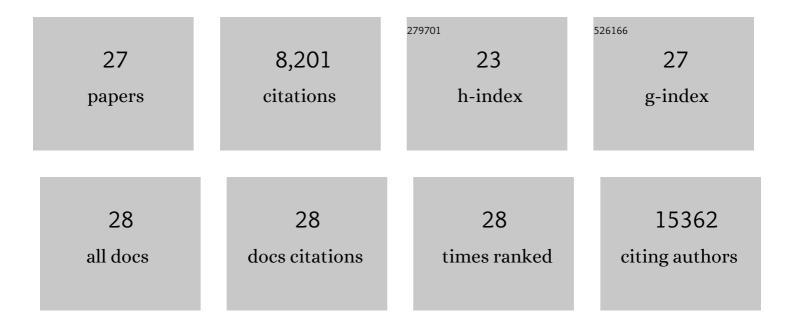
## David P Enot

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11805197/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Sustained Type I interferon signaling as a mechanism of resistance to PD-1 blockade. Cell Research, 2019, 29, 846-861.	5.7	160
2	α-Ketoglutarate inhibits autophagy. Aging, 2019, 11, 3418-3431.	1.4	30
3	Aspirin Recapitulates Features of Caloric Restriction. Cell Reports, 2018, 22, 2395-2407.	2.9	98
4	TumGrowth: An open-access web tool for the statistical analysis of tumor growth curves. Oncolmmunology, 2018, 7, e1462431.	2.1	82
5	Immune biomarkers for prognosis and prediction of responses to immune checkpoint blockade in cutaneous melanoma. Oncolmmunology, 2017, 6, e1299303.	2.1	20
6	Caloric Restriction Mimetics Enhance Anticancer Immunosurveillance. Cancer Cell, 2016, 30, 147-160.	7.7	410
7	Impact of Pattern Recognition Receptors on the Prognosis of Breast Cancer Patients Undergoing Adjuvant Chemotherapy. Cancer Research, 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> . Cell Cycle, 2015, 14, 2399-2407.	1.3	27
9	Anticancer immunotherapy by CTLA-4 blockade relies on the gut microbiota. Science, 2015, 350, 1079-1084.	6.0	2,539
10	Chemotherapy-induced antitumor immunity requires formyl peptide receptor 1. Science, 2015, 350, 972-978.	6.0	367
11	Regulation of Autophagy by Cytosolic Acetyl-Coenzyme A. Molecular Cell, 2014, 53, 710-725.	4.5	412
12	Cancer cell–autonomous contribution of type I interferon signaling to the efficacy of chemotherapy. Nature Medicine, 2014, 20, 1301-1309.	15.2	823
13	The Intestinal Microbiota Modulates the Anticancer Immune Effects of Cyclophosphamide. Science, 2013, 342, 971-976.	6.0	1,580
14	Bioinformatics for Mass Spectrometry-Based Metabolomics. Methods in Molecular Biology, 2011, 719, 351-375.	0.4	19
15	Targeted Metabolomics for Biomarker Discovery. Angewandte Chemie - International Edition, 2010, 49, 5426-5445.	7.2	310
16	Metabolite fingerprinting of urine suggests breed-specific dietary metabolism differences in domestic dogs. British Journal of Nutrition, 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'. BMC Bioinformatics, 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> . Plant Journal, 2009, 59, 723-737.	2.8	209

DAVID P ENOT

#	Article	IF	CITATIONS
19	Rice blast infection of Brachypodium distachyon as a model system to study dynamic host/pathogen interactions. Nature Protocols, 2008, 3, 435-445.	5.5	95
20	High-throughput, nontargeted metabolite fingerprinting using nominal mass flow injection electrospray mass spectrometry. Nature Protocols, 2008, 3, 486-504.	5.5	115
21	Preprocessing, classification modeling and feature selection using flow injection electrospray mass spectrometry metabolite fingerprint data. Nature Protocols, 2008, 3, 446-470.	5.5	114
22	Explanatory signal interpretation and metabolite identification strategies for nominal mass FIE-MS metabolite fingerprints. Nature Protocols, 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. Journal of Agricultural and Food Chemistry, 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. Metabolomics, 2007, 3, 335-347.	1.4	24
25	Statistical measures for validating plant genotype similarity assessments following multivariate analysis of metabolome fingerprint data. Metabolomics, 2007, 3, 349-355.	1.4	15
26	Predicting interpretability of metabolome models based on behavior, putative identity, and biological relevance of explanatory signals. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14865-14870.	3.3	44
27	Hierarchical metabolomics demonstrates substantial compositional similarity between genetically modified and conventional potato crops. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 14458-14462.	3.3	367