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 MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. Nucleic Acids Research, 2014, 42, D358-D363.	14.5	1,634
2	MINT, the molecular interaction database: 2012 update. Nucleic Acids Research, 2012, 40, D857-D861.	14.5	917
3	IntAct: an open source molecular interaction database. Nucleic Acids Research, 2004, 32, 452D-455.	14.5	864
4	MINT: the Molecular INTeraction database. Nucleic Acids Research, 2007, 35, D572-D574.	14.5	795
5	MINT: a Molecular INTeraction database. FEBS Letters, 2002, 513, 135-140.	2.8	665
6	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
7	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	19.0	500
8	MINT, the molecular interaction database: 2009 update. Nucleic Acids Research, 2010, 38, D532-D539.	14.5	458
9	Linear Motif Atlas for Phosphorylation-Dependent Signaling. Science Signaling, 2008, 1, ra2.	3.6	418
10	KinomeXplorer: an integrated platform for kinome biology studies. Nature Methods, 2014, 11, 603-604.	19.0	304
11	mentha: a resource for browsing integrated protein-interaction networks. Nature Methods, 2013, 10, 690-691.	19.0	291
12	The minimum information required for reporting a molecular interaction experiment (MIMIx). Nature Biotechnology, 2007, 25, 894-898.	17.5	274
13	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	19.0	274
14	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
15	SIGNOR: a database of causal relationships between biological entities. Nucleic Acids Research, 2016, 44, D548-D554.	14.5	243
16	Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions. BMC Biology, 2007, 5, 44.	3.8	237
17	The human phosphatase interactome: An intricate family portrait. FEBS Letters, 2012, 586, 2732-2739.	2.8	184
18	VirusMINT: a viral protein interaction database. Nucleic Acids Research, 2009, 37, D669-D673.	14.5	180

#	Article	IF	Citations
19	SIGNOR 2.0, the SIGnaling Network Open Resource 2.0: 2019 update. Nucleic Acids Research, 2020, 48, D504-D510.	14.5	160
20	VirusMentha: a new resource for virus-host protein interactions. Nucleic Acids Research, 2015, 43, D588-D592.	14.5	141
21	Conjugation to Nedd8 Instigates Ubiquitylation and Down-regulation of Activated Receptor Tyrosine Kinases. Journal of Biological Chemistry, 2006, 281, 21640-21651.	3.4	135
22	HomoMINT: an inferred human network based on orthology mapping of protein interactions discovered in model organisms. BMC Bioinformatics, 2005, 6, S21.	2.6	128
23	Can we infer peptide recognition specificity mediated by SH3 domains?. FEBS Letters, 2002, 513, 38-44.	2.8	124
24	Tools and data services registry: a community effort to document bioinformatics resources. Nucleic Acids Research, 2016, 44, D38-D47.	14.5	113
25	Single-cell mass cytometry and transcriptome profiling reveal the impact of graphene on human immune cells. Nature Communications, 2017, 8, 1109.	12.8	111
26	The SH2 Domain Interaction Landscape. Cell Reports, 2013, 3, 1293-1305.	6.4	110
27	Gene Regulatory Network Modeling of Macrophage Differentiation Corroborates the Continuum Hypothesis of Polarization States. Frontiers in Physiology, 2018, 9, 1659.	2.8	102
28	3D hydrogel environment rejuvenates aged pericytes for skeletal muscle tissue engineering. Frontiers in Physiology, 2014, 5, 203.	2.8	90
29	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	14.5	89
30	Comparative interactomics: comparing apples and pears?. Trends in Biotechnology, 2007, 25, 448-454.	9.3	81
31	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
32	DOMINO: a database of domain-peptide interactions. Nucleic Acids Research, 2007, 35, D557-D560.	14.5	76
33	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
34	Glucose-regulated and drug-perturbed phosphoproteome reveals molecular mechanisms controlling insulin secretion. Nature Communications, 2016, 7, 13250.	12.8	74
35	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
36	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

#	Article	IF	Citations
37	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
38	Linking entries in protein interaction database to structured text: The FEBS Letters experiment. FEBS Letters, 2008, 582, 1171-1177.	2.8	62
39	IKAP: A heuristic framework for inference of kinase activities from Phosphoproteomics data. Bioinformatics, 2016, 32, 424-431.	4.1	62
40	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
41	HuPho: the human phosphatase portal. FEBS Journal, 2013, 280, 379-387.	4.7	55
42	COVID19 Disease Map, a computational knowledge repository of virusâ€"host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	7.2	53
43	The 4G10, pY20 and p-TYR-100 antibody specificity: profiling by peptide microarrays. New Biotechnology, 2012, 29, 571-577.	4.4	52
44	The protein interaction network mediated by human SH3 domains. Biotechnology Advances, 2012, 30, 4-15.	11.7	49
45	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	12.8	49
46	Activation of the Pro-Oxidant PKCÎ²II-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
47	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
48	Metformin Protects Skeletal Muscle from Cardiotoxin Induced Degeneration. PLoS ONE, 2014, 9, e114018.	2.5	45
49	Comparative interactomics. FEBS Letters, 2005, 579, 1828-1833.	2.8	44
50	Probing Protein-tyrosine Phosphatase Substrate Specificity Using a Phosphotyrosine-containing Phage Library. Journal of Biological Chemistry, 2004, 279, 311-318.	3.4	42
51	The FEBS Letters/BioCreative II.5 experiment: making biological information accessible. Nature Biotechnology, 2010, 28, 897-899.	17.5	42
52	DISNOR: a disease network open resource. Nucleic Acids Research, 2018, 46, D527-D534.	14.5	42
53	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
54	Fibro-adipogenic progenitors of dystrophic mice are insensitive to NOTCH regulation of adipogenesis. Life Science Alliance, 2019, 2, e201900437.	2.8	41

#	Article	IF	Citations
55	Metabolic reprogramming of fibro/adipogenic progenitors facilitates muscle regeneration. Life Science Alliance, 2020, 3, e202000646.	2.8	36
56	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
57	Protein interactions: integration leads to belief. Trends in Biochemical Sciences, 2008, 33, 241-242.	7.5	33
58	Metformin Delays Satellite Cell Activation and Maintains Quiescence. Stem Cells International, 2019, 2019, 1-19.	2.5	32
59	Phage Displayed Peptide Libraries. Combinatorial Chemistry and High Throughput Screening, 1999, 2, 1-17.	1.1	30
60	CancerGeneNet: linking driver genes to cancer hallmarks. Nucleic Acids Research, 2020, 48, D416-D421.	14.5	29
61	Methods to reveal domain networks. Drug Discovery Today, 2005, 10, 1111-1117.	6.4	28
62	Regulation of myoblast differentiation by metabolic perturbations induced by metformin. PLoS ONE, 2017, 12, e0182475.	2.5	28
63	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
64	Mapping the human phosphatome on growth pathways. Molecular Systems Biology, 2012, 8, 603.	7.2	24
65	The cell-autonomous mechanisms underlying the activity of metformin as an anticancer drug. British Journal of Cancer, 2016, 115, 1451-1456.	6.4	23
66	Selectivity of the CUBAN domain in the recognition of ubiquitin and NEDD8. FEBS Journal, 2019, 286, 653-677.	4.7	22
67	SCA-1 micro-heterogeneity in the fate decision of dystrophic fibro/adipogenic progenitors. Cell Death and Disease, 2021, 12, 122.	6.3	21
68	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
69	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
70	High-Dimensional Single-Cell Quantitative Profiling of Skeletal Muscle Cell Population Dynamics during Regeneration. Cells, 2020, 9, 1723.	4.1	18
71	Janus effect of glucocorticoids on differentiation of muscle fibro/adipogenic progenitors. Scientific Reports, 2020, 10, 5363.	3.3	18
72	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

#	Article	IF	Citations
73	Domain repertoires as a tool to derive protein recognition rules. FEBS Letters, 2000, 480, 49-54.	2.8	16
74	Combining Phosphoproteomics Datasets and Literature Information to Reveal the Functional Connections in a Cell Phosphorylation Network. Proteomics, 2018, 18, 1700311.	2.2	15
75	SIGNOR: A Database of Causal Relationships Between Biological Entitiesâ€"A Short Guide to Searching and Browsing. Current Protocols in Bioinformatics, 2017, 58, 8.23.1-8.23.16.	25.8	14
76	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
77	Dissection of CD20 regulation in lymphoma using RNAi. Leukemia, 2016, 30, 2409-2412.	7.2	13
78	SPV: a JavaScript Signaling Pathway Visualizer. Bioinformatics, 2018, 34, 2684-2686.	4.1	12
79	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
80	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
81	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
82	Characterization of the Skeletal Muscle Secretome Reveals a Role for Extracellular Vesicles and IL1Î±/IL1Î² in Restricting Fibro/Adipogenic Progenitor Adipogenesis. Biomolecules, 2021, 11, 1171.	4.0	10
83	Enriching the viralâ€"host interactomes with interactions mediated by SH3 domains. Amino Acids, 2010, 38, 1541-1547.	2.7	9
84	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
85	Characterization by mass cytometry of different methods for the preparation of muscle mononuclear cells. New Biotechnology, 2016, 33, 514-523.	4.4	9
86	iSPOT: A Web Tool for the Analysis and Recognition of Protein Domain Specificity. Comparative and Functional Genomics, 2001, 2, 314-318.	2.0	8
87	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
88	Myo-REG: A Portal for Signaling Interactions in Muscle Regeneration. Frontiers in Physiology, 2019, 10, 1216.	2.8	8
89	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
90	A Resource for the Network Representation of Cell Perturbations Caused by SARS-CoV-2 Infection. Genes, 2021, 12, 450.	2.4	7

#	Article	IF	Citations
91	SIGNORApp: a Cytoscape 3 application to access SIGNOR data. Bioinformatics, 2022, 38, 1764-1766.	4.1	7
92	The hierarchical organization of natural protein interaction networks confers self-organization properties on pseudocells. BMC Systems Biology, 2015, 9, S3.	3.0	5
93	A subset of RAB proteins modulates PP2A phosphatase activity. Scientific Reports, 2016, 6, 32857.	3.3	5
94	Skeletal Muscle Subpopulation Rearrangements upon Rhabdomyosarcoma Development through Single-Cell Mass Cytometry. Journal of Clinical Medicine, 2021, 10, 823.	2.4	4
95	Combining Mass Spectrometry-Based Phosphoproteomics with a Network-Based Approach to Reveal FLT3-Dependent Mechanisms of Chemoresistance. Proteomes, 2021, 9, 19.	3.5	4
96	Assembling Disease Networks From Causal Interaction Resources. Frontiers in Genetics, 2021, 12, 694468.	2.3	4
97	Profiling Phosphopeptide-Binding Domain Recognition Specificity Using Peptide Microarrays. Methods in Molecular Biology, 2017, 1518, 177-193.	0.9	3
98	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
99	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
100	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
101	A Resource to Infer Molecular Paths Linking Cancer Mutations to Perturbation of Cell Metabolism. Frontiers in Molecular Biosciences, 2022, 9, .	3.5	3
102	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
103	Phosphoproteomics and Organelle Proteomics in Pancreatic Islets. Methods in Molecular Biology, 2022, , 123-140.	0.9	1
104	Approaches to Analyze Protein Interactions. Scientific World Journal, The, 2002, 2, 93-94.	2.1	0
105	HiPPO and PANDA: Two Bioinformatics Tools to Support Analysis of Mass Cytometry Data. Journal of Computational Biology, 2020, 27, 1283-1294.	1.6	0
106	Transcription Factor Activation Profiles (TFAP) identify compounds promoting differentiation of Acute Myeloid Leukemia cell lines. Cell Death Discovery, 2022, 8, 16.	4.7	0