

Mark N. Wass

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/204797/publications.pdf>

Version: 2024-02-01

51
papers

12,511
citations

270111

25
h-index

198040

52
g-index

67
all docs

67
docs citations

67
times ranked

31202
citing authors

#	ARTICLE	IF	CITATIONS
1	3DLigandSite: structure-based prediction of protein-ligand binding sites. <i>Nucleic Acids Research</i> , 2022, 50, W13-W20.	6.5	25
2	Differentially conserved amino acid positions may reflect differences in SARS-CoV-2 and SARS-CoV behaviour. <i>Bioinformatics</i> , 2021, 37, 2282-2288.	1.8	9
3	Constitutive Cell Proliferation Regulating Inhibitor of Protein Phosphatase 2A (CIP2A) Mediates Drug Resistance to Erlotinib in an EGFR Activating Mutated NSCLC Cell Line. <i>Cells</i> , 2021, 10, 716.	1.8	7
4	Identification of sequence changes in myosin II that adjust muscle contraction velocity. <i>PLoS Biology</i> , 2021, 19, e3001248.	2.6	9
5	A Potential Role of the CD47/SIRPalpha Axis in COVID-19 Pathogenesis. <i>Current Issues in Molecular Biology</i> , 2021, 43, 1212-1225.	1.0	9
6	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	6.5	87
7	Thiourea and Guanidine Compounds and Their Iridium Complexes in Drug-Resistant Cancer Cell Lines: Structure-Activity Relationships and Direct Luminescent Imaging. <i>ChemMedChem</i> , 2020, 15, 349-353.	1.6	21
8	COVID-19-Related Coagulopathy—Is Transferrin a Missing Link?. <i>Diagnostics</i> , 2020, 10, 539.	1.3	32
9	Aprotinin Inhibits SARS-CoV-2 Replication. <i>Cells</i> , 2020, 9, 2377.	1.8	72
10	YM155-Adapted Cancer Cell Lines Reveal Drug-Induced Heterogeneity and Enable the Identification of Biomarker Candidates for the Acquired Resistance Setting. <i>Cancers</i> , 2020, 12, 1080.	1.7	5
11	Testing of the Survivin Suppressant YM155 in a Large Panel of Drug-Resistant Neuroblastoma Cell Lines. <i>Cancers</i> , 2020, 12, 577.	1.7	7
12	SAMHD1 is a key regulator of the lineage-specific response of acute lymphoblastic leukaemias to nelarabine. <i>Communications Biology</i> , 2020, 3, 324.	2.0	23
13	Non-Phosphorylatable PEA-15 Sensitises SKOV-3 Ovarian Cancer Cells to Cisplatin. <i>Cells</i> , 2020, 9, 515.	1.8	5
14	Miyabeacin: A new cyclodimer presents a potential role for willow in cancer therapy. <i>Scientific Reports</i> , 2020, 10, 6477.	1.6	8
15	Environmental conditions shape the nature of a minimal bacterial genome. <i>Nature Communications</i> , 2019, 10, 3100.	5.8	43
16	Incorporation of doxorubicin in different polymer nanoparticles and their anticancer activity. <i>Beilstein Journal of Nanotechnology</i> , 2019, 10, 2062-2072.	1.5	20
17	Doxorubicin-loaded human serum albumin nanoparticles overcome transporter-mediated drug resistance in drug-adapted cancer cells. <i>Beilstein Journal of Nanotechnology</i> , 2019, 10, 1707-1715.	1.5	48
18	Intact-Cell MALDI-ToF Mass Spectrometry for the Authentication of Drug-Adapted Cancer Cell Lines. <i>Cells</i> , 2019, 8, 1194.	1.8	3

#	ARTICLE	IF	CITATIONS
19	Is the Bombali virus pathogenic in humans?. <i>Bioinformatics</i> , 2019, 35, 3553-3558.	1.8	16
20	Understanding of researcher behavior is required to improve data reliability. <i>GigaScience</i> , 2019, 8, .	3.3	12
21	Omeprazole Increases the Efficacy of Acyclovir Against Herpes Simplex Virus Type 1 and 2. <i>Frontiers in Microbiology</i> , 2019, 10, 2790.	1.5	11
22	Herd Immunity to Ebolaviruses Is Not a Realistic Target for Current Vaccination Strategies. <i>Frontiers in Immunology</i> , 2018, 9, 1025.	2.2	12
23	<i>Desulfovibrio vulgaris</i> CbiK P cobaltochelataase: evolution of a haem binding protein orchestrated by the incorporation of two histidine residues. <i>Environmental Microbiology</i> , 2017, 19, 106-118.	1.8	9
24	Investigating Ebola virus pathogenicity using molecular dynamics. <i>BMC Genomics</i> , 2017, 18, 566.	1.2	10
25	Associating mutations causing cystinuria with disease severity with the aim of providing precision medicine. <i>BMC Genomics</i> , 2017, 18, 550.	1.2	16
26	Acquired resistance to oxaliplatin is not directly associated with increased resistance to DNA damage in SK-N-ASrOXALI4000, a newly established oxaliplatin-resistant sub-line of the neuroblastoma cell line SK-N-AS. <i>PLoS ONE</i> , 2017, 12, e0172140.	1.1	6
27	The Role of Protein Modelling in Predicting the Disease Severity of Cystinuria. <i>European Urology</i> , 2016, 69, 543-544.	0.9	7
28	Computational analysis of Ebolavirus data: prospects, promises and challenges. <i>Biochemical Society Transactions</i> , 2016, 44, 973-978.	1.6	8
29	Effects of YM155 on survivin levels and viability in neuroblastoma cells with acquired drug resistance. <i>Cell Death and Disease</i> , 2016, 7, e2410-e2410.	2.7	40
30	Substrate-specific effects of pirinixic acid derivatives on ABCB1-mediated drug transport. <i>Oncotarget</i> , 2016, 7, 11664-11676.	0.8	7
31	The genetic diversity of cystinuria in a <sc>UK</sc> population of patients. <i>BJU International</i> , 2015, 116, 109-116.	1.3	39
32	Ten Simple Rules for a Community Computational Challenge. <i>PLoS Computational Biology</i> , 2015, 11, e1004150.	1.5	9
33	The Phyre2 web portal for protein modeling, prediction and analysis. <i>Nature Protocols</i> , 2015, 10, 845-858.	5.5	8,366
34	VarMod: modelling the functional effects of non-synonymous variants. <i>Nucleic Acids Research</i> , 2014, 42, W331-W336.	6.5	16
35	Proteomic analysis of the Plasmodium male gamete reveals the key role for glycolysis in flagellar motility. <i>Malaria Journal</i> , 2014, 13, 315.	0.8	50
36	The South Asian Genome. <i>PLoS ONE</i> , 2014, 9, e102645.	1.1	43

#	ARTICLE	IF	CITATIONS
37	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013, 10, 221-227.	9.0	789
38	CombFunc: predicting protein function using heterogeneous data sources. <i>Nucleic Acids Research</i> , 2012, 40, W466-W470.	6.5	63
39	Proteomic analysis of <i>Plasmodium</i> in the mosquito: progress and pitfalls. <i>Parasitology</i> , 2012, 139, 1131-1145.	0.7	35
40	Protein-protein interaction sites are hot spots for disease-associated nonsynonymous SNPs. <i>Human Mutation</i> , 2012, 33, 359-363.	1.1	149
41	Towards the prediction of protein interaction partners using physical docking. <i>Molecular Systems Biology</i> , 2011, 7, 469.	3.2	102
42	Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. <i>Nature Genetics</i> , 2011, 43, 1131-1138.	9.4	501
43	Challenges for the prediction of macromolecular interactions. <i>Current Opinion in Structural Biology</i> , 2011, 21, 382-390.	2.6	84
44	Genetic variation in SCN10A influences cardiac conduction. <i>Nature Genetics</i> , 2010, 42, 149-152.	9.4	248
45	Genetic loci influencing kidney function and chronic kidney disease. <i>Nature Genetics</i> , 2010, 42, 373-375.	9.4	246
46	3DLigandSite: predicting ligand-binding sites using similar structures. <i>Nucleic Acids Research</i> , 2010, 38, W469-W473.	6.5	549
47	The flagellum in malarial parasites. <i>Current Opinion in Microbiology</i> , 2010, 13, 491-500.	2.3	87
48	Prediction of ligand binding sites using homologous structures and conservation at CASP8. <i>Proteins: Structure, Function and Bioinformatics</i> , 2009, 77, 147-151.	1.5	45
49	Genome-wide association study identifies variants in TMPRSS6 associated with hemoglobin levels. <i>Nature Genetics</i> , 2009, 41, 1170-1172.	9.4	217
50	ConFunc—functional annotation in the twilight zone. <i>Bioinformatics</i> , 2008, 24, 798-806.	1.8	95
51	Convergent Evolution of Enzyme Active Sites Is not a Rare Phenomenon. <i>Journal of Molecular Biology</i> , 2007, 372, 817-845.	2.0	109