## ENTRAF is free for academic/noncommercial use

User is not entitled to change or erase data sets of the ENTRAF database or to eliminate copyright notices from ENTRAF. Furthermore user is not entitled to expand ENTRAF or to integrate ENTRAF partly or as a whole into other databank systems without prior written consent from IIMAS-UNAM.

## Citation:

Tenorio-Salgado S. et al (2025) ENcyclopedia of TRAnscription Factors in Bacteria and Archaea genomes (ENTRAF) version 2.0.

## Contact

**ENTRAF** Team

Web Page: entraf.iimas.unam.mx (ernesto.perez@iimas.unam.mx)

Release: 2.0. Date: XX/XX/2025

Experimental evidences

Definition	Description	Quality of evidence	Comments
APPH	Assay of Protein Purified to	strong	In vitro transcription assay
	Homogeneity		
BPP	Binding of Purified Proteins	strong	Footprinting assay (DNase I, DMS, etc.). Physical
			binding of the regulator to the regulated promoter
			proved by using footprinting assay
CHS	ChIP-seq	strong	Physical binding of the regulator to the regulated
			promoter proved by using electrophoretic Chromatin
			inmuno precipitation assay
IDA	Inferred from Direct Assay	strong	Inferred from direct assay
qRT-PCR	mRNA expression levels measured	strong	mRNA expression levels of regulated element
	by qRT-PCR technique	_	measured and compared between wild-type and trans-

			element mutation (knockout, over expression etc.) performed by using qRT-PCR technique
OHRs	One Hybrid Reporter system	strong	Physical binding of the regulator to the regulated promoter proved by using electrophoretic mobility shift assay
PRM	Primer Extension Analysis	strong	Transcription initiation mapping (used in combination with transcript concentrations measurements to compare mutant vs wild type expression levels)
PROT	Proteomic studies	Strong	Proteomics techniques. Regulated gene product concentrations measured and compared between wild-type and trans-element mutation (knockout, over expression etc.)
PDB	Protein structural determination	strong	The regulation is infered after the observation of protein structure
FURTA	Fur titration assay	strong	
SM	Site Mutation	Strong	Site-directed mutagenesis in the DNA binding site. A cis-mutation in the DNA sequence of the TF binding site interferes with the operation of the regulatory function
BCE	Binding of Cellular Extracts	weak	Electrophoretic mobility shift assays EMSA. Physical binding of the regulator to the regulated promoter proved by using electrophoretic mobility shift assay
GEA	Gene expression analysis	weak	LacZ-promoter fusion; Gfp-promoter fusion. Expression levels of LacZ- regulated promoter fusion measured and compared between wild-type and transelement mutation (knockout, over expression etc.); expression levels of gfp-regulated promoter fusion measured and compared between wild-type and transelement mutation (knockout, over expression etc.)
AS	Author Statement	weak	Traceable author statement to experimental support and associated with literature
IEP	Inferred from Expression Pattern	weak	Inferred from expression pattern

IMP	Inferred from mutant phenotype	weak	Inferred from mutant phenotype. A mutation of a transcription factor has a visible cell phenotype, and it is inferred that the regulator might be regulating the genes responsible for the phenotype
IGI	Inferred from Genetic interaction	weak	Inferred from genetic interaction. In vitro titration assay
RBM	Reaction Blocked in Mutant	weak	Gene Disruption
MIC	Microarrays	weak	mRNA levels of regulated element measured and compared between wild-type and trans-element mutation (knockout, over expression etc.) performed by using microarray (or macroarray) experiments.
RACE	High throughput transcription initiation	weak	High throughput transcription initiation mapping (used in combination with transcript concentrations measurements to compare mutant vs wild type expression levels)
2D-PAGE	Polyacrylamide gel electrophoresis (PAGE)	weak	Two-dimensional gels