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Bioinformatics

37, 2473-2475

DOI: [10.1093/bioinformatics/btab007](https://doi.org/10.1093/bioinformatics/btab007)

Citation Report

#	ARTICLE	IF	CITATIONS
1	cblaster: a remote search tool for rapid identification and visualization of homologous gene clusters. <i>Bioinformatics Advances</i> , 2021, 1, .	0.9	101
2	The confluence of big data and evolutionary genome mining for the discovery of natural products. <i>Natural Product Reports</i> , 2021, 38, 2024-2040.	5.2	30
3	The year 2020 in natural product bioinformatics: an overview of the latest tools and databases. <i>Natural Product Reports</i> , 2021, 38, 301-306.	5.2	44
4	Genome Mining and Evolutionary Analysis Reveal Diverse Type III Polyketide Synthase Pathways in Cyanobacteria. <i>Genome Biology and Evolution</i> , 2021, 13, .	1.1	8
7	Unexpected distribution of the 4-formylaminoxyvinylglycine (FVG) biosynthetic pathway in <i>Pseudomonas</i> and beyond. <i>PLoS ONE</i> , 2021, 16, e0247348.	1.1	8
8	Comparative genomics of the ADA clade within the Nostocales. <i>Harmful Algae</i> , 2021, 104, 102037.	2.2	11
9	Grincamycins Pâ€™T: Rearranged Angucyclines from the Marine Sediment-Derived <i>Streptomyces</i> sp. CNZ-748 Inhibit Cell Lines of the Rare Cancer <i>Pseudomyxoma Peritonei</i> . <i>Journal of Natural Products</i> , 2021, 84, 1638-1648.	1.5	9
11	A functional bacteria-derived restriction modification system in the mitochondrion of a heterotrophic protist. <i>PLoS Biology</i> , 2021, 19, e3001126.	2.6	6
12	Prophage Genomics and Ecology in the Family Rhodobacteraceae. <i>Microorganisms</i> , 2021, 9, 1115.	1.6	22
14	Discovery and Biosynthesis of a Structurally Dynamic Antibacterial Diterpenoid. <i>Angewandte Chemie - International Edition</i> , 2021, 60, 14163-14170.	7.2	20
18	Secondary metabolite biosynthetic diversity in the fungal family <i>Hypoxylaceae</i> and <i>Xylaria hypoxylon</i> . <i>Studies in Mycology</i> , 2021, 99, 100118-100118.	4.5	27
19	Bioinformatic Analysis of the <i>Campylobacter jejuni</i> Type VI Secretion System and Effector Prediction. <i>Frontiers in Microbiology</i> , 2021, 12, 694824.	1.5	10
20	<i>Burkholderia</i> from Fungus Gardens of Fungus-Growing Ants Produces Antifungals That Inhibit the Specialized Parasite <i>Escovopsis</i> . <i>Applied and Environmental Microbiology</i> , 2021, 87, e0017821.	1.4	8
21	Identification and Genomic Characterization of Two Previously Unknown Magnetotactic Nitrospirae. <i>Frontiers in Microbiology</i> , 2021, 12, 690052.	1.5	7
23	Comparative analyses of the <i>Hymenoscyphus fraxineus</i> and <i>Hymenoscyphus albidus</i> genomes reveals potentially adaptive differences in secondary metabolite and transposable element repertoires. <i>BMC Genomics</i> , 2021, 22, 503.	1.2	6
25	Genomic characterization of three marine fungi, including <i>Emericellopsis atlantica</i> sp. nov. with signatures of a generalist lifestyle and marine biomass degradation. <i>IMA Fungus</i> , 2021, 12, 21.	1.7	23
31	Investigating the Role of Vanadium-Dependent Haloperoxidase Enzymology in Microbial Secondary Metabolism and Chemical Ecology. <i>MSystems</i> , 2021, 6, e0078021.	1.7	5
32	Genomic Stability and Genetic Defense Systems in <i>Dolosigranulum pigrum</i> , a Candidate Beneficial Bacterium from the Human Microbiome. <i>MSystems</i> , 2021, 6, e0042521.	1.7	11

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33	Azaphilone Pigments from <i>Hypoxylon rubiginosum</i> and <i>H. texense</i> : Absolute Configuration, Bioactivity, and Biosynthesis. <i>European Journal of Organic Chemistry</i> , 2021, 2021, 5094-5103.	1.2	5
34	Skyllamycins D and E, Non-Ribosomal Cyclic Depsipeptides from Lichen-Sourced <i>Streptomyces anulatus</i> . <i>Journal of Natural Products</i> , 2021, 84, 2536-2543.	1.5	15
36	Diversification of the Type VI Secretion System in <i>Agrobacteria</i> . <i>MBio</i> , 2021, 12, e0192721.	1.8	15
37	Infant gut strain persistence is associated with maternal origin, phylogeny, and traits including surface adhesion and iron acquisition. <i>Cell Reports Medicine</i> , 2021, 2, 100393.	3.3	39
38	Plasmidome of <i>Listeria</i> spp. – The repA-Family Business. <i>International Journal of Molecular Sciences</i> , 2021, 22, 10320.	1.8	7
39	Final Destination? Pinpointing <i>Hyella disjuncta</i> sp. nov. PCC 6712 (Cyanobacteria) Based on Taxonomic Aspects, Multicellularity, Nitrogen Fixation and Biosynthetic Gene Clusters. <i>Life</i> , 2021, 11, 916.	1.1	2
40	Microdiversity of <i>Enterococcus faecalis</i> isolates in cases of infective endocarditis: selection of non-synonymous mutations and large deletions is associated with phenotypic modifications. <i>Emerging Microbes and Infections</i> , 2021, 10, 929-938.	3.0	9
42	Phage tail-like nanostructures affect microbial interactions between <i>Streptomyces</i> and fungi. <i>Scientific Reports</i> , 2021, 11, 20116.	1.6	9
43	Episymbiotic <i>Saccharibacteria</i> suppresses gingival inflammation and bone loss in mice through host bacterial modulation. <i>Cell Host and Microbe</i> , 2021, 29, 1649-1662.e7.	5.1	39
44	Genome Study of a Novel Virulent Phage vB_SspS_KASIA and Mu-like Prophages of <i>Shewanella</i> sp. M16 Provides Insights into the Genetic Diversity of the <i>Shewanella</i> Virome. <i>International Journal of Molecular Sciences</i> , 2021, 22, 11070.	1.8	2
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51	Bilateral symmetry of linear streptomycete chromosomes. <i>Microbial Genomics</i> , 2021, 7, .	1.0	8
53	A <i>Campylobacter</i> integrative and conjugative element with a CRISPR-Cas9 system targeting competing plasmids: a history of plasmid warfare?. <i>Microbial Genomics</i> , 2021, 7, .	1.0	6
54	Mobile Genetic Elements Drive Antimicrobial Resistance Gene Spread in <i>Pasteurellaceae</i> Species. <i>Frontiers in Microbiology</i> , 2021, 12, 773284.	1.5	11
56	The CbbQO-type rubisco activases encoded in carboxysome gene clusters can activate carboxysomal form IA rubiscos. <i>Journal of Biological Chemistry</i> , 2022, 298, 101476.	1.6	5
57	Bacteriophages Roam the Wheat Phyllosphere. <i>Viruses</i> , 2022, 14, 244.	1.5	13

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58	Isolation and Characterization of a Novel Autographiviridae Phage and Its Combined Effect with Tigecycline in Controlling Multidrug-Resistant <i>Acinetobacter baumannii</i> -Associated Skin and Soft Tissue Infections. <i>Viruses</i> , 2022, 14, 194.	1.5	14
59	Oxidative desulfurization pathway for complete catabolism of sulfoquinovose by bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	18
60	Acquisition of the arginine deiminase system benefits epiparasitic <i>Saccharibacteria</i> and their host bacteria in a mammalian niche environment. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	30
61	MagCluster: a Tool for Identification, Annotation, and Visualization of Magnetosome Gene Clusters. <i>Microbiology Resource Announcements</i> , 2022, 11, e0103121.	0.3	5
62	Genomic Diversity of Bacteriophages Infecting the Genus <i>Acinetobacter</i> . <i>Viruses</i> , 2022, 14, 181.	1.5	12
64	Domoic acid biosynthesis in the red alga <i>Chondria armata</i> suggests a complex evolutionary history for toxin production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	16
65	<i>Bacteroides thetaiotaomicron</i> uses a widespread extracellular DNase to promote bile-dependent biofilm formation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	11
67	Cargo Genes of Tn <i>7</i> -Like Transposons Comprise an Enormous Diversity of Defense Systems, Mobile Genetic Elements, and Antibiotic Resistance Genes. <i>MBio</i> , 2021, 12, e0293821.	1.8	34
68	Genome Mining and Analysis of PKS Genes in <i>Eurotium cristatum</i> E1 Isolated from Fuzhuan Brick Tea. <i>Journal of Fungi (Basel, Switzerland)</i> , 2022, 8, 193.	1.5	3
69	Nigericin and Geldanamycin Are Phytotoxic Specialized Metabolites Produced by the Plant Pathogen <i>Streptomyces</i> sp. 11-1-2. <i>Microbiology Spectrum</i> , 2022, 10, e0231421.	1.2	11
70	Sexual reproduction contributes to the evolution of resistance-breaking isolates of the spinach pathogen <i>Peronospora effusa</i> . <i>Environmental Microbiology</i> , 2022, 24, 1622-1637.	1.8	8
71	First identification of bla NDM-5 producing <i>Escherichia coli</i> from neonates and a HIV infected adult in Tanzania. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	6
72	Discovery of actinomycin L, a new member of the actinomycin family of antibiotics. <i>Scientific Reports</i> , 2022, 12, 2813.	1.6	15
73	In silico analyses of maleidride biosynthetic gene clusters. <i>Fungal Biology and Biotechnology</i> , 2022, 9, 2.	2.5	4
74	An inventory of early branch points in microbial phosphonate biosynthesis. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
75	Dual adhesive unipolar polysaccharides synthesized by overlapping biosynthetic pathways in <i>Agrobacterium tumefaciens</i> . <i>Molecular Microbiology</i> , 2022, 117, 1023-1047.	1.2	9
76	Taxonomic distribution and evolutionary analysis of the equol biosynthesis gene cluster. <i>BMC Genomics</i> , 2022, 23, 182.	1.2	10
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78	Healthcare-associated infections caused by chlorhexidine-tolerant <i>Serratia marcescens</i> carrying a promiscuous IncHI2 multi-drug resistance plasmid in a veterinary hospital. <i>PLoS ONE</i> , 2022, 17, e0264848.	1.1	6
79	Genetic analysis of the cold-sensitive growth phenotype of <i>Burkholderia pseudomallei/thailandensis</i> bacteriophage AMP1. <i>Scientific Reports</i> , 2022, 12, 4288.	1.6	0
80	Phages and their satellites encode hotspots of antiviral systems. <i>Cell Host and Microbe</i> , 2022, 30, 740-753.e5.	5.1	129
81	Complete Genome Assemblies of All <i>Xanthomonas translucens</i> Pathotype Strains Reveal Three Genetically Distinct Clades. <i>Frontiers in Microbiology</i> , 2021, 12, 817815.	1.5	19
82	Genomic Characterisation of UFJF_PfDIW6: A Novel Lytic <i>Pseudomonas fluorescens</i> -Phage with Potential for Biocontrol in the Dairy Industry. <i>Viruses</i> , 2022, 14, 629.	1.5	3
83	The genomic basis of the <i>Streptococcus thermophilus</i> health-promoting properties. <i>BMC Genomics</i> , 2022, 23, 210.	1.2	18
84	Kaptive 2.0: updated capsule and lipopolysaccharide locus typing for the <i>Klebsiella pneumoniae</i> species complex. <i>Microbial Genomics</i> , 2022, 8, .	1.0	52
85	The molecular basis of FimT-mediated DNA uptake during bacterial natural transformation. <i>Nature Communications</i> , 2022, 13, 1065.	5.8	10
86	A New Variant of the <i>aadE-sat4-aphA-3</i> Gene Cluster Found in a Conjugative Plasmid from a MDR <i>Campylobacter jejuni</i> Isolate. <i>Antibiotics</i> , 2022, 11, 466.	1.5	6
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92	Investigation of the Molecular Landscape of Bacterial Aromatic Polyketides by Global Analysis of Type II Polyketide Synthases. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	16
93	Investigation of the Molecular Landscape of Bacterial Aromatic Polyketides by Global Analysis of Type II Polyketide Synthases. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	2
96	In situ visualization of glycoside hydrolase family 92 genes in marine flavobacteria. <i>ISME Communications</i> , 2021, 1, .	1.7	1
97	<i>Trichoderma reesei</i> Contains a Biosynthetic Gene Cluster That Encodes the Antifungal Agent Ilicicolin H. <i>Journal of Fungi</i> (Basel, Switzerland), 2021, 7, 1034.	1.5	6
98	Glycoside hydrolase from the GH76 family indicates that marine <i>Salegendibacter</i> sp. Hel_I_6 consumes alpha-mannan from fungi. <i>ISME Journal</i> , 2022, 16, 1818-1830.	4.4	8

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100	Prediction of Prophages and Their Host Ranges in Pathogenic and Commensal <i>Neisseria</i> Species. <i>MSystems</i> , 2022, 7, e0008322.	1.7	9
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102	Genome Mining of Î±-Pyrone Natural Products from Ascidian-Derived Fungus <i>Amphichordafelina</i> SYSU-MS7908. <i>Marine Drugs</i> , 2022, 20, 294.	2.2	6
103	A Novel Isolate of Spherical Multicellular Magnetotactic Prokaryotes Has Two Magnetosome Gene Clusters and Synthesizes Both Magnetite and Greigite Crystals. <i>Microorganisms</i> , 2022, 10, 925.	1.6	1
105	Genomic diversity across the <i>Rickettsia</i> and <i>Candidatus Megaira</i> ™ genera and proposal of genus status for the Torix group. <i>Nature Communications</i> , 2022, 13, 2630.	5.8	22
106	Unusual Lipid Components of <i>Legionella gormanii</i> Membranes. <i>Metabolites</i> , 2022, 12, 418.	1.3	5
108	Characterization of Three Novel Virulent <i>Aeromonas</i> Phages Provides Insights into the Diversity of the Autographiviridae Family. <i>Viruses</i> , 2022, 14, 1016.	1.5	3
109	Poxvirus infection in house finches (<i>Haemorhous mexicanus</i>): Genome sequence analysis and patterns of infection in wild birds. <i>Transboundary and Emerging Diseases</i> , 2022, 69, .	1.3	4
110	The development of extracellular vesicle markers for the fungal phytopathogen <i>Colletotrichum higginsianum</i> . <i>Journal of Extracellular Vesicles</i> , 2022, 11, e12216.	5.5	8
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114	Evolution-Informed Discovery of the Naphthalenone Biosynthetic Pathway in Fungi. <i>MBio</i> , 0, , .	1.8	5
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119	Genome Mining and Metabolomics Unveil Pseudonochelin: A Siderophore Containing 5-Aminosalicylate from a Marine-Derived <i>Pseudonocardia</i> sp. <i>Bacterium. Organic Letters</i> , 2022, 24, 3998-4002.	2.4	7
120	2- <i>Fucosyllactose</i> Increases the Abundance of <i>Blautia</i> in the Presence of Extracellular Fucosidase-Possessing Bacteria. <i>Frontiers in Microbiology</i> , 2022, 13, .	1.5	5
122	High sorbic acid resistance of <i>Penicillium roqueforti</i> is mediated by the SORBUS gene cluster. <i>PLoS Genetics</i> , 2022, 18, e1010086.	1.5	4

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123	Isolation and Characterization of Lytic Proteus Virus 309. <i>Viruses</i> , 2022, 14, 1309.	1.5	4
124	Integrated Metabolomic, Molecular Networking, and Genome Mining Analyses Uncover Novel Angucyclines From <i>Streptomyces</i> sp. RO-S4 Strain Isolated From Bejaia Bay, Algeria. <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	2
125	Characterization of <i>Stenotrophomonas maltophilia</i> phage AXL1 as a member of the genus Pamexvirus encoding resistance to trimethoprimâ€“sulfamethoxazole. <i>Scientific Reports</i> , 2022, 12, .	1.6	5
127	Isolation of Novel <i>Xanthomonas</i> Phages Infecting the Plant Pathogens <i>X. translucens</i> and <i>X. campestris</i> . <i>Viruses</i> , 2022, 14, 1449.	1.5	6
128	Genomic Diversity of <i>Bradyrhizobium</i> from the Tree Legumes <i>Inga</i> and <i>Lysiloma</i> (<i>Caesalpinioideae</i> - <i>Mimosoid</i> Clade). <i>Diversity</i> , 2022, 14, 518.	0.7	3
129	<i>Salmonella</i> phage akira, infecting selected <i>Salmonella enterica</i> Enteritidis and Typhimurium strains, represents a new lineage of bacteriophages. <i>Archives of Virology</i> , 2022, 167, 2049-2056.	0.9	5
131	Expanded Dataset Reveals the Emergence and Evolution of DNA Gyrase in Archaea. <i>Molecular Biology and Evolution</i> , 2022, 39, .	3.5	4
133	Genomic surveillance reveals antibiotic resistance gene transmission via phage recombinases within sheep mastitis-associated <i>Streptococcus uberis</i> . <i>BMC Veterinary Research</i> , 2022, 18, .	0.7	9
134	<i>Streptomyces</i> sp. BV410 : Interspecies cross-talk for staurosporine production. <i>Journal of Applied Microbiology</i> , 0, , .	1.4	0
136	A potato late blight resistance gene protects against multiple <i>Phytophthora</i> species by recognizing a broadly conserved RXLR-WY effector. <i>Molecular Plant</i> , 2022, 15, 1457-1469.	3.9	27
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142	<i>Lightella neohaematopini</i> : A new lineage of highly reduced endosymbionts coevolving with chipmunk lice of the genus <i>Neohaematopinus</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	4
143	ExplorePipolin: reconstruction and annotation of piPolB-encoding bacterial mobile elements from draft genomes. <i>Bioinformatics Advances</i> , 0, , .	0.9	0
144	Wide distribution of <i>Escherichia coli</i> carrying IncF plasmids containing bla NDM-5 and rmtB resistance genes from hospitalized patients in England. <i>Journal of Medical Microbiology</i> , 2022, 71, .	0.7	4
145	Copper starvation induces antimicrobial isocyanide integrated into two distinct biosynthetic pathways in fungi. <i>Nature Communications</i> , 2022, 13, .	5.8	9
146	Viruses Ubiquity and Diversity in Atacama Desert Endolithic Communities. <i>Viruses</i> , 2022, 14, 1983.	1.5	3

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148	Stereochemical and Biosynthetic Rationalisation of the Tropolone Sesquiterpenoids. <i>Journal of Fungi</i> (Basel, Switzerland), 2022, 8, 929.	1.5	4
149	Identification of the Biosynthetic Gene Cluster for Pyracrimycin A, an Antibiotic Produced by <i>Streptomyces</i> sp.. <i>ACS Chemical Biology</i> , 2022, 17, 2411-2417.	1.6	3
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153	Viruses inhibit TIR gcADPR signalling to overcome bacterial defence. <i>Nature</i> , 2022, 611, 326-331.	13.7	66
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155	A novel function of the key nitrogen-fixation activator NifA in beta-rhizobia: Repression of bacterial auxin synthesis during symbiosis. <i>Frontiers in Plant Science</i> , 0, 13, .	1.7	6
157	Naryaviridae, Nenyaviridae, and Vilyaviridae: three new families of single-stranded DNA viruses in the phylum Cressdnarivicota. <i>Archives of Virology</i> , 2022, 167, 2907-2921.	0.9	10
159	Comparative genomics of <i>Rothia</i> species reveals diversity in novel biosynthetic gene clusters and ecological adaptation to different eukaryotic hosts and host niches. <i>Microbial Genomics</i> , 2022, 8, .	1.0	4
160	Identification of a novel aminoglycoside O-nucleotidyltransferase AadA33 in <i>Providencia vermicola</i> . <i>Frontiers in Microbiology</i> , 0, 13, .	1.5	1
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163	Multiple phage resistance systems inhibit infection via SIR2-dependent NAD ⁺ depletion. <i>Nature Microbiology</i> , 2022, 7, 1849-1856.	5.9	64
165	Chromosome-Level Genome Sequences, Comparative Genomic Analyses, and Secondary-Metabolite Biosynthesis Evaluation of the Medicinal Edible Mushroom <i>Laetiporus sulphureus</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	12
166	Pan-genomic and comparative analysis of <i>Pediococcus pentosaceus</i> focused on the in silico assessment of pediocin-like bacteriocins. <i>Computational and Structural Biotechnology Journal</i> , 2022, 20, 5595-5606.	1.9	2
167	<i>Wolbachia</i> causes cytoplasmic incompatibility but not male-killing in a grain pest beetle. <i>Molecular Ecology</i> , 2022, 31, 6570-6587.	2.0	6
168	The –emodin family™ of fungal natural products– amalgamating a century of research with recent genomics-based advances. <i>Natural Product Reports</i> , 2023, 40, 174-201.	5.2	9

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171	Complete Coding Sequences of Rhinovirus Types A46, A39, C56, and C48. <i>Microbiology Resource Announcements</i> , 0, , .	0.3	0
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174	Genome-centric analysis of short and long read metagenomes reveals uncharacterized microbiome diversity in Southeast Asians. <i>Nature Communications</i> , 2022, 13, .	5.8	16
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