolixus DNA Zoo Sample1912B
1 ILLUMINA (NextSeq 500) run: 65.3M spots, 10.5G bases, 3.7Gb downloads

Design: Rao, Huntley et al., 2014

Submitted by: Baylor College of Medicine

Study: DNA Zoo
PRJNA512907 • SRP175152 • All experiments • All runs
show Abstract

Metodologia de montagem *Rhodnius prolixus*




Methodology Article | Open access | Published: 12 July 2017

Scaffolding of long read assemblies using long range contact information

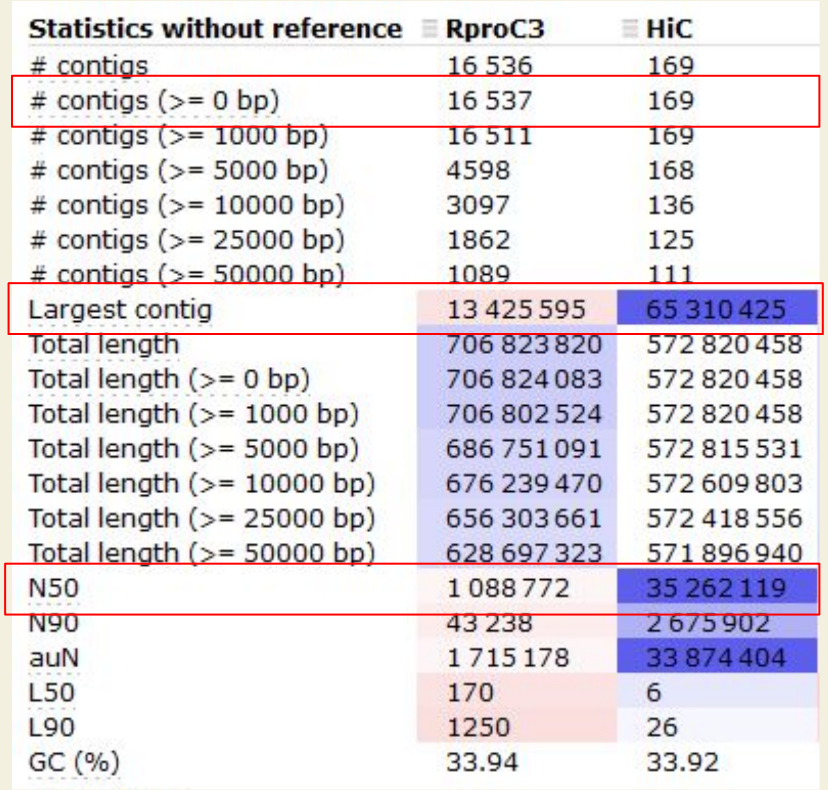
Jay Ghurye, Mihai Pop, Sergey Koren, Derek Bickhart & Chen-Shan Chin

BMC Genomics **18**, Article number: 527 (2017) | Cite this article

11k Accesses | **163** Citations | **11** Altmetric | Metrics

Montagem *Rhodnius prolixus*: Resultados preliminares

- Sequenciamento Oxford Nanopore
- Sequenciamento Illumina
- Incorporação de dados de Hi-C
- Aumentar cobertura

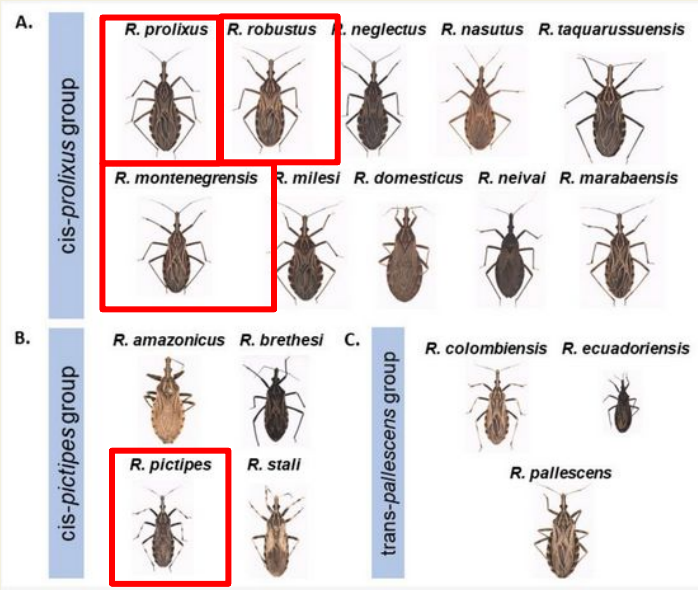


Statistics without reference	RproC3	HiC
# contigs	16 536	169
# contigs (>= 0 bp)	16 537	169
# contigs (>= 1000 bp)	16 511	169
# contigs (>= 5000 bp)	4598	168
# contigs (>= 10000 bp)	3097	136
# contigs (>= 25000 bp)	1862	125
# contigs (>= 50000 bp)	1089	111
Largest contig	13 425 595	65 310 425
Total length	706 823 820	572 820 458
Total length (>= 0 bp)	706 824 083	572 820 458
Total length (>= 1000 bp)	706 802 524	572 820 458
Total length (>= 5000 bp)	686 751 091	572 815 531
Total length (>= 10000 bp)	676 239 470	572 609 803
Total length (>= 25000 bp)	656 303 661	572 418 556
Total length (>= 50000 bp)	628 697 323	571 896 940
N50	1 088 772	35 262 119
N90	43 238	2 675 902
auN	1 715 178	33 874 404
L50	170	6
L90	1250	26
GC (%)	33.94	33.92

Viroma de Triatomíneos

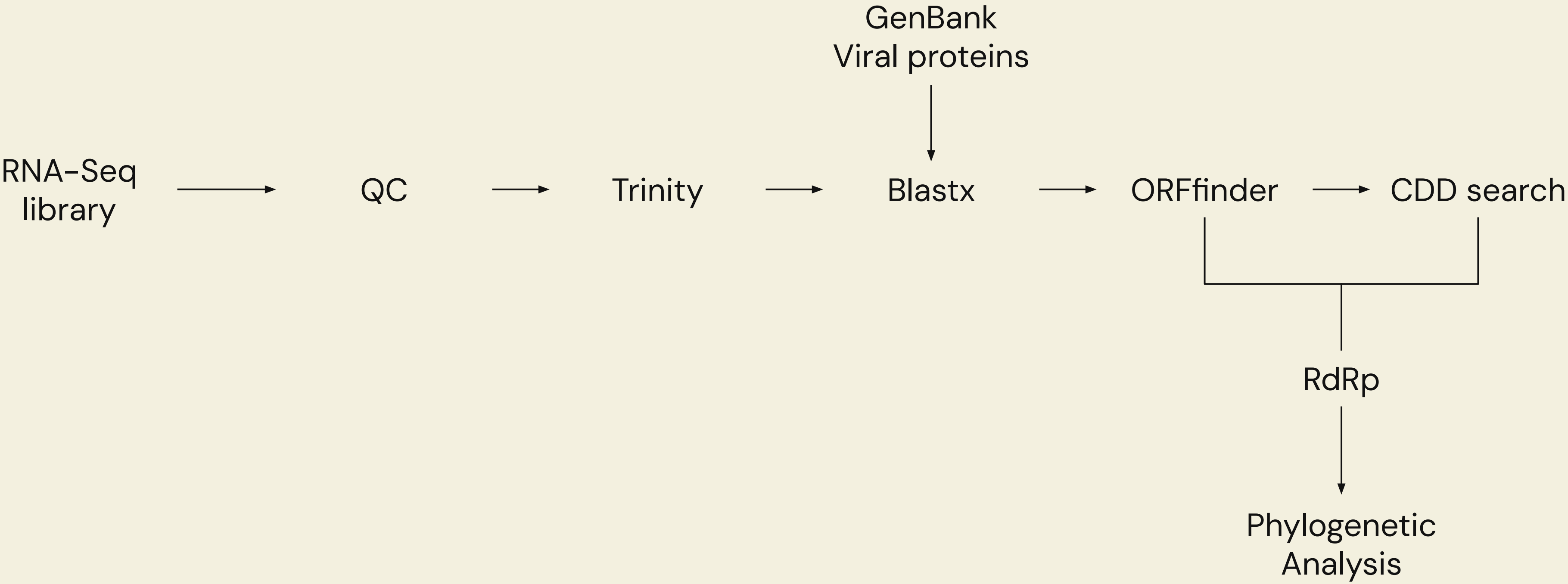
- Triatomíneos selvagens
- Diversas regiões do Brasil (SP, PA, RJ)
- Análise de Transcriptoma
- Identificação de vírus de RNA
- Anotação do genoma viral
- Estabelecer relações evolutivas

Professor Attilio Pane
(ICB-UFRJ)



Hernández, C.; Aristeu da Rosa, J.; Vallejo, G.A.; Guhl, F.; Ramírez, J.D. Taxonomy, Evolution, and Biogeography of the Rhodniini Tribe (Hemiptera: Reduviidae). *Diversity* **2020**, *12*, 97. https://doi.org/10.3390/d12030097

Viroma de Triatomíneos: Metodologia



RNA-Seq library

QC

Trinity

GenBank Viral proteins

Blastx

ORFfinder

CDD search

RdRp

Phylogenetic Analysis

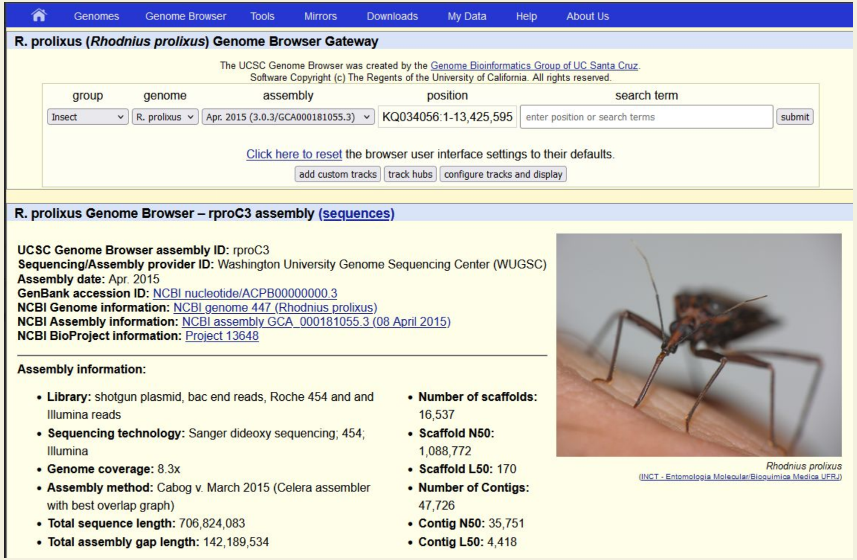
Infraestrutura para pesquisa e ensino em Bioinformática

- Servidor para processamento de dados
- Expansível
- Ferramentas multi-usuário online
- Pesquisa e ensino
- Democratização da bioinformática

Servidor para processamento de dados junto com outros servidores do ICB

Infraestrutura para pesquisa e ensino em Bioinformática

UCSC Genome Browser Local



R. prolixus (*Rhodnius prolixus*) Genome Browser Gateway

The UCSC Genome Browser was created by the Genome Bioinformatics Group of UC Santa Cruz.
Software Copyright (c) The Regents of the University of California. All rights reserved.

group	genome	assembly	position	search term
Insect	R. prolixus	Apr. 2015 (3.0.3/GCA000181055.3)	KQ034056:1-13,425,595	enter position or search terms

Click here to reset the browser user interface settings to their defaults.

R. prolixus Genome Browser – rproC3 assembly (sequences)

UCSC Genome Browser assembly ID: rproC3
Sequencing/Assembly provider ID: Washington University Genome Sequencing Center (WUGSC)
Assembly date: Apr. 2015
GenBank accession ID: NCBI nucleotide/ACPB00000000.3
NCBI Genome information: NCBI genome 447 (Rhodnius prolixus)
NCBI Assembly information: NCBI assembly GCA_000181055.3 (08 April 2015)
NCBI BioProject information: Project 13648

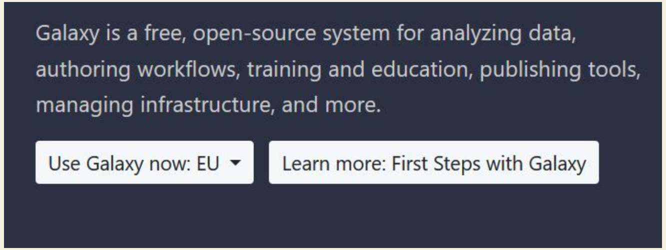
Assembly information:

- **Library:** shotgun plasmid, bac end reads, Roche 454 and and Illumina reads
- **Sequencing technology:** Sanger dideoxy sequencing; 454; Illumina
- **Genome coverage:** 8.3x
- **Assembly method:** Cabog v. March 2015 (Celera assembler with best overlap graph)
- **Total sequence length:** 706,824,083
- **Total assembly gap length:** 142,189,534
- **Number of scaffolds:** 16,537
- **Scaffold N50:** 1,088,772
- **Scaffold L50:** 170
- **Number of Contigs:** 47,726
- **Contig N50:** 35,751
- **Contig L50:** 4,418

Rhodnius prolixus
(INCT - Entomologia Molecular/Bioquimica Medica UFRJ)

Servidor Galaxy

Galaxy
COMMUNITY HUB

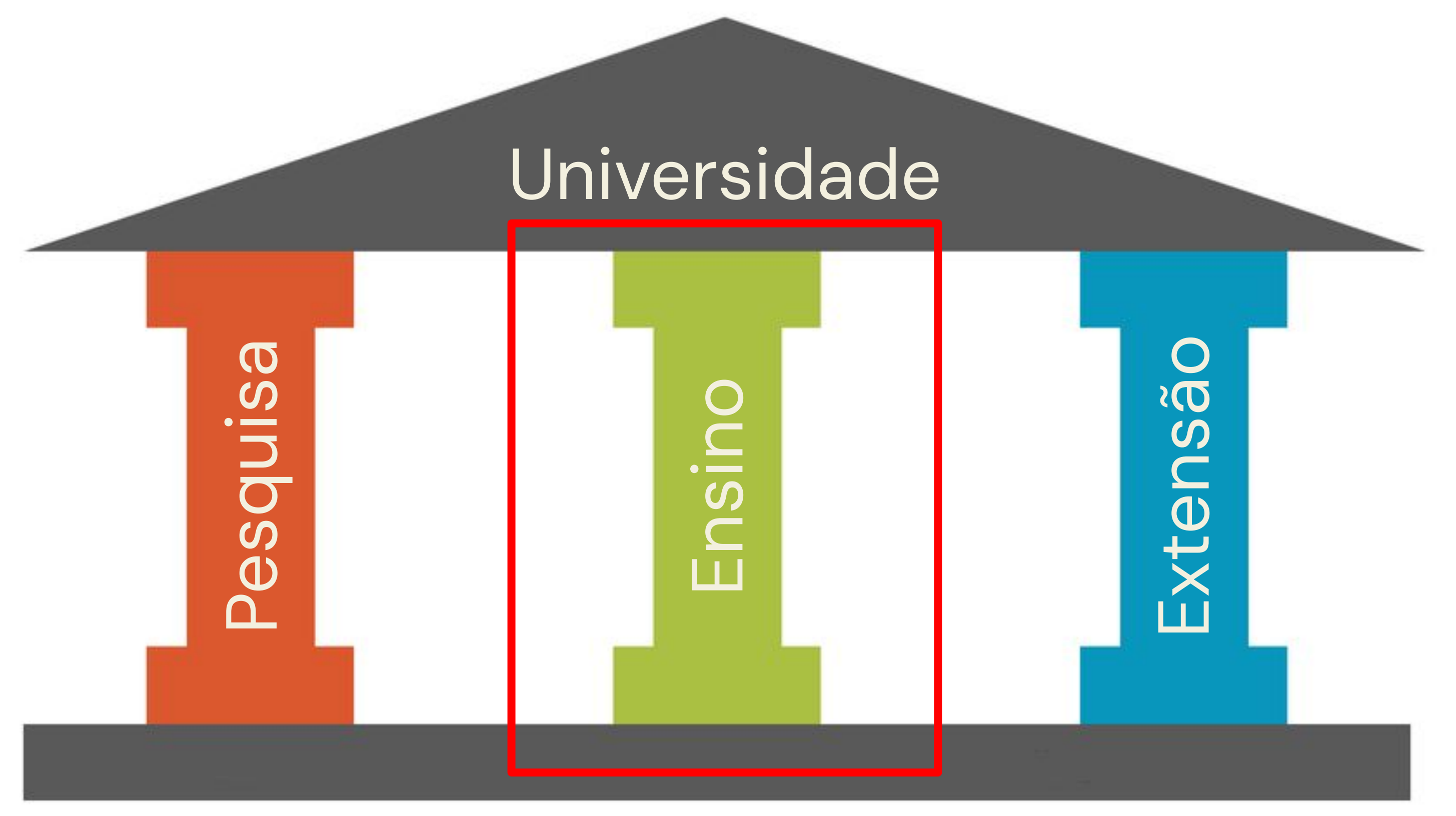


Galaxy is a free, open-source system for analyzing data, authoring workflows, training and education, publishing tools, managing infrastructure, and more.

Fortalecer e estabelecer novas colaborações

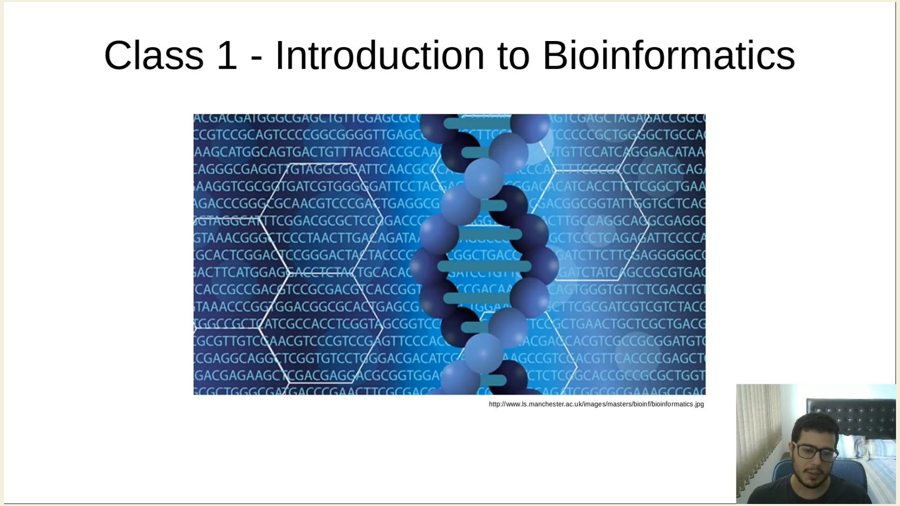
- Prof. Kátia Carneiro (ICB-UFRJ)
  - Linfoma de células do manto
    - WES
  - Gliomas (LGG e GBL)
    - TCGA: WES, DNAme
- Prof. Ana Bahia (IBCCF-UFRJ)
  - Infecções Mayaro e Dengue Virus em *Aedes aegypti*
    - RNA-Seq

Art. 207 - princípio da indissociabilidade



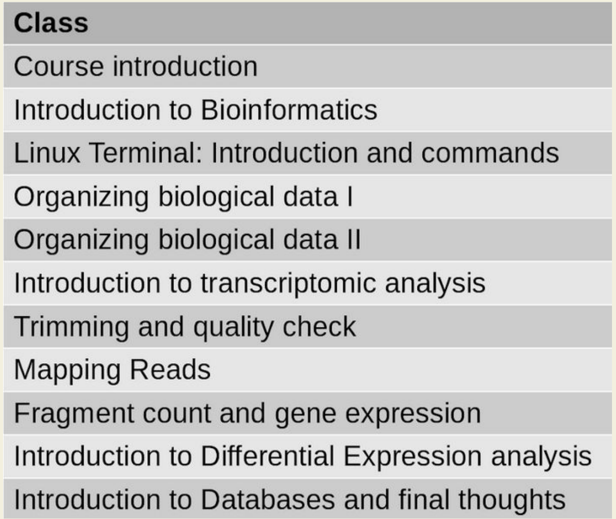
Ensino

- Disciplinas existentes
  - BMH(193/127/119) – Embriologia
  - BMM762 – Bioinformática Básica (português e inglês)
- Proposição de novas disciplinas
  - Epigenômica
  - Introdução a análise de dados com R



Class 1 - Introduction to Bioinformatics

http://www.ls.manchester.ac.uk/images/masters/bioinf/bioinformatics.jpg

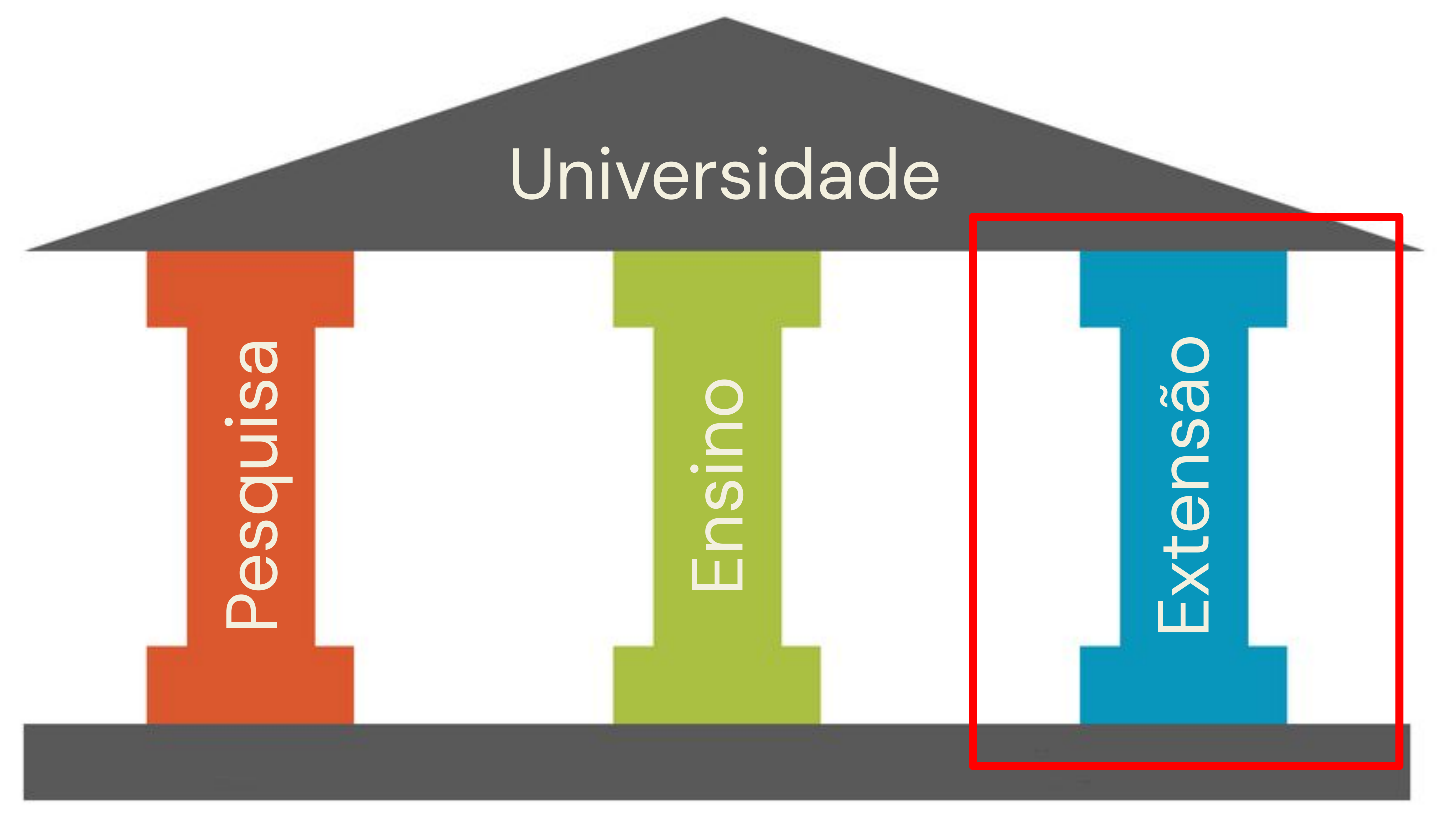


Class
Course introduction
Introduction to Bioinformatics
Linux Terminal: Introduction and commands
Organizing biological data I
Organizing biological data II
Introduction to transcriptomic analysis
Trimming and quality check
Mapping Reads
Fragment count and gene expression
Introduction to Differential Expression analysis
Introduction to Databases and final thoughts

Ensino

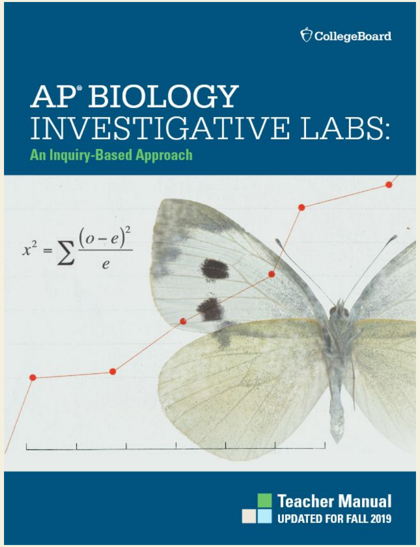
- Curso de Verão do PCM
- Propor oficinas
- Engajar alunos para ingresso na pós-graduação

Art. 207 - princípio da indissociabilidade



Laboratórios de Bioinformática em escolas

- Advanced Placement (AP)
- Adaptação do material e práticas
- Laboratórios Práticos
- Ensino Médio
- Envolvimento de Escolas



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$$x^2 = \sum \frac{(o-e)^2}{e}$$

Teacher Manual
UPDATED FOR FALL 2019

CollegeBoard

CollegeBoard
Advanced Placement
Program

LEADING PROFESSIONAL SOCIETY FOR
COMPUTATIONAL BIOLOGY AND BIOINFORMATICS
CONNECTING, TRAINING, EMPOWERING, WORLDWIDE

Bioinformatics Resources for High Schools

Extensão com envolvimento estudantil

- Engajamento estudantil no desenvolvimento da bioinformática
- Projetos de extensão com alunos protagonistas
- Projetos de extensão na UFRJ podem ser liderados por alunos

iSCB
INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY

iSCB REGIONAL Student GROUP
Brazil

BIOINFO
FORA DA BOLHA
RSG-BRAZIL

Tem alguma ideia interessante pra fomentar a Bioinformática no Brasil?

Envie sua ideia: Clique Aqui

Conclusão

- Formação Acadêmica
- Experiência Científica
- Experiência Técnica
- Experiência Didática
- Experiência internacional
- Experiência no setor privado

Obrigado!

1. **Pesquisa**
2. Ensino
3. Extensão

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2. Ensino
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1. **Pesquisa**
2. **Ensino**
3. **Extensão**

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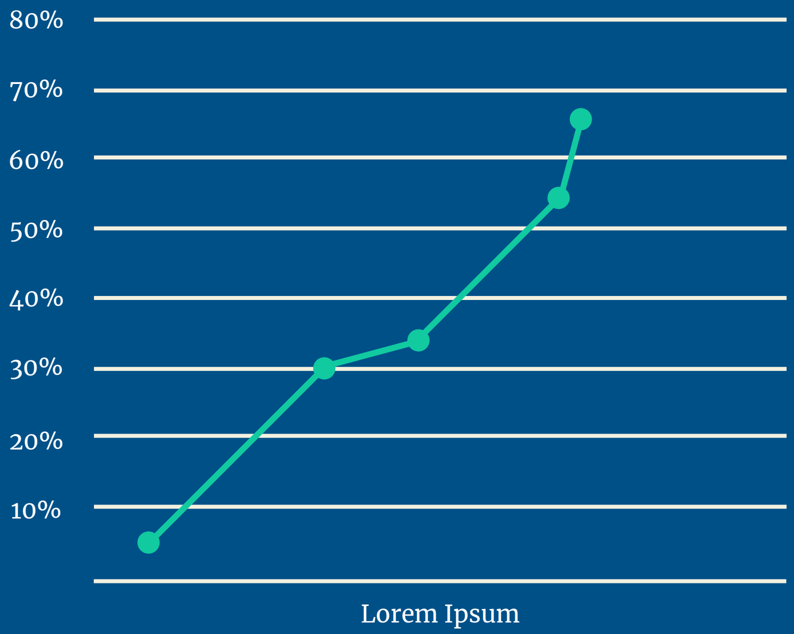

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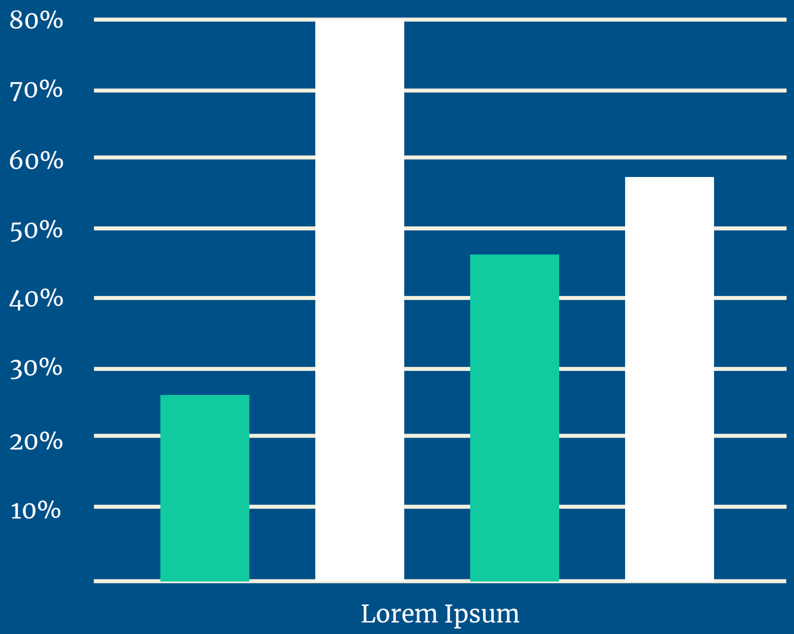

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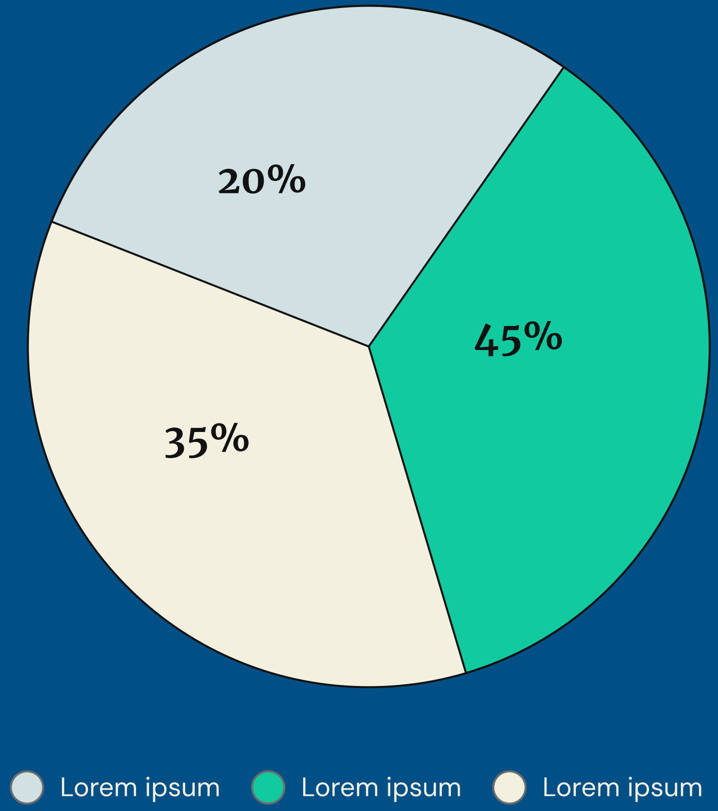

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Experiment Results (Bar Chart)

Curso de Verão do PCM

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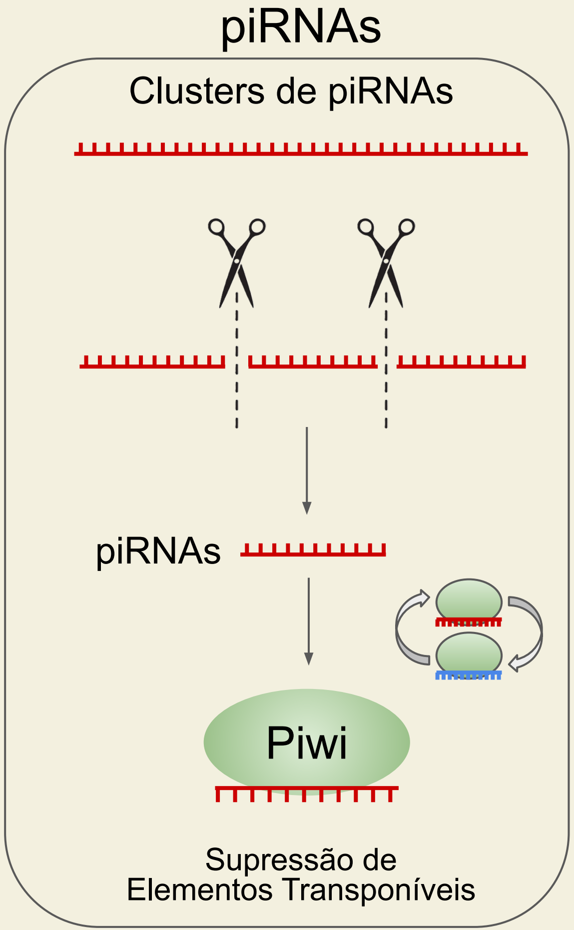
Via de piRNAs

- 23 a 30 nt de tamanho
- Proteínas PIWI
- Tradicionalmente associados ao silenciamento de Elementos Transponíveis



piRNAs

Clusters de piRNAs

piRNAs

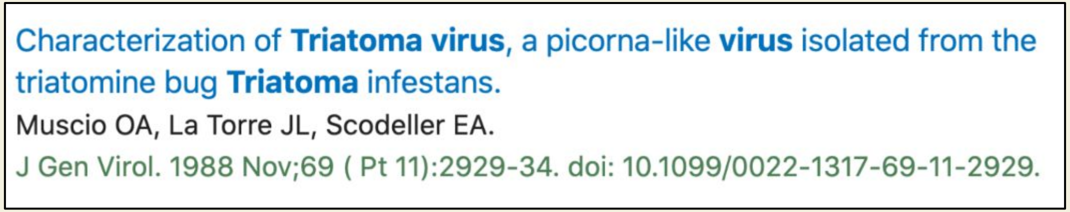
Piwi

Supressão de
Elementos Transponíveis

“Art. 207. As universidades gozam, na forma da lei, de autonomia didático-científica, administrativa e de gestão financeira e patrimonial e obedecerão ao princípio da **indissociabilidade** entre <u>ensino</u>, <u>pesquisa</u> e <u>extensão</u>.”

Vírus em Triatomíneos

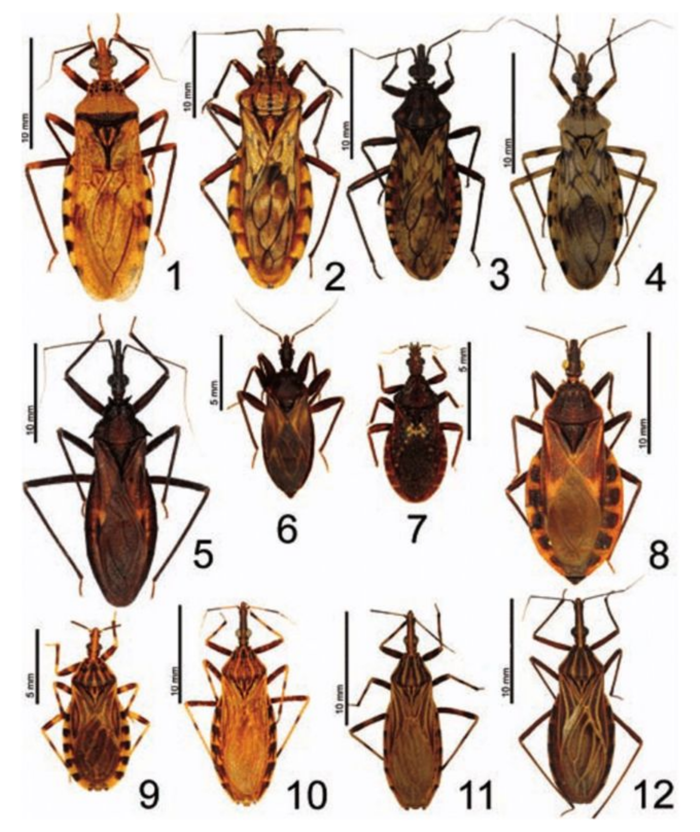
- Mais de 150 espécies de Triatomíneos
- Apenas **UM** vírus até então conhecido
- Triatoma Virus (TrV)



Characterization of **Triatoma virus**, a picorna-like **virus** isolated from the triatomine bug **Triatoma** infestans.

Muscio OA, La Torre JL, Scodeller EA.

J Gen Virol. 1988 Nov;69 (Pt 11):2929-34. doi: 10.1099/0022-1317-69-11-2929.



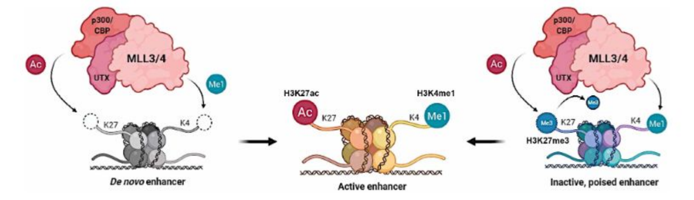
Histórico

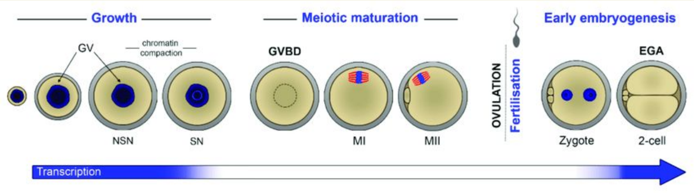
- Graduação
- Doutorado direto

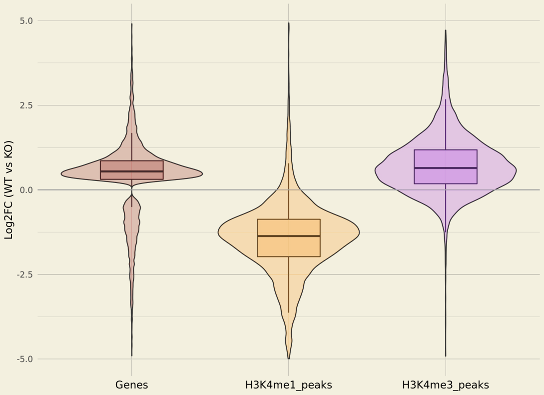
UFRJ

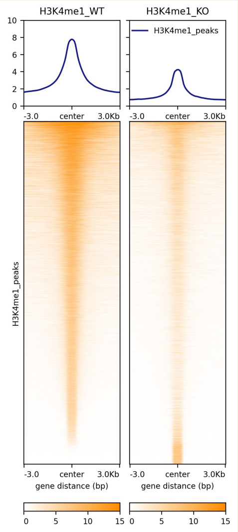
INSTITUTO DE CIÊNCIAS BIOMÉDICAS

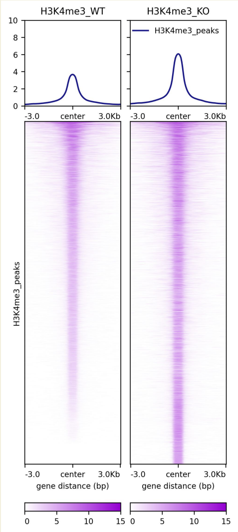
MAX PLANCK INSTITUTE
OF IMMUNOBIOLOGY AND EPIGENETICS





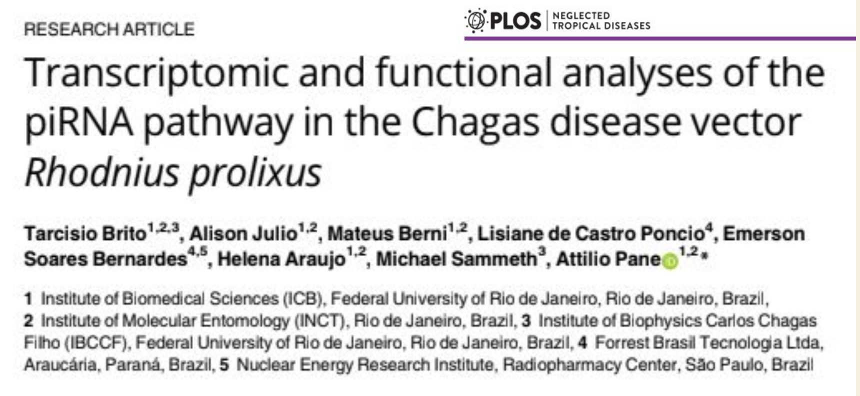






Via de piRNAs em *Rhodnius prolixus*

- Componentes da via de piRNA são conservados e expressos durante a ovogênese
- *Rp-piwi2*, *Rp-piwi3* e *Rp-ago3* são importantes para a fertilidade em fêmeas adultas



RESEARCH ARTICLE

PLOS | NEGLECTED TROPICAL DISEASES

Transcriptomic and functional analyses of the piRNA pathway in the Chagas disease vector *Rhodnius prolixus*

Tarcisio Brito[1,2,3], Alison Julio[1,2], Mateus Berni[1,2], Lisiane de Castro Poncio[4], Emerson Soares Bernardes[4,5], Helena Araujo[1,2], Michael Sammeth[3], Attilio Pane[1,2]*

1 Institute of Biomedical Sciences (ICB), Federal University of Rio de Janeiro, Rio de Janeiro, Brazil, **2** Institute of Molecular Entomology (INCT), Rio de Janeiro, Brazil, **3** Institute of Biophysics Carlos Chagas Filho (IBCCF), Federal University of Rio de Janeiro, Rio de Janeiro, Brazil, **4** Forrest Brasil Tecnologia Ltda, Araucária, Paraná, Brazil, **5** Nuclear Energy Research Institute, Radiopharmacy Center, São Paulo, Brazil