

Figure S1 - Snapshot of the relational database structure of CollecTF.

(A)

collecTF | Admin page | .tbl export |

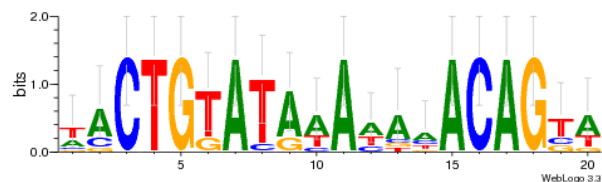
logged in as tfnut | logout

Split view Ensemble view Non-motif-associated sites ▾ Export data

LexA binding site collection of *Vibrio parahaemolyticus*

Binding sites Aligned binding sites Sequence logo Detailed view

To generate the weblogo, aligned binding sites are used.



LexA binding site collection of *Pseudomonas putida*

Binding sites Aligned binding sites Sequence logo Detailed view

To generate the weblogo, aligned binding sites are used.

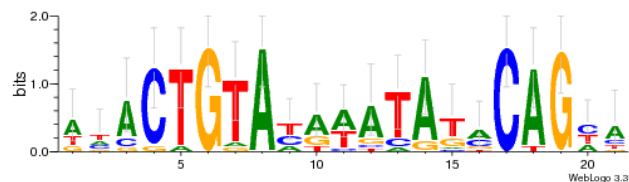


Figure S2 – Screenshot of a dynamically generated report of LexA-binding sites in the Gammaproteobacteria as **(A)** individual TF/species pair (split) reports and **(B)** an ensemble report integrating all Gammaproteobacteria sites of LexA.

(B)

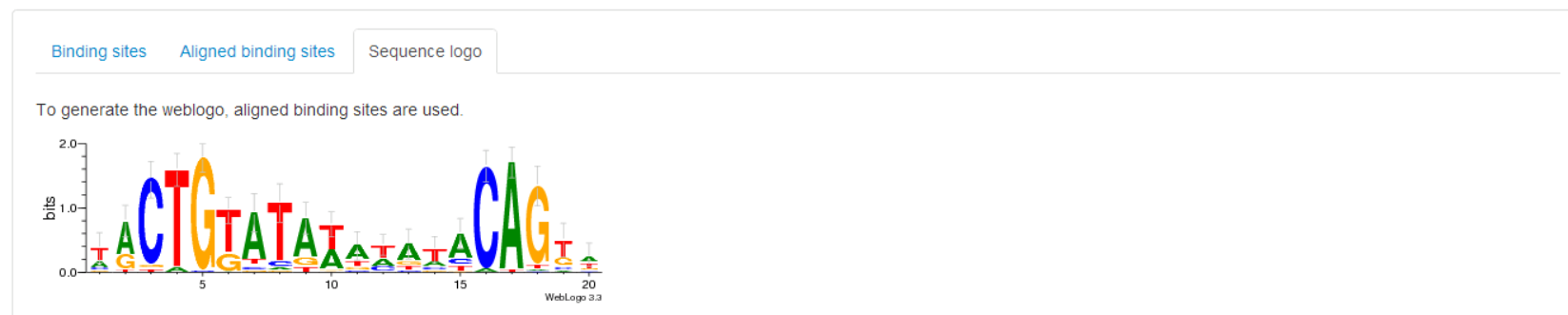
collecTF | Admin page | .tbl export |

logged in as tfnut | logout

Split view Ensemble view Non-motif-associated sites ▼ Export data

Ensemble view

All binding sites in split view are combined and a sequence logo is generated. Note that it may contain binding site sequences from different transcription factors and different species. To see individual sequence logos and curation details go to split view.



Please send comments to sefa1@umbc.edu. For help, visit [CollecTF wiki](#).

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