

Manuela Helmer-Citterich

List of Publications by Year in descending order

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Version: 2024-02-01

100
papers

5,525
citations

126907

33
h-index

85541

71
g-index

102
all docs

102
docs citations

102
times ranked

10527
citing authors

#	ARTICLE	IF	CITATIONS
1	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	14.5	46
2	Evaluation of potential sponge effects of SARS genomes in human. <i>Non-coding RNA Research</i> , 2022, , .	4.6	7
3	Conserved exchange of paralog proteins during neuronal differentiation. <i>Life Science Alliance</i> , 2022, 5, e202201397.	2.8	0
4	Variation in the co-expression profile highlights a loss of miRNA-mRNA regulation in multiple cancer types. <i>Non-coding RNA Research</i> , 2022, 7, 98-105.	4.6	2
5	Dissecting the Genome for Drug Response Prediction. <i>Methods in Molecular Biology</i> , 2022, 2449, 187-196.	0.9	1
6	Motif Discovery from CLIP Experiments. <i>Methods in Molecular Biology</i> , 2021, 2284, 43-50.	0.9	2
7	Relative Information Gain: Shannon entropy-based measure of the relative structural conservation in RNA alignments. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab007.	3.2	3
8	BRIO: a web server for RNA sequence and structure motif scan. <i>Nucleic Acids Research</i> , 2021, 49, W67-W71.	14.5	10
9	Variants in MHY7 Gene Cause Arrhythmogenic Cardiomyopathy. <i>Genes</i> , 2021, 12, 793.	2.4	4
10	A eutherian-specific microRNA controls the translation of Satb2 in a model of cortical differentiation. <i>Stem Cell Reports</i> , 2021, 16, 1496-1509.	4.8	8
11	COTAN: scRNA-seq data analysis based on gene co-expression. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab072.	3.2	11
12	Early life adversity affecting the attachment bond alters ventral tegmental area transcriptomic patterning and behavior almost exclusively in female mice. <i>Neurobiology of Stress</i> , 2021, 15, 100406.	4.0	5
13	PDBe-KB: a community-driven resource for structural and functional annotations. <i>Nucleic Acids Research</i> , 2020, 48, D344-D353.	14.5	87
14	WWP1 germline variants are associated with normocephalic autism spectrum disorder. <i>Cell Death and Disease</i> , 2020, 11, 529.	6.3	5
15	COVID-19 and Genetic Variants of Protein Involved in the SARS-CoV-2 Entry into the Host Cells. <i>Genes</i> , 2020, 11, 1010.	2.4	88
16	RISC RNA sequencing in the Dorsal Raphe ⁺ reveals microRNAs regulatory activities associated with behavioral and functional adaptations to chronic stress. <i>Brain Research</i> , 2020, 1736, 146763.	2.2	4
17	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq1 1 0.784314 rrgBT /Overlock 10 Tj	1.6	12
18	Kinome-wide identification of phosphorylation networks in eukaryotic proteomes. <i>Bioinformatics</i> , 2019, 35, 372-379.	4.1	9

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19	Modeling cancer drug response through drug-specific informative genes. <i>Scientific Reports</i> , 2019, 9, 15222.	3.3	42
20	Discovering sequence and structure landscapes in RNA interaction motifs. <i>Nucleic Acids Research</i> , 2019, 47, 4958-4969.	14.5	17
21	BEAM web server: a tool for structural RNA motif discovery. <i>Bioinformatics</i> , 2018, 34, 1058-1060.	4.1	10
22	Structural Defects of Laminin Î²3 N-terminus Underlie Junctional Epidermolysis Bullosa with Altered Granulation Tissue Response. <i>Acta Dermato-Venereologica</i> , 2016, 96, 954-958.	1.3	5
23	c-MYC inhibition impairs hypoxia response in glioblastoma multiforme. <i>Oncotarget</i> , 2016, 7, 33257-33271.	1.8	24
24	Genome-wide methylation analysis demonstrates that 5-aza-2-deoxycytidine treatment does not cause random DNA demethylation in fragile X syndrome cells. <i>Epigenetics and Chromatin</i> , 2016, 9, 12.	3.9	28
25	A novel method for the identification of conserved structural patterns in RNA: From small scale to high-throughput applications. <i>Nucleic Acids Research</i> , 2016, 44, 8600-8609.	14.5	19
26	The human rs1050286 polymorphism alters <i>LOX</i> expression through modifying miR-24 binding. <i>Journal of Cellular and Molecular Medicine</i> , 2016, 20, 181-187.	3.6	19
27	Revealing protein-lncRNA interaction. <i>Briefings in Bioinformatics</i> , 2016, 17, 106-116.	6.5	536
28	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	14.5	113
29	Preface: BITS2014, the annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2015, 16, S1.	2.6	0
30	Web-Beagle: a web server for the alignment of RNA secondary structures: Figure 1.. <i>Nucleic Acids Research</i> , 2015, 43, W493-W497.	14.5	29
31	Kinome-wide Decoding of Network-Attacking Mutations Rewiring Cancer Signaling. <i>Cell</i> , 2015, 163, 202-217.	28.9	168
32	AMBRA1 links autophagy to cell proliferation and tumorigenesis by promoting c-Myc dephosphorylation and degradation. <i>Nature Cell Biology</i> , 2015, 17, 20-30.	10.3	200
33	A Simple Protocol for the Inference of RNA Global Pairwise Alignments. <i>Methods in Molecular Biology</i> , 2015, 1269, 39-47.	0.9	1
34	Exploiting holistic approaches to model specificity in protein phosphorylation. <i>Frontiers in Genetics</i> , 2014, 5, 315.	2.3	14
35	Computational methods for analysis and inference of kinase/inhibitor relationships. <i>Frontiers in Genetics</i> , 2014, 5, 196.	2.3	16
36	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2198-2212.	3.8	5

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37	A novel approach to represent and compare RNA secondary structures. <i>Nucleic Acids Research</i> , 2014, 42, 6146-6157.	14.5	43
38	Regulation Dynamics of <i>Leishmania</i> Differentiation: Deconvoluting Signals and Identifying Phosphorylation Trends. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1787-1799.	3.8	72
39	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. <i>BMC Bioinformatics</i> , 2013, 14, S1.	2.6	1
40	Alternative splicing tends to avoid partial removals of protein-protein interaction sites. <i>BMC Genomics</i> , 2013, 14, 379.	2.8	4
41	Experimental and computational methods for the analysis and modeling of signaling networks. <i>New Biotechnology</i> , 2013, 30, 327-332.	4.4	3
42	Enrichment of <i>Leishmania donovani</i> ATP-binding proteins using a staurosporine capture compound. <i>Journal of Proteomics</i> , 2013, 86, 97-104.	2.4	3
43	Peamaclein – A new peach allergenic protein: similarities, differences and misleading features compared to Pru p 3. <i>Clinical and Experimental Allergy</i> , 2013, 43, 128-140.	2.9	85
44	Phosphoproteomic Analysis of Differentiating <i>Leishmania</i> Parasites Reveals a Unique Stage-Specific Phosphorylation Motif. <i>Journal of Proteome Research</i> , 2013, 12, 3405-3412.	3.7	67
45	Exploring the diversity of SPRY/B30.2-mediated interactions. <i>Trends in Biochemical Sciences</i> , 2013, 38, 38-46.	7.5	67
46	DBATE: database of alternative transcripts expression. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat050.	3.0	11
47	webPDBinder: a server for the identification of ligand binding sites on protein structures. <i>Nucleic Acids Research</i> , 2013, 41, W308-W313.	14.5	5
48	Role of CTCF Protein in Regulating FMR1 Locus Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003601.	3.5	38
49	Nucleos: a web server for the identification of nucleotide-binding sites in protein structures. <i>Nucleic Acids Research</i> , 2013, 41, W281-W285.	14.5	7
50	Deciphering a global network of functionally associated post-translational modifications. <i>Molecular Systems Biology</i> , 2012, 8, 599.	7.2	216
51	Mapping the human phosphatome on growth pathways. <i>Molecular Systems Biology</i> , 2012, 8, 603.	7.2	24
52	What has proteomics taught us about <i>Leishmania</i> development?. <i>Parasitology</i> , 2012, 139, 1146-1157.	1.5	31
53	Identification of binding pockets in protein structures using a knowledge-based potential derived from local structural similarities. <i>BMC Bioinformatics</i> , 2012, 13, S17.	2.6	14
54	Modeling gene regulatory network motifs using statecharts. <i>BMC Bioinformatics</i> , 2012, 13, S20.	2.6	8

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55	Bioinformatics in Italy: BITS2011, the Eighth Annual Meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2012, 13, 11.	2.6	2
56	B-Pred, a structure based B-cell epitopes prediction server. Advances and Applications in Bioinformatics and Chemistry, 2012, 5, 11.	2.6	14
57	Identification of Nucleotide-Binding Sites in Protein Structures: A Novel Approach Based on Nucleotide Modularity. PLoS ONE, 2012, 7, e50240.	2.5	6
58	From sequence to structural analysis in protein phosphorylation motifs. Frontiers in Bioscience - Landmark, 2011, 16, 1261.	3.0	18
59	PhosTryp: a phosphorylation site predictor specific for parasitic protozoa of the family trypanosomatidae. BMC Genomics, 2011, 12, 614.	2.8	19
60	Adaptation of a 2D in-gel kinase assay to trace phosphotransferase activities in the human pathogen Leishmania donovani. Journal of Proteomics, 2011, 74, 1644-1651.	2.4	7
61	Phosfinder: a web server for the identification of phosphate-binding sites on protein structures. Nucleic Acids Research, 2011, 39, W278-W282.	14.5	13
62	Phospho3D 2.0: an enhanced database of three-dimensional structures of phosphorylation sites. Nucleic Acids Research, 2011, 39, D268-D271.	14.5	45
63	Phosphate binding sites identification in protein structures. Nucleic Acids Research, 2011, 39, 1231-1242.	14.5	15
64	Identification of <i>Leishmania</i> -specific protein phosphorylation sites by LC-ESI-MS/MS and comparative genomics analyses. Proteomics, 2010, 10, 3868-3883.	2.2	35
65	Superpose3D: A Local Structural Comparison Program That Allows for User-Defined Structure Representations. PLoS ONE, 2010, 5, e11988.	2.5	14
66	ELM: the status of the 2010 eukaryotic linear motif resource. Nucleic Acids Research, 2010, 38, D167-D180.	14.5	217
67	Cyclosporin A Treatment of <i>Leishmania donovani</i> Reveals Stage-Specific Functions of Cyclophilins in Parasite Proliferation and Viability. PLoS Neglected Tropical Diseases, 2010, 4, e729.	3.0	34
68	Modular architecture of nucleotide-binding pockets. Nucleic Acids Research, 2010, 38, 3809-3816.	14.5	24
69	Structural motifs recurring in different folds recognize the same ligand fragments. BMC Bioinformatics, 2009, 10, 182.	2.6	13
70	A structure filter for the Eukaryotic Linear Motif Resource. BMC Bioinformatics, 2009, 10, 351.	2.6	40
71	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. BMC Bioinformatics, 2008, 9, S2.	2.6	31
72	Structure-based function prediction: approaches and applications. Briefings in Functional Genomics & Proteomics, 2008, 7, 291-302.	3.8	67

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73	Phospho3D: a database of three-dimensional structures of protein phosphorylation sites. <i>Nucleic Acids Research</i> , 2007, 35, D229-D231.	14.5	43
74	3dLOGO: a web server for the identification, analysis and use of conserved protein substructures. <i>Nucleic Acids Research</i> , 2007, 35, W416-W419.	14.5	6
75	SH3-Hunter: discovery of SH3 domain interaction sites in proteins. <i>Nucleic Acids Research</i> , 2007, 35, W451-W454.	14.5	35
76	Convergent Evolution of Enzyme Active Sites Is not a Rare Phenomenon. <i>Journal of Molecular Biology</i> , 2007, 372, 817-845.	4.2	109
77	False occurrences of functional motifs in protein sequences highlight evolutionary constraints. <i>BMC Bioinformatics</i> , 2007, 8, 68.	2.6	8
78	Local comparison of protein structures highlights cases of convergent evolution in analogous functional sites. <i>BMC Bioinformatics</i> , 2007, 8, S24.	2.6	17
79	Functional annotation by identification of local surface similarities: a novel tool for structural genomics. <i>BMC Bioinformatics</i> , 2005, 6, 194.	2.6	27
80	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. <i>BMC Bioinformatics</i> , 2005, 6, S1.	2.6	8
81	A neural strategy for the inference of SH3 domain-peptide interaction specificity. <i>BMC Bioinformatics</i> , 2005, 6, S13.	2.6	10
82	Query3d: a new method for high-throughput analysis of functional residues in protein structures. <i>BMC Bioinformatics</i> , 2005, 6, S5.	2.6	47
83	Seq2Struct: a resource for establishing sequence-structure links. <i>Bioinformatics</i> , 2005, 21, 551-553.	4.1	10
84	pdbFun: mass selection and fast comparison of annotated PDB residues. <i>Nucleic Acids Research</i> , 2005, 33, W133-W137.	14.5	31
85	SURFACE: a database of protein surface regions for functional annotation. <i>Nucleic Acids Research</i> , 2004, 32, 240D-244.	14.5	59
86	A structural study for the optimisation of functional motifs encoded in protein sequences. <i>BMC Bioinformatics</i> , 2004, 5, 50.	2.6	6
87	Development of Computational Tools for the Inference of Protein Interaction Specificity Rules and Functional Annotation Using Structural Information. <i>Comparative and Functional Genomics</i> , 2003, 4, 416-419.	2.0	1
88	iSPOT: a web tool to infer the interaction specificity of families of protein modules. <i>Nucleic Acids Research</i> , 2003, 31, 3709-3711.	14.5	30
89	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	14.5	555
90	Searching the MINT Database for Protein Interaction Information. <i>Current Protocols in Bioinformatics</i> , 2003, 2, Unit 8.5.	25.8	0

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91	The SH3 domain of nebulin binds selectively to type II peptides: theoretical prediction and experimental validation. <i>Journal of Molecular Biology</i> , 2002, 316, 305-315.	4.2	22
92	MINT: a Molecular INTERaction database. <i>FEBS Letters</i> , 2002, 513, 135-140.	2.8	665
93	iSPOT: A Web Tool for the Analysis and Recognition of Protein Domain Specificity. <i>Comparative and Functional Genomics</i> , 2001, 2, 314-318.	2.0	8
94	Identification of a Putative Binding Site for Negatively Charged Surfaces in the Fibronectin Type II Domain of Human Factor XII. <i>Thrombosis and Haemostasis</i> , 2000, 84, 1057-1065.	3.4	40
95	Three-dimensional view of the surface motif associated with the P-loop structure: cis and trans cases of convergent evolution 1 Edited by J. Thornton. <i>Journal of Molecular Biology</i> , 2000, 303, 455-465.	4.2	78
96	Design and properties of a Myc derivative that efficiently homodimerizes. <i>Oncogene</i> , 1998, 17, 2463-2472.	5.9	154
97	Three-dimensional profiles: a new tool to identify protein surface similarities. <i>Journal of Molecular Biology</i> , 1998, 284, 1211-1221.	4.2	49
98	Correlated mutations contain information about protein-protein interaction 1 Edited by A. R. Fersht. <i>Journal of Molecular Biology</i> , 1997, 271, 511-523.	4.2	498
99	Modelling antibody-antigen interactions: ferritin as a case study. <i>Molecular Immunology</i> , 1995, 32, 1001-1010.	2.2	15
100	PUZZLE: A New Method for Automated Protein Docking Based on Surface Shape Complementarity. <i>Journal of Molecular Biology</i> , 1994, 235, 1021-1031.	4.2	91