Kristoffer Forslund

List of Publications by Year
in descending order

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81
papers

34,469
citations

53660
45
h-index

56606
83
g-index

93
all docs

93
docs citations

93
times ranked

55550
citing authors

#	Article	IF	Citations
1	Skin Sodium Accumulates in Psoriasis and Reflects Disease Severity. Journal of Investigative Dermatology, 2022, 142, 166-178.e8.	0.3	20
2	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
3	Increased Salt Intake Decreases Diet-Induced Thermogenesis in Healthy Volunteers: A Randomized Placebo-Controlled Study. Nutrients, 2022, 14, 253.	1.7	3
4	Towards the biogeography of prokaryotic genes. Nature, 2022, 601, 252-256.	13.7	85
5	Metabolomic and microbiome profiling reveals personalized risk factors for coronary artery disease. Nature Medicine, 2022, 28, 295-302.	15.2	74
6	Microbiome and metabolome features of the cardiometabolic disease spectrum. Nature Medicine, 2022, 28, 303-314.	15.2	102
7	Landscape of mobile genetic elements and their antibiotic resistance cargo in prokaryotic genomes. Nucleic Acids Research, 2022, 50, 3155-3168.	6.5	34
8	Gut Microbiome Composition in Obese and Non-Obese Persons: A Systematic Review and Meta-Analysis. Nutrients, 2022, 14, 12.	1.7	121
9	Quantifying technical confounders in microbiome studies. Cardiovascular Research, 2021, 117, 863-875.	1.8	40
10	Fasting alters the gut microbiome reducing blood pressure and body weight in metabolic syndrome patients. Nature Communications, 2021, 12, 1970.	5.8	108
11	Dynamic Changes in Microbiome Composition Following Mareâ€™s Milk Intake for Prevention of Collateral Antibiotic Effect. Frontiers in Cellular and Infection Microbiology, 2021, 11, 622735.	1.8	3
12	The Gut Microbiome in Hypertension. Circulation Research, 2021, 128, 934-950.	2.0	86
13	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
14	Enhanced Ca²⁺signaling, mild primary aldosteronism, and hypertension in a familial hyperaldosteronism mouse model (<i>Cacna1h</i>^{<i>M1560V/+</i>}). Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	15
15	Human and preclinical studies of the hostâ€“gut microbiome co-metabolite hippurate as a marker and mediator of metabolic health. Gut, 2021, 70, 2105-2114.	6.1	58
16	Salt Transiently Inhibits Mitochondrial Energetics in Mononuclear Phagocytes. Circulation, 2021, 144, 144-158.	1.6	32
17	Protein Intake, Metabolic Status and the Gut Microbiota in Different Ethnicities: Results from Two Independent Cohorts. Nutrients, 2021, 13, 3159.	1.7	6
18	Identification and Characterization of Human Observational Studies in Nutritional Epidemiology on Gut Microbiomics for Joint Data Analysis. Nutrients, 2021, 13, 3292.	1.7	6

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19	Unravelling the collateral damage of antibiotics on gut bacteria. Nature, 2021, 599, 120-124.	13.7	159
20	Reporting guidelines for human microbiome research: the STORMS checklist. Nature Medicine, 2021, 27, 1885-1892.	15.2	170
21	The Gut Microbiome in Myalgic Encephalomyelitis (ME)/Chronic Fatigue Syndrome (CFS). Frontiers in Immunology, 2021, 12, 628741.	2.2	42
22	Combinatorial, additive and dose-dependent drugâ€“microbiome associations. Nature, 2021, 600, 500-505.	13.7	102
23	B-cell lymphoma/leukaemia 10 and angiotensin II-induced kidney injury. Cardiovascular Research, 2020, 116, 1059-1070.	1.8	12
24	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
25	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
26	Hitchhikerâ€™s guide to microbiome studies. Cardiovascular Research, 2020, 116, e44-e47.	1.8	1
27	Imidazole propionate is increased in diabetes and associated with dietary patterns and altered microbial ecology. Nature Communications, 2020, 11, 5881.	5.8	122
28	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
29	Statin therapy is associated with lower prevalence of gut microbiota dysbiosis. Nature, 2020, 581, 310-315.	13.7	283
30	Phosphodiesterase 3A and Arterial Hypertension. Circulation, 2020, 142, 133-149.	1.6	35
31	Propionic Acid Shapes the Multiple Sclerosis Disease Course by an Immunomodulatory Mechanism. Cell, 2020, 180, 1067-1080.e16.	13.5	367
32	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
33	Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2019, 1910, 469-504.	0.4	30
34	Domainoid: domain-oriented orthology inference. BMC Bioinformatics, 2019, 20, 523.	1.2	17
35	Elevated aldosterone and blood pressure in a mouse model of familial hyperaldosteronism with ClC-2 mutation. Nature Communications, 2019, 10, 5155.	5.8	34
36	Antibiotics-induced monodominance of a novel gut bacterial order. Gut, 2019, 68, 1781-1790.	6.1	73

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37	Precarious Symbiosis Between Host and Microbiome in Cardiovascular Health. Hypertension, 2019, 73, 926-935.	1.3	10
38	Short-Chain Fatty Acid Propionate Protects From Hypertensive Cardiovascular Damage. Circulation, 2019, 139, 1407-1421.	1.6	452
39	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
40	Transposase-DNA Complex Structures Reveal Mechanisms for Conjugative Transposition of Antibiotic Resistance. Cell, 2018, 173, 208-220.e20.	13.5	51
41	A computational framework to integrate high-throughput â€˜-omicsâ€™ datasets for the identification of potential mechanistic links. Nature Protocols, 2018, 13, 2781-2800.	5.5	82
42	Recovery of gut microbiota of healthy adults following antibiotic exposure. Nature Microbiology, 2018, 3, 1255-1265.	5.9	483
43	Gearing up to handle the mosaic nature of life in the quest for orthologs. Bioinformatics, 2018, 34, 323-329.	1.8	36
44	Structure and function of the global topsoil microbiome. Nature, 2018, 560, 233-237.	13.7	1,370
45	Metagenomic analysis of gut microbial communities from a Central Asian population. BMJ Open, 2018, 8, e021682.	0.8	31
46	A Semi-supervised Approach to Discover Bivariate Causality in Large Biological Data. Lecture Notes in Computer Science, 2018, , 406-420.	1.0	1
47	Similarity of the dog and human gut microbiomes in gene content and response to diet. Microbiome, 2018, 6, 72.	4.9	211
48	Abstract P372: The Effect of Periodic Fasting on Patients With Hypertension and Metabolic Syndrome. Hypertension, 2018, 72, .	1.3	0
49	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
50	RTK: efficient rarefaction analysis of large datasets. Bioinformatics, 2017, 33, 2594-2595.	1.8	100
51	Fast Genome-Wide Functional Annotation through Orthology Assignment by eggNOG-Mapper. Molecular Biology and Evolution, 2017, 34, 2115-2122.	3.5	2,156
52	Subspecies in the global human gut microbiome. Molecular Systems Biology, 2017, 13, 960.	3.2	115
53	Salt-responsive gut commensal modulates TH17 axis and disease. Nature, 2017, 551, 585-589.	13.7	896
54	proGenomes: a resource for consistent functional and taxonomic annotations of prokaryotic genomes. Nucleic Acids Research, 2017, 45, D529-D534.	6.5	131

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55	Standardized benchmarking in the quest for orthologs. Nature Methods, 2016, 13, 425-430.	9.0	198
56	MOCAT2: a metagenomic assembly, annotation and profiling framework. Bioinformatics, 2016, 32, 2520-2523.	1.8	172
57	Benchmarking the next generation of homology inference tools. Bioinformatics, 2016, 32, 2636-2641.	1.8	14
58	Human gut microbes impact host serum metabolome and insulin sensitivity. Nature, 2016, 535, 376-381.	13.7	1,506
59	Intestinal microbiome is related to lifetime antibiotic use in Finnish pre-school children. Nature Communications, 2016, 7, 10410.	5.8	557
60	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
61	STRING v10: proteinâ€“protein interaction networks, integrated over the tree of life. Nucleic Acids Research, 2015, 43, D447-D452.	6.5	9,029
62	Disentangling type 2 diabetes and metformin treatment signatures in the human gut microbiota. Nature, 2015, 528, 262-266.	13.7	1,627
63	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
64	A Phylogeny-Based Benchmarking Test for Orthology Inference Reveals the Limitations of Function-Based Validation. PLoS ONE, 2014, 9, e111122.	1.1	14
65	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
66	Metagenomic insights into the human gut resistome and the forces that shape it. BioEssays, 2014, 36, 316-329.	1.2	76
67	Country-specific antibiotic use practices impact the human gut resistome. Genome Research, 2013, 23, 1163-1169.	2.4	356
68	Individuality and temporal stability of the human gut microbiome. Central Asian Journal of Global Health, 2013, 2, 120.	0.6	6
69	The Pfam protein families database. Nucleic Acids Research, 2012, 40, D290-D301.	6.5	3,306
70	Evolution of Protein Domain Architectures. Methods in Molecular Biology, 2012, 856, 187-216.	0.4	47
71	Domain architecture conservation in orthologs. BMC Bioinformatics, 2011, 12, 326.	1.2	54
72	OrthoDisease: tracking disease gene orthologs across 100 species. Briefings in Bioinformatics, 2011, 12, 463-473.	3.2	16

#	Article	IF	Citations
73	Orthology confers intron position conservation. BMC Genomics, 2010, 11, 412.	1.2	29
74	InParanoid 7: new algorithms and tools for eukaryotic orthology analysis. Nucleic Acids Research, 2010, 38, D196-D203.	6.5	576
75	The Pfam protein families database. Nucleic Acids Research, 2010, 38, D211-D222.	6.5	2,693
76	Benchmarking homology detection procedures with low complexity filters. Bioinformatics, 2009, 25, 2500-2505.	1.8	11
77	Domain Tree-Based Analysis of Protein Architecture Evolution. Molecular Biology and Evolution, 2008, 25, 254-264.	3.5	98
78	Predicting protein function from domain content. Bioinformatics, 2008, 24, 1681-1687.	1.8	83
79	Constructing Phylogenetic Supernetworks from Quartets. Lecture Notes in Computer Science, 2008, , 284-295.	1.0	4
80	QNet: An Agglomerative Method for the Construction of Phylogenetic Networks from Weighted Quartets. Molecular Biology and Evolution, 2006, 24, 532-538.	3.5	56
81	A novel exploratory method for visual recombination detection. Genome Biology, 2003, 4, R33.	13.9	19