

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

MuIPSSM

RRID:SCR_007812

Type: Tool

Proper Citation

MuIPSSM (RRID:SCR_007812)

Resource Information

URL: <http://crick.mbu.iisc.ernet.in/~mulpssm>

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Description: A database of multiple position specific scoring matrices of protein domain families with constant alignments. Representation of multiple sequence alignments of protein families in terms of position-specific scoring matrices (PSSMs) is commonly used in the detection of remote homologues. A PSSM is generated with respect to one of the sequences involved in the multiple sequence alignment as a reference. We have shown recently that the use of multiple PSSMs corresponding to an alignment, with several sequences in the family used as reference, improves the sensitivity of the remote homology detection dramatically. MuIPSSM contains PSSMs for a large number of sequence and structural families of protein domains with multiple PSSMs for every family. The approach involves use of a clustering algorithm to identify most distinct sequences corresponding to a family. With each one of the distinct sequences as reference, multiple PSSMs have been generated. The current release of MuIPSSM contains ~33 000 and ~38 000 PSSMs corresponding to 7868 sequence and 2625 structural families. A RPS_BLAST interface allows sequence search against PSSMs of sequence or structural families or both. An analysis interface allows display and convenient navigation of alignments and domain hits.

Synonyms: MuIPSSM

Resource Type: data or information resource, database

Resource Name: MuIPSSM

Resource ID: SCR_007812

Alternate IDs: nif-0000-03172

Record Creation Time: 20220129T080243+0000

Record Last Update: 20260905T133146+0000

Ratings and Alerts

No rating or validation information has been found for MulPSSM.

No alerts have been found for MulPSSM.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at [Kravitz](#) .

Janaki C, et al. (2021) Master Blaster: an approach to sensitive identification of remotely related proteins. Scientific reports, 11(1), 8746.

Gowri VS, et al. (2006) Recent trends in remote homology detection: an Indian Medley. Bioinformation, 1(3), 94.