## Kristoffer Forslund

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/9233440/publications.pdf

Version: 2024-02-01

81 papers 34,469 citations

45 h-index 83 g-index

93 all docs 93 docs citations 93 times ranked 55550 citing authors

#	Article	IF	CITATIONS
1	STRING v10: protein–protein interaction networks, integrated over the tree of life. Nucleic Acids Research, 2015, 43, D447-D452.	6.5	9,029
2	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	6.5	3,306
3	The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222.	6.5	2,693
4	eggNOG 5.0: a hierarchical, functionally and phylogenetically annotated orthology resource based on 5090 organisms and 2502 viruses. Nucleic Acids Research, 2019, 47, D309-D314.	6.5	2,575
5	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	3.5	2,156
6	eggNOG 4.5: a hierarchical orthology framework with improved functional annotations for eukaryotic, prokaryotic and viral sequences. Nucleic Acids Research, 2016, 44, D286-D293.	6.5	1,937
7	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	13.7	1,627
8	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	13.7	1,506
9	Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237.	13.7	1,370
10	Salt-responsive gut commensal modulates TH17 axis and disease. Nature, 2017, 551, 585-589.	13.7	896
11	InParanoid 7: new algorithms and tools for eukaryotic orthology analysis. Nucleic Acids Research, 2010, 38, D196-D203.	6.5	576
12	Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children. Nature Communications, 2016, 7, 10410.	5.8	557
13	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
14	Recovery of gut microbiota of healthy adults following antibiotic exposure. Nature Microbiology, 2018, 3, 1255-1265.	5.9	483
15	Short-Chain Fatty Acid Propionate Protects From Hypertensive Cardiovascular Damage. Circulation, 2019, 139, 1407-1421.	1.6	452
16	Propionic Acid Shapes the Multiple Sclerosis Disease Course by an Immunomodulatory Mechanism. Cell, 2020, 180, 1067-1080.e16.	13.5	367
17	Country-specific antibiotic use practices impact the human gut resistome. Genome Research, 2013, 23, 1163-1169.	2.4	356
18	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	13.7	283

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19	Similarity of the dog and human gut microbiomes in gene content and response to diet. Microbiome, 2018, 6, 72.	4.9	211
20	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
21	MOCAT2: a metagenomic assembly, annotation and profiling framework. Bioinformatics, 2016, 32, 2520-2523.	1.8	172
22	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
23	Unravelling the collateral damage of antibiotics on gut bacteria. Nature, 2021, 599, 120-124.	13.7	159
24	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. Nucleic Acids Research, 2017, 45, D529-D534.	6.5	131
25	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. Nature Communications, 2020, 11, 5881.	5.8	122
26	Gut Microbiome Composition in Obese and Non-Obese Persons: A Systematic Review and Meta-Analysis. Nutrients, 2022, 14, 12.	1.7	121
27	Subspecies in the global human gut microbiome. Molecular Systems Biology, 2017, 13, 960.	3.2	115
28	Fasting alters the gut microbiome reducing blood pressure and body weight in metabolic syndrome patients. Nature Communications, 2021, 12, 1970.	5.8	108
29	Combinatorial, additive and dose-dependent drug–microbiome associations. Nature, 2021, 600, 500-505.	13.7	102
30	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	15.2	102
31	RTK: efficient rarefaction analysis of large datasets. Bioinformatics, 2017, 33, 2594-2595.	1.8	100
32	Domain Tree-Based Analysis of Protein Architecture Evolution. Molecular Biology and Evolution, 2008, 25, 254-264.	3.5	98
33	The Gut Microbiome in Hypertension. Circulation Research, 2021, 128, 934-950.	2.0	86
34	Towards the biogeography of prokaryotic genes. Nature, 2022, 601, 252-256.	13.7	85
35	Predicting protein function from domain content. Bioinformatics, 2008, 24, 1681-1687.	1.8	83
36	A computational framework to integrate high-throughput '-omics' datasets for the identification of potential mechanistic links. Nature Protocols, 2018, 13, 2781-2800.	5.5	82

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37	Metagenomic insights into the human gut resistome and the forces that shape it. BioEssays, 2014, 36, 316-329.	1.2	76
38	Metabolomic and microbiome profiling reveals personalized risk factors for coronary artery disease. Nature Medicine, 2022, 28, 295-302.	15.2	74
39	Antibiotics-induced monodominance of a novel gut bacterial order. Gut, 2019, 68, 1781-1790.	6.1	73
40	Gut microbiota differs between children with Inflammatory Bowel Disease and healthy siblings in taxonomic and functional composition: a metagenomic analysis. American Journal of Physiology - Renal Physiology, 2017, 312, G327-G339.	1.6	69
41	S100A8 and S100A9 Are Important for Postnatal Development of Gut Microbiota and Immune System in Mice and Infants. Gastroenterology, 2020, 159, 2130-2145.e5.	0.6	64
42	proGenomes2: an improved database for accurate and consistent habitat, taxonomic and functional annotations of prokaryotic genomes. Nucleic Acids Research, 2020, 48, D621-D625.	6.5	60
43	Human and preclinical studies of the host–gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. Gut, 2021, 70, 2105-2114.	6.1	58
44	QNet: An Agglomerative Method for the Construction of Phylogenetic Networks from Weighted Quartets. Molecular Biology and Evolution, 2006, 24, 532-538.	3.5	56
45	Domain architecture conservation in orthologs. BMC Bioinformatics, 2011, 12, 326.	1.2	54
46	Impairment of gut microbial biotin metabolism and host biotin status in severe obesity: effect of biotin and prebiotic supplementation on improved metabolism. Gut, 2022, 71, 2463-2480.	6.1	53
47	Transposase-DNA Complex Structures Reveal Mechanisms for Conjugative Transposition of Antibiotic Resistance. Cell, 2018, 173, 208-220.e20.	13.5	51
48	Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2012, 856, 187-216.	0.4	47
49	The Gut Microbiome in Myalgic Encephalomyelitis (ME)/Chronic Fatigue Syndrome (CFS). Frontiers in Immunology, 2021, 12, 628741.	2.2	42
50	Quantifying technical confounders in microbiome studies. Cardiovascular Research, 2021, 117, 863-875.	1.8	40
51	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	1.8	36
52	Phosphodiesterase 3A and Arterial Hypertension. Circulation, 2020, 142, 133-149.	1.6	35
53	Elevated aldosterone and blood pressure in a mouse model of familial hyperaldosteronism with ClC-2 mutation. Nature Communications, 2019, 10, 5155.	5.8	34
54	The gut microbiota is associated with the small intestinal paracellular permeability and the development of the immune system in healthy children during the first two years of life. Journal of Translational Medicine, 2021, 19, 177.	1.8	34

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55	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. Nucleic Acids Research, 2022, 50, 3155-3168.	6.5	34
56	Salt Transiently Inhibits Mitochondrial Energetics in Mononuclear Phagocytes. Circulation, 2021, 144, 144-158.	1.6	32
57	Metagenomic analysis of gut microbial communities from a Central Asian population. BMJ Open, 2018, 8, e021682.	0.8	31
58	Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2019, 1910, 469-504.	0.4	30
59	Orthology confers intron position conservation. BMC Genomics, 2010, 11, 412.	1.2	29
60	Quest for Orthologs Entails Quest for Tree of Life: In Search of the Gene Stream. Genome Biology and Evolution, 2015, 7, 1988-1999.	1.1	25
61	Skin Sodium Accumulates in Psoriasis and Reflects Disease Severity. Journal of Investigative Dermatology, 2022, 142, 166-178.e8.	0.3	20
62	A novel exploratory method for visual recombination detection. Genome Biology, 2003, 4, R33.	13.9	19
63	Domainoid: domain-oriented orthology inference. BMC Bioinformatics, 2019, 20, 523.	1.2	17
64	OrthoDisease: tracking disease gene orthologs across 100 species. Briefings in Bioinformatics, 2011, 12, 463-473.	3.2	16
65	Enhanced Ca <sup>2+</sup> signaling, mild primary aldosteronism, and hypertension in a familial hyperaldosteronism mouse model ( <i>Cacna1h</i> < <sup><i>M1560V/+</i></sup> ). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
66	A Phylogeny-Based Benchmarking Test for Orthology Inference Reveals the Limitations of Function-Based Validation. PLoS ONE, 2014, 9, e111122.	1.1	14
67	Benchmarking the next generation of homology inference tools. Bioinformatics, 2016, 32, 2636-2641.	1.8	14
68	B-cell lymphoma/leukaemia 10 and angiotensin II-induced kidney injury. Cardiovascular Research, 2020, 116, 1059-1070.	1.8	12
69	Benchmarking homology detection procedures with low complexity filters. Bioinformatics, 2009, 25, 2500-2505.	1.8	11
70	Precarious Symbiosis Between Host and Microbiome in Cardiovascular Health. Hypertension, 2019, 73, 926-935.	1.3	10
71	Blood pressure changes correlate with short-chain fatty acid production potential shifts under a synbiotic intervention. Cardiovascular Research, 2020, 116, 1252-1253.	1.8	10
72	Protein Intake, Metabolic Status and the Gut Microbiota in Different Ethnicities: Results from Two Independent Cohorts. Nutrients, 2021, 13, 3159.	1.7	6

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73	Identification and Characterization of Human Observational Studies in Nutritional Epidemiology on Gut Microbiomics for Joint Data Analysis. Nutrients, 2021, 13, 3292.	1.7	6
74	Individuality and temporal stability of the human gut microbiome. Central Asian Journal of Global Health, 2013, 2, 120.	0.6	6
75	Constructing Phylogenetic Supernetworks from Quartets. Lecture Notes in Computer Science, 2008, , 284-295.	1.0	4
76	Dynamic Changes in Microbiome Composition Following Mare's Milk Intake for Prevention of Collateral Antibiotic Effect. Frontiers in Cellular and Infection Microbiology, 2021, 11, 622735.	1.8	3
77	Increased Salt Intake Decreases Diet-Induced Thermogenesis in Healthy Volunteers: A Randomized Placebo-Controlled Study. Nutrients, 2022, 14, 253.	1.7	3
78	A Semi-supervised Approach to Discover Bivariate Causality in Large Biological Data. Lecture Notes in Computer Science, 2018, , 406-420.	1.0	1
79	Hitchhiker's guide to microbiome studies. Cardiovascular Research, 2020, 116, e44-e47.	1.8	1
80	Using Unlabeled Data to Discover Bivariate Causality with Deep Restricted Boltzmann Machines. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 358-364.	1.9	0
81	Abstract P372: The Effect of Periodic Fasting on Patients With Hypertension and Metabolic Syndrome. Hypertension, 2018, 72, .	1.3	0