



Departamento de Microbiologia - ICBII
BMM5729 - Análise sistêmica e engenharia do
metabolismo microbiano

Reconstrução de rede metabólica com base em dados genômicos

Pseudomonas sp. LFM046

Juliana Cardinali Rezende
Esp. MSc e PhD em Genética de Microrganismos

3 de Junho de 2020

Rede Metabólica

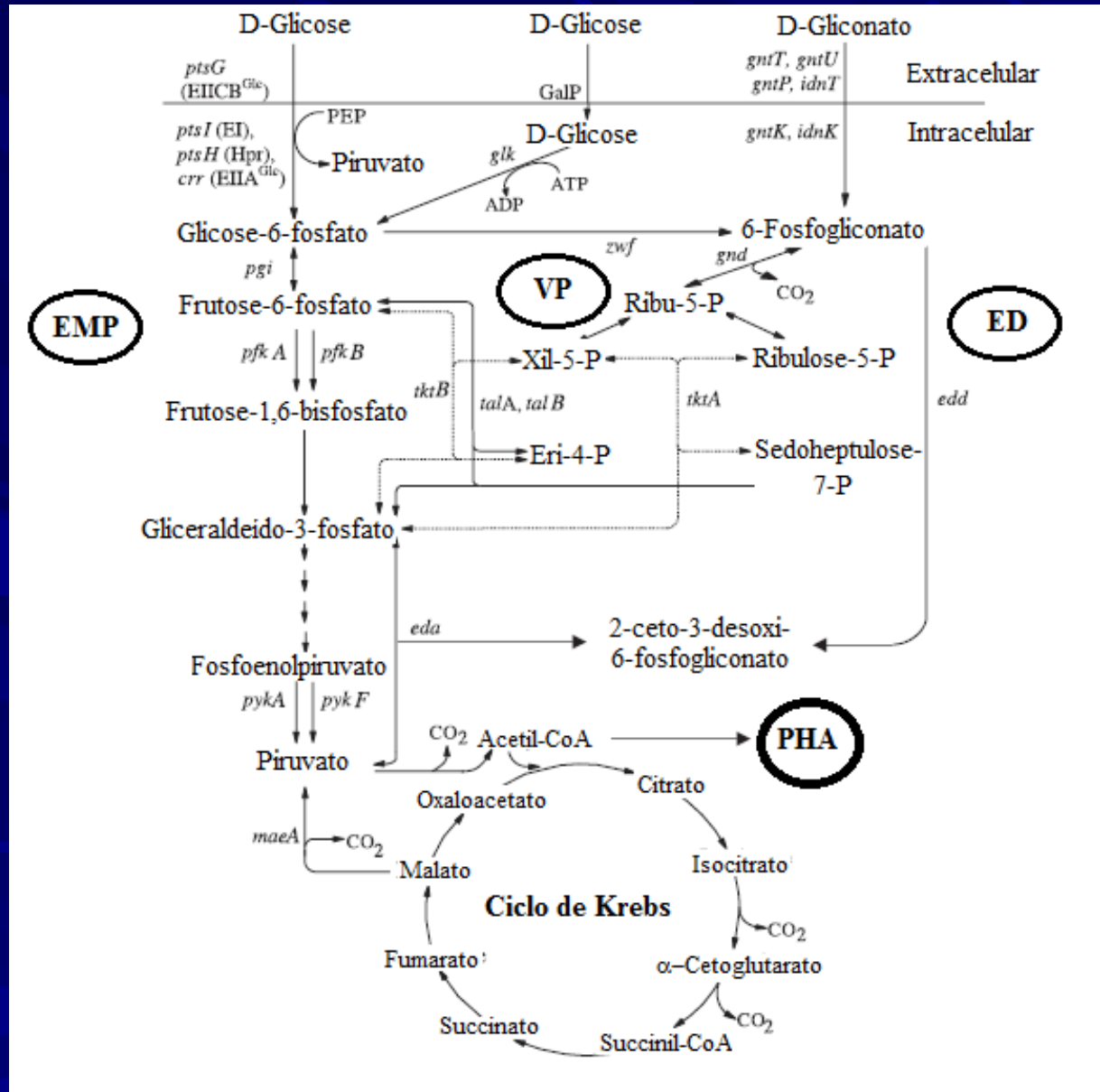
Genes:

1. Glicólise (EMP)
2. VP
3. VED
4. Ciclo de Krebs
5. Síntese de:

- . Aa
- . Ác. Graxos
- . DNA/RNA

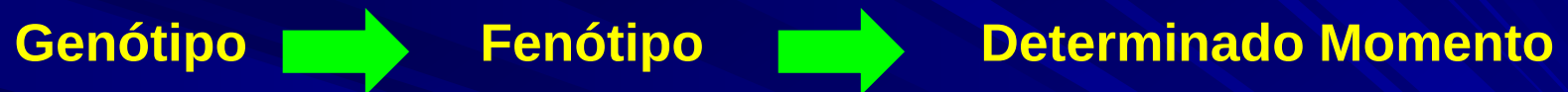


BIOMASSA
PHA



Por que construir redes metabólicas?

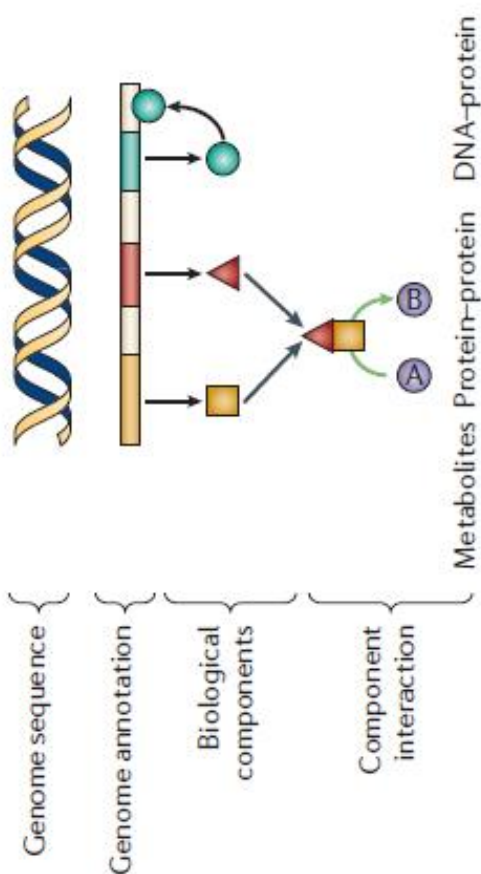
A análise e simulações *in silico* dos modelos fornecerão informações:



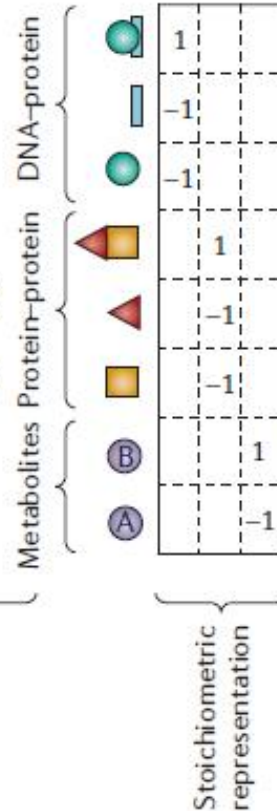
- Doenças humanas, como câncer e diabetes, etc.;
- Doenças infecciosas - microrganismos x hospedeiro;
- Análises genômicas - identificar alvos de drogas para patógenos;
- Projetar e produzir organismos geneticamente melhorados;
- Desenvolver organismos geneticamente modificados (OGMs) – Biofábricas - produtos com alto valor agregado; etc.

Anotação para reconstrução do modelo metabólico

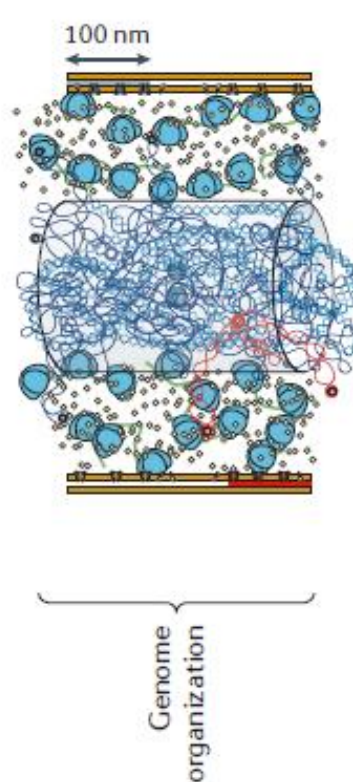
One-dimensional
annotation:
component enumeration



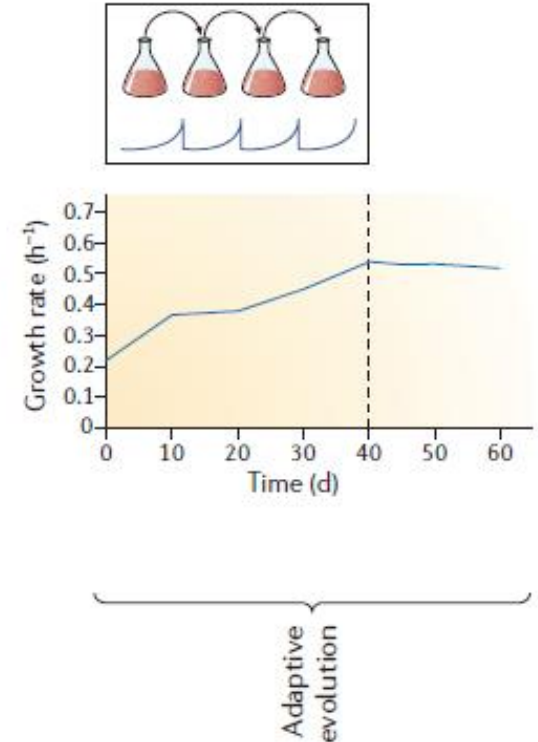
Two-dimensional
annotation:
network reconstruction



Three-dimensional
annotation:
ultrastructural reconstruction



Four-dimensional annotation:
genome plasticity and
new network states



Reed et al. 2006

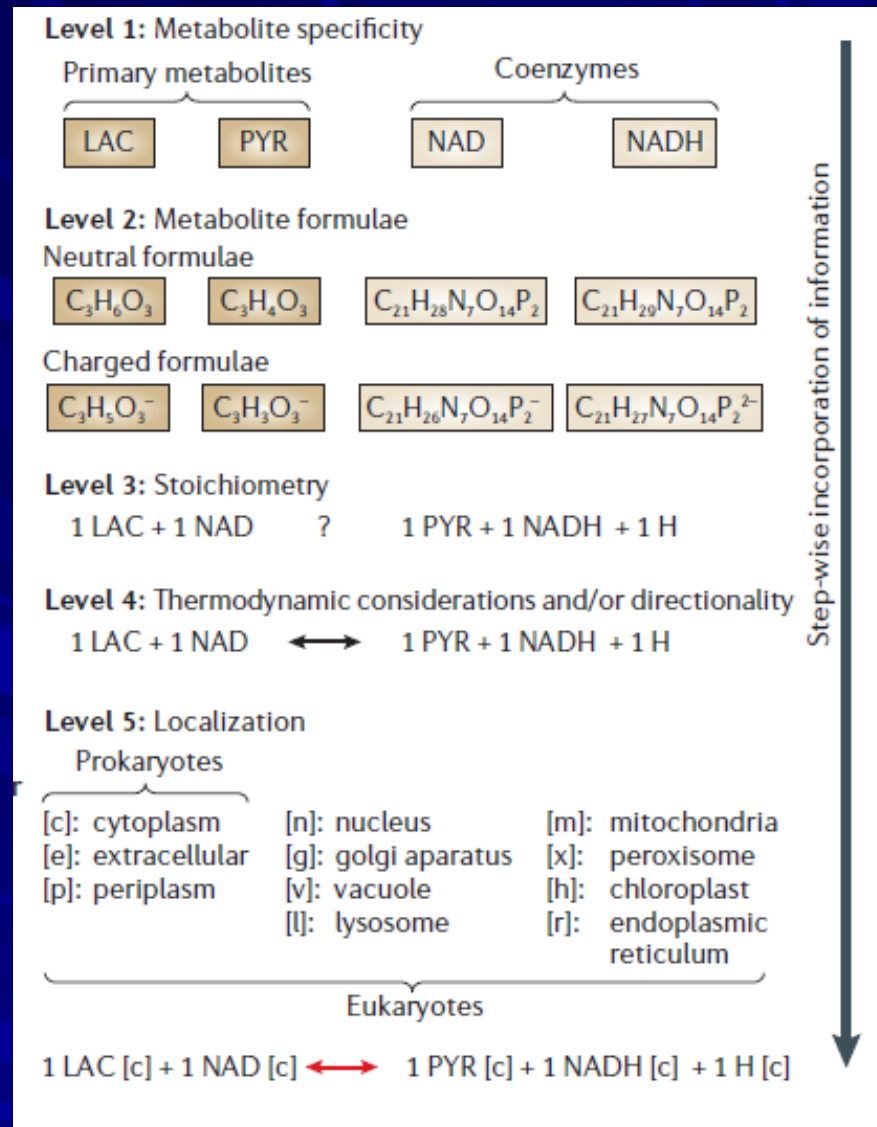
A relação genótipo-fenótipo deve ser bioquimicamente, genomicamente e geneticamente acurado.

Reações Metabólicas

Diferentes níveis de informação são necessários para que ocorra uma transformação bioquímica.

A reação bioquímica é correta se a representação matemática da reconstrução pode ser usada para cálculos subsequentes, caso contrário as propriedades da rede calculadas são incorretas.

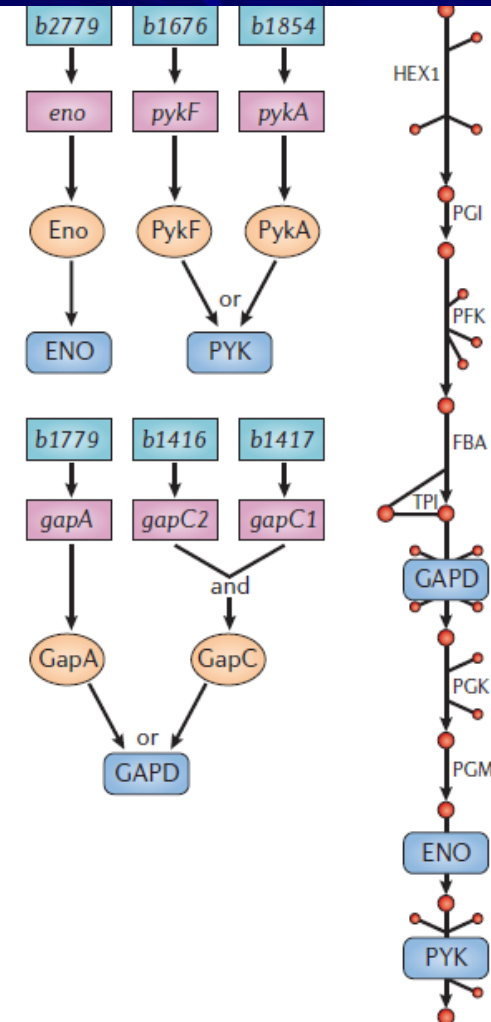
Reconstruct biochemical-reaction networks



Modelo metabólico representado em texto, reação estequiométrica ou gráfico

Abbreviation	Glycolytic reactions	Genes
HEX1	$[c] \text{GLC} + \text{ATP} \rightarrow \text{G6P} + \text{ADP} + \text{H}$	<i>glk</i>
PGI	$[c] \text{G6P} \rightleftharpoons \text{F6P}$	<i>pgi</i>
PFK	$[c] \text{ATP} + \text{F6P} \rightarrow \text{ADP} + \text{FDP} + \text{H}$	<i>pfkA, pfkB</i>
FBA	$[c] \text{FDP} \rightleftharpoons \text{DHAP} + \text{G3P}$	<i>fbaA, fbaB</i>
TPI	$[c] \text{DHAP} \rightleftharpoons \text{G3P}$	<i>tpiA</i>
GAPD	$[c] \text{G3P} + \text{NAD} + \text{PI} \rightleftharpoons 13\text{DPG} + \text{H} + \text{NADH}$	<i>gapA, gapC1, gapC2</i>
PGK	$[c] 13\text{DPG} + \text{ADP} \rightleftharpoons 3\text{PG} + \text{ATP}$	<i>pgk</i>
PGM	$[c] 3\text{PG} \rightleftharpoons 2\text{PG}$	<i>gpmA, gpmB</i>
ENO	$[c] 2\text{PG} \rightleftharpoons \text{H}_2\text{O} + \text{PEP}$	<i>eno</i>
PYK	$[c] \text{ADP} + \text{H} + \text{PEP} \rightarrow \text{ATP} + \text{PYR}$	<i>pykA, pykF</i>

ATP	-1	0	-1	0	0	0	1	0	0	1
GLC	-1	0	0	0	0	0	0	0	0	0
ADP	1	0	1	0	0	0	-1	0	0	-1
G6P	1	-1	0	0	0	0	0	0	0	0
H	1	0	1	0	0	1	0	0	0	-1
F6P	0	1	-1	0	0	0	0	0	0	0
FDP	0	0	1	-1	0	0	0	0	0	0
DHAP	0	0	0	1	-1	0	0	0	0	0
G3P	0	0	0	1	1	-1	0	0	0	0
NAD	0	0	0	0	0	-1	0	0	0	0
PI	0	0	0	0	0	-1	0	0	0	0
13DPG	0	0	0	0	0	1	-1	0	0	0
NADH	0	0	0	0	0	1	0	0	0	0
3PG	0	0	0	0	0	0	1	-1	0	0
2PG	0	0	0	0	0	0	0	1	-1	0
PEP	0	0	0	0	0	0	0	0	1	-1
H ₂ O	0	0	0	0	0	0	0	0	1	0
PYR	0	0	0	0	0	0	0	0	0	1
	HEX1	PGI	PFK	FBA	TPI	GAPD	PGK	PGM	ENO	PYK



Como construir um modelo metabólico em escala genômica?

Sequenciamento e montagem *de novo* do genoma



Anotação dos genes

Ferramentas de bioinformática + Bancos de dados + Dados da literatura + Análises experimentais



Reconstrução da rede metabólica

Ferramentas de bioinformática + Bancos de dados +
Dados da literatura + Dados experimentais

Etapa 1.

**Sequenciamento, montagem *de novo*
e anotação genômica de
Pseudomonas sp. LFM046**

Sequenciamento de Nova Geração - NGS

Acelerar o processo de sequenciamento

Baixar os custos

Aumentar a acurácia



**Processamento paralelo massivo
de fragmentos de DNA**

Sequenciadores de nova geração

Roche: 454 Piro GS FLX Titanium
GS Júnior

Illumina : Genetic Analyzer
MiSeq
NextSeq
Hi Seq 2000
NextSeq 1000 and NextSeq 2000

Thermo Fisher Scientific: Genetic Analyzer
Solid 5500XL
PGM Ion Torrent
Ion Próton
Ion Chef System

Pacific Biosciences: Sequel system
PacBio RSII

Características das plataformas disponíveis no mercado

High-end sequencing- Platform†	Sequencing chemistry	Read lengths/through put	Run time	Template prep	Application
Roche 454 -Titanium FLX	Pyrosequencing	400 bp 400 Mb/run	10 hours	Emulsion PCR	Denovo WGS of microbes, pathogen discovery, Exome seq
Illumina/Solexa -HiSeq 2000	Reversible terminator chemistry	2×100bp 600 GB/run (dual cell)	11.5 days	Solid-phase	Human WGS, exome seq, RNA-seq, Methylation
ABI/LifeTechnology-SOLiD 5550XL	Sequencing by ligation	2×60bp 15 GB/day	8 days	Emulsion PCR	Human WGS, exome seq, RNA-seq, Methylation
HelicosBiotechnologies	Reversible Terminator chemistry	25-55 bp 28 GB/run (avg)	>1 GB/hour	Single molecule	Human WGS, exome seq, RNA-seq, Methylation
Roche 454- GS Junior	Pyrosequencing	400 bp 50 Mb/run	10 hours	Emulsion PCR	Denovo WGS of microbes, pathogen discovery, Exome seq
Illumina/Solexa- MiSeq	Reversible terminator chemistry	2×150bp 1.0-1.4 Gb	26 hours	Solid-phase	Microbial discovery, Exome seq, Targeted capture
ABI/Lifetechnology- Iontorrent	H ⁺ Ion sensitive transistor	320 Mb/run	8 hours*	Emulsion PCR	Microbial discovery, Exome seq, Targeted capture

Sequenciamento

1) Preparação da Amostra: Fragmentação do DNA

2) Preparação da biblioteca: Ligação dos adaptadores

Possível combinar diferentes amostras!

3) Validação da biblioteca

4) Sequenciamento utilizando o MiSeq Illumina

5) Análise dos dados

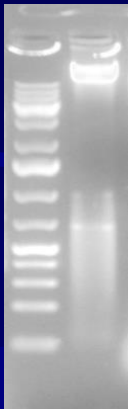
1) Preparação da Amostra

1.0. Cultivo da *Pseudomonas* sp. LFM046

Luria-Bertani (LB) a 30 °C por 24 horas no incubador TE-420 a 150 rpm.

1.1. Extração e quantificação do DNA genômico

DNeasy Blood and Tissue Kit (Qiagen)



Qubit® 3.0 Fluorometer



NanoVue – Espectofotometer

Abs. 260/280 e 260/230

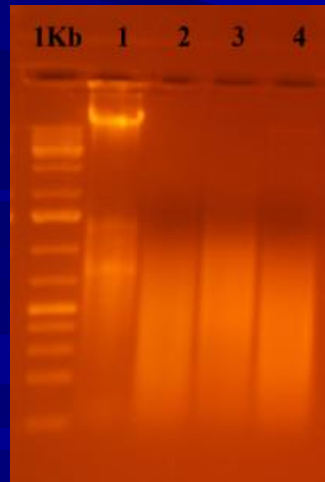
1.2. Amplificação e sequenciamento do gene de rRNA 16S

- 100% de identidade a sequência parcial do gene de rRNA16 de *Pseudomonas* sp. IPT 046 depositado no GenBank: JF922302.1

1.3. Fragmentação do DNA genômico



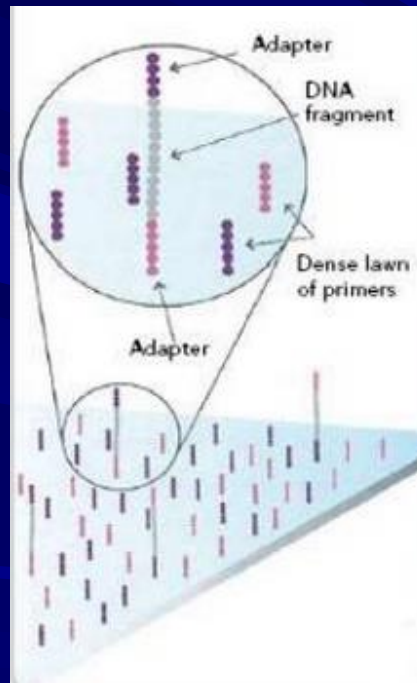
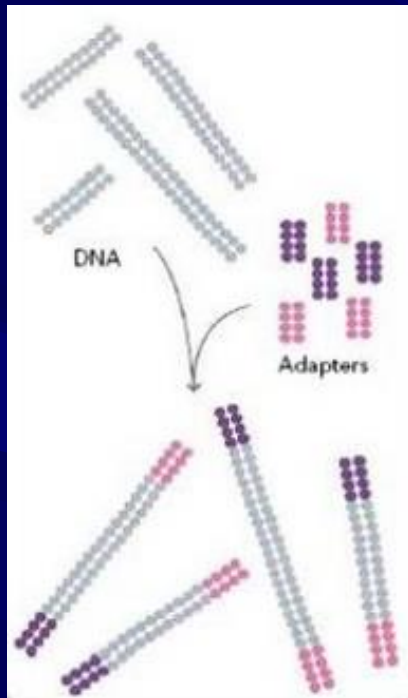
2,5 µg do DNA genômico



Tamanho médio de 550pb

2) Preparação da biblioteca

Ligação dos adaptadores e Barcodes nas pontas dos fragmentos de DNA.



TruSeq DNA PCR-Free LT Sample Preparation Kit – Set A (Illumina, San Diego, CA).

Adapter	Sequence	Set	Adapter	Sequence	Set
AD001	ATCACG(A)	B	AD013	AGTCAA(C)	A
AD002	CGATGT(A)	A	AD014	AGTTCC(G)	A
AD003	TTAGGC(A)	B	AD015	ATGTCA(G)	A
AD004	TGACCA(A)	A	AD016	CCGTCC(C)	A
AD005	ACAGTG(A)	A	AD018	GTCCGC(A)	A
AD006	GCCAAT(A)	A	AD019	GTGAAA(C)	A
AD007	CAGATC(A)	A	AD020	GTGGCC(T)	B
AD008	ACTTGA(A)	B	AD021	GTTTCG(G)	B

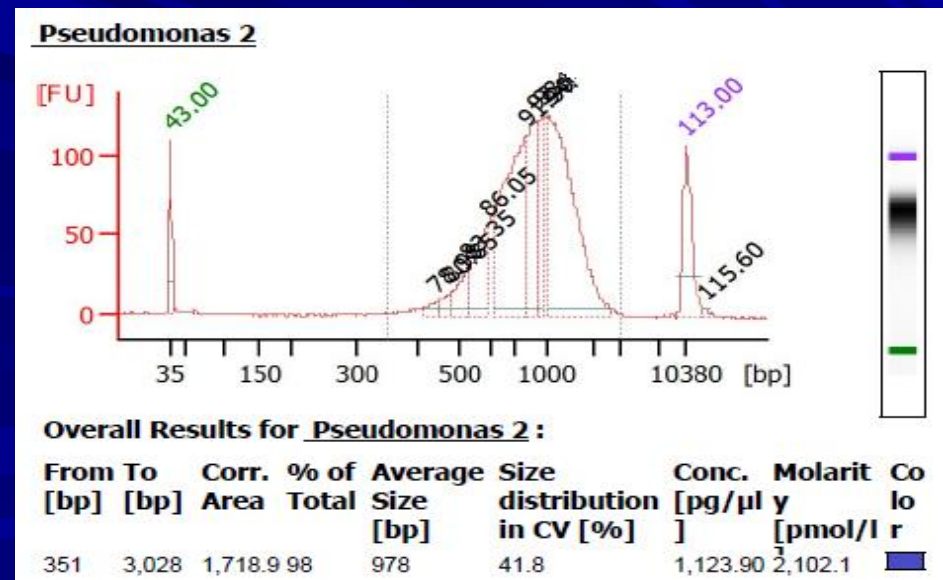
3) Validação da biblioteca

3.1. Quantificação e análise em relação ao tamanhos dos fragmentos de DNA genômico ligados ao adaptadores.

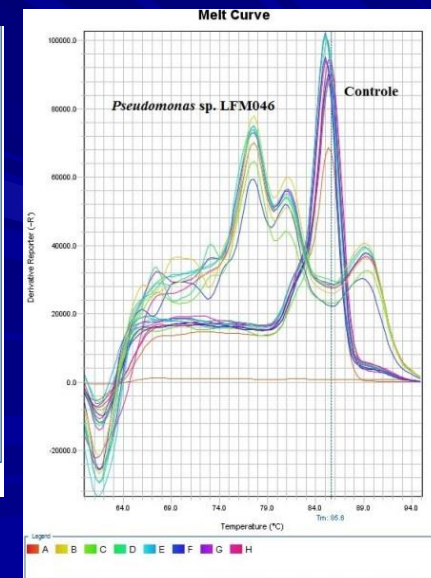
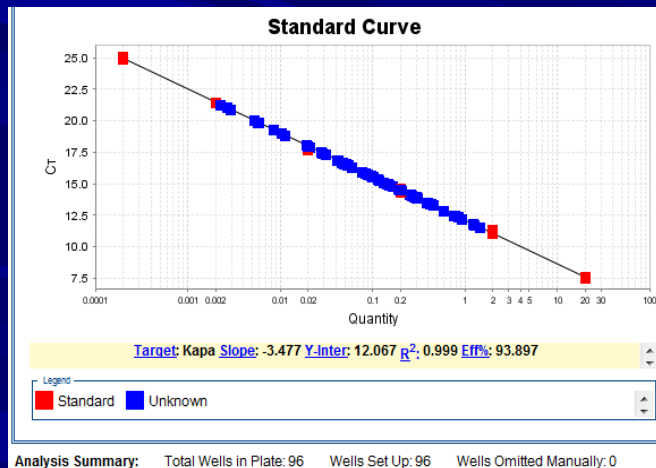
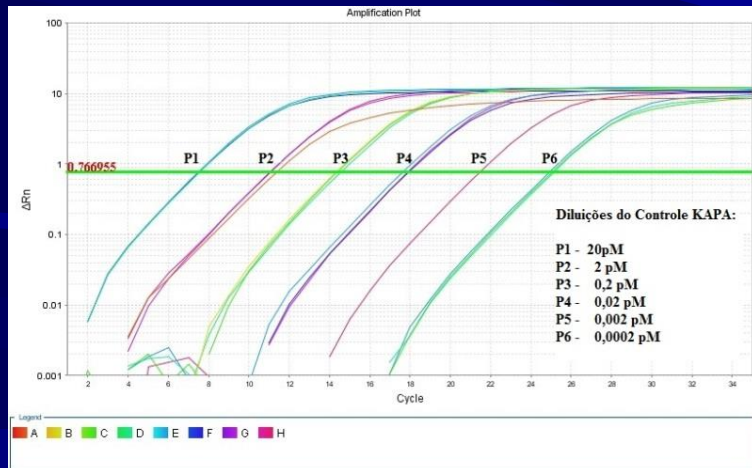
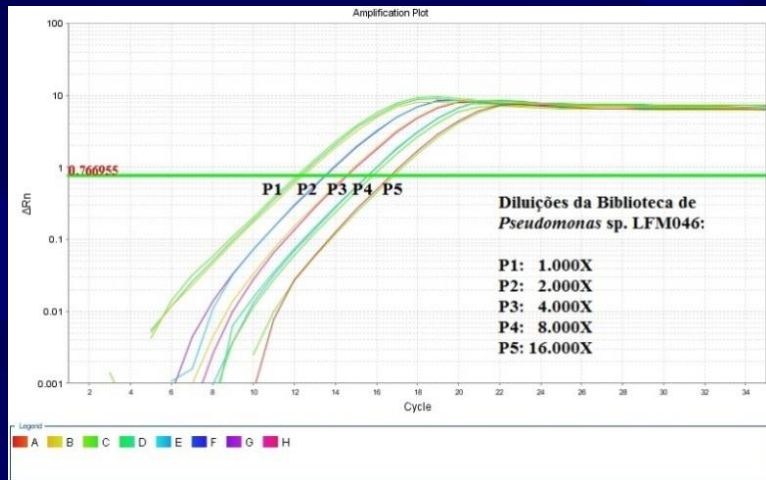


Qubit® 3.0 Fluorometer

Agilent Bioanalyzer 2100



3.1. Quantificação dos fragmentos da biblioteca de *Pseudomonas* sp. LFM046 por Real-time PCR



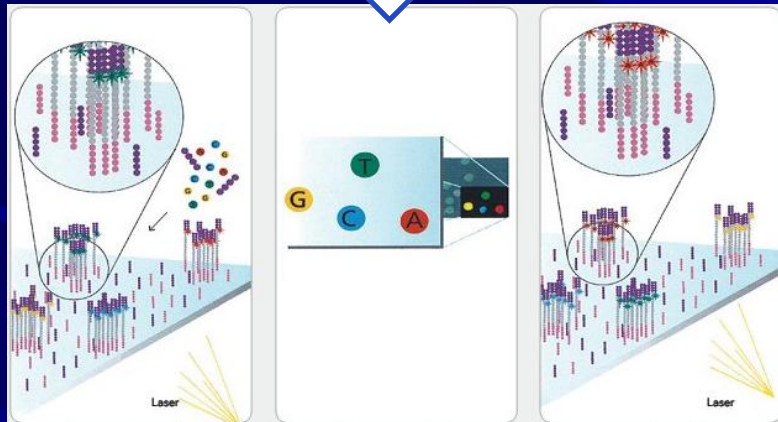
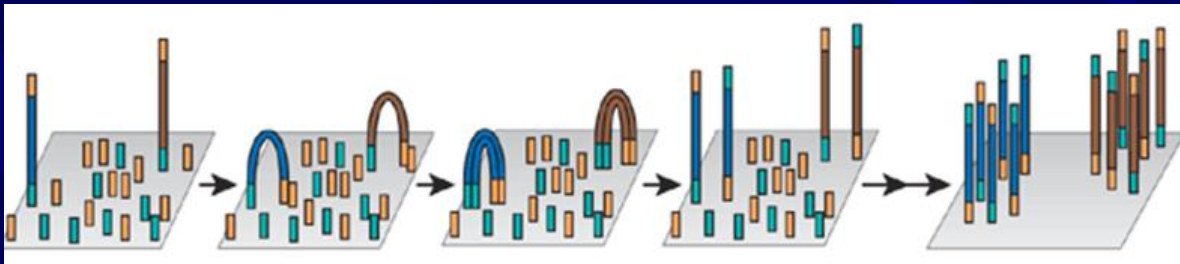
KAPA Library Quantification kit (KapaBiosystems, USA)

4. Sequenciamento - Illumina MiSeq

MiSeq Reagent Kit v3
(Illumina, San Diego, CA)

Seq. paired-end de 2 x 300 pb

Amplificação por Ponte



Sequenciamento por método de
terminação de cadeia reversível

5) Análise dos dados do Sequenciamento

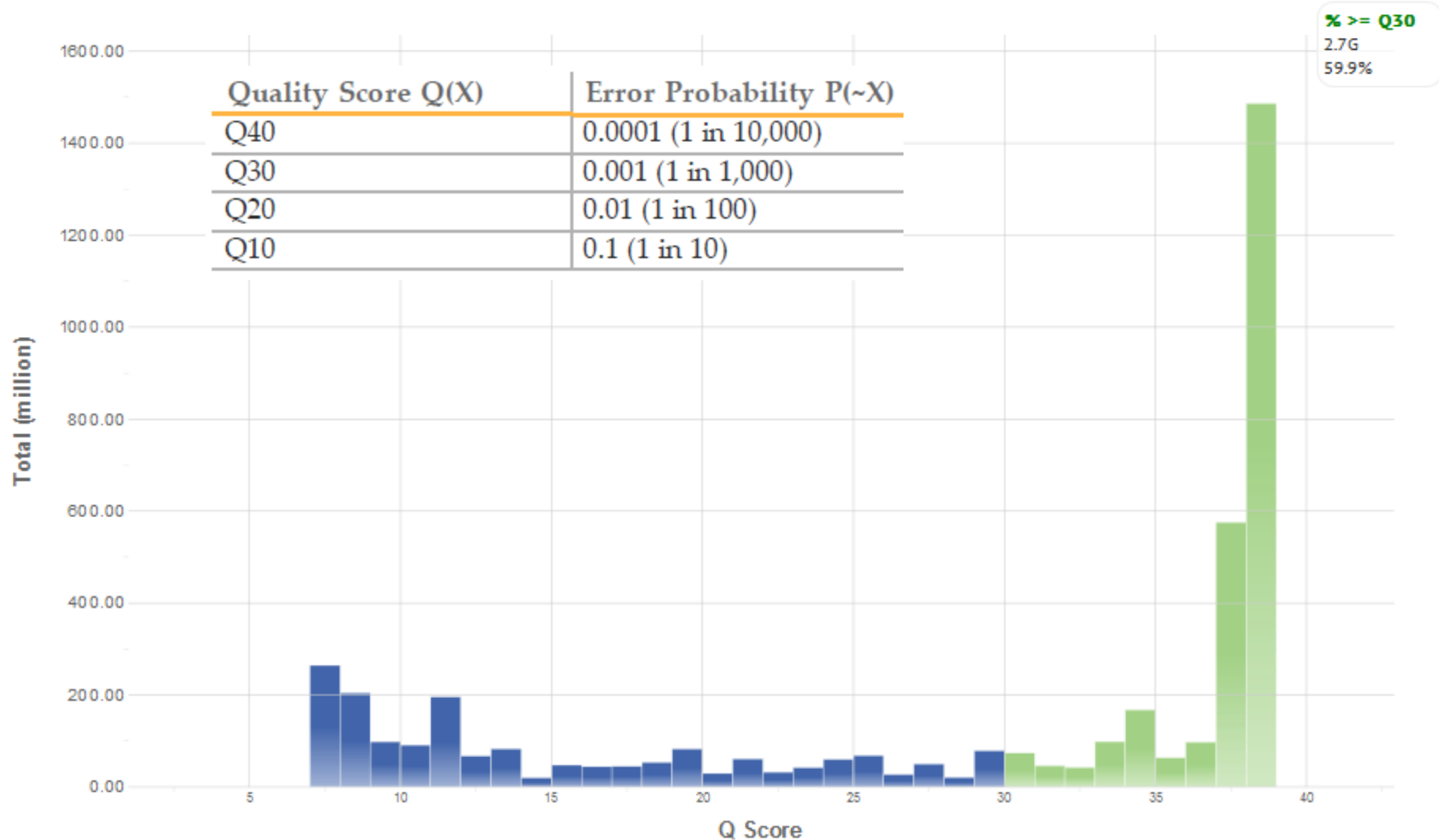


Data

Sample_ID	Sample_Name	Sample_Plate	Sample_Well	I7_Index_ID	index
1	Pseudomonas			A005	ACAGTG
2	Burkholderia			A006	GCCAAT
3	Halomonas			A012	CTTGTA

BaseSpace NGS Data Analysis (<https://basespace.illumina.com/>)

Análise de qualidade dos reads



Montagem *de novo* do genoma de *Pseudomonas* sp. LFM046

Controle de qualidade dos reads e montagem

	Número de Reads	
	Forward	Reverse
Total Bruto de Reads	1.950.218	1.900.789
Após Filtragem (QV>20 90%)	1.632.546 (-13,3%)	1.519.391 (-21,8%)
Juntou reads	1.516.647 (-7,6%)	1.516.647 (-0,2%)
Eliminou Reads < 200pb	1.516.491 (-0,01%)	1.516.491 (-0,01%)
Total de Reads	3.032.982	
Cobertura	60%	

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(<https://usegalaxy.org/>; Velvet (Bruijn graph assemblers))

Draft do Genoma

- 3.032.982 reads após triagem por qualidade (Galaxy software)
- Draft genoma: 34 contigs
- Contig: 1,038,386 pb , sendo N50 contig of 640,128 bp.
- 5.970.318 pb
- Cobertura: 60X
- G+C: 64%.
- 5.440 sequências codificadoras
- 75 = RNAs
- 204 genes - Metabolismo Central dos Carboidratos

Nucleotide

Nucleotide [Advanced](#)[Display Settings:](#) ☒ GenBank[Send to:](#) ☐

Pseudomonas sp. LFM046, whole genome shotgun sequencing project

GenBank: JYK000000000.1

i This entry is the master record for a whole genome shotgun sequencing project and contains no sequence data.

[Go to:](#) ☐

LOCUS	JYK001000000	33 rc	DNA	linear	BCT 09-MAR-2015
DEFINITION	Pseudomonas sp. LFM046, whole genome shotgun sequencing project.				
ACCESSION	JYK000000000				
VERSION	JYK000000000.1 GI:766658315				
DBLINK	BioProject: PRJNA274268 BioSample: SAMN03299269				
KEYWORDS	WGS.				
SOURCE	Pseudomonas sp. LFM046				
ORGANISM	Pseudomonas sp. LFM046 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.				
REFERENCE	1 (bases 1 to 33)				
AUTHORS	Cardinali-Rezende, J., Alexandrino, P.M., Taciro, M.K., Silva, L.F. and Gomez, J.G.				
TITLE	Draft genome sequence of Pseudomonas sp. LFM046: A great producer of medium-chain-length polyhydroxyalkanoate (PHAMCL) from glucose and fructose				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 33)				
AUTHORS	Cardinali-Rezende, J., Alexandrino, P.M., Taciro, M.K., Silva, L.F. and Gomez, J.G.				

- Montagem *de novo* do genoma

Dra. Marie-France Sagot, Inria-Lion, França.

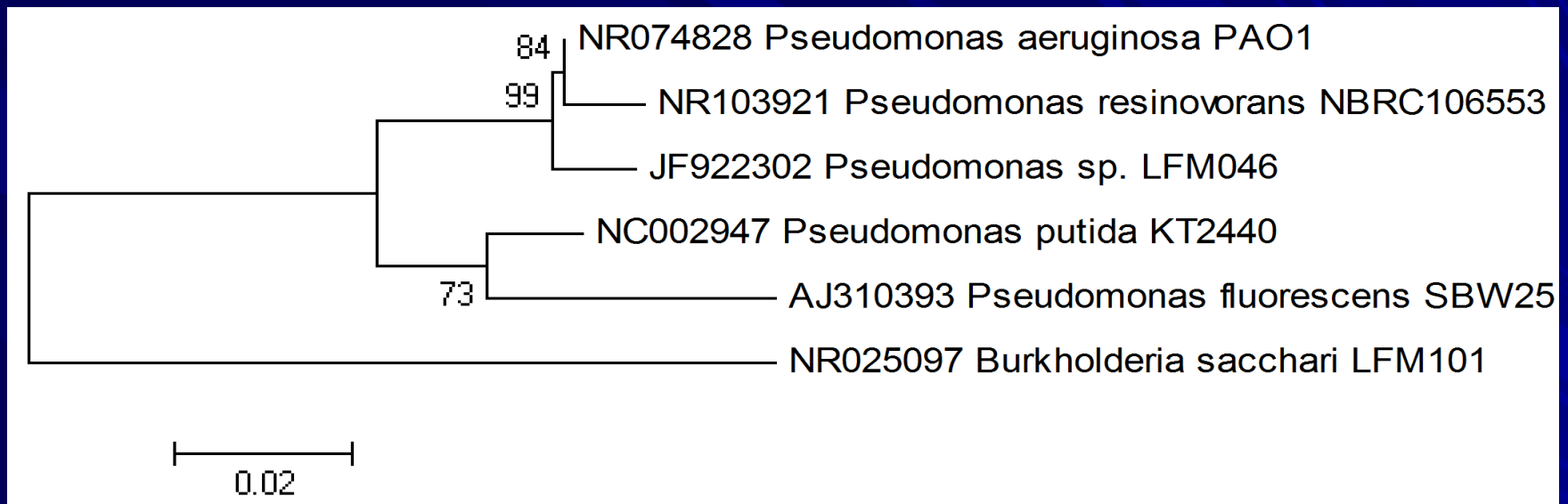
1. DiscoVar *de novo* assembly

(<https://www.broadinstitute.org/software/discovar/blog/>).

20 contigs com um N50 de 641Kb

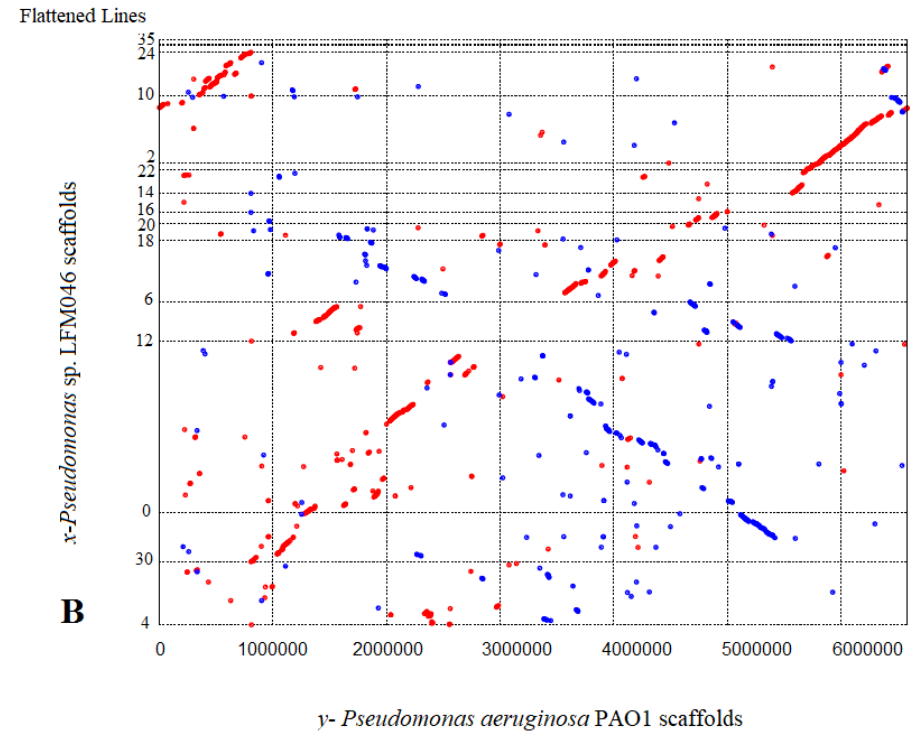
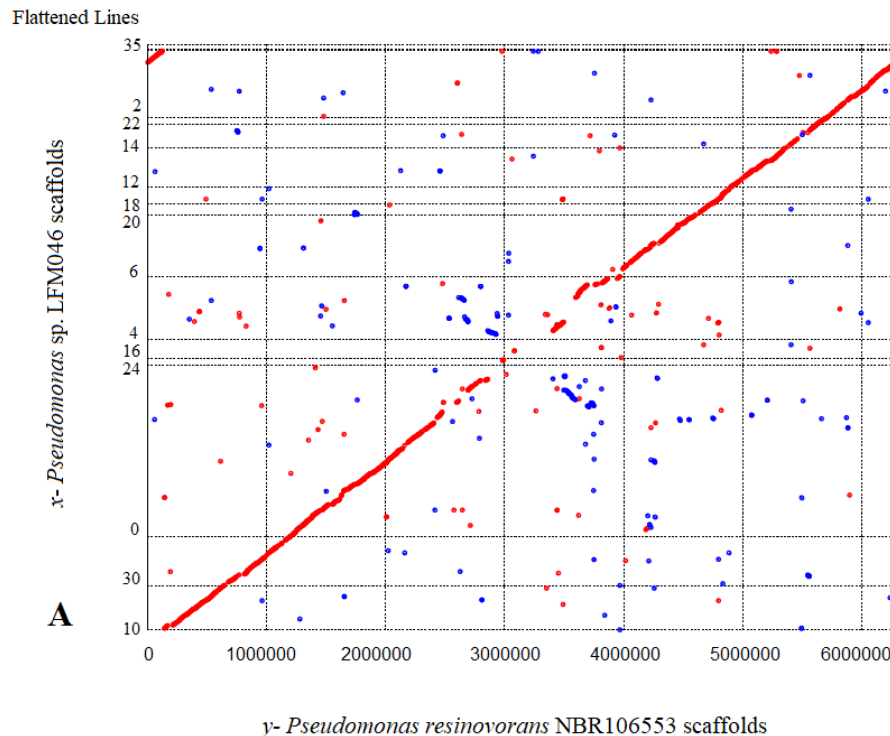
2. MEDUSA - Multi-Draft based Scaffold, V. MeDuSa++

Com base em sequências de genes de rRNA16S, espécies de *Pseudomonas* filogeneticamente próximas a *Pseudomonas* sp. LFM046 foram identificadas .



O gene de rRNA 16S de *Pseudomonas* sp. LFM046 apresentou:
98% de identidade com *P. resinovorans* NBRC106553 e *P. aeruginosa* PAO1.

Alinhamento dos scaffolds de *Pseudomonas* sp. LFM046 com genoma de espécies mais próximas



A) x- *Pseudomonas* sp. LFM046 e y- *P. resinovorans* NBR106553

B) B) x- *Pseudomonas* sp. LFM046 e y- *P. aeruginosa* PAO1.

MEDUSA - Multi-Draft based Scaffold, V. MeDuSa++

- Montagem *de novo* do genoma

2. MEDUSA (Multi-Draft based Scaffold, V. MeDuSa++)

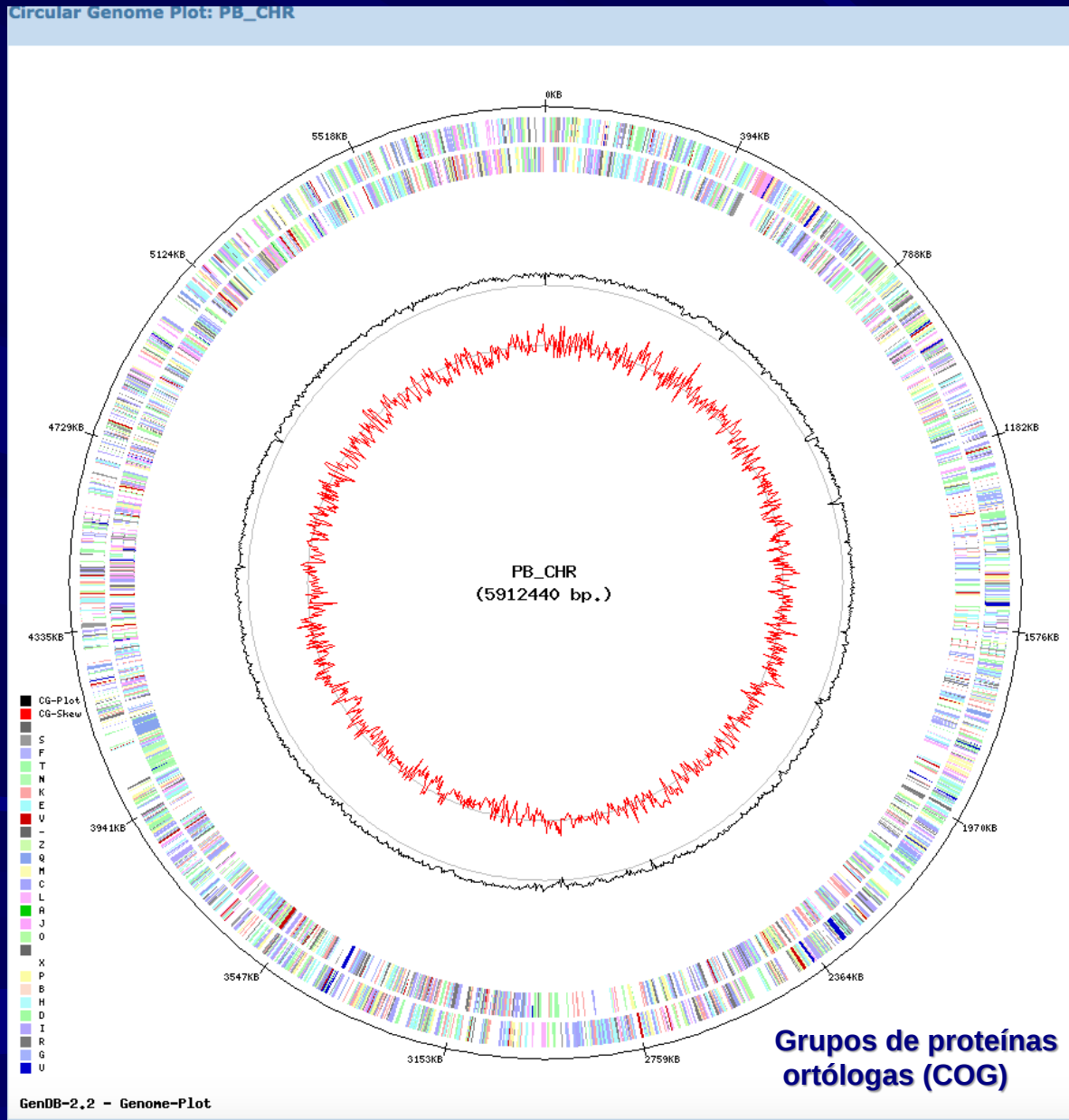
- Alinhamento com *Pseudomonas resinovorans*
NBR106553:

7 scaffolds com N50 de 2.671 Kb:
13 gaps e 1.550 bases desconhecidas

- Gapfilling usando reads brutas do sequenciamento:

135 bases desconhecidas

Genoma da *Pseudomonas* sp. LFM046



➤ Cobertura: 150 X

➤ 1 scaffold:

5.972.904 bp

5.419 genes

1 cromossomo e

3 plasmídios (60kb)

1) 13.100 pb

2) 45.000 pb

3) 1.900 pb

Grupos de proteínas
ortólogas (COG)

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Info: To monitor RAST's load and view other news and statistics for RAST and the SEED, please visit ["The Daily SEED."](#)

As of Wed Apr 6 15:30:02 2016, there are 31 jobs in the RAST queue

Job Load is Moderate

Jobs Overview

The overview below list all genomes currently processed and the progress on the annotation. To get a more detailed report on an annotation job, please click on the progress bar graphic in the overview.

In case of questions or problems using this service, please contact: rast@mcs.anl.gov.

Progress bar color key:

- not started
- queued for computation
- in progress
- requires user input
- failed with an error
- successfully completed

Jobs you have access to :

Job ▲▼	Owner ▲▼	ID ▲▼	Name ▲▼	Num contigs ▲▼	Size (bp) ▲▼	Creation Date	Annotation Progress	Status comple ▼
336691	REZENDE, JULIANA	159450.99	Burkholderia sacchari LMG 19450	47	7276343	2016-03-26 11:08:01	 [view details]	complete
336690	REZENDE, JULIANA	1609967.4	Halomonas sp. HG01	1	3666044	2016-03-26 11:02:05	 [view details]	complete
333770	REZENDE, JULIANA	1093222.6	Pseudomonas sp. LFM046	6	5972817	2016-03-14 19:42:32	 [view details]	complete



Job Details #333770

» [Browse annotated genome in SEED Viewer](#)

» [View metabolic model](#)

» Available downloads for this job: Genbank Download Update download files

» [Share this genome with selected users](#)

» View [Close Strains for this job](#)

» [Back to the Jobs Overview](#)

✓ Genome Upload has been successfully completed.

Genome ID - Name:	1093222.6 - Pseudomonas sp. LFM046
Job:	#333770
User:	jcardinali
Date:	Mon Mar 14 19:42:32 2016
Genetic code:	11
Annotation scheme:	ClassicRAST
Preserve gene calls:	no
Automatically fix errors:	yes
Fix frameshifts:	yes
Backfill gaps:	yes

✓ Rapid Propagation has been successfully completed.



The SEED Viewer

SEED Viewer version 2.0

Welcome to the SEED Viewer - a read-only browser of the curated SEED data.
For more information about The SEED please visit theSEED.org.

»Navigate »Organism »Comparative Tools »Help

find



JULIANA REZENDE

Organism Overview for *Pseudomonas* sp. LFM046 (1093222.6)

Genome	 <i>Pseudomonas</i> sp. LFM046 (Taxonomy ID: 1093222)
Domain	Bacteria
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; <i>Pseudomonas</i> ; <i>Pseudomonas</i> sp. LFM046
Neighbors	View closest neighbors
Size and G+C	5,972,904, (bp)
Number of Contigs (with PEGs)	4
Number of Subsystems	497
Number of Coding Sequences	5419
Number of RNAs	70

For each genome we offer a wide set of information to browse, compare and download.

Browse Compare Download Annotate

Browse through the features of [Pseudomonas](#) sp. LFM046 both graphically and through a table. Both allow quick navigation and filtering for features of your interest. Each feature is linked to its own detail page.

Click [here](#) to get to the Genome Browser

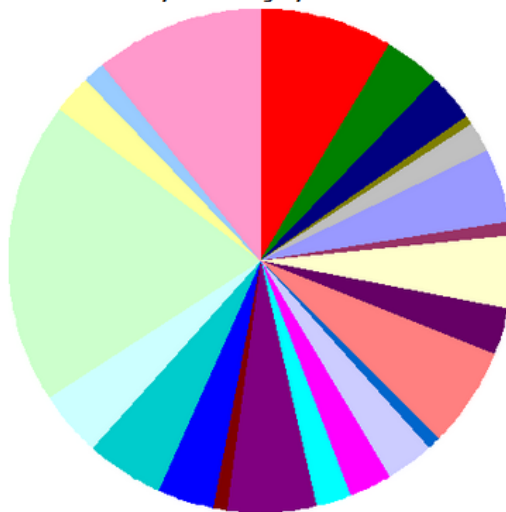
Subsystem Information

Subsystem Statistics Features in Subsystems

Subsystem Coverage



Subsystem Category Distribution



Subsystem Feature Counts

- ☐ Cofactors, Vitamins, Prosthetic Groups, Pigments (375)
- ☐ Cell Wall and Capsule (160)
- ☐ Virulence, Disease and Defense (121)
- ☐ Potassium metabolism (30)
- ☐ Photosynthesis (0)
- ☐ Miscellaneous (85)
- ☐ Phages, Prophages, Transposable elements, Plasmids (4)
- ☐ Membrane Transport (199)
- ☐ Iron acquisition and metabolism (33)
- ☐ RNA Metabolism (207)
- ☐ Nucleosides and Nucleotides (131)
- ☐ Protein Metabolism (272)
- ☐ Cell Division and Cell Cycle (33)
- ☐ Motility and Chemotaxis (130)
- ☐ Regulation and Cell signaling (118)
- ☐ Secondary Metabolism (5)
- ☐ DNA Metabolism (96)
- ☐ Fatty Acids, Lipids, and Isoprenoids (253)
- ☐ Nitrogen Metabolism (37)
- ☐ Dormancy and Sporulation (5)
- ☐ Respiration (158)
- ☐ Stress Response (208)
- ☐ Metabolism of Aromatic Compounds (184)
- ☐ Amino Acids and Derivatives (834)
- ☐ Sulfur Metabolism (107)
- ☐ Phosphorus Metabolism (54)
- ☐ Carbohydrates (446)

»Navigate »Organism »Comparative Tools »Help

Organism *Pseudomonas* sp. LFM 046 (1093222.5)

Genome	General Information
Domain	Feature Table
Taxonomy	Genome Browser
	Scenarios
	Subsystems
	Export
Neighbors	View closest neighbors
Size	5,970,318 bp
Number of Contigs (with PEGs)	34
Number of Subsystems	504
Number of Coding Sequences	5440
Number of RNAs	75

For each genome we offer a wide set of information to browse, compare and download.

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Browse through the features of [Pseudomonas sp. LFM 046](#) both graphically and through a table. Both allow quick navigation and filtering for features of your interest. Each feature is linked to its own detail page.

Click [here](#) to get to the Genome Browser

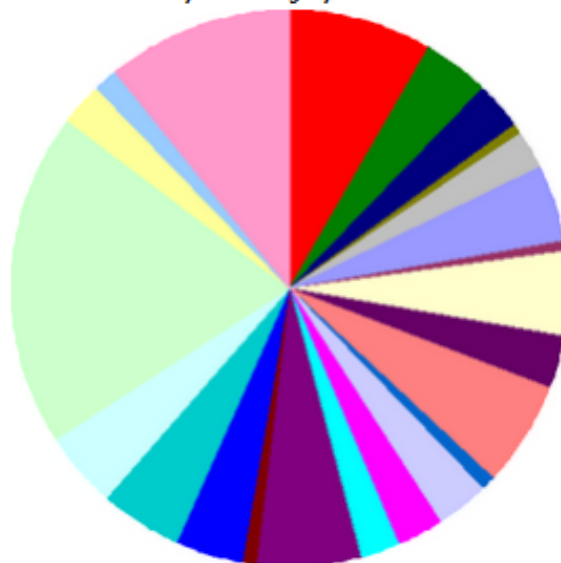
Subsystem Information

[Subsystem Statistics](#) [Features in Subsystems](#)

Subsystem Coverage



Subsystem Category Distribution



Subsystem Feature Counts

- ☐ Cofactors, Vitamins, Prosthetic Groups, Pigments (371)
- ☐ Cell Wall and Capsule (160)
- ☐ Virulence, Disease and Defense (121)
- ☐ Potassium metabolism (30)
- ☐ Photosynthesis (0)
- ☐ Miscellaneous (86)
- ☐ Phages, Prophages, Transposable elements, Plasmids (9)
- ☐ Membrane Transport (199)
- ☐ Iron acquisition and metabolism (16)
- ☐ RNA Metabolism (222)
- ☐ Nucleosides and Nucleotides (133)
- ☐ Protein Metabolism (261)
- ☐ Cell Division and Cell Cycle (34)
- ☐ Motility and Chemotaxis (134)
- ☐ Regulation and Cell signaling (119)
- ☐ Secondary Metabolism (5)
- ☐ DNA Metabolism (96)
- ☐ Fatty Acids, Lipids, and Isoprenoids (259)
- ☐ Nitrogen Metabolism (38)
- ☐ Dormancy and Sporulation (5)
- ☐ Respiration (167)
- ☐ Stress Response (211)
- ☐ Metabolism of Aromatic Compounds (189)
- ☐ Amino Acids and Derivatives (841)
- ☐ Sulfur Metabolism (107)
- ☐ Phosphorus Metabolism (55)
- ☐ Carbohydrates (445)



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SEED Viewer version 2.0

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[»Navigate](#) [»Organism](#) [»Comparative Tools](#) [»Help](#)

Organism Overview for *Pseudomonas* sp. LFM046 (1093222.6)

Genome	<i>Pseudomonas</i> sp. LFM046 (Taxonomy ID: 1093222) 
Domain	Bacteria
Taxonomy	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas; Pseudomonas sp. LFM046
Neighbors	View closest neighbors
Size and G+C	5,972,904, (bp
Number of Contigs (with PEGs)	4
Number of Subsystems	497
Number of Coding Sequences	5419
Number of RNAs	70

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Browse through the features of [Pseudomonas](#) sp. LFM046 both graphically and through a table. Both allow quick navigation and filtering for features of your interest. Each feature is linked to its own detail page.

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Subsystem Information

[Subsystem Statistics](#) [Features in Subsystems](#)

[export to file](#)

[clear all filters](#)

display items per page

displaying 1 - 2 of 2

Category ▲▼	Subcategory ▲▼	Subsystem ▲▼	Role ▲▼	Features
Carbohydrates ▼	Central carbohydrate metabolism ▼		PHOSPHOGLUCONATE	
Carbohydrates	Central carbohydrate metabolism	Entner-Doudoroff Pathway 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)		fig 1093222.6.peq.1279 , fig 1093222.6.peq.1830
Carbohydrates	Central carbohydrate metabolism	Entner-Doudoroff Pathway Phosphogluconate dehydratase (EC 4.2.1.12)		fig 1093222.6.peq.1266

displaying 1 - 2 of 2

Annotation Overview for [fig|1093222.6.peg.1266](#) in [Pseudomonas sp. LFM046](#): Phosphogluconate dehydratase (EC 4.2.1.12)

current assignment	Phosphogluconate dehydratase (EC 4.2.1.12)
taxonomy id	1093222
internal links	genome browser feature evidence sequence
annotation history	show
CDD link	show cdd
edit functional role	Phosphogluconate dehydratase (EC 4.2.1.12)
propagation lock	Unlocked Toggle lock

EC Number	4.2.1.12
contig	Pseudomonas-Brazil-Chromosome (5,912,440bp) ▾
run tool	Psi-Blast ▾ run tool

This feature is part of a subsystem

- In *Entner-Doudoroff Pathway* its role is *Phosphogluconate dehydratase (EC 4.2.1.12)*.

Compare Regions For [fig|1093222.6.peg.1266](#)

The chromosomal region of the focus gene (top) is compared with four similar organisms. The graphic is centered on the focus gene, which is red and numbered 1. Sets of genes with similar sequence are grouped with the same number and color. Genes whose relative position is conserved in at least four other species are functionally coupled and share gray background boxes. The size of the region and the number of genomes may be reset. Click on any arrow in the display to refocus the comparison on that gene. The focus gene always points to the right, even if it is located on the minus strand.

Display options [Regular](#) [Advanced](#)

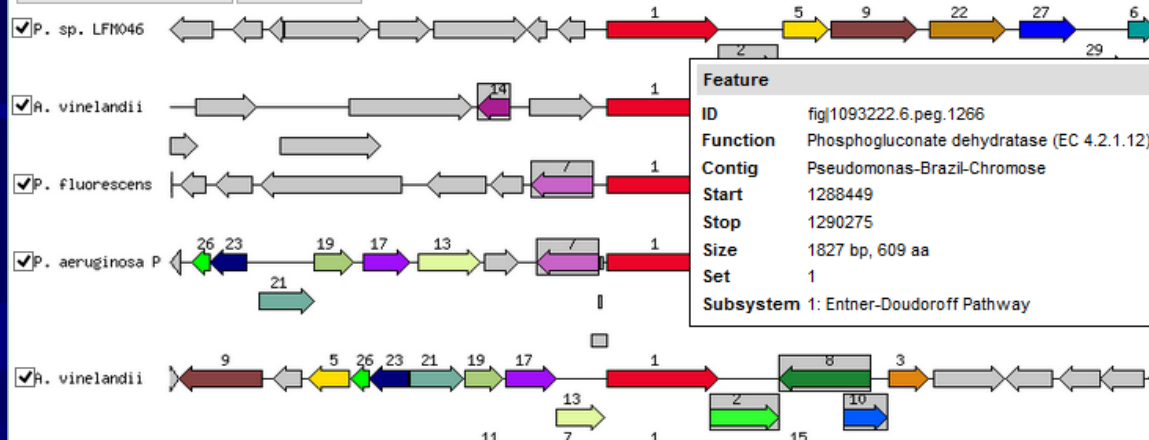
Region Size (bp)

Number of Regions

[<<](#) [<](#) [draw](#) [>](#) [>>](#)

Visual Region Information [Tabular Region Information](#) [Sequences](#)

[update with selected](#) [uncheck all](#)





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- »Organism
- »Comp
- General Information
- Feature Table
- Genome Browser
- Scenarios
- Subsystems
- Export

»Navigate »Organism »Comparative Tools »Help

Browse Genome: [Pseudomonas sp. LFM046 \(1093222.6\)](#)

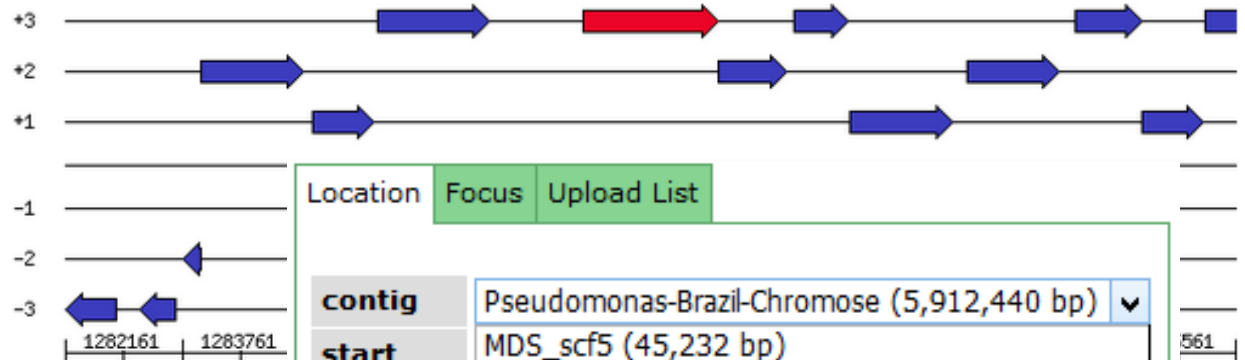
Location Focus Upload List

ID fig|1093222.6.peg.1266
Contig Pseudomonas-Brazil-Chromose
Type CDS
Function Phosphogluconate dehydratase (EC 4.2.1.12)
Subsystem Entner-Doudoroff Pathway
Start 1288449
Stop 1290275
Length 1827

[zoom to sequence](#)

[details page](#)

[evidence page](#)



Location Focus Upload List

contig Pseudomonas-Brazil-Chromose (5,912,440 bp) ▾
start base MDS_scf5 (45,232 bp)
MDS_scf6 (13,302 bp)
MDS_scf7 (1,930 bp)
window Pseudomonas-Brazil-Chromose (5,912,440 bp)
Color features by focus ▾

<==

draw

==>

display 15 items per page

displaying 1 - 1 of 1

Feature ID ▲▼	Type ▲▼	Contig ▲▼	Start ▲▼	Stop ▲▼	Length (bp) ▲▼	Function ▲▼	Subsystems ▲▼	Region
	CDS ▾	Pseudomor ▾	< ▾	< ▾	< ▾	6- phosphoglucon		
fig 1093222.6.peg.1266	CDS	Pseudomonas-Brazil-Chromose	1288449	1290275	1827	Phosphogluconate dehydratase (EC 4.2.1.12)	Entner-Doudoroff Pathway	show



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»Navigate »Organism »Comparative Tools »Feature »Feature Tools »Help

Annotation Overview for [fig|109322](#)

Phosphogluconate dehydratase (EC

current assignment	Phosphogluconate dehydratase
taxonomy id	1093222
internal links	genome browser feature evidence
annotation history	show
CDD link	show cdd
edit functional role	Phosphogluconate dehydratase
propagation lock	Unlocked Toggle lock

»Feature »Feature Tools

Feature Overview
DNA Sequence
DNA Sequence w/ flanking
Protein Sequence
Feature Evidence vs. FIG
Feature Evidence vs. all DB
Add to PEGcart
Ross UI

Pseudomonas sp. LFM046:

EC Number [4.2.1.12](#)

contig [Pseudomonas-Brazil-Chromosome \(5,912,440bp\)](#) ▾

run tool [Psi-Blast](#) ▾

This feature is part of a subsystem

- In Entner-Doudoroff Pathway its role is Phosphogluconate dehydratase (EC 4.2.1.12).

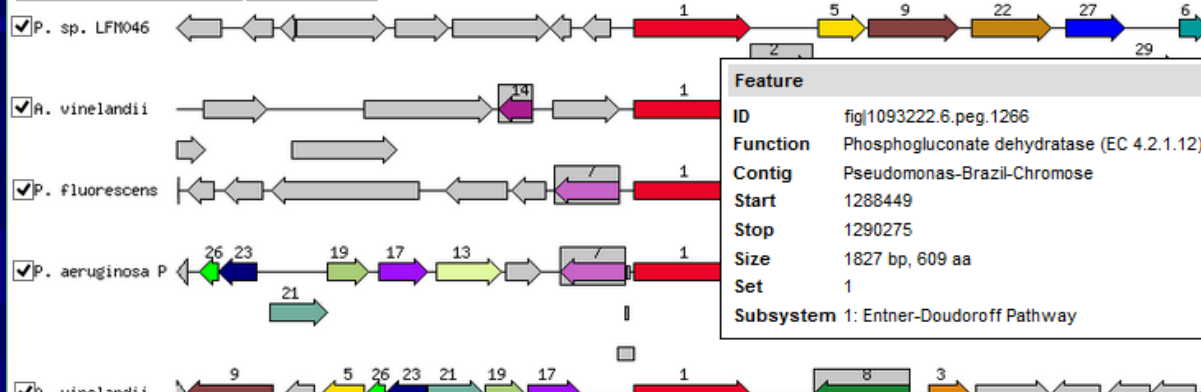
Compare Regions For [fig|1093222.6.peg.1266](#)

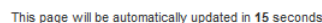
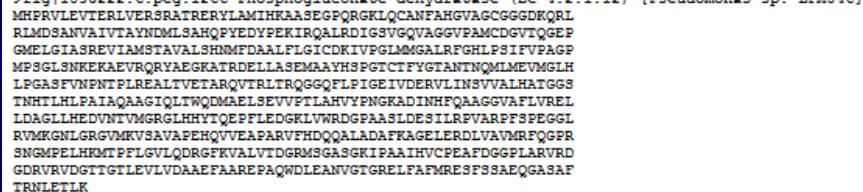
Display options [Regular](#) [Advanced](#)

Region Size (bp)

Number of Regions

Visual Region Information [Tabular Region Information](#) [Sequences](#)







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find JULIANA REZENDE

» Organism » Comp

Select organisms to show whether paths are present
 annotations in subsystems.

www.genome.jp/kegg-bin/show_pathway?rn00030+R01049+R01056+R01070+R01529+R01641+R01737+R01827+R01830+R02035+R02036

Pesquisar

KF_{GG}

[\[Pathway menu | Organism menu | Pathway entry | Download KGML | Show description | User data mapping \]](#)

Reference pathway (Reaction)

Go

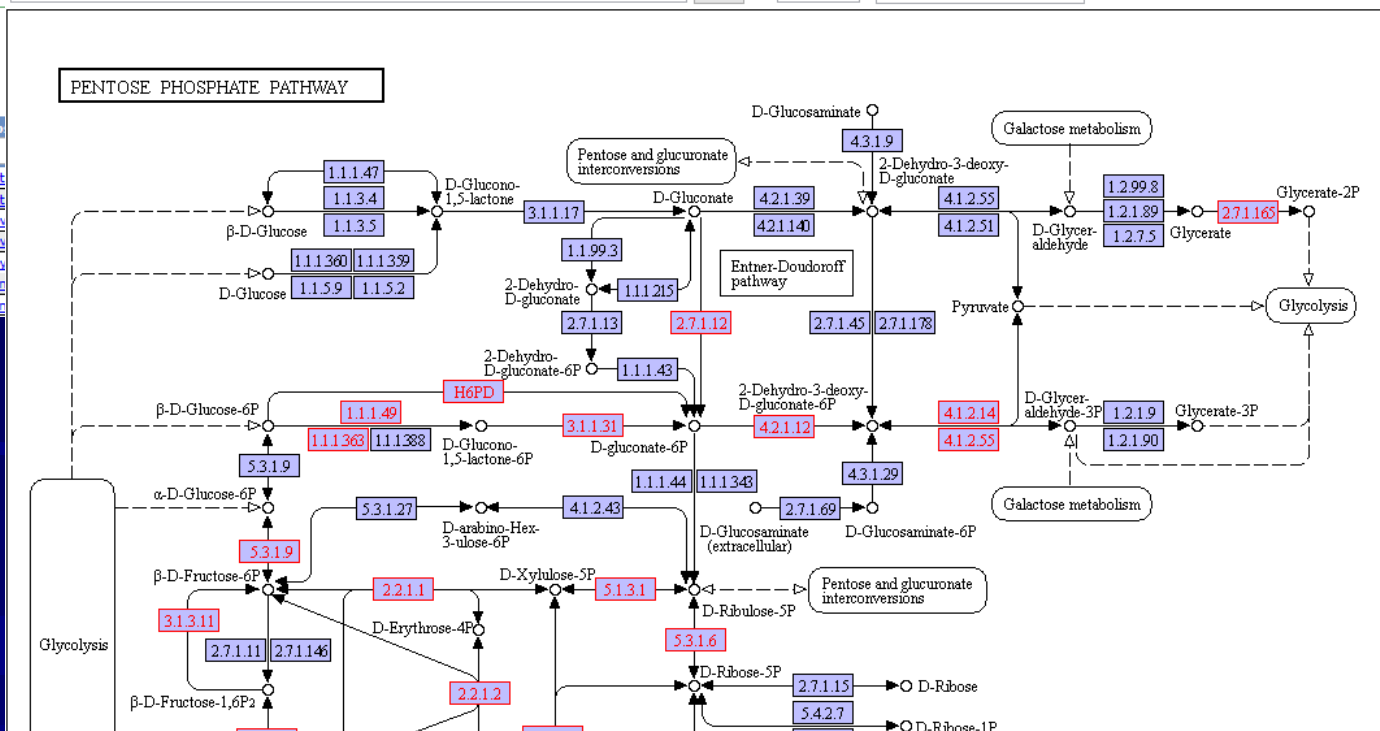
100% ▾

Go

Scenarios in Subsystems

clear all filters

Category ▲▼	Subcategory ▲▼	Subcategory
Carbohydrates ▼	all ▼	
Carbohydrates	Aminosugars	Chitin
Carbohydrates	Aminosugars	Chitin
Carbohydrates	CO2 fixation	Calvin cycle
Carbohydrates	CO2 fixation	Calvin cycle
Carbohydrates	Central carbohydrate metabolism	Dihydroxyacetone
Carbohydrates	Central carbohydrate metabolism	Entner-Doudoroff
Carbohydrates	Central carbohydrate metabolism	Entner-Doudoroff





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»Navigate »Organism »Comparative Tools »Help

Compare Metabolic Reconstruction of *Pseudomonas* sp. LFM046

Please select an organism to compare to.

start typing to narrow selection

Proteus mirabilis H4320 [B] (384.1)
Pseudoalteromonas atlantica T6c [B] (342610.3)
Pseudoalteromonas haloplanktis TAC125 [B] (326442.4)
Pseudoalteromonas tunicata D2 [B] (87626.3)
Pseudomonas aeruginosa 2192 [B] (350703.3)
Pseudomonas aeruginosa LESB58 [B] (557722.3)
Pseudomonas aeruginosa PA7 [B] (381754.5)
Pseudomonas aeruginosa PAO1 [B] (208964.1)
Pseudomonas aeruginosa UCBPP-PA14 [B] (208963.3)
Pseudomonas entomophila L48 [B] (384676.6)
Pseudomonas fluorescens Pf-5 [B] (220664.3)
Pseudomonas fluorescens Pf0-1 [B] (205022.3)

select

Completeness

- ☒ complete
☐ incomplete
☐ fragment

sort

- ☒ alphabetical
☐ genome id
☐ phylogeny

Domains

- ☒ Archaea
☒ Bacteria
☐ Environmental Sample
☒ Eukaryota
☐ Plasmid
☐ Virus

»Comparative Tools

Function based
Comparison

Sequence based
Comparison

Kegg

BLAST

Compare Metabolic Reconstruction of *Pseudomonas* sp. LFM046 (A) and *Pseudomonas putida* KT2440 (B)

select other

The comparison of metabolic reconstruction will allow you to compare the **functioning parts** of two organisms. The notion of functioning is defined by having genes for all the functional roles that compose a variant of a subsystem.

The table below will list all genes which were associated with a subsystem in the respective organism. The first column will allow you to filter those that are unique to one organism, to the other, or common to both. The column 'SS active' will show you whether the subsystem this gene has been classified into was found to have an active variant in this organism.

If the gene cannot be found, you can click the find button in that cell to search for it.

save to file

clear all filters

display 15 items per page

displaying 1 - 15 of 3385

Presence	Category	Subcategory	Subsystem	Role	Organism A	SS active	Organism B
all	all	all				all	all
A and B	Amino Acids and Derivatives	Alanine, serine, and glycine	Alanine biosynthesis	Alanine racemase (EC 5.1.1.1)	figl1093222.6.peq.4827 , figl1093222.6.peq.5179	yes	figl160488.1.peq.3685 , figl160488.1.peq.5200
A and B	Amino Acids and Derivatives	Alanine, serine, and glycine	Alanine biosynthesis	Branched-chain amino acid aminotransferase (EC 2.6.1.42)	figl1093222.6.peq.4905	yes	figl160488.1.peq.3478
A and B	Amino Acids and Derivatives	Alanine, serine, and glycine	Alanine biosynthesis	Chaperone protein HscA	figl1093222.6.peq.974	yes	figl160488.1.peq.837
A and B	Amino Acids and Derivatives	Alanine, serine, and glycine	Alanine biosynthesis	Cysteine desulfurase (EC 2.8.1.7)	figl1093222.6.peq.3088 , figl1093222.6.peq.3554	yes	figl160488.1.peq.2413 , figl160488.1.peq.4295

Presence	Category	Subcategory	Subsystem	Role	Organism A	SS active A	Organism B
1 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Alanine racemase (EC 5.1.1.1)	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
2 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Branched-chain amino acid amir	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
3 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Chaperone protein HscA	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
4 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Cysteine desulfurase (EC 2.8.1.7)	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
5 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Cysteine desulfurase (EC 2.8.1.7)	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
6 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Cysteine desulfurase CsdA-CsdE	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
7 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Ferredoxin, 2Fe-2S	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
8 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Iron binding protein IscA for iron	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
9 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Iron-sulfur cluster assembly sca	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
10 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Iron-sulfur cluster regulator IscR	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
11 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Serine hydroxymethyltransferase	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
12 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Serine hydroxymethyltransferase	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
13 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Serine hydroxymethyltransferase	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
14 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Serine hydroxymethyltransferase	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes
15 A and B	Amino Acids and Derivatives	Alanine, serine, and glyci	Alanine biosynthesis	Serine hydroxymethyltransferase	ca href=&#39;?page=yes	ca href=&#39;?page=yes	ca href=&#39;?page=yes



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»Comparative Tools

Function based
Comparison

Sequence based
Comparison

Kegg Metabolic Analysis

BLAST search

»Navigate »Organism »Comparative Tools »Help

KEGG map *Glycolysis / Gluconeogenesis* for *Pseudomonas sp. LFM046* (1093222.6)

Select KEGG metabolic map:

Glycolysis / Gluconeogenesis

Geraniol degradation

Glucosinolate biosynthesis

Glutathione metabolism

Glycerolipid metabolism

Glycerophospholipid metabolism

Glycine, serine and threonine metabolism

Glycolysis / Gluconeogenesis

Select upto 4 organisms for comparison:

Columns not in display

Public: Palaeococcus ferrophilus DSM
Public: thermococcus barophilus MP
Private: Burkholderia sacchari LMG 19
Private: Burkholderia sacchari LMG45C
Private: Halomonas sp. H601 (66666)
Private: Halomonas sp. HG01 (16099)
Private: Pseudomonas sp. IPT 046 (1
Private: Pseudomonas sp. IPT 046 (1

->

<-

clear selection

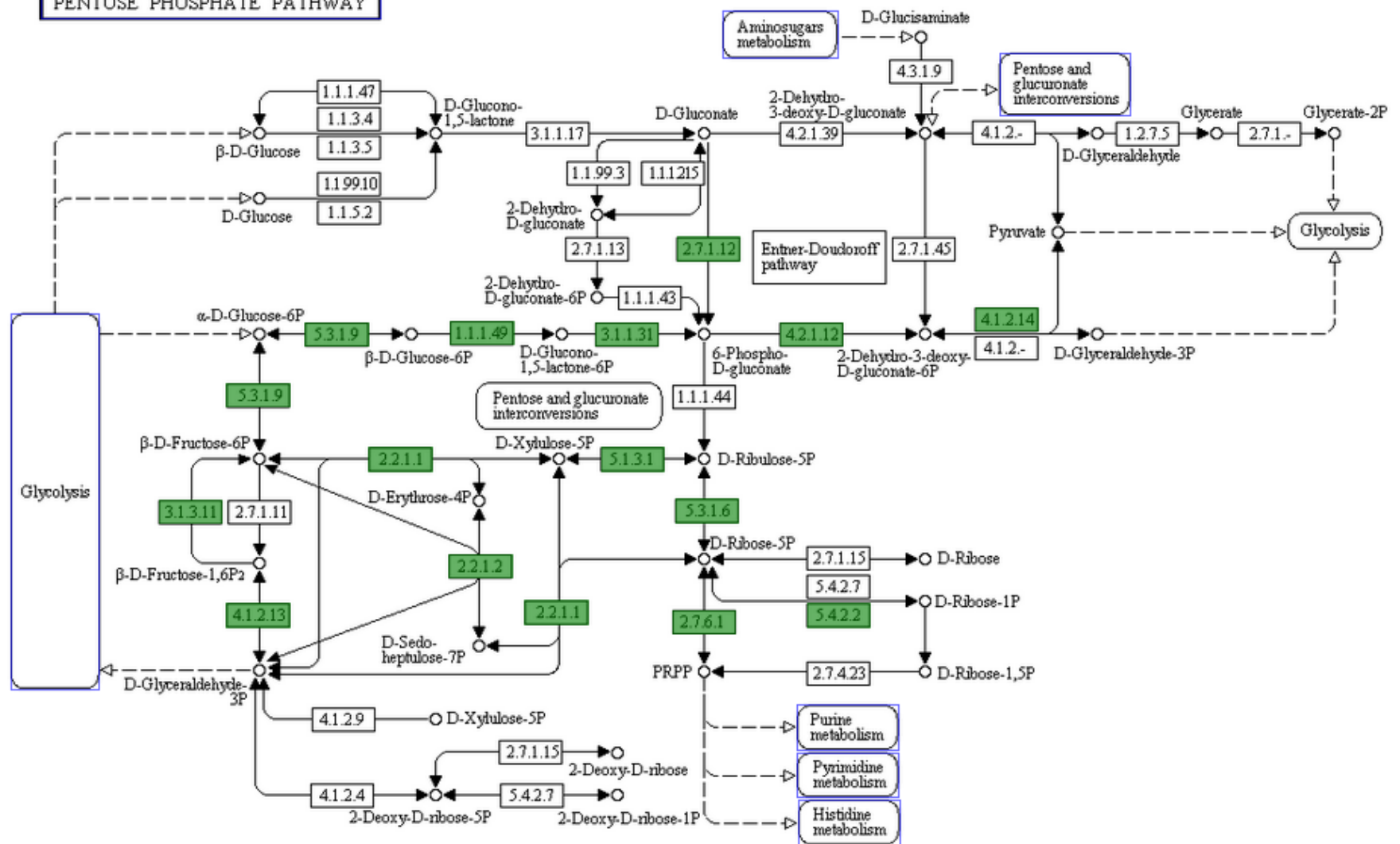
Columns in display

Pseudomonas aeruginosa PA01 (208
Pseudomonas putida KT2440 (16048

Select

KEGG map	Distinct ECs	Pseudomonas sp. LFM046	Pseudomonas aeruginosa PA01	Pseudomonas putida KT2440
Carbon fixation in photosynthetic organisms	25	14 (56.0 %)	16 (64.0 %)	15 (60.0 %)
Citrate cycle (TCA cycle)	22	15 (68.2 %)	14 (63.6 %)	14 (63.6 %)
Glycolysis / Gluconeogenesis	41	19 (46.3 %)	20 (48.8 %)	20 (48.8 %)
Pentose phosphate pathway	37	15 (40.5 %)	23 (62.2 %)	23 (62.2 %)
Propanoate metabolism	47	20 (42.6 %)	20 (42.6 %)	19 (40.4 %)
Pyruvate metabolism	64	26 (40.6 %)	29 (45.3 %)	27 (42.2 %)
Starch and sucrose metabolism	71	9 (12.7 %)	15 (21.1 %)	16 (22.5 %)

PENTOSE PHOSPHATE PATHWAY





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Export for sp. LFM046 (1093222.6)

We support the following information about our organisms. All this information is
Scenarios: The data they created is freely available on our ftp site at:
Subsystems: <http://ftp.theseed.org/>

This is a RAST job details page for Pseudomonas sp. LFM046
link to get to the according RAST page:

- [RAST job details page for Pseudomonas sp. LFM046](#)

The table below includes all features of this genome. You have multiple options of filtering that
button, you can export the table in it's currently filtered form into tab separated format,
application.

export table clear all filters

display 20 items per page

displaying 1 - 20 of 5489

next last

Feature ID	Type	Contig	Start	Stop	Frame	Strand	Length (bp)	Function	Subsystem	NCBI GI	locus
fig 1093222.6.peg.1	CDS	MDS_scf5	1430	1077							
fig 1093222.6.peg.2	CDS	MDS_scf5	1919	1449							
fig 1093222.6.peg.3	CDS	MDS_scf5	3733	1916							
fig 1093222.6.peg.4	CDS	MDS_scf5	4800	3730							
fig 1093222.6.peg.5	CDS	MDS_scf5	4954	4820							
fig 1093222.6.peg.6	CDS	MDS_scf5	5485	5123							
fig 1093222.6.peg.7	CDS	MDS_scf5	6160	5543							
fig 1093222.6.peg.8	CDS	MDS_scf5	6221	6896							
fig 1093222.6.peg.9	CDS	MDS_scf5	6835	6221							
fig 1093222.6.peg.10	CDS	MDS_scf5	7399	6896							
fig 1093222.6.peg.11	CDS	MDS_scf5	7972	7427							
fig 1093222.6.peg.12	CDS	MDS_scf5	9084	7969							
fig 1093222.6.peg.13	CDS	MDS_scf5	9899	9141							
fig 1093222.6.peg.14	CDS	MDS_scf5	10778	9966							
fig 1093222.6.peg.15	CDS	MDS_scf5	11173	10829							
fig 1093222.6.peg.16	CDS	MDS_scf5	11460	11221							
fig 1093222.6.peg.17	CDS	MDS_scf5	11822	11457							
fig 1093222.6.peg.18	CDS	MDS_scf5	12100	11819							
fig 1093222.6.peg.19	CDS	MDS_scf5	13001	12105							
fig 1093222.6.peg.20	CDS	MDS_scf5	13204	12998							
fig 1093222.6.peg.21	CDS	MDS_scf5	13746	13330							
fig 1093222.6.peg.22	CDS	MDS_scf5	14554	15039							
fig 1093222.6.peg.23	CDS	MDS_scf5	15032	15244							

Abrir "table.tsv"

Você selecionou abrir:

☒ table.tsv

tipo: tsv File (875 KB)

de: http://rast.nmpdr.org

O que o Firefox deve fazer?

☒ Abrir com o:

☐ Download

☐ Memorizar a decisão para este tipo de arquivo

OK Cancelar

table [Read-Only] - Excel											
File Home Insert Page Layout Formulas Data Review View Tell me what you want to do											
Clipboard			Font			Alignment			Number		
Cells			Styles			Cells			Formulas		
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23											
Feature ID	Type	Contig	Start	Stop	Frame	Strand	length (bp)	Function	Subsystem	NCBI GI	locus
fig 1093222.6.peg.1	CDS	MDS_scf5	1430	1077	-2	-	354	hypothetical protein	- none -		
fig 1093222.6.peg.2	CDS	MDS_scf5	1919	1449	-2	-	471	hypothetical protein	- none -		
fig 1093222.6.peg.3	CDS	MDS_scf5	3733	1916	-1	-	1818	DNA cytosine methyltransferase fami	- none -		
fig 1093222.6.peg.4	CDS	MDS_scf5	4800	3730	-3	-	1071	Retron-type RNA-directed DNA polymrout II intron-associated gene	- none -		
fig 1093222.6.peg.5	CDS	MDS_scf5	4954	4820	-1	-	135	hypothetical protein	- none -		
fig 1093222.6.peg.6	CDS	MDS_scf5	5485	5123	-1	-	363	hypothetical protein	- none -		
fig 1093222.6.peg.7	CDS	MDS_scf5	6160	5543	-1	-	618	hypothetical protein	- none -		
fig 1093222.6.peg.8	CDS	MDS_scf5	6835	6221	-1	-	615	hypothetical protein	- none -		
fig 1093222.6.peg.9	CDS	MDS_scf5	7399	6896	-1	-	504	hypothetical protein	- none -		
fig 1093222.6.peg.10	CDS	MDS_scf5	7972	7427	-1	-	546	COG1896: Predicted hydrolases of HD	- none -		
fig 1093222.6.peg.11	CDS	MDS_scf5	9084	7969	-3	-	1116	FIG146085: 3'-to-5'-oligoribc19; RNA processing and c	- none -		
fig 1093222.6.peg.12	CDS	MDS_scf5	9899	9141	-2	-	759	hypothetical protein	- none -		
fig 1093222.6.peg.13	CDS	MDS_scf5	10778	9966	-2	-	813	Phage protein	- none -		
fig 1093222.6.peg.14	CDS	MDS_scf5	11173	10829	-1	-	345	Translation elongation factors (GTPase	- none -		
fig 1093222.6.peg.15	CDS	MDS_scf5	11460	11221	-3	-	240	hypothetical protein	- none -		
fig 1093222.6.peg.16	CDS	MDS_scf5	11822	11457	-2	-	366	hypothetical protein	- none -		
fig 1093222.6.peg.17	CDS	MDS_scf5	12100	11819	-1	-	282	hypothetical protein	- none -		
fig 1093222.6.peg.18	CDS	MDS_scf5	13001	12105	-2	-	897	hypothetical protein	- none -		
fig 1093222.6.peg.19	CDS	MDS_scf5	13204	12998	-1	-	207	hypothetical protein	- none -		
fig 1093222.6.peg.20	CDS	MDS_scf5	13746	13330	-3	-	417	putative phage repressor	- none -		
fig 1093222.6.peg.21	CDS	MDS_scf5	14554	15039	1	+	486	hypothetical protein	- none -		
fig 1093222.6.peg.22	CDS	MDS_scf5	15032	15244	2	+	213	hypothetical protein	- none -		

- Conferência da anotação automática dos genes:

Nucleotide BLAST: Search ...

blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&BLAST_SPEC=&LINK_LOC=blasttab&LAST_PAGE=bl

Mais visitados Últimas notícias https://mail.google.co... FAPESP :: Pós-Doutora... Entrada (1.349) - jujuc... Catho On

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ blastn suite

Standard Nucleotide BLAST

blastn blastp blastx tblastn tblastx

BLASTN programs

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

Or, upload file

Selecionar arquivo... Nenhum arquivo selecionado.

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database

☐ Human genomic + transcript ☐ Mouse genomic + transcript

Nucleotide collection (nr/nt)

BLAST® Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ blastx

Translated BLAST: blastx

blastn blastp blastx tblastn tblastx

BLASTX search protein databases using a translated nucleotide sequence

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

Clear Query subrange

From

To

Or, upload file

Selecionar arquivo... Nenhum arquivo selecionado.

Genetic code

Standard (1)

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

Choose Search Set

Database

Non-redundant protein sequences (nr)

Organism

Optional

Enter organism name or id--completions will be suggested

Exclude

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Softwares utilizados

	KEGG	BRENDA	UniProtKB	Entrez Gene	PubChem	MetaCyc	Transport DB
<i>Information about the definition of metabolic reactions</i>							
Substrate specificity	✓	✓	✓			✓	✓
Metabolite formulae	✓	✓			✓	✓	✓
Stoichiometry	✓	✓	✓			✓	
Reaction directionality	✓	✓				✓	✓
Subcellular localization				✓		✓	
<i>Other information about metabolic-reaction properties</i>							
Genome sequence and annotation	✓		✓	✓			
GPR associations	✓	✓				✓	✓
Literature	✓	✓	✓	✓		✓	✓
GPR associations, gene–protein–reaction associations.							

PSEUDOMONAS GENOME DATABASE

Improving Disease Treatment Through Genome Research



cystic fibrosis foundation
THERAPEUTICS inc.



Please note that we will be retiring this old site on Tuesday, August 25th, 2015.

At that point, the URL for www.pseudomonas.com will bring you to our new site currently hosted at beta.pseudomonas.com. We encourage you to visit the new site now and see a more recent set of updated gene annotations and MANY more *Pseudomonas* strains.

[Home](#) [About](#) [News](#) [Database Overview](#) [Database Search](#) [Tools](#) [BLAST](#) [GBrowse](#) [PseudoCyc](#) [Updates Log](#) [Download](#) [View My Clipboard](#) [Contact Us](#)



Since 2001, the Pseudomonas Genome database has been a resource for peer-reviewed, continually-updated annotations for the *Pseudomonas aeruginosa* PAO1 reference strain's genome and, more recently, comparative analyses of several related *Pseudomonas* species.

Funding for this work is gratefully provided by [Cystic Fibrosis Foundation Therapeutics Inc.](#), a non-profit drug discovery and development affiliate of the Cystic Fibrosis Foundation ([learn more](#)).

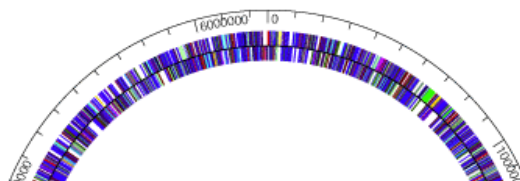
Quick Search?

for

Latest News

June 3, 2015

Fixed a recently introduced bug that was causing some BLAST search results to be empty.



Strain-Specific Summaries and Analyses

Choose from Complete Genomes

Choose from Incomplete/Draft Genomes

By linking from here, one can go to an overview of any reference strain's chromosome or plasmids with a summary of their genes, broken down by feature type or its product's primary subcellular localization.

Submit an Annotation Update

[Submit](#) an update to the continually-updated *Pseudomonas aeruginosa* PAO1 or LESB58 genome annotations.



KEGG

4.1.3.16

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KEGG: Kyoto Encyclopedia of Genes and Genomes

KEGG is a database resource for understanding high-level functions and utilities of the biological system, such as the cell, the organism and the ecosystem, from molecular-level information, especially large-scale molecular datasets generated by genome sequencing and other high-throughput experimental technologies (See [Release notes](#) for new and updated features).

New service [GhostKOALA](#) for metagenome annotation is available.

Main entry point to the KEGG web service[KEGG2](#)[KEGG Table of Contents](#)[Update notes](#)**Data-oriented entry points****KEGG PATHWAY**[KEGG pathway maps](#) [[Pathway list](#)]**KEGG BRITE**[BRITE functional hierarchies](#) [[Brite list](#)]**KEGG MODULE**[KEGG modules](#) [[Module list](#) | [Statistics](#)]**KEGG ORTHOLOGY**[Ortholog groups](#) [[KO system](#) | [Annotation](#)]**KEGG GENOME**[Genomes](#) [[KEGG organisms](#)]**KEGG GENES**[Genes and proteins](#) [[Release history](#)]**KEGG COMPOUND**[Small molecules](#) [[Compound classification](#)]**KEGG REACTION**[Biochemical reactions](#) [[Reaction modules](#)]**KEGG DISEASE**[Human diseases](#) [[Cancer](#) | [Pathogen](#)]**KEGG DRUG**[Drugs](#) [[ATC drug classification](#)]**KEGG MEDICUS**[Health information resource](#) [[Drug labels search](#)]**Organism-specific entry points****KEGG Organisms**

Enter org code(s)

Go

[hsa](#) [hsa eco](#)

BioCyc Database Collection

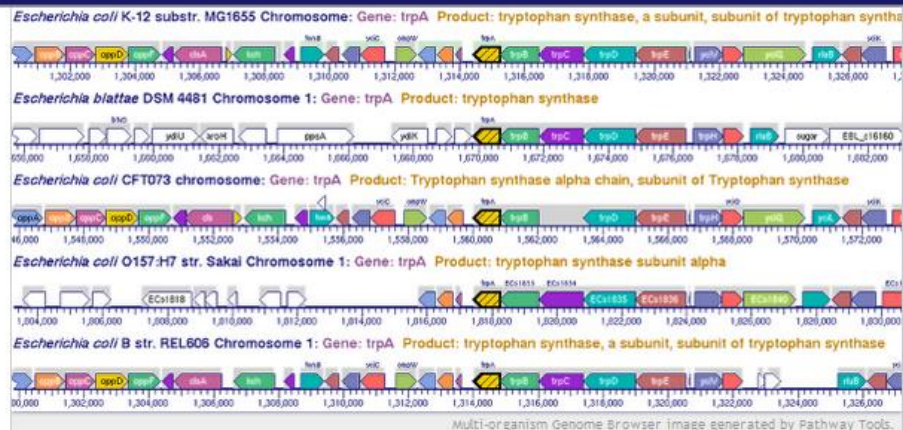
BioCyc is a collection of 5500 Pathway/Genome Databases (PGDBs), plus software tools for understanding their data.

Getting Started

New to BioCyc? Typical usage is:

- Select one or more databases (genomes) to search. To do so, click "change organism database" in the box in the top right of every page. By default, BioCyc searches *Escherichia coli* K-12 substr. MG1655.
- Search for a gene or pathway using the Quick Search, or see the Search menu for more options.

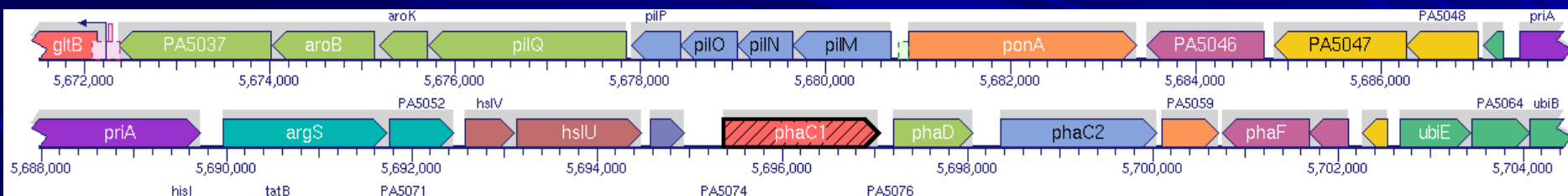
[New User Guide >>](#)



Comparative Genome Analysis

Multiple comparative analysis tools are available in this website.

[Learn More](#)



BRENDA - informações sobre especificidades do substrato da enzima para uma série de organismos e links para relevantes Publicações.

BRENDA home

History

how all | hide all No of entries

Enzyme Nomenclature 80

Enzyme-Ligand Interactions 217

Diseases 0

Functional Parameters 165

Organism related Information 41

General Information 4

Enzyme Structure 6369

Molecular Properties 37

Applications 7

References 47

External Links

**BRENDA**
The Comprehensive Enzyme Information System

Information on EC 4.1.2.14 - 2-dehydro-3-deoxy-phosphogluconate aldolase

for references in articles please use BRENDA:EC4.1.2.14

EC Tree

- 4 Lyases
 - 4.1 Carbon-carbon lyases
 - 4.1.2 Aldehyde-lyases
 - 4.1.2.14 2-dehydro-3-deoxy-phosphogluconate aldolase

IUBMB Comments

The enzyme shows no activity with 2-dehydro-3-deoxy-6-phosphate-D-galactonate. cf. EC 4.1.2.55, 2-dehydro-3-deoxy-phosphogluconate/2-dehydro-3-deoxy-6-phosphogalactonate

Specify your search results

Mark a special word or phrase in this record: **Mark!**

Search Reference ID: **Search**

Search UniProt Accession: **Search**

Select one or more organisms in this record:

All organisms

Acidiphilium cryptum

animal

Archaea

Aureobasidium pullulans

Submit

Show additional data

☒ Do not include text mining results

☐ Include **AMENDA** (text mining) results

☐ Include **BRENDA** results (AMENDA + additional results, but less precise)

Word Map hide

emden-meyeroth schiff-base

entner-doudoroff

synthesis 4.1.2.14

dehydratases

bromopyruvate

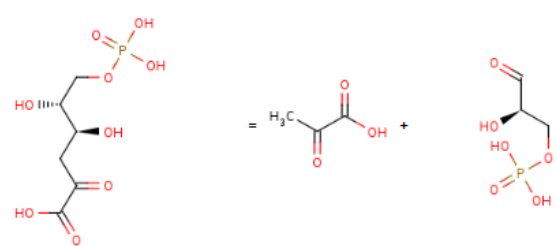
aldolases

medicine

carbinolamine

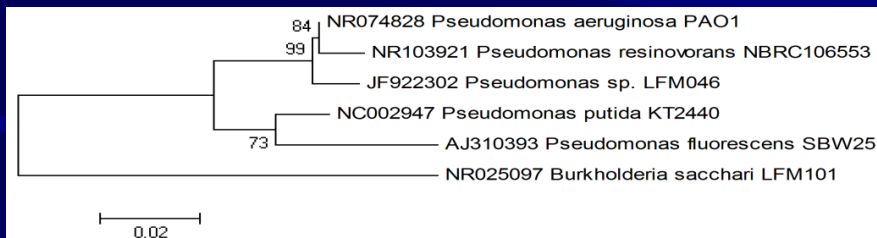
Reaction Schemes hide

2-dehydro-3-deoxy-6-phospho-D-gluconate = pyruvate + D-glyceraldehyde 3-phosphate



Core de *Pseudomonas* sp. LFM046

Análise comparativa dos genes do metabolismo de carboidratos a partir da anotação gênica de genomas espécies de *Pseudomonas* disponíveis em bases de dados.



Árvore filogenética representando as espécies de *Pseudomonas* mais próximas à *Pseudomonas* sp. LFM046

Cardinali Rezende et al. 2020

Gene	<i>Pseudomonas</i> sp. LFM046	<i>P. putida</i> KT2440	<i>P. resinovorans</i> NBRC106553	<i>P. fluorescens</i> SW25	<i>P. aeruginosa</i> PAO1
PHA synthesis					
<i>phaA</i>	NO	NO	NO	PFLU-0396	NO
<i>phaB</i>	NO	NO	NO	PFLU-0395	NO
<i>phaI1</i>	OK	NO	PCA10-41660	NO	NO
<i>phaI</i>	OK	PP5008	PCA10-52820	PFLU-0391	PA-5061
<i>phaF</i>	OK	PP5007	NO	NO	PA-5060
<i>phaC1</i>	OK	PP5003	PCA10-52770	PFLU-0394	PA-5056
<i>phaC2</i>	OK	PP5005	PCA10-52790	NO	PA-5058
<i>phaC</i>	OK				
<i>phaC</i>	OK				
<i>phaZ</i>	OK	PP5004	PCA10-52780	NO	NO
<i>phaD</i>	OK	PP5006	NO	NO	PA-5057
<i>phaG</i>	OK	PP1408	PCA10-15380	PFLU-1434	NO
<i>phaK</i>	OK	P3271	PCA10-16370	NO	NO
<i>bdhA</i>	OK	PP3073	17640/35300	NO	PA-2003
Embden-Meyerhof-Parnas (EMP) / Glycolysis/Gluconeogenesis					
<i>glk</i>	OK	PP1011	NO	PFLU-4963	PA-3193
<i>pgi</i>	OK	PP1808	PCA10-48920	PFLU-5243	PA-4732
<i>fbp</i>	OK	PP5040	PCA10-53170	0355/0527B	PA-5110
<i>pfk</i>	NO	NO	NO	NO	NO
<i>sdh</i>	OK	OPP4960	PCA10-03780	NO	PA-0555
<i>tpiA</i>	OK	PP4715	PCA10-49150	PFLU-5257	PA-4748
<i>gap1</i>	OK	PP1009	PCA10-16110	PFLU-1566	PA-3195
<i>gap2</i>	OK	PP2149	PCA10-35760	NO	NO
<i>pgk</i>	OK	PP4963	PCA10-03750	PFLU-5705	PA-0552
<i>pgm</i>	OK	PP5056	NO	NO	PA-5131
<i>eno</i>	OK	PP1612	PCA10-45140	PFLU-1291/1903	PA-3635
<i>pyk</i>	OK	PP1362	PCA10-19080	PFLU-1799	PA-1498 (pykF)
<i>PykA</i>	OK	NO	PCA10-46450	NO	PA-4329
<i>aceE</i>	OK	PP0339	PCA10-52400	PFLU-0460	PA-2634
Pentose phosphate pathways (PPP)					
<i>zwf1</i>	OK	PP1022	PCA10-14620	NO	PA-3183
<i>zwf2</i>	OK	PP4042	PCA10-56010	NO	NO
<i>zwf3</i>	NO	PP5351	NO	NO	NO
<i>gnd</i>	NO	PP4043	NO	NO	NO
<i>rpiA</i>	OK	PP5150	PCA10-03260	PFLU-5824	PA-0330
<i>rpe</i>	OK	PP0415	PCA10-05530	PFLU-5563	PA-0607
<i>tktA</i>	OK	PP4965	PCA10-03730	PFLU-5707	PA-0548
<i>tal</i>	OK	PP2168	PCA10-35900	PFLU-1585B	PA-2796
Entner-Doudoroff Pathway (EDP)					
<i>edd</i>	OK	PP1010	PCA10-14590	NO	PA-3194
<i>eda</i>	OK	PP1024	PCA10-14640	NO	PA-3181
Tricarboxylic acid Cycle (TCA cycle)					
<i>glcA</i>	OK	PP4194	NO	PFLU-1815	PA-1580
<i>acnA</i>	OK	PP2112	PCA10-38140	PFLU-1542	PA-1562
<i>acnB</i>	NO	PP2339	27520/36960	NO	PA-1787
<i>icd</i>	OK	PP4011	NO	NO	NO
<i>icd2</i>	OK	NO	PCA10-25100	NO	OK
<i>sucA</i>	OK	PP4189	PCA10-21680	PFLU-1820	PA-1585
<i>sucB</i>	OK	NO	PCA10-21690	PFLU-1821	PA-1586
<i>sucD</i>	OK	PP4185	PCA10-21720	PFLU-1824	PA-1589
<i>sucC</i>	OK	PP4186	PCA10-21710	PFLU-1823	PA-1588
<i>sdhA</i>	OK	PP4191	PCA10-21660	PFLU-1818	PA-1583
<i>sdhB</i>	OK	PP4191	PCA10-21670	PFLU-1819	PA-1584
<i>sdhC</i>	OK	NO	PCA10-21640	PFLU-1816	PA-1581
<i>fumA</i>	OK	NO	PCA10-46490	PFLU-4314/4952	NO
<i>fumC</i>	OK	PP0944	10210/13230	PFLU-0874	PA-4470/0854
<i>mdh</i>	OK	PP0654	PCA10-23230	NO	NO

Rede metabólica - Core

Genome sequence and annotation



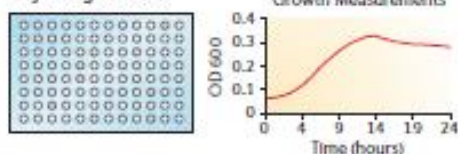
Available literature



Phylogenetic data



Physiological data



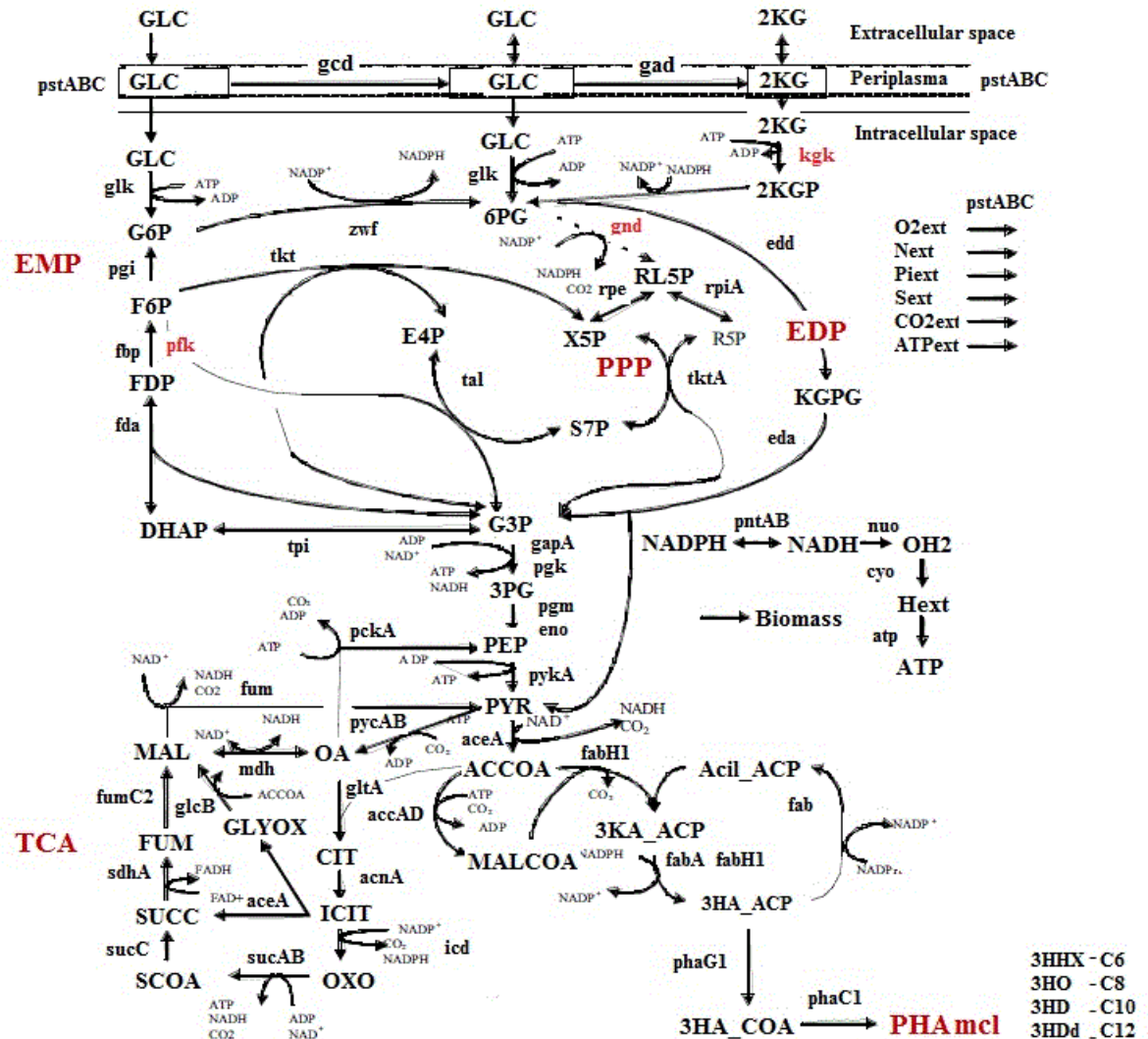
Databases



Localization



Signal sequences: PLILIPISGSALP



Construção da rede metabólica em escala genômica de *Pseudomonas* sp.LFM046

Etapa 2. Construção e refinamento manual do core



NIH Public Access Author Manuscript

Nat Protoc. Author manuscript; available in PMC 2011 June 28.

Published in final edited form as:

Nat Protoc. 2010 ; 5(1): 93–121. doi:10.1038/nprot.2009.203.

A protocol for generating a high-quality genome-scale metabolic reconstruction

Ines Thiele^{1,2} and Bernhard Ø. Palsson^{1,*}

¹Department of Bioengineering University of California, San Diego 9500 Gilman Drive La Jolla, CA 92093-0412 United States of America

Etapa 2. Construção e refinamento manual do Core

- Conferência da anotação dos genes da *Pseudomonas* sp. LFM046.
- Rede metabólica em escala genômica de *Pseudomonas aeruginosa* PA01.
- Reconstrução e refinamento do core a partir de dados presentes na literatura e nos bancos de dados:
RAST, KBase, NCBI, Pseudomonas Genome Database, KEGG, BioCyc, UniProt, COG (ptns ortólogas), STRING (Interações entre ptns), BRENDA (informações enzimáticas), etc.

Core da *Pseudomonas* sp. LFM046

- Texto composto por 380 reações e 230 metabólitos:

Copy of 2_REAÇÕES E METABÓLITOS_LFM046 - Excel

FileHomeInsertPage LayoutFormulasDataReviewViewTell me what you want to do

CutCopyFormat Painter

Clipboard

Calibri11

B*I*U

Font

Wrap Text

Alignment

General

Number

Conditional Formatting

Format as Table

Cell Styles

Styles

Insert

Delete

Format

Cells

Σ Auto

Fill

Clear

K3

	A	B	C	D	E	F	G	H	I
1	LFM046	Metabolite	Metabolite Name	Neutral Formula	Charged Formula	Alternate compound names	KeggID	Compartment	EXCHANGE
2	1	10fthf	10-Formyltetrahydrofolate	C20H21N7O7	C20H23N7O7	10-Formyl-THF	C00234	cytosol	EX
3	2	13dpg	3-Phospho-D-glyceroyl phosphate	C3H4O10P2	C3H8O10P2	1,3-bis-phosphoglycerate/ 3-Phospho	C00236	cytosol	EX
4	3	23dhdp	2,3-Dihydrodipicolinate	C7H5NO4	C7H7NO4	Dihydrodipicolinic acid	C03340	cytosol	-
5	4	23dhmb	(R)-2,3-Dihydroxy-3-methylbutanoate	C5H9O4	C5H10O4	(R)-2,3-Dihydroxy-isovalerate/ (R)-2,3	C04272	cytosol	-
6	5	23dhmp	(R)-2,3-Dihydroxy-3-methylpentanoate	C6H11O4	C6H12O4	2,3-Dihydroxy-3-methylvalerate	C06007	cytosol	-
7	6	25aics	(S)-2-[5-Amino-1-(5-phospho-D-ribosyl	C13H15N4O12P	C13H19N4O12P	1-(5'-Phosphoribosyl)-5-amino-4-(N-s	C04823	cytosol	-
8	7	26dap-LL	LL-2,6-Diaminoheptanedioate	C7H14N2O4	C7H14N2O4	LL-2,6-Diaminopimelic acid/ LL-2,6-Dia	C00666	cytosol	-
9	8	26dap-M	meso-2,6-Diaminoheptanedioate	C7H14N2O4	C7H14N2O4	meso-2,6-Diaminopimelic acid/ meso-	C00680	cytosol	EX
10	9	2ahbut	(S)-2-Aceto-2-hydroxybutanoate	C6H9O4	C6H10O4	(S)-2-Hydroxy-2-ethyl-3-oxobutanoate	C06006	cytosol	EX
11	10	2beACP	But-2-enoyl-[acyl-carrier protein]	C4H5OX	C4H5OX	But-2-enoyl-[acyl-carrier protein]	C04246	cytosol	-
12	11	2dda7p	2-Dehydro-3-deoxy-D-arabino-heptona	C7H10O10P	C7H13O10P	3-Deoxy-D-arabino-hept-2-ulosonate	C04691	cytosol	-
13	12	2ddg6p	2-Dehydro-3-deoxy-D-gluconate 6-pho	C6H8O9P	C6H11O9P	2-Dehydro-3-deoxy-6-phospho-D-gluc	C04442	cytosol	-
14	13	2ippm	2-Isopropylmaleate	C7H8O4	C7H10O4	beta-isopropylmaleate	C02631	cytosol	-
15	14	2maacoa	2-Methyl-3-acetoacetyl-CoA	C26H38N7O18P3S	C26H42N7O18P3S	2-Methylacetoacetyl-CoA	C03344	cytosol	EX
16	15	2o3mpt	(R)-2-Oxo-3-methylpentanoate	C6H9O3	C6H10O3	(R)-2-Oxo-3-methylpentanoic acid/ (3	C06008	cytosol	EX
17	16	2obut	2-Oxobutanoate	C4H5O3	C4H6O3	2-Ketobutyric acid/ 2-Oxobutyric acid/	C00109	cytosol	EX
18	17	2pg	D-Glycerate 2-phosphate	C3H4O7P	C3H7O7P	2-Phospho-D-glycerate/ 2-phosphogly	C00631	cytosol	EX
19	18	2tddACP	trans-Dodec-2-enoyl-[acyl-carrier prote	C12H21OX	C12H21OX	trans-Dodec-2-enoyl-[acp]	C05758	cytosol	-
20	19	2tdeACP	trans-Dec-2-enoyl-[acyl-carrier protein	C10H17OX	C10H17OX	trans-Dec-2-enoyl-[acp]/ (2E)-Deceno	C05754	cytosol	-
21	20	2theACP	trans-Hex-2-enoyl-[acp]	C6H9OX	C6H9OX	trans-Hex-2-enoyl-[acyl-carrier protei	C05748	cytosol	-
22	21	2tocdACP	trans-Octadec-2-enoyl-[acyl-carrier-pro	C18H33OX	C18H33OX	(2E)-Octadecenoyl-[acp]	C16221	cytosol	-
23	22	2toceACP	trans-Oct-2-enoyl-facvl-carrier protein	C8H13OX	C8H13OX	trans-Oct-2-enoyl-facvl-carrier protein	C05751	cytosol	-

Anotação RAST

Reações

Metabólitos

046XPA01

046XKT2440

PA01XKT2440

Unique to 046 (f ...)

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BioModels Database is a repository of computational models of biological processes. Models described from literature are manually curated and enriched with cross-references. All models are provided in the [Public Domain](#). More information about BioModels Database can be found in the [FAQ](#).

Models published in the literature

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(591 models)



[Non curated](#)
(877 models)

Alternative access



[Gene Ontology classification](#)
(new)



[Gene Ontology tree](#)



[Advanced search](#)

Models automatically generated from pathway resources (Path2Models)

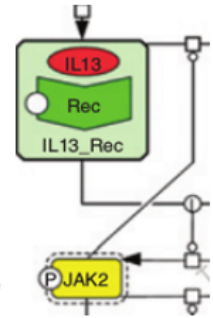
Browse

Alternative access

Model of the month

April, 2016

The JAK/STAT signalling pathway is hyper-activated in several lymphomas. Here, the conditions prevailing the two types of lymphomas (PMBL and cHL) has been described using a mathematical model, and signalling components in the JAK/STAT pathway that can be a potential drug target has been identified and validated experimentally.



[Access this model of the month.](#)

News

 **18 Feb 2016** [New Models in BioModels](#)

BioModels now provides 1457 literature-based models, with the new addition of 78 models.

bigg.ucsd.edu/models

Pesquisar

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BiGG Models

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Search DatabaseSearch

Search Results ?

Models

BiGG ID	Organism	Metabolites	Reactions	Genes
e_coli_core	Escherichia coli str. K-12 substr. MG1655	72	95	137
IAB_RBC_283	Homo sapiens	342	469	346
iAF1260	Escherichia coli str. K-12 substr. MG1655	1668	2382	1261
iAF1260b	Escherichia coli str. K-12 substr. MG1655	1668	2388	1261
iAF692	Methanosarcina barkeri str. Fusaro	628	690	692
iAF987	Geobacter metallireducens GS-15	1109	1285	987
IAPECO1_1312	Escherichia coli APEC O1	1944	2736	1313
iAT_PLT_636	Homo sapiens	738	1008	636
iB21_1397	Escherichia coli BL21(DE3)	1945	2742	1337
IBWG_1329	Escherichia coli BW2952	1949	2742	1328
ic_1306	Escherichia coli CFT073	1938	2727	1307
IE2348C_1286	Escherichia coli O127:H6 str. E2348/69	1919	2704	1284
IEC042_1314	Escherichia coli 042	1926	2715	1314

HomeAdvanced SearchModel ValidatorData Access

Search DatabaseSearch

Model: e_coli_core

Organism:
Escherichia coli str. K-12 substr. MG1655

Genome:
[NC_000913.3](#)

Model metrics:

Component	Count
Metabolites	72
Reactions	95
Genes	137

Download COBRA model from the BiGG Database:
SBML ? : [e_coli_core.xml.gz](#) (uncompressed)
JSON ? : [e_coli_core.json](#)
MAT ? : [e_coli_core.mat](#)

Construção automática da rede metabólica em escala genômica de *Pseudomonas* sp. LFM046



The Model SEED

Model SEED version 1.0

Welcome to the Model SEED - a resource for the generation, optimization, curation, and analysis of genome-scale metabolic models. For more information about The SEED please visit theSEED.org.

»SEED Resources »Account management

Pathway Tools

Information

Pathway Tools Overview
Academic Download
Commercial Download
Publications
Release Note History
Contributions
Pathway Tools Blog
Technical Datasheet
Contact Us

Technical Specs

Web Services
Pathway Tools APIs
Installation Guide
Ontologies
Operations
File Formats

Support

PATHWAY TOOLS SOFTWARE

Pathway Tools is a comprehensive symbolic systems biology software system that is associated with systems biology:

- Development of organism-specific databases (also called model-organism databases) that include:
 - Metabolic reconstruction and modeling.
- Scientific Visualization, web publishing, and dissemination of those organism-specific data:
 - Automatic display of metabolic pathways and full metabolic networks
 - A genome browser
 - Display of operons, regulons, and full transcriptional regulatory networks
- Visual analysis of gene-expression and metabolomics datasets, such as painting omics data onto diagrams of the full metabolic network, full regulatory network, and full genome.
- Computational inferences including prediction of metabolic pathways, prediction of metabolic pathway hole fillers, and prediction of operons, that can be used for genome analysis.
- Comparative genome and pathway analyses
- Analysis of biological networks:
 - Search for routes between specified metabolites
 - Find dead-end metabolites
 - Identify choke points (potential drug targets) in metabolic networks



KBBase

PREDICTIVE BIOLOGY

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KBBase: The Department of Energy Systems Biology Knowledgebase

A collaborative environment for computational experiments

▼ DATA

-  **FBA Model**
FBA Model
Oct 6, 2015 by jankabbase
-  **FBA Model**
FBA Model
Oct 6, 2015 by jankabbase
-  **FBA Model**
FBA Model
Oct 6, 2015 by jankabbase
-  **FBA Model**
FBA Model
Oct 6, 2015 by jankabbase
-  **FBA Model**
FBA Model
Oct 6, 2015 by jankabbase

▼ Run Flux Balance Analysis

Use Flux Balance Analysis (FBA) to predict metabolic fluxes in a metabolic model of an organism.

FBA Model: **BthetaVPI-5482_GapFilled_Glucose**

Media: **Btheta_minimal_media**

Output FBA Results: **BthetaVPI-5482_GapFilled.FBA.GlucoseMinimal**

[Edit profile-run](#) submitted on 13:38:28, 10/06/2015 by jankabbase

[Run Flux Balance Analysis](#)

KBBase's Narrative user interface lets you create and share sophisticated analytical workflows that include data, results and commentary.

cherry141373289994.BthetaVPI-5482_GapFilled.FBA
KBBase/BA.FBA-12.0

New to KBBase?

Search Data

Sign In

KBBase is an open platform for comparative functional genomics and systems biology for microbes, plants and their communities, and for sharing results and methods with other scientists.

- Adição da narrativa

The screenshot displays the KBase Narrative Interface in a web browser. The browser's address bar shows the URL <https://narrative.kbase.us/narrative/ws.13710.obj.1>. The page title is "GENOMA COMPLETO PSEUDOMONAS LFM046", created by Juliana Cardinali Rezende (jcardinali). The interface includes a sidebar with navigation tabs for "Analyze", "Narratives", and "Jobs". Under the "Narratives" tab, there are buttons for "+ New Narrative" and "Copy This Narrative". The "My Narratives" section lists several narratives, including "GENOMA COMPLETO PSEUDOMONAS LFM046 v47" (Mar 16, 2016), "2_Pseudomonas_sp_LFM046 - Copy v166" (Mar 14, 2016), "2_Pseudomonas_sp_LFM046 - Copy - Copy v148" (Sep 18, 2015), and "Pseudomonas_sp_LFM046 v37" (Jul 17, 2015). A link for "Show Advanced Controls" is also present. The main content area features the KBase logo and a welcome message: "Welcome to the Narrative Interface!". It includes sections for "What's a Narrative?" (describing collaborative computational experiments), "Get Some Data" (explaining how to browse or upload data), "Analyze It" (describing how to run analyses), and "Save and Share Your Narrative". The interface is clean and modern, with a blue and green color scheme.

(<http://kbase.us/compare-two-metabolic-models-method>)

2_Pseudomonas_sp_LFM0...

GENOMA COMPLETO PSE...

GENOMA COMPLETO PSE...

KB

GENOMA COMPLETO PSEUDOMONAS LFM046

Created by: Juliana Cardinali Rezende (jcardinali)

Analyze

Narratives

Hide / Show data browser

Data

Shared With Me

Public

Example

Import

DATA

ANOTACAO_PSEUDOMONAS_LFM046 v1

Genome: Pseudomonas_sp_LFM046

24 days ago

Carbon-D-Fructose v1

Media

24 days ago

Carbon-D-Glucose-Palsson v1

Media

24 days ago

Pseudomonas_LFM046 v1

+

APPS & METHODS

Domains

Annotate Domains in a Genome

★ v1.0.0

RAST

Annotate Microbial Contigs

★ v1.0.0

RAST

Annotate Microbial Genome

★ v1.0.0

Plant

Annotate Plant Coding Sequences with Metabolic

Search data...

All types...

All Narratives...

Genome

Pseudomonas_sp_LFM046

Jul 17, 2015 by jcardinali

Genome_scale_metabolic_model_Pseudomonas_sp_LFM046 v1

FBAModel

Pseudomonas_sp_LFM046

Jul 17, 2015 by jcardinali

Genome_scale_metabolic_model_Pseudomonas_sp_LFM046... v2

FBAModel

Pseudomonas_sp_LFM046

Jul 16, 2015 by jcardinali

Carbon-D-Glucose-Palsson v1

Media

Pseudomonas_sp_LFM046

Jul 15, 2015 by jcardinali

Carbon-D-Fructose v1

Media

Pseudomonas_sp_LFM046

Jul 15, 2015 by jcardinali

Anotation_Pseudomonas_sp_LFM046 v1

Genome: Pseudomonas sp. LFM046

Pseudomonas_sp_LFM046

Jul 15, 2015 by jcardinali

JYK000000000.1 v1

ContigSet

Pseudomonas_sp_LFM046

Jul 14, 2015 by jcardinali



GENOMA COMPLETO PSEUDOMONAS LFM046

Created by: Juliana Cardinali Rezende (jcardinali)

Analyze Narratives Jobs My Data Shared With Me Public Example Import

DATA



Search data...

All types...

All Narratives...

No data found



ANOTACAO_PSEUDOMONAS_LFM046 v1

Genome: Pseudomonas_sp_LFM046
24 days ago



Carbon-D-Fructose v1

Media
24 days ago



Carbon-D-Glucose-Palsson v1

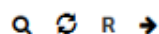
Media
24 days ago



Pseudomonas_LFM046 v1



APPS & METHODS



Annotate Domains in a Genome

★ v1.0.0



Annotate Microbial Contigs

★ v1.0.0



Annotate Microbial Genome

★ v1.0.0



Annotate Plant Coding
Sequences with Metabolic



GENOMA COMPLETO PSEUDOMONAS LFM046

Created by: Juliana Cardinali Rezende (jcardinali)

Analyze

Narratives

Jobs

My Data

Shared With Me

Public

Example

Import

DATA



ANOTACAO_PSEUDOMONAS_LFM046 v1

Genome: Pseudomonas_sp_LFM046
24 days ago



Carbon-D-Fructose v1

Media
24 days ago



Carbon-D-Glucose-Palsson v1

Media
24 days ago



Pseudomonas_LFM046 v1



APPS & METHODS



Annotate Domains in a Genome

★ v1.0.0



Annotate Microbial Contigs

★ v1.0.0



Annotate Microbial Genome

★ v1.0.0



Annotate Plant Coding Sequences with Metabolic

Genomes

Search data...

Total results: 28372 (40 shown)



Yersinia pestis biovar Microtus str. 91001

Domain: Bacteria
Contigs: 5
Genes: 4887



Gibberella zeae PH-1

Domain: Eukaryota
Contigs: 512
Genes: 11640



Synechococcus sp. CB0101

Domain: Bacteria
Contigs: 94
Genes: 2862



Synechococcus sp. CB0205

Domain: Bacteria
Contigs: 78
Genes: 2644



Acidovorax sp. JS42

Domain: Bacteria
Contigs: 3
Genes: 4392



Mycoplasma gallisepticum R

Domain: Bacteria
Contigs: 1
Genes: 816



Haemophilus ducreyi 35000HP

Domain: Bacteria

DATA 🔍 📄 📊 🔄 ➡️

-  **ANOTACAO_PSEUDOMONAS_LFM046** *v1*
Genome: *Pseudomonas_sp_LFM046*
24 days ago
 -  **Carbon-D-Fructose** *v1*
Media
24 days ago
 -  **Carbon-D-Glucose-Palsson** *v1*
Media
24 days ago
 -  **Pseudomonas_LFM046** *v1*

▼ APPS & METHODS

- Domains** **Annotate Domains in a Genome** ★ v1.0.0
 - RAST** **Annotate Microbial Contigs** ★ v1.0.0
 - RAST** **Annotate Microbial Genome** ★ v1.0.0
 - Plant** **Annotate Plant Coding Sequences with Metabolic**

My Data Shared With Me Public **Example** Import

Example Sequence Assembly Inputs

Various types of read data configured for sequence assembly.

-  **rhodo.art.q20.int.PE.reads**
PairedEndLibrary
-  **rhodo.art.q10.PE.reads**
PairedEndLibrary

Example Contig Sets

A set of DNA sequences

- Shewanella_oneidensis_MR-1_contigs
ContigSet
 - Rhodobacter_CACIA_14H1_contigs
ContigSet

Example Genomes

Genomic sequence generally with attached functional annotations

-  **Shewanella_oneidensis_MR-1**
Genome: *Shewanella oneidensis* MR-1
 -  **Sbicolor JGI-v2.1**
Genome: *Sorghum bicolor*
 -  **Rhodobacter_sphaeroides_2.4.1_KBas**
Genome
 -  **Rhodobacter_sphaeroides_2.4.1**
Genome
 -  **Rhodobacter_CACIA_14HI**
Genome

Example FBAModels

A metabolic model of an organism

-  **iRsp1140**
FBAModel
-  **CACIA_model_kbase**
FBAModel
-  **CACIA_14H1_model_translated**
FBAModel

Example Media

Specification of an environmental condition

- LB_4C_24h
Media
 - C-D-Lactate
Media
 - C-Butyrate
Media
 - C-acetate
Media
 - Rsp-minimal
Media
 - PlantHeterotrophicMedia
Media

- Submissão da sequência do genoma para anotação

The screenshot displays the KBase web interface for the 'GENOMA COMPLETO PSEUDOMONAS LFM046' project. The left sidebar lists various analysis jobs, including 'Run Flux Balance Analysis', 'Simulate Growth on Phenotype Data', 'Build Metabolic Model', and 'Annotate Microbial Contigs'. The 'Annotate Microbial Contigs' job is highlighted, showing its status as 'Completed 24.6 days ago'.

The main panel shows the 'Annotate Microbial Contigs' configuration. The job was submitted on 22:06:30, 3/14/2016 by jcardinali. The configuration includes the following fields:

Field	Value	Description
Contig Set	Pseudomonas_LFM046	The set of contig sequences to annotate
Scientific Name	Pseudomonas_sp_LFM046	The scientific name to assign to the genome
Domain	B (Bacteria)	The domain of life of the organism being annotated
Genetic Code	11 (Archaea, most Bacteria, most Virii, and some Mitocho...	The genetic code used in translating to protein sequences
Output Genome Name	ANOTACAO_PSEUDOMONAS_LFM046	Name to assign the output genome

Below the configuration, the job status is shown as 'In-progress'.



▼ ANOTACAO_PSEUDOMONAS_LFM046

[Overview](#)[Contigs](#)[Genes](#)

Show 10 entries

Search contig:

Contig name	Length	Genes
Pseudomonas-Brazil-Chromosome	5912441	5605
MDS_scf5	45233	55
MDS_scf6	13303	11
MDS_scf7	1931	3

Showing 1 to 4 of 4 entries

[First](#) [Previous](#) [1](#) [Next](#) [Last](#)

▼ ANOTACAO_PSEUDOMONAS_LFM046

[Overview](#)[Contigs](#)[Genes](#)

Show 50 entries

Search gene: phosphogluconate

Gene ID	Contig	Start	Strand	Length	Type	Function
ANOTACAO_PSEUDOMONAS_LFM046.CDS.6809	Pseudomonas-Brazil-Chromosome	1288449	+	1827	CDS	Phosphogluconate dehydratase (EC 4.2.1.12)
ANOTACAO_PSEUDOMONAS_LFM046.CDS.6819	Pseudomonas-Brazil-Chromosome	1301238	-	870	CDS	Phosphogluconate repressor HexR, RpiR family
ANOTACAO_PSEUDOMONAS_LFM046.CDS.6822	Pseudomonas-Brazil-Chromosome	1303598	+	690	CDS	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)
ANOTACAO_PSEUDOMONAS_LFM046.CDS.7360	Pseudomonas-Brazil-Chromosome	1896883	+	648	CDS	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10794	Pseudomonas-Brazil-Chromosome	5736179	-	915	CDS	Phosphogluconate repressor HexR, RpiR family

Showing 1 to 5 of 5 entries (filtered from 5,674 total entries)

[First](#) [Previous](#) [1](#) [Next](#) [Last](#)



Data View for ANOTACAO_PSEUDOMONAS_LFM046

Feature Overview

Function	LSU rRNA ## 23S rRNA, large subunit ribosomal RNA
Genome	Pseudomonas_sp_LFM046 jcardinali:1458003481132/ANOTACAO_PSEUDOMONAS_LFM046
Length	2892 bp
Location	449238 to 452129 (+)
Aliases	No known aliases

Biochemistry

Function	LSU rRNA ## 23S rRNA, large subunit ribosomal RNA
Subsystems	No subsystem data found.
Annotation Comments	No annotation comments found.

Sequence

Protein

ANOTACAO_PSEUDOMONAS_LFM046



Overview

Contigs

Genes

Pseudomonas-Brazil-Chromosome ☐

ANOTACAO_PSEUDOMONAS_LFM046.CDS.5670 ☐

Contig name	Pseudomonas-Brazil-Chromosome
Length	5912441
Gene count	5605



ANOTACAO_PSEUDOMONAS_LFM046.CDS.5762: Cystathionine gamma-lyase (EC 4.4.1.1)

First

Previous

Zoom In

Zoom Out

Next

Last

- Anotação automática

2_Pseudomonas_sp_LFM0... GENOMA COMPLETO PSE... GENOMA COMPLETO PSE... +

https://narrative.kbase.us/narrative/ws.13710.obj.1

Pesquisar

KBase Data View for ANOTACAO_PSEUDOMONAS_LFM046

Copy Download

Assembly and Annotation

MDS_scf5 - 45232 bp Show Contig

Click on a feature to view details

Functional Categories

- 378 Carbohydrates
- 24 Organic acids
- 30 Monosaccharides
- 24 Sugar alcohols
- 11 Di- and oligosaccharides
- 1 Aminosugars
- 166 Central carbohydrate metabolism
- 26 One-carbon Metabolism
- 0 Polysaccharides
- 42 CO2 fixation
- 50 Fermentation
- 0 Glycoside hydrolases
- 4 --- Carbohydrates ---
- 131 Respiration
- 80 Nucleosides and Nucleotides
- 150 Stress Response
- 178 Protein Metabolism
- 63 Regulation and Cell signaling
- 142 Cell Wall and Capsule
- 25 Miscellaneous
- 0 Photosynthesis
- 84 RNA Metabolism
- 143 Metabolism of Aromatic Compounds
- 64 Clustering-based subsystems
- 39 Phosphorus Metabolism
- 0 Phages, Prophages, Transposable elements
- 10 Secondary Metabolism

Gene ID	Contig	Start	Strand	Length	Type	Function
ANOTACAO_PSEUDOMONAS_LFM046.repeat.1	MDS_scf5	1	+	342	repeat	repeat region
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5553	MDS_scf5	1053	-	1053	CDS	integrase, putative
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5554	MDS_scf5	1430	-	354	CDS	-
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5555	MDS_scf5	1919	-	471	CDS	-
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5556	MDS_scf5	3733	-	1818	CDS	DNA cytosine methyltransferase family protein
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5557	MDS_scf5	4800	-	1071	CDS	Retron-type RNA-directed DNA polymerase (EC 2.7.7.49)
ANOTACAO_PSEUDOMONAS_LFM046.CDS.4	MDS_scf5	4954	-	135	CDS	-
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5558	MDS_scf5	5485	-	363	CDS	-
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5559	MDS_scf5	6160	-	618	CDS	hypothetical protein
ANOTACAO_PSEUDOMONAS_LFM046.CDS.5560	MDS_scf5	6835	-	615	CDS	hypothetical protein

- Construção do modelo metabólico em escala genômica a partir de glicose

The screenshot displays the KBase GENOMA interface for the Pseudomonas LFM046 genome. The main panel shows the 'Build Metabolic Model' workflow with the following configuration:

- Genome:** ANOTACAO_PSEUDOMONAS_LFM046
- Media:** Carbon-D-Glucose-Palsson
- Output model:** Pseudomonas_using_glucose
- Template for reconstruction:** Gram negative
- ☒ Gapfill model?

The workflow status is 'Completed' (submitted on 23:42:07, 3/14/2016 by jcardinali). The console log shows the job ID, status, submission time, and execution details.

On the left, a sidebar lists recent jobs, including 'Run Flux Balance Analysis', 'Simulate Growth on Phenotype Data', and 'Build Metabolic Model' (multiple instances).

On the right, a 'DATA' panel shows the output model 'Pseudomonas_using_glucose v2' (FBAModel) and provides export options (SBML, TSV, EXCEL, JSON) and a 'Cancel' button.

Build Metabolic Model (method output)



Overview

Reactions

Compounds

Genes

Compartments

Biomass

Gapfilling

Pathways

Show 10 entries

Search Reactions

Reaction	Name	Equation	Genes	Gapfilling
rxn00001[c0]	Pyrophosphate phosphohydrolase	$H_2O[c0] + PPi[c0] \Rightarrow (2) H^+[c0] + (2) Phosphate[c0]$	ANOTACAO_PSEUDOMONAS_LFM046.CDS.6148	
rxn00002[c0]	Urea-1-carboxylate amidohydrolase	$(3) H^+[c0] + Allophanate[c0] + H_2O[c0] \Rightarrow (2) NH_3[c0] + (2) CO_2[c0]$	ANOTACAO_PSEUDOMONAS_LFM046.CDS.7582, ANOTACAO_PSEUDOMONAS_LFM046.CDS.6376, ANOTACAO_PSEUDOMONAS_LFM046.CDS.7748, ANOTACAO_PSEUDOMONAS_LFM046.CDS.7747, ANOTACAO_PSEUDOMONAS_LFM046.CDS.6377	
rxn00006[c0]	hydrogen-peroxide:hydrogen-peroxide oxidoreductase	$(2) H_2O_2[c0] \Rightarrow (2) H_2O[c0] + O_2[c0]$	ANOTACAO_PSEUDOMONAS_LFM046.CDS.6070, ANOTACAO_PSEUDOMONAS_LFM046.CDS.7861, ANOTACAO_PSEUDOMONAS_LFM046.CDS.7881, ANOTACAO_PSEUDOMONAS_LFM046.CDS.7977	
rxn00010[c0]	Glyoxylate carboxy-lyase (dimerizing)	$H^+[c0] + (2) Glyoxalate[c0] \Rightarrow Tartronate semialdehyde[c0] + CO_2[c0]$	ANOTACAO_PSEUDOMONAS_LFM046.CDS.7259	
rxn00011[c0]	pyruvate:thiamin diphosphate acetaldehydetransferase	$2-Hydroxyethyl-ThPP[c0] + CO_2[c0] \leq H^+[c0] + Pyruvate[c0] + TPP[c0]$	ANOTACAO_PSEUDOMONAS_LFM046.CDS.4645, ANOTACAO_PSEUDOMONAS_LFM046.CDS.10079, ANOTACAO_PSEUDOMONAS_LFM046.CDS.8575, ANOTACAO_PSEUDOMONAS_LFM046.CDS.10436	
rxn00029[c0]	5-Aminolevulinate hydro-lyase(adding 5-aminolevulinate and	$(2) 5-Aminolevulinate[c0] \Rightarrow H^+[c0] + (2) H_2O[c0] + Porphobilinogen[c0]$	ANOTACAO_PSEUDOMONAS_LFM046.CDS.10655	
rxn00048[c0]	6,7-Dimethyl-8-(1-D-riboityl)lumazine:6,7-	$(2) 6,7-Dimethyl-8-(1-D-riboityl)lumazine[c0] \Rightarrow 4-(1-D-$	ANOTACAO_PSEUDOMONAS_LFM046.CDS.6114	



▼ Build Metabolic Model (method output)



Overview Reactions Compounds **Genes** Compartments Biomass Gapfilling Pathways

Show 10 ▼ entries

Search Genes

Gene	Reactions
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10001	rxn09674[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10014	rxn08900[c0], rxn08901[c0], rxn00935[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10019	rxn00915[c0], rxn00836[c0], rxn01544[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10020	rxn00711[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10021	rxn05197[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10023	rxn00224[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10030	rxn00193[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10034	rxn06591[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10037	rxn03908[c0]
ANOTACAO_PSEUDOMONAS_LFM046.CDS.10042	rxn09692[c0]

Showing 1 to 10 of 1,237 entries

Previous 1 2 3 4 5 ... 124 Next

▼ Build Metabolic Model (method output)



Overview Reactions Compounds Genes **Compartments** Biomass Gapfilling Pathways

Show 10 ▼ entries

Search Compartments

Compartment	Name	pH	Potential
c0	Cytosol	7	0
e0	Extracellular	7	0

Showing 1 to 2 of 2 entries

Previous 1 Next

▼ Build Metabolic Model (method output)



Overview Reactions Compounds Genes Compartments **Biomass** Gapfilling Pathways

Show 10 ▼ entries

Search Biomass

Biomass	Compound	Name	Coefficient	Compartment
bio1	cpd15723[c0]	Dianteisoheptadecanoylphosphatidylglycerol	-0.0106480421341882	c0
bio1	cpd00008[c0]	ADP	40	c0
bio1	cpd00015[c0]	FAD	-0.00309646685192537	c0
bio1	cpd15352[c0]	2-Demethylmenaquinone 8	-0.00309646685192537	c0
bio1	cpd00322[c0]	L-Isoleucine	-0.241798510337235	c0
bio1	cpd00033[c0]	Glycine	-0.509869786991038	c0
bio1	cpd15695[c0]	Diisoheptadecanoylphosphatidylethanolamine	-0.0106480421341882	c0
bio1	cpd00006[c0]	NADP	-0.00309646685192537	c0
bio1	cpd00035[c0]	L-Alanine	-0.427934380173264	c0
bio1	cpd17041[c0]	Protein biosynthesis	-1	c0

Showing 1 to 10 of 85 entries

Previous 1 2 3 4 5 ... 9 Next

Analyze Narratives Jobs

Run Flux Balance Analysis

method:56e9d49760b2433b100895c9

Status: Completed 22.8 days ago
Run Time: 37.5 sec
Started: 22.8 days ago

Simulate Growth on Phenotype Data

method:56e9d45d60b2433b100895c8

Status: Completed 22.8 days ago
Run Time: 31.4 sec
Started: 22.8 days ago

Build Metabolic Model

method:56e7783d60b2433b10089461

Status: Completed 24.6 days ago
Run Time: 1.7 min
Started: 24.6 days ago

Build Metabolic Model

method:56e7768660b2433b10089460

Status: Completed 24.6 days ago
Run Time: 1.7 min
Started: 24.6 days ago

Annotate Microbial Contigs

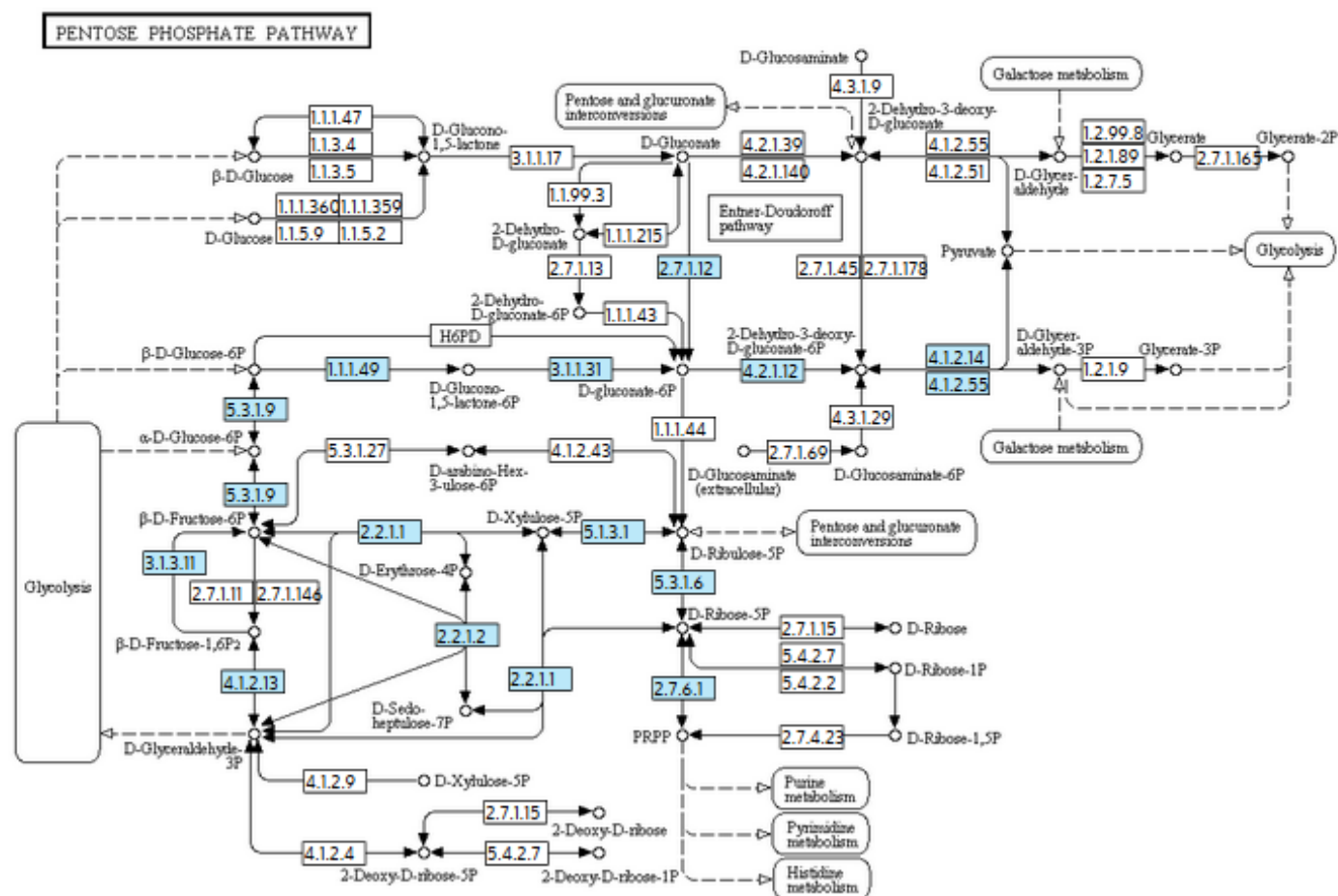
method:d833b23d-9ec2-4f2a-8bf9-344372929244

Status: Completed 24.6 days ago
Run Time: 11.9 min
Started: 24.6 days ago

Build Metabolic Model (method output)

Overview Reactions Compounds Genes Compartments Biomass Gapfilling Pathways

Selection Pentose phosphate pathway %



- Construção do modelo metabólico em escala genômica a partir de frutose

KBbase

GENOMA COMPLETO PSEUDOMONAS LFM046

Created by: Juliana Cardinali Rezende (jcardinali)

kernel

share

save

Analyze

Narratives

Jobs

Model SEED

Build Metabolic Model

Generate a draft metabolic model based on an annotated genome. [more...](#)

Genome

ANOTACAO_PSEUDOMONAS_LFM046

A genome with functional annotations generated by Kbase

Media

Carbon-D-Fructose

Media specifies the set of chemical compounds organism can use for its growth. In this function, the media is used as the growth condition for gapfilling, if gapfilling is performed.

Output model

Pseudomonas_using_fructose

Enter a name for the metabolic model to be created

Template for reconstruction

Gram negative

Models are generated based on a default template model in KBase. Template models capture the necessary biochemical information based on user-defined scope. KBase primarily uses four template models: (i) Gram positive microbe, (ii) Gram negative microbe, (iii) Core pathways microbe, and (iv) Plant. These template models differ from each other by biomass composition and biochemical reaction functional associations.

Gapfill model?

Identify the minimal set of biochemical reactions to add to a draft metabolic model to enable it to produce biomass in a specified media.

show advanced options

Edit and Re-Run

submitted on 23:49:26, 3/14/2016 by jcardinali

Status

Console Log

Job Id:	method:56e7783d60b2433b10089461
Status:	Completed
Submitted:	23:49:34, 3/14/2016
Time in queue:	1.574 sec.
Execution Started:	23:49:35, 3/14/2016
Execution Finished:	23:51:17, 3/14/2016
Execution Time:	101.84 sec.

Run Flux Balance Analysis

method:56c9d49760b2433b100895c9

Status: Completed 22.8 days ago

Run Time: 37.5 sec

Started: 22.8 days ago

Simulate Growth on Phenotype Data

method:56c9d49760b2433b100895c8

Status: Completed 22.8 days ago

Run Time: 31.4 sec

Started: 22.8 days ago

Build Metabolic Model

method:56e7783d60b2433b10089461

Status: Completed 24.6 days ago

Run Time: 1.7 min

Started: 24.6 days ago

Build Metabolic Model

method:56e7783d60b2433b10089460

Status: Completed 24.6 days ago

Run Time: 1.7 min

Started: 24.6 days ago

Annotate Microbial Contigs

method:28113b23d90c2462a18d934437292444

Status: Completed 24.6 days ago

Run Time: 11.9 min

Started: 24.6 days ago

Analyze

Narratives

Jobs

DATA

24 days ago

Carbon-D-Fructose

Media

24 days ago

Drag onto narrative

Permanent Id

13710/4/1

Full Type

KBaseBiochem.Media-1.0

Saved by

Juliana Cardinali Rezende (jcardinali)

- Comparação entre modelos metabólicos de espécies diferentes

Output Compare Two Metabolic Models 10:13:50, 7/22/2015

Statistics Common reactions Genome_scale_metabolic_model_Pseudomonas_sp_LFM046 only
Genome_Scale_Metabolic_Model_P_aeruginosa_PA01 only

Genome_scale_metabolic_model_Pseudomonas_sp_LFM046 genome	Anontation_Pseudomonas_sp_LFM046 (Pseudomonas sp. LFM046)
Genome_Scale_Metabolic_Model_P_aeruginosa_PA01 genome	P_aeruginosa_PA01_ANNOTATION (Pseudomonas aeruginosa PA01)
Reactions in Genome_scale_metabolic_model_Pseudomonas_sp_LFM046	1231
Reactions in Genome_Scale_Metabolic_Model_P_aeruginosa_PA01	1219
Common reactions	1143
Reactions with same features	833
Unique reactions in Genome_scale_metabolic_model_Pseudomonas_sp_LFM046	88
Unique reactions in Genome_Scale_Metabolic_Model_P_aeruginosa_PA01	76

Output Compare Two Metabolic Models 11:46:40, 7/21/2015

Statistics Common reactions Genome_Scale_Metabolic_Model_Pseudomonas_putida_KT2440 only
Genome_scale_metabolic_model_Pseudomonas_sp_LFM046 only

Genome_Scale_Metabolic_Model_Pseudomonas_putida_KT2440 genome	Pseudomonas_putida_KT2440 (Pseudomonas putida KT2440)
Genome_scale_metabolic_model_Pseudomonas_sp_LFM046 genome	Anontation_Pseudomonas_sp_LFM046 (Pseudomonas sp. LFM046)
Reactions in Genome_Scale_Metabolic_Model_Pseudomonas_putida_KT2440	1185
Reactions in Genome_scale_metabolic_model_Pseudomonas_sp_LFM046	1231
Common reactions	1126
Reactions with same features	778
Unique reactions in Genome_Scale_Metabolic_Model_Pseudomonas_putida_KT2440	59
Unique reactions in Genome_scale_metabolic_model_Pseudomonas_sp_LFM046	105

- Simulação de crescimento em diferentes fontes de carbono

KBose

GENOMA COMPLETO PSEUDOMONAS LFM046

Created by: Juliana Cardinali Rezende (jcardinali)

kernel

share

save

Analyze

Narratives

Jobs

Run Flux Balance Analysis
method:56e9d49760b2433b100895c9

Status: Completed 22.8 days ago

Run Time: 37.5 sec

Started: 22.8 days ago

Simulate Growth on Phenotype Data
method:56e9d45d60b2433b100895c8

Status: Completed 22.8 days ago

Run Time: 31.4 sec

Started: 22.8 days ago

Build Metabolic Model
method:56e7783d60b2433b10089461

Status: Completed 24.5 days ago

Run Time: 1.7 min

Started: 24.5 days ago

Build Metabolic Model
method:56e7768660b2433b10089460

Status: Completed 24.6 days ago

Run Time: 1.7 min

Started: 24.6 days ago

Annotate Microbial Contigs
method:d833b23d-9ec2-4f2a-8bf9-344372929244

Status: Completed 24.6 days ago

Run Time: 11.9 min

Started: 24.6 days ago

Simulate Growth on Phenotype Data (method output)

Overview

Phenotypes

Show 10 entries

Search Phenotypes

Growth condition	Gene KO	Additional compounds	Observed normalized growth	Simulated growth	Prediction class
Rsp-minimal-CN		D-Ribose, NH3	1	1	CP
Rsp-minimal-CN		D-Galacturonate, NH3	1	1	CP
Rsp-minimal-CN		Uridine, NH3	1	1	CP
Rsp-minimal-CN		L-Proline, NH3	1	1	CP
Rsp-minimal-CN		D-Mannose, NH3	1	1	CP
Rsp-minimal-CN		delta-aminovalerate, NH3	1	1	CP
Rsp-minimal-CN		D-Glucose, NH3	1	1	CP
Rsp-minimal-CN		D- Psicose, NH3	1	1	CP
Rsp-minimal-CN		D-Fructose, NH3	1	1	CP
Rsp-minimal-CN		L-Lyxose, NH3	1	1	CP

Showing 31 to 40 of 208 entries

Previous 1 2 3 4 5 ... 21 Next

time in queue: 1.255 sec.

Substratos utilizados pela *Pseudomonas* sp. LFM046 simulados pelo KBase.

Xylose, NH3	Palatinose, NH3	L-Isoleucine, Succinate	Gly-Met, Succinate	D-Galacturonate, NH3
Xanthosine, Succinate	NH3, Succinate	L-Isoleucine, NH3	gly-glu-L, NH3	D-Fructose, NH3
XAN, Succinate				
4-hydroxyphenylacetate, NH3	N-Acetyl-D-glucosamine, Succinate	L-Histidine, Succinate	Gly-Gln, Succinate	D-Chondrosamine, Succinate
		2-Oxovalerate, NH3	Oxoglutarate, NH3	2-Oxobutyrate, NH3
Uridine, Succinate	L-Valine, NH3	L-Glutamine, Succinate	GABA, NH3	D-Aspartate, Succinate
Uridine, NH3	L-Tyrosine, Succinate	L-Glutamine, NH3	Fumarate, NH3	D-Asparagine, Succinate
Urea, Succinate	L-Tryptophan, Succinate	L-Glutamate, Succinate	Aminoethanol, Succinate	D-Alanine, Succinate
Urate, Succinate	L-Serine, Succinate	L-Glutamate, NH3	Formate, NH3	Cytosine, Succinate
Uracil, Succinate	L-Serine, NH3	L-Cysteine, Succinate	Dextrin, NH3	Cytidine, Succinate
Tyramine, NH3	L-Proline, Succinate	L-Aspartate, Succinate	Delta-aminovalerate, NH3	Citrulline, Succinate
Tween 20, NH3	L-Proline, NH3	L-Asparagine, Succinate	D-Serine, Succinate	Butyrate, NH3
Thymine, Succinate	L-Malate, NH3	L-Asparagine, NH3	D-Ribose, NH3	Aminoethanol, NH3
Thymidine, Succinate	L-Malate, NH3	L-Arginine, Succinate	D-Psicose, NH3	Allantoin, Succinate
Thymidine, NH3	L-Lyxose, NH3	L-alanylglycine, NH3	D-Mannose, NH3	Ala-Leu, Succinate
Tartrate, NH3	L-Lysine, Succinate	L-Alanine, Succinate	D-Mannosamine, Succinate	Ala-His, Succinate
Succinate, NH3	L-Lysine, NH3	L-Alanine, NH3	D-Mannitol, NH3	Ala-Gln, Succinate
Sorbitol, NH3	L-Leucine, Succinate	Histamine, Succinate	D-Malate, NH3	Agmatine, Succinate
Ribitol, NH3	L-Leucine, NH3	Guanosine, Succinate	D-Lyxitol, NH3	ACTN, NH3
Pyruvate, NH3	L-Lactate, NH3	Guanine, Succinate	D-Lysine, Succinate	Acetoacetate, NH3
Putrescine, Succinate	L-Isoleucine, Succinate	Glyoxalate, NH3	D-Glutamate, Succinate	Acetate, NH3
Xylose, NH3	L-Isoleucine, NH3	Glycine, Succinate	D-Glucose, NH3	5-Oxoproline, Succinate

Extensiva curação manual e validação do modelo são necessários.

The screenshot displays the KBase web interface for the GENOMA COMPLETO PSEUDOMONAS LFM046 project. The left sidebar shows a list of data objects and apps. The main panel is titled 'Check Model Mass Balance' and shows a failed FBA run for the model 'Pseudomonas_using_glucose'.

DATA

- maximizando_eda v1 FBA 22 days ago
- teste_maximizando_edd v1 PhenotypeSimulationSet 22 days ago
- Pseudomonas_using_glucose.gffba v1 FBA 24 days ago
- Pseudomonas_using_glucose v2 FBAModel

APPS & METHODS

- FBA** Check Model Mass Balance ★ fba_tools v1.0.0
- KB EXPR** Cluster Expression Data - Hierarchical ★ v1.0.0
- KB EXPR** Cluster Expression Data - K-Means ★ v1.0.0
- Compare FBA Solutions

Check Model Mass Balance

Check the mass balanced of all reactions in a model [more...](#)

Model ID: **Pseudomonas_using_glucose** ✓ ID of model to check the mass balance of

no advanced options

Edit and Re-Run submitted on 17:20:53, 4/08/2016 by jcardinali

Status Console Log **Report** New Data Objects

Image received from catalog: dockerhub-pub.kbase.us/kbase:fba_tools.c90b2e8045439504333a88d2f88517da155b778e
Use of uninitialized value in concatenation (.) or string at /kb/module/bin/./lib/fba_tools/fba_toolsServer.pm line 378.
Starting check_model_mass_balance method.
Retrieving input parameters.
Retrieving model.
Checking model mass balance.
Model failed to grow. Could not produce the following biomass compounds:

cpd15723_c0	Dianteischoeptadecanoylphosphatidylglycerol_c0
cpd00015_c0	FAD_c0
cpd15352_c0	2-Demethylmenaquinone 8_c0
cpd15695_c0	Diischoeptadecanoylphosphatidylethanolamine_c0
cpd15722_c0	Diischoeptadecanoylphosphatidylglycerol_c0
cpd15432_c0	core oligosaccharide lipid A_c0
cpd00241_c0	dGTP_c0
cpd15665_c0	Peptidoglycan polymer (n subunits)_c0
cpd15696_c0	Dianteischoeptadecanoylphosphatidylethanolamine_c0
cpd00557_c0	Siroheme_c0
cpd00038_c0	GTP_c0
cpd00345_c0	5-Methyltetrahydrofolate_c0
cpd00062_c0	UTP_c0

Etapa 3. Validação do modelo, cálculo de biomassa e simulações

- Identificar e resolver erros no modelo - gaps

Muitos genes no genoma sem função conhecida – lista de enzimas é incompleta;
Especificidade incorreta do substrato; reversibilidade de reação; uso de cofatores;
Tratamento de subunidades enzimas como enzimas separadas.

- Definir a equação da biomassa

- * Composição macromolecular da célula (proteínas, DNAs, RNAs e lipídeos ...)
- * Requerimentos energéticos da célula para produzir biomassa (ATP)

- Validar o modelo com dados experimentais

Taxa de crescimento, utilização do substrato, formação do produto, rendimento

1. Draft Reconstruction

- 1| Obtain genome annotation.
- 2| Identify candidate metabolic functions.
- 3| Obtain candidate metabolic reactions.
- 4| Assembly of draft reconstruction.
- 5| Collect of experimental data.



2. Refinement of reconstruction

- 6| Determine and verify substrate and cofactor usage
- 7| Obtain neutral formula for each metabolite.
- 8| Determine the charged formula.
- 9| Calculate reaction stoichiometry.
- 10| Determine reaction directionality.
- 11| Add information for gene and reaction localization.
- 12| Add subsystems information.
- 13| Verify gene-protein-reaction association.
- 14| Add metabolite identifier.
- 15| Determine and add confidence score.
- 16| Add references and notes.
- 17| Flag information from other organisms.
- 18| Repeat Step 6 to 17 for all genes.
- 19| Add spontaneous reactions to the reconstruction.
- 20| Add extracellular and periplasmic transport reactions.
- 21| Add exchange reactions.
- 22| Add intracellular transport reactions.
- 23| Draw metabolic map (optional).
- 24-32| Determine biomass composition.
- 33| Add biomass reaction.
- 34| Add ATP maintenance reaction (ATPM).
- 35| Add demand reactions.
- 36| Add sink reactions.
- 37| Determine growth medium requirements.



4. Network evaluation

- 43-44| Test if network is mass- and charge balanced.
- 45| Identify metabolic dead-ends.
- 46-48| Gap analysis.
- 49| Add missing exchange reactions to model.
- 50| Set exchange constraints for a simulation condition.
- 51-58| Test for stoichiometrically balanced cycles.
- 59| Re-compute gap list.
- 60-65| Test if biomass precursors can be produced in standard medium
- 66| Test if biomass precursors can be produced in other growth media.
- 67-75| Test if model can produce known secretion products
- 76-78| Check for blocked reactions.
- 79-80| Compute single gene deletion phenotypes
- 81-82| Test for known incapacities of the organism.
- 83| Compare predicted physiological properties with known properties.
- 84-87| Test if the model can grow fast enough.
- 88-94| Test if the model grows too fast.



Data assembly and Dissemination

- 95| Print Matlab model content.
- 96| Add gap information to the reconstruction output.



3. Conversion of reconstruction into computable format

- 38| Initialize the COBRA toolbox.
- 39| Load reconstruction into Matlab.
- 40| Verify S matrix.
- 41| Set objective function.
- 42| Set simulation constraints.



Thiele e Palsson, 2010

A combinação de esforços automatizados e manuais de reconstrução é necessária para gerar reconstruções precisas!

Table 2 | Organisms and network properties for which genome-scale metabolic reconstructions have been generated*

Organism	Genes	SKI	N _g	N _m	N _r	Status	Refs
<i>Bacteria</i>							
<i>Bacillus subtilis</i>	4,225	4.8	614	637	754	C, E	95
<i>Escherichia coli</i>	4,405	55.1	904	625	931	C, E	39
			720	438	627	C, E	92
			961	NA	1,107	C	53
<i>Francisella tularensis</i>	1,804	ND	350 [‡]	NA	429	C	68
<i>Geobacter sulfurreducens</i>	3,530	ND	588	541	523	C, E	105
<i>Haemophilus influenzae</i>	1,775	8.9	296	343	488	C, E	96
			400	451	461	C, E	97
<i>Helicobacter pylori</i>	1,632	13	341	485	476	C, E	61
			291	340	388	C, E	98
			301 [‡]	442	533	C	63
<i>Lactococcus lactis</i>	2,310	ND	358	422	621	C, E	99
<i>Mannheimia succiniciproducens</i>	2,463	ND	335	352	373	C, E	100
<i>Pseudomonas aeruginosa</i>	5,640	5.7	546	467	542	C, E	1
			718	623	800	C	67
<i>Staphylococcus aureus</i>	2,702	16	619	571	641	C, E	4
<i>Streptomyces coelicolor</i>	8,042	0.13	700	500	700	C, E	36
<i>Archaea</i>							
<i>Methanococcus jannaschii</i>	1,821	0.3	436 [‡]	510	609	C	64
<i>Methanosarcina barkeri</i>	5,072	ND	692	558	619	C, E	106
<i>Eukarya</i>							
<i>Arabidopsis thaliana</i>	28,848	ND	1,418	NA	894	C	66
<i>Homo sapiens</i>	28,783	48.5	2,709 [‡]	661	1,093	C	65
<i>Mus musculus</i>	28,287	15.6	1,156 [§]	872	1,220	C, E	94
<i>Plasmodium falciparum</i>	5,342	ND	737 [‡]	525	697	C	3
<i>Saccharomyces cerevisiae</i>	6,183	10.6	750	646	1,149	C, E	45
			708	584	1,175	C, E	93

*Several non-curated automated reconstructions are also available from KEGG⁶² and BioCyc⁶⁹. [‡]Only enzyme numbers were reported. [§]Genes as reported¹⁰¹.

^{||}Latest numbers from HpCyc⁶³. [¶]J. Edwards, personal communication. C, a curated network; E, a network that is evaluated using computational modelling methods that are based on a stoichiometric matrix; NA, not available; ND, not determined; N_g, number of genes; N_m, number of metabolites; N_r, number of reactions; SKI, reported species knowledge index¹².