



APRENDE R  
Y HAGAMOS  
COMUNIDAD



# Entre Pares 2018

## DATOS Y LOS PRINCIPIOS FAIR

and Julio Comodo-Vides  
"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12  
beyond transcription, active (experimental) annotated promoters and  
textpresso navigation"  
Nucleic Acids Research, 2008, vol 36, D120-D124  
Release: 6.4 Date: 10-AUG-09

Transcription Factor Matrix  
The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3  
Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2  
AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAACAATGTTTAG19.78

Delfino García Alonso  
Shirley Alquicira Hernández

Centro de Ciencias Genómicas-UNAM



Licenciatura en  
CIENCIAS  
GENÓMICAS



# Contenido

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## Citation

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Socorro Gama-Castro, Verónica Jiménez-Jacinto, Martín Peralta-Gil, Alberto Santos-Zavaleta, Monica I. Peñalosa-Spindola, Bruno Contreras-Moreira, Juan Segura-Salazar, Luis Muñoz-Rascado, Irma Martínez-Flores, Heladia Salgado, César Bonavides-Martínez, Cel Abreu-Goodger, Carlos Rodríguez-Penagos, Juan Miranda-Ries, Enrique Morett, Enrique Merino, Araceli M. Huerta, Luis Treviño-Quintanilla and Julio Collado-Veces.  
"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and textpresso navigation"  
Nucleic Acids Research, 2008, vol 36, D120-D124

Release: 6.4 Date: 10-AUG-09

## Transcription Factor Matrix and Alignments

The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix

A	2	3	1	1	3	2	3	0	0	1	1	2	0	0	1	0	2	2	0	3	2	0	1	1	0	0	0	1	0
C	1	0	0	1	0	1	0	0	1	0	2	0	0	2	0	1	1	0	0	0	0	0	0	0	1	0	0	0	0
G	0	0	1	0	0	0	0	1	0	2	0	0	3	1	2	0	0	0	3	0	0	0	2	0	0	2	1	0	1
T	0	0	1	1	0	0	0	2	2	0	0	1	0	0	0	2	0	1	0	0	1	3	0	2	2	1	2	2	2

AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGAATGTTTAG19.78





# Antes de aplicar los principios FAIR, el primer paso es....

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"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and textpresso navigation"  
Nucleic Acids Research, 2008, vol 36, D120-D124  
Release: 6.4 Date: 10-AUG-09

Transcription Factor

The consensus and position of the  
Transcription Factor Name  
Total of unique binding sites

Motif

G

T

Alignment

AAGCAAAGC

AAAAAATTAA

CATTACATTGCT

## Buena organización y uso de los Principios FAIR



Buenas prácticas

Situación actual

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En el trabajo diario manejamos demasiada información, y en la mayoría de las ocasiones se vuelve complicado tener un orden de la misma.



Transcription

The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0 0  
G 0 0 1 0 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1 1  
T 0 0 1 1 0 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
AAGCAAAGCGCAGCGCTGGAATAACGTTT20.66  
AAAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAACAATGTTTAGT19.78

# Cuando trabajamos en un proyecto colaborativo...

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Citation

User is committed to cite update publication como Sicoiro, Gama-Castro, Alberto Santos-Zavaleta, Moreira, Juan Segura-Salazar, Li Salgado, Cesar Bonnavides-Martin, Juan Miranda-Rios, Enrique Morett, Enrique and Julio Colado-Vides. "Regulador (Version 6) beyond transcription, ad... (proceso navigation)"



Regulador  
TRANSCRIPTIONAL NETWORK



Artículos

Participante 1

- Programas
- Resultados de ejecuciones de programas
- Copia de archivos de datos

Participante 2

- Servidor con aplicaciones
- Análisis de datos
- Reportes



Participante 3

- Versión original de los datos en excel
- DB de pdfs



email

Internet

**Responsable**

- Reportes



Los que quedan les toca integrar al nuevo miembro del equipo:

Nuevo integrante

**Jefe**

- Biólogo
- Programador
- Analista
- Estudiante



Discutiendo el proyecto



¿Dónde están los programas?  
 ¿Dónde están los datos?  
 ¿A quién le reporto?  
 ¿Y qué reporto?



Retrasos en entregas  
 Trabajos a la carrera  
 Pérdida de información  
 Estrés, frustración, enojo, etc...

¡Muy interesante por cierto!

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"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and textpresso navigation"  
Nucleic Acids Research, 2003, vol 36, D120-D124

Release: 6.4 Date: 10-AUG-09

# RegulonDB

## Base de Conocimiento (BC)

Transcription Factor Matrix and Alignments

The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
AAGCAAAGCGCAGCGCTGAATAACGTTT20.66  
AAAAAATTTAAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGAATGTTTAG19.78



Modelo de Procesos para la Industria del Software en México, desarrollado a solicitud de la Secretaría de Economía en convenio con la Facultad de Ciencias de la UNAM



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\*RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription: active (experimental) annotated promoters and textpresso navigation  
Nucleic Acids Res.

Release: 6.4 Date: 2010-01-01

Transcription Factor Name

The consensus and patser programs were used to create the matrix and alignment

Transcription Factor Name

Total of uniq bins

Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAATTAAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGAATGTTTAG19.78

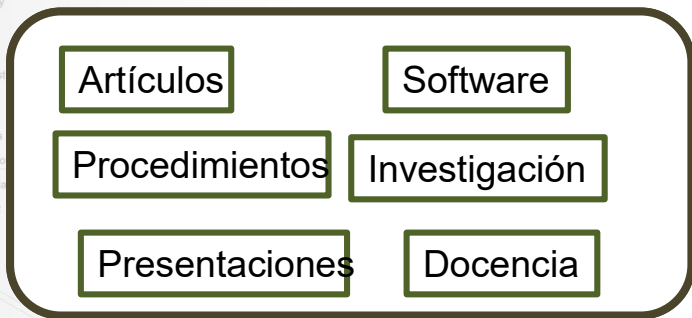
Repositorio de **todos los productos de trabajo** resultado de los proyectos: software, planes, reportes, registros, lecciones aprendidas, tesis, artículos, plantillas, seminarios, datos, imágenes, etc.\*

\*NYCE, Norma Mexicana NMX-I-059/01-NYCE-2005, 2005. Definición de Conceptos y Productos

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 Nucleic Acids Research, 2008, vol 36, D120-D124  
 Release: 6.4 Date: 10-AUG-09

**PROYECTO**

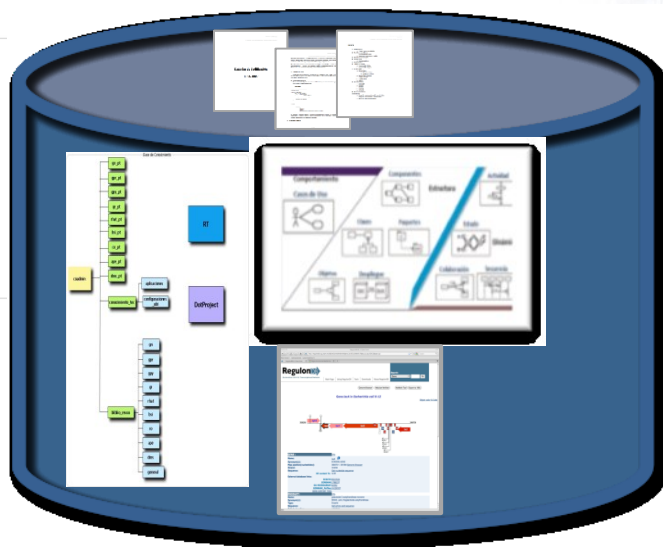


Colaborador



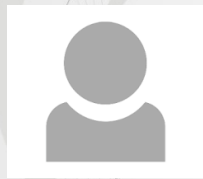
**Alimentación/  
poblado**

¿Dónde están los programas?  
 ¿Dónde están los datos?  
 ¿A quién le reporto?  
 ¿Y qué reporto?



Administrador

**Mantenimiento  
Respaldo**



Investigador



**Consulta**

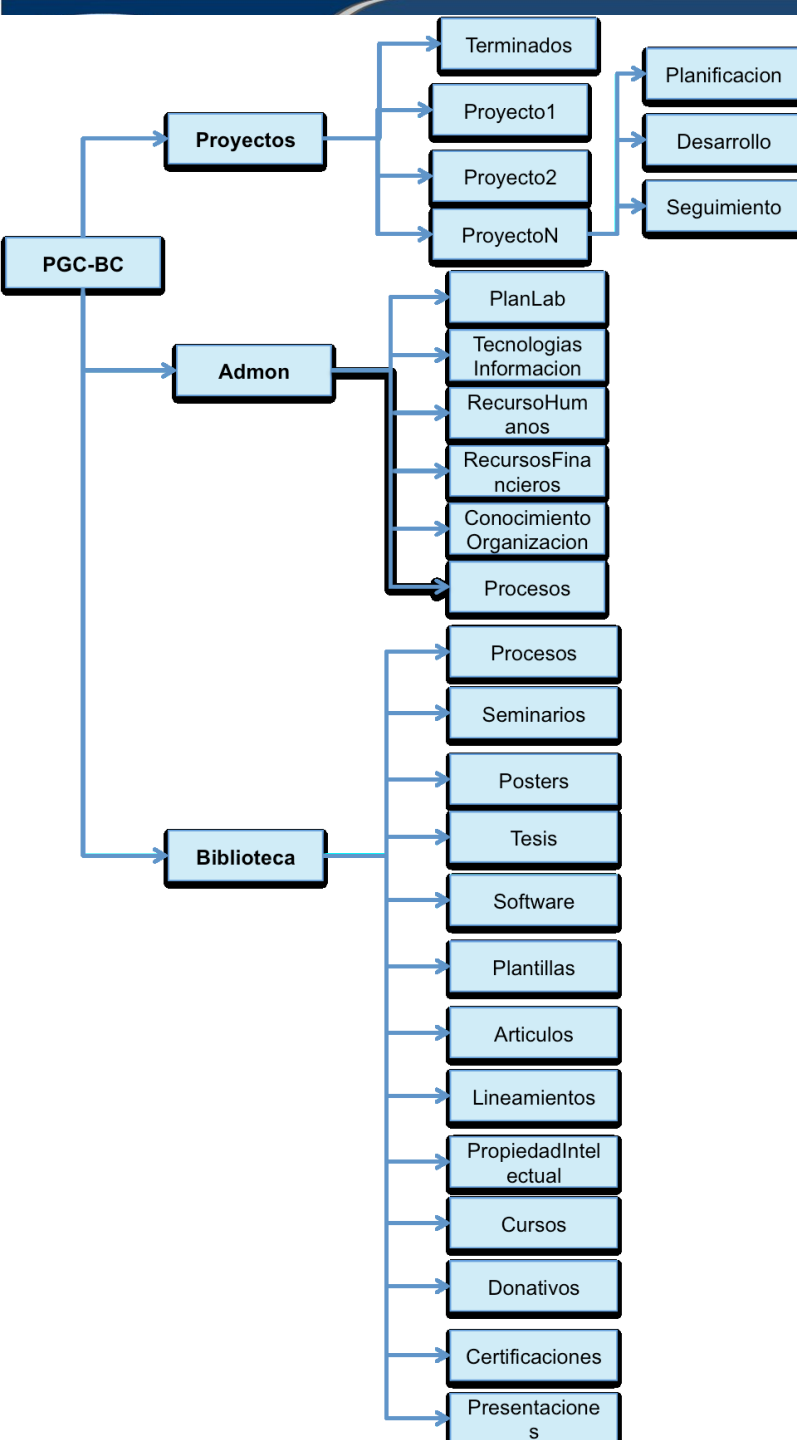
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
 AAAAAAATTAAGCGCAAGATTGTTGGTT21.42  
 CATTACATTGCTGGATAAGCAATGTTTAG19.78

# Sugerencia de herramientas para crear una BC



- Almacenamiento de archivos y carpetas
- Compartir de archivos y carpetas
- Control de cambios y versiones
- Recuperación de archivos/carpetas eliminadas
- Manejo de usuarios
- Disponibilidad en dispositivos móviles
- Multi-plataforma
- **Trabajo colaborativo** permite la edición de múltiples usuarios sobre un mismo documento

# Ejemplo



## Directorios de trabajo en una BC



**Administrador**

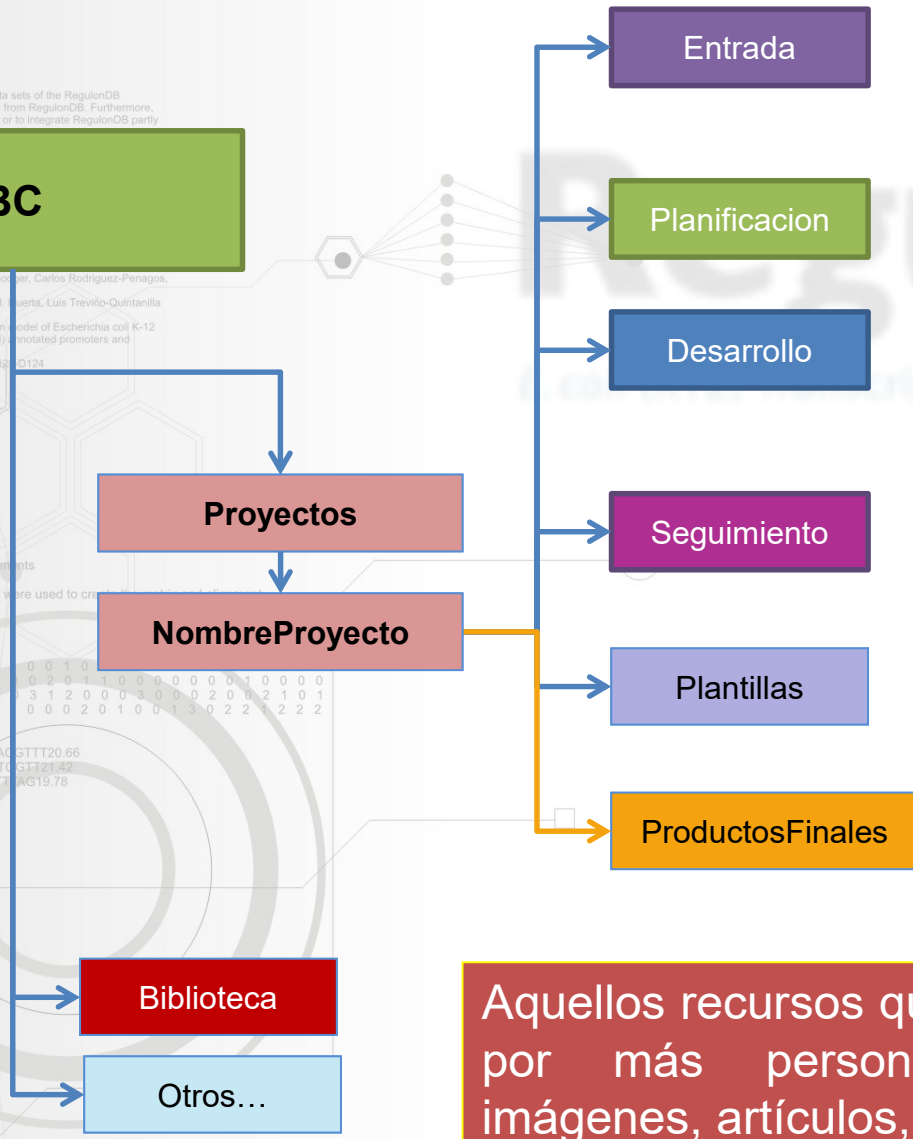
# Mi carpeta de trabajo

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**BC**

César Hernández-Martínez, Col Abreu-Grobois, Carlos Rodríguez-Penagos, Juan Miranda-Ries, Enrique Morett, Enrique Merino, Araceli M. Cuarta, Luis Treviño-Quintanilla and Julio Collado-Vides  
"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and textpresso navigation"  
Nucleic Acids Research, 2008, vol 36, D52-D124  
Release: 6.4 Date: 10-AUG-09

Transcription Factor Matrix and Alignments  
The consensus and patser programs were used to create  
Transcription Factor NameAda  
Total of uniq binding sites3  
Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 0 0 0 2 2 0 0 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2  
AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAAGTTT20.66  
AAAAAATTAAGCGCAAGATTGTTGTT21.42  
CATTACATTGCTGGATAAAGAATGTTTAG19.78



**Entrada**  
Datos fuente de Bases de datos, documentación externa, programas de otros, datos, etc..

**Planificación**  
Repositorio para el resguardo de planes de, Cronograma, Descripción del proyecto

**Desarrollo**  
Repositorio para el resguardo de toda la información generada en la ejecución del proyecto:  
Documentación, Diagramas, Programas, Manuales, etc.

**Seguimiento**  
Repositorio para el resguardo de reportes sobre el estado del proyecto., Minutas

**Plantillas**  
Material guía para la elaboración de la documentación del proyecto.

**Productos Finales**  
Versiones finales de TODO, en el cierre

Aquellos recursos que pueden ser reutilizados por más personas: plantillas, posters, imágenes, artículos, programas, etc.



Correo electrónico: Cuenta institucional, gmail, hotmail, etc.



**“Asunto” en correos electrónicos**

**Usar palabras clave para localizar su búsqueda y localización.**

**Asignar un “identificador” o “nombre corto” del proyecto, el cual es utilizado para localizar todos los correos relacionados al proyecto.**

**Ejemplo:**

**[NombreCortoProyecto] Palabras clave**

[TIB2018-CDSB] Niveles de patrocinio ▶ Inbox x

[RICG] Validacion de ficha de metadatos para datasets ▶ Inbox x

[Conogasi] Reporte avances bimestre may-jun ▶ Inbox x

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Moreira,  
Juan Segura-  
Salgado,  
César Bonnavides-M... Penagos,  
Juan Miranda-Rios,  
Enrique Morett, Enrique Merino, Araceli M. Huerta, Luis Treviño-Quintanilla  
and Julio Collado-Meneses  
"RegulonDB (v8.0): new regulatory model of Escherichia coli K-12  
beyond transac...  
textpresso nam...  
Nucleic Acids Research, 2008, Vol 36, E170-D124  
Release: 6.4 Date: 10-AUG-09

Transcription  
The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0 0  
G 0 0 1 1 0 1 0 1 0 1 0 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAATTAAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAACAATGTTTAGS19.7

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Sorensen, Claus, Pines, Steffen, Lindmark, Larsen, Martin, Brune, Christensen, Hez-Flores, Malin, Rodriguez-Penagos, i Travisa, spheric, romoloni.



**Trello:** Herramienta para la administración de proyectos. Representa un **tablero** virtual en el que se pueden **definir** ideas, **tareas**, imágenes o enlaces.

Transcription Factor Matrix and Alignments  
The consensus and patscr programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3  
Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2



**Slack:** Herramienta de comunicación en equipo, ofrece canales de chat organizados por temas, así como grupos privados y mensajes directos.





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Nucleic Acids Research, 2008, vol 36, D120-D124

Release: 6.4 Date: 10-AUG-09



# Versionamiento

Transcription Factor Matrix and Alignments

The consensus and patser programs were used to create the matrix and all  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGAATGTTTAG19.78



Contar con un *control de versiones* ayuda a gestionar y manejar los cambios realizados en un producto de trabajo.

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\*RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription: active, integrated, and promotional regulation in textpresso navigational interface.  
Nucleic Acids Res 36(12):3606-3615, 2008.  
Release: 6.4 Database: 2010-01-15

Transcription Factor Matrix and Alignments  
The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3  
Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2  
AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGAATGTTTAG19.78



# ¿Por qué es útil?

La razón por la cual el control de versiones es universal es porque **ayuda** en todos los aspectos **al dirigir un proyecto:**



- Comunicación entre los participantes del proyecto, todos los participantes saben a que documento se refieren
- Control entre aquellos documentos liberados y los nuevos cambios en la documentación
- Identificación de los cambios realizados por los participantes del proyecto

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 "RegulonDB (Version 6.0): gene regulon database beyond transcription, active (experimental) textpresso navigation"  
 Nucleic Acids Research, 2008; vol 36  
 Release: 6.4 Date: 10-AUG-09



FINAL.doc!



FINAL\_rev.2.doc

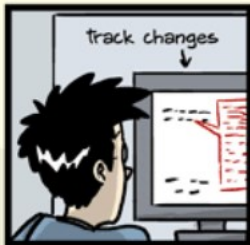


FINAL\_rev.6.COMMENTS.doc



FINAL\_rev.8.comments5.CORRECTIONS.doc

Transcription Factor Matrix and A  
 The consensus and patser progr  
 Transcription Factor NameAda  
 Total of uniq binding sites3  
 Matrix  
 A 2 3 1 1 3 2 3 0 0 1  
 C 1 0 0 1 0 1 0 0 1 4  
 G 0 0 1 0 0 0 0 1 0 0  
 T 0 0 1 1 0 0 0 0 2 2 0



FINAL\_rev.18.comments7.corrections9.MORE.30.doc



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**Proceso Extraccion\_datos\_v0.5.ppt**

Gómez-Castro, Yvonne Jiménez-Jacobs, María Penilla-Gil, María Soledad López-Cabrera, María Soledad Salgado, César Bonavides-Martínez, Cel Abreu-Goodger, Carlos Rodríguez-Penagos, Juan Miranda-Ríos, Enrique Morett, Enrique Merino, Araceli M. Huerta, Luis Treviño-Quintanilla and Julio Collado-Vides  
"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and textpresso navigation"  
Nucleic Acids Research, 2008, vol 36, D120-D124

Release: 6.4 Date: 10-AUG-09

**Expo\_Admon\_Proyectos\_v2.0.ppt**

The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix		2	0	1	4	0	0	0	1	1
A	2	3	1	1	3	2	3	0	0	1
C	1	0	0	1	0	1	0	0	1	0
G	0	0	1	0	0	0	1	0	2	0
T	0	0	1	1	0	0	0	2	2	0

AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAAC  
AAAAAATTAAGCGCAAGATTGTTCC  
CATTACATTGCTGGATAACAATGTTTAG19.78

**Analisis\_Experimento1\_v1.0.xls**



# Uso de metadatos

• **Los metadatos ayudan a describir el contenido de un recurso (archivo de datos/literatura). El uso de metadatos:**

- Facilita la localización y posicionamiento de los recursos en internet
- Nos ayuda a que nuestros datos puedan ser referenciados por otros
- Que otras personas puedan acceder a nuestros datos y puedan trabajar con ellos

Existen normas y estándares internacionales\* dedicados a promover el uso e intercambio de información por medio del uso de **metadatos**.

\*Dublin Core, OpenAIRE, Lineamientos FAIR

# Ejemplo

## • Antes y después del uso de los metadatos

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Citation  
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 \*RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) annotated promoters and textpresso navigation"  
 Nucleic Acids Research, 2008, vol 36, D120-D124

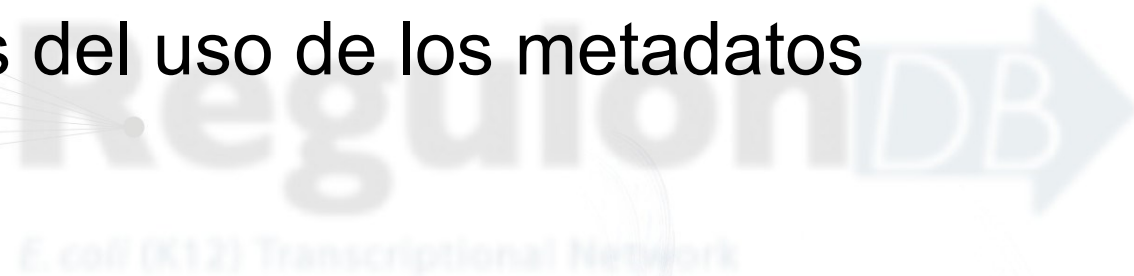
Release: 6.4 Date: 10-AUG-09

### Transcription Factor Matrix and Alignments

The consensus and patser programs were used to create the matrix and alignment  
 Transcription Factor NameAda  
 Total of uniq binding sites3

Matrix  
 A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
 C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
 G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
 T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
 AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
 AAAAAAATTAAGCGCAAGATTGTTGGTT21.42  
 CATTACATTGCTGGATAAGAATGTTTAG19.78







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 \*RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription, active (experimental) promoters and the textpresso navigation\*  
 Nucleic Acids Research, 2008, volume 36, issue 1, pages 119-123  
 Release: 6.4 Date: 10-AUG-09

- Buenas prácticas aplicadas a mi proyecto y ambiente de trabajo....



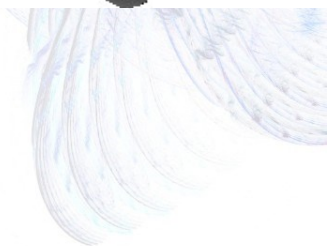
Transcription Factor Matrix and Alignment

The consensus and patser programs were used to create the matrix and alignment  
 Transcription Factor NameAda  
 Total of uniq binding sites3

Matrix  
 A 2 3 1 1 3 2 3 0 0 1  
 C 1 0 0 1 0 1 0 0 1 0 2 0 0 1 0 1 0 0 0 1 0 0 1  
 G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 1 0 1  
 T 0 0 1 1 0 0 0 2 2 0 0 1 0 0 2 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
 AAGCAAAGCGCAGCGTCTGAATAACGTT  
 AAAAAAATTAAGCGCAAGATTGTTGGTT21.42  
 CATTACATTGCTGGATAAGAATGTTTAG19.78

- Tengo una Base de Conocimiento
- Uso adecuadamente herramientas de comunicación
- Versiono mis datos y archivos



Ahora que he terminado mi proyecto (investigación) y que tengo datos y resultados finales...

¿Qué tengo que hacer para publicar mis datos/resultados?

¿Qué características deben tener mis datos/resultados para que puedan ser utilizados por los demás?



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Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 1 0 1  
T 0 0 1 0 0 0 0 0 0 0 1 0 0 0 0 2 0 1 0 0 0 0 0 2 2 2 2 2

# Principio: FINDABLE (F)

- Selecciona algún repositorio para colocar mis datos
- Asegurarme de que puedan asignar un **IDENTIFICADOR** (doi, handle, purl, etc) a mis datos
- Describir mis datos por medio de **METADATOS**



Host Dataverse      Repositorio Institucional de Conocimiento Genómico

\*Asterisks indicate required fields

Citation Metadata

**Title \***

Enter title...

Add "Replication Data for" to Title

**Author \***

Name      Affiliation

FamilyName, GivenName or Organization

Identifier Scheme      Identifier

Select...

Agregar

**Description \***

This field supports only certain HTML tags.

Text

Date      Description Type

YYYY-MM-DD      Select...

Agregar



Metadatos  
Dublin Core

# Ortólogos del organismo *Bacillus pseudofirmus* OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus. Version 1.0

Description Files **Metadata** Versions Terms

Add + Edit Metadata Export Metadata

## Citation Metadata

**Dataset Persistent ID** doi:10.5072/FK2/6HS2RU

**Publication Date** 2018-01-16

**Title** Ortólogos del organismo *Bacillus pseudofirmus* OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.

**Author** MORENO HAGELSIEB, GABRIEL  
Wilfrid Laurier University  
ORCID  
0000-0002-2457-4450

**Description** Ortólogos bidireccionales del genoma organismo *Bacillus pseudofirmus* OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus. comparado con otros genomas.

**Keyword** GENÉTICA

**Related Publication** Gabriel Moreno-Hagelsieb, Kristen Latimer; Choosing BLAST options for better detection of orthologs as reciprocal best hits, *Bioinformatics*, Volume 24, Issue 3, 1 February 2008, Pages 319-324.

**Producer** Centro de Ciencias Genómicas

**Production Date** 2017-10-30

**Contributor** Programa de Genómica Computacional

**Depositor** curators, curator

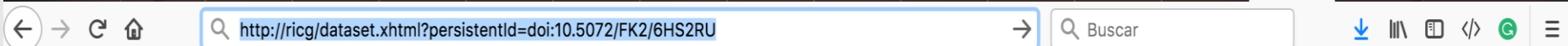
**Kind of Data** Documentación técnica

CITE Export

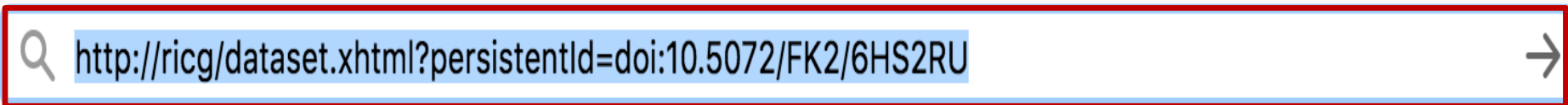
MORENO HAGELSIEB, GABRIEL; Wilfrid Laurier University; ORCID; 0000-0002-2457-4450, 2018, "Ortólogos del organismo *Bacillus pseudofirmus* OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.", doi:10.5072/FK2/6HS2RU, Repositorio Institucional de Conocimiento Genómico, V1

Identificador persistente

# Ejemplo: Principio-Accesible (A)



About Documentation Support Dashboard **Dataverse Admin**



Ortólogos del organismo *Bacillus pseudofirmus* OF4, Bacteria, Firmicutes, Bacilli, Bacillales, Bacillaceae; Bacillus. Version 1.0

Description

Files

Metadata

Versions

Terms

### Description

Ortólogos bidireccionales del genoma organismo *Bacillus pseudofirmus* OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus. comparado con otros genomas.

### Keyword

GENÉTICA

### Related Publication

Gabriel Moreno-Hagelsieb, Kristen Latimer; Choosing BLAST options for better detection of orthologs as reciprocal best hits, *Bioinformatics*, Volume 24, Issue 3, 1 February 2008, Pages 319-324.

CITE

Export

MORENO HAGELSIEB, GABRIEL; Wilfrid Laurier University; ORCID: 0000-0002-2457-4450, 2018, "Ortólogos del organismo *Bacillus pseudofirmus* OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.", doi:10.5072/FK2/6HS2RU, Repositorio Institucional de Conocimiento Genómico, V1

Internet

Protocolo de comunicación  
(HTTP (S) FTP SMTP)

132.248.220.47/dataset.xhtml?persistentId=doi:10.5072/FK2/6HS2RU



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### Citation

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### ID Type

doi

### URL

mic.oup.com/bioinformatics/article/24/3/319/252715

Agregar

### ID Number

10.1093/bioinformatics/btm585

## Related Type \*

- References
- IsNewVersionOf
- IsPreviousVersionOf
- IsPartOf
- IsReferencedBy
- References
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Release: 6.4 Date: 10-AUG-09

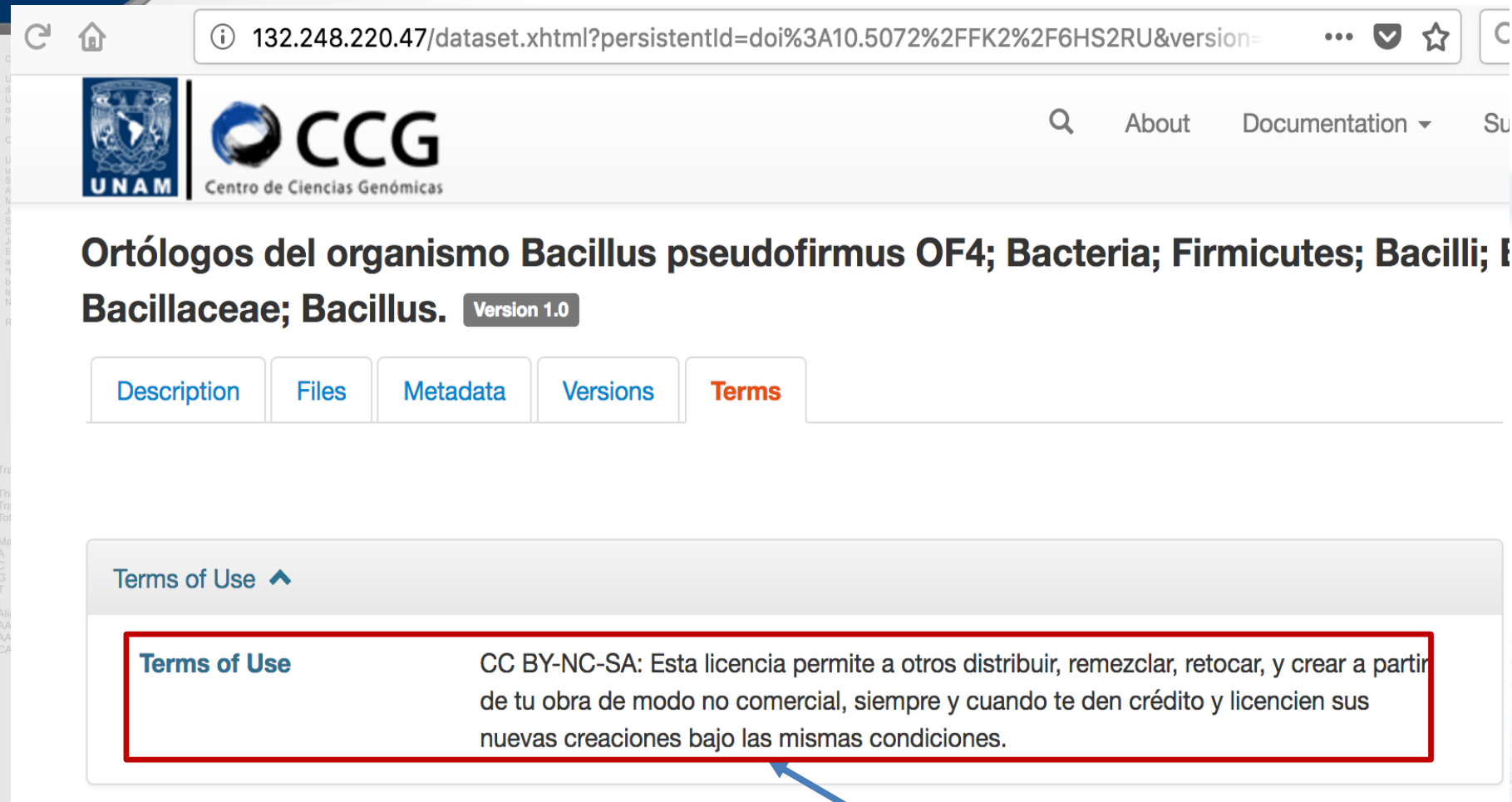
Transcription Factor Matrix and Alignments

The consensus and patser programs were used  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0  
C 1 0 0 1 0 1 0 0 1 1 2 0 0 2  
G 0 0 1 0 0 0 0 1 1 2 0 0 3 1  
T 0 0 1 1 0 0 0 1 1 2 0 0 0 0



# Ejemplo: Principio-Reusable (R)



132.248.220.47/dataset.xhtml?persistentId=doi%3A10.5072%2FFK2%2F6HS2RU&version=

UNAM CCG Centro de Ciencias Genómicas

Ortólogos del organismo **Bacillus pseudofirmus OF4; Bacteria; Firmicutes; Bacilli; Firmicutes; Bacillaceae; Bacillus.** **Version 1.0**

Description Files Metadata Versions **Terms**

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Licencia de uso  
de los datos



# Al final tenemos!!!

http://ricg/dataset.xhtml?persistentId=doi%3A10.5072%2FFK2%2F6HS2RU&version=1.0

← Link Edit

## Ortólogos del organismo Bacillus pseudofirmus OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus. Version 1.0

1 Add + Edit Metadata Export Metadata

2 Dataset Persistent ID doi:10.5072/FK2/6HS2RU

4 Description Ortólogos bidireccionales del genoma organismo Bacillus pseudofirmus OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.

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CITE Export

MORENO HAGELSIEB, GABRIEL; Wilfrid Laurier University; ORCID; 0000-0002-2457-4450, 2018, "Ortólogos del organismo Bacillus pseudofirmus OF4; Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.", doi:10.5072/FK2/6HS2RU, Repositorio Institucional de Conocimiento Genómico, V1



- 1. Metadatos F
- 2. Identificador
- 3. Protocolo de comunicación A
- 4. Referencias I
- 5. Licencia R

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"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 beyond transcription (experimental) annotated promoters and textpresso navigation".  
Nucleic Acids Research 41(12):2212-2222, 2013.  
Release: 6.4 Date: 10-AUG-2013

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*The chain, whereby new scientific discoveries are built on previously established results, can only work optimally if all research results are made openly available to the scientific community.*

Transcription Factor

The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor NameAda  
Total of uniq binding sites3

Matrix  
A 2 3 1 1 3 2 3 0 0 1 1 2 0 0 1 0 2 2 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0 1 0 0 1 0 2 0 0 2 0 1 1 0 0 0 0 0 0 0 1 0 0 0 0  
G 0 0 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 2 0 0 2 1 0 1  
T 0 0 1 0 0 0 0 2 2 0 0 1 0 0 0 2 0 1 0 0 1 3 0 2 2 1 2 2 2

AlignmentScore  
AAGCAAAGCG...  
AAAAAATTAAAGCGCAAGATTGTTGGTTT21.42  
CATTACATTGCTGATAACAATGTTTAGT19.78

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Suzanne Garma-Castillo, Alberto Santos-Zamora, Mariana Moreno, Juan Segura-Salazar, Leticia Rascado, and Martínez-Flores, Heladia Salgado, César Bonavides-Martínez, Cel Abreu-Goodger, Carlos Rodríguez-Penagos, Juan Miranda-Ríos, Enrique Morett, Enrique Merino, Araceli M. Huerta, Luis Treviño-Quintanilla and Julio Colado-Vides.  
"RegulonDB (Version 6.0): gene regulation model of Escherichia coli K-12 (beyond transcriptional regulation): experimental design and promotion and textpresso navigation".  
Nucleic Acids Research  
Release: 6.4 Date: 10-AUG-09

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Transcription Factor Matrix and Alignments

The consensus and patser programs were used to create the matrix and alignment  
Transcription Factor Matrix  
Total of uniq bins

Matrix  
A 2 3 1 1 3 2 3 0 0 1 2 0 0 1 0 2 0 0 3 2 0 1 1 0 0 0 1 0  
C 1 0 0 1 0  
G 0 0 1 0  
T 0 0 1 0

AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGATAACAATGTTTAGT19.78

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