

# Protein Sequence Analysis Using the MPI Bioinformatics

Current Protocols in Bioinformatics

72, e108

DOI: [10.1002/cpbi.108](https://doi.org/10.1002/cpbi.108)

Citation Report

#	ARTICLE	IF	CITATIONS
1	Development of a fluorogenic ADAMTS-7 substrate. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2021, 36, 2160-2169.	2.5	4
2	Advances in Understanding of the Copper Homeostasis in <i>Pseudomonas aeruginosa</i> . <i>International Journal of Molecular Sciences</i> , 2021, 22, 2050.	1.8	14
5	Bioinformatic Analysis of the Nicotinamide Binding Site in Poly(ADP-Ribose) Polymerase Family Proteins. <i>Cancers</i> , 2021, 13, 1201.	1.7	11
6	Structural and Biochemical Analysis of OrfC: The VirB8-like Component of the Conjugative Type IV Secretion System of ICESt3 From <i>Streptococcus thermophilus</i> . <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 642606.	1.6	3
9	Assessing the functional relevance of splice isoforms. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab044.	1.5	13
10	Regulatory Light Chains in Cardiac Development and Disease. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4351.	1.8	13
15	REP2: A Web Server to Detect Common Tandem Repeats in Protein Sequences. <i>Journal of Molecular Biology</i> , 2021, 433, 166895.	2.0	7
17	Interdomain horizontal gene transfer of nickel-binding superoxide dismutase. <i>Geobiology</i> , 2021, 19, 450-459.	1.1	11
18	Fungal Ice2p is in the same superfamily as <scp>SERINC</scp>, restriction factors for <scp>HIV</scp> and other viruses. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1240-1250.	1.5	9
19	Interleukins and Interleukin Receptors Evolutionary History and Origin in Relation to CD4+ T Cell Evolution. <i>Genes</i> , 2021, 12, 813.	1.0	21
20	Characterization of an Endolysin Targeting <i>Clostridioides difficile</i> That Affects Spore Outgrowth. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5690.	1.8	14
23	Some Dietary Phenolic Compounds Can Activate Thyroid Peroxidase and Inhibit Lipoxygenase-Preliminary Study in the Model Systems. <i>International Journal of Molecular Sciences</i> , 2021, 22, 5108.	1.8	8
28	Remote Homology Detection Identifies a Eukaryotic RPA DBD-C-like DNA Binding Domain as a Conserved Feature of Archaeal Rpa1-Like Proteins. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 675229.	1.6	2
29	Pantoea Bacteriophage vB_PagS_MED16A Siphovirus Containing a 2-Deoxy-7-amido-7-deazaguanosine-Modified DNA. <i>International Journal of Molecular Sciences</i> , 2021, 22, 7333.	1.8	2
30	An Ancient Clade of <i>Penelope</i> -Like Retroelements with Permuted Domains Is Present in the Green Lineage and Protists, and Dominates Many Invertebrate Genomes. <i>Molecular Biology and Evolution</i> , 2021, 38, 5005-5020.	3.5	12
31	Loss of C2orf69 defines a fatal autoinflammatory syndrome in humans and zebrafish that evokes a glycogen-storage-associated mitochondriopathy. <i>American Journal of Human Genetics</i> , 2021, 108, 1301-1317.	2.6	11
32	Comprehensive in silico Characterization of Universal Stress Proteins in Rice ( <i>Oryza sativa</i> L.) With Insight Into Their Stress-Specific Transcriptional Modulation. <i>Frontiers in Plant Science</i> , 2021, 12, 712607.	1.7	11
33	The clinical importance of tandem exon duplication-derived substitutions. <i>Nucleic Acids Research</i> , 2021, 49, 8232-8246.	6.5	11

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35	An Obligate Peptidyl Brominase Underlies the Discovery of Highly Distributed Biosynthetic Gene Clusters in Marine Sponge Microbiomes. <i>Journal of the American Chemical Society</i> , 2021, 143, 10221-10231.	6.6	22
37	cGAS-like receptors sense RNA and control 3'UTR-cGAMP signalling in <i>Drosophila</i> . <i>Nature</i> , 2021, 597, 109-113.	13.7	104
38	Accurate prediction of protein structures and interactions using a three-track neural network. <i>Science</i> , 2021, 373, 871-876.	6.0	2,843
40	New insights into the diversity and evolution of the archaeal mobilome from three complete genomes of <i>Saccharolobus shibatae</i> . <i>Environmental Microbiology</i> , 2021, 23, 4612-4630.	1.8	5
42	<i>Caenorhabditis elegans</i> RMI2 functional homolog-2 (RMIF-2) and RMI1 (RMH-1) have both overlapping and distinct meiotic functions within the BTR complex. <i>PLoS Genetics</i> , 2021, 17, e1009663.	1.5	5
43	Structural and Functional Elucidation of IF-3 Protein of <i>Chloroflexus aurantiacus</i> Involved in Protein Biosynthesis: An In Silico Approach. <i>BioMed Research International</i> , 2021, 2021, 1-10.	0.9	5
46	Iron Oxidation by a Fused Cytochrome-Porin Common to Diverse Iron-Oxidizing Bacteria. <i>MBio</i> , 2021, 12, e0107421.	1.8	34
48	Large-scale computational discovery and analysis of virus-derived microbial nanocompartments. <i>Nature Communications</i> , 2021, 12, 4748.	5.8	28
49	Substitutions in SurA and BamA Lead to Reduced Susceptibility to Broad Range Antibiotics in <i>Gonococci</i> . <i>Genes</i> , 2021, 12, 1312.	1.0	0
50	Impact of natural mutations on the riboflavin transporter 2 and their relevance to human riboflavin transporter deficiency 2. <i>IUBMB Life</i> , 2022, 74, 618-628.	1.5	6
51	Unexpected organellar locations of ESCRT machinery in <i>Giardia intestinalis</i> and complex evolutionary dynamics spanning the transition to parasitism in the lineage <i>Fornicata</i> . <i>BMC Biology</i> , 2021, 19, 167.	1.7	8
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53	Target classification in the 14th round of the critical assessment of protein structure prediction (CASP14). <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1618-1632.	1.5	32
54	TMEM106B in humans and Vac7 and Tag1 in yeast are predicted to be lipid transfer proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, 90, 164-175.	1.5	13
55	Assessment of the CASP14 assembly predictions. <i>Proteins: Structure, Function and Bioinformatics</i> , 2021, 89, 1787-1799.	1.5	35
56	How do I get the most out of my protein sequence using bioinformatics tools?. <i>Acta Crystallographica Section D: Structural Biology</i> , 2021, 77, 1116-1126.	1.1	8
57	Gene-teratogen interactions influence the penetrance of birth defects by altering Hedgehog signaling strength. <i>Development (Cambridge)</i> , 2021, 148, .	1.2	4
58	Characterization and genomic analysis of the first <i>Oceanospirillum</i> phage, vB_OliS_CJ44, representing a novel siphoviral cluster. <i>BMC Genomics</i> , 2021, 22, 675.	1.2	7

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59	Enumeration and comprehensive in-silico modeling of three-helix bundle structures composed of typical $\beta$ -hairpins. BMC Bioinformatics, 2021, 22, 465.	1.2	0
60	Investigation of Evolutionary History and Origin of the Tre1 Family Suggests a Role in Regulating Hemocytes Cells Infiltration of the Bloodâ€”Brain Barrier. Insects, 2021, 12, 882.	1.0	3
63	Novel Hemizygous Mutations of TEX11 Cause Meiotic Arrest and Non-obstructive Azoospermia in Chinese Han Population. Frontiers in Genetics, 2021, 12, 741355.	1.1	8
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68	Microalgal protein AstaP is a potent carotenoid solubilizer and delivery module with a broad carotenoid binding repertoire. FEBS Journal, 2022, 289, 999-1022.	2.2	23
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70	Ty1 integrase is composed of an active N-terminal domain and a large disordered C-terminal module dispensable for its activity inÂvitro. Journal of Biological Chemistry, 2021, 297, 101093.	1.6	4
71	A novel lineage of polyomaviruses identified in bark scorpions. Virology, 2021, 563, 58-63.	1.1	9
72	Revisiting the CooJ family, a potential chaperone for nickel delivery to [NiFe]â€”carbon monoxide dehydrogenase. Journal of Inorganic Biochemistry, 2021, 225, 111588.	1.5	1
75	The Honey Bee Gene Bee Antiviral Protein-1 Is a Taxonomically Restricted Antiviral Immune Gene. Frontiers in Insect Science, 2021, 1, .	0.9	3
79	Cloning, Characterization, Expression Analysis, and Agglutination Studies of Novel Gene Encoding Î²-d-Galactose, N-Acetyl-d-Glucosamine and Lactose-Binding Lectin from Rice Bean (Vigna umbellata). Molecular Biotechnology, 2022, 64, 293-310.	1.3	2
80	The structure of neurofibromin isoform 2 reveals different functional states. Nature, 2021, 599, 315-319.	13.7	22
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82	Discovery of novel fish papillomaviruses: From the Antarctic to the commercial fish market. Virology, 2022, 565, 65-72.	1.1	10
83	Computed structures of core eukaryotic protein complexes. Science, 2021, 374, eabm4805.	6.0	316
85	Diversity, taxonomy, and evolution of archaeal viruses of the class Caudoviricetes. PLoS Biology, 2021, 19, e3001442.	2.6	44
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88	Cryo-EM structure of native human thyroglobulin. <i>Nature Communications</i> , 2022, 13, 61.	5.8	9
89	Gp29 LysA of mycobacteriophage TM4 can hydrolyze peptidoglycan through an N-acetyl-muramoyl-L-alanine amidase activity. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2022, 1870, 140745.	1.1	2
90	A Micrarchaeon Isolate Is Covered by a Proteinaceous S-Layer. <i>Applied and Environmental Microbiology</i> , 2022, 88, AEM0155321.	1.4	4
91	African Swine Fever Virus and Host Response: Transcriptome Profiling of the Georgia 2007/1 Strain and Porcine Macrophages. <i>Journal of Virology</i> , 2022, 96, jvi0193921.	1.5	40
92	Development of an Anti-Acinetobacter baumannii Biofilm Phage Cocktail: Genomic Adaptation to the Host. <i>Antimicrobial Agents and Chemotherapy</i> , 2022, 66, AAC0192321.	1.4	12
93	Three Novel Bacteriophages, J5a, F16Ba, and z1a, Specific for Bacillus anthracis, Define a New Clade of Historical Wbeta Phage Relatives. <i>Viruses</i> , 2022, 14, 213.	1.5	8
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95	Gene expression alterations from reversible to irreversible stages during coral metamorphosis. <i>Zoological Letters</i> , 2022, 8, 4.	0.7	2
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100	<scp>SxsA</scp>, a novel surface protein mediating cell aggregation and adhesive biofilm formation of <i>Staphylococcus xylosus</i>. <i>Molecular Microbiology</i> , 2022, 117, 986-1001.	1.2	5
101	Understanding saffron biology using omics- and bioinformatics tools: stepping towards a better Crocus phenome. <i>Molecular Biology Reports</i> , 2022, 49, 5325-5340.	1.0	10
102	Transcription regulation of iron carrier transport genes by ECF sigma factors through signaling from the cell surface into the cytoplasm. <i>FEMS Microbiology Reviews</i> , 2022, 46, .	3.9	4
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106	Treponema pallidum genome sequencing from six continents reveals variability in vaccine candidate genes and dominance of Nichols clade strains in Madagascar. <i>PLoS Neglected Tropical Diseases</i> , 2021, 15, e0010063.	1.3	30

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109	<i>Curtobacterium</i> spp. and <i>Curtobacterium flaccumfaciens</i> : Phylogeny, Genomics-Based Taxonomy, Pathogenicity, and Diagnostics. <i>Current Issues in Molecular Biology</i> , 2022, 44, 889-927.	1.0	15
110	<i>Legionella pneumophila</i> regulates host cell motility by targeting Phldb2 with a 14-3-3 $\sigma$ -dependent protease effector. <i>ELife</i> , 2022, 11, .	2.8	15
111	Genomic and Phenotypic Characterization of the Nontoxigenic <i>Clostridioides difficile</i> Strain CCUG37785 and Demonstration of Its Therapeutic Potential for the Prevention of <i>C. difficile</i> Infection. <i>Microbiology Spectrum</i> , 2022, 10, e0178821.	1.2	7
113	A mobile restriction- $\epsilon$ -modification system provides phage defence and resolves an epigenetic conflict with an antagonistic endonuclease. <i>Nucleic Acids Research</i> , 2022, 50, 3348-3361.	6.5	17
114	Bacteriophage Control of <i>Pseudomonas</i> $\Delta$ avastanoi pv. <i>glycinea</i> in Soybean. <i>Plants</i> , 2022, 11, 938.	1.6	8
116	New Insights into the Structure and Assembly of Bacteriophage P1. <i>Viruses</i> , 2022, 14, 678.	1.5	6
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124	Using Genomics to Shape the Definition of the Agglutinin-Like Sequence (ALS) Family in the Saccharomycetales. <i>Frontiers in Cellular and Infection Microbiology</i> , 2021, 11, 794529.	1.8	9
125	Novel <i>Klebsiella pneumoniae</i> virulent bacteriophage KPPK108.1 capable of infecting the K108 serotype strains. <i>Bulletin of Russian State Medical University</i> , 2021, , .	0.3	1
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136	Evolutionary Principles of Bacterial Signaling Capacity and Complexity. <i>MBio</i> , 2022, 13, e0076422.	1.8	12
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138	A novel superfamily of bridge-like lipid transfer proteins. <i>Trends in Cell Biology</i> , 2022, 32, 962-974.	3.6	44
139	Homology-based classification of accessory proteins in coronavirus genomes uncovers extremely dynamic evolution of gene content. <i>Molecular Ecology</i> , 2022, 31, 3672-3692.	2.0	11
141	Profile of the in silico secretome of the palm dieback pathogen, <i>Fusarium oxysporum</i> f. sp. <i>albedinis</i> , a fungus that puts natural oases at risk. <i>PLoS ONE</i> , 2022, 17, e0260830.	1.1	4
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146	Evolution of Phage Tail Sheath Protein. <i>Viruses</i> , 2022, 14, 1148.	1.5	8
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149	An antibacterial <i>T6SS</i> in <i>Pantoea agglomerans</i> pv. <i>betae</i> delivers a lysozyme-like effector to antagonize competitors. <i>Environmental Microbiology</i> , 2022, 24, 4787-4802.	1.8	10
150	Archaeal bundling pili of <i>Pyrobaculum calidifontis</i> reveal similarities between archaeal and bacterial biofilms. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	13
151	Relating SARS-CoV-2 variants using cellular automata imaging. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
152	To kill or to be killed: pangenome analysis of <i>Escherichia coli</i> strains reveals a tailocin specific for pandemic ST131. <i>BMC Biology</i> , 2022, 20, .	1.7	10
153	The Ankyrin Repeat Protein RARP-1 Is a Periplasmic Factor That Supports <i>Rickettsia parkeri</i> Growth and Host Cell Invasion. <i>Journal of Bacteriology</i> , 2022, 204, .	1.0	5
154	Tertiary and Quaternary Structure Organization in GMP Synthetases: Implications for Catalysis. <i>Biomolecules</i> , 2022, 12, 871.	1.8	2
155	A Novel Flavi-like Virus in Alfalfa ( <i>Medicago sativa</i> L.) Crops along the Snake River Valley. <i>Viruses</i> , 2022, 14, 1320.	1.5	7
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159	The Biosynthetic Landscape of Triceptides Reveals Radical SAM Enzymes That Catalyze Cyclophane Formation on Tyr- and His-Containing Motifs. <i>Journal of the American Chemical Society</i> , 2022, 144, 11580-11593.	6.6	22
160	Systematic overexpression of genes encoded by mycobacteriophage Waterfoul reveals novel inhibitors of mycobacterial growth. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	7
161	Plasmodium berghei Brca2 is required for normal development and differentiation in mice and mosquitoes. <i>Parasites and Vectors</i> , 2022, 15, .	1.0	4
163	Structure Prediction, Evaluation, and Validation of GPR18 Lipid Receptor Using Free Programs. <i>International Journal of Molecular Sciences</i> , 2022, 23, 7917.	1.8	0
164	Comparative phylogeny and evolutionary analysis of Dicer-like protein family in two plant monophyletic lineages. <i>Journal of Genetic Engineering and Biotechnology</i> , 2022, 20, 103.	1.5	0
170	The evolutionary path of chemosensory and flagellar macromolecular machines in Campylobacterota. <i>PLoS Genetics</i> , 2022, 18, e1010316.	1.5	8
171	In Search of a Dynamical Vocabulary: A Pipeline to Construct a Basis of Shared Traits in Large-Scale Motions of Proteins. <i>Applied Sciences (Switzerland)</i> , 2022, 12, 7157.	1.3	1
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181	Cohesin ATPase activities regulate DNA binding and coiled-coil configuration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	2
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183	New putative phenol oxidase in ascidian blood cells. <i>Scientific Reports</i> , 2022, 12, .	1.6	1
184	A Specialized Polythioamideâ€Binding Protein Confers Antibiotic Selfâ€Resistance in Anaerobic Bacteria. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	0



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186	Pre-Treatment With Polysaccharide Depolymerase Enhances the Infective Performance of Klebsiella Phage KP1079. , 2022, , .		0
187	A Novel Acinetobacter Phage Cato: Lytic Myovirus Containing Tailspike Depolymerase. , 2022, , .		1
188	TurboID Identification of Evolutionarily Divergent Components of the Nuclear Pore Complex in the Malaria Model <i>Plasmodium berghei</i> . <i>MBio</i> , 2022, 13, .	1.8	5
189	Molecular architecture of the autoinhibited kinesin-1 lambda particle. <i>Science Advances</i> , 2022, 8, .	4.7	13
190	The SPARC complex defines RNAPII promoters in <i>Trypanosoma brucei</i> . <i>ELife</i> , 0, 11, .	2.8	7
191	APPRIS principal isoforms and MANE Select transcripts define reference splice variants. <i>Bioinformatics</i> , 2022, 38, ii89-ii94.	1.8	6
194	Domain function and predicted structure of three heterodimeric endonuclease subunits of RNA editing catalytic complexes in <i>Trypanosoma brucei</i> . <i>Nucleic Acids Research</i> , 2022, 50, 10123-10139.	6.5	3
195	Group II intron-like reverse transcriptases function in double-strand break repair. <i>Cell</i> , 2022, 185, 3671-3688.e23.	13.5	7
196	Adhesion of <i>Bartonella henselae</i> to Fibronectin Is Mediated via Repetitive Motifs Present in the Stalk of <i>Bartonella</i> Adhesin A. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	3
197	Methotrexate recognition by the human reduced folate carrier SLC19A1. <i>Nature</i> , 2022, 609, 1056-1062.	13.7	21
198	Endoplasmic Reticulum Membrane Contact Sites, Lipid Transport, and Neurodegeneration. <i>Cold Spring Harbor Perspectives in Biology</i> , 2023, 15, a041257.	2.3	12
199	Naryaviridae, Nenyaviridae, and Vilyaviridae: three new families of single-stranded DNA viruses in the phylum Cressdnaviricota. <i>Archives of Virology</i> , 2022, 167, 2907-2921.	0.9	10
200	Purification, crystallization and crystallographic analysis of the PorX response regulator associated with the type IX secretion system. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2022, 78, 354-362.	0.4	2
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