

# Sayed-Amir Marashi

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

82

papers

660

citations

14

h-index

20

g-index

89

ext. papers

811

ext. citations

3.7

avg, IF

4.39

L-index

#	Paper	IF	Citations
82	A Constraint-based modeling approach to reach an improved chemically defined minimal medium for recombinant antiEpEX-scFv production by Escherichia coli. <i>Biochemical Engineering Journal</i> , <b>2022</b> , 179, 108339	4.2	0
81	prediction of enzymatic reactions catalyzed by acid phosphatases. <i>Journal of Biomolecular Structure and Dynamics</i> , <b>2021</b> , 39, 3900-3911	3.6	3
80	Systematically gap-filling the genome-scale metabolic model of CHO cells. <i>Biotechnology Letters</i> , <b>2021</b> , 43, 73-87	3	5
79	EIA-CNDP: An exact iterative algorithm for critical node detection problem. <i>Computers and Operations Research</i> , <b>2021</b> , 127, 105138	4.6	3
78	CAMAMED: a pipeline for composition-aware mapping-based analysis of metagenomic data. <i>NAR Genomics and Bioinformatics</i> , <b>2021</b> , 3, lqaa107	3.7	2
77	Structural systems pharmacology: A framework for integrating metabolic network and structure-based virtual screening for drug discovery against bacteria.. <i>PLoS ONE</i> , <b>2021</b> , 16, e0261267	3.7	
76	A reconciliation of genome-scale metabolic network model of Zymomonas mobilis ZM4. <i>Scientific Reports</i> , <b>2020</b> , 10, 7782	4.9	5
75	A Systems-Based Approach for Cyanide Overproduction by for Gold Bioleaching Enhancement. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2020</b> , 8, 528	5.8	11
74	Regulation of photosynthesis and vegetative growth of plants by small RNAs <b>2020</b> , 247-275		
73	A metabolic network-based approach for developing feeding strategies for CHO cells to increase monoclonal antibody production. <i>Bioprocess and Biosystems Engineering</i> , <b>2020</b> , 43, 1381-1389	3.7	17
72	Impact of hfq and sigE on the tolerance of Zymomonas mobilis ZM4 to furfural and acetic acid stresses. <i>PLoS ONE</i> , <b>2020</b> , 15, e0240330	3.7	7
71	A meta-analysis of gene expression data highlights synaptic dysfunction in the hippocampus of brains with Alzheimer's disease. <i>Scientific Reports</i> , <b>2020</b> , 10, 8384	4.9	9
70	A system architecture for parallel analysis of flux-balanced metabolic pathways. <i>Computational Biology and Chemistry</i> , <b>2020</b> , 88, 107309	3.6	
69	NDDSA: A network- and domain-based method for predicting drug-side effect associations. <i>Information Processing and Management</i> , <b>2020</b> , 57, 102357	6.3	1
68	Rps27a might act as a controller of microglia activation in triggering neurodegenerative diseases. <i>PLoS ONE</i> , <b>2020</b> , 15, e0239219	3.7	8
67	Impact of hfq and sigE on the tolerance of Zymomonas mobilis ZM4 to furfural and acetic acid stresses <b>2020</b> , 15, e0240330		
66	Impact of hfq and sigE on the tolerance of Zymomonas mobilis ZM4 to furfural and acetic acid stresses <b>2020</b> , 15, e0240330		

65	Impact of hfq and sigE on the tolerance of <i>Zymomonas mobilis</i> ZM4 to furfural and acetic acid stresses <b>2020</b> , 15, e0240330		
64	Impact of hfq and sigE on the tolerance of <i>Zymomonas mobilis</i> ZM4 to furfural and acetic acid stresses <b>2020</b> , 15, e0240330		
63	Impact of hfq and sigE on the tolerance of <i>Zymomonas mobilis</i> ZM4 to furfural and acetic acid stresses <b>2020</b> , 15, e0240330		
62	Impact of hfq and sigE on the tolerance of <i>Zymomonas mobilis</i> ZM4 to furfural and acetic acid stresses <b>2020</b> , 15, e0240330		
61	The metabolic network model of primed/naive human embryonic stem cells underlines the importance of oxidation-reduction potential and tryptophan metabolism in primed pluripotency. <i>Cell and Bioscience</i> , <b>2019</b> , 9, 71	9.8	3
60	A genome-scale metabolic network reconstruction of extremely halophilic bacterium <i>Salinibacter ruber</i> . <i>PLoS ONE</i> , <b>2019</b> , 14, e0216336	3.7	2
59	Beyond Taxonomic Analysis of Microbiomes: A Functional Approach for Revisiting Microbiome Changes in Colorectal Cancer. <i>Frontiers in Microbiology</i> , <b>2019</b> , 10, 3117	5.7	3
58	Acetic acid uptake rate controls H <sub>2</sub> production in <i>Chlamydomonas</i> -bacteria co-cultures. <i>Algal Research</i> , <b>2019</b> , 42, 101605	5	10
57	Cancer driver gene discovery in transcriptional regulatory networks using influence maximization approach. <i>Computers in Biology and Medicine</i> , <b>2019</b> , 114, 103362	7	6
56	Manually curated genome-scale reconstruction of the metabolic network of <i>Bacillus megaterium</i> DSM319. <i>Scientific Reports</i> , <b>2019</b> , 9, 18762	4.9	6
55	Three-way interaction model with switching mechanism as an effective strategy for tracing functionally-related genes. <i>Expert Review of Proteomics</i> , <b>2019</b> , 16, 161-169	4.2	4
54	A graph-based approach to analyze flux-balanced pathways in metabolic networks. <i>BioSystems</i> , <b>2018</b> , 165, 40-51	1.9	6
53	Applications of a metabolic network model of mesenchymal stem cells for controlling cell proliferation and differentiation. <i>Cytotechnology</i> , <b>2018</b> , 70, 331-338	2.2	7
52	Genome-Scale Metabolic Network Models of <i>Bacillus</i> Species Suggest that Model Improvement is Necessary for Biotechnological Applications. <i>Iranian Journal of Biotechnology</i> , <b>2018</b> , 16, e1684	1	1
51	Genome-Scale Metabolic Network Models of <i>Bacillus</i> Species Suggest that Model Improvement is Necessary for Biotechnological Applications. <i>Iranian Journal of Biotechnology</i> , <b>2018</b> , 16, 164-172	1	2
50	Accounting for robustness in modeling signal transduction responses. <i>Journal of Receptor and Signal Transduction Research</i> , <b>2018</b> , 38, 442-447	2.6	
49	A sperm-specific proteome-scale metabolic network model identifies non-glycolytic genes for energy deficiency in asthenozoospermia. <i>Systems Biology in Reproductive Medicine</i> , <b>2017</b> , 63, 100-112	2.9	21
48	Biomedical applications of cell- and tissue-specific metabolic network models. <i>Journal of Biomedical Informatics</i> , <b>2017</b> , 68, 35-49	10.2	24

47	Discovering missing reactions of metabolic networks by using gene co-expression data. <i>Scientific Reports</i> , <b>2017</b> , 7, 41774	4.9	9
46	A multiscale agent-based framework integrated with a constraint-based metabolic network model of cancer for simulating avascular tumor growth. <i>Molecular BioSystems</i> , <b>2017</b> , 13, 1888-1897		11
45	A network biology approach to understanding the importance of chameleon proteins in human physiology and pathology. <i>Amino Acids</i> , <b>2017</b> , 49, 303-315	3.5	2
44	Three-way interaction model to trace the mechanisms involved in Alzheimer's disease transgenic mice. <i>PLoS ONE</i> , <b>2017</b> , 12, e0184697	3.7	8
43	In silico prediction of specific pathways that regulate mesangial cell proliferation in IgA nephropathy. <i>Medical Hypotheses</i> , <b>2016</b> , 97, 38-45	3.8	4
42	A kidney-specific genome-scale metabolic network model for analyzing focal segmental glomerulosclerosis. <i>Mammalian Genome</i> , <b>2016</b> , 27, 158-67	3.2	9
41	On correlated reaction sets and coupled reaction sets in metabolic networks. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2015</b> , 13, 1571003	1	1
40	PCD-GED: Protein complex detection considering PPI dynamics based on time series gene expression data. <i>Journal of Theoretical Biology</i> , <b>2015</b> , 378, 31-8	2.3	12
39	Genome-scale reconstruction of the metabolic network in <i>Pseudomonas stutzeri</i> A1501. <i>Molecular BioSystems</i> , <b>2015</b> , 11, 3022-32		10
38	Reconstruction and validation of a constraint-based metabolic network model for bone marrow-derived mesenchymal stem cells. <i>Cell Proliferation</i> , <b>2015</b> , 48, 475-85	7.9	12
37	CAMWI: Detecting protein complexes using weighted clustering coefficient and weighted density. <i>Computational Biology and Chemistry</i> , <b>2015</b> , 58, 231-40	3.6	8
36	Can scientific journals be classified based on their citation profiles? <i>South African Journal of Science</i> , <b>2015</b> , 111,	1.3	1
35	Evidence for the relationship between the regulatory effects of microRNAs and attack robustness of biological networks. <i>Computers in Biology and Medicine</i> , <b>2015</b> , 63, 83-91	7	2
34	Hierarchical organization of fluxes in <i>Escherichia coli</i> metabolic network: using flux coupling analysis for understanding the physiological properties of metabolic genes. <i>Gene</i> , <b>2015</b> , 561, 199-208	3.8	5
33	FCDECOMP: decomposition of metabolic networks based on flux coupling relations. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2014</b> , 12, 1450028	1	1
32	Reconstruction of a generic metabolic network model of cancer cells. <i>Molecular BioSystems</i> , <b>2014</b> , 10, 3014-21		16
31	Reconstruction of phylogenetic trees of prokaryotes using maximal common intervals. <i>BioSystems</i> , <b>2014</b> , 124, 86-94	1.9	1
30	A mathematical approach to emergent properties of metabolic networks: partial coupling relations, hyperarcs and flux ratios. <i>Journal of Theoretical Biology</i> , <b>2014</b> , 355, 185-93	2.3	9

29	Modeling the differences in biochemical capabilities of pseudomonas species by flux balance analysis: how good are genome-scale metabolic networks at predicting the differences?. <i>Scientific World Journal, The</i> , <b>2014</b> , 2014, 416289	2.2	9
28	Evolutionarily conserved motifs and modules in mitochondrial protein-protein interaction networks. <i>Mitochondrion</i> , <b>2013</b> , 13, 668-75	4.9	11
27	Finding elementary flux modes in metabolic networks based on flux balance analysis and flux coupling analysis: application to the analysis of Escherichia coli metabolism. <i>Biotechnology Letters</i> , <b>2013</b> , 35, 2039-44	3	13
26	Exploring biological processes involved in embryonic stem cell differentiation by analyzing proteomic data. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2013</b> , 1834, 1063-9	4	12
25	Studying the relationship between robustness against mutations in metabolic networks and lifestyle of organisms. <i>Scientific World Journal, The</i> , <b>2013</b> , 2013, 615697	2.2	3
24	Impact of Wikipedia on citation trends. <i>EXCLI Journal</i> , <b>2013</b> , 12, 15-9	2.4	4
23	On flux coupling analysis of metabolic subsystems. <i>Journal of Theoretical Biology</i> , <b>2012</b> , 302, 62-9	2.3	9
22	Analysis of metabolic subnetworks by flux cone projection. <i>Algorithms for Molecular Biology</i> , <b>2012</b> , 7, 17	1.8	20
21	FFCA: a feasibility-based method for flux coupling analysis of metabolic networks. <i>BMC Bioinformatics</i> , <b>2011</b> , 12, 236	3.6	19
20	Flux coupling analysis of metabolic networks is sensitive to missing reactions. <i>BioSystems</i> , <b>2011</b> , 103, 57-66	1.9	16
19	A tale of two symmetrical tails: structural and functional characteristics of palindromes in proteins. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 274	3.6	15
18	Impact of residue accessible surface area on the prediction of protein secondary structures. <i>BMC Bioinformatics</i> , <b>2008</b> , 9, 357	3.6	25
17	Beta-sheet capping: signals that initiate and terminate beta-sheet formation. <i>Journal of Structural Biology</i> , <b>2008</b> , 161, 101-10	3.4	24
16	Binding of Tris to Bacillus licheniformis alpha-amylase can affect its starch hydrolysis activity. <i>Protein and Peptide Letters</i> , <b>2008</b> , 15, 212-4	1.9	22
15	Evolution of 'ligand-diffusion chreodes' on protein-surface models: a genetic-algorithm study. <i>Chemistry and Biodiversity</i> , <b>2007</b> , 4, 2766-71	2.5	1
14	Adaptation of proteins to different environments: a comparison of proteome structural properties in Bacillus subtilis and Escherichia coli. <i>Journal of Theoretical Biology</i> , <b>2007</b> , 244, 127-32	2.3	8
13	On the mechanism of apoptosis-inducing activity of human calprotectin: zinc sequestration, induction of a signaling pathway, or something else?. <i>Medical Hypotheses</i> , <b>2007</b> , 68, 1012-5	3.8	8
12	Impact of RNA structure on the prediction of donor and acceptor splice sites. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 297	3.6	13

11	Application of beta-lactamase-dependent prodrugs in clostridial-directed enzyme therapy (CDEPT): a proposal. <i>Medical Hypotheses</i> , <b>2006</b> , 67, 998-9	3.8	0
10	Importance of RNA secondary structure information for yeast donor and acceptor splice site predictions by neural networks. <i>Computational Biology and Chemistry</i> , <b>2006</b> , 30, 50-7	3.6	11
9	Conformational study of human serum albumin in pre-denaturation temperatures by differential scanning calorimetry, circular dichroism and UV spectroscopy. <i>BMB Reports</i> , <b>2006</b> , 39, 530-6	5.5	56
8	Why major nonenzymatic glycation sites of human serum albumin are preferred to other residues?. <i>Medical Hypotheses</i> , <b>2005</b> , 64, 881	3.8	6
7	Nanotechnology helps medicine: nanoscale swimmers and their future applications. <i>Medical Hypotheses</i> , <b>2005</b> , 65, 198-9	3.8	17
6	On the identity of "citers": are papers promptly recognized by other investigators?. <i>Medical Hypotheses</i> , <b>2005</b> , 65, 822	3.8	7
5	Modeling directed ligand passage toward enzyme active site by a 'double cellular automata' model. <i>Biochemical and Biophysical Research Communications</i> , <b>2005</b> , 333, 1-4	3.4	7
4	How reliable re-adjustment is: correspondence regarding A. Fuglsang, "The 'effective number of codons' revisited". <i>Biochemical and Biophysical Research Communications</i> , <b>2004</b> , 324, 1-2	3.4	8
3	Correlations between genomic GC levels and optimal growth temperatures are not 'robust'. <i>Biochemical and Biophysical Research Communications</i> , <b>2004</b> , 325, 381-3	3.4	25
2	Systematically gap-filling the genome-scale metabolic model of CHO cells		2
1	A metabolic network-based approach for developing feeding strategies for CHO cells to increase monoclonal antibody production		2