

Manuela Helmer-Citterich

List of Publications by Year in descending order

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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	MINT: a Molecular INTERaction database. FEBS Letters, 2002, 513, 135-140.	2.8	665
2	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. Nucleic Acids Research, 2003, 31, 3625-3630.	14.5	555
3	Revealing proteinâ€“lncRNA interaction. Briefings in Bioinformatics, 2016, 17, 106-116.	6.5	536
4	Correlated mutations contain information about protein-protein interaction 1 1Edited by A. R. Fersht. Journal of Molecular Biology, 1997, 271, 511-523.	4.2	498
5	ELM: the status of the 2010 eukaryotic linear motif resource. Nucleic Acids Research, 2010, 38, D167-D180.	14.5	217
6	Deciphering a global network of functionally associated postâ€“translational modifications. Molecular Systems Biology, 2012, 8, 599.	7.2	216
7	AMBRA1 links autophagy to cell proliferation and tumorigenesis by promoting c-Myc dephosphorylation and degradation. Nature Cell Biology, 2015, 17, 20-30.	10.3	200
8	Kinome-wide Decoding of Network-Attacking Mutations Rewiring Cancer Signaling. Cell, 2015, 163, 202-217.	28.9	168
9	Design and properties of a Myc derivative that efficiently homodimerizes. Oncogene, 1998, 17, 2463-2472.	5.9	154
10	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
11	Convergent Evolution of Enzyme Active Sites Is not a Rare Phenomenon. Journal of Molecular Biology, 2007, 372, 817-845.	4.2	109
12	PUZZLE: A New Method for Automated Protein Docking Based on Surface Shape Complementarity. Journal of Molecular Biology, 1994, 235, 1021-1031.	4.2	91
13	COVID-19 and Genetic Variants of Protein Involved in the SARS-CoV-2 Entry into the Host Cells. Genes, 2020, 11, 1010.	2.4	88
14	PDBe-KB: a community-driven resource for structural and functional annotations. Nucleic Acids Research, 2020, 48, D344-D353.	14.5	87
15	Peamaclein â€“ A new peach allergenic protein: similarities, differences and misleading features compared to Pru p 3. Clinical and Experimental Allergy, 2013, 43, 128-140.	2.9	85
16	Three-dimensional view of the surface motif associated with the P-loop structure: cis and trans cases of convergent evolution 1 1Edited by J. Thornton. Journal of Molecular Biology, 2000, 303, 455-465.	4.2	78
17	Regulation Dynamics of Leishmania Differentiation: Deconvoluting Signals and Identifying Phosphorylation Trends. Molecular and Cellular Proteomics, 2014, 13, 1787-1799.	3.8	72
18	Structure-based function prediction: approaches and applications. Briefings in Functional Genomics & Proteomics, 2008, 7, 291-302.	3.8	67

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19	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
20	Exploring the diversity of SPRY/B30.2-mediated interactions. <i>Trends in Biochemical Sciences</i> , 2013, 38, 38-46.	7.5	67
21	SURFACE: a database of protein surface regions for functional annotation. <i>Nucleic Acids Research</i> , 2004, 32, 240D-244.	14.5	59
22	Three-dimensional profiles: a new tool to identify protein surface similarities. <i>Journal of Molecular Biology</i> , 1998, 284, 1211-1221.	4.2	49
23	Query3d: a new method for high-throughput analysis of functional residues in protein structures. <i>BMC Bioinformatics</i> , 2005, 6, S5.	2.6	47
24	PDBe-KB: collaboratively defining the biological context of structural data. <i>Nucleic Acids Research</i> , 2022, 50, D534-D542.	14.5	46
25	Phospho3D 2.0: an enhanced database of three-dimensional structures of phosphorylation sites. <i>Nucleic Acids Research</i> , 2011, 39, D268-D271.	14.5	45
26	Phospho3D: a database of three-dimensional structures of protein phosphorylation sites. <i>Nucleic Acids Research</i> , 2007, 35, D229-D231.	14.5	43
27	A novel approach to represent and compare RNA secondary structures. <i>Nucleic Acids Research</i> , 2014, 42, 6146-6157.	14.5	43
28	Modeling cancer drug response through drug-specific informative genes. <i>Scientific Reports</i> , 2019, 9, 15222.	3.3	42
29	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
30	A structure filter for the Eukaryotic Linear Motif Resource. <i>BMC Bioinformatics</i> , 2009, 10, 351.	2.6	40
31	Role of CTCF Protein in Regulating FMR1 Locus Transcription. <i>PLoS Genetics</i> , 2013, 9, e1003601.	3.5	38
32	SH3-Hunter: discovery of SH3 domain interaction sites in proteins. <i>Nucleic Acids Research</i> , 2007, 35, W451-W454.	14.5	35
33	Identification of <i>Leishmania</i> specific protein phosphorylation sites by LC-ESI-MS/MS and comparative genomics analyses. <i>Proteomics</i> , 2010, 10, 3868-3883.	2.2	35
34	Cyclosporin A Treatment of <i>Leishmania donovani</i> Reveals Stage-Specific Functions of Cyclophilins in Parasite Proliferation and Viability. <i>PLoS Neglected Tropical Diseases</i> , 2010, 4, e729.	3.0	34
35	pdBFun: mass selection and fast comparison of annotated PDB residues. <i>Nucleic Acids Research</i> , 2005, 33, W133-W137.	14.5	31
36	FunClust: a web server for the identification of structural motifs in a set of non-homologous protein structures. <i>BMC Bioinformatics</i> , 2008, 9, S2.	2.6	31

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37	What has proteomics taught us about <i>Leishmania</i> development?. <i>Parasitology</i> , 2012, 139, 1146-1157.	1.5	31
38	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
39	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
40	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
41	Functional annotation by identification of local surface similarities: a novel tool for structural genomics. <i>BMC Bioinformatics</i> , 2005, 6, 194.	2.6	27
42	Modular architecture of nucleotide-binding pockets. <i>Nucleic Acids Research</i> , 2010, 38, 3809-3816.	14.5	24
43	Mapping the human phosphatome on growth pathways. <i>Molecular Systems Biology</i> , 2012, 8, 603.	7.2	24
44	c-MYC inhibition impairs hypoxia response in glioblastoma multiforme. <i>Oncotarget</i> , 2016, 7, 33257-33271.	1.8	24
45	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
46	PhosTryp: a phosphorylation site predictor specific for parasitic protozoa of the family trypanosomatidae. <i>BMC Genomics</i> , 2011, 12, 614.	2.8	19
47	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
48	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
49	From sequence to structural analysis in protein phosphorylation motifs. <i>Frontiers in Bioscience - Landmark</i> , 2011, 16, 1261.	3.0	18
50	Local comparison of protein structures highlights cases of convergent evolution in analogous functional sites. <i>BMC Bioinformatics</i> , 2007, 8, S24.	2.6	17
51	Discovering sequence and structure landscapes in RNA interaction motifs. <i>Nucleic Acids Research</i> , 2019, 47, 4958-4969.	14.5	17
52	Computational methods for analysis and inference of kinase/inhibitor relationships. <i>Frontiers in Genetics</i> , 2014, 5, 196.	2.3	16
53	Modelling antibody-antigen interactions: ferritin as a case study. <i>Molecular Immunology</i> , 1995, 32, 1001-1010.	2.2	15
54	Phosphate binding sites identification in protein structures. <i>Nucleic Acids Research</i> , 2011, 39, 1231-1242.	14.5	15

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55	Superpose3D: A Local Structural Comparison Program That Allows for User-Defined Structure Representations. PLoS ONE, 2010, 5, e11988.	2.5	14
56	Identification of binding pockets in protein structures using a knowledge-based potential derived from local structural similarities. BMC Bioinformatics, 2012, 13, S17.	2.6	14
57	B-Pred, a structure based B-cell epitopes prediction server. Advances and Applications in Bioinformatics and Chemistry, 2012, 5, 11.	2.6	14
58	Exploiting holistic approaches to model specificity in protein phosphorylation. Frontiers in Genetics, 2014, 5, 315.	2.3	14
59	Structural motifs recurring in different folds recognize the same ligand fragments. BMC Bioinformatics, 2009, 10, 182.	2.6	13
60	Phosfinder: a web server for the identification of phosphate-binding sites on protein structures. Nucleic Acids Research, 2011, 39, W278-W282.	14.5	13
61	A community proposal to integrate structural bioinformatics activities in ELIXIR (3D-Bioinfo) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tj ETQq1 1 0.784314 rgBT /Overlock 10	0.784314	12
62	DBATE: database of alternative transcripts expression. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat050.	3.0	11
63	COTAN: scRNA-seq data analysis based on gene co-expression. NAR Genomics and Bioinformatics, 2021, 3, lqab072.	3.2	11
64	A neural strategy for the inference of SH3 domain-peptide interaction specificity. BMC Bioinformatics, 2005, 6, S13.	2.6	10
65	Seq2Struct: a resource for establishing sequence-structure links. Bioinformatics, 2005, 21, 551-553.	4.1	10
66	BEAM web server: a tool for structural RNA motif discovery. Bioinformatics, 2018, 34, 1058-1060.	4.1	10
67	BRIO: a web server for RNA sequence and structure motif scan. Nucleic Acids Research, 2021, 49, W67-W71.	14.5	10
68	Kinome-wide identification of phosphorylation networks in eukaryotic proteomes. Bioinformatics, 2019, 35, 372-379.	4.1	9
69	iSPOT: A Web Tool for the Analysis and Recognition of Protein Domain Specificity. Comparative and Functional Genomics, 2001, 2, 314-318.	2.0	8
70	Overview of BITS2005, the Second Annual Meeting of the Italian Bioinformatics Society. BMC Bioinformatics, 2005, 6, S1.	2.6	8
71	False occurrences of functional motifs in protein sequences highlight evolutionary constraints. BMC Bioinformatics, 2007, 8, 68.	2.6	8
72	Modeling gene regulatory network motifs using statecharts. BMC Bioinformatics, 2012, 13, S20.	2.6	8

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73	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
74	Adaptation of a 2D in-gel kinase assay to trace phosphotransferase activities in the human pathogen <i>Leishmania donovani</i> . <i>Journal of Proteomics</i> , 2011, 74, 1644-1651.	2.4	7
75	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
76	Evaluation of potential sponge effects of SARS genomes in human. <i>Non-coding RNA Research</i> , 2022, , .	4.6	7
77	A structural study for the optimisation of functional motifs encoded in protein sequences. <i>BMC Bioinformatics</i> , 2004, 5, 50.	2.6	6
78	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
79	Identification of Nucleotide-Binding Sites in Protein Structures: A Novel Approach Based on Nucleotide Modularity. <i>PLoS ONE</i> , 2012, 7, e50240.	2.5	6
80	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
81	A Proteome-wide Domain-centric Perspective on Protein Phosphorylation. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2198-2212.	3.8	5
82	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
83	WWP1 germline variants are associated with normocephalic autism spectrum disorder. <i>Cell Death and Disease</i> , 2020, 11, 529.	6.3	5
84	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
85	Alternative splicing tends to avoid partial removals of protein-protein interaction sites. <i>BMC Genomics</i> , 2013, 14, 379.	2.8	4
86	RISC RNA sequencing in the Dorsal Raphe nucleus reveals microRNAs regulatory activities associated with behavioral and functional adaptations to chronic stress. <i>Brain Research</i> , 2020, 1736, 146763.	2.2	4
87	Variants in MHY7 Gene Cause Arrhythmogenic Cardiomyopathy. <i>Genes</i> , 2021, 12, 793.	2.4	4
88	Experimental and computational methods for the analysis and modeling of signaling networks. <i>New Biotechnology</i> , 2013, 30, 327-332.	4.4	3
89	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
90	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

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91	Bioinformatics in Italy: BITS2011, the Eighth Annual Meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2012, 13, 11.	2.6	2
92	Motif Discovery from CLIP Experiments. Methods in Molecular Biology, 2021, 2284, 43-50.	0.9	2
93	Variation in the co-expression profile highlights a loss of miRNA-mRNA regulation in multiple cancer types. Non-coding RNA Research, 2022, 7, 98-105.	4.6	2
94	Development of Computational Tools for the Inference of Protein Interaction Specificity Rules and Functional Annotation Using Structural Information. Comparative and Functional Genomics, 2003, 4, 416-419.	2.0	1
95	Bioinformatics in Italy: BITS2012, the ninth annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2013, 14, S1.	2.6	1
96	A Simple Protocol for the Inference of RNA Global Pairwise Alignments. Methods in Molecular Biology, 2015, 1269, 39-47.	0.9	1
97	Dissecting the Genome for Drug Response Prediction. Methods in Molecular Biology, 2022, 2449, 187-196.	0.9	1
98	Searching the MINT Database for Protein Interaction Information. Current Protocols in Bioinformatics, 2003, 2, Unit 8.5.	25.8	0
99	Preface: BITS2014, the annual meeting of the Italian Society of Bioinformatics. BMC Bioinformatics, 2015, 16, S1.	2.6	0
100	Conserved exchange of paralog proteins during neuronal differentiation. Life Science Alliance, 2022, 5, e202201397.	2.8	0