

# Gianni Cesareni

## List of Publications by Year in descending order

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135  
papers

16,673  
citations

23567

58  
h-index

16183

124  
g-index

145  
all docs

145  
docs citations

145  
times ranked

19558  
citing authors

#	ARTICLE	IF	CITATIONS
1	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	14.5	89
2	Transcription Factor Activation Profiles (TFAP) identify compounds promoting differentiation of Acute Myeloid Leukemia cell lines. <i>Cell Death Discovery</i> , 2022, 8, 16.	4.7	0
3	SIGNORApp: a Cytoscape 3 application to access SIGNOR data. <i>Bioinformatics</i> , 2022, 38, 1764-1766.	4.1	7
4	A Resource to Infer Molecular Paths Linking Cancer Mutations to Perturbation of Cell Metabolism. <i>Frontiers in Molecular Biosciences</i> , 2022, 9, .	3.5	3
5	SCA-1 micro-heterogeneity in the fate decision of dystrophic fibro/adipogenic progenitors. <i>Cell Death and Disease</i> , 2021, 12, 122.	6.3	21
6	Skeletal Muscle Subpopulation Rearrangements upon Rhabdomyosarcoma Development through Single-Cell Mass Cytometry. <i>Journal of Clinical Medicine</i> , 2021, 10, 823.	2.4	4
7	Biofabricating murine and human myoâ€ substitutes for rapid volumetric muscle loss restoration. <i>EMBO Molecular Medicine</i> , 2021, 13, e12778.	6.9	29
8	A Resource for the Network Representation of Cell Perturbations Caused by SARS-CoV-2 Infection. <i>Genes</i> , 2021, 12, 450.	2.4	7
9	Assembling Disease Networks From Causal Interaction Resources. <i>Frontiers in Genetics</i> , 2021, 12, 694468.	2.3	4
10	Characterization of the Skeletal Muscle Secretome Reveals a Role for Extracellular Vesicles and IL1±/IL1² in Restricting Fibro/Adipogenic Progenitor Adipogenesis. <i>Biomolecules</i> , 2021, 11, 1171.	4.0	10
11	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. <i>Nucleic Acids Research</i> , 2020, 48, D504-D510.	14.5	160
12	CancerGeneNet: linking driver genes to cancer hallmarks. <i>Nucleic Acids Research</i> , 2020, 48, D416-D421.	14.5	29
13	HiPPO and PANDA: Two Bioinformatics Tools to Support Analysis of Mass Cytometry Data. <i>Journal of Computational Biology</i> , 2020, 27, 1283-1294.	1.6	0
14	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020, 11, 6144.	12.8	49
15	High-Dimensional Single-Cell Quantitative Profiling of Skeletal Muscle Cell Population Dynamics during Regeneration. <i>Cells</i> , 2020, 9, 1723.	4.1	18
16	Adipogenesis of skeletal muscle fibro/adipogenic progenitors is affected by the WNT5a/GSK3/²-catenin axis. <i>Cell Death and Differentiation</i> , 2020, 27, 2921-2941.	11.2	69
17	Janus effect of glucocorticoids on differentiation of muscle fibro/adipogenic progenitors. <i>Scientific Reports</i> , 2020, 10, 5363.	3.3	18
18	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.	10.0	10

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19	The IMEx coronavirus interactome: an evolving map of <i>Coronaviridae</i> host molecular interactions. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	3.0	34
20	Metabolic reprogramming of fibro/adipogenic progenitors facilitates muscle regeneration. Life Science Alliance, 2020, 3, e202000646.	2.8	36
21	CoCUN, a Novel Ubiquitin Binding Domain Identified in N4BP1. Biomolecules, 2019, 9, 284.	4.0	12
22	Lowe syndrome-linked endocytic adaptors direct membrane cycling kinetics with OCRL in <i>Dictyostelium discoideum</i> . Molecular Biology of the Cell, 2019, 30, 2268-2282.	2.1	2
23	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. Frontiers in Physiology, 2019, 10, 1216.	2.8	8
24	Selectivity of the CUBAN domain in the recognition of ubiquitin and NEDD8. FEBS Journal, 2019, 286, 653-677.	4.7	22
25	Metformin Delays Satellite Cell Activation and Maintains Quiescence. Stem Cells International, 2019, 2019, 1-19.	2.5	32
26	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. Bioinformatics, 2019, 35, 3779-3785.	4.1	32
27	CUBAN, a Case Study of Selective Binding: Structural Details of the Discrimination between Ubiquitin and NEDD8. International Journal of Molecular Sciences, 2019, 20, 1185.	4.1	3
28	The immunosuppressant drug azathioprine restrains adipogenesis of muscle Fibro/Adipogenic Progenitors from dystrophic mice by affecting AKT signaling. Scientific Reports, 2019, 9, 4360.	3.3	20
29	Osteogenic differentiation of skeletal muscle progenitor cells is activated by the DNA damage response. Scientific Reports, 2019, 9, 5447.	3.3	11
30	Fibro-adipogenic progenitors of dystrophic mice are insensitive to NOTCH regulation of adipogenesis. Life Science Alliance, 2019, 2, e201900437.	2.8	41
31	Combining Phosphoproteomics Datasets and Literature Information to Reveal the Functional Connections in a Cell Phosphorylation Network. Proteomics, 2018, 18, 1700311.	2.2	15
32	SPV: a JavaScript Signaling Pathway Visualizer. Bioinformatics, 2018, 34, 2684-2686.	4.1	12
33	DISNOR: a disease network open resource. Nucleic Acids Research, 2018, 46, D527-D534.	14.5	42
34	Gene Regulatory Network Modeling of Macrophage Differentiation Corroborates the Continuum Hypothesis of Polarization States. Frontiers in Physiology, 2018, 9, 1659.	2.8	102
35	Group I Paks support muscle regeneration and counteract cancer-associated muscle atrophy. Journal of Cachexia, Sarcopenia and Muscle, 2018, 9, 727-746.	7.3	20
36	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. BMC Bioinformatics, 2018, 19, 134.	2.6	47

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37	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.	3.4	8
38	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.	11.4	252
39	Single-cell mass cytometry and transcriptome profiling reveal the impact of graphene on human immune cells. <i>Nature Communications</i> , 2017, 8, 1109.	12.8	111
40	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
41	Profiling Phosphopeptide-Binding Domain Recognition Specificity Using Peptide Microarrays. <i>Methods in Molecular Biology</i> , 2017, 1518, 177-193.	0.9	3
42	Regulation of myoblast differentiation by metabolic perturbations induced by metformin. <i>PLoS ONE</i> , 2017, 12, e0182475.	2.5	28
43	Structural studies and SH3 domain binding properties of a human antiviral salivary proline-rich peptide. <i>Biopolymers</i> , 2016, 106, 714-725.	2.4	6
44	SH3 and SH2: Prototypic Domains to Mediate Regulatory Mechanisms in the Cell. , 2016, , 112-121.		0
45	A subset of RAB proteins modulates PP2A phosphatase activity. <i>Scientific Reports</i> , 2016, 6, 32857.	3.3	5
46	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.	6.2	76
47	The cell-autonomous mechanisms underlying the activity of metformin as an anticancer drug. <i>British Journal of Cancer</i> , 2016, 115, 1451-1456.	6.4	23
48	Tools and data services registry: a community effort to document bioinformatics resources. <i>Nucleic Acids Research</i> , 2016, 44, D38-D47.	14.5	113
49	Characterization by mass cytometry of different methods for the preparation of muscle mononuclear cells. <i>New Biotechnology</i> , 2016, 33, 514-523.	4.4	9
50	Alterations in the phosphoproteomic profile of cells expressing a non-functional form of the SHP2 phosphatase. <i>New Biotechnology</i> , 2016, 33, 524-536.	4.4	7
51	SIGNOR: a database of causal relationships between biological entities. <i>Nucleic Acids Research</i> , 2016, 44, D548-D554.	14.5	243
52	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
53	VirusMentha: a new resource for virus-host protein interactions. <i>Nucleic Acids Research</i> , 2015, 43, D588-D592.	14.5	141
54	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.	5.9	15

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55	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.	1.7	17
56	Metformin Protects Skeletal Muscle from Cardiotoxin Induced Degeneration. <i>PLoS ONE</i> , 2014, 9, e114018.	2.5	45
57	3D hydrogel environment rejuvenates aged pericytes for skeletal muscle tissue engineering. <i>Frontiers in Physiology</i> , 2014, 5, 203.	2.8	90
58	Combining affinity proteomics and network context to identify new phosphatase substrates and adapters in growth pathways. <i>Frontiers in Genetics</i> , 2014, 5, 115.	2.3	13
59	The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. <i>Nucleic Acids Research</i> , 2014, 42, D358-D363.	14.5	1,634
60	KinomeXplorer: an integrated platform for kinome biology studies. <i>Nature Methods</i> , 2014, 11, 603-604.	19.0	304
61	mentha: a resource for browsing integrated protein-interaction networks. <i>Nature Methods</i> , 2013, 10, 690-691.	19.0	291
62	HuPho: the human phosphatase portal. <i>FEBS Journal</i> , 2013, 280, 379-387.	4.7	55
63	The SH2 Domain Interaction Landscape. <i>Cell Reports</i> , 2013, 3, 1293-1305.	6.4	110
64	Exploring the diversity of SPRY/B30.2-mediated interactions. <i>Trends in Biochemical Sciences</i> , 2013, 38, 38-46.	7.5	67
65	MINT, the molecular interaction database: 2012 update. <i>Nucleic Acids Research</i> , 2012, 40, D857-D861.	14.5	917
66	Mapping the human phosphatome on growth pathways. <i>Molecular Systems Biology</i> , 2012, 8, 603.	7.2	24
67	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	19.0	500
68	Reactive Oxygen Species and Epidermal Growth Factor Are Antagonistic Cues Controlling SHP-2 Dimerization. <i>Molecular and Cellular Biology</i> , 2012, 32, 1998-2009.	2.3	9
69	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.	3.4	35
70	The human phosphatase interactome: An intricate family portrait. <i>FEBS Letters</i> , 2012, 586, 2732-2739.	2.8	184
71	The 4G10, pY20 and p-TYR-100 antibody specificity: profiling by peptide microarrays. <i>New Biotechnology</i> , 2012, 29, 571-577.	4.4	52
72	The protein interaction network mediated by human SH3 domains. <i>Biotechnology Advances</i> , 2012, 30, 4-15.	11.7	49

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73	PSICQUIC and PSIScore: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	19.0	274
74	Structural and functional protein network analyses predict novel signaling functions for rhodopsin. <i>Molecular Systems Biology</i> , 2011, 7, 551.	7.2	33
75	Benchmarking of the 2010 BioCreative Challenge III text-mining competition by the BioGRID and MINT interaction databases. <i>BMC Bioinformatics</i> , 2011, 12, S8.	2.6	11
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.	2.2	34
77	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.	3.4	41
78	Enriching the viral-host interactomes with interactions mediated by SH3 domains. <i>Amino Acids</i> , 2010, 38, 1541-1547.	2.7	9
79	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.	2.8	8
80	The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. <i>Nature Biotechnology</i> , 2010, 28, 897-899.	17.5	42
81	An Overview of BioCreative II.5. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 385-399.	3.0	83
82	MINT, the molecular interaction database: 2009 update. <i>Nucleic Acids Research</i> , 2010, 38, D532-D539.	14.5	458
83	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.	3.4	68
84	Bayesian Modeling of the Yeast SH3 Domain Interactome Predicts Spatiotemporal Dynamics of Endocytosis Proteins. <i>PLoS Biology</i> , 2009, 7, e1000218.	5.6	172
85	VirusMINT: a viral protein interaction database. <i>Nucleic Acids Research</i> , 2009, 37, D669-D673.	14.5	180
86	Recurated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 860-861.	19.0	58
87	Linear Motif Atlas for Phosphorylation-Dependent Signaling. <i>Science Signaling</i> , 2008, 1, ra2.	3.6	418
88	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.	2.3	32
89	Linking entries in protein interaction database to structured text: The FEBS Letters experiment. <i>FEBS Letters</i> , 2008, 582, 1171-1177.	2.8	62
90	Spotlight on Gianni Cesareni. <i>FEBS Letters</i> , 2008, 582, 1291-1292.	2.8	0

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91	Protein interactions: integration leads to belief. <i>Trends in Biochemical Sciences</i> , 2008, 33, 241-242.	7.5	33
92	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.	2.9	79
93	Domains Mediate Protein-Protein Interactions and Nucleate Protein Assemblies. <i>Handbook of Experimental Pharmacology</i> , 2008, , 383-405.	1.8	6
94	MINT: the Molecular INTERaction database. <i>Nucleic Acids Research</i> , 2007, 35, D572-D574.	14.5	795
95	DOMINO: a database of domain-peptide interactions. <i>Nucleic Acids Research</i> , 2007, 35, D557-D560.	14.5	76
96	Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	3.8	237
97	WI-PHI: A weighted yeast interactome enriched for direct physical interactions. <i>Proteomics</i> , 2007, 7, 932-943.	2.2	83
98	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	17.5	274
99	Comparative interactomics: comparing apples and pears?. <i>Trends in Biotechnology</i> , 2007, 25, 448-454.	9.3	81
100	Conjugation to Nedd8 Instigates Ubiquitylation and Down-regulation of Activated Receptor Tyrosine Kinases. <i>Journal of Biological Chemistry</i> , 2006, 281, 21640-21651.	3.4	135
101	The ubiquitin–protein ligase Itch regulates p73 stability. <i>EMBO Journal</i> , 2005, 24, 836-848.	7.8	286
102	Methods to reveal domain networks. <i>Drug Discovery Today</i> , 2005, 10, 1111-1117.	6.4	28
103	HomoMINT: an inferred human network based on orthology mapping of protein interactions discovered in model organisms. <i>BMC Bioinformatics</i> , 2005, 6, S21.	2.6	128
104	Comparative interactomics. <i>FEBS Letters</i> , 2005, 579, 1828-1833.	2.8	44
105	Probing Protein-tyrosine Phosphatase Substrate Specificity Using a Phosphotyrosine-containing Phage Library. <i>Journal of Biological Chemistry</i> , 2004, 279, 311-318.	3.4	42
106	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	14.5	864
107	Protein Interaction Networks by Proteome Peptide Scanning. <i>PLoS Biology</i> , 2004, 2, e14.	5.6	197
108	The HUPO PSI's Molecular Interaction format – a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	17.5	581

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109	Selectivity and promiscuity in the interaction network mediated by protein recognition modules. FEBS Letters, 2004, 567, 74-79.	2.8	65
110	ELM server: a new resource for investigating short functional sites in modular eukaryotic proteins. Nucleic Acids Research, 2003, 31, 3625-3630.	14.5	555
111	In Vitro Evolution of Recognition Specificity Mediated by SH3 Domains Reveals Target Recognition Rules. Journal of Biological Chemistry, 2002, 277, 21666-21674.	3.4	47
112	A Combined Experimental and Computational Strategy to Define Protein Interaction Networks for Peptide Recognition Modules. Science, 2002, 295, 321-324.	12.6	668
113	MINT: a Molecular INTERaction database. FEBS Letters, 2002, 513, 135-140.	2.8	665
114	Normalization of nomenclature for peptide motifs as ligands of modular protein domains. FEBS Letters, 2002, 513, 141-144.	2.8	118
115	Can we infer peptide recognition specificity mediated by SH3 domains?. FEBS Letters, 2002, 513, 38-44.	2.8	124
116	Making decisions in G1. FEBS Letters, 2001, 490, 109-109.	2.8	0
117	Distinct Binding Specificity of the Multiple PDZ Domains of INADL, a Human Protein with Homology to INAD from Drosophila melanogaster. Journal of Biological Chemistry, 2001, 276, 42122-42130.	3.4	58
118	SH3-SPOT: an algorithm to predict preferred ligands to different members of the SH3 gene family. Journal of Molecular Biology, 2000, 298, 313-328.	4.2	86
119	Domain repertoires as a tool to derive protein recognition rules. FEBS Letters, 2000, 480, 49-54.	2.8	16
120	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. Journal of Biological Chemistry, 1999, 274, 32001-32007.	3.4	122
121	A novel peptide-SH3 interaction. EMBO Journal, 1999, 18, 5300-5309.	7.8	172
122	Phage displayed peptide libraries. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 1-17.	1.1	5
123	Phage Displayed Peptide Libraries. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 1-17.	1.1	30
124	Intersectin, a Novel Adaptor Protein with Two Eps15 Homology and Five Src Homology 3 Domains. Journal of Biological Chemistry, 1998, 273, 31401-31407.	3.4	264
125	Recognition specificity of individual EH domains of mammals and yeast. EMBO Journal, 1998, 17, 6541-6550.	7.8	106
126	Binding specificity and in vivo targets of the EH domain, a novel proteinâ€“protein interactionâ€“module. Genes and Development, 1997, 11, 2239-2249.	5.9	293



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127	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.	2.5	30
128	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.	4.2	74
129	Escher: A new docking procedure applied to the reconstruction of protein tertiary structure. <i>Proteins: Structure, Function and Bioinformatics</i> , 1997, 28, 556-567.	2.6	74
130	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.	4.2	400
131	Control of ColE1 plasmid replication by antisense RNA. <i>Trends in Genetics</i> , 1991, 7, 230-235.	6.7	91
132	Recombinant H-chain ferritins: Effects of changes in the 3-fold channels. <i>FEBS Letters</i> , 1989, 247, 268-272.	2.8	69
133	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.	2.3	75
134	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
135	Adipogenesis of Skeletal Muscle Fibro/Adipogenic Progenitors is Controlled by the WNT5a/GSK3 $\beta$ -Catenin Axis. <i>SSRN Electronic Journal</i> , 0, , .	0.4	7