

# Steven P Gygi

## List of Publications by Citations

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392  
papers

60,018  
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107  
h-index

242  
g-index

459  
ext. papers

71,222  
ext. citations

15.7  
avg, IF

7.82  
L-index

#	Paper	IF	Citations
392	Quantitative analysis of complex protein mixtures using isotope-coded affinity tags. <i>Nature Biotechnology</i> , <b>1999</b> , 17, 994-9	44.5	4239
391	Correlation between protein and mRNA abundance in yeast. <i>Molecular and Cellular Biology</i> , <b>1999</b> , 19, 1720-30	4.8	3171
390	The impact of microRNAs on protein output. <i>Nature</i> , <b>2008</b> , 455, 64-71	50.4	2911
389	Target-decoy search strategy for increased confidence in large-scale protein identifications by mass spectrometry. <i>Nature Methods</i> , <b>2007</b> , 4, 207-14	21.6	2838
388	Absolute quantification of proteins and phosphoproteins from cell lysates by tandem MS. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 6940-5	11.5	1547
387	Identification of a unique TGF- $\beta$ -dependent molecular and functional signature in microglia. <i>Nature Neuroscience</i> , <b>2014</b> , 17, 131-43	25.5	1532
386	Evaluation of multidimensional chromatography coupled with tandem mass spectrometry (LC/LC-MS/MS) for large-scale protein analysis: the yeast proteome. <i>Journal of Proteome Research</i> , <b>2003</b> , 2, 43-50	5.6	1406
385	Large-scale characterization of HeLa cell nuclear phosphoproteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2004</b> , 101, 12130-5	11.5	1339
384	A proteomics approach to understanding protein ubiquitination. <i>Nature Biotechnology</i> , <b>2003</b> , 21, 921-6	44.5	1300
383	A tissue-specific atlas of mouse protein phosphorylation and expression. <i>Cell</i> , <b>2010</b> , 143, 1174-89	56.2	1218
382	A probability-based approach for high-throughput protein phosphorylation analysis and site localization. <i>Nature Biotechnology</i> , <b>2006</b> , 24, 1285-92	44.5	1212
381	Network organization of the human autophagy system. <i>Nature</i> , <b>2010</b> , 466, 68-76	50.4	1185
380	Systematic and quantitative assessment of the ubiquitin-modified proteome. <i>Molecular Cell</i> , <b>2011</b> , 44, 325-40	17.6	1163
379	Defining the human deubiquitinating enzyme interaction landscape. <i>Cell</i> , <b>2009</b> , 138, 389-403	56.2	1163
378	The BioPlex Network: A Systematic Exploration of the Human Interactome. <i>Cell</i> , <b>2015</b> , 162, 425-440	56.2	908
377	Architecture of the human interactome defines protein communities and disease networks. <i>Nature</i> , <b>2017</b> , 545, 505-509	50.4	755
376	MultiNotch MS3 enables accurate, sensitive, and multiplexed detection of differential expression across cancer cell line proteomes. <i>Analytical Chemistry</i> , <b>2014</b> , 86, 7150-8	7.8	706

375	Landscape of the PARKIN-dependent ubiquitylome in response to mitochondrial depolarization. <i>Nature</i> , <b>2013</b> , 496, 372-6	50.4	689
374	MS3 eliminates ratio distortion in isobaric multiplexed quantitative proteomics. <i>Nature Methods</i> , <b>2011</b> , 8, 937-40	21.6	689
373	Quantitative proteomics identifies NCOA4 as the cargo receptor mediating ferritinophagy. <i>Nature</i> , <b>2014</b> , 509, 105-9	50.4	684
372	A conserved MST-FOXO signaling pathway mediates oxidative-stress responses and extends life span. <i>Cell</i> , <b>2006</b> , 125, 987-1001	56.2	653
371	Large-scale phosphorylation analysis of mouse liver. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2007</b> , 104, 1488-93	11.5	627
370	Comparative evaluation of mass spectrometry platforms used in large-scale proteomics investigations. <i>Nature Methods</i> , <b>2005</b> , 2, 667-75	21.6	612
369	Meteorin-like is a hormone that regulates immune-adipose interactions to increase beige fat thermogenesis. <i>Cell</i> , <b>2014</b> , 157, 1279-1291	56.2	540
368	Complementary profiling of gene expression at the transcriptome and proteome levels in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Proteomics</i> , <b>2002</b> , 1, 323-33	7.6	525
367	The SCX/IMAC enrichment approach for global phosphorylation analysis by mass spectrometry. <i>Nature Protocols</i> , <b>2008</b> , 3, 1630-8	18.8	500
366	Proteomics: the move to mixtures. <i>Journal of Mass Spectrometry</i> , <b>2001</b> , 36, 1083-91	2.2	496
365	A protein complex network of <i>Drosophila melanogaster</i> . <i>Cell</i> , <b>2011</b> , 147, 690-703	56.2	471
364	The absolute quantification strategy: a general procedure for the quantification of proteins and post-translational modifications. <i>Methods</i> , <b>2005</b> , 35, 265-73	4.6	471
363	Distinct phosphorylation sites on the $\beta_2$ -adrenergic receptor establish a barcode that encodes differential functions of $\beta$ arrestin. <i>Science Signaling</i> , <b>2011</b> , 4, ra51	8.8	418
362	The CASTOR Proteins Are Arginine Sensors for the mTORC1 Pathway. <i>Cell</i> , <b>2016</b> , 165, 153-164	56.2	411
361	Increasing the multiplexing capacity of TMTs using reporter ion isotopologues with isobaric masses. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 7469-78	7.8	409
360	Quantitative proteomics reveal a feedforward mechanism for mitochondrial PARKIN translocation and ubiquitin chain synthesis. <i>Molecular Cell</i> , <b>2014</b> , 56, 360-375	17.6	401
359	Target-decoy search strategy for mass spectrometry-based proteomics. <i>Methods in Molecular Biology</i> , <b>2010</b> , 604, 55-71	1.4	399
358	Dual inhibition of sister chromatid separation at metaphase. <i>Cell</i> , <b>2001</b> , 107, 715-26	56.2	389

357	Semiquantitative proteomic analysis of rat forebrain postsynaptic density fractions by mass spectrometry. <i>Journal of Biological Chemistry</i> , <b>2004</b> , 279, 21003-11	5.4	373
356	Multi-omics analysis identifies ATF4 as a key regulator of the mitochondrial stress response in mammals. <i>Journal of Cell Biology</i> , <b>2017</b> , 216, 2027-2045	7.3	349
355	iPSC-derived neurons from GBA1-associated Parkinson disease patients show autophagic defects and impaired calcium homeostasis. <i>Nature Communications</i> , <b>2014</b> , 5, 4028	17.4	324
354	Proteome analysis of low-abundance proteins using multidimensional chromatography and isotope-coded affinity tags. <i>Journal of Proteome Research</i> , <b>2002</b> , 1, 47-54	5.6	312
353	Detection and Quantitation of Circulating Human Irisin by Tandem Mass Spectrometry. <i>Cell Metabolism</i> , <b>2015</b> , 22, 734-740	24.6	310
352	The Sestrins interact with GATOR2 to negatively regulate the amino-acid-sensing pathway upstream of mTORC1. <i>Cell Reports</i> , <b>2014</b> , 9, 1-8	10.6	305
351	Quantitative temporal viromics: an approach to investigate host-pathogen interaction. <i>Cell</i> , <b>2014</b> , 157, 1460-1472	56.2	292
350	Purification and characterization of native spliceosomes suitable for three-dimensional structural analysis. <i>Rna</i> , <b>2002</b> , 8, 426-39	5.8	276
349	Dynamics of cullin-RING ubiquitin ligase network revealed by systematic quantitative proteomics. <i>Cell</i> , <b>2010</b> , 143, 951-65	56.2	270
348	A mass-tolerant database search identifies a large proportion of unassigned spectra in shotgun proteomics as modified peptides. <i>Nature Biotechnology</i> , <b>2015</b> , 33, 743-9	44.5	261
347	Intensity-based protein identification by machine learning from a library of tandem mass spectra. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 214-9	44.5	256
346	BRCA1-dependent ubiquitination of gamma-tubulin regulates centrosome number. <i>Molecular and Cellular Biology</i> , <b>2004</b> , 24, 8457-66	4.8	248
345	Optimization and use of peptide mass measurement accuracy in shotgun proteomics. <i>Molecular and Cellular Proteomics</i> , <b>2006</b> , 5, 1326-37	7.6	241
344	Steps in assembly of silent chromatin in yeast: Sir3-independent binding of a Sir2/Sir4 complex to silencers and role for Sir2-dependent deacetylation. <i>Molecular and Cellular Biology</i> , <b>2002</b> , 22, 4167-80	4.8	238
343	mTOR inhibition activates overall protein degradation by the ubiquitin proteasome system as well as by autophagy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2015</b> , 112, 15790-7	11.5	236
342	SAMTOR is an -adenosylmethionine sensor for the mTORC1 pathway. <i>Science</i> , <b>2017</b> , 358, 813-818	33.3	235
341	A large-scale method to measure absolute protein phosphorylation stoichiometries. <i>Nature Methods</i> , <b>2011</b> , 8, 677-83	21.6	233
340	Cell-cycle-regulated activation of Akt kinase by phosphorylation at its carboxyl terminus. <i>Nature</i> , <b>2014</b> , 508, 541-5	50.4	232

339	Proteomics of Primary Cilia by Proximity Labeling. <i>Developmental Cell</i> , <b>2015</b> , 35, 497-512	10.2	225
338	The Parkinson disease-associated DJ-1 protein is a transcriptional co-activator that protects against neuronal apoptosis. <i>Human Molecular Genetics</i> , <b>2005</b> , 14, 1231-41	5.6	216
337	Quantitative Proteomics of the Cancer Cell Line Encyclopedia. <i>Cell</i> , <b>2020</b> , 180, 387-402.e16	56.2	210
336	Defining the consequences of genetic variation on a proteome-wide scale. <i>Nature</i> , <b>2016</b> , 534, 500-5	50.4	209
335	Quantitative Proteomic Atlas of Ubiquitination and Acetylation in the DNA Damage Response. <i>Molecular Cell</i> , <b>2015</b> , 59, 867-81	17.6	206
334	Accumulation of succinate controls activation of adipose tissue thermogenesis. <i>Nature</i> , <b>2018</b> , 560, 102-106	16.4	204
333	RNAi-dependent and -independent RNA turnover mechanisms contribute to heterochromatic gene silencing. <i>Cell</i> , <b>2007</b> , 129, 707-21	56.2	201
332	An ERK/Cdk5 axis controls the diabetogenic actions of PPAR $\alpha$ . <i>Nature</i> , <b>2015</b> , 517, 391-5	50.4	196
331	Amyloid-like Self-Assembly of a Cellular Compartment. <i>Cell</i> , <b>2016</b> , 166, 637-650	56.2	194
330	The metabolic function of cyclin D3-CDK6 kinase in cancer cell survival. <i>Nature</i> , <b>2017</b> , 546, 426-430	50.4	189
329	Weighing in on ubiquitin: the expanding role of mass-spectrometry-based proteomics. <i>Nature Cell Biology</i> , <b>2005</b> , 7, 750-7	23.4	187
328	Chemical genetic screen for AMPK substrates uncovers a network of proteins involved in mitosis. <i>Molecular Cell</i> , <b>2011</b> , 44, 878-92	17.6	182
327	Quantitative cancer proteomics: stable isotope labeling with amino acids in cell culture (SILAC) as a tool for prostate cancer research. <i>Molecular and Cellular Proteomics</i> , <b>2004</b> , 3, 729-35	7.6	179
326	Mitochondrial Biogenesis and Proteome Remodeling Promote One-Carbon Metabolism for T Cell Activation. <i>Cell Metabolism</i> , <b>2016</b> , 24, 104-17	24.6	178
325	Protein profiling with cleavable isotope-coded affinity tag (cICAT) reagents: the yeast salinity stress response. <i>Molecular and Cellular Proteomics</i> , <b>2003</b> , 2, 1198-204	7.6	177
324	Identification of a protein mediating respiratory supercomplex stability. <i>Cell Metabolism</i> , <b>2012</b> , 15, 348-60	14.6	176
323	Quantitative proteomic analysis using a MALDI quadrupole time-of-flight mass spectrometer. <i>Analytical Chemistry</i> , <b>2001</b> , 73, 978-86	7.8	171
322	Phosphoproteome analysis of fission yeast. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 1088-97	5.6	161

321	Differential Glutamate Metabolism in Proliferating and Quiescent Mammary Epithelial Cells. <i>Cell Metabolism</i> , <b>2016</b> , 23, 867-80	24.6	161
320	Cdk1-dependent regulation of the mitotic inhibitor Wee1. <i>Cell</i> , <b>2005</b> , 122, 407-20	56.2	159
319	Deep proteomics of the <i>Xenopus laevis</i> egg using an mRNA-derived reference database. <i>Current Biology</i> , <b>2014</b> , 24, 1467-1475	6.3	158
318	Mitochondrial Sirtuin Network Reveals Dynamic SIRT3-Dependent Deacetylation in Response to Membrane Depolarization. <i>Cell</i> , <b>2016</b> , 167, 985-1000.e21	56.2	157
317	Quantitative proteomic analysis reveals posttranslational responses to aneuploidy in yeast. <i>ELife</i> , <b>2014</b> , 3, e03023	8.9	156
316	Recruitment of <i>Xenopus</i> Scc2 and cohesin to chromatin requires the pre-replication complex. <i>Nature Cell Biology</i> , <b>2004</b> , 6, 991-6	23.4	151
315	Compensatory metabolic networks in pancreatic cancers upon perturbation of glutamine metabolism. <i>Nature Communications</i> , <b>2017</b> , 8, 15965	17.4	148
314	Structurally distinct Ca(2+) signaling domains of sperm flagella orchestrate tyrosine phosphorylation and motility. <i>Cell</i> , <b>2014</b> , 157, 808-22	56.2	147
313	METABOLISM. S-Nitrosylation links obesity-associated inflammation to endoplasmic reticulum dysfunction. <i>Science</i> , <b>2015</b> , 349, 500-6	33.3	146
312	The intraflagellar transport protein IFT27 promotes BBSome exit from cilia through the GTPase ARL6/BBS3. <i>Developmental Cell</i> , <b>2014</b> , 31, 265-278	10.2	145
311	Multidimensional Tracking of GPCR Signaling via Peroxidase-Catalyzed Proximity Labeling. <i>Cell</i> , <b>2017</b> , 169, 338-349.e11	56.2	140
310	The Secreted Enzyme PM20D1 Regulates Lipidated Amino Acid Uncouplers of Mitochondria. <i>Cell</i> , <b>2016</b> , 166, 424-435	56.2	140
309	A subset of membrane-associated proteins is ubiquitinated in response to mutations in the endoplasmic reticulum degradation machinery. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2003</b> , 100, 12735-40	11.5	139
308	Correct interpretation of comprehensive phosphorylation dynamics requires normalization by protein expression changes. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M111.009654	7.6	138
307	Prolonged Mek1/2 suppression impairs the developmental potential of embryonic stem cells. <i>Nature</i> , <b>2017</b> , 548, 219-223	50.4	135
306	Ubiquitylation by Trim32 causes coupled loss of desmin, Z-bands, and thin filaments in muscle atrophy. <i>Journal of Cell Biology</i> , <b>2012</b> , 198, 575-89	7.3	134
305	An Ancient, Unified Mechanism for Metformin Growth Inhibition in <i>C. elegans</i> and Cancer. <i>Cell</i> , <b>2016</b> , 167, 1705-1718.e13	56.2	134
304	A cullin E3 ubiquitin ligase complex associates with Rik1 and the Clr4 histone H3-K9 methyltransferase and is required for RNAi-mediated heterochromatin formation. <i>RNA Biology</i> , <b>2005</b> , 2, 106-11	4.8	131

303	Inhibition of homologous recombination by a cohesin-associated clamp complex recruited to the rDNA recombination enhancer. <i>Genes and Development</i> , <b>2006</b> , 20, 2887-901	12.6	129
302	An integrated microfluidics-tandem mass spectrometry system for automated protein analysis. <i>Analytical Chemistry</i> , <b>1998</b> , 70, 3728-34	7.8	128
301	On the Relationship of Protein and mRNA Dynamics in Vertebrate Embryonic Development. <i>Developmental Cell</i> , <b>2015</b> , 35, 383-94	10.2	126
300	Identification of protein components in in vivo human acquired enamel pellicle using LC-ESI-MS/MS. <i>Journal of Proteome Research</i> , <b>2007</b> , 6, 2152-60	5.6	126
299	USP14 deubiquitinates proteasome-bound substrates that are ubiquitinated at multiple sites. <i>Nature</i> , <b>2016</b> , 532, 398-401	50.4	126
298	TMTpro reagents: a set of isobaric labeling mass tags enables simultaneous proteome-wide measurements across 16 samples. <i>Nature Methods</i> , <b>2020</b> , 17, 399-404	21.6	123
297	Proteome analysis: biological assay or data archive?. <i>Electrophoresis</i> , <b>1998</b> , 19, 1862-71	3.6	121
296	Streamlined Tandem Mass Tag (SL-TMT) Protocol: An Efficient Strategy for Quantitative (Phospho)proteome Profiling Using Tandem Mass Tag-Synchronous Precursor Selection-MS3. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 2226-2236	5.6	120
295	Evaluating multiplexed quantitative phosphopeptide analysis on a hybrid quadrupole mass filter/linear ion trap/orbitrap mass spectrometer. <i>Analytical Chemistry</i> , <b>2015</b> , 87, 1241-9	7.8	117
294	Autoubiquitination of the 26S proteasome on Rpn13 regulates breakdown of ubiquitin conjugates. <i>EMBO Journal</i> , <b>2014</b> , 33, 1159-76	13	116
293	Hyperplexing: a method for higher-order multiplexed quantitative proteomics provides a map of the dynamic response to rapamycin in yeast. <i>Science Signaling</i> , <b>2012</b> , 5, rs2	8.8	116
292	Highly Multiplexed Quantitative Mass Spectrometry Analysis of Ubiquitylomes. <i>Cell Systems</i> , <b>2016</b> , 3, 395-403.e4	10.6	115
291	Global analysis of protein expression and phosphorylation of three stages of Plasmodium falciparum intraerythrocytic development. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 4028-45	5.6	114
290	Msp1/ATAD1 maintains mitochondrial function by facilitating the degradation of mislocalized tail-anchored proteins. <i>EMBO Journal</i> , <b>2014</b> , 33, 1548-64	13	113
289	Obesity Shapes Metabolism in the Tumor Microenvironment to Suppress Anti-Tumor Immunity. <i>Cell</i> , <b>2020</b> , 183, 1848-1866.e26	56.2	112
288	Latency-associated degradation of the MRP1 drug transporter during latent human cytomegalovirus infection. <i>Science</i> , <b>2013</b> , 340, 199-202	33.3	112
287	Accurate multiplexed proteomics at the MS2 level using the complement reporter ion cluster. <i>Analytical Chemistry</i> , <b>2012</b> , 84, 9214-21	7.8	111
286	Hexameric assembly of the proteasomal ATPases is templated through their C termini. <i>Nature</i> , <b>2009</b> , 459, 866-70	50.4	110

285	APC/C-mediated multiple monoubiquitylation provides an alternative degradation signal for cyclin B1. <i>Nature Cell Biology</i> , <b>2012</b> , 14, 168-76	23.4	106
284	A Quantitative Tissue-Specific Landscape of Protein Redox Regulation during Aging. <i>Cell</i> , <b>2020</b> , 180, 968-983.e24	56.2	105
283	QIL1 is a novel mitochondrial protein required for MICOS complex stability and cristae morphology. <i>ELife</i> , <b>2015</b> , 4,	8.9	104
282	Quantitative mass spectrometry-based multiplexing compares the abundance of 5000 <i>S. cerevisiae</i> proteins across 10 carbon sources. <i>Journal of Proteomics</i> , <b>2016</b> , 148, 85-93	3.9	102
281	The mitochondrial acyl carrier protein (ACP) coordinates mitochondrial fatty acid synthesis with iron sulfur cluster biogenesis. <i>ELife</i> , <b>2016</b> , 5,	8.9	99
280	A perturbed ubiquitin landscape distinguishes between ubiquitin in trafficking and in proteolysis. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M111.009753	7.6	98
279	The impact of peptide abundance and dynamic range on stable-isotope-based quantitative proteomic analyses. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 4756-65	5.6	98
278	A Triple Knockout (TKO) Proteomics Standard for Diagnosing Ion Interference in Isobaric Labeling Experiments. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2016</b> , 27, 1620-5	3.5	97
277	Dynamics of PARKIN-Dependent Mitochondrial Ubiquitylation in Induced Neurons and Model Systems Revealed by Digital Snapshot Proteomics. <i>Molecular Cell</i> , <b>2018</b> , 70, 211-227.e8	17.6	95
276	PCIF1 Catalyzes m6Am mRNA Methylation to Regulate Gene Expression. <i>Molecular Cell</i> , <b>2019</b> , 75, 620-630.e9	17.6	95
275	Cyclin C is a haploinsufficient tumour suppressor. <i>Nature Cell Biology</i> , <b>2014</b> , 16, 1080-91	23.4	94
274	The Nuclear Proteome of a Vertebrate. <i>Current Biology</i> , <b>2015</b> , 25, 2663-71	6.3	93
273	A Secreted Slit2 Fragment Regulates Adipose Tissue Thermogenesis and Metabolic Function. <i>Cell Metabolism</i> , <b>2016</b> , 23, 454-66	24.6	92
272	Quantitative phosphoproteomic analysis reveals system-wide signaling pathways downstream of SDF-1/CXCR4 in breast cancer stem cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, E2182-90	11.5	91
271	Protein analysis by mass spectrometry and sequence database searching: tools for cancer research in the post-genomic era. <i>Electrophoresis</i> , <b>1999</b> , 20, 310-9	3.6	90
270	Mek1 kinase is regulated to suppress double-strand break repair between sister chromatids during budding yeast meiosis. <i>Molecular and Cellular Biology</i> , <b>2007</b> , 27, 5456-67	4.8	89
269	Sensitive multiplexed analysis of kinase activities and activity-based kinase identification. <i>Nature Biotechnology</i> , <b>2009</b> , 27, 933-40	44.5	88
268	A Strategy to Combine Sample Multiplexing with Targeted Proteomics Assays for High-Throughput Protein Signature Characterization. <i>Molecular Cell</i> , <b>2017</b> , 65, 361-370	17.6	87



267	UCP1 deficiency causes brown fat respiratory chain depletion and sensitizes mitochondria to calcium overload-induced dysfunction. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 7981-7986	11.5	86
266	Mechanism of adrenergic Ca1.2 stimulation revealed by proximity proteomics. <i>Nature</i> , <b>2020</b> , 577, 695-706	9.4	86
265	Dual proteome-scale networks reveal cell-specific remodeling of the human interactome. <i>Cell</i> , <b>2021</b> , 184, 3022-3040.e28	56.2	86
264	Prolyl hydroxylation by EglN2 destabilizes FOXO3a by blocking its interaction with the USP9x deubiquitinase. <i>Genes and Development</i> , <b>2014</b> , 28, 1429-44	12.6	85
263	Tissue-Specific Oncogenic Activity of KRAS. <i>Cancer Discovery</i> , <b>2019</b> , 9, 738-755	24.4	84
262	Electrophoresis combined with novel mass spectrometry techniques: powerful tools for the analysis of proteins and proteomes. <i>Electrophoresis</i> , <b>1998</b> , 19, 1811-8	3.6	84
261	Proteasomal control of cytokinin synthesis protects Mycobacterium tuberculosis against nitric oxide. <i>Molecular Cell</i> , <b>2015</b> , 57, 984-994	17.6	81
260	Toward a high-throughput approach to quantitative proteomic analysis: expression-dependent protein identification by mass spectrometry. <i>Journal of the American Society for Mass Spectrometry</i> , <b>2001</b> , 12, 1238-46	3.5	80
259	Extraproteasomal Rpn10 restricts access of the polyubiquitin-binding protein Dsk2 to proteasome. <i>Molecular Cell</i> , <b>2008</b> , 32, 415-25	17.6	79
258	GENE-19. DEEP PROTEOMIC SURVEY ACROSS SEVEN CHILDHOOD BRAIN TUMORS. <i>Neuro-Oncology</i> , <b>2019</b> , 21, ii85-ii85	1	78
257	Characterization and Optimization of Multiplexed Quantitative Analyses Using High-Field Asymmetric-Waveform Ion Mobility Mass Spectrometry. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 4010-4016	7.8	77
256	UBE2O remodels the proteome during terminal erythroid differentiation. <i>Science</i> , <b>2017</b> , 357,	33.3	77
255	G1 cyclins link proliferation, pluripotency and differentiation of embryonic stem cells. <i>Nature Cell Biology</i> , <b>2017</b> , 19, 177-188	23.4	76
254	Evaluation of the utility of neutral-loss-dependent MS3 strategies in large-scale phosphorylation analysis. <i>Proteomics</i> , <b>2008</b> , 8, 4444-52	4.8	76
253	Proteome-Wide Evaluation of Two Common Protein Quantification Methods. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 1934-1942	5.6	75
252	PHD3 Loss in Cancer Enables Metabolic Reliance on Fatty Acid Oxidation via Deactivation of ACC2. <i>Molecular Cell</i> , <b>2016</b> , 63, 1006-20	17.6	75
251	Malaria. A forward genetic screen identifies erythrocyte CD55 as essential for Plasmodium falciparum invasion. <i>Science</i> , <b>2015</b> , 348, 711-4	33.3	74
250	An inhibitor of the proteasomal deubiquitinating enzyme USP14 induces tau elimination in cultured neurons. <i>Journal of Biological Chemistry</i> , <b>2017</b> , 292, 19209-19225	5.4	73

249	G protein-coupled receptor 56 regulates mechanical overload-induced muscle hypertrophy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2014</b> , 111, 15756-61	11.5	73
248	Post-transcriptional regulation of meiotic genes by a nuclear RNA silencing complex. <i>Rna</i> , <b>2014</b> , 20, 867-88	8.8	70
247	Promoter decommissioning by the NuRD chromatin remodeling complex triggers synaptic connectivity in the mammalian brain. <i>Neuron</i> , <b>2014</b> , 83, 122-34	13.9	69
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245	RFWD3-Dependent Ubiquitination of RPA Regulates Repair at Stalled Replication Forks. <i>Molecular Cell</i> , <b>2015</b> , 60, 280-93	17.6	68
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