# Sébastien Moretti

## List of Publications by Year
## in descending order

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|---|---|---|---|
| **26**<br>papers | **4,785**<br>citations | 361045<br>**20**<br>h-index | 580395<br>**25**<br>g-index |
| **30**<br>all docs | **30**<br>docs citations | **30**<br>times ranked | **10008**<br>citing authors |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 1 | Ni2+-Assisted Hydrolysis May Affect the Human Proteome; Filaggrin Degradation Ex Vivo as an Example of Possible Consequences. Frontiers in Molecular Biosciences, 2022, 9, 828674. | 1.6 | 1 |
| 2 | The Bgee suite: integrated curated expression atlas and comparative transcriptomics in animals. Nucleic Acids Research, 2021, 49, D831-D847. | 6.5 | 112 |
| 3 | MetaNetX/MNXref: unified namespace for metabolites and biochemical reactions in the context of metabolic models. Nucleic Acids Research, 2021, 49, D570-D574. | 6.5 | 91 |
| 4 | Condition-specific series of metabolic sub-networks and its application for gene set enrichment analysis. Bioinformatics, 2019, 35, 2258-2266. | 1.8 | 12 |
| 5 | Updates in Rhea â€" an expert curated resource of biochemical reactions. Nucleic Acids Research, 2017, 45, D415-D418. | 6.5 | 56 |
| 6 | MetaNetX/MNXref â€" reconciliation of metabolites and biochemical reactions to bring together genome-scale metabolic networks. Nucleic Acids Research, 2016, 44, D523-D526. | 6.5 | 160 |
| 7 | Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47. | 6.5 | 113 |
| 8 | The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37. | 6.5 | 64 |
| 9 | Patterns of Positive Selection in Seven Ant Genomes. Molecular Biology and Evolution, 2014, 31, 1661-1685. | 3.5 | 138 |
| 10 | Selectome update: quality control and computational improvements to a database of positive selection. Nucleic Acids Research, 2014, 42, D917-D921. | 6.5 | 65 |
| 11 | Reconciliation of metabolites and biochemical reactions for metabolic networks. Briefings in Bioinformatics, 2014, 15, 123-135. | 3.2 | 64 |
| 12 | The Hourglass and the Early Conservation Modelsâ€"Co-Existing Patterns of Developmental Constraints in Vertebrates. PLoS Genetics, 2013, 9, e1003476. | 1.5 | 73 |
| 13 | MetaNetX.org: a website and repository for accessing, analysing and manipulating metabolic networks. Bioinformatics, 2013, 29, 815-816. | 1.8 | 120 |
| 14 | Developmental and Environmental Regulation of Aquaporin Gene Expression across Populus Species: Divergence or Redundancy?. PLoS ONE, 2013, 8, e55506. | 1.1 | 32 |
| 15 | ExPASy: SIB bioinformatics resource portal. Nucleic Acids Research, 2012, 40, W597-W603. | 6.5 | 1,737 |
| 16 | gcodeml: a Grid-enabled tool for detecting positive selection in biological evolution. Studies in Health Technology and Informatics, 2012, 175, 59-68. | 0.2 | 5 |
| 17 | T-Coffee: a web server for the multiple sequence alignment of protein and RNA sequences using structural information and homology extension. Nucleic Acids Research, 2011, 39, W13-W17. | 6.5 | 982 |
| 18 | Selectome: a database of positive selection. Nucleic Acids Research, 2009, 37, D404-D407. | 6.5 | 38 |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 19 | R-Coffee: a web server for accurately aligning noncoding RNA sequences. Nucleic Acids Research, 2008, 36, W10-W13. | 6.5 | 53 |
| 20 | Bgee: Integrating and Comparing Heterogeneous Transcriptome Data Among Species. Lecture Notes in Computer Science, 2008, , 124-131. | 1.0 | 137 |
| 21 | The M-Coffee web server: a meta-method for computing multiple sequence alignments by combining alternative alignment methods. Nucleic Acids Research, 2007, 35, W645-W648. | 6.5 | 209 |
| 22 | Expresso: automatic incorporation of structural information in multiple sequence alignments using 3D-Coffee. Nucleic Acids Research, 2006, 34, W604-W608. | 6.5 | 448 |
| 23 | PROTOGENE: turning amino acid alignments into bona fide CDS nucleotide alignments. Nucleic Acids Research, 2006, 34, W600-W603. | 6.5 | 13 |
| 24 | APDB: a web server to evaluate the accuracy of sequence alignments using structural information. Bioinformatics, 2006, 22, 2439-2440. | 1.8 | 1 |
| 25 | The iRMSD: a local measure of sequence alignment accuracy using structural information. Bioinformatics, 2006, 22, e35-e39. | 1.8 | 34 |
| 26 | Comparative analysis of early embryonic sunflower cDNA libraries. Plant Molecular Biology, 2005, 57, 255-270. | 2.0 | 18 |