# Sayed-Amir Marashi

List of Publications by Year
in descending order

| 82 papers | 982 citations | 471371 17 h-index | 610775 24 g-index |
|---|---|---|---|
| 89 all docs | 89 docs citations | 89 times ranked | 1261 citing authors |

| # | ARTICLE | IF | CITATIONS |
|---|---------|-----|-----------|
| 1 | Conformational Study of Human Serum Albumin in Pre-denaturation Temperatures by Differential Scanning Calorimetry, Circular Dichroism and UV Spectroscopy. BMB Reports, 2006, 39, 530-536. | 1.1 | 67 |
| 2 | Impact of residue accessible surface area on the prediction of protein secondary structures. BMC Bioinformatics, 2008, 9, 357. | 1.2 | 38 |
| 3 | A metabolic network-based approach for developing feeding strategies for CHO cells to increase monoclonal antibody production. Bioprocess and Biosystems Engineering, 2020, 43, 1381-1389. | 1.7 | 36 |
| 4 | A sperm-specific proteome-scale metabolic network model identifies non-glycolytic genes for energy deficiency in asthenozoospermia. Systems Biology in Reproductive Medicine, 2017, 63, 100-112. | 1.0 | 32 |
| 5 | Correlations between genomic GC levels and optimal growth temperatures are not â€˜robustâ€™. Biochemical and Biophysical Research Communications, 2004, 325, 381-383. | 1.0 | 31 |
| 6 | Biomedical applications of cell- and tissue-specific metabolic network models. Journal of Biomedical Informatics, 2017, 68, 35-49. | 2.5 | 29 |
| 7 | Î²-Sheet capping: Signals that initiate and terminate Î²-sheet formation. Journal of Structural Biology, 2008, 161, 101-110. | 1.3 | 28 |
| 8 | Analysis of Metabolic Subnetworks by Flux Cone Projection. Algorithms for Molecular Biology, 2012, 7, 17. | 0.3 | 28 |
| 9 | Rps27a might act as a controller of microglia activation in triggering neurodegenerative diseases. PLoS ONE, 2020, 15, e0239219. | 1.1 | 27 |
| 10 | Binding of Tris to Bacillus licheniformis &amp;#945;-Amylase Can Affect Its Starch Hydrolysis Activity. Protein and Peptide Letters, 2008, 15, 212-214. | 0.4 | 26 |
| 11 | FFCA: a feasibility-based method for flux coupling analysis of metabolic networks. BMC Bioinformatics, 2011, 12, 236. | 1.2 | 24 |
| 12 | Nanotechnology helps medicine: Nanoscale swimmers and their future applications. Medical Hypotheses, 2005, 65, 198-199. | 0.8 | 22 |
| 13 | Flux coupling analysis of metabolic networks is sensitive to missing reactions. BioSystems, 2011, 103, 57-66. | 0.9 | 22 |
| 14 | A meta-analysis of gene expression data highlights synaptic dysfunction in the hippocampus of brains with Alzheimerâ€™s disease. Scientific Reports, 2020, 10, 8384. | 1.6 | 22 |
| 15 | Manually curated genome-scale reconstruction of the metabolic network of Bacillus megaterium DSM319. Scientific Reports, 2019, 9, 18762. | 1.6 | 21 |
| 16 | Reconstruction of a generic metabolic network model of cancer cells. Molecular BioSystems, 2014, 10, 3014-3021. | 2.9 | 20 |
| 17 | A Systems-Based Approach for Cyanide Overproduction by Bacillus megaterium for Gold Bioleaching Enhancement. Frontiers in Bioengineering and Biotechnology, 2020, 8, 528. | 2.0 | 19 |
| 18 | Importance of RNA secondary structure information for yeast donor and acceptor splice site predictions by neural networks. Computational Biology and Chemistry, 2006, 30, 50-57. | 1.1 | 18 |

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|---|---------|----|-----------|
| 19 | Impact of RNA structure on the prediction of donor and acceptor splice sites. BMC Bioinformatics, 2006, 7, 297. | 1.2 | 18 |
| 20 | A tale of two symmetrical tails: Structural and functional characteristics of palindromes in proteins. BMC Bioinformatics, 2008, 9, 274. | 1.2 | 18 |
| 21 | Finding elementary flux modes in metabolic networks based on flux balance analysis and flux coupling analysis: application to the analysis of Escherichia coli metabolism. Biotechnology Letters, 2013, 35, 2039-2044. | 1.1 | 18 |
| 22 | Reconstruction and validation of a constraint€based metabolic network model for bone marrow€derived mesenchymal stem cells. Cell Proliferation, 2015, 48, 475-485. | 2.4 | 17 |
| 23 | Acetic acid uptake rate controls H2 production in Chlamydomonas-bacteria co-cultures. Algal Research, 2019, 42, 101605. | 2.4 | 17 |
| 24 | A multiscale agent-based framework integrated with a constraint-based metabolic network model of cancer for simulating avascular tumor growth. Molecular BioSystems, 2017, 13, 1888-1897. | 2.9 | 16 |
| 25 | Evolutionarily conserved motifs and modules in mitochondrial protein€"protein interaction networks. Mitochondrion, 2013, 13, 668-675. | 1.6 | 15 |
| 26 | Modeling the Differences in Biochemical Capabilities ofPseudomonasSpecies by Flux Balance Analysis: How Good Are Genome-Scale Metabolic Networks at Predicting the Differences?. Scientific World Journal, The, 2014, 2014, 1-11. | 0.8 | 15 |
| 27 | A kidney-specific genome-scale metabolic network model for analyzing focal segmental glomerulosclerosis. Mammalian Genome, 2016, 27, 158-167. | 1.0 | 15 |
| 28 | A reconciliation of genome-scale metabolic network model of Zymomonas mobilis ZM4. Scientific Reports, 2020, 10, 7782. | 1.6 | 15 |
| 29 | PCD-GED: Protein complex detection considering PPI dynamics based on time series gene expression data. Journal of Theoretical Biology, 2015, 378, 31-38. | 0.8 | 14 |
| 30 | Genome-scale reconstruction of the metabolic network in Pseudomonas stutzeri A1501. Molecular BioSystems, 2015, 11, 3022-3032. | 2.9 | 13 |
| 31 | Cancer driver gene discovery in transcriptional regulatory networks using influence maximization approach. Computers in Biology and Medicine, 2019, 114, 103362. | 3.9 | 13 |
| 32 | Three-way interaction model to trace the mechanisms involved in Alzheimer€™s disease transgenic mice. PLoS ONE, 2017, 12, e0184697. | 1.1 | 13 |
| 33 | Impact of hfq and sigE on the tolerance of Zymomonas mobilis ZM4 to furfural and acetic acid stresses. PLoS ONE, 2020, 15, e0240330. | 1.1 | 13 |
| 34 | On flux coupling analysis of metabolic subsystems. Journal of Theoretical Biology, 2012, 302, 62-69. | 0.8 | 12 |
| 35 | Exploring biological processes involved in embryonic stem cell differentiation by analyzing proteomic data. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2013, 1834, 1063-1069. | 1.1 | 12 |
| 36 | NDDSA: A network- and domain-based method for predicting drug-side effect associations. Information Processing and Management, 2020, 57, 102357. | 5.4 | 12 |

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| 37 | A mathematical approach to emergent properties of metabolic networks: Partial coupling relations, hyperarcs and flux ratios. Journal of Theoretical Biology, 2014, 355, 185-193. | 0.8 | 11 |
| 38 | Discovering missing reactions of metabolic networks by using gene co-expression data. Scientific Reports, 2017, 7, 41774. | 1.6 | 11 |
| 39 | How reliable re-adjustment is: correspondence regarding A. Fuglsang, â€œThe â€˜effective number of codonsâ€™ revisitedâ€. Biochemical and Biophysical Research Communications, 2004, 324, 1-2. | 1.0 | 10 |
| 40 | On the identity of â€œcitersâ€: Are papers promptly recognized by other investigators?. Medical Hypotheses, 2005, 65, 822. | 0.8 | 10 |
| 41 | CAMWI: Detecting protein complexes using weighted clustering coefficient and weighted density. Computational Biology and Chemistry, 2015, 58, 231-240. | 1.1 | 10 |
| 42 | Systematically gap-filling the genome-scale metabolic model of CHO cells. Biotechnology Letters, 2021, 43, 73-87. | 1.1 | 10 |
| 43 | On the mechanism of apoptosis-inducing activity of human calprotectin: Zinc sequestration, induction of a signaling pathway, or something else?. Medical Hypotheses, 2007, 68, 1012-1015. | 0.8 | 9 |
| 44 | Adaptation of proteins to different environments: A comparison of proteome structural properties in Bacillus subtilis and Escherichia coli. Journal of Theoretical Biology, 2007, 244, 127-132. | 0.8 | 9 |
| 45 | Applications of a metabolic network model of mesenchymal stem cells for controlling cell proliferation and differentiation. Cytotechnology, 2018, 70, 331-338. | 0.7 | 9 |
| 46 | Modeling directed ligand passage toward enzyme active site by a â€˜double cellular automataâ€™ model. Biochemical and Biophysical Research Communications, 2005, 333, 1-4. | 1.0 | 8 |
| 47 | A graph-based approach to analyze flux-balanced pathways in metabolic networks. BioSystems, 2018, 165, 40-51. | 0.9 | 8 |
| 48 | *In silico* prediction of enzymatic reactions catalyzed by acid phosphatases. Journal of Biomolecular Structure and Dynamics, 2021, 39, 3900-3911. | 2.0 | 8 |
| 49 | A genome-scale metabolic network reconstruction of extremely halophilic bacterium Salinibacter ruber. PLoS ONE, 2019, 14, e0216336. | 1.1 | 7 |
| 50 | Why major nonenzymatic glycation sites of human serum albumin are preferred to other residues?. Medical Hypotheses, 2005, 64, 881. | 0.8 | 6 |
| 51 | Hierarchical organization of fluxes in Escherichia coli metabolic network: Using flux coupling analysis for understanding the physiological properties of metabolic genes. Gene, 2015, 561, 199-208. | 1.0 | 6 |
| 52 | The metabolic network model of primed/naive human embryonic stem cells underlines the importance of oxidation-reduction potential and tryptophan metabolism in primed pluripotency. Cell and Bioscience, 2019, 9, 71. | 2.1 | 6 |
| 53 | Beyond Taxonomic Analysis of Microbiomes: A Functional Approach for Revisiting Microbiome Changes in Colorectal Cancer. Frontiers in Microbiology, 2019, 10, 3117. | 1.5 | 6 |
| 54 | EIA-CNDP: An exact iterative algorithm for critical node detection problem. Computers and Operations Research, 2021, 127, 105138. | 2.4 | 6 |

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|---|---------|----|-----------|
| 55 | In silico prediction of specific pathways that regulate mesangial cell proliferation in IgA nephropathy. Medical Hypotheses, 2016, 97, 38-45. | 0.8 | 5 |
| 56 | Three-way interaction model with switching mechanism as an effective strategy for tracing functionally-related genes. Expert Review of Proteomics, 2019, 16, 161-169. | 1.3 | 5 |
| 57 | Impact of Wikipedia on citation trends. EXCLI Journal, 2013, 12, 15-9. | 0.5 | 5 |
| 58 | CAMAMED: a pipeline for composition-aware mapping-based analysis of metagenomic data. NAR Genomics and Bioinformatics, 2021, 3, lqaa107. | 1.5 | 4 |
| 59 | Genome-Scale Metabolic Network Models of Bacillus Species Suggest that Model Improvement is Necessary for Biotechnological Applications. Iranian Journal of Biotechnology, 2018, 16, 164-172. | 0.3 | 4 |
| 60 | Structural systems pharmacology: A framework for integrating metabolic network and structure-based virtual screening for drug discovery against bacteria. PLoS ONE, 2021, 16, e0261267. | 1.1 | 4 |
| 61 | Studying the Relationship between Robustness against Mutations in Metabolic Networks and Lifestyle of Organisms. Scientific World Journal, The, 2013, 2013, 1-6. | 0.8 | 3 |
| 62 | A network biology approach to understanding the importance of chameleon proteins in human physiology and pathology. Amino Acids, 2017, 49, 303-315. | 1.2 | 3 |
| 63 | Evolution of 'Ligand-Diffusion Chreodes' on Protein-Surface Models: A Genetic-Algorithm Study. Chemistry and Biodiversity, 2007, 4, 2766-2771. | 1.0 | 2 |
| 64 | FCDECOMP: Decomposition of metabolic networks based on flux coupling relations. Journal of Bioinformatics and Computational Biology, 2014, 12, 1450028. | 0.3 | 2 |
| 65 | Can scientific journals be classified based on their 'citation profiles'?. South African Journal of Science, 2015, 111, 1-3. | 0.3 | 2 |
| 66 | Evidence for the relationship between the regulatory effects of microRNAs and attack robustness of biological networks. Computers in Biology and Medicine, 2015, 63, 83-91. | 3.9 | 2 |
| 67 | On correlated reaction sets and coupled reaction sets in metabolic networks. Journal of Bioinformatics and Computational Biology, 2015, 13, 1571003. | 0.3 | 2 |
| 68 | Glucose Metabolism: Optimizing Regenerative Functionalities of Mesenchymal Stromal Cells Postimplantation. Tissue Engineering - Part B: Reviews, 2023, 29, 47-61. | 2.5 | 2 |
| 69 | Application of $\beta$-lactamase-dependent prodrugs in clostridial-directed enzyme therapy (CDEPT): A proposal. Medical Hypotheses, 2006, 67, 998-999. | 0.8 | 1 |
| 70 | Reconstruction of phylogenetic trees of prokaryotes using maximal common intervals. BioSystems, 2014, 124, 86-94. | 0.9 | 1 |
| 71 | Genome-Scale Metabolic Network Models of Bacillus Species Suggest that Model Improvement is Necessary for Biotechnological Applications. Iranian Journal of Biotechnology, 2018, 16, e1684. | 0.3 | 1 |
| 72 | A Constraint-based modeling approach to reach an improved chemically defined minimal medium for recombinant antiEpEX-scFv production by Escherichia coli. Biochemical Engineering Journal, 2022, 179, 108339. | 1.8 | 1 |

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| 73 | Critical assessment of genome-scale metabolic models of Arabidopsis thaliana. Molecular Omics, 2022, , . | 1.4 | 1 |
| 74 | Accounting for robustness in modeling signal transduction responses. Journal of Receptor and Signal Transduction Research, 2018, 38, 442-447. | 1.3 | 0 |
| 75 | A system architecture for parallel analysis of flux-balanced metabolic pathways. Computational Biology and Chemistry, 2020, 88, 107309. | 1.1 | 0 |
| 76 | Regulation of photosynthesis and vegetative growth of plants by small RNAs. , 2020, , 247-275. | | 0 |
| 77 | Title is missing!. , 2020, 15, e0240330. | | 0 |
| 78 | Title is missing!. , 2020, 15, e0240330. | | 0 |
| 79 | Title is missing!. , 2020, 15, e0240330. | | 0 |
| 80 | Title is missing!. , 2020, 15, e0240330. | | 0 |
| 81 | Title is missing!. , 2020, 15, e0240330. | | 0 |
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