

Daniel Lundin

List of Publications by Year in descending order

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69
papers

3,337
citations

147801

31
h-index

161849

54
g-index

81
all docs

81
docs citations

81
times ranked

4718
citing authors

#	ARTICLE	IF	CITATIONS
1	Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. PLoS ONE, 2014, 9, e95567.	2.5	218
2	Identification and characterization of a novel botulinum neurotoxin. Nature Communications, 2017, 8, 14130.	12.8	196
3	Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. PLoS ONE, 2014, 9, e89549.	2.5	184
4	Disentangling seasonal bacterioplankton population dynamics by high-frequency sampling. Environmental Microbiology, 2015, 17, 2459-2476.	3.8	142
5	Comparative Genomic Evidence for a Complete Nuclear Pore Complex in the Last Eukaryotic Common Ancestor. PLoS ONE, 2010, 5, e13241.	2.5	132
6	Gut microbiome and innate immune response patterns in eczema-associated eczema. Clinical and Experimental Allergy, 2015, 45, 1419-1429.	2.9	131
7	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. BMC Evolutionary Biology, 2013, 13, 33.	3.2	123
8	Which sequencing depth is sufficient to describe patterns in bacterial diversity?. Environmental Microbiology Reports, 2012, 4, 367-372.	2.4	117
9	Biodegradation as an important sink of aromatic hydrocarbons in the oceans. Nature Geoscience, 2019, 12, 119-125.	12.9	114
10	Microbial metagenomes from three aquifers in the Fennoscandian shield terrestrial deep biosphere reveal metabolic partitioning among populations. ISME Journal, 2016, 10, 1192-1203.	9.8	113
11	RNRdb, a curated database of the universal enzyme family ribonucleotide reductase, reveals a high level of misannotation in sequences deposited to Genbank. BMC Genomics, 2009, 10, 589.	2.8	109
12	Metagenomic De Novo Assembly of an Aquatic Representative of the Verrucomicrobial Class Spartobacteria. MBio, 2013, 4, e00569-12.	4.1	107
13	Endosymbiont gene functions impaired and rescued by polymerase infidelity at poly(A) tracts. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 14934-14939.	7.1	92
14	Transplant experiments uncover Baltic Sea basin-specific responses in bacterioplankton community composition and metabolic activities. Frontiers in Microbiology, 2015, 6, 223.	3.5	90
15	Phylogenetic Signals of Salinity and Season in Bacterial Community Composition Across the Salinity Gradient of the Baltic Sea. Frontiers in Microbiology, 2016, 7, 1883.	3.5	81
16	Deregulation of the A-to-I RNA editing mechanism in psychiatric disorders. Human Molecular Genetics, 2012, 21, 311-321.	2.9	80
17	The Origin and Evolution of Ribonucleotide Reduction. Life, 2015, 5, 604-636.	2.4	74
18	Consequences of increased terrestrial dissolved organic matter and temperature on bacterioplankton community composition during a Baltic Sea mesocosm experiment. Ambio, 2015, 44, 402-412.	5.5	70

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19	Response of marine bacterioplankton pH homeostasis gene expression to elevated CO ₂ . <i>Nature Climate Change</i> , 2016, 6, 483-487.	18.8	68
20	Use of Structural Phylogenetic Networks for Classification of the Ferritin-like Superfamily. <i>Journal of Biological Chemistry</i> , 2012, 287, 20565-20575.	3.4	66
21	Ribonucleotide reduction - horizontal transfer of a required function spans all three domains. <i>BMC Evolutionary Biology</i> , 2010, 10, 383.	3.2	61
22	Basic Leucine Zipper Protein Cnc-C Is a Substrate and Transcriptional Regulator of the <i>Drosophila</i> 26S Proteasome. <i>Molecular and Cellular Biology</i> , 2011, 31, 897-909.	2.3	54
23	BARM and BalticMicrobeDB, a reference metagenome and interface to meta-omic data for the Baltic Sea. <i>Scientific Data</i> , 2018, 5, 180146.	5.3	54
24	Metal-free ribonucleotide reduction powered by a DOPA radical in <i>Mycoplasma</i> pathogens. <i>Nature</i> , 2018, 563, 416-420.	27.8	50
25	A Metagenomics Transect into the Deepest Point of the Baltic Sea Reveals Clear Stratification of Microbial Functional Capacities. <i>PLoS ONE</i> , 2013, 8, e74983.	2.5	48
26	Prokaryotic Responses to Ammonium and Organic Carbon Reveal Alternative CO ₂ Fixation Pathways and Importance of Alkaline Phosphatase in the Mesopelagic North Atlantic. <i>Frontiers in Microbiology</i> , 2016, 7, 1670.	3.5	47
27	Microbial consumption of organophosphate esters in seawater under phosphorus limited conditions. <i>Scientific Reports</i> , 2019, 9, 233.	3.3	44
28	Novel ATP-cone-driven allosteric regulation of ribonucleotide reductase via the radical-generating subunit. <i>ELife</i> , 2018, 7, .	6.0	40
29	Diversity in Overall Activity Regulation of Ribonucleotide Reductase. <i>Journal of Biological Chemistry</i> , 2015, 290, 17339-17348.	3.4	39
30	Metapopulation theory identifies biogeographical patterns among core and satellite marine bacteria scaling from tens to thousands of kilometers. <i>Environmental Microbiology</i> , 2017, 19, 1222-1236.	3.8	38
31	A computational screen for site selective A-to-I editing detects novel sites in neuron specific Hu proteins. <i>BMC Bioinformatics</i> , 2010, 11, 6.	2.6	35
32	High-resolution crystal structures of the flavoprotein NrdI in oxidized and reduced states – an unusual flavodoxin. <i>FEBS Journal</i> , 2010, 277, 4265-4277.	4.7	33
33	The POU/Oct Transcription Factor Pdm1/nub Is Necessary for a Beneficial Gut Microbiota and Normal Lifespan of <i>Drosophila</i> . <i>Journal of Innate Immunity</i> , 2016, 8, 412-426.	3.8	31
34	Comparative proteomics reveals signature metabolisms of exponentially growing and stationary phase marine bacteria. <i>Environmental Microbiology</i> , 2017, 19, 2301-2319.	3.8	30
35	Structural Mechanism of Allosteric Activity Regulation in a Ribonucleotide Reductase with Double ATP Cones. <i>Structure</i> , 2016, 24, 906-917.	3.3	28
36	Microbial responses to anthropogenic dissolved organic carbon in the Arctic and Antarctic coastal seawaters. <i>Environmental Microbiology</i> , 2019, 21, 1466-1481.	3.8	28

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37	Labile Dissolved Organic Matter Compound Characteristics Select for Divergence in Marine Bacterial Activity and Transcription. <i>Frontiers in Microbiology</i> , 2020, 11, 588778.	3.5	26
38	Reconstructing ecosystem functions of the active microbial community of the Baltic Sea oxygen depleted sediments. <i>PeerJ</i> , 2016, 4, e1593.	2.0	25
39	Direct effects of organic pollutants on the growth and gene expression of the Baltic Sea model bacterium <i>Rheinheimera</i> sp. BAL341. <i>Microbial Biotechnology</i> , 2019, 12, 892-906.	4.2	19
40	Cobalamin and microbial plankton dynamics along a coastal to offshore transect in the Eastern North Atlantic Ocean. <i>Environmental Microbiology</i> , 2021, 23, 1559-1583.	3.8	19
41	The Fennoscandian Shield deep terrestrial virosphere suggests slow motion "boom and burst" cycles. <i>Communications Biology</i> , 2021, 4, 307.	4.4	19
42	Rapid bacterioplankton transcription cascades regulate organic matter utilization during phytoplankton bloom progression in a coastal upwelling system. <i>ISME Journal</i> , 2022, 16, 2360-2372.	9.8	17
43	Characterization of a REG/PA28 Proteasome Activator Homolog in <i>Dictyostelium discoideum</i> Indicates that the Ubiquitin- and ATP-Independent REG ³ Proteasome Is an Ancient Nuclear Protease. <i>Eukaryotic Cell</i> , 2009, 8, 844-851.	3.4	16
44	Responses of Coastal Marine Microbiomes Exposed to Anthropogenic Dissolved Organic Carbon. <i>Environmental Science & Technology</i> , 2021, 55, 9609-9621.	10.0	16
45	A glutaredoxin domain fused to the radical-generating subunit of ribonucleotide reductase (RNR) functions as an efficient RNR reductant. <i>Journal of Biological Chemistry</i> , 2018, 293, 15889-15900.	3.4	15
46	Microbial Plankton Community Structure and Function Responses to Vitamin B ₁₂ and B ₁ Amendments in an Upwelling System. <i>Applied and Environmental Microbiology</i> , 2021, 87, e0152521.	3.1	15
47	Oxygen-deficient water zones in the Baltic Sea promote uncharacterized Hg methylating microorganisms in underlying sediments. <i>Limnology and Oceanography</i> , 2022, 67, 135-146.	3.1	15
48	A unique cysteine-rich zinc finger domain present in a majority of class II ribonucleotide reductases mediates catalytic turnover. <i>Journal of Biological Chemistry</i> , 2017, 292, 19044-19054.	3.4	14
49	A Rare Combination of Ribonucleotide Reductases in the Social Amoeba <i>Dictyostelium discoideum</i> . <i>Journal of Biological Chemistry</i> , 2013, 288, 8198-8208.	3.4	12
50	Comparative Analysis of the Nodule Transcriptomes of <i>Ceanothus thyrsiflorus</i> (Rhamnaceae, Rosales) and <i>Datisca glomerata</i> (Datisceae, Cucurbitales). <i>Frontiers in Plant Science</i> , 2018, 9, 1629.	3.6	12
51	A ribonucleotide reductase from <i>Clostridium botulinum</i> reveals distinct evolutionary pathways to regulation via the overall activity site. <i>Journal of Biological Chemistry</i> , 2020, 295, 15576-15587.	3.4	12
52	Fish Skin Microbiomes Are Highly Variable Among Individuals and Populations but Not Within Individuals. <i>Frontiers in Microbiology</i> , 2021, 12, 767770.	3.5	12
53	Diversity and Host Interactions among Virulent and Temperate Baltic Sea <i>Flavobacterium</i> Phages. <i>Viruses</i> , 2020, 12, 158.	3.3	11
54	Class I d ribonucleotide reductase utilizes a Mn ² (IV,III) cofactor and undergoes large conformational changes on metal loading. <i>Journal of Biological Inorganic Chemistry</i> , 2019, 24, 863-877.	2.6	10

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55	The Crystal Structure of <i>Thermotoga maritima</i> Class III Ribonucleotide Reductase Lacks a Radical Cysteine Pre-Positioned in the Active Site. <i>PLoS ONE</i> , 2015, 10, e0128199.	2.5	10
56	Chemical flexibility of heterobimetallic Mn/Fe cofactors: R2lox and R2c proteins. <i>Journal of Biological Chemistry</i> , 2019, 294, 18372-18386.	3.4	8
57	Non-host class II ribonucleotide reductase in <i>Thermus</i> viruses: sequence adaptation and host interaction. <i>PeerJ</i> , 2019, 7, e6700.	2.0	8
58	Microbial Community and Metabolic Activity in Thiocyanate Degrading Low Temperature Microbial Fuel Cells. <i>Frontiers in Microbiology</i> , 2018, 9, 2308.	3.5	7
59	Seasonal Dynamics in Carbon Cycling of Marine Bacterioplankton Are Lifestyle Dependent. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	7
60	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. <i>Scientific Data</i> , 2019, 6, 207.	5.3	6
61	Structural and Biochemical Investigation of Class I Ribonucleotide Reductase from the Hyperthermophile <i>Aquifex aeolicus</i> . <i>Biochemistry</i> , 2022, 61, 92-106.	2.5	6
62	Dynamics of Baltic Sea phages driven by environmental changes. <i>Environmental Microbiology</i> , 2021, 23, 4576-4594.	3.8	5
63	Structural determinants and distribution of phosphate specificity in ribonucleotide reductases. <i>Journal of Biological Chemistry</i> , 2021, 297, 101008.	3.4	4
64	Freeze-drying can replace cold-chains for transport and storage of fecal microbiome samples. <i>PeerJ</i> , 2022, 10, e13095.	2.0	3
65	H3ABioNet computational metagenomics workshop in Mauritius: training to analyse microbial diversity for Africa. <i>Standards in Genomic Sciences</i> , 2015, 10, .	1.5	2
66	The evolution of early cellular systems viewed through the lens of biological interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 1144.	3.5	2
67	A nucleotide-sensing oligomerization mechanism that controls NrdR-dependent transcription of ribonucleotide reductases. <i>Nature Communications</i> , 2022, 13, 2700.	12.8	2
68	Taxon-Specific Shifts in Bacterial and Archaeal Transcription of Dissolved Organic Matter Cycling Genes in a Stratified Fjord. <i>MSystems</i> , 2021, 6, e0057521.	3.8	1
69	Microbial metabolic routes in metagenome assembled genomes are mirrored by the mass balance of polycyclic aromatic hydrocarbons in a high altitude lake. <i>Environmental Pollution</i> , 2022, 308, 119592.	7.5	0