Michael J E Sternberg

List of Publications by Year
in descending order

69 papers	16,346 citations	172207 29 h-index	114278 63 g-index
82 all docs	82 docs citations	82 times ranked	31785 citing authors

#	Article	IF	Citations
1	The Phyre2 web portal for protein modeling, prediction and analysis. Nature Protocols, 2015, 10, 845-858.	5.5	8,366
2	Protein structure prediction on the Web: a case study using the Phyre server. Nature Protocols, 2009, 4, 363-371.	5.5	3,815
3	3DLigandSite: predicting ligand-binding sites using similar structures. Nucleic Acids Research, 2010, 38, W469-W473.	6.5	549
4	A Highly Conserved Program of Neuronal Microexons Is Misregulated in Autistic Brains. Cell, 2014, 159, 1511-1523.	13.5	546
5	Can Predicted Protein 3D Structures Provide Reliable Insights into whether Missense Variants Are Disease Associated?. Journal of Molecular Biology, 2019, 431, 2197-2212.	2.0	344
6	ePlant: Visualizing and Exploring Multiple Levels of Data for Hypothesis Generation in Plant Biology. Plant Cell, 2017, 29, 1806-1821.	3.1	316
7	An expanded evaluation of protein function prediction methods shows an improvement in accuracy. Genome Biology, 2016, 17, 184.	3.8	308
8	SuSPect: Enhanced Prediction of Single Amino Acid Variant (SAV) Phenotype Using Network Features. Journal of Molecular Biology, 2014, 426, 2692-2701.	2.0	189
9	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.	2.0	145
10	The AlphaFold Database of Protein Structures: A Biologistâ€™s Guide. Journal of Molecular Biology, 2022, 434, 167336.	2.0	126
11	The Contribution of Missense Mutations in Core and Rim Residues of Proteinâ€“Protein Interfaces to Human Disease. Journal of Molecular Biology, 2015, 427, 2886-2898.	2.0	105
12	Similarity in membrane proteins. Nature, 1989, 342, 624-624.	13.7	90
13	Structure-based prediction of protein allostery. Current Opinion in Structural Biology, 2018, 50, 1-8.	2.6	90
14	AlloPred: prediction of allosteric pockets on proteins using normal mode perturbation analysis. BMC Bioinformatics, 2015, 16, 335.	1.2	88
15	Protein Folding Requires Crowd Control in a Simulated Cell. Journal of Molecular Biology, 2010, 397, 1329-1338.	2.0	76
16	Structural Characterization of the Human Proteome. Genome Research, 2002, 12, 1625-1641.	2.4	66
17	Relating chemical activity to structure: An examination of ILP successes. New Generation Computing, 1995, 13, 411-433.	2.5	65
18	ArchDB: automated protein loop classification as a tool for structural genomics. Nucleic Acids Research, 2004, 32, 185D-188.	6.5	61

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19	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, 421-432.	1.3	55
20	Genome3D: a UK collaborative project to annotate genomic sequences with predicted 3D structures based on SCOP and CATH domains. Nucleic Acids Research, 2012, 41, D499-D507.	6.5	53
21	k-SLAM: accurate and ultra-fast taxonomic classification and gene identification for large metagenomic data sets. Nucleic Acids Research, 2017, 45, gkw1248.	6.5	50
22	Thienopyrimidinone Based Sirtuin-2 (SIRT2)-Selective Inhibitors Bind in the Ligand Induced Selectivity Pocket. Journal of Medicinal Chemistry, 2017, 60, 1928-1945.	2.9	49
23	Predicting Protein Dynamics and Allostery Using Multi-Protein Atomic Distance Constraints. Structure, 2017, 25, 546-558.	1.6	45
24	Genome3D: exploiting structure to help users understand their sequences. Nucleic Acids Research, 2015, 43, D382-D386.	6.5	42
25	In Silico Analysis of the Small Molecule Content of Outer Membrane Vesicles Produced by Bacteroides thetaiotaomicron Indicates an Extensive Metabolic Link between Microbe and Host. Frontiers in Microbiology, 2017, 8, 2440.	1.5	42
26	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, 269-280.	1.3	40
27	Missense3D-DB web catalogue: an atom-based analysis and repository of 4M human protein-coding genetic variants. Human Genetics, 2021, 140, 805-812.	1.8	39
28	Protein surface area defined. Nature, 1993, 366, 638-638.	13.7	35
29	COMPARISON OF ARTIFICIAL INTELLIGENCE METHODS FOR MODELING PHARMACEUTICAL QSARS. Applied Artificial Intelligence, 1995, 9, 213-233.	2.0	30
30	PhenoRank: reducing study bias in gene prioritization through simulation. Bioinformatics, 2018, 34, 2087-2095.	1.8	30
31	A general approach for developing systemâ€specific functions to score proteinâ€“ligand docked complexes using support vector inductive logic programming. Proteins: Structure, Function and Bioinformatics, 2007, 69, 823-831.	1.5	29
32	Recognition of remote protein homologies using three-dimensional information to generate a position specific scoring matrix in the program 3D-PSSM. , 1999, , .		27
33	New approaches to QSAR: Neural networks and machine learning. Journal of Computer - Aided Molecular Design, 1993, 1, 279-290.	1.0	26
34	Landscape of Pleiotropic Proteins Causing Human Disease: Structural and System Biology Insights. Human Mutation, 2017, 38, 289-296.	1.1	26
35	3DLigandSite: structure-based prediction of proteinâ€“ligand binding sites. Nucleic Acids Research, 2022, 50, W13-W20.	6.5	25
36	The Automatic Discovery of Structural Principles Describing Protein Fold Space. Journal of Molecular Biology, 2003, 330, 839-850.	2.0	22

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37	Application of docking methodologies to modeled proteins. Proteins: Structure, Function and Bioinformatics, 2020, 88, 1180-1188.	1.5	22
38	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, 746-757.	1.5	21
39	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.	2.0	21
40	Gene Function Hypotheses for the Campylobacter jejuni Glycome Generated by a Logic-Based Approach. Journal of Molecular Biology, 2013, 425, 186-197.	2.0	20
41	Application of inductive logic programming to discover rules governing the three-dimensional topology of protein structure. Lecture Notes in Computer Science, 1998, , 53-64.	1.0	18
42	The proteome: structure, function and evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2006, 361, 441-451.	1.8	18
43	PhyreStorm: A Web Server for Fast Structural Searches Against the PDB. Journal of Molecular Biology, 2016, 428, 702-708.	2.0	15
44	Phylotranscriptomic Insights into the Diversification of EndothermicThunnusTunas. Molecular Biology and Evolution, 2019, 36, 84-96.	3.5	15
45	3D-GENOMICS: a database to compare structural and functional annotations of proteins between sequenced genomes. Nucleic Acids Research, 2004, 32, 245D-250.	6.5	14
46	Exploring the cellular basis of human disease through a large-scale mapping of deleterious genes to cell types. Genome Medicine, 2015, 7, 95.	3.6	13
47	Properties of human genes guided by their enrichment in rare and common variants. Human Mutation, 2018, 39, 365-370.	1.1	13
48	Genome3D: integrating a collaborative data pipeline to expand the depth and breadth of consensus protein structure annotation. Nucleic Acids Research, 2020, 48, D314-D319.	6.5	13
49	Library of common protein motifs. Nature, 1991, 349, 111-111.	13.7	12
50	Clustering of Protein Domains in the Human Genome. Journal of Molecular Biology, 2004, 340, 991-1004.	2.0	12
51	Partial protein domains: evolutionary insights and bioinformatics challenges. Genome Biology, 2015, 16, 100.	3.8	10
52	Identification of disease-associated loci using machine learning for genotype and network data integration. Bioinformatics, 2019, 35, 5182-5190.	1.8	7
53	A polygenic biomarker to identify patients with severe hypercholesterolemia of polygenic origin. Molecular Genetics & Genomic Medicine, 2020, 8, e1248.	0.6	5
54	The fine details of evolution. Biochemical Society Transactions, 2009, 37, 723-726.	1.6	3

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55	The Genome3D Consortium for Structural Annotations of Selected Model Organisms. Methods in Molecular Biology, 2020, 2165, 27-67.	0.4	3
56	A Common TMPRSS2 Variant Protects Against Severe COVID-19. SSRN Electronic Journal, 0, , .	0.4	2
57	Multi-class Prediction Using Stochastic Logic Programs. Lecture Notes in Computer Science, 2006, , 109-124.	1.0	2
58	Computational Resources for Molecular Biology 2022. Journal of Molecular Biology, 2022, 434, 167625.	2.0	2
59	Protein Fold Discovery Using Stochastic Logic Programs. Lecture Notes in Computer Science, 2008, , 244-262.	1.0	1
60	Variation of Background Knowledge in an Industrial Application of ILP. Lecture Notes in Computer Science, 2011, , 158-170.	1.0	1
61	Does Multi-Clause Learning Help in Real-World Applications?. Lecture Notes in Computer Science, 2012, , 221-237.	1.0	1
62	Including Functional Annotations and Extending the Collection of Structural Classifications of Protein Loops (ArchDB). Bioinformatics and Biology Insights, 2009, 1, 77-90.	1.0	1
63	Computation Resources for Molecular Biology: A Special Issue. Journal of Molecular Biology, 2016, 428, 669-670.	2.0	0
64	Computation Resources for Molecular Biology: Special Issue 2017. Journal of Molecular Biology, 2017, 429, 345-347.	2.0	0
65	Computation Resources for Molecular Biology: Special Issue 2018. Journal of Molecular Biology, 2018, 430, 2181-2183.	2.0	0
66	Computation Resources for Molecular Biology: Special Issue 2019. Journal of Molecular Biology, 2019, 431, 2395-2397.	2.0	0
67	Computational Resources for Molecular Biology: Special Issue 2020. Journal of Molecular Biology, 2020, 432, 3361-3363.	2.0	0
68	Computational Resources for Molecular Biology 2021. Journal of Molecular Biology, 2021, 433, 166962.	2.0	0
69	Recent Developments in Applying Machine Learning to Drug Design. , 1998, , 151-162.		0