

Daniel Lundin

List of Publications by Year in descending order

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Version: 2024-02-01

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	Oxygenâ€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
2	Freeze-drying can replace cold-chains for transport and storage of fecal microbiome samples. <i>PeerJ</i> , 2022, 10, e13095.	2.0	3
3	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
4	A nucleotide-sensing oligomerization mechanism that controls NrdR-dependent transcription of ribonucleotide reductases. <i>Nature Communications</i> , 2022, 13, 2700.	12.8	2
5	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
6	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
7	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
8	Responses of Coastal Marine Microbiomes Exposed to Anthropogenic Dissolved Organic Carbon. <i>Environmental Science & Technology</i> , 2021, 55, 9609-9621.	10.0	16
9	The Fennoscandian Shield deep terrestrial virosphere suggests slow motion â€boom and burstâ€™ cycles. <i>Communications Biology</i> , 2021, 4, 307.	4.4	19
10	Dynamics of Baltic Sea phages driven by environmental changes. <i>Environmental Microbiology</i> , 2021, 23, 4576-4594.	3.8	5
11	Structural determinants and distribution of phosphate specificity in ribonucleotide reductases. <i>Journal of Biological Chemistry</i> , 2021, 297, 101008.	3.4	4
12	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
13	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
14	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
15	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
16	Diversity and Host Interactions among Virulent and Temperate Baltic Sea <i>Flavobacterium</i> Phages. <i>Viruses</i> , 2020, 12, 158.	3.3	11
17	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
18	Class Id 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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19	Direct effects of organic pollutants on the growth and gene expression of the Baltic Sea model bacterium Rheinheimerasp. BAL341. <i>Microbial Biotechnology</i> , 2019, 12, 892-906.	4.2	19
20	Metagenomes and metatranscriptomes from boreal potential and actual acid sulfate soil materials. <i>Scientific Data</i> , 2019, 6, 207.	5.3	6
21	Microbial consumption of organophosphate esters in seawater under phosphorus limited conditions. <i>Scientific Reports</i> , 2019, 9, 233.	3.3	44
22	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
23	Chemical flexibility of heterobimetallic Mn/Fe cofactors: R2lox and R2c proteins. <i>Journal of Biological Chemistry</i> , 2019, 294, 18372-18386.	3.4	8
24	Biodegradation as an important sink of aromatic hydrocarbons in the oceans. <i>Nature Geoscience</i> , 2019, 12, 119-125.	12.9	114
25	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
26	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
27	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
28	Microbial Community and Metabolic Activity in Thiocyanate Degrading Low Temperature Microbial Fuel Cells. <i>Frontiers in Microbiology</i> , 2018, 9, 2308.	3.5	7
29	Metal-free ribonucleotide reduction powered by a DOPA radical in <i>Mycoplasma</i> pathogens. <i>Nature</i> , 2018, 563, 416-420.	27.8	50
30	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
31	Novel ATP-cone-driven allosteric regulation of ribonucleotide reductase via the radical-generating subunit. <i>ELife</i> , 2018, 7, .	6.0	40
32	Comparative proteomics reveals signature metabolisms of exponentially growing and stationary phase marine bacteria. <i>Environmental Microbiology</i> , 2017, 19, 2301-2319.	3.8	30
33	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
34	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
35	Identification and characterization of a novel botulinum neurotoxin. <i>Nature Communications</i> , 2017, 8, 14130.	12.8	196
36	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

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37	Phylogenetic Signals of Salinity and Season in Bacterial Community Composition Across the Salinity Gradient of the Baltic Sea. <i>Frontiers in Microbiology</i> , 2016, 7, 1883.	3.5	81
38	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
39	Structural Mechanism of Allosteric Activity Regulation in a Ribonucleotide Reductase with Double ATP Cones. <i>Structure</i> , 2016, 24, 906-917.	3.3	28
40	Response of marine bacterioplankton pH homeostasis gene expression to elevated CO ₂ . <i>Nature Climate Change</i> , 2016, 6, 483-487.	18.8	68
41	Microbial metagenomes from three aquifers in the Fennoscandian shield terrestrial deep biosphere reveal metabolic partitioning among populations. <i>ISME Journal</i> , 2016, 10, 1192-1203.	9.8	113
42	Reconstructing ecosystem functions of the active microbial community of the Baltic Sea oxygen depleted sediments. <i>PeerJ</i> , 2016, 4, e1593.	2.0	25
43	H3ABioNet computational metagenomics workshop in Mauritius: training to analyse microbial diversity for Africa. <i>Standards in Genomic Sciences</i> , 2015, 10, .	1.5	2
44	Transplant experiments uncover Baltic Sea basin-specific responses in bacterioplankton community composition and metabolic activities. <i>Frontiers in Microbiology</i> , 2015, 6, 223.	3.5	90
45	The evolution of early cellular systems viewed through the lens of biological interactions. <i>Frontiers in Microbiology</i> , 2015, 6, 1144.	3.5	2
46	Consequences of increased terrestrial dissolved organic matter and temperature on bacterioplankton community composition during a Baltic Sea mesocosm experiment. <i>Ambio</i> , 2015, 44, 402-412.	5.5	70
47	Diversity in Overall Activity Regulation of Ribonucleotide Reductase. <i>Journal of Biological Chemistry</i> , 2015, 290, 17339-17348.	3.4	39
48	Disentangling seasonal bacterioplankton population dynamics by high-frequency sampling. <i>Environmental Microbiology</i> , 2015, 17, 2459-2476.	3.8	142
49	The Origin and Evolution of Ribonucleotide Reduction. <i>Life</i> , 2015, 5, 604-636.	2.4	74
50	Gut microbiome and innate immune response patterns in <i>Helicobacter pylori</i> -associated eczema. <i>Clinical and Experimental Allergy</i> , 2015, 45, 1419-1429.	2.9	131
51	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
52	Functional Tradeoffs Underpin Salinity-Driven Divergence in Microbial Community Composition. <i>PLoS ONE</i> , 2014, 9, e89549.	2.5	184
53	Systematic Design of 18S rRNA Gene Primers for Determining Eukaryotic Diversity in Microbial Consortia. <i>PLoS ONE</i> , 2014, 9, e95567.	2.5	218
54	A bioinformatic analysis of ribonucleotide reductase genes in phage genomes and metagenomes. <i>BMC Evolutionary Biology</i> , 2013, 13, 33.	3.2	123

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55	Metagenomic <i>De Novo</i> Assembly of an Aquatic Representative of the Verrucomicrobial Class <i>Spartobacteria</i> . <i>MBio</i> , 2013, 4, e00569-12.	4.1	107
56	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
57	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
58	Deregulation of the A-to-I RNA editing mechanism in psychiatric disorders. <i>Human Molecular Genetics</i> , 2012, 21, 311-321.	2.9	80
59	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
60	Which sequencing depth is sufficient to describe patterns in bacterial α - and β -diversity?. <i>Environmental Microbiology Reports</i> , 2012, 4, 367-372.	2.4	117
61	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
62	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
63	Ribonucleotide reduction - horizontal transfer of a required function spans all three domains. <i>BMC Evolutionary Biology</i> , 2010, 10, 383.	3.2	61
64	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
65	Comparative Genomic Evidence for a Complete Nuclear Pore Complex in the Last Eukaryotic Common Ancestor. <i>PLoS ONE</i> , 2010, 5, e13241.	2.5	132
66	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
67	RNRdb, a curated database of the universal enzyme family ribonucleotide reductase, reveals a high level of misannotation in sequences deposited to Genbank. <i>BMC Genomics</i> , 2009, 10, 589.	2.8	109
68	Endosymbiont gene functions impaired and rescued by polymerase infidelity at poly(A) tracts. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 14934-14939.	7.1	92
69	Seasonal Dynamics in Carbon Cycling of Marine Bacterioplankton Are Lifestyle Dependent. <i>Frontiers in Microbiology</i> , 0, 13, .	3.5	7