

Paul F Long

List of Publications by Year in descending order

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54
papers

1,706
citations

304743

22
h-index

289244

40
g-index

56
all docs

56
docs citations

56
times ranked

2513
citing authors

#	ARTICLE	IF	CITATIONS
1	ClustScan : an integrated program package for the semi-automatic annotation of modular biosynthetic gene clusters and in silico prediction of novel chemical structures. <i>Nucleic Acids Research</i> , 2008, 36, 6882-6892.	14.5	181
2	Shotgun Cloning and Heterologous Expression of the Patellamide Gene Cluster as a Strategy to Achieving Sustained Metabolite Production. <i>ChemBioChem</i> , 2005, 6, 1760-1765.	2.6	165
3	Enzymes of the shikimic acid pathway encoded in the genome of a basal metazoan, <i>Nematostella vectensis</i> , have microbial origins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 2533-2537.	7.1	119
4	Effect of Antibiotics for Otitis Media on Mastoiditis in Children: A Retrospective Cohort Study Using the United Kingdom General Practice Research Database. <i>Pediatrics</i> , 2009, 123, 424-430.	2.1	112
5	Mycosporine-Like Amino Acids for Skin Photoprotection. <i>Current Medicinal Chemistry</i> , 2019, 25, 5512-5527.	2.4	99
6	Proteomic characterisation of toxins isolated from nematocysts of the South Atlantic jellyfish <i>Olindias sambaquiensis</i> . <i>Toxicon</i> , 2013, 71, 11-17.	1.6	65
7	Gene duplications are extensive and contribute significantly to the toxic proteome of nematocysts isolated from <i>Acropora digitifera</i> (Cnidaria: Anthozoa: Scleractinia). <i>BMC Genomics</i> , 2015, 16, 774.	2.8	58
8	The mycosporine-like amino acids porphyra-334 and shinorine are antioxidants and direct antagonists of Keap1-Nrf2 binding. <i>Biochimie</i> , 2018, 154, 35-44.	2.6	54
9	Rising levels of atmospheric oxygen and evolution of Nrf2. <i>Scientific Reports</i> , 2016, 6, 27740.	3.3	52
10	KEGG orthology-based annotation of the predicted proteome of <i>Acropora digitifera</i> : ZoophyteBase - an open access and searchable database of a coral genome. <i>BMC Genomics</i> , 2013, 14, 509.	2.8	51
11	Methyltransferase Is Shared between the Pentose Phosphate and Shikimate Pathways and Is Essential for Mycosporine-Like Amino Acid Biosynthesis in <i>Anabaena variabilis</i> ATCC 29413. <i>ChemBioChem</i> , 2015, 16, 320-327.	2.6	48
12	A Profile of an Endosymbiont-enriched Fraction of the Coral <i>Stylophora pistillata</i> Reveals Proteins Relevant to Microbial-Host Interactions. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.015487.	3.8	46
13	Bacterial diversity of polluted surface sediments in the northern Adriatic Sea. <i>Systematic and Applied Microbiology</i> , 2015, 38, 189-197.	2.8	45
14	Plasticity of the <i>Streptomyces</i> Genome-Evolution and Engineering of New Antibiotics. <i>Current Medicinal Chemistry</i> , 2005, 12, 1697-1704.	2.4	39
15	Redundant Pathways of Sunscreen Biosynthesis in a Cyanobacterium. <i>ChemBioChem</i> , 2012, 13, 531-533.	2.6	39
16	Proteomics Links the Redox State to Calcium Signaling During Bleaching of the Scleractinian Coral <i>Acropora microphthalmum</i> on Exposure to High Solar Irradiance and Thermal Stress. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 585-595.	3.8	38
17	Machine learning can differentiate venom toxins from other proteins having non-toxic physiological functions. <i>PeerJ Computer Science</i> , 0, 2, e90.	4.5	38
18	Predicting substrate specificity of adenylation domains of nonribosomal peptide synthetases and other protein properties by latent semantic indexing. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 461-467.	3.0	37

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19	Gene Expression in the Scleractinian <i>Acropora microphthalma</i> Exposed to High Solar Irradiance Reveals Elements of Photoprotection and Coral Bleaching. <i>PLoS ONE</i> , 2010, 5, e13975.	2.5	32
20	Characterising the enzymatic profile of crude tentacle extracts from the South Atlantic jellyfish <i>Olindias sambaquiensis</i> (Cnidaria: Hydrozoa). <i>Toxicon</i> , 2016, 119, 1-7.	1.6	25
21	Global genome analysis of the shikimic acid pathway reveals greater gene loss in host-associated than in free-living bacteria. <i>BMC Genomics</i> , 2010, 11, 628.	2.8	24
22	Comparative proteomics reveals recruitment patterns of some protein families in the venoms of Cnidaria. <i>Toxicon</i> , 2017, 137, 19-26.	1.6	24
23	Development and validation of a rapid LC-MS/MS method for the quantification of mycosporines and mycosporine-like amino acids (MAAs) from cyanobacteria. <i>Algal Research</i> , 2020, 46, 101796.	4.6	24
24	Horizontal gene transfer and gene conversion drive evolution of modular polyketide synthases. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 1541-1547.	3.0	22
25	Databases of the thiotemplate modular systems (CSDB) and their in silico recombinants (r-CSDB). <i>Journal of Industrial Microbiology and Biotechnology</i> , 2013, 40, 653-659.	3.0	22
26	Bioinformatics analyses provide insight into distant homology of the Keap1-Nrf2 pathway. <i>Free Radical Biology and Medicine</i> , 2015, 88, 373-380.	2.9	18
27	“Beyond Primary Sequence” Proteomic Data Reveal Complex Toxins in Cnidarian Venoms. <i>Integrative and Comparative Biology</i> , 2019, 59, 777-785.	2.0	18
28	Dosing of oral penicillins in children: is big child=half an adult, small child=half a big child, baby=half a small child still the best we can do?. <i>BMJ: British Medical Journal</i> , 2011, 343, d7803-d7803.	2.3	17
29	Predicting the Nature and Timing of Epimerisation on a Modular Polyketide Synthase. <i>ChemBioChem</i> , 2007, 8, 28-31.	2.6	16
30	Evolutionary concepts in natural products discovery: what actinomycetes have taught us. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2014, 41, 211-217.	3.0	16
31	Structural and functional diversity of asparaginases: Overview and recommendations for a revised nomenclature. <i>Biotechnology and Applied Biochemistry</i> , 2022, 69, 503-513.	3.1	14
32	Evolutionary dynamics of modular polyketide synthases, with implications for protein design and engineering. <i>Journal of Antibiotics</i> , 2011, 64, 89-92.	2.0	13
33	A novel docking domain interface model predicting recombination between homoeologous modular biosynthetic gene clusters. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2011, 38, 1295-1304.	3.0	13
34	Diversification of Animal Venom Peptides—Were Jellyfish Amongst the First Combinatorial Chemists?. <i>ChemBioChem</i> , 2013, 14, 1407-1409.	2.6	13
35	Oral penicillin prescribing for children in the UK: a comparison with NICE for Children age-band recommendations. <i>British Journal of General Practice</i> , 2014, 64, e217-e222.	1.4	12
36	Recombinatorial biosynthesis of polyketides. <i>Journal of Industrial Microbiology and Biotechnology</i> , 2012, 39, 503-511.	3.0	10

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37	Combinations of long peptide sequence blocks can be used to describe toxin diversification in venomous animals. <i>Toxicon</i> , 2015, 95, 84-92.	1.6	9
38	Bioprospecting for Genes Encoding Hydrocarbon-Degrading Enzymes from Metagenomic Samples Isolated from Northern Adriatic Sea Sediments. <i>Food Technology and Biotechnology</i> , 2018, 56, 270-277.	2.1	9
39	Stress-Free Evolution: The Nrf-Coordinated Oxidative Stress Response in Early Diverging Metazoans. <i>Integrative and Comparative Biology</i> , 2019, 59, 799-810.	2.0	9
40	Venom Composition Does Not Vary Greatly Between Different Nematocyst Types Isolated from the Primary Tentacles of <i>Olindias sambaquiensis</i> (Cnidaria: Hydrozoa). <i>Biological Bulletin</i> , 2019, 237, 26-35.	1.8	7
41	Interferences that impact measuring optimal L-asparaginase activity and consequent errors interpreting these data. <i>Applied Microbiology and Biotechnology</i> , 2019, 103, 5161-5166.	3.6	7
42	An improved method for simple and accurate colorimetric determination of L-asparaginase enzyme activity using Nessler's reagent. <i>Journal of Chemical Technology and Biotechnology</i> , 2021, 96, 1326-1332.	3.2	7
43	Genetic and biochemical evidence for redundant pathways leading to mycosporine-like amino acid biosynthesis in the cyanobacterium <i>Sphaerospermopsis torques-reginae</i> ; ITP-024. <i>Algae</i> , 2020, 35, 177-187.	2.3	7
44	Clustering of protein domains for functional and evolutionary studies. <i>BMC Bioinformatics</i> , 2009, 10, 335.	2.6	6
45	Recruitment of toxin-like proteins with ancestral venom function supports endoparasitic lifestyles of Myxozoa. <i>PeerJ</i> , 2021, 9, e11208.	2.0	6
46	Reciprocal transplantation of the heterotrophic coral <i>Tubastraea coccinea</i> (Scleractinia): Evolution, 2020, 10, 1794-1803.	1.9	5
47	2-epi-5-epi-Valiolone synthase activity is essential for maintaining phycobilisome composition in the cyanobacterium <i>Anabaena variabilis</i> ATCC 29413 when grown in the presence of a carbon source. <i>Photosynthesis Research</i> , 2013, 116, 33-43.	2.9	4
48	Did the accuracy of oral amoxicillin dosing of children improve after British National Formulary dose revisions in 2014? National cross-sectional survey in England. <i>BMJ Open</i> , 2017, 7, e016363.	1.9	4
49	Epidemiology of <i>Polypodium hydriforme</i> in American Paddlefish. <i>Journal of Fish Diseases</i> , 2020, 43, 979-989.	1.9	3
50	The Efficacy of Antibacterial Travel Wash Soaps. <i>Journal of Travel Medicine</i> , 2006, 13, 114-114.	3.0	1
51	Chemical Responses to the Biotic and Abiotic Environment by Early Diverging Metazoans Revealed in the Post-Genomic Age. <i>Integrative and Comparative Biology</i> , 2019, 59, 731-738.	2.0	1
52	MEGGASENSE - the Metagenome/Genome Annotated Sequence Natural Language Search Engine: a Platform for the Construction of Sequence Data Warehouses. <i>Food Technology and Biotechnology</i> , 2017, 55, 251-257.	2.1	1
53	Horizontal transfer of a natterin-like toxin encoding gene within the holobiont of the reef building coral (Cnidaria: Anthozoa: Scleractinia) and across multiple animal lineages. <i>Journal of Venom Research</i> , 2020, 10, 7-12.	0.6	1
54	Early origins of oral penicillin dosing for children. <i>Archives of Disease in Childhood</i> , 2020, 105, 1118-1119.	1.9	0