Michael J E Sternberg

List of Publications by Year in Descending Order

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Version: 2024-04-20

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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.

62 papers	11,927 citations	27 h-index	82 g-index
82 ext. papers	14,838 ext. citations	10.2 avg, IF	6.91 L-index

#	Paper	IF	Citations
62	The AlphaFold Database of Protein Structures: A BiologistUs Guide. *Journal of Molecular Biology*, **2021**, 434, 167336	6.5	17
61	Missense3D-DB web catalogue: an atom-based analysis and repository of 4M human protein-coding genetic variants. *Human Genetics*, **2021**, 140, 805-812	6.3	7
60	A polygenic biomarker to identify patients with severe hypercholesterolemia of polygenic origin. *Molecular Genetics & Genomic Medicine*, **2020**, 8, e1248	2.3	2
59	Application of docking methodologies to modeled proteins. *Proteins: Structure, Function and Bioinformatics*, **2020**, 88, 1180-1188	4.2	4
58	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. *Methods in Molecular Biology*, **2020**, 2165, 27-67	1.4	1
57	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. *Nucleic Acids Research*, **2020**, 48, D314-D319	20.1	7
56	Identification of disease-associated loci using machine learning for genotype and network data integration. *Bioinformatics*, **2019**, 35, 5182-5190	7.2	7
55	Can Predicted Protein 3D Structures Provide Reliable Insights into whether Missense Variants Are Disease Associated?. *Journal of Molecular Biology*, **2019**, 431, 2197-2212	6.5	138
54	PhyreRisk: A Dynamic Web Application to Bridge Genomics, Proteomics and 3D Structural Data to Guide Interpretation of Human Genetic Variants. *Journal of Molecular Biology*, **2019**, 431, 2460-2466	6.5	13
53	Phylotranscriptomic Insights into the Diversification of Endothermic Thunnus Tunas. *Molecular Biology and Evolution*, **2019**, 36, 84-96	8.3	11
52	EzMol: A Web Server Wizard for the Rapid Visualization and Image Production of Protein and Nucleic Acid Structures. *Journal of Molecular Biology*, **2018**, 430, 2244-2248	6.5	82
51	PhenoRank: reducing study bias in gene prioritization through simulation. *Bioinformatics*, **2018**, 34, 2087-2095	7.2	15
50	Properties of human genes guided by their enrichment in rare and common variants. *Human Mutation*, **2018**, 39, 365-370	4.7	9
49	Structure-based prediction of protein allostery. *Current Opinion in Structural Biology*, **2018**, 50, 1-8	8.1	57
48	Thienopyrimidinone Based Sirtuin-2 (SIRT2)-Selective Inhibitors Bind in the Ligand Induced Selectivity Pocket. *Journal of Medicinal Chemistry*, **2017**, 60, 1928-1945	8.3	39
47	Predicting Protein Dynamics and Allostery Using Multi-Protein Atomic Distance Constraints. *Structure*, **2017**, 25, 546-558	5.2	31
46	Landscape of Pleiotropic Proteins Causing Human Disease: Structural and System Biology Insights. *Human Mutation*, **2017**, 38, 289-296	4.7	16

(2010-2017)

45	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. *Plant Cell*, **2017**, 29, 1806-1821	11.6	150
44	Analysis of the Small Molecule Content of Outer Membrane Vesicles Produced by Indicates an Extensive Metabolic Link between Microbe and Host. *Frontiers in Microbiology*, **2017**, 8, 2440	5.7	28
43	k-SLAM: accurate and ultra-fast taxonomic classification and gene identification for large metagenomic data sets. *Nucleic Acids Research*, **2017**, 45, 1649-1656	20.1	32
42	PhyreStorm: A Web Server for Fast Structural Searches Against the PDB. *Journal of Molecular Biology*, **2016**, 428, 702-708	6.5	9
41	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. *Genome Biology*, **2016**, 17, 184	18.3	218
40	The Contribution of Missense Mutations in Core and Rim Residues of Protein-Protein Interfaces to Human Disease. *Journal of Molecular Biology*, **2015**, 427, 2886-98	6.5	69
39	The Phyre2 web portal for protein modeling, prediction and analysis. *Nature Protocols*, **2015**, 10, 845-58	18.8	5622
38	AlloPred: prediction of allosteric pockets on proteins using normal mode perturbation analysis. *BMC Bioinformatics*, **2015**, 16, 335	3.6	55
37	Exploring the cellular basis of human disease through a large-scale mapping of deleterious genes to cell types. *Genome Medicine*, **2015**, 7, 95	14.4	9
36	Genome3D: exploiting structure to help users understand their sequences. *Nucleic Acids Research*, **2015**, 43, D382-6	20.1	33
35	Partial protein domains: evolutionary insights and bioinformatics challenges. *Genome Biology*, **2015**, 16, 100	18.3	9
34	A highly conserved program of neuronal microexons is misregulated in autistic brains. *Cell*, **2014**, 159, 1511-23	56.2	356
33	SuSPect: enhanced prediction of single amino acid variant (SAV) phenotype using network features. *Journal of Molecular Biology*, **2014**, 426, 2692-701	6.5	140
32	Gene function hypotheses for the Campylobacter jejuni glycome generated by a logic-based approach. *Journal of Molecular Biology*, **2013**, 425, 186-97	6.5	19
31	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. *Nucleic Acids Research*, **2013**, 41, D499-507	20.1	48
30	Does Multi-Clause Learning Help in Real-World Applications?. *Lecture Notes in Computer Science*, **2012**, 221-237	0.9	1
29	Variation of Background Knowledge in an Industrial Application of ILP. *Lecture Notes in Computer Science*, **2011**, 158-170	0.9	1
28	3DLigandSite: predicting ligand-binding sites using similar structures. *Nucleic Acids Research*, **2010**, 38, W469-73	20.1	456

27	Protein folding requires crowd control in a simulated cell. *Journal of Molecular Biology*, **2010**, 397, 1329-38	6.5	70
26	Protein structure prediction on the Web: a case study using the Phyre server. *Nature Protocols*, **2009**, 4, 363-71	18.8	3569
25	Including Functional Annotations and Extending the Collection of Structural Classifications of Protein Loops (ArchDB). *Bioinformatics and Biology Insights*, **2009**, 1, 77-90	5.3	1
24	Protein Fold Discovery Using Stochastic Logic Programs. *Lecture Notes in Computer Science*, **2008**, 244-262	0.9	
23	A general approach for developing system-specific functions to score protein-ligand docked complexes using support vector inductive logic programming. *Proteins: Structure, Function and Bioinformatics*, **2007**, 69, 823-31	4.2	25
22	Support vector inductive logic programming outperforms the naive Bayes classifier and inductive logic programming for the classification of bioactive chemical compounds. *Journal of Computer-Aided Molecular Design*, **2007**, 21, 269-80	4.2	31
21	The proteome: structure, function and evolution. *Philosophical Transactions of the Royal Society B: Biological Sciences*, **2006**, 361, 441-51	5.8	18
20	Multi-class Prediction Using Stochastic Logic Programs. *Lecture Notes in Computer Science*, **2006**, 109-124	0.9	1
19	Prediction of the conformation and geometry of loops in globular proteins: testing ArchDB, a structural classification of loops. *Proteins: Structure, Function and Bioinformatics*, **2005**, 60, 746-57	4.2	17
18	Support Vector Inductive Logic Programming. *Lecture Notes in Computer Science*, **2005**, 163-175	0.9	28
17	3D-GENOMICS: a database to compare structural and functional annotations of proteins between sequenced genomes. *Nucleic Acids Research*, **2004**, 32, D245-50	20.1	13
16	ArchDB: automated protein loop classification as a tool for structural genomics. *Nucleic Acids Research*, **2004**, 32, D185-8	20.1	54
15	Clustering of protein domains in the human genome. *Journal of Molecular Biology*, **2004**, 340, 991-1004	6.5	9
14	The automatic discovery of structural principles describing protein fold space. *Journal of Molecular Biology*, **2003**, 330, 839-50	6.5	20
13	Structural characterization of the human proteome. *Genome Research*, **2002**, 12, 1625-41	9.7	57
12	Recognition of remote protein homologies using three-dimensional information to generate a position specific scoring matrix in the program 3D-PSSM **1999**,		21
11	Application of inductive logic programming to discover rules governing the three-dimensional topology of protein structure. *Lecture Notes in Computer Science*, **1998**, 53-64	0.9	14
10	Recent Developments in Applying Machine Learning to Drug Design **1998**, 151-162		

9	Relating chemical activity to structure: An examination of ILP successes. *New Generation Computing* , **1995**, 13, 411-433	0.9	58
8	COMPARISON OF ARTIFICIAL INTELLIGENCE METHODS FOR MODELING PHARMACEUTICAL QSARS. *Applied Artificial Intelligence*, **1995**, 9, 213-233	2.3	21
7	Quantitative structure-activity relationships by neural networks and inductive logic programming. II. The inhibition of dihydrofolate reductase by triazines. *Journal of Computer-Aided Molecular Design*, **1994**, 8, 421-32	4.2	38
6	Protein surface area defined. *Nature*, **1993**, 366, 638-638	50.4	29
5	New approaches to QSAR: Neural networks and machine learning. *Journal of Computer - Aided Molecular Design*, **1993**, 1, 279-290		22
4	Library of common protein motifs. *Nature*, **1991**, 349, 111	50.4	9
3	Similarity in membrane proteins. *Nature*, **1989**, 342, 624	50.4	78
2	Structure, function and variants analysis of the androgen-regulatedTMPRSS2, a drug target candidate for COVID-19 infection		3
1	A Common TMPRSS2 Variant Protects Against Severe COVID-19. *SSRN Electronic Journal*,	1	1