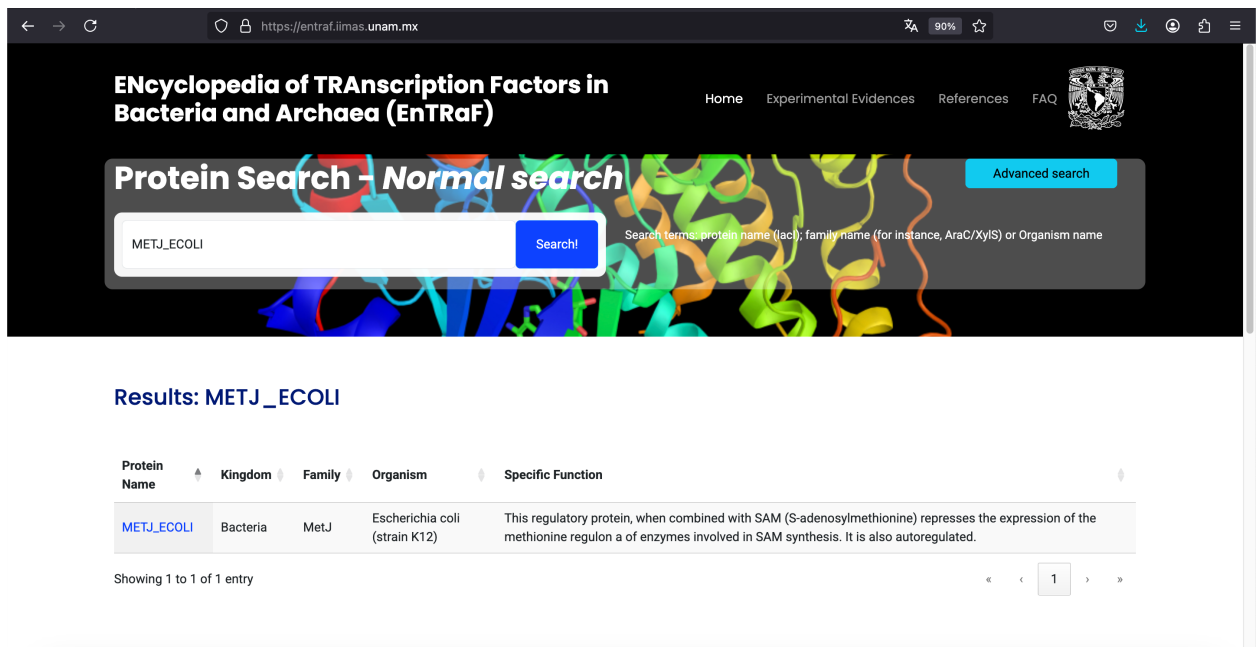


README of ENcyclopedia of TRAnscription Factors in Bacteria and Archaea genomes (ENTRAF) version 2.0.

There are two forms, to search into the database:

1. Input the keyword for the transcription factor: AraC/XylS, MetJ, LacI/GalR or Bacillus subtilis



The screenshot shows the ENcyclopedia of TRAnscription Factors in Bacteria and Archaea (EnTRaF) website. The header includes the site name and navigation links: Home, Experimental Evidences, References, and FAQ. A search bar is prominently displayed with the text "Protein Search - Normal search" and a "Search!" button. The search term "METJ_ECOLI" is entered in the search bar. Below the search bar, the results are displayed under the heading "Results: METJ_ECOLI". A table lists the search results, showing the protein name, kingdom, family, organism, and specific function. The table has one entry for METJ_ECOLI, which is a protein from Escherichia coli (strain K12) that represses the expression of the methionine regulon and is involved in SAM synthesis.

Protein Name	Kingdom	Family	Organism	Specific Function
METJ_ECOLI	Bacteria	MetJ	Escherichia coli (strain K12)	This regulatory protein, when combined with SAM (S-adenosylmethionine) represses the expression of the methionine regulon a of enzymes involved in SAM synthesis. It is also autoregulated.

Showing 1 to 1 of 1 entry

2. Display the Transcription factor (protein) ID

[←](#)
[→](#)
[↺](#)

[https://entraf.iimas.unam.mx](#)

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ENcyclopedia of TRANscription Factors in Bacteria and Archaea (EnTRaF)

[Home](#)
[Experimental Evidences](#)
[References](#)
[FAQ](#)

Id Entraf

ENTRAF0561

Entry name

METJ_ECOLI

Organism

Escherichia coli (strain K12)

Global Function

Amino-acid metabolism

Specific Function

This regulatory protein, when combined with SAM (S-adenosylmethionine) represses the expression of the methionine regulon a of enzymes involved in SAM synthesis. It is also autoregulated.

Subunits

Homodimer.

Ligand

methyl-5'-thioadenosine; adenine

Sequence

MAEWSGEYIS

PYAEHGKKSE

QVKKITVSIP

LKVLKILTDE

RTRRQVNNLR

HATNSELLCE

AFLHAFTGQP

LPDDADLRKE

RSDEIPEAAK

EIMRENGINP

ETWEY

State Tree

https://alphafold.ebi.ac.uk/...

Model 1

Model 853 elements

Polymer 853 elements

Cartoon

Sequence of

https://alphafold.ebi.ac.uk/files/AF-...

Chain

1: MET REPR...

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GENE Ontology


Taxonomy


Useful links

id GO	Description
GO:0003677	DNA binding
GO:0003677	DNA binding
GO:0003677	DNA binding
GO:0003700	DNA-binding transcription factor activity
GO:0003700	DNA-binding transcription factor activity
GO:0003700	DNA-binding transcription factor activity
GO:0005829	cytosol
GO:0009086	methionine biosynthetic process
GO:0045892	negative regulation of DNA-templated transcription
GO:0045892	negative regulation of DNA-templated transcription

- Phylum: Pseudomonadota
- Order: Enterobacterales
- Family: Enterobacteriaceae
- Class: Gammaproteobacteria
- Genus: Escherichia

PDB

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- Alternatively, for advance searches; we included diverse fields to be considered: Gene ontology; Global regulation and/or taxonomy. For instance, for the term “bent DNA-binding”, we get the following result:

[entraf.iimas.unam.mx/advancedSearch.php](#)

[easyROC](#)
[ggplot2 Based Plots...](#)
[GitHub - u-genoma/...](#)
[scExplorer](#)
[Downloads](#)
[Algorithm](#)
[Boxy SVG Editor](#)
[Rickettsia: Taxonom...](#)
[Rickettsia: Taxonom...](#)
[KBase: App Catalog](#)

Entraf

[Home](#)
[Experimental Evidences](#)
[References](#)
[FAQ](#)

idEntraf	Kingdom	Family	Organism	Specific Function
ENTRAF0535	Procariota	Histone_HNS	Escherichia coli (strain K12)	<p>A DNA-binding protein implicated in transcriptional repression (silencing). Also involved in bacterial chromosome organization a compaction. H-NS binds tightly to AT-rich dsDNA and inhibits transcription. Binds upstream and downstream of initiating RNA polymerase, trapping it in a loop and preventing transcription. Binds to hundreds of sites, approximately half of which are in non-coding DNA, which only accounts for about 10% of the genome. Many of these loci were horizontally transferred (HTG); this offers the selective advantage of silencing foreign DNA while keeping it in the genome in case of need. Suppresses transcription at many intragenic sites as well as transcription of spurious, non-coding RNAs genome-wide. Repression of HTG by H-NS is thought to allow their DNA to evolve faster than non-H-NS-bound regions, a facilitates integration of HTG into transcriptional regulatory networks. A subset of H-NS/StpA-regulated genes also require Hha (a/or Cnu, ydgT) for repression; Hha and Cnu increase the number of genes DNA bound by H-NS/StpA and may also modulate the oligomerization of the H-NS/StpA-complex. The protein forms 2 clusters in the nucleoid which gather hns-bound loci together, bridging non-contiguous DNA, a causes DNA substantial coensation. Binds DNA better at low temperatures than at 37 degrees Celsius; AT-rich sites nucleate H-NS binding, further DNA-binding is cooperative and this cooperativity decreases with rising temperature. Transcriptional repression can be inhibited by dominant-negative mutants of StpA or itself. May effect transcriptional elongation. Can increase translational efficiency of mRNA with suboptimal Shine-Dalgarno sequences. Plays a role in the thermal control of pili and adhesive curli fimbriae production, by inducing transcription of csgD. Plays a role in flagellar function. Represses the CRISPR-cas promoters, permits only weak transcription of the crRNA precursor; its repression is antagonized by LeuO. Binds preferentially to the upstream region of its own gene recognizing two segments of DNA on both sides of a binding site centered around -150. Overexpression suppresses secY24, a temperature-sensitive mutation. Has also been reported to activate transcription of some genes.</p> <p>Controls the transcription of genes involved in arginine and lysine metabolism. Activates transcription of several genes, including argO, lysP, lysC, asd, dapB, dapD, lysA, gadA and argK. Acts by binding directly to their promoter or control region. ArgP dimer by itself is able to bind the argO promoter-operator region to form a binary complex, but the formation of a ternary complex with RNA polymerase is greatly stimulated only in presence of a coeffector.</p>

And as in the original search, the protein record can be displayed to check all the functional information.