
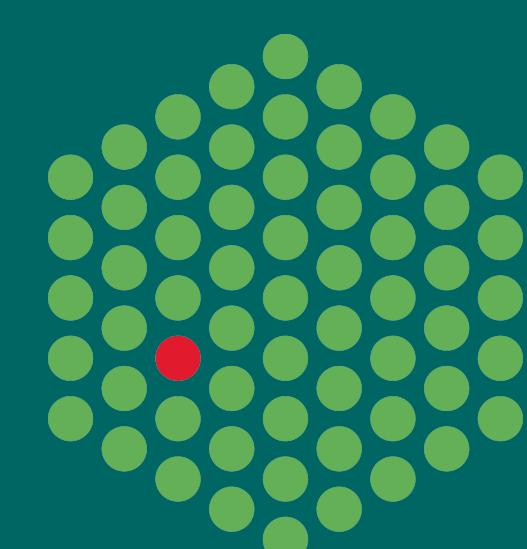


Identifying novel functional linear motifs using host-viral protein interactions and the principle of convergent evolution

**References:**

- All analyses were performed in R. IMEx consortium databases such as IntAct, MINT, DIP, BHF-UCL, MPIDB, MatrixDB, HPIDb, I2D-IMEx, InnateDB-IMEx, MolCon, UniProt, MBLInfo are currently integrated into IntAct [1].
- Orchard S, Ammari M, Aranda B, et al. The MlnAct project—IntAct as a common curation platform for 11 molecular interaction databases. *Nucleic Acids Research*. 2014;42(Database issue):D358–D363.
 - Jones P, Birns D, Chang HY, et al. InterProScan 5: genome-scale protein function classification. *Bioinformatics (Oxford, England)*. 2014;30(9):1236–1240.
 - Palopoli N, Lythgow KT, Edwards RJ. QSLIMFinder: improved short linear motif prediction using specific query protein data. *Bioinformatics (Oxford, England)*. 2015;31(14):2284–2293.
 - Pawson T, Gish GD, Nash P. SH2 domains, interaction modules and cellular wiring. *Trends in Cell Biology*. 2001;11(12):504–511.

- Hagai T, Azia A, Babu MM, Andino R. Use of host-like peptide motifs in viral proteins is a prevalent strategy in host-virus interactions. *Cell Reports*. 2014;7(5):1729–1739.
- Edwards RJ, Palopoli N. Computational prediction of short linear motifs from protein sequences. *Methods in Molecular Biology (Clifton, N.J.)*. 2015;1268:89–141.
- Dinkel H, Van Roey K, Michael S, et al. ELM 2016—data update and new functionality of the eukaryotic linear motif resource. *Nucleic Acids Research*. 2015;44(D1):D294–300.