Anne-Claude Gingras

List of Publications by Year in Descending Order

Source: https://exaly.com/author-pdf/5310556/anne-claude-gingras-publications-by-year.pdf
Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.
The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

303 papers	33,378 citations	88 h-index	179 g-index
359 ext. papers	39,953 ext. citations	12.4 avg, IF	6.97 L-index

#	Paper	IF	Citations
303	Identification and functional characterization of transcriptional activators in human cells.. *Molecular Cell*, **2022**,	17.6	4
302	Preclinical evaluation of a SARS-CoV-2 mRNA vaccine PTX-COVID19-B.. *Science Advances*, **2022**, 8, eabj9815	14.3	6
301	Diferences in mRNA-1273 (Moderna) and BNT162b2 (Pfizer-BioNTech) SARS-CoV-2 vaccine immunogenicity among patients undergoing dialysis.. *Cmaj*, **2022**,	3.5	3
300	Defining the interactomes of proteins involved in cytoskeletal dynamics using high-throughput proximity-dependent biotinylation .. *STAR Protocols*, **2022**, 3, 101075	1.4	0
299	A scalable serology solution for profiling humoral immune responses to SARS-CoV-2 infection and vaccination.. *Clinical and Translational Immunology*, **2022**, 11, e1380	6.8	3
298	SARS-CoV-2 Virus-Like Particle Neutralizing Capacity in Blood Donors Depends on Serological Profile and Donor-Declared SARS-CoV-2 Vaccination History.. *Microbiology Spectrum*, **2022**, e0226221	8.9	1
297	Assessment of SARS-CoV-2 Seropositivity During the First and Second Viral Waves in 2020 and 2021 Among Canadian Adults.. *JAMA Network Open*, **2022**, 5, e2146798	10.4	4
296	Estimating SARS-CoV-2 Seroprevalence in Canadian Blood Donors, April 2020 to March 2021: Improving Accuracy with Multiple Assays.. *Microbiology Spectrum*, **2022**, 10, e0256321	8.9	3
295	Proximity-Dependent Biotinylation Approaches to Explore the Dynamic Compartmentalized Proteome.. *Frontiers in Molecular Biosciences*, **2022**, 9, 852911	5.6	1
294	Neutralization against Omicron variant in transplant recipients after three-doses of mRNA vaccine.. *American Journal of Transplantation*, **2022**,	8.7	8
293	Adapting Serosurveys for the SARS-CoV-2 Vaccine Era.. *Open Forum Infectious Diseases*, **2022**, 9, ofab632	1	4
292	Systemic and mucosal IgA responses are variably induced in response to SARS-CoV-2 mRNA vaccination and are associated with protection against subsequent infection.. *Mucosal Immunology*, **2022**,	9.2	10
291	Understudied proteins: opportunities and challenges for functional proteomics.. *Nature Methods*, **2022**,	21.6	6
290	An open invitation to the Understudied Proteins Initiative.. *Nature Biotechnology*, **2022**,	44.5	2
289	Omicron BA.1/1.1 SARS-CoV-2 Infection among Vaccinated Canadian Adults.. *New England Journal of Medicine*, **2022**,	59.2	2
288	Retention of hemostatic and immunological properties of frozen plasma and COVID-19 convalescent apheresis fresh-frozen plasma produced and freeze-dried in Canada.. *Transfusion*, **2021**,	2.9	1
287	Leveraging machine learning essentiality predictions and chemogenomic interactions to identify antifungal targets. *Nature Communications*, **2021**, 12, 6497	17.4	4

286	Neutralization of SARS-CoV-2 Variants in Transplant Recipients After Two and Three Doses of mRNA-1273 Vaccine : Secondary Analysis of a Randomized Trial. *Annals of Internal Medicine*, **2021**,	8	9
285	ATRX proximal protein associations boast roles beyond histone deposition. *PLoS Genetics*, **2021**, 17, e1009909	6	0
284	Evaluating Humoral Immunity against SARS-CoV-2: Validation of a Plaque-Reduction Neutralization Test and a Multilaboratory Comparison of Conventional and Surrogate Neutralization Assays. *Microbiology Spectrum*, **2021**, e0088621	8.9	6
283	Membrane-dependent relief of translation elongation arrest on pseudouridine- and N1-methyl-pseudouridine-modified mRNAs.. *Nucleic Acids Research*, **2021**,	20.1	1
282	Palmitoylation targets the calcineurin phosphatase to the phosphatidylinositol 4-kinase complex at the plasma membrane. *Nature Communications*, **2021**, 12, 6064	17.4	4
281	Endofin is required for HD-PTP and ESCRT-0 interdependent endosomal sorting of ubiquitinated transmembrane cargoes. *IScience*, **2021**, 24, 103274	6.1	1
280	Resistance of SARS-CoV-2 beta and gamma variants to plasma collected from Canadian blood donors during the spring of 2020. *Transfusion*, **2021**,	2.9	3
279	TAZ-CAMTA1 and YAP-TFE3 alter the TAZ/YAP transcriptome by recruiting the ATAC histone acetyltransferase complex. *ELife*, **2021**, 10,	8.9	4
278	Subcellular proteomics. *Nature Reviews Methods Primers*, **2021**, 1,		13
277	Comprehensive interactome profiling of the human Hsp70 network highlights functional differentiation of J domains. *Molecular Cell*, **2021**, 81, 2549-2565.e8	17.6	9
276	Nanoluciferase complementation-based bioreporter reveals the importance of N-linked glycosylation of SARS-CoV-2 S for viral entry. *Molecular Therapy*, **2021**, 29, 1984-2000	11.7	13
275	A proximity-dependent biotinylation map of a human cell. *Nature*, **2021**, 595, 120-124	50.4	60
274	Systematic Examination of Antigen-Specific Recall T Cell Responses to SARS-CoV-2 versus Influenza Virus Reveals a Distinct Inflammatory Profile. *Journal of Immunology*, **2021**, 206, 37-50	5.3	12
273	Mitochondrial Threonyl-tRNA Synthetase TARS2 Is Required for Threonine-Sensitive mTORC1 Activation. *Molecular Cell*, **2021**, 81, 398-407.e4	17.6	8
272	Rag GTPases and phosphatidylinositol 3-phosphate mediate recruitment of the AP-5/SPG11/SPG15 complex. *Journal of Cell Biology*, **2021**, 220,	7.3	1
271	A Toolbox for Efficient Proximity-Dependent Biotinylation in Zebrafish Embryos. *Molecular and Cellular Proteomics*, **2021**, 20, 100128	7.6	2
270	The PHLPP1 N-Terminal Extension is a Mitotic Cdk1 Substrate and Controls an Interactome Switch. *Molecular and Cellular Biology*, **2021**,	4.8	3
269	The macrophage-derived protein PTMA induces filamentation of the human fungal pathogen Candida albicans. *Cell Reports*, **2021**, 36, 109584	10.6	0

268	Early warning and rapid public health response to prevent COVID-19 outbreaks in long-term care facilities (LTCF) by monitoring SARS-CoV-2 RNA in LTCF site-specific sewage samples and assessment of antibodies response in this population: prospective study protocol. *BMJ Open*, **2021**, 11, e052282	3	2
267	Implementation of serological and molecular tools to inform COVID-19 patient management: protocol for the GENCOV prospective cohort study. *BMJ Open*, **2021**, 11, e052842	3	0
266	Evaluation of the SARS-CoV-2 Antibody Response to the BNT162b2 Vaccine in Patients Undergoing Hemodialysis. *JAMA Network Open*, **2021**, 4, e2123622	10.4	16
265	Clionamines stimulate autophagy, inhibit Mycobacterium tuberculosis survival in macrophages, and target Pik1. *Cell Chemical Biology*, **2021**,	8.2	2
264	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) seroprevalence: Navigating the absence of a gold standard. *PLoS ONE*, **2021**, 16, e0257743	3.7	7
263	TRK-Fused Gene (TFG), a protein involved in protein secretion pathways, is an essential component of the antiviral innate immune response. *PLoS Pathogens*, **2021**, 17, e1009111	7.6	4
262	Dried blood spot specimens for SARS-CoV-2 antibody testing: A multi-site, multi-assay comparison. *PLoS ONE*, **2021**, 16, e0261003	3.7	5
261	A novel role for NUAK1 in promoting ovarian cancer metastasis through regulation of fibronectin production in spheroids. *Cancers*, **2020**, 12,	6.6	8
260	Proteomic Analysis Reveals a Role for RSK in p120-catenin Phosphorylation and Melanoma Cell-Cell Adhesion. *Molecular and Cellular Proteomics*, **2020**, 19, 50-64	7.6	5
259	Systematic mapping of genetic interactions for de novo fatty acid synthesis identifies C12orf49 as a regulator of lipid metabolism. *Nature Metabolism*, **2020**, 2, 499-513	14.6	22
258	Pharmacological inhibition of PRMT7 links arginine monomethylation to the cellular stress response. *Nature Communications*, **2020**, 11, 2396	17.4	29
257	Systems analysis of RhoGEF and RhoGAP regulatory proteins reveals spatially organized RAC1 signalling from integrin adhesions. *Nature Cell Biology*, **2020**, 22, 498-511	23.4	58
256	Rare driver mutations in head and neck squamous cell carcinomas converge on NOTCH signaling. *Science*, **2020**, 367, 1264-1269	33.3	112
255	Systematic Discovery of Short Linear Motifs Decodes Calcineurin Phosphatase Signaling. *Molecular Cell*, **2020**, 79, 342-358.e12	17.6	22
254	Variability in Streptavidin-Sepharose Matrix Quality Can Significantly Affect Proximity-Dependent Biotinylation (BioID) Data. *Journal of Proteome Research*, **2020**, 19, 3554-3561	5.6	3
253	Autism-Misregulated eIF4G Microexons Control Synaptic Translation and Higher Order Cognitive Functions. *Molecular Cell*, **2020**, 77, 1176-1192.e16	17.6	32
252	Proximity Dependent Biotinylation: Key Enzymes and Adaptation to Proteomics Approaches. *Molecular and Cellular Proteomics*, **2020**, 19, 757-773	7.6	63
251	A simple protein-based surrogate neutralization assay for SARS-CoV-2. *JCI Insight*, **2020**, 5,	9.9	95

250	Uncovering The Unique Functions And Regulation Of The Palmitoylated Calcineurin Isoform, CN1. *FASEB Journal*, **2020**, 34, 1-1	0.9	
249	CDK1-dependent Phosphorylation of the Tumor Suppressor Phosphatase, PHLPP1, Regulates the Mitotic PHLPP1 Interactome. *FASEB Journal*, **2020**, 34, 1-1	0.9	
248	Robust, reproducible and quantitative analysis of thousands of proteomes by micro-flow LC-MS/MS. *Nature Communications*, **2020**, 11, 157	17.4	105
247	Mapping the proximity interaction network of the Rho-family GTPases reveals signalling pathways and regulatory mechanisms. *Nature Cell Biology*, **2020**, 22, 120-134	23.4	60
246	Connecting proteins: shareable tools for reproducible interaction mapping. *Biochemistry and Cell Biology*, **2020**, 98, 309-313	3.6	
245	Persistence of serum and saliva antibody responses to SARS-CoV-2 spike antigens in COVID-19 patients. *Science Immunology*, **2020**, 5,	28	396
244	The GATOR-Rag GTPase pathway inhibits mTORC1 activation by lysosome-derived amino acids. *Science*, **2020**, 370, 351-356	33.3	15
243	Human GTPBP5 (MTG2) fuels mitoribosome large subunit maturation by facilitating 16S rRNA methylation. *Nucleic Acids Research*, **2020**, 48, 7924-7943	20.1	18
242	AXL confers cell migration and invasion by hijacking a PEAK1-regulated focal adhesion protein network. *Nature Communications*, **2020**, 11, 3586	17.4	13
241	Functional characterization of a PROTAC directed against BRAF mutant V600E. *Nature Chemical Biology*, **2020**, 16, 1170-1178	11.7	34
240	The NEMP family supports metazoan fertility and nuclear envelope stiffness. *Science Advances*, **2020**, 6, eabb4591	14.3	3
239	A High-Density Human Mitochondrial Proximity Interaction Network. *Cell Metabolism*, **2020**, 32, 479-497.e9	24.6	43
238	A Comprehensive, Flexible Collection of SARS-CoV-2 Coding Regions. *G3: Genes, Genomes, Genetics*, **2020**, 10, 3399-3402	3.2	22
237	IRX3/5 regulate mitotic chromatid segregation and limb bud shape. *Development (Cambridge)*, **2020** , 147,	6.6	2
236	Inactivation of PP2A by a recurrent mutation drives resistance to MEK inhibitors. *Oncogene*, **2020**, 39, 703-717	9.2	16
235	Gene Information eXtension (GIX): effortless retrieval of gene product information on any website. *Nature Methods*, **2019**, 16, 665-666	21.6	3
234	A conserved CCM complex promotes apoptosis non-autonomously by regulating zinc homeostasis. *Nature Communications*, **2019**, 10, 1791	17.4	13
233	FAM105A/OTULINL Is a Pseudodeubiquitinase of the OTU-Class that Localizes to the ER Membrane. *Structure*, **2019**, 27, 1000-1012.e6	5.2	5

232	A novel protein domain in an ancestral splicing factor drove the evolution of neural microexons. *Nature Ecology and Evolution*, **2019**, 3, 691-701	12.3	33
231	Proteomic Analysis of Histones H2A/H2B and Variant Hv1 in Tetrahymena thermophila Reveals an Ancient Network of Chaperones. *Molecular Biology and Evolution*, **2019**, 36, 1037-1055	8.3	9
230	BRN2 suppresses apoptosis, reprograms DNA damage repair, and is associated with a high somatic mutation burden in melanoma. *Genes and Development*, **2019**, 33, 310-332	12.6	16
229	The endosomal sorting adaptor HD-PTP is required for ephrin-B:EphB signalling in cellular collapse and spinal motor axon guidance. *Scientific Reports*, **2019**, 9, 11945	4.9	8
228	Global proteomic analyses define an environmentally contingent Hsp90 interactome and reveal chaperone-dependent regulation of stress granule proteins and the R2TP complex in a fungal pathogen. *PLoS Biology*, **2019**, 17, e3000358	9.7	18
227	Properties of Stress Granule and P-Body Proteomes. *Molecular Cell*, **2019**, 76, 286-294	17.6	105
226	Interactome Rewiring Following Pharmacological Targeting of BET Bromodomains. *Molecular Cell*, **2019**, 73, 621-638.e17	17.6	77
225	Getting to know the neighborhood: using proximity-dependent biotinylation to characterize protein complexes and map organelles. *Current Opinion in Chemical Biology*, **2019**, 48, 44-54	9.7	122
224	Functional divergence of a global regulatory complex governing fungal filamentation. *PLoS Genetics*, **2019**, 15, e1007901	6	8
223	Molecular architecture of LSM14 interactions involved in the assembly of mRNA silencing complexes. *EMBO Journal*, **2018**, 37,	13	27
222	High-Density Proximity Mapping Reveals the Subcellular Organization of mRNA-Associated Granules and Bodies. *Molecular Cell*, **2018**, 69, 517-532.e11	17.6	331
221	KIBRA (WWC1) Is a Metastasis Suppressor Gene Affected by Chromosome 5q Loss in Triple-Negative Breast Cancer. *Cell Reports*, **2018**, 22, 3191-3205	10.6	25
220	Translational control of ERK signaling through miRNA/4EHP-directed silencing. *ELife*, **2018**, 7,	8.9	28
219	Functions of the COPII gene paralogs SEC23A and SEC23B are interchangeable in vivo. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E7748-E7757	11.5	46
218	Global Interactomics Uncovers Extensive Organellar Targeting by Zika Virus. *Molecular and Cellular Proteomics*, **2018**, 17, 2242-2255	7.6	78
217	The shieldin complex mediates 53BP1-dependent DNA repair. *Nature*, **2018**, 560, 117-121	50.4	277
216	A Versatile Lentiviral Delivery Toolkit for Proximity-dependent Biotinylation in Diverse Cell Types. *Molecular and Cellular Proteomics*, **2018**, 17, 2256-2269	7.6	16
215	The bromodomain-containing protein Ibd1 links multiple chromatin-related protein complexes to highly expressed genes in Tetrahymena thermophila. *Epigenetics and Chromatin*, **2018**, 11, 10	5.8	11

214	In planta proximity dependent biotin identification (BioID). *Scientific Reports*, **2018**, 8, 9212	4.9	42
213	The cargo receptor SURF4 promotes the efficient cellular secretion of PCSK9. *ELife*, **2018**, 7,	8.9	42
212	CDK1-dependent Phosphorylation of the Tumor Suppressor Phosphatase, PHLPP1, Regulates the Mitotic PHLPP1 Interactome. *FASEB Journal*, **2018**, 32, 687.2	0.9	
211	Human MARF1 is an endoribonuclease that interacts with the DCP1:2 decapping complex and degrades target mRNAs. *Nucleic Acids Research*, **2018**, 46, 12008-12021	20.1	12
210	Genome-wide CRISPR-Cas9 Interrogation of Splicing Networks Reveals a Mechanism for Recognition of Autism-Misregulated Neuronal Microexons. *Molecular Cell*, **2018**, 72, 510-524.e12	17.6	51
209	A feed forward loop enforces YAP/TAZ signaling during tumorigenesis. *Nature Communications*, **2018**, 9, 3510	17.4	37
208	Proteomic and Biochemical Comparison of the Cellular Interaction Partners of Human VPS33A and VPS33B. *Journal of Molecular Biology*, **2018**, 430, 2153-2163	6.5	12
207	Structural Basis for Auto-Inhibition of the NDR1 Kinase Domain by an Atypically Long Activation Segment. *Structure*, **2018**, 26, 1101-1115.e6	5.2	12
206	Parallel Exploration of Interaction Space by BioID and Affinity Purification Coupled to Mass Spectrometry. *Methods in Molecular Biology*, **2017**, 1550, 115-136	1.4	39
205	Cap-binding protein 4EHP effects translation silencing by microRNAs. *Proceedings of the National Academy of Sciences of the United States of America*, **2017**, 114, 5425-5430	11.5	56
204	Acetylation of PCNA Sliding Surface by Eco1 Promotes Genome Stability through Homologous Recombination. *Molecular Cell*, **2017**, 65, 78-90	17.6	28
203	CLMSVault: A Software Suite for Protein Cross-Linking Mass-Spectrometry Data Analysis and Visualization. *Journal of Proteome Research*, **2017**, 16, 2645-2652	5.6	14
202	Regulation of Protein Interactions by ps ne inder (MOB1) Phosphorylation. *Molecular and Cellular Proteomics*, **2017**, 16, 1111-1125	7.6	20
201	MOB1 Mediated Phospho-recognition in the Core Mammalian Hippo Pathway. *Molecular and Cellular Proteomics*, **2017**, 16, 1098-1110	7.6	30
200	CCM-3 Promotes C. elegans Germline Development by Regulating Vesicle Trafficking Cytokinesis and Polarity. *Current Biology*, **2017**, 27, 868-876	6.3	32
199	Activation of Mitochondrial Protein Phosphatase SLP2 by MIA40 Regulates Seed Germination. *Plant Physiology*, **2017**, 173, 956-969	6.6	18
198	A Global Analysis of the Receptor Tyrosine Kinase-Protein Phosphatase Interactome. *Molecular Cell*, **2017**, 65, 347-360	17.6	73
197	A pseudouridine synthase module is essential for mitochondrial protein synthesis and cell viability. *EMBO Reports*, **2017**, 18, 28-38	6.5	79

196	Evolution of AF6-RAS association and its implications in mixed-lineage leukemia. *Nature Communications*, **2017**, 8, 1099	17.4	15
195	MARK3-mediated phosphorylation of ARHGEF2 couples microtubules to the actin cytoskeleton to establish cell polarity. *Science Signaling*, **2017**, 10,	8.8	28
194	C. elegans SUP-46, an HNRNPM family RNA-binding protein that prevents paternally-mediated epigenetic sterility. *BMC Biology*, **2017**, 15, 61	7.3	4
193	Selective Targeting of Bromodomains of the Bromodomain-PHD Fingers Family Impairs Osteoclast Differentiation. *ACS Chemical Biology*, **2017**, 12, 2619-2630	4.9	20
192	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry. *Nature Communications*, **2017**, 8, 291	17.4	252
191	Regulatory Expansion in Mammals of Multivalent hnRNP Assemblies that Globally Control Alternative Splicing. *Cell*, **2017**, 170, 324-339.e23	56.2	72
190	ProHits-viz: a suite of web tools for visualizing interaction proteomics data. *Nature Methods*, **2017**, 14, 645-646	21.6	90
189	CEP19 cooperates with FOP and CEP350 to drive early steps in the ciliogenesis programme. *Open Biology*, **2017**, 7,	7	25
188	Plk4 Promotes Cancer Invasion and Metastasis through Arp2/3 Complex Regulation of the Actin Cytoskeleton. *Cancer Research*, **2017**, 77, 434-447	10.1	87
187	Proteomic analysis of the human KEOPS complex identifies C14ORF142 as a core subunit homologous to yeast Gon7. *Nucleic Acids Research*, **2017**, 45, 805-817	20.1	31
186	Ydj1 governs fungal morphogenesis and stress response, and facilitates mitochondrial protein import via Mas1 and Mas2. *Microbial Cell*, **2017**, 4, 342-361	3.9	21
185	AIRE is a critical spindle-associated protein in embryonic stem cells. *ELife*, **2017**, 6,	8.9	14
184	Dual action antifungal small molecule modulates multidrug efflux and TOR signaling. *Nature Chemical Biology*, **2016**, 12, 867-75	11.7	50
183	The RNF146 and tankyrase pathway maintains the junctional Crumbs complex through regulation of angiomotin. *Journal of Cell Science*, **2016**, 129, 3396-411	5.3	16
182	Phenotypic and Interaction Profiling of the Human Phosphatases Identifies Diverse Mitotic Regulators. *Cell Reports*, **2016**, 17, 2488-2501	10.6	58
181	Promiscuous targeting of bromodomains by bromosporine identifies BET proteins as master regulators of primary transcription response in leukemia. *Science Advances*, **2016**, 2, e1600760	14.3	64
180	Exploring genetic suppression interactions on a global scale. *Science*, **2016**, 354,	33.3	103
179	Topoisomerase II beta interacts with cohesin and CTCF at topological domain borders. *Genome Biology*, **2016**, 17, 182	18.3	143

178	HELB Is a Feedback Inhibitor of DNA End Resection. *Molecular Cell*, **2016**, 61, 405-418	17.6	92
177	Heart of glass anchors Rasip1 at endothelial cell-cell junctions to support vascular integrity. *ELife*, **2016**, 5, e11394	8.9	25
176	SAINTq: Scoring protein-protein interactions in affinity purification - mass spectrometry experiments with fragment or peptide intensity data. *Proteomics*, **2016**, 16, 2238-45	4.8	23
175	Multivalent Histone and DNA Engagement by a PHD/BRD/PWWP Triple Reader Cassette Recruits ZMYND8 to K14ac-Rich Chromatin. *Cell Reports*, **2016**, 17, 2724-2737	10.6	54
174	BRPF3-HBO1 regulates replication origin activation and histone H3K14 acetylation. *EMBO Journal*, **2016**, 35, 176-92	13	61
173	SLC25A46 is required for mitochondrial lipid homeostasis and cristae maintenance and is responsible for Leigh syndrome. *EMBO Molecular Medicine*, **2016**, 8, 1019-38	12	105
172	Crystal structures and mutagenesis of PPP-family ser/thr protein phosphatases elucidate the selectivity of cantharidin and novel norcantharidin-based inhibitors of PP5C. *Biochemical Pharmacology*, **2016**, 109, 14-26	6	16
171	Data Independent Acquisition analysis in ProHits 4.0. *Journal of Proteomics*, **2016**, 149, 64-68	3.9	37
170	The TIP60 Complex Regulates Bivalent Chromatin Recognition by 53BP1 through Direct H4K20me Binding and H2AK15 Acetylation. *Molecular Cell*, **2016**, 62, 409-421	17.6	136
169	Inborn Error of Cobalamin Metabolism Associated with the Intracellular Accumulation of Transcobalamin-Bound Cobalamin and Mutations in ZNF143, Which Codes for a Transcriptional Activator. *Human Mutation*, **2016**, 37, 976-82	4.7	21
168	A global genetic interaction network maps a wiring diagram of cellular function. *Science*, **2016**, 353,	33.3	626
167	Proteomics approaches to decipher new signaling pathways. *Current Opinion in Structural Biology*, **2016**, 41, 128-134	8.1	5
166	DIA-Umpire: comprehensive computational framework for data-independent acquisition proteomics. *Nature Methods*, **2015**, 12, 258-64, 7 p following 264	21.6	371
165	Myotubularin-related proteins 3 and 4 interact with polo-like kinase 1 and centrosomal protein of 55 kDa to ensure proper abscission. *Molecular and Cellular Proteomics*, **2015**, 14, 946-60	7.6	13
164	A web-tool for visualizing quantitative protein-protein interaction data. *Proteomics*, **2015**, 15, 1432-6	4.8	24
163	Systematic investigation of hierarchical phosphorylation by protein kinase CK2. *Journal of Proteomics*, **2015**, 118, 49-62	3.9	41
162	Assessment of a method to characterize antibody selectivity and specificity for use in immunoprecipitation. *Nature Methods*, **2015**, 12, 725-31	21.6	86
161	Proteomic analysis of the palmitoyl protein thioesterase 1 interactome in SH-SY5Y human neuroblastoma cells. *Journal of Proteomics*, **2015**, 123, 42-53	3.9	38

160	Combinatorial proteomic analysis of intercellular signaling applied to the CD28 T-cell costimulatory receptor. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E1594-603	11.5	44
159	BioID-based Identification of Skp Cullin F-box (SCF)TrCP1/2 E3 Ligase Substrates. *Molecular and Cellular Proteomics*, **2015**, 14, 1781-95	7.6	108
158	CCM-3/STRIPAK promotes seamless tube extension through endocytic recycling. *Nature Communications*, **2015**, 6, 6449	17.4	57
157	The Human Adenovirus Type 5 E4orf4 Protein Targets Two Phosphatase Regulators of the Hippo Signaling Pathway. *Journal of Virology*, **2015**, 89, 8855-70	6.6	8
156	mapDIA: Preprocessing and statistical analysis of quantitative proteomics data from data independent acquisition mass spectrometry. *Journal of Proteomics*, **2015**, 129, 108-120	3.9	101
155	An alternative splicing event amplifies evolutionary differences between vertebrates. *Science*, **2015** , 349, 868-73	33.3	89
154	Quantitative analysis of PPT1 interactome in human neuroblastoma cells. *Data in Brief*, **2015**, 4, 207-16	1.2	8
153	MSPLIT-DIA: sensitive peptide identification for data-independent acquisition. *Nature Methods*, **2015**, 12, 1106-8	21.6	86
152	Proximity biotinylation and affinity purification are complementary approaches for the interactome mapping of chromatin-associated protein complexes. *Journal of Proteomics*, **2015**, 118, 81-94	3.9	173
151	A Dynamic Protein Interaction Landscape of the Human Centrosome-Cilium Interface. *Cell*, **2015**, 163, 1484-99	56.2	316
150	The eIF4E-Binding Protein 4E-T Is a Component of the mRNA Decay Machinery that Bridges the 5’ and 3’ Termini of Target mRNAs. *Cell Reports*, **2015**, 11, 1425-36	10.6	56
149	Incorporating DNA shearing in standard affinity purification allows simultaneous identification of both soluble and chromatin-bound interaction partners. *Journal of Proteomics*, **2014**, 100, 55-9	3.9	24
148	Cell cycle-regulated oscillator coordinates core histone gene transcription through histone acetylation. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 14124-9	11.5	20
147	A global regulatory mechanism for activating an exon network required for neurogenesis. *Molecular Cell*, **2014**, 56, 90-103	17.6	85
146	A quantitative chaperone interaction network reveals the architecture of cellular protein homeostasis pathways. *Cell*, **2014**, 158, 434-448	56.2	258
145	Assessing cellular efficacy of bromodomain inhibitors using fluorescence recovery after photobleaching. *Epigenetics and Chromatin*, **2014**, 7, 14	5.8	58
144	Endosomal sorting of VAMP3 is regulated by PI4K2A. *Journal of Cell Science*, **2014**, 127, 3745-56	5.3	36
143	The RhoGEF GEF-H1 is required for oncogenic RAS signaling via KSR-1. *Cancer Cell*, **2014**, 25, 181-95	24.3	64

142	Mechanistic insight into GPCR-mediated activation of the microtubule-associated RhoA exchange factor GEF-H1. *Nature Communications*, **2014**, 5, 4857	17.4	42
141	SETD6 controls the expression of estrogen-responsive genes and proliferation of breast carcinoma cells. *Epigenetics*, **2014**, 9, 942-50	5.7	22
140	SAINTexpress: improvements and additional features in Significance Analysis of INTeractome software. *Journal of Proteomics*, **2014**, 100, 37-43	3.9	296
139	Protein phosphatase PP1/GLC7 interaction domain in yeast eIF2□bypasses targeting subunit requirement for eIF2□dephosphorylation. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, E1344-53	11.5	18
138	Src homology 2 domain containing protein 5 (SH2D5) binds the breakpoint cluster region protein, BCR, and regulates levels of Rac1-GTP. *Journal of Biological Chemistry*, **2014**, 289, 35397-408	5.4	10
137	Role of the SIK2-p35-PJA2 complex in pancreatic □cell functional compensation. *Nature Cell Biology*, **2014**, 16, 234-44	23.4	52
136	The PPFIA1-PP2A protein complex promotes trafficking of Kif7 to the ciliary tip and Hedgehog signaling. *Science Signaling*, **2014**, 7, ra117	8.8	34
135	(R)-PFI-2 is a potent and selective inhibitor of SETD7 methyltransferase activity in cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 12853-8	11.5	120
134	Control of the hippo pathway by Set7-dependent methylation of Yap. *Developmental Cell*, **2013**, 26, 188-94	10.2	100
133	The CRAPome: a contaminant repository for affinity purification-mass spectrometry data. *Nature Methods*, **2013**, 10, 730-6	21.6	894
132	Temporal regulation of EGF signalling networks by the scaffold protein Shc1. *Nature*, **2013**, 499, 166-71	50.4	199
131	Profiling the kinome: current capabilities and future challenges. *Journal of Proteomics*, **2013**, 81, 43-55	3.9	25
130	Mapping differential interactomes by affinity purification coupled with data-independent mass spectrometry acquisition. *Nature Methods*, **2013**, 10, 1239-45	21.6	207
129	Protein interaction network of the mammalian Hippo pathway reveals mechanisms of kinase-phosphatase interactions. *Science Signaling*, **2013**, 6, rs15	8.8	305
128	Drafting the CLN3 protein interactome in SH-SY5Y human neuroblastoma cells: a label-free quantitative proteomics approach. *Journal of Proteome Research*, **2013**, 12, 2101-15	5.6	38
127	Construction of human activity-based phosphorylation networks. *Molecular Systems Biology*, **2013**, 9, 655	12.2	134
126	Conserved Asf1-importin □physical interaction in growth and sexual development in the ciliate Tetrahymena thermophila. *Journal of Proteomics*, **2013**, 94, 311-26	3.9	15
125	Label-free quantitative proteomics trends for protein-protein interactions. *Journal of Proteomics*, **2013**, 81, 91-101	3.9	47

124	The linear ubiquitin-specific deubiquitinase gumby regulates angiogenesis. *Nature*, **2013**, 498, 318-24	50.4	184
123	LuciPHOr: algorithm for phosphorylation site localization with false localization rate estimation using modified target-decoy approach. *Molecular and Cellular Proteomics*, **2013**, 12, 3409-19	7.6	53
122	Lnk adaptor suppresses radiation resistance and radiation-induced B-cell malignancies by inhibiting IL-11 signaling. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 20599-604	11.5	13
121	Regulation of CD133 by HDAC6 promotes catenin signaling to suppress cancer cell differentiation. *Cell Reports*, **2012**, 2, 951-63	10.6	131
120	Mass spectrometry approaches to study mammalian kinase and phosphatase associated proteins. *Methods*, **2012**, 57, 400-8	4.6	53
119	Global gene deletion analysis exploring yeast filamentous growth. *Science*, **2012**, 337, 1353-6	33.3	141
118	Beyond hairballs: The use of quantitative mass spectrometry data to understand protein-protein interactions. *FEBS Letters*, **2012**, 586, 2723-31	3.8	23
117	Histone recognition and large-scale structural analysis of the human bromodomain family. *Cell*, **2012**, 149, 214-31	56.2	1054
116	A novel whole-cell lysate kinase assay identifies substrates of the p38 MAPK in differentiating myoblasts. *Skeletal Muscle*, **2012**, 2, 5	5.1	30
115	Selective proteasomal degradation of the B'subunit of protein phosphatase 2A by the E3 ubiquitin ligase adaptor Kelch-like 15. *Journal of Biological Chemistry*, **2012**, 287, 43378-89	5.4	24
114	Analyzing protein-protein interactions from affinity purification-mass spectrometry data with SAINT. *Current Protocols in Bioinformatics*, **2012**, Chapter 8, Unit8.15	24.2	90
113	Using ProHits to store, annotate, and analyze affinity purification-mass spectrometry (AP-MS) data. *Current Protocols in Bioinformatics*, **2012**, Chapter 8, Unit8.16	24.2	17
112	Mass spectrometric tools for systematic analysis of protein phosphorylation. *Progress in Molecular Biology and Translational Science*, **2012**, 106, 3-32	4	11
111	Affinity-purification coupled to mass spectrometry: basic principles and strategies. *Proteomics*, **2012**, 12, 1576-90	4.8	202
110	Mapping physical interactions within chromatin by proteomic approaches. *Proteomics*, **2012**, 12, 1609-22	4.8	15
109	History of protein-protein interactions: from egg-white to complex networks. *Proteomics*, **2012**, 12, 1478-98	4.8	139
108	Proteomic profiling of the TRAF3 interactome network reveals a new role for the ER-to-Golgi transport compartments in innate immunity. *PLoS Pathogens*, **2012**, 8, e1002747	7.6	42
107	High-resolution protein interaction map of the Drosophila melanogaster p38 mitogen-activated protein kinases reveals limited functional redundancy. *Molecular and Cellular Biology*, **2012**, 32, 3695-706	4.8	20

106	Novel NEDD1 phosphorylation sites regulate □-tubulin binding and mitotic spindle assembly. *Journal of Cell Science*, **2012**, 125, 3745-51	5.3	29
105	STK25 protein mediates TrkA and CCM2 protein-dependent death in pediatric tumor cells of neural origin. *Journal of Biological Chemistry*, **2012**, 287, 29285-9	5.4	17
104	Interaction proteomics identify NEURL4 and the HECT E3 ligase HERC2 as novel modulators of centrosome architecture. *Molecular and Cellular Proteomics*, **2012**, 11, M111.014233	7.6	47
103	CEP192 interacts physically and functionally with the K63-deubiquitinase CYLD to promote mitotic spindle assembly. *Cell Cycle*, **2012**, 11, 3555-8	4.7	21
102	A novel 4EHP-GIGYF2 translational repressor complex is essential for mammalian development. *Molecular and Cellular Biology*, **2012**, 32, 3585-93	4.8	107
101	Two phosphatidylinositol 4-kinases control lysosomal delivery of the Gaucher disease enzyme, □-glucocerebrosidase. *Molecular Biology of the Cell*, **2012**, 23, 1533-45	3.5	75
100	OpenFreezer: a reagent information management software system. *Nature Methods*, **2011**, 8, 612-3	21.6	22
99	Identification and characterization of AtI-2, an Arabidopsis homologue of an ancient protein phosphatase 1 (PP1) regulatory subunit. *Biochemical Journal*, **2011**, 435, 73-83	3.8	33
98	SAINT: probabilistic scoring of affinity purification-mass spectrometry data. *Nature Methods*, **2011**, 8, 70-3	21.6	480
97	Systematic exploration of essential yeast gene function with temperature-sensitive mutants. *Nature Biotechnology*, **2011**, 29, 361-7	44.5	258
96	A cost-benefit analysis of multidimensional fractionation of affinity purification-mass spectrometry samples. *Proteomics*, **2011**, 11, 2603-12	4.8	27
95	Label-free quantitative proteomics and SAINT analysis enable interactome mapping for the human Ser/Thr protein phosphatase 5. *Proteomics*, **2011**, 11, 1508-16	4.8	59
94	CCM3/PDCD10 heterodimerizes with germinal center kinase III (GCKIII) proteins using a mechanism analogous to CCM3 homodimerization. *Journal of Biological Chemistry*, **2011**, 286, 25056-64	5.4	50
93	Structure-function analysis of core STRIPAK Proteins: a signaling complex implicated in Golgi polarization. *Journal of Biological Chemistry*, **2011**, 286, 25065-75	5.4	95
92	Non-canonical inhibition of DNA damage-dependent ubiquitination by OTUB1. *Nature*, **2010**, 466, 941-6	50.4	256
91	ProHits: integrated software for mass spectrometry-based interaction proteomics. *Nature Biotechnology*, **2010**, 28, 1015-7	44.5	156
90	Quantitative analysis of fitness and genetic interactions in yeast on a genome scale. *Nature Methods*, **2010**, 7, 1017-24	21.6	251
89	A novel mechanism for SUMO system control: regulated Ulp1 nucleolar sequestration. *Molecular and Cellular Biology*, **2010**, 30, 4452-62	4.8	33

88	A lentiviral functional proteomics approach identifies chromatin remodeling complexes important for the induction of pluripotency. *Molecular and Cellular Proteomics*, **2010**, 9, 811-23	7.6	77
87	Postnatal deamidation of 4E-BP2 in brain enhances its association with raptor and alters kinetics of excitatory synaptic transmission. *Molecular Cell*, **2010**, 37, 797-808	17.6	66
86	The MMS22L-TONSL complex mediates recovery from replication stress and homologous recombination. *Molecular Cell*, **2010**, 40, 619-31	17.6	85
85	Analysis of protein complexes through model-based biclustering of label-free quantitative AP-MS data. *Molecular Systems Biology*, **2010**, 6, 385	12.2	30
84	A global protein kinase and phosphatase interaction network in yeast. *Science*, **2010**, 328, 1043-6	33.3	523
83	The genetic landscape of a cell. *Science*, **2010**, 327, 425-31	33.3	1627
82	A PP2A phosphatase high density interaction network identifies a novel striatin-interacting phosphatase and kinase complex linked to the cerebral cavernous malformation 3 (CCM3) protein. *Molecular and Cellular Proteomics*, **2009**, 8, 157-71	7.6	257
81	HAUS, the 8-subunit human Augmin complex, regulates centrosome and spindle integrity. *Current Biology*, **2009**, 19, 816-26	6.3	186
80	Journal Club: 35 years later, mRNA caps still matter. *Nature Reviews Molecular Cell Biology*, **2009**, 10, 734	48.7	2
79	PP4 is a gamma H2AX phosphatase required for recovery from the DNA damage checkpoint. *EMBO Reports*, **2008**, 9, 1019-26	6.5	163
78	Control of eIF4E cellular localization by eIF4E-binding proteins, 4E-BPs. *Rna*, **2008**, 14, 1318-27	5.8	90
77	PP4R4/KIAA1622 forms a novel stable cytosolic complex with phosphoprotein phosphatase 4. *Journal of Biological Chemistry*, **2008**, 283, 29273-84	5.4	59
76	Analysis of protein complexes using mass spectrometry. *Nature Reviews Molecular Cell Biology*, **2007**, 8, 645-54	48.7	553
75	Identification of putative androgen receptor interaction protein modules: cytoskeleton and endosomes modulate androgen receptor signaling in prostate cancer cells. *Molecular and Cellular Proteomics*, **2007**, 6, 252-71	7.6	46
74	Wilms tumor suppressor WTX negatively regulates WNT/beta-catenin signaling. *Science*, **2007**, 316, 1043-6	33.3	341
73	Affinity-purification mass spectrometry (AP-MS) of serine/threonine phosphatases. *Methods*, **2007**, 42, 298-305	4.6	85
72	Advances in protein complex analysis using mass spectrometry. *Journal of Physiology*, **2005**, 563, 11-21	3.9	148
71	Eukaryotic translation initiation factor 4E availability controls the switch between cap-dependent and internal ribosomal entry site-mediated translation. *Molecular and Cellular Biology*, **2005**, 25, 10556-65	4.8	143

70	A novel, evolutionarily conserved protein phosphatase complex involved in cisplatin sensitivity. *Molecular and Cellular Proteomics*, **2005**, 4, 1725-40	7.6	148
69	Phosphorylation of eucaryotic translation initiation factor 4B Ser422 is modulated by S6 kinases. *EMBO Journal*, **2004**, 23, 1761-9	13	363
68	Phosphorylation of eIF4E attenuates its interaction with mRNA 5’ cap analogs by electrostatic repulsion: intein-mediated protein ligation strategy to obtain phosphorylated protein. *Rna*, **2003**, 9, 52-61	5.8	107
67	Activation of GCN2 in UV-irradiated cells inhibits translation. *Current Biology*, **2002**, 12, 1279-86	6.3	209
66	A rapamycin-sensitive signaling pathway contributes to long-term synaptic plasticity in the hippocampus. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 467-72	11.5	589
65	Translational control of cell fate: availability of phosphorylation sites on translational repressor 4E-BP1 governs its proapoptotic potency. *Molecular and Cellular Biology*, **2002**, 22, 2853-61	4.8	91
64	Biophysical studies of eIF4E cap-binding protein: recognition of mRNA 5’ cap structure and synthetic fragments of eIF4G and 4E-BP1 proteins. *Journal of Molecular Biology*, **2002**, 319, 615-35	6.5	322
63	Insulin regulation of protein translation repressor 4E-BP1, an eIF4E-binding protein, in renal epithelial cells. *Kidney International*, **2001**, 59, 866-75	9.9	67
62	Adipose tissue reduction in mice lacking the translational inhibitor 4E-BP1. *Nature Medicine*, **2001**, 7, 1128-32	50.5	310
61	Regulation of translation initiation by FRAP/mTOR. *Genes and Development*, **2001**, 15, 807-26	12.6	1230
60	FRAP/mTOR is required for proliferation and patterning during embryonic development in the mouse. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 13796-801	11.5	135
59	The target of rapamycin (TOR) proteins. *Proceedings of the National Academy of Sciences of the United States of America*, **2001**, 98, 7037-44	11.5	492
58	Control of translation by the target of rapamycin proteins. *Progress in Molecular and Subcellular Biology*, **2001**, 27, 143-74	3	76
57	Hierarchical phosphorylation of the translation inhibitor 4E-BP1. *Genes and Development*, **2001**, 15, 2852-64	12.6	595
56	Serum-stimulated, rapamycin-sensitive phosphorylation sites in the eukaryotic translation initiation factor 4GI. *EMBO Journal*, **2000**, 19, 434-44	13	225
55	Translational control of the antiapoptotic function of Ras. *Journal of Biological Chemistry*, **2000**, 275, 24776-80	5.4	80
54	Regulation of the rapamycin and FKBP-target 1/mammalian target of rapamycin and cap-dependent initiation of translation by the c-Abl protein-tyrosine kinase. *Journal of Biological Chemistry*, **2000**, 275, 10779-87	5.4	49
53	Requirement for Akt (protein kinase B) in insulin-induced activation of glycogen synthase and phosphorylation of 4E-BP1 (PHAS-1). *Journal of Biological Chemistry*, **1999**, 274, 20611-8	5.4	80

52	A potential role for extracellular signal-regulated kinases in prostaglandin F2alpha-induced protein synthesis in smooth muscle cells. *Journal of Biological Chemistry*, **1999**, 274, 12925-32	5.4	45
51	Human eukaryotic translation initiation factor 4G (eIF4G) recruits mnk1 to phosphorylate eIF4E. *EMBO Journal*, **1999**, 18, 270-9	13	507
50	Protein analysis by mass spectrometry and sequence database searching: tools for cancer research in the post-genomic era. *Electrophoresis*, **1999**, 20, 310-9	3.6	90
49	eIF4E activity is regulated at multiple levels. *International Journal of Biochemistry and Cell Biology*, **1999**, 31, 43-57	5.6	241
48	Cap-dependent translation initiation in eukaryotes is regulated by a molecular mimic of eIF4G. *Molecular Cell*, **1999**, 3, 707-16	17.6	406
47	eIF4 initiation factors: effectors of mRNA recruitment to ribosomes and regulators of translation. *Annual Review of Biochemistry*, **1999**, 68, 913-63	29.1	1729
46	Translational homeostasis: eukaryotic translation initiation factor 4E control of 4E-binding protein 1 and p70 S6 kinase activities. *Molecular and Cellular Biology*, **1999**, 19, 4302-10	4.8	95
45	Regulation of 4E-BP1 phosphorylation: a novel two-step mechanism. *Genes and Development*, **1999**, 13, 1422-37	12.6	947
44	Gastrin induces phosphorylation of eIF4E binding protein 1 and translation initiation of ornithine decarboxylase mRNA. *Oncogene*, **1998**, 16, 2219-27	9.2	34
43	The mRNA 5' cap-binding protein eIF4E and control of cell growth. *Current Opinion in Cell Biology*, **1998**, 10, 268-75	9	506
42	4E binding proteins inhibit the translation factor eIF4E without folded structure. *Biochemistry*, **1998** , 37, 9-15	3.2	107
41	mu-Opioid receptor activates signaling pathways implicated in cell survival and translational control. *Journal of Biological Chemistry*, **1998**, 273, 23534-41	5.4	156
40	4E-BP3, a new member of the eukaryotic initiation factor 4E-binding protein family. *Journal of Biological Chemistry*, **1998**, 273, 14002-7	5.4	220
39	Cloning and characterization of 4EHP, a novel mammalian eIF4E-related cap-binding protein. *Journal of Biological Chemistry*, **1998**, 273, 13104-9	5.4	100
38	4E-BP1, a repressor of mRNA translation, is phosphorylated and inactivated by the Akt(PKB) signaling pathway. *Genes and Development*, **1998**, 12, 502-13	12.6	691
37	Rapamycin and wortmannin enhance replication of a defective encephalomyocarditis virus. *Journal of Virology*, **1998**, 72, 5811-9	6.6	37
36	Angiotensin II stimulates phosphorylation of the translational repressor 4E-binding protein 1 by a mitogen-activated protein kinase-independent mechanism. *Journal of Biological Chemistry*, **1997**, 272, 4006-12	5.4	33
35	The insulin-induced signalling pathway leading to S6 and initiation factor 4E binding protein 1 phosphorylation bifurcates at a rapamycin-sensitive point immediately upstream of p70s6k. *Molecular and Cellular Biology*, **1997**, 17, 5426-36	4.8	215

34	Cocrystal structure of the messenger RNA 5’ cap-binding protein (eIF4E) bound to 7-methyl-GDP. *Cell*, **1997**, 89, 951-61	56.2	574
33	Adenovirus infection inactivates the translational inhibitors 4E-BP1 and 4E-BP2. *Virology*, **1997**, 237, 182-6	3.6	46
32	Macrophage Inflammatory Protein-1□and Interferon-Inducible Protein 10 Inhibit Synergistically Induced Growth Factor Stimulation of MAP Kinase Activity and Suppress Phosphorylation of Eukaryotic Initiation Factor 4E and 4E Binding Protein 1. *Blood*, **1997**, 89, 3582-3595	2.2	24
31	Structure of translation factor eIF4E bound to m7GDP and interaction with 4E-binding protein. *Nature Structural Biology*, **1997**, 4, 717-24		309
30	Macrophage Inflammatory Protein-1□and Interferon-Inducible Protein 10 Inhibit Synergistically Induced Growth Factor Stimulation of MAP Kinase Activity and Suppress Phosphorylation of Eukaryotic Initiation Factor 4E and 4E Binding Protein 1. *Blood*, **1997**, 89, 3582-3595	2.2	2
29	Tissue distribution, genomic structure, and chromosome mapping of mouse and human eukaryotic initiation factor 4E-binding proteins 1 and 2. *Genomics*, **1996**, 38, 353-63	4.3	46
28	IDENTIFICATION OF POTENTIAL ANTI-ONCOGENIC PROPERTIES OF elF-4E BINDING PROTEINS 1 AND 2. *Biology of the Cell*, **1996**, 88, 69-69	3.5	
27	4E-BP1 phosphorylation is mediated by the FRAP-p70s6k pathway and is independent of mitogen-activated protein kinase. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 4076-80	11.5	230
26	Activation of the translational suppressor 4E-BP1 following infection with encephalomyocarditis virus and poliovirus. *Proceedings of the National Academy of Sciences of the United States of America*, **1996**, 93, 5578-83	11.5	185
25	Phosphorylation of eIF-4E on serine 209 by protein kinase C is inhibited by the translational repressors, 4E-binding proteins. *Journal of Biological Chemistry*, **1996**, 271, 11831-7	5.4	81
24	Expression of a translationally regulated, dominant-negative CCAAT/enhancer-binding protein beta isoform and up-regulation of the eukaryotic translation initiation factor 2alpha are correlated with neoplastic transformation of mammary epithelial cells. *Cancer Research*, **1996**, 56, 4382-6	10.1	82
23	The eIF4E-binding proteins 1 and 2 are negative regulators of cell growth. *Oncogene*, **1996**, 13, 2415-20	9.2	156
22	Insulin-dependent stimulation of protein synthesis by phosphorylation of a regulator of 5’-cap function. *Nature*, **1994**, 371, 762-7	50.4	1079
21	Safety and Efficacy of Preventative COVID Vaccines: The StopCoV Study		1
20	Structure of mammalian V-ATPase with the TLDc domain protein mEAK7 bound		2
19	A □Made-in-Canada□serology solution for profiling humoral immune responses to SARS-CoV-2 infection and vaccination		4
18	A high-density human mitochondrial proximity interaction network		4
17	A simple protein-based surrogate neutralization assay for SARS-CoV-2		3

16	Mucosal versus systemic antibody responses to SARS-CoV-2 antigens in COVID-19 patients		30
15	A SARS-CoV-2 BioID-based virus-host membrane protein interactome and virus peptide compendium: new proteomics resources for COVID-19 research		11
14	Global BioID-based SARS-CoV-2 proteins proximal interactome unveils novel ties between viral polypeptides and host factors involved in multiple COVID19-associated mechanisms		29
13	A SARS-CoV-2 host proximity interactome		34
12	TAZ-CAMTA1 and YAP-TFE3 modulate the basal TAZ/YAP transcriptional program by recruiting the ATAC histone acetyltransferase complex		1
11	Endogenous BioID elucidates TCF7L1 interactome modulation upon GSK-3 inhibition in mouse ESCs		2
10	Systematic discovery of Short Linear Motifs decodes calcineurin phosphatase signaling		2
9	A proximity-dependent biotinylation map of a human cell: an interactive web resource		28
8	Multi-laboratory assessment of reproducibility, qualitative and quantitative performance of SWATH-mass spectrometry		3
7	Dried blood spot specimens for SARS-CoV-2 antibody testing: A multi-site, multi-assay comparison		3
6	Preclinical evaluation of a SARS-CoV-2 mRNA vaccine PTX-COVID19-B		2
5	The Humoral Response to the BNT162b2 Vaccine in Hemodialysis Patients		2
4	Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) seroprevalence: Navigating the absence of a gold standard		1
3	SARS-CoV-2 Seroprevalence During the First and Second Pandemic Waves in Canada. *SSRN Electronic Journal*,	1	2
2	Neutralizing antibody responses to SARS-CoV-2 variants in vaccinated Ontario long-term care home residents and workers		13
1	A mucosal antibody response is induced by intra-muscular SARS-CoV-2 mRNA vaccination		10