



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.  
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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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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  
AAAAAATTAAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGAATGTTTAGT9.78



# 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 Bonavides-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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 Citation  
 RegulonDB. The current most updated version is RegulonDB 6.0. Martin Peralt-Gil, María J. de la Hoz, Bruno Contreras, María J. Martínez-Flores, Heberto Martínez-Flores, Carlos Rodríguez-Pérez, Carlos Rodríguez-Pérez, Luis Treviño-Quintanilla and "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  
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 Total of uniq binding sites3  
 Matrix  
 0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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Nucleic Acids Research, 2003, vol 36, D120-D124

Release: 6.4 Date: 10-AUG-09

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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

# RegulonDB

## Base de Conocimiento (BC)



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

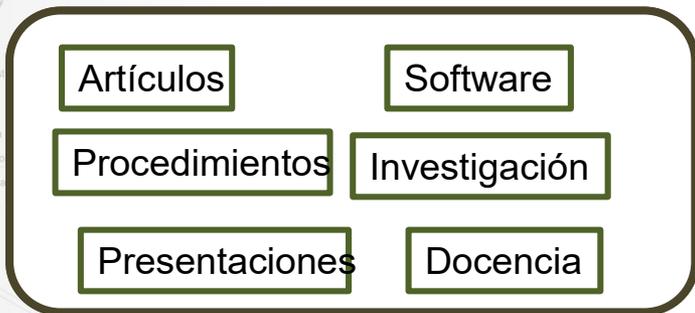
Repositorio de **todos los productos de trabajo** resultado de los proyectos: software, planes, reportes, registros, lecciones aprendidas, tesis, artículos, plantillas, seminarios, datos, imágenes, etc.\*

\*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

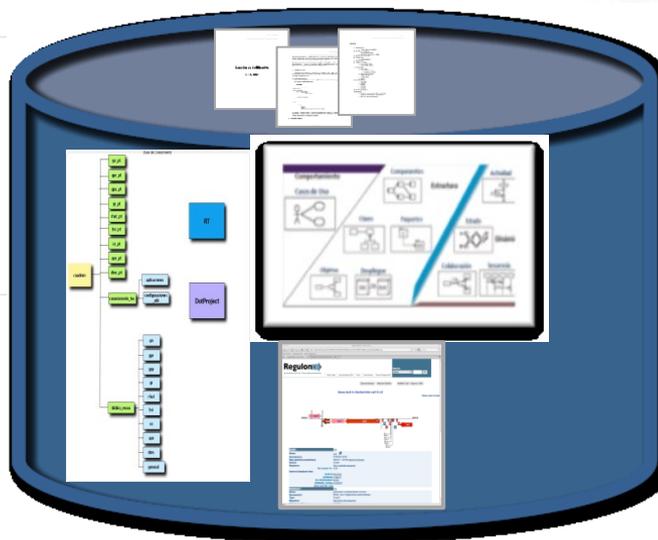


Colaborador



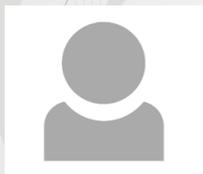
Alimentación/  
poblado

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



Administrador

Mantenimiento  
Respaldo



Investigador

Consulta



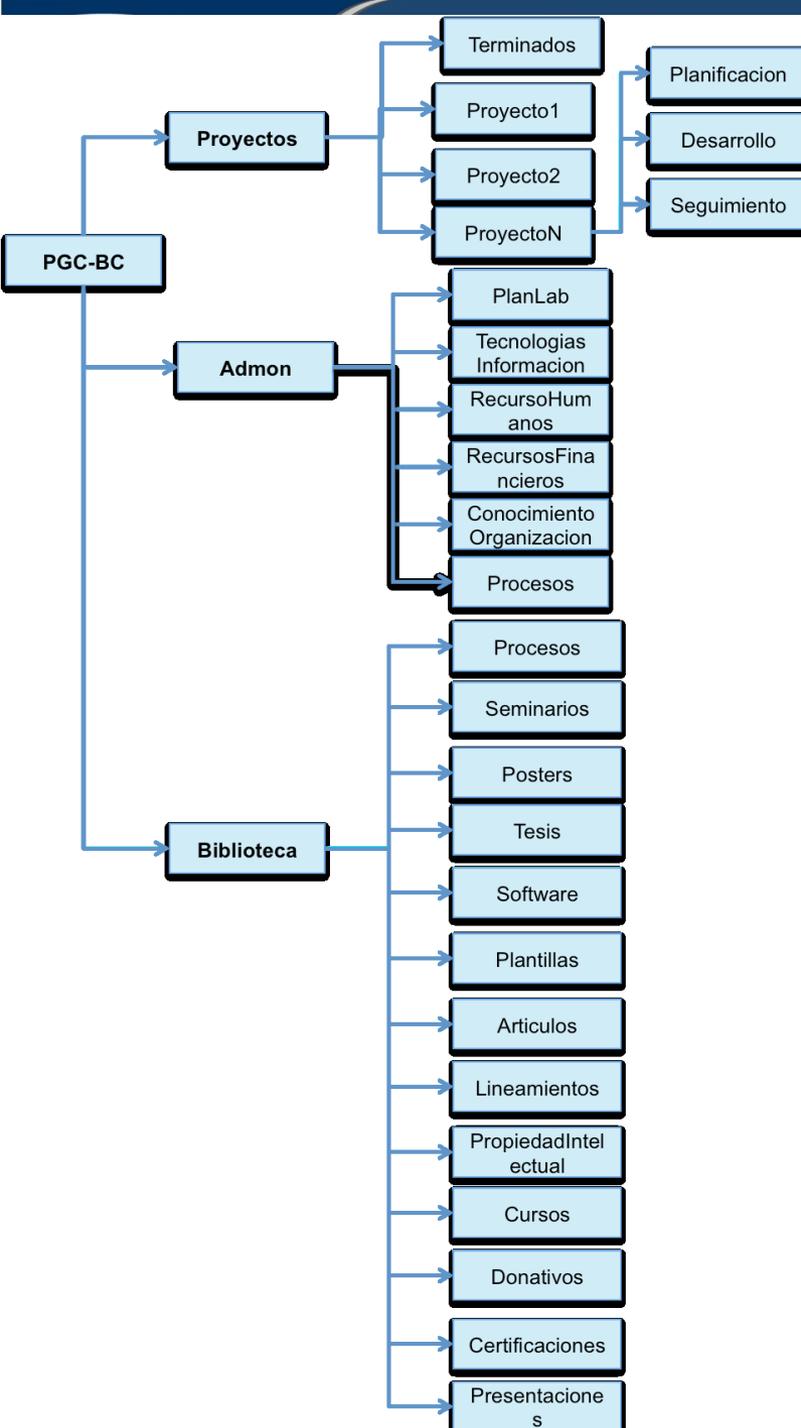
ATGTTTGGCCG  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAATTAAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGCAATGTTTAG19.78

# 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**

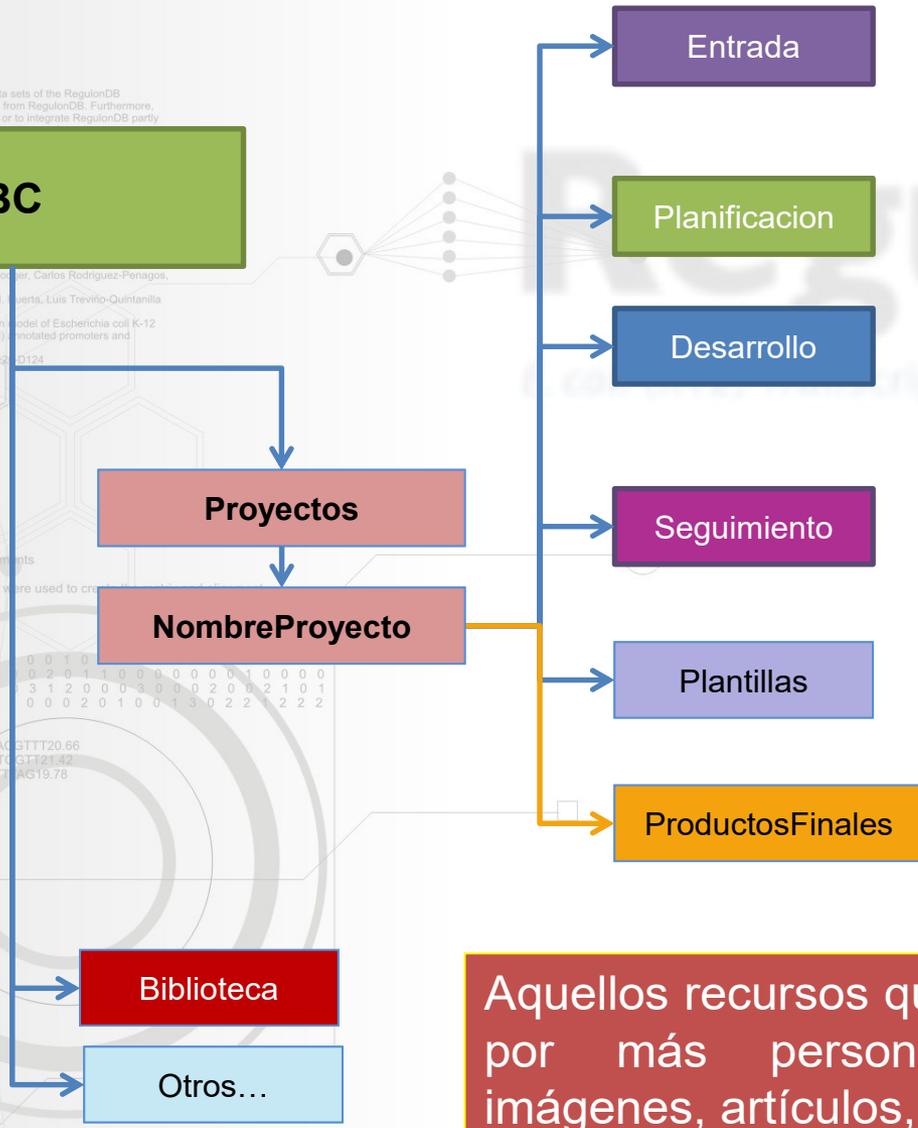
# Mi carpeta de trabajo

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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  
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Nucleic Acids Research, 2008, vol 36, D52-D124  
Release: 6.4 Date: 10-AUG-09

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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  
CATTACATTGCTGGATAAAGATGTTTAG19.78



**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.

**ProductosFinales**  
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  
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beyond transac...  
textpresso nam...  
Nucleic Acids Research, 2008, Vol 36, E177-D124  
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G 0 0 1 1 0 1 0 1 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  
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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



# 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



# Versionamiento

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

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Citation  
User is committed to cite the current most update publication concerning RegulonDB. Sincerely, Socorro Garza-Castro, Verónica Jiménez-Jasinto, Marín Pérez-Gil, Alberto Santos-Zavaleta, Monica I. Peñafoza-Spindola, Bruno Contreras-Moreira, Juan Segura-Salazar, Cesar Bonnavides-Gottelli, Juan Miranda-Rico, Enrique Morett, E. Guerrero, Araceli M. Huerta, Luis Treviño-Quintanilla and Julio Colado-Vides.  
\*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. 2009; 37(12):4168-4176.  
Release: 6.4 Database: 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 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



# ¿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

# "FINAL".doc



FINAL.doc!



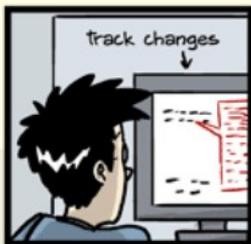
FINAL\_rev.2.doc



FINAL\_rev.6.COMMENTS.doc



FINAL\_rev.8.comments5.  
CORRECTIONS.doc



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



FINAL\_rev.22.comments49.  
corrections.10. #@\$%WHYDID  
ICOMETOGRADSCHOOL?????.doc

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Socorro Gama-Castro, Verónica Jiménez-Jasinto, Mari Alberto Santos-Zavaleta, Monica I. Peñalzoza-Spindola, Morena, Juan Segura-Salazar, Luis Muñoz-Rascado, Irma Martín Salgado, César Bonavides-Martínez, Cel Abreu-Goodger, Carlos Juan Miranda-Ríos, Enrique Morett, Enrique Merino, Araceli M. Huerta, Luis Treviño-Quintanilla and Julio Collado-Vides.  
"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

Transcription Factor Matrix and Analysis  
The consensus and patser program  
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 2 2 0

AlignmentScore  
AAGCAAAGCCAGCG  
AAAAAATTAAGCGC  
CATTACATTGCTGGAT

JORGE CHAM © 2012

# Ejemplos

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Citation

User is committed to cite properly in most update publication concerning RegulonDB is:

**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-Ries, 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

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

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  
User is committed to cite properly in any future update publication concerning RegulonDB. *Journal of Bacteriology*, 191(12):3523-3531, 2009. S. Garza-Castro, Verónica Jiménez-Jacinto, Marín Peralta-Gu, Alberto Santos-Zavaleta, Monica I. Peñaloza-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-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 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  
AAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGGATAAGAATGTTTAG19.78





# En resumen...

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

- 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 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 0  
G 0 0 1 1 0 0 0 0 1 0 2 0 0 3 1 2 0 0 0 3 0 0 0 0 2 1 0 1 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 0 0 2 2 0 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

FamilyName, GivenName or Organization

Affiliation

Identifier Scheme

Select...

Identifier

Agregar

**Description \***

This field supports only certain HTML tags.

Text

Date

YYYY-MM-DD

Description Type

Select...

Agregar

onDB

**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



About Documentation Support

## Date Type \*

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- Updated
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## Related Publication \*

### 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 \*

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- IsNewVersionOf
- IsPreviousVersionOf
- IsPartOf
- IsReferencedBy
- References
- IsDocumentedBy
- Issued
- Documents



Referencias

Vocabulario controlado  
Ontologías  
Diccionarios

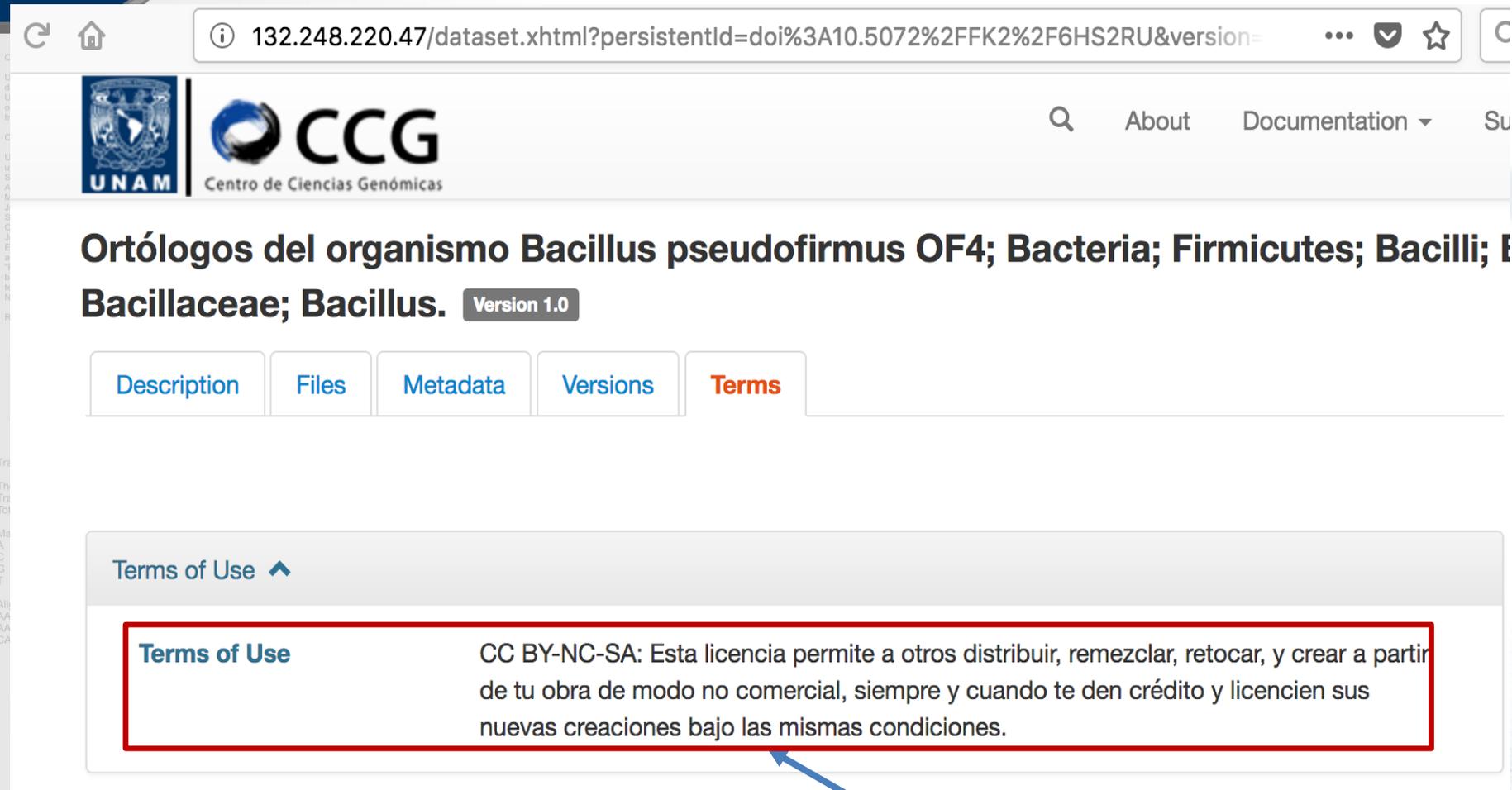
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"RegulonDB (Version 6.0): gene regulation model of E. coli beyond transcription, active (experimental) annotated textpresso navigation"  
*Nucleic Acids Research*, 2008, vol 36, D120-D124  
Release: 6.4 Date: 10-AUG-09

Transcription Factor Matrix and Alignments  
The consensus and patser programs were used  
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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*Monetising the access to new and existing research results is profoundly at odds with the ethos of science (Merton, 1973).*

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. comparado con otros genomas.

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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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Citation

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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 textpresso navigation".  
Nucleic Acids Research  
Release: 6.4 Date: 10-AUG-09

*Only results that can be discussed, challenged, and, where appropriate, tested, and reproduced by others qualify as scientific.*

*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 Matrix and Alignments

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

Transcription Factor: HcrA

Total of uniq bins: 1

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

AlignmentScore  
AAGCAAAGCGCAGCGTCTGAATAACGTTT20.66  
AAAAAAATTAAGCGCAAGATTGTTGGTT21.42  
CATTACATTGCTGATAACAATGTTTAGT19.78

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