Francesca Sacco

List of Publications by Year
in descending order

106 papers	12,509 citations	57758 44 h-index	29157 104 g-index
115 all docs	115 docs citations	115 times ranked	16362 citing authors

#	Article	IF	Citations
1	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	14.5	89
2	Transcription Factor Activation Profiles (TFAP) identify compounds promoting differentiation of Acute Myeloid Leukemia cell lines. Cell Death Discovery, 2022, 8, 16.	4.7	0
3	SIGNORApp: a Cytoscape 3 application to access SIGNOR data. Bioinformatics, 2022, 38, 1764-1766.	4.1	7
4	Phosphoproteomics and Organelle Proteomics in Pancreatic Islets. Methods in Molecular Biology, 2022, , 123-140.	0.9	1
5	A Resource to Infer Molecular Paths Linking Cancer Mutations to Perturbation of Cell Metabolism. Frontiers in Molecular Biosciences, 2022, 9, .	3.5	3
6	SCA-1 micro-heterogeneity in the fate decision of dystrophic fibro/adipogenic progenitors. Cell Death and Disease, 2021, 12, 122.	6.3	21
7	Integrating Patient-Specific Information into Logic Models of Complex Diseases: Application to Acute Myeloid Leukemia. Journal of Personalized Medicine, 2021, 11, 117.	2.5	3
8	Skeletal Muscle Subpopulation Rearrangements upon Rhabdomyosarcoma Development through Single-Cell Mass Cytometry. Journal of Clinical Medicine, 2021, 10, 823.	2.4	4
9	A Resource for the Network Representation of Cell Perturbations Caused by SARS-CoV-2 Infection. Genes, 2021, 12, 450.	2.4	7
10	Combining Mass Spectrometry-Based Phosphoproteomics with a Network-Based Approach to Reveal FLT3-Dependent Mechanisms of Chemoresistance. Proteomes, 2021, 9, 19.	3.5	4
11	Assembling Disease Networks From Causal Interaction Resources. Frontiers in Genetics, 2021, 12, 694468.	2.3	4
12	Characterization of the Skeletal Muscle Secretome Reveals a Role for Extracellular Vesicles and IL1α/IL1β in Restricting Fibro/Adipogenic Progenitor Adipogenesis. Biomolecules, 2021, 11, 1171.	4.0	10
13	COVID19 Disease Map, a computational knowledge repository of virus–host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
14	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. Nucleic Acids Research, 2020, 48, D504-D510.	14.5	160
15	CancerGeneNet: linking driver genes to cancer hallmarks. Nucleic Acids Research, 2020, 48, D416-D421.	14.5	29
16	HiPPO and PANDA: Two Bioinformatics Tools to Support Analysis of Mass Cytometry Data. Journal of Computational Biology, 2020, 27, 1283-1294.	1.6	0
17	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	12.8	49
18	High-Dimensional Single-Cell Quantitative Profiling of Skeletal Muscle Cell Population Dynamics during Regeneration. Cells, 2020, 9, 1723.	4.1	18

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19	MiT/ <scp>TFE</scp> factors control <scp>ER</scp> â€phagy via transcriptional regulation of <scp>FAM</scp> 134B. EMBO Journal, 2020, 39, e105696.	7.8	60
20	Adipogenesis of skeletal muscle fibro/adipogenic progenitors is affected by the WNT5a/GSK3/Î²-catenin axis. Cell Death and Differentiation, 2020, 27, 2921-2941.	11.2	69
21	Singleâ€Cell Analysis: Toward Highâ€Dimensional Singleâ€Cell Analysis of Graphene Oxide Biological Impact: Tracking on Immune Cells by Singleâ€Cell Mass Cytometry (Small 21/2020). Small, 2020, 16, 2070117.	10.0	3
22	Janus effect of glucocorticoids on differentiation of muscle fibro/adipogenic progenitors. Scientific Reports, 2020, 10, 5363.	3.3	18
23	Ring Finger Protein 11 acts on ligandâ€activated EGFR via the direct interaction with the UIM region of ANKRD13 protein family. FEBS Journal, 2020, 287, 3526-3550.	4.7	12
24	Toward Highâ€Dimensional Singleâ€Cell Analysis of Graphene Oxide Biological Impact: Tracking on Immune Cells by Singleâ€Cell Mass Cytometry. Small, 2020, 16, 2000123.	10.0	10
25	Metabolic reprogramming of fibro/adipogenic progenitors facilitates muscle regeneration. Life Science Alliance, 2020, 3, e202000646.	2.8	36
26	Lowe syndromeâ€"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
27	SILAC-based quantitative mass spectrometry-based proteomics quantifies endoplasmic reticulum stress in whole HeLa cells. DMM Disease Models and Mechanisms, 2019, 12, .	2.4	10
28	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. Frontiers in Physiology, 2019, 10, 1216.	2.8	8
29	Selectivity of the CUBAN domain in the recognition of ubiquitin and NEDD8. FEBS Journal, 2019, 286, 653-677.	4.7	22
30	Metformin Delays Satellite Cell Activation and Maintains Quiescence. Stem Cells International, 2019, 2019, 1-19.	2.5	32
31	Phosphoproteomics Reveals the GSK3-PDX1 Axis as a Key Pathogenic Signaling Node in Diabetic Islets. Cell Metabolism, 2019, 29, 1422-1432.e3.	16.2	65
32	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
33	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
34	Fibro-adipogenic progenitors of dystrophic mice are insensitive to NOTCH regulation of adipogenesis. Life Science Alliance, 2019, 2, e201900437.	2.8	41
35	Combining Phosphoproteomics Datasets and Literature Information to Reveal the Functional Connections in a Cell Phosphorylation Network. Proteomics, 2018, 18, 1700311.	2.2	15
36	SPV: a JavaScript Signaling Pathway Visualizer. Bioinformatics, 2018, 34, 2684-2686.	4.1	12

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37	DISNOR: a disease network open resource. Nucleic Acids Research, 2018, 46, D527-D534.	14.5	42
38	Gene Regulatory Network Modeling of Macrophage Differentiation Corroborates the Continuum Hypothesis of Polarization States. Frontiers in Physiology, 2018, 9, 1659.	2.8	102
39	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
40	Both Intrinsic Substrate Preference and Network Context Contribute to Substrate Selection of Classical Tyrosine Phosphatases. Journal of Biological Chemistry, 2017, 292, 4942-4952.	3.4	8
41	Microfluidic-enhanced 3D bioprinting of aligned myoblast-laden hydrogels leads to functionally organized myofibers inÂvitro and inÂvivo. Biomaterials, 2017, 131, 98-110.	11.4	252
42	Single-cell mass cytometry and transcriptome profiling reveal the impact of graphene on human immune cells. Nature Communications, 2017, 8, 1109.	12.8	111
43	SIGNOR: A Database of Causal Relationships Between Biological Entities—A Short Guide to Searching and Browsing. Current Protocols in Bioinformatics, 2017, 58, 8.23.1-8.23.16.	25.8	14
44	Profiling Phosphopeptide-Binding Domain Recognition Specificity Using Peptide Microarrays. Methods in Molecular Biology, 2017, 1518, 177-193.	0.9	3
45	Regulation of myoblast differentiation by metabolic perturbations induced by metformin. PLoS ONE, 2017, 12, e0182475.	2.5	28
46	A subset of RAB proteins modulates PP2A phosphatase activity. Scientific Reports, 2016, 6, 32857.	3.3	5
47	Deep Proteomics of Breast Cancer Cells Reveals that Metformin Rewires Signaling Networks Away from a Pro-growth State. Cell Systems, 2016, 2, 159-171.	6.2	76
48	Activation of the Pro-Oxidant PKCβII-p66Shc Signaling Pathway Contributes to Pericyte Dysfunction in Skeletal Muscles of Patients With Diabetes With Critical Limb Ischemia. Diabetes, 2016, 65, 3691-3704.	0.6	48
49	Dissection of CD20 regulation in lymphoma using RNAi. Leukemia, 2016, 30, 2409-2412.	7.2	13
50	The cell-autonomous mechanisms underlying the activity of metformin as an anticancer drug. British Journal of Cancer, 2016, 115, 1451-1456.	6.4	23
51	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. Nature Communications, 2016, 7, 13250.	12.8	74
52	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. Bioinformatics, 2016, 32, 424-431.	4.1	62
53	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
54	Characterization by mass cytometry of different methods for the preparation of muscle mononuclear cells. New Biotechnology, 2016, 33, 514-523.	4.4	9

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55	Alterations in the phosphoproteomic profile of cells expressing a non-functional form of the SHP2 phosphatase. New Biotechnology, 2016, 33, 524-536.	4.4	7
56	SIGNOR: a database of causal relationships between biological entities. Nucleic Acids Research, 2016, 44, D548-D554.	14.5	243
57	The hierarchical organization of natural protein interaction networks confers self-organization properties on pseudocells. BMC Systems Biology, 2015, 9, S3.	3.0	5
58	VirusMentha: a new resource for virus-host protein interactions. Nucleic Acids Research, 2015, 43, D588-D592.	14.5	141
59	The adapter protein CD2AP binds to p53 protein in the cytoplasm and can discriminate its polymorphic variants P72R. Journal of Biochemistry, 2015, 157, 101-111.	1.7	17
60	Metformin Protects Skeletal Muscle from Cardiotoxin Induced Degeneration. PLoS ONE, 2014, 9, e114018.	2.5	45
61	3D hydrogel environment rejuvenates aged pericytes for skeletal muscle tissue engineering. Frontiers in Physiology, 2014, 5, 203.	2.8	90
62	Combining affinity proteomics and network context to identify new phosphatase substrates and adapters in growth pathways. Frontiers in Genetics, 2014, 5, 115.	2.3	13
63	The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. Nucleic Acids Research, 2014, 42, D358-D363.	14.5	1,634
64	KinomeXplorer: an integrated platform for kinome biology studies. Nature Methods, 2014, 11, 603-604.	19.0	304
65	mentha: a resource for browsing integrated protein-interaction networks. Nature Methods, 2013, 10, 690-691.	19.0	291
66	HuPho: the human phosphatase portal. FEBS Journal, 2013, 280, 379-387.	4.7	55
67	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	6.4	110
68	MINT, the molecular interaction database: 2012 update. Nucleic Acids Research, 2012, 40, D857-D861.	14.5	917
69	Mapping the human phosphatome on growth pathways. Molecular Systems Biology, 2012, 8, 603.	7.2	24
70	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	19.0	500
71	Reactive Oxygen Species and Epidermal Growth Factor Are Antagonistic Cues Controlling SHP-2 Dimerization. Molecular and Cellular Biology, 2012, 32, 1998-2009.	2.3	9
72	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*. Journal of Biological Chemistry, 2012, 287, 27066-27077.	3.4	35

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73	The human phosphatase interactome: An intricate family portrait. FEBS Letters, 2012, 586, 2732-2739.	2.8	184
74	The 4G10, pY20 and p-TYR-100 antibody specificity: profiling by peptide microarrays. New Biotechnology, 2012, 29, 571-577.	4.4	52
75	The protein interaction network mediated by human SH3 domains. Biotechnology Advances, 2012, 30, 4-15.	11.7	49
76	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	19.0	274
77	Identification of New Substrates of the Protein-tyrosine Phosphatase PTP1B by Bayesian Integration of Proteome Evidence. Journal of Biological Chemistry, 2011, 286, 4173-4185.	3.4	41
78	Enriching the viral–host interactomes with interactions mediated by SH3 domains. Amino Acids, 2010, 38, 1541-1547.	2.7	9
79	The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. Nature Biotechnology, 2010, 28, 897-899.	17.5	42
80	MINT, the molecular interaction database: 2009 update. Nucleic Acids Research, 2010, 38, D532-D539.	14.5	458
81	Tumor Suppressor Density-enhanced Phosphatase-1 (DEP-1) Inhibits the RAS Pathway by Direct Dephosphorylation of ERK1/2 Kinases. Journal of Biological Chemistry, 2009, 284, 22048-22058.	3.4	68
82	VirusMINT: a viral protein interaction database. Nucleic Acids Research, 2009, 37, D669-D673.	14.5	180
83	Linear Motif Atlas for Phosphorylation-Dependent Signaling. Science Signaling, 2008, 1, ra2.	3.6	418
84	Linking entries in protein interaction database to structured text: The FEBS Letters experiment. FEBS Letters, 2008, 582, 1171-1177.	2.8	62
85	Protein interactions: integration leads to belief. Trends in Biochemical Sciences, 2008, 33, 241-242.	7.5	33
86	Diverse driving forces underlie the invariant occurrence of the T42A, E139D, I282V and T468M SHP2 amino acid substitutions causing Noonan and LEOPARD syndromes. Human Molecular Genetics, 2008, 17, 2018-2029.	2.9	79
87	MINT: the Molecular INTeraction database. Nucleic Acids Research, 2007, 35, D572-D574.	14.5	795
88	DOMINO: a database of domain-peptide interactions. Nucleic Acids Research, 2007, 35, D557-D560.	14.5	76
89	Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions. BMC Biology, 2007, 5, 44.	3.8	237
90	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	17.5	274

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91	Comparative interactomics: comparing apples and pears?. Trends in Biotechnology, 2007, 25, 448-454.	9.3	81
92	Conjugation to Nedd8 Instigates Ubiquitylation and Down-regulation of Activated Receptor Tyrosine Kinases. Journal of Biological Chemistry, 2006, 281, 21640-21651.	3.4	135
93	Methods to reveal domain networks. Drug Discovery Today, 2005, 10, 1111-1117.	6.4	28
94	HomoMINT: an inferred human network based on orthology mapping of protein interactions discovered in model organisms. BMC Bioinformatics, 2005, 6, S21.	2.6	128
95	Comparative interactomics. FEBS Letters, 2005, 579, 1828-1833.	2.8	44
96	Probing Protein-tyrosine Phosphatase Substrate Specificity Using a Phosphotyrosine-containing Phage Library. Journal of Biological Chemistry, 2004, 279, 311-318.	3.4	42
97	IntAct: an open source molecular interaction database. Nucleic Acids Research, 2004, 32, 452D-455.	14.5	864
98	The HUPO PSI's Molecular Interaction format—a community standard for the representation of protein interaction data. Nature Biotechnology, 2004, 22, 177-183.	17.5	581
99	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
100	MINT: a Molecular INTeraction database. FEBS Letters, 2002, 513, 135-140.	2.8	665
101	Can we infer peptide recognition specificity mediated by SH3 domains?. FEBS Letters, 2002, 513, 38-44.	2.8	124
102	Approaches to Analyze Protein Interactions. Scientific World Journal, The, 2002, 2, 93-94.	2.1	0
103	iSPOT: A Web Tool for the Analysis and Recognition of Protein Domain Specificity. Comparative and Functional Genomics, 2001, 2, 314-318.	2.0	8
104	Contribution of the different modules in the utrophin carboxy-terminal region to the formation and regulation of the DAP complex. FEBS Letters, 2000, 471, 229-234.	2.8	26
105	Domain repertoires as a tool to derive protein recognition rules. FEBS Letters, 2000, 480, 49-54.	2.8	16
106	Phage Displayed Peptide Libraries. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 1-17.	1.1	30