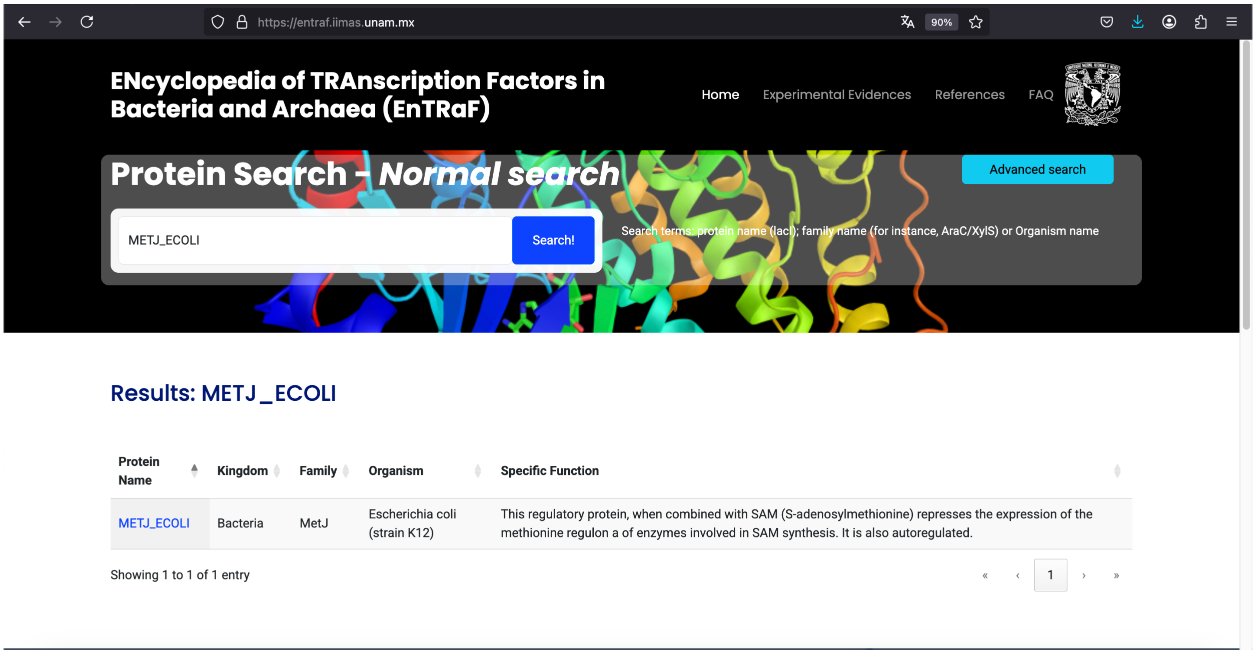
README of ENcyclopedia of TRAnscription Factors in Bacteria and Archaea genomes (ENTRAF) version 2.0.

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



ENcyclopedia of TRAnscription Factors in Bacteria and Archaea (EnTRaF)

Protein Search - *Normal search*

METJ_ECOLI

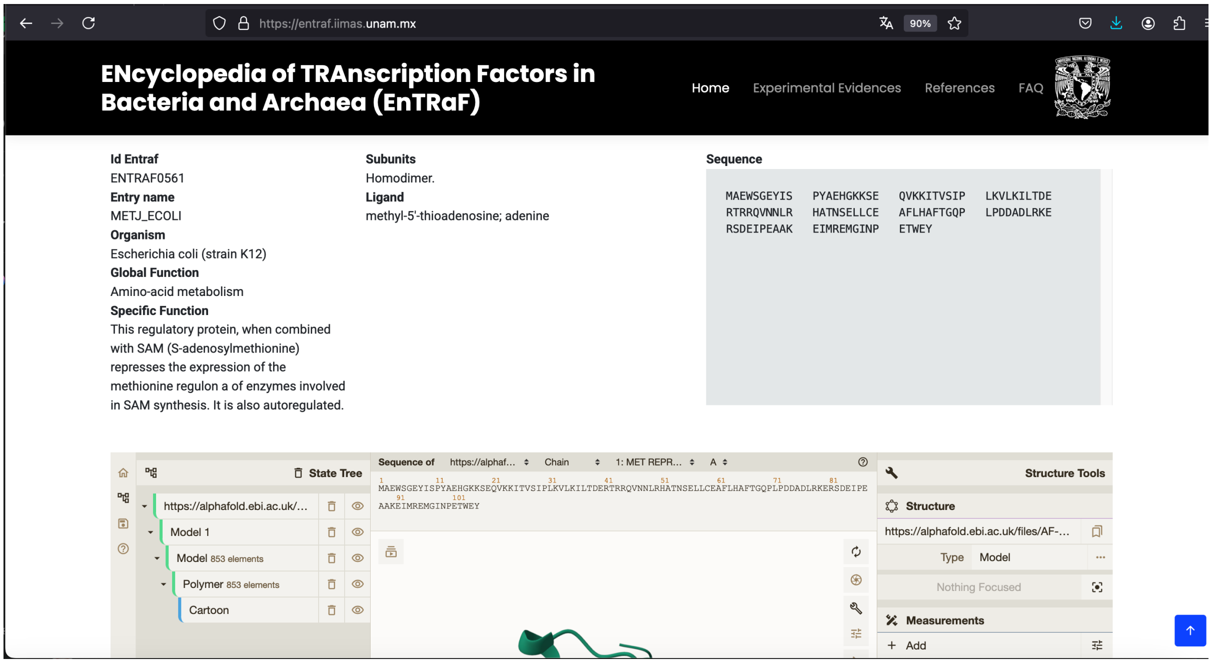
Search terms: protein name (lacI); family name (for instance, AraC/XylS) or Organism name

Results: METJ_ECOLI

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



ENcyclopedia of TRAnscription Factors in Bacteria and Archaea (EnTRaF)

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.

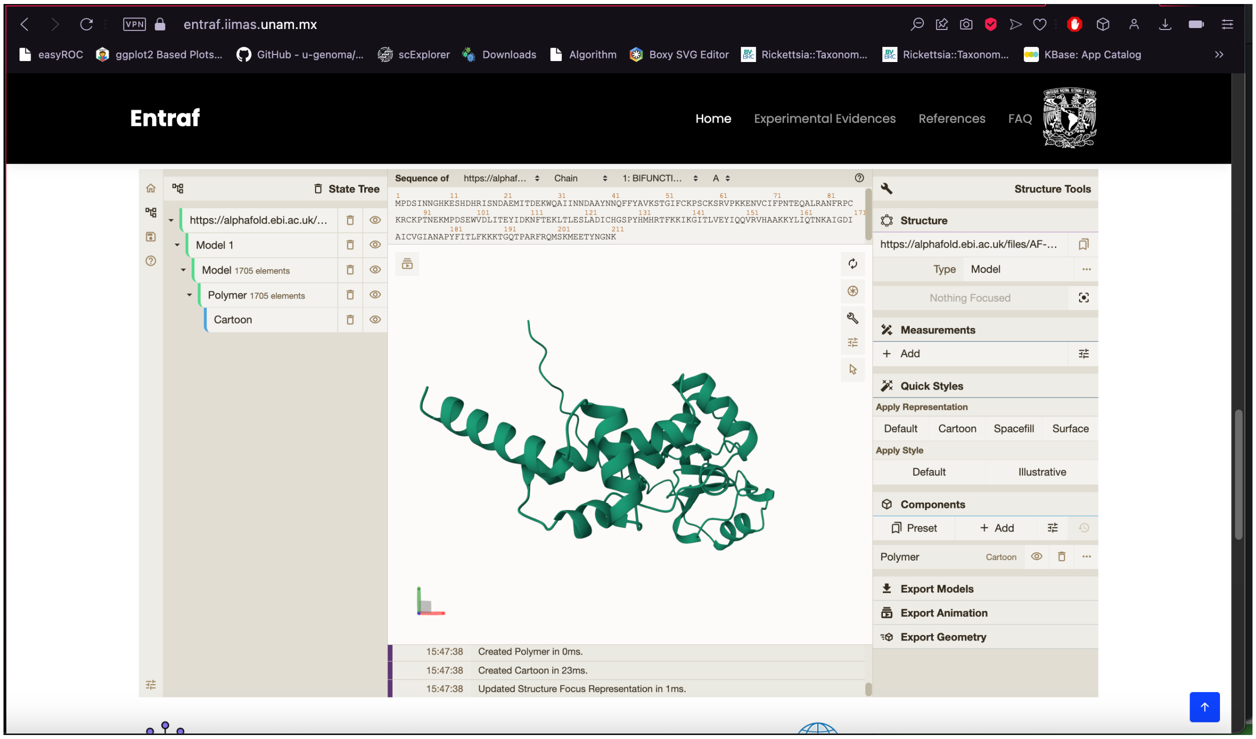
Subunits
Homodimer.
Ligand
methyl-5'-thioadenosine; adenine

Sequence

```
MAEWSGEYIS   PYAEHGKKSE   QVKKITVSIP   LKVLKILTDE
RTRRQVNNLR   HATNSELLCE   AFLHAFTGQP   LPDDADLRKE
RSDEIPEAAK   EIMREMGINP   ETWEY
```

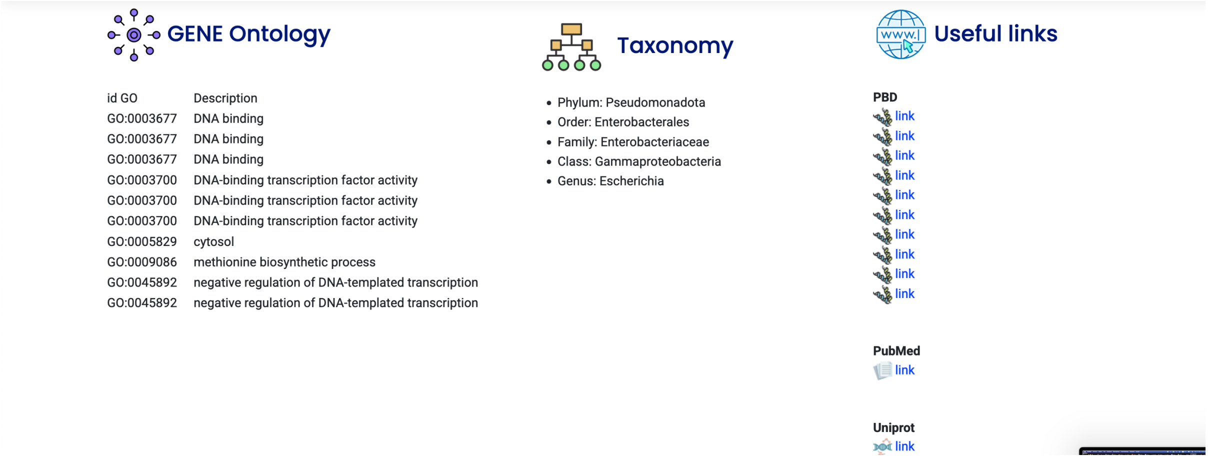
```
1         11        21        31        41        51        61        71        81
MAEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHAFTGQPLPDDADLRKERSDEIPE
   91        101
AAKEIMREMGINPETWEY
```

For this entry (MetJ_Ecoli) we display the protein ID (internal database identificator); entry name; Organism; Global function; Specific function; Subunits; Ligand molecule; protein sequence; alpha fold model; Gene ontology; bacterial or archaeal taxonomy and external links to PDB, PubMed and Uniprot databases.



```
1         11        21        31        41        51        61        71        81
MPDSINNGHKESHDHRISNDAEMITDEKWQAIINNDAAYNNQFFYAVKSTGIFCKPSCKSRVPKKENVCIFPNTEQALRANFRPC
   91        101       111       121       131       141       151       161       171
KRCKPTNEKMPDSEWVDLITEYIDKNFTEKLTLESLADICHGSPYHMHRTFKKIKGITLVEYIQQVRVHAAKKYLIQTNKAIGDI
     181       191       201       211
AICVGIANAPYFITLFKKKTGQTPARFRQMSKMEETYNGNK
```

```
15:47:38   Created Polymer in 0ms.
15:47:38   Created Cartoon in 23ms.
15:47:38   Updated Structure Focus Representation in 1ms.
```



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

PBD
link
link
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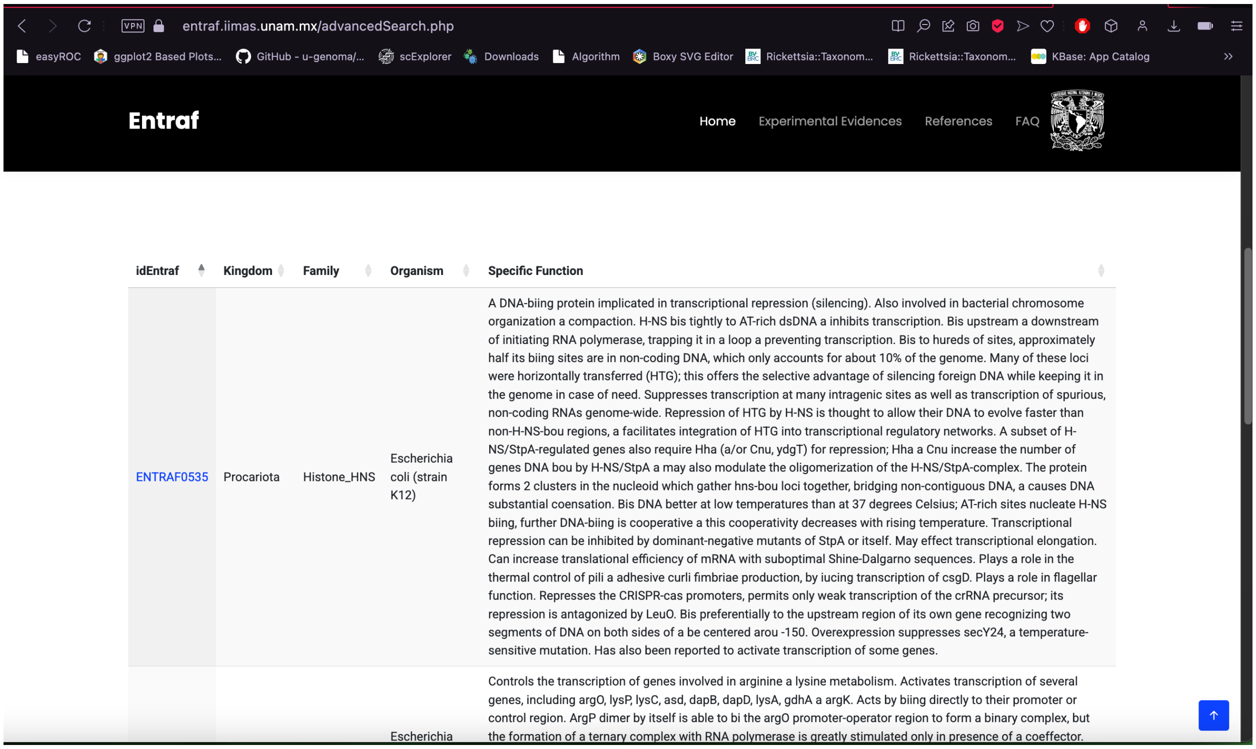
PubMed
link

Uniprot
link

1. 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:



idEntraf	Kingdom	Family	Organism	Specific Function
ENTRAF0535	Procariota	Histone_HNS	Escherichia coli (strain K12)	A DNA-biing protein implicated in transcriptional repression (silencing). Also involved in bacterial chromosome organization a compaction. H-NS bis tightly to AT-rich dsDNA a inhibits transcription. Bis upstream a downstream of initiating RNA polymerase, trapping it in a loop a preventing transcription. Bis to hureds of sites, approximately half its biing sites 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-bou 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 a Cnu increase the number of genes DNA bou by H-NS/StpA a may also modulate the oligomerization of the H-NS/StpA-complex. The protein forms 2 clusters in the nucleoid which gather hns-bou loci together, bridging non-contiguous DNA, a causes DNA substantial coensation. Bis DNA better at low temperatures than at 37 degrees Celsius; AT-rich sites nucleate H-NS biing, further DNA-biing is cooperative a 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 a adhesive curli fimbriae production, by iucing 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. Bis preferentially to the upstream region of its own gene recognizing two segments of DNA on both sides of a be centered arou -150. Overexpression suppresses secY24, a temperature-sensitive mutation. Has also been reported to activate transcription of some genes.
			Escherichia	Controls the transcription of genes involved in arginine a lysine metabolism. Activates transcription of several genes, including argO, lysP, lysC, asd, dapB, dapD, lysA, gdhA a argK. Acts by biing directly to their promoter or control region. ArgP dimer by itself is able to bi 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.

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