

# CITATION REPORT

List of articles citing

**Minimotif Miner 3.0: database expansion and significantly improved reduction of false-positive predictions from consensus sequences**

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**Nucleic Acids Research, 2012, 40, D252-60.**

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| #  | Paper  | IF   | Citations |
|----|--|------|-----------|
| 51 | The identification of short linear motif-mediated interfaces within the human interactome. <i>Bioinformatics</i> , <b>2012</b> , 28, 976-82  | 7.2  | 50        |
| 50 | SLiMPrints: conservation-based discovery of functional motif fingerprints in intrinsically disordered protein regions. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, 10628-41        | 20.1 | 57        |
| 49 | Uncovering new aspects of protein interactions through analysis of specificity landscapes in peptide recognition domains. <i>FEBS Letters</i> , <b>2012</b> , 586, 2764-72               | 3.8  | 11        |
| 48 | Efficient algorithms for biological stems search. <i>BMC Bioinformatics</i> , <b>2013</b> , 14, 161  | 3.6  | 2         |
| 47 | Variable-Length Protein Sequence Motif Extraction Using Hierarchically-Clustered Hidden Markov Models. <b>2013</b> ,   |      |           |
| 46 | Exploring the binding diversity of intrinsically disordered proteins involved in one-to-many binding. <i>Protein Science</i> , <b>2013</b> , 22, 258-73                                  | 6.3  | 132       |
| 45 | A model based on minimotifs for classification of stable protein-protein complexes. <b>2014</b> ,  |      | 1         |
| 44 | What's that gene (or protein)? Online resources for exploring functions of genes, transcripts, and proteins. <i>Molecular Biology of the Cell</i> , <b>2014</b> , 25, 1187-201           | 3.5  | 10        |
| 43 | Predicting protein-ligand and protein-peptide interfaces. <i>European Physical Journal Plus</i> , <b>2014</b> , 129, 1   | 3.1  | 4         |
| 42 | Classification of intrinsically disordered regions and proteins. <i>Chemical Reviews</i> , <b>2014</b> , 114, 6589-631   | 68.1 | 1141      |
| 41 | Intrinsically disordered proteins and intrinsically disordered protein regions. <i>Annual Review of Biochemistry</i> , <b>2014</b> , 83, 553-84  | 29.1 | 584       |
| 40 | Mass spectrometry-driven phosphoproteomics: patterning the systems biology mosaic. <i>Wiley Interdisciplinary Reviews: Developmental Biology</i> , <b>2014</b> , 3, 83-112               | 5.9  | 56        |
| 39 | Short linear motifs: ubiquitous and functionally diverse protein interaction modules directing cell regulation. <i>Chemical Reviews</i> , <b>2014</b> , 114, 6733-78                     | 68.1 | 254       |
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| 37 | Conserved Functional Motifs and Homology Modeling to Predict Hidden Moonlighting Functional Sites. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2015</b> , 3, 82            | 5.8  | 44        |
| 36 | An Efficient Exact Algorithm for the Motif Stem Search Problem over Large Alphabets. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2015</b> , 12, 384-97 | 3    | 12        |
| 35 | Natural variability of minimotifs in 1092 people indicates that minimotifs are targets of evolution. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, 6399-412                          | 20.1 | 6         |

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| 33 | The minimotif synthesis hypothesis for the origin of life. <i>Journal of Translational Science</i> , <b>2016</b> , 2, 289-296.2   |      | 6  |
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| 31 | Bioinformatics Approaches to the Structure and Function of Intrinsically Disordered Proteins. <b>2017</b> , 167-203   |      | 2  |
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| 27 | SLiMSearch: a framework for proteome-wide discovery and annotation of functional modules in intrinsically disordered regions. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, W464-W469   | 20.1 | 54 |
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| 23 | Minimotif Miner 4: a million peptide minimotifs and counting. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D465-D470.1   | 20.1 | 9  |
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| 19 | Human Cytomegalovirus UL135 Interacts with Host Adaptor Proteins To Regulate Epidermal Growth Factor Receptor and Reactivation from Latency. <i>Journal of Virology</i> , <b>2018</b> , 92,   | 6.6  | 20 |
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| 16 | Computational Investigation of Structural Interfaces of Protein Complexes with Short Linear Motifs. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 3254-3263  | 5.6 | 1  |
| 15 | IDPs and their complexes in GPCR and nuclear receptor signaling. <i>Progress in Molecular Biology and Translational Science</i> , <b>2020</b> , 174, 105-155   | 4   | 3  |
| 14 | Unique and exclusive peptide signatures directly identify intrinsically disordered proteins from sequences without structural information. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2021</b> , 39, 2885-2893 | 3.6 | 3  |
| 13 | Pathogen Moonlighting Proteins: From Ancestral Key Metabolic Enzymes to Virulence Factors. <i>Microorganisms</i> , <b>2021</b> , 9,  | 4.9 | 3  |
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| 4  | Computational Investigation Of Structural Interfaces Of Protein Complexes With Short Linear Motifs.  |     |    |
| 3  | MotSASI: Functional short linear motifs (SLiMs) prediction based on genomic single nucleotide variants and structural data.. <i>Biochimie</i> , <b>2022</b> , 197, 59-73   | 4.6 | 0  |
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