Pablo Mier

List of Publications by Year
in descending order

45 papers	910 citations	687335 13 h-index	526264 27 g-index
49 all docs	49 docs citations	49 times ranked	1258 citing authors

#	Article	IF	Citations
1	PolyX2: Fast Detection of Homorepeats in Large Protein Datasets. Genes, 2022, 13, 758.	2.4	5
2	Annotation and Analysis of 3902 Odorant Receptor Protein Sequences from 21 Insect Species Provide Insights into the Evolution of Odorant Receptor Gene Families in Solitary and Social Insects. Genes, 2022, 13, 919.	2.4	2
3	Analysis of Huntington's Disease Modifiers Using the Hyperbolic Mapping of the Protein Interaction Network. International Journal of Molecular Sciences, 2022, 23, 5853.	4.1	5
4	The Role of Low Complexity Regions in Protein Interaction Modes: An Illustration in Huntingtin. International Journal of Molecular Sciences, 2021, 22, 1727.	4.1	10
5	Avoided motifs: short amino acid strings missing from protein datasets. Biological Chemistry, 2021, 402, 945-951.	2.5	1
6	The Conservation of Low Complexity Regions in Bacterial Proteins Depends on the Pathogenicity of the Strain and Subcellular Location of the Protein. Genes, 2021, 12, 451.	2.4	5
7	REP2: A Web Server to Detect Common Tandem Repeats in Protein Sequences. Journal of Molecular Biology, 2021, 433, 166895.	4.2	7
8	Between Interactions and Aggregates: The PolyQ Balance. Genome Biology and Evolution, 2021, 13, .	2.5	9
9	Disentangling the complexity of low complexity proteins. Briefings in Bioinformatics, 2020, 21, 458-472.	6.5	70
10	Evolutionary Study of Disorder in Protein Sequences. Biomolecules, 2020, 10, 1413.	4.0	16
11	MAGA: A Supervised Method to Detect Motifs From Annotated Groups in Alignments. Evolutionary Bioinformatics, 2020, 16, 117693432091619.	1.2	1
12	Flanking Regions Determine the Structure of the Poly-Glutamine in Huntingtin through Mechanisms Common among Glutamine-Rich Human Proteins. Structure, 2020, 28, 733-746.e5.	3.3	45
13	A novel approach to investigate the evolution of structured tandem repeat protein families by exon duplication. Journal of Structural Biology, 2020, 212, 107608.	2.8	8
14	PlaToLoCo: the first web meta-server for visualization and annotation of low complexity regions in proteins. Nucleic Acids Research, 2020, 48, W77-W84.	14.5	71
15	The 18S ribosomal RNA m^{6}A methyltransferase Mettl5 is required for normal walking behavior in *Drosophila*. EMBO Reports, 2020, 21, e49443.	4.5	52
16	The features of polyglutamine regions depend on their evolutionary stability. BMC Evolutionary Biology, 2020, 20, 59.	3.2	6
17	The importance of definitions in the study of polyQ regions: A tale of thresholds, impurities and sequence context. Computational and Structural Biotechnology Journal, 2020, 18, 306-313.	4.1	18
18	CRISPR sequences are sometimes erroneously translated and can contaminate public databases with spurious proteins containing spaced repeats. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	4

#	ARTICLE	IF	CITATIONS
19	Assessing the low complexity of protein sequences via the low complexity triangle. PLoS ONE, 2020, 15, e0239154.	2.5	6
20	Assessing the low complexity of protein sequences via the low complexity triangle. , 2020, 15, e0239154.		0
21	Assessing the low complexity of protein sequences via the low complexity triangle. , 2020, 15, e0239154.		0
22	Assessing the low complexity of protein sequences via the low complexity triangle. , 2020, 15, e0239154.		0
23	Assessing the low complexity of protein sequences via the low complexity triangle. , 2020, 15, e0239154.		0
24	Traitpedia: a collaborative effort to gather species traits. Bioinformatics, 2019, 35, 1079-1081.	4.1	0
25	Repeatability in protein sequences. Journal of Structural Biology, 2019, 208, 86-91.	2.8	12
26	Tandem repeats lead to sequence assembly errors and impose multi-level challenges for genome and protein databases. Nucleic Acids Research, 2019, 47, 10994-11006.	14.5	236
27	AnABlast: Re-searching for Protein-Coding Sequences in Genomic Regions. Methods in Molecular Biology, 2019, 1962, 207-214.	0.9	4
28	Large expert-curated database for benchmarking document similarity detection in biomedical literature search. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	3.0	15
29	Toward completion of the Earth's proteome: an update a decade later. Briefings in Bioinformatics, 2019, 20, 463-470.	6.5	3
30	The latent geometry of the human protein interaction network. Bioinformatics, 2018, 34, 2826-2834.	4.1	24
31	Proteome-wide comparison between the amino acid composition of domains and linkers. BMC Research Notes, 2018, 11, 117.	1.4	25
32	Automated selection of homologs to track the evolutionary history of proteins. BMC Bioinformatics, 2018, 19, 431.	2.6	7
33	Glutamine Codon Usage and polyQ Evolution in Primates Depend on the Q Stretch Length. Genome Biology and Evolution, 2018, 10, 816-825.	2.5	15
34	dAPE: a web server to detect homorepeats and follow their evolution. Bioinformatics, 2017, 33, 1221-1223.	4.1	12
35	<scp>C</scp>ontext characterization of amino acid homorepeats using evolution, position, and order. Proteins: Structure, Function and Bioinformatics, 2017, 85, 709-719.	2.6	36
36	Protein-protein interactions can be predicted using coiled coil co-evolution patterns. Journal of Theoretical Biology, 2017, 412, 198-203.	1.7	18

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37	Reading the Evolution of Compartmentalization in the Ribosome Assembly Toolbox: The YRG Protein Family. PLoS ONE, 2017, 12, e0169750.	2.5	6
38	The Protein Structure Context of PolyQ Regions. PLoS ONE, 2017, 12, e0170801.	2.5	40
39	Efficient embedding of complex networks to hyperbolic space via their Laplacian. Scientific Reports, 2016, 6, 30108.	3.3	56
40	Manifold learning and maximum likelihood estimation for hyperbolic network embedding. Applied Network Science, 2016, 1, 10.	1.5	31
41	CABRA: Cluster and Annotate Blast Results Algorithm. BMC Research Notes, 2016, 9, 253.	1.4	0
42	FastaHerder2: Four Ways to Research Protein Function and Evolution with Clustering and Clustered Databases. Journal of Computational Biology, 2016, 23, 270-278.	1.6	13
43	orthoFind Facilitates the Discovery of Homologous and Orthologous Proteins. PLoS ONE, 2015, 10, e0143906.	2.5	3
44	Fungal Smn and Spf30 homologues are mainly present in filamentous fungi and genomes with many introns: Implications for spinal muscular atrophy. Gene, 2012, 491, 135-141.	2.2	11
45	Mpg2 interacts and cooperates with Mpg1 to maintain yeast glycosylation. FEMS Yeast Research, 2012, 12, 511-520.	2.3	2