

Gianni Cesareni

List of Publications by Year in descending order

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135
papers

16,673
citations

23500

58
h-index

16127

124
g-index

145
all docs

145
docs citations

145
times ranked

19558
citing authors

#	ARTICLE	IF	CITATIONS
1	The MIntAct projectâ€”IntAct as a common curation platform for 11 molecular interaction databases. <i>Nucleic Acids Research</i> , 2014, 42, D358-D363.	6.5	1,634
2	MINT, the molecular interaction database: 2012 update. <i>Nucleic Acids Research</i> , 2012, 40, D857-D861.	6.5	917
3	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	6.5	864
4	MINT: the Molecular INTERaction database. <i>Nucleic Acids Research</i> , 2007, 35, D572-D574.	6.5	795
5	A Combined Experimental and Computational Strategy to Define Protein Interaction Networks for Peptide Recognition Modules. <i>Science</i> , 2002, 295, 321-324.	6.0	668
6	MINT: a Molecular INTERaction database. <i>FEBS Letters</i> , 2002, 513, 135-140.	1.3	665
7	The HUPO PSI's Molecular Interaction formatâ€”a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	9.4	581
8	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. <i>Nucleic Acids Research</i> , 2003, 31, 3625-3630.	6.5	555
9	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	9.0	500
10	MINT, the molecular interaction database: 2009 update. <i>Nucleic Acids Research</i> , 2010, 38, D532-D539.	6.5	458
11	Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2.	1.6	418
12	Selection of antibody ligands from a large library of oligopeptides expressed on a multivalent exposition vector. <i>Journal of Molecular Biology</i> , 1991, 222, 301-310.	2.0	400
13	KinomeXplorer: an integrated platform for kinome biology studies. <i>Nature Methods</i> , 2014, 11, 603-604.	9.0	304
14	Binding specificity and in vivo targets of the EH domain, a novel proteinâ€”protein interaction module. <i>Genes and Development</i> , 1997, 11, 2239-2249.	2.7	293
15	mentha: a resource for browsing integrated protein-interaction networks. <i>Nature Methods</i> , 2013, 10, 690-691.	9.0	291
16	The ubiquitinâ€”protein ligase Itch regulates p73 stability. <i>EMBO Journal</i> , 2005, 24, 836-848.	3.5	286
17	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	9.4	274
18	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	9.0	274

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19	Intersectin, a Novel Adaptor Protein with Two Eps15 Homology and Five Src Homology 3 Domains. <i>Journal of Biological Chemistry</i> , 1998, 273, 31401-31407.	1.6	264
20	Microfluidic-enhanced 3D bioprinting of aligned myoblast-laden hydrogels leads to functionally organized myofibers in vitro and in vivo. <i>Biomaterials</i> , 2017, 131, 98-110.	5.7	252
21	SIGNOR: a database of causal relationships between biological entities. <i>Nucleic Acids Research</i> , 2016, 44, D548-D554.	6.5	243
22	Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	1.7	237
23	Protein Interaction Networks by Proteome Peptide Scanning. <i>PLoS Biology</i> , 2004, 2, e14.	2.6	197
24	The human phosphatase interactome: An intricate family portrait. <i>FEBS Letters</i> , 2012, 586, 2732-2739.	1.3	184
25	VirusMINT: a viral protein interaction database. <i>Nucleic Acids Research</i> , 2009, 37, D669-D673.	6.5	180
26	A novel peptide-SH3 interaction. <i>EMBO Journal</i> , 1999, 18, 5300-5309.	3.5	172
27	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. <i>PLoS Biology</i> , 2009, 7, e1000218.	2.6	172
28	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D504-D510.	6.5	160
29	VirusMentha: a new resource for virus-host protein interactions. <i>Nucleic Acids Research</i> , 2015, 43, D588-D592.	6.5	141
30	Conjugation to Nedd8 Instigates Ubiquitylation and Down-regulation of Activated Receptor Tyrosine Kinases. <i>Journal of Biological Chemistry</i> , 2006, 281, 21640-21651.	1.6	135
31	HomoMINT: an inferred human network based on orthology mapping of protein interactions discovered in model organisms. <i>BMC Bioinformatics</i> , 2005, 6, S21.	1.2	128
32	Can we infer peptide recognition specificity mediated by SH3 domains?. <i>FEBS Letters</i> , 2002, 513, 38-44.	1.3	124
33	The SH3 Domains of Endophilin and Amphiphysin Bind to the Proline-rich Region of Synaptojanin 1 at Distinct Sites That Display an Unconventional Binding Specificity. <i>Journal of Biological Chemistry</i> , 1999, 274, 32001-32007.	1.6	122
34	Normalization of nomenclature for peptide motifs as ligands of modular protein domains. <i>FEBS Letters</i> , 2002, 513, 141-144.	1.3	118
35	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	6.5	113
36	Single-cell mass cytometry and transcriptome profiling reveal the impact of graphene on human immune cells. <i>Nature Communications</i> , 2017, 8, 1109.	5.8	111

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37	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	2.9	110
38	Recognition specificity of individual EH domains of mammals and yeast. <i>EMBO Journal</i> , 1998, 17, 6541-6550.	3.5	106
39	Gene Regulatory Network Modeling of Macrophage Differentiation Corroborates the Continuum Hypothesis of Polarization States. <i>Frontiers in Physiology</i> , 2018, 9, 1659.	1.3	102
40	Control of ColE1 plasmid replication by antisense RNA. <i>Trends in Genetics</i> , 1991, 7, 230-235.	2.9	91
41	3D hydrogel environment rejuvenates aged pericytes for skeletal muscle tissue engineering. <i>Frontiers in Physiology</i> , 2014, 5, 203.	1.3	90
42	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	6.5	89
43	SH3-SPOT: an algorithm to predict preferred ligands to different members of the SH3 gene family. <i>Journal of Molecular Biology</i> , 2000, 298, 313-328.	2.0	86
44	WI-PHI: A weighted yeast interactome enriched for direct physical interactions. <i>Proteomics</i> , 2007, 7, 932-943.	1.3	83
45	An Overview of BioCreative II.5. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 385-399.	1.9	83
46	Comparative interactomics: comparing apples and pears?. <i>Trends in Biotechnology</i> , 2007, 25, 448-454.	4.9	81
47	Diverse driving forces underlie the invariant occurrence of the T42A, E139D, I282V and T468M SHP2 amino acid substitutions causing Noonan and LEOPARD syndromes. <i>Human Molecular Genetics</i> , 2008, 17, 2018-2029.	1.4	79
48	DOMINO: a database of domain-peptide interactions. <i>Nucleic Acids Research</i> , 2007, 35, D557-D560.	6.5	76
49	Deep Proteomics of Breast Cancer Cells Reveals that Metformin Rewires Signaling Networks Away from a Pro-growth State. <i>Cell Systems</i> , 2016, 2, 159-171.	2.9	76
50	The Most Abundant Small Cytoplasmic RNA of <i>Saccharomyces cerevisiae</i> Has an Important Function Required for Normal Cell Growth. <i>Molecular and Cellular Biology</i> , 1989, 9, 3260-3268.	1.1	75
51	Modified phage peptide libraries as a tool to study specificity of phosphorylation and recognition of tyrosine containing peptides 1 Edited by J. Karn. <i>Journal of Molecular Biology</i> , 1997, 269, 694-703.	2.0	74
52	Escher: A new docking procedure applied to the reconstruction of protein tertiary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 28, 556-567.	1.5	74
53	Recombinant H-chain ferritins: Effects of changes in the 3-fold channels. <i>FEBS Letters</i> , 1989, 247, 268-272.	1.3	69
54	Adipogenesis of skeletal muscle fibro/adipogenic progenitors is affected by the WNT5a/GSK3 β -catenin axis. <i>Cell Death and Differentiation</i> , 2020, 27, 2921-2941.	5.0	69

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55	Tumor Suppressor Density-enhanced Phosphatase-1 (DEP-1) Inhibits the RAS Pathway by Direct Dephosphorylation of ERK1/2 Kinases. <i>Journal of Biological Chemistry</i> , 2009, 284, 22048-22058.	1.6	68
56	Exploring the diversity of SPRY/B30.2-mediated interactions. <i>Trends in Biochemical Sciences</i> , 2013, 38, 38-46.	3.7	67
57	Selectivity and promiscuity in the interaction network mediated by protein recognition modules. <i>FEBS Letters</i> , 2004, 567, 74-79.	1.3	65
58	Linking entries in protein interaction database to structured text: The FEBS Letters experiment. <i>FEBS Letters</i> , 2008, 582, 1171-1177.	1.3	62
59	Distinct Binding Specificity of the Multiple PDZ Domains of INADL, a Human Protein with Homology to INAD from <i>Drosophila melanogaster</i> . <i>Journal of Biological Chemistry</i> , 2001, 276, 42122-42130.	1.6	58
60	Recurated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 860-861.	9.0	58
61	HuPho: the human phosphatase portal. <i>FEBS Journal</i> , 2013, 280, 379-387.	2.2	55
62	The 4G10, pY20 and p-TYR-100 antibody specificity: profiling by peptide microarrays. <i>New Biotechnology</i> , 2012, 29, 571-577.	2.4	52
63	The protein interaction network mediated by human SH3 domains. <i>Biotechnology Advances</i> , 2012, 30, 4-15.	6.0	49
64	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020, 11, 6144.	5.8	49
65	In Vitro Evolution of Recognition Specificity Mediated by SH3 Domains Reveals Target Recognition Rules. <i>Journal of Biological Chemistry</i> , 2002, 277, 21666-21674.	1.6	47
66	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. <i>BMC Bioinformatics</i> , 2018, 19, 134.	1.2	47
67	Metformin Protects Skeletal Muscle from Cardiotoxin Induced Degeneration. <i>PLoS ONE</i> , 2014, 9, e114018.	1.1	45
68	Comparative interactomics. <i>FEBS Letters</i> , 2005, 579, 1828-1833.	1.3	44
69	Probing Protein-tyrosine Phosphatase Substrate Specificity Using a Phosphotyrosine-containing Phage Library. <i>Journal of Biological Chemistry</i> , 2004, 279, 311-318.	1.6	42
70	The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. <i>Nature Biotechnology</i> , 2010, 28, 897-899.	9.4	42
71	DISNOR: a disease network open resource. <i>Nucleic Acids Research</i> , 2018, 46, D527-D534.	6.5	42
72	Identification of New Substrates of the Protein-tyrosine Phosphatase PTP1B by Bayesian Integration of Proteome Evidence. <i>Journal of Biological Chemistry</i> , 2011, 286, 4173-4185.	1.6	41

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73	Fibro-adipogenic progenitors of dystrophic mice are insensitive to NOTCH regulation of adipogenesis. <i>Life Science Alliance</i> , 2019, 2, e201900437.	1.3	41
74	Metabolic reprogramming of fibro/adipogenic progenitors facilitates muscle regeneration. <i>Life Science Alliance</i> , 2020, 3, e202000646.	1.3	36
75	Counteracting Effects Operating on Src Homology 2 Domain-containing Protein-tyrosine Phosphatase 2 (SHP2) Function Drive Selection of the Recurrent Y62D and Y63C Substitutions in Noonan Syndrome*. <i>Journal of Biological Chemistry</i> , 2012, 287, 27066-27077.	1.6	35
76	Combining peptide recognition specificity and context information for the prediction of the 14-3-3-mediated interactome in <i>S. cerevisiae</i> and <i>H. sapiens</i> . <i>Proteomics</i> , 2011, 11, 128-143.	1.3	34
77	The IMEx coronavirus interactome: an evolving map of <i>Coronaviridae</i> 's host molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	34
78	Protein interactions: integration leads to belief. <i>Trends in Biochemical Sciences</i> , 2008, 33, 241-242.	3.7	33
79	Structural and functional protein network analyses predict novel signaling functions for rhodopsin. <i>Molecular Systems Biology</i> , 2011, 7, 551.	3.2	33
80	Role of 14-3-3 proteins in the regulation of neutral trehalase in the yeast <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2008, 8, 53-63.	1.1	32
81	Metformin Delays Satellite Cell Activation and Maintains Quiescence. <i>Stem Cells International</i> , 2019, 2019, 1-19.	1.2	32
82	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. <i>Bioinformatics</i> , 2019, 35, 3779-3785.	1.8	32
83	Construction, Exploitation and Evolution of a New Peptide Library Displayed at High Density by Fusion to the Major Coat Protein of Filamentous Phage. <i>Biological Chemistry</i> , 1997, 378, 517-21.	1.2	30
84	Phage Displayed Peptide Libraries. <i>Combinatorial Chemistry and High Throughput Screening</i> , 1999, 2, 1-17.	0.6	30
85	CancerGeneNet: linking driver genes to cancer hallmarks. <i>Nucleic Acids Research</i> , 2020, 48, D416-D421.	6.5	29
86	Biofabricating murine and human myoblasts substitutes for rapid volumetric muscle loss restoration. <i>EMBO Molecular Medicine</i> , 2021, 13, e12778.	3.3	29
87	Methods to reveal domain networks. <i>Drug Discovery Today</i> , 2005, 10, 1111-1117.	3.2	28
88	Regulation of myoblast differentiation by metabolic perturbations induced by metformin. <i>PLoS ONE</i> , 2017, 12, e0182475.	1.1	28
89	Mapping the human phosphatome on growth pathways. <i>Molecular Systems Biology</i> , 2012, 8, 603.	3.2	24
90	The cell-autonomous mechanisms underlying the activity of metformin as an anticancer drug. <i>British Journal of Cancer</i> , 2016, 115, 1451-1456.	2.9	23

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91	Selectivity of the CUBAN domain in the recognition of ubiquitin and NEDD8. <i>FEBS Journal</i> , 2019, 286, 653-677.	2.2	22
92	SCA-1 micro-heterogeneity in the fate decision of dystrophic fibro/adipogenic progenitors. <i>Cell Death and Disease</i> , 2021, 12, 122.	2.7	21
93	Group I Paks support muscle regeneration and counteract cancer-associated muscle atrophy. <i>Journal of Cachexia, Sarcopenia and Muscle</i> , 2018, 9, 727-746.	2.9	20
94	The immunosuppressant drug azathioprine restrains adipogenesis of muscle Fibro/Adipogenic Progenitors from dystrophic mice by affecting AKT signaling. <i>Scientific Reports</i> , 2019, 9, 4360.	1.6	20
95	The target of the negative regulator of pMB1 replication overlaps with part of the repressor coding sequence. <i>Molecular Genetics and Genomics</i> , 1981, 184, 40-45.	2.4	19
96	High-Dimensional Single-Cell Quantitative Profiling of Skeletal Muscle Cell Population Dynamics during Regeneration. <i>Cells</i> , 2020, 9, 1723.	1.8	18
97	Janus effect of glucocorticoids on differentiation of muscle fibro/adipogenic progenitors. <i>Scientific Reports</i> , 2020, 10, 5363.	1.6	18
98	The adapter protein CD2AP binds to p53 protein in the cytoplasm and can discriminate its polymorphic variants P72R. <i>Journal of Biochemistry</i> , 2015, 157, 101-111.	0.9	17
99	Domain repertoires as a tool to derive protein recognition rules. <i>FEBS Letters</i> , 2000, 480, 49-54.	1.3	16
100	RNF11 is a GGA protein cargo and acts as a molecular adaptor for GGA3 ubiquitination mediated by Itch. <i>Oncogene</i> , 2015, 34, 3377-3390.	2.6	15
101	Combining Phosphoproteomics Datasets and Literature Information to Reveal the Functional Connections in a Cell Phosphorylation Network. <i>Proteomics</i> , 2018, 18, 1700311.	1.3	15
102	SIGNOR: A Database of Causal Relationships Between Biological Entities—A Short Guide to Searching and Browsing. <i>Current Protocols in Bioinformatics</i> , 2017, 58, 8.23.1-8.23.16.	25.8	14
103	Combining affinity proteomics and network context to identify new phosphatase substrates and adapters in growth pathways. <i>Frontiers in Genetics</i> , 2014, 5, 115.	1.1	13
104	SPV: a JavaScript Signaling Pathway Visualizer. <i>Bioinformatics</i> , 2018, 34, 2684-2686.	1.8	12
105	CoCUN, a Novel Ubiquitin Binding Domain Identified in N4BP1. <i>Biomolecules</i> , 2019, 9, 284.	1.8	12
106	Benchmarking of the 2010 BioCreative Challenge III text-mining competition by the BioGRID and MINT interaction databases. <i>BMC Bioinformatics</i> , 2011, 12, S8.	1.2	11
107	Osteogenic differentiation of skeletal muscle progenitor cells is activated by the DNA damage response. <i>Scientific Reports</i> , 2019, 9, 5447.	1.6	11
108	Toward High-Dimensional Single-Cell Analysis of Graphene Oxide Biological Impact: Tracking on Immune Cells by Single-Cell Mass Cytometry. <i>Small</i> , 2020, 16, 2000123.	5.2	10

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109	Characterization of the Skeletal Muscle Secretome Reveals a Role for Extracellular Vesicles and IL1 β /IL1 γ in Restricting Fibro/Adipogenic Progenitor Adipogenesis. <i>Biomolecules</i> , 2021, 11, 1171.	1.8	10
110	Enriching the viralâ€‘host interactomes with interactions mediated by SH3 domains. <i>Amino Acids</i> , 2010, 38, 1541-1547.	1.2	9
111	Reactive Oxygen Species and Epidermal Growth Factor Are Antagonistic Cues Controlling SHP-2 Dimerization. <i>Molecular and Cellular Biology</i> , 2012, 32, 1998-2009.	1.1	9
112	Characterization by mass cytometry of different methods for the preparation of muscle mononuclear cells. <i>New Biotechnology</i> , 2016, 33, 514-523.	2.4	9
113	The FEBS Letters SDA corpus: A collection of protein interaction articles with high quality annotations for the BioCreative II.5 online challenge and the text mining community. <i>FEBS Letters</i> , 2010, 584, 4129-4130.	1.3	8
114	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. <i>Journal of Biological Chemistry</i> , 2017, 292, 4942-4952.	1.6	8
115	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. <i>Frontiers in Physiology</i> , 2019, 10, 1216.	1.3	8
116	Alterations in the phosphoproteomic profile of cells expressing a non-functional form of the SHP2 phosphatase. <i>New Biotechnology</i> , 2016, 33, 524-536.	2.4	7
117	A Resource for the Network Representation of Cell Perturbations Caused by SARS-CoV-2 Infection. <i>Genes</i> , 2021, 12, 450.	1.0	7
118	Adipogenesis of Skeletal Muscle Fibro/Adipogenic Progenitors is Controlled by the WNT5a/GSK3 β -Catenin Axis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	7
119	SIGNORApp: a Cytoscape 3 application to access SIGNOR data. <i>Bioinformatics</i> , 2022, 38, 1764-1766.	1.8	7
120	Structural studies and SH3 domain binding properties of a human antiviral salivary prolineâ€‘rich peptide. <i>Biopolymers</i> , 2016, 106, 714-725.	1.2	6
121	Domains Mediate Protein-Protein Interactions and Nucleate Protein Assemblies. <i>Handbook of Experimental Pharmacology</i> , 2008, , 383-405.	0.9	6
122	The hierarchical organization of natural protein interaction networks confers self-organization properties on pseudocells. <i>BMC Systems Biology</i> , 2015, 9, S3.	3.0	5
123	A subset of RAB proteins modulates PP2A phosphatase activity. <i>Scientific Reports</i> , 2016, 6, 32857.	1.6	5
124	Phage displayed peptide libraries. <i>Combinatorial Chemistry and High Throughput Screening</i> , 1999, 2, 1-17.	0.6	5
125	Skeletal Muscle Subpopulation Rearrangements upon Rhabdomyosarcoma Development through Single-Cell Mass Cytometry. <i>Journal of Clinical Medicine</i> , 2021, 10, 823.	1.0	4
126	Assembling Disease Networks From Causal Interaction Resources. <i>Frontiers in Genetics</i> , 2021, 12, 694468.	1.1	4

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127	Profiling Phosphopeptide-Binding Domain Recognition Specificity Using Peptide Microarrays. <i>Methods in Molecular Biology</i> , 2017, 1518, 177-193.	0.4	3
128	CUBAN, a Case Study of Selective Binding: Structural Details of the Discrimination between Ubiquitin and NEDD8. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1185.	1.8	3
129	A Resource to Infer Molecular Paths Linking Cancer Mutations to Perturbation of Cell Metabolism. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	1.6	3
130	Lowe syndromeâ€“linked endocytic adaptors direct membrane cycling kinetics with OCRL in <i>Dictyostelium discoideum</i> . <i>Molecular Biology of the Cell</i> , 2019, 30, 2268-2282.	0.9	2
131	Making decisions in G1. <i>FEBS Letters</i> , 2001, 490, 109-109.	1.3	0
132	Spotlight onâ€“Gianni Cesareni. <i>FEBS Letters</i> , 2008, 582, 1291-1292.	1.3	0
133	SH3 and SH2: Prototypic Domains to Mediate Regulatory Mechanisms in the Cell. , 2016, , 112-121.		0
134	HiPPO and PANDA: Two Bioinformatics Tools to Support Analysis of Mass Cytometry Data. <i>Journal of Computational Biology</i> , 2020, 27, 1283-1294.	0.8	0
135	Transcription Factor Activation Profiles (TFAP) identify compounds promoting differentiation of Acute Myeloid Leukemia cell lines. <i>Cell Death Discovery</i> , 2022, 8, 16.	2.0	0