

David P Enot

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11805197/publications.pdf>

Version: 2024-02-01

27
papers

8,201
citations

279701

23
h-index

526166

27
g-index

28
all docs

28
docs citations

28
times ranked

15362
citing authors

#	ARTICLE	IF	CITATIONS
1	Sustained Type I interferon signaling as a mechanism of resistance to PD-1 blockade. <i>Cell Research</i> , 2019, 29, 846-861.	5.7	160
2	Î±-Ketoglutarate inhibits autophagy. <i>Aging</i> , 2019, 11, 3418-3431.	1.4	30
3	Aspirin Recapitulates Features of Caloric Restriction. <i>Cell Reports</i> , 2018, 22, 2395-2407.	2.9	98
4	TumGrowth: An open-access web tool for the statistical analysis of tumor growth curves. <i>Oncolmmunology</i> , 2018, 7, e1462431.	2.1	82
5	Immune biomarkers for prognosis and prediction of responses to immune checkpoint blockade in cutaneous melanoma. <i>Oncolmmunology</i> , 2017, 6, e1299303.	2.1	20
6	Caloric Restriction Mimetics Enhance Anticancer Immunosurveillance. <i>Cancer Cell</i> , 2016, 30, 147-160.	7.7	410
7	Impact of Pattern Recognition Receptors on the Prognosis of Breast Cancer Patients Undergoing Adjuvant Chemotherapy. <i>Cancer Research</i> , 2016, 76, 3122-3126.	0.4	47
8	Metabolomic analyses reveal that anti-aging metabolites are depleted by palmitate but increased by oleate <i>in vivo</i> . <i>Cell Cycle</i> , 2015, 14, 2399-2407.	1.3	27
9	Anticancer immunotherapy by CTLA-4 blockade relies on the gut microbiota. <i>Science</i> , 2015, 350, 1079-1084.	6.0	2,539
10	Chemotherapy-induced antitumor immunity requires formyl peptide receptor 1. <i>Science</i> , 2015, 350, 972-978.	6.0	367
11	Regulation of Autophagy by Cytosolic Acetyl-Coenzyme A. <i>Molecular Cell</i> , 2014, 53, 710-725.	4.5	412
12	Cancer cellâ€™s autonomous contribution of type I interferon signaling to the efficacy of chemotherapy. <i>Nature Medicine</i> , 2014, 20, 1301-1309.	15.2	823
13	The Intestinal Microbiota Modulates the Anticancer Immune Effects of Cyclophosphamide. <i>Science</i> , 2013, 342, 971-976.	6.0	1,580
14	Bioinformatics for Mass Spectrometry-Based Metabolomics. <i>Methods in Molecular Biology</i> , 2011, 719, 351-375.	0.4	19
15	Targeted Metabolomics for Biomarker Discovery. <i>Angewandte Chemie - International Edition</i> , 2010, 49, 5426-5445.	7.2	310
16	Metabolite fingerprinting of urine suggests breed-specific dietary metabolism differences in domestic dogs. <i>British Journal of Nutrition</i> , 2010, 103, 1127-1138.	1.2	37
17	Metabolite signal identification in accurate mass metabolomics data with MZedDB, an interactive m/z annotation tool utilising predicted ionisation behaviour 'rules'. <i>BMC Bioinformatics</i> , 2009, 10, 227.	1.2	142
18	Metabolomic analysis reveals a common pattern of metabolic reâ€™programming during invasion of three host plant species by <i>Magnaporthe grisea</i> . <i>Plant Journal</i> , 2009, 59, 723-737.	2.8	209

#	ARTICLE	IF	CITATIONS
19	Rice blast infection of <i>Brachypodium distachyon</i> as a model system to study dynamic host/pathogen interactions. <i>Nature Protocols</i> , 2008, 3, 435-445.	5.5	95
20	High-throughput, nontargeted metabolite fingerprinting using nominal mass flow injection electrospray mass spectrometry. <i>Nature Protocols</i> , 2008, 3, 486-504.	5.5	115
21	Preprocessing, classification modeling and feature selection using flow injection electrospray mass spectrometry metabolite fingerprint data. <i>Nature Protocols</i> , 2008, 3, 446-470.	5.5	114
22	Explanatory signal interpretation and metabolite identification strategies for nominal mass FIE-MS metabolite fingerprints. <i>Nature Protocols</i> , 2008, 3, 471-485.	5.5	44
23	Representation, Comparison, and Interpretation of Metabolome Fingerprint Data for Total Composition Analysis and Quality Trait Investigation in Potato Cultivars. <i>Journal of Agricultural and Food Chemistry</i> , 2007, 55, 3444-3451.	2.4	71
24	Detecting a difference “ assessing generalisability when modelling metabolome fingerprint data in longer term studies of genetically modified plants. <i>Metabolomics</i> , 2007, 3, 335-347.	1.4	24
25	Statistical measures for validating plant genotype similarity assessments following multivariate analysis of metabolome fingerprint data. <i>Metabolomics</i> , 2007, 3, 349-355.	1.4	15
26	Predicting interpretability of metabolome models based on behavior, putative identity, and biological relevance of explanatory signals. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14865-14870.	3.3	44
27	Hierarchical metabolomics demonstrates substantial compositional similarity between genetically modified and conventional potato crops. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 14458-14462.	3.3	367