

Michael J E Sternberg

List of Publications by Citations

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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 Phyre2 web portal for protein modeling, prediction and analysis. <i>Nature Protocols</i> , 2015 , 10, 845-58	18.8	5622
61	Protein structure prediction on the Web: a case study using the Phyre server. <i>Nature Protocols</i> , 2009 , 4, 363-71	18.8	3569
60	3DLigandSite: predicting ligand-binding sites using similar structures. <i>Nucleic Acids Research</i> , 2010 , 38, W469-73	20.1	456
59	A highly conserved program of neuronal microexons is misregulated in autistic brains. <i>Cell</i> , 2014 , 159, 1511-23	56.2	356
58	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. <i>Genome Biology</i> , 2016 , 17, 184	18.3	218
57	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. <i>Plant Cell</i> , 2017 , 29, 1806-1821	11.6	150
56	SuSPect: enhanced prediction of single amino acid variant (SAV) phenotype using network features. <i>Journal of Molecular Biology</i> , 2014 , 426, 2692-701	6.5	140
55	Can Predicted Protein 3D Structures Provide Reliable Insights into whether Missense Variants Are Disease Associated?. <i>Journal of Molecular Biology</i> , 2019 , 431, 2197-2212	6.5	138
54	EzMol: A Web Server Wizard for the Rapid Visualization and Image Production of Protein and Nucleic Acid Structures. <i>Journal of Molecular Biology</i> , 2018 , 430, 2244-2248	6.5	82
53	Similarity in membrane proteins. <i>Nature</i> , 1989 , 342, 624	50.4	78
52	Protein folding requires crowd control in a simulated cell. <i>Journal of Molecular Biology</i> , 2010 , 397, 1329-38	18.5	70
51	The Contribution of Missense Mutations in Core and Rim Residues of Protein-Protein Interfaces to Human Disease. <i>Journal of Molecular Biology</i> , 2015 , 427, 2886-98	6.5	69
50	Relating chemical activity to structure: An examination of ILP successes. <i>New Generation Computing</i> , 1995 , 13, 411-433	0.9	58
49	Structural characterization of the human proteome. <i>Genome Research</i> , 2002 , 12, 1625-41	9.7	57
48	Structure-based prediction of protein allostery. <i>Current Opinion in Structural Biology</i> , 2018 , 50, 1-8	8.1	57
47	AlloPred: prediction of allosteric pockets on proteins using normal mode perturbation analysis. <i>BMC Bioinformatics</i> , 2015 , 16, 335	3.6	55
46	ArchDB: automated protein loop classification as a tool for structural genomics. <i>Nucleic Acids Research</i> , 2004 , 32, D185-8	20.1	54

45	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. <i>Nucleic Acids Research</i> , 2013 , 41, D499-507	20.1	48
44	Thienopyrimidinone Based Sirtuin-2 (SIRT2)-Selective Inhibitors Bind in the Ligand Induced Selectivity Pocket. <i>Journal of Medicinal Chemistry</i> , 2017 , 60, 1928-1945	8.3	39
43	Quantitative structure-activity relationships by neural networks and inductive logic programming. II. The inhibition of dihydrofolate reductase by triazines. <i>Journal of Computer-Aided Molecular Design</i> , 1994 , 8, 421-32	4.2	38
42	Genome3D: exploiting structure to help users understand their sequences. <i>Nucleic Acids Research</i> , 2015 , 43, D382-6	20.1	33
41	k-SLAM: accurate and ultra-fast taxonomic classification and gene identification for large metagenomic data sets. <i>Nucleic Acids Research</i> , 2017 , 45, 1649-1656	20.1	32
40	Predicting Protein Dynamics and Allostery Using Multi-Protein Atomic Distance Constraints. <i>Structure</i> , 2017 , 25, 546-558	5.2	31
39	Support vector inductive logic programming outperforms the naive Bayes classifier and inductive logic programming for the classification of bioactive chemical compounds. <i>Journal of Computer-Aided Molecular Design</i> , 2007 , 21, 269-80	4.2	31
38	Protein surface area defined. <i>Nature</i> , 1993 , 366, 638-638	50.4	29
37	Analysis of the Small Molecule Content of Outer Membrane Vesicles Produced by Indicates an Extensive Metabolic Link between Microbe and Host. <i>Frontiers in Microbiology</i> , 2017 , 8, 2440	5.7	28
36	Support Vector Inductive Logic Programming. <i>Lecture Notes in Computer Science</i> , 2005 , 163-175	0.9	28
35	A general approach for developing system-specific functions to score protein-ligand docked complexes using support vector inductive logic programming. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007 , 69, 823-31	4.2	25
34	New approaches to QSAR: Neural networks and machine learning. <i>Journal of Computer - Aided Molecular Design</i> , 1993 , 1, 279-290		22
33	Recognition of remote protein homologies using three-dimensional information to generate a position specific scoring matrix in the program 3D-PSSM 1999 ,		21
32	COMPARISON OF ARTIFICIAL INTELLIGENCE METHODS FOR MODELING PHARMACEUTICAL QSARS. <i>Applied Artificial Intelligence</i> , 1995 , 9, 213-233	2.3	21
31	The automatic discovery of structural principles describing protein fold space. <i>Journal of Molecular Biology</i> , 2003 , 330, 839-50	6.5	20
30	Gene function hypotheses for the Campylobacter jejuni glycome generated by a logic-based approach. <i>Journal of Molecular Biology</i> , 2013 , 425, 186-97	6.5	19
29	The proteome: structure, function and evolution. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , 2006 , 361, 441-51	5.8	18
28	Prediction of the conformation and geometry of loops in globular proteins: testing ArchDB, a structural classification of loops. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005 , 60, 746-57	4.2	17

27	The AlphaFold Database of Protein Structures: A Biologist's Guide. <i>Journal of Molecular Biology</i> , 2021 , 434, 167336	6.5	17
26	Landscape of Pleiotropic Proteins Causing Human Disease: Structural and System Biology Insights. <i>Human Mutation</i> , 2017 , 38, 289-296	4.7	16
25	PhenoRank: reducing study bias in gene prioritization through simulation. <i>Bioinformatics</i> , 2018 , 34, 2087-2095	7.2	15
24	Application of inductive logic programming to discover rules governing the three-dimensional topology of protein structure. <i>Lecture Notes in Computer Science</i> , 1998 , 53-64	0.9	14
23	PhyreRisk: A Dynamic Web Application to Bridge Genomics, Proteomics and 3D Structural Data to Guide Interpretation of Human Genetic Variants. <i>Journal of Molecular Biology</i> , 2019 , 431, 2460-2466	6.5	13
22	3D-GENOMICS: a database to compare structural and functional annotations of proteins between sequenced genomes. <i>Nucleic Acids Research</i> , 2004 , 32, D245-50	20.1	13
21	Phylotranscriptomic Insights into the Diversification of Endothermic Thunnus Tunas. <i>Molecular Biology and Evolution</i> , 2019 , 36, 84-96	8.3	11
20	PhyreStorm: A Web Server for Fast Structural Searches Against the PDB. <i>Journal of Molecular Biology</i> , 2016 , 428, 702-708	6.5	9
19	Exploring the cellular basis of human disease through a large-scale mapping of deleterious genes to cell types. <i>Genome Medicine</i> , 2015 , 7, 95	14.4	9
18	Partial protein domains: evolutionary insights and bioinformatics challenges. <i>Genome Biology</i> , 2015 , 16, 100	18.3	9
17	Clustering of protein domains in the human genome. <i>Journal of Molecular Biology</i> , 2004 , 340, 991-1004	6.5	9
16	Library of common protein motifs. <i>Nature</i> , 1991 , 349, 111	50.4	9
15	Properties of human genes guided by their enrichment in rare and common variants. <i>Human Mutation</i> , 2018 , 39, 365-370	4.7	9
14	Identification of disease-associated loci using machine learning for genotype and network data integration. <i>Bioinformatics</i> , 2019 , 35, 5182-5190	7.2	7
13	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. <i>Nucleic Acids Research</i> , 2020 , 48, D314-D319	20.1	7
12	Missense3D-DB web catalogue: an atom-based analysis and repository of 4M human protein-coding genetic variants. <i>Human Genetics</i> , 2021 , 140, 805-812	6.3	7
11	Application of docking methodologies to modeled proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2020 , 88, 1180-1188	4.2	4
10	Structure, function and variants analysis of the androgen-regulated TMPRSS2, a drug target candidate for COVID-19 infection		3

9	A polygenic biomarker to identify patients with severe hypercholesterolemia of polygenic origin. <i>Molecular Genetics & Genomic Medicine</i> , 2020 , 8, e1248	2.3	2
8	Multi-class Prediction Using Stochastic Logic Programs. <i>Lecture Notes in Computer Science</i> , 2006 , 109-124.	0.9	1
7	Including Functional Annotations and Extending the Collection of Structural Classifications of Protein Loops (ArchDB). <i>Bioinformatics and Biology Insights</i> , 2009 , 1, 77-90	5.3	1
6	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. <i>Methods in Molecular Biology</i> , 2020 , 2165, 27-67	1.4	1
5	Variation of Background Knowledge in an Industrial Application of ILP. <i>Lecture Notes in Computer Science</i> , 2011 , 158-170	0.9	1
4	Does Multi-Clause Learning Help in Real-World Applications?. <i>Lecture Notes in Computer Science</i> , 2012 , 221-237	0.9	1
3	A Common TMPRSS2 Variant Protects Against Severe COVID-19. <i>SSRN Electronic Journal</i> ,	1	1
2	Protein Fold Discovery Using Stochastic Logic Programs. <i>Lecture Notes in Computer Science</i> , 2008 , 244-262.	0.9	1
1	Recent Developments in Applying Machine Learning to Drug Design 1998 , 151-162		