

Matthias Gstaiger

List of Publications by Year in descending order

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65
papers

7,954
citations

87888

38
h-index

114465

63
g-index

69
all docs

69
docs citations

69
times ranked

13570
citing authors

#	ARTICLE	IF	CITATIONS
1	Covalent Proximity Scanning of a Distal Cysteine to Target PI3K. <i>Journal of the American Chemical Society</i> , 2022, 144, 6326-6342.	13.7	27
2	System-Wide Profiling of Protein Complexes Via Size Exclusion Chromatography-Mass Spectrometry (SEC-MS). <i>Methods in Molecular Biology</i> , 2021, 2259, 269-294.	0.9	11
3	Inhibition of endothelin-B receptor signaling synergizes with MAPK pathway inhibitors in BRAF mutated melanoma. <i>Oncogene</i> , 2021, 40, 1659-1673.	5.9	8
4	Mapping specificity, cleavage entropy, allosteric changes and substrates of blood proteases in a high-throughput screen. <i>Nature Communications</i> , 2021, 12, 1693.	12.8	17
5	PCprophet: a framework for protein complex prediction and differential analysis using proteomic data. <i>Nature Methods</i> , 2021, 18, 520-527.	19.0	32
6	Complex-centric proteome profiling by SEC-SWATH-MS for the parallel detection of hundreds of protein complexes. <i>Nature Protocols</i> , 2020, 15, 2341-2386.	12.0	34
7	Multi-layered proteomic analyses decode compositional and functional effects of cancer mutations on kinase complexes. <i>Nature Communications</i> , 2020, 11, 3563.	12.8	26
8	Kinase Interaction Network Expands Functional and Disease Roles of Human Kinases. <i>Molecular Cell</i> , 2020, 79, 504-520.e9.	9.7	74
9	A Global Screen for Assembly State Changes of the Mitotic Proteome by SEC-SWATH-MS. <i>Cell Systems</i> , 2020, 10, 133-155.e6.	6.2	57
10	NuRD subunit CHD4 regulates super-enhancer accessibility in rhabdomyosarcoma and represents a general tumor dependency. <i>ELife</i> , 2020, 9, .	6.0	36
11	The Leukemogenic TCF3-HLF Complex Rewires Enhancers Driving Cellular Identity and Self-Renewal Conferring EP300 Vulnerability. <i>Cancer Cell</i> , 2019, 36, 630-644.e9.	16.8	35
12	BRAF inhibition sensitizes melanoma cells to Î±-amanitin via decreased RNA polymerase II assembly. <i>Scientific Reports</i> , 2019, 9, 7779.	3.3	9
13	Quantitative Interactomics in Primary T Cells Provides a Rationale for Concomitant PD-1 and BTLA Coinhibitor Blockade in Cancer Immunotherapy. <i>Cell Reports</i> , 2019, 27, 3315-3330.e7.	6.4	106
14	ASPP proteins discriminate between PP1 catalytic subunits through their SH3 domain and the PP1 C-tail. <i>Nature Communications</i> , 2019, 10, 771.	12.8	44
15	Elucidating essential kinases of endothelin signalling by logic modelling of phosphoproteomics data. <i>Molecular Systems Biology</i> , 2019, 15, e8828.	7.2	11
16	Complex-centric proteome profiling by SEC-SWATH-MS. <i>Molecular Systems Biology</i> , 2019, 15, e8438.	7.2	109
17	AP-SWATH Reveals Direct Involvement of VCP/p97 in Integrated Stress Response Signaling Through Facilitating CReP/PPP1R15B Degradation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1295-1307.	3.8	26
18	Contribution of Mass Spectrometry-Based Proteomics to the Understanding of TNF-Î± Signaling. <i>Journal of Proteome Research</i> , 2017, 16, 14-33.	3.7	11

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19	Precise Temporal Profiling of Signaling Complexes in Primary Cells Using SWATH Mass Spectrometry. <i>Cell Reports</i> , 2017, 18, 3219-3226.	6.4	28
20	Systematic Analysis of Human Protein Phosphatase Interactions and Dynamics. <i>Cell Systems</i> , 2017, 4, 430-444.e5.	6.2	65
21	Meru couples planar cell polarity with apical-basal polarity during asymmetric cell division. <i>ELife</i> , 2017, 6, .	6.0	14
22	A High-Density Map for Navigating the Human Polycomb Complexome. <i>Cell Reports</i> , 2016, 17, 583-595.	6.4	234
23	An Inducible Retroviral Expression System for Tandem Affinity Purification Mass-Spectrometry-Based Proteomics Identifies Mixed Lineage Kinase Domain-like Protein (MLKL) as an Heat Shock Protein 90 (HSP90) Client. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1139-1150.	3.8	23
24	An Inducible Retroviral Expression System for Tandem Affinity Purification Mass-Spectrometry-Based Proteomics Identifies Mixed Lineage Kinase Domain-like Protein (MLKL) as an Heat Shock Protein 90 (HSP90) Client. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1139-1150.	3.8	9
25	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. <i>Nature Methods</i> , 2015, 12, 725-731.	19.0	109
26	Quantitative proteomics analysis of signalosome dynamics in primary T cells identifies the surface receptor CD6 as a Lat adaptor-independent TCR signaling hub. <i>Nature Immunology</i> , 2014, 15, 384-392.	14.5	119
27	The CRAPome: a contaminant repository for affinity purification mass spectrometry data. <i>Nature Methods</i> , 2013, 10, 730-736.	19.0	1,353
28	Quantifying protein interaction dynamics by SWATH mass spectrometry: application to the 14-3-3 system. <i>Nature Methods</i> , 2013, 10, 1246-1253.	19.0	302
29	A method to resolve the composition of heterogeneous affinity-purified protein complexes assembled around a common protein by chemical cross-linking, gel electrophoresis and mass spectrometry. <i>Nature Protocols</i> , 2013, 8, 75-97.	12.0	27
30	Human RECQ1 promotes restart of replication forks reversed by DNA topoisomerase I inhibition. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 347-354.	8.2	370
31	Interlaboratory reproducibility of large-scale human protein-complex analysis by standardized AP-MS. <i>Nature Methods</i> , 2013, 10, 307-314.	19.0	192
32	Genotype-phenotype relationships in light of a modular protein interaction landscape. <i>Molecular BioSystems</i> , 2013, 9, 1064.	2.9	11
33	The Protein Interaction Landscape of the Human CMGC Kinase Group. <i>Cell Reports</i> , 2013, 3, 1306-1320.	6.4	178
34	EphA2 cleavage by MT1-MMP triggers single cancer cell invasion via homotypic cell repulsion. <i>Journal of Cell Biology</i> , 2013, 201, 467-484.	5.2	75
35	Interaction proteome of human Hippo signaling: modular control of the coactivator YAP1. <i>Molecular Systems Biology</i> , 2013, 9, 713.	7.2	82
36	Bacterial effector binds host cell adenylyl cyclase to potentiate G β s-dependent cAMP production. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 9581-9586.	7.1	35

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37	Regulation of PTEN activity by p38 β -PKD1 signaling in neutrophils confers inflammatory responses in the lung. <i>Journal of Experimental Medicine</i> , 2012, 209, 2229-2246.	8.5	80
38	Regulation of PTEN activity by p38 δ -PKD1 signaling in neutrophils confers inflammatory responses in the lung. <i>Journal of Cell Biology</i> , 2012, 199, i6-i6.	5.2	0
39	Tandem affinity purification combined with inducible shRNA expression as a tool to study the maturation of macromolecular assemblies. <i>Rna</i> , 2011, 17, 189-200.	3.5	42
40	The oxygen sensor PHD3 limits glycolysis under hypoxia via direct binding to pyruvate kinase. <i>Cell Research</i> , 2011, 21, 983-986.	12.0	26
41	Modularity and hormone sensitivity of the <i>Drosophila melanogaster</i> insulin receptor/target of rapamycin interaction proteome. <i>Molecular Systems Biology</i> , 2011, 7, 547.	7.2	60
42	Endolysosomal sorting of ubiquitylated caveolin-1 is regulated by VCP and UBXD1 and impaired by VCP disease mutations. <i>Nature Cell Biology</i> , 2011, 13, 1116-1123.	10.3	213
43	Combined Functional Genomic and Proteomic Approaches Identify a PP2A Complex as a Negative Regulator of Hippo Signaling. <i>Molecular Cell</i> , 2010, 39, 521-534.	9.7	212
44	AN INTEGRATED EXPERIMENTAL WORKFLOW TO INCREASE THROUGHPUT AND DATA ROBUSTNESS FOR ANALYSIS OF MAMMALIAN PROTEIN INTERACTION NETWORKS. <i>FASEB Journal</i> , 2010, 24, 1b165.	0.5	0
45	The dASPP-dRASSF8 Complex Regulates Cell-Cell Adhesion during <i>Drosophila</i> Retinal Morphogenesis. <i>Current Biology</i> , 2009, 19, 1969-1978.	3.9	41
46	Comparative profiling identifies C13orf3 as a component of the Ska complex required for mammalian cell division. <i>EMBO Journal</i> , 2009, 28, 1453-1465.	7.8	89
47	Quantitative interaction proteomics using mass spectrometry. <i>Nature Methods</i> , 2009, 6, 203-205.	19.0	136
48	Applying mass spectrometry-based proteomics to genetics, genomics and network biology. <i>Nature Reviews Genetics</i> , 2009, 10, 617-627.	16.3	410
49	An integrated workflow for charting the human interaction proteome: insights into the PP2A system. <i>Molecular Systems Biology</i> , 2009, 5, 237.	7.2	253
50	NSs Protein of Rift Valley Fever Virus Induces the Specific Degradation of the Double-Stranded RNA-Dependent Protein Kinase. <i>Journal of Virology</i> , 2009, 83, 4365-4375.	3.4	216
51	PIMS Modulates Immune Tolerance by Negatively Regulating <i>Drosophila</i> Innate Immune Signaling. <i>Cell Host and Microbe</i> , 2008, 4, 147-158.	11.0	224
52	Quantitative Proteomic Analysis of Protein Complexes. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 326-346.	3.8	99
53	S6K1-Mediated Disassembly of Mitochondrial URI/PP1 β Complexes Activates a Negative Feedback Program that Counters S6K1 Survival Signaling. <i>Molecular Cell</i> , 2007, 28, 28-40.	9.7	101
54	An integrated mass spectrometric and computational framework for the analysis of protein interaction networks. <i>Nature Biotechnology</i> , 2007, 25, 345-352.	17.5	156

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55	Analysis of protein complexes using mass spectrometry. <i>Nature Reviews Molecular Cell Biology</i> , 2007, 8, 645-654.	37.0	634
56	The HRPT2 Tumor Suppressor Gene Product Parafibromin Associates with Human PAF1 and RNA Polymerase II. <i>Molecular and Cellular Biology</i> , 2005, 25, 5052-5060.	2.3	184
57	Control of Nutrient-Sensitive Transcription Programs by the Unconventional Prefoldin URI. <i>Science</i> , 2003, 302, 1208-1212.	12.6	164
58	Open Reading Frame UL26 of Human Cytomegalovirus Encodes a Novel Tegument Protein That Contains a Strong Transcriptional Activation Domain. <i>Journal of Virology</i> , 2002, 76, 4836-4847.	3.4	70
59	Loss of Cul1 results in early embryonic lethality and dysregulation of cyclin E. <i>Nature Genetics</i> , 1999, 23, 245-248.	21.4	164
60	Association of Human SCFSKP2 Subunit p19SKP1 with Interphase Centrosomes and Mitotic Spindle Poles. <i>Experimental Cell Research</i> , 1999, 247, 554-562.	2.6	52
61	Oct-1 POU and octamer DNA co-operate to recognise the Bob-1 transcription co-activator via induced folding. <i>Journal of Molecular Biology</i> , 1999, 288, 941-952.	4.2	48
62	Two versatile eukaryotic expression vectors permitting epitope tagging, radiolabelling and nuclear localisation of expressed proteins. <i>Gene</i> , 1996, 168, 165-167.	2.2	53
63	Fine mapping of protein interaction surfaces with a PCR-based mutagenesis screen in yeast. <i>Trends in Genetics</i> , 1996, 12, 393-394.	6.7	5
64	A B-cell coactivator of octamer-binding transcription factors. <i>Nature</i> , 1995, 373, 360-362.	27.8	307
65	Strong transcriptional activators isolated from viral DNA by the $\hat{\epsilon}$ -activator trap [™] , a novel selection system in mammalian cells. <i>Nucleic Acids Research</i> , 1994, 22, 4031-4038.	14.5	14