

Mathias Uhlen

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

333
papers

29,027
citations

64
h-index

166
g-index

362
ext. papers

38,509
ext. citations

9.5
avg, IF

6.75
L-index

#	Paper	IF	Citations
333	Proteomics. Tissue-based map of the human proteome. <i>Science</i> , 2015 , 347, 1260419	33.3	6576
332	Analysis of the human tissue-specific expression by genome-wide integration of transcriptomics and antibody-based proteomics. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 397-406	7.6	1730
331	Towards a knowledge-based Human Protein Atlas. <i>Nature Biotechnology</i> , 2010 , 28, 1248-50	44.5	1653
330	A pathology atlas of the human cancer transcriptome. <i>Science</i> , 2017 , 357,	33.3	1481
329	A subcellular map of the human proteome. <i>Science</i> , 2017 , 356,	33.3	1183
328	A sequencing method based on real-time pyrophosphate. <i>Science</i> , 1998 , 281, 363, 365	33.3	1070
327	A human protein atlas for normal and cancer tissues based on antibody proteomics. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 1920-32	7.6	976
326	Binding proteins selected from combinatorial libraries of an alpha-helical bacterial receptor domain. <i>Nature Biotechnology</i> , 1997 , 15, 772-7	44.5	509
325	A genecentric Human Protein Atlas for expression profiles based on antibodies. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2019-27	7.6	462
324	The protein expression profile of ACE2 in human tissues. <i>Molecular Systems Biology</i> , 2020 , 16, e9610	12.2	405
323	How many human proteoforms are there?. <i>Nature Chemical Biology</i> , 2018 , 14, 206-214	11.7	324
322	Correlations between RNA and protein expression profiles in 23 human cell lines. <i>BMC Genomics</i> , 2009 , 10, 365	4.5	323
321	Genome-scale metabolic modelling of hepatocytes reveals serine deficiency in patients with non-alcoholic fatty liver disease. <i>Nature Communications</i> , 2014 , 5, 3083	17.4	320
320	A proposal for validation of antibodies. <i>Nature Methods</i> , 2016 , 13, 823-7	21.6	312
319	Defining the transcriptome and proteome in three functionally different human cell lines. <i>Molecular Systems Biology</i> , 2010 , 6, 450	12.2	269
318	Prediction of the human membrane proteome. <i>Proteomics</i> , 2010 , 10, 1141-9	4.8	250
317	The human proteome project: current state and future direction. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.009993	7.6	249

316	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012 , 30, 221-3	44.5	244
315	Novel asymmetrically localizing components of human centrosomes identified by complementary proteomics methods. <i>EMBO Journal</i> , 2011 , 30, 1520-35	13	235
314	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8503	12.2	235
313	Gene-specific correlation of RNA and protein levels in human cells and tissues. <i>Molecular Systems Biology</i> , 2016 , 12, 883	12.2	230
312	Antibody-based proteomics for human tissue profiling. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 384-93.6	9.6	224
311	Identification of anticancer drugs for hepatocellular carcinoma through personalized genome-scale metabolic modeling. <i>Molecular Systems Biology</i> , 2014 , 10, 721	12.2	223
310	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. <i>Nature Methods</i> , 2007 , 4, 13-7	21.6	207
309	Towards a human proteome atlas: high-throughput generation of mono-specific antibodies for tissue profiling. <i>Proteomics</i> , 2005 , 5, 4327-37	4.8	196
308	An Integrated Understanding of the Rapid Metabolic Benefits of a Carbohydrate-Restricted Diet on Hepatic Steatosis in Humans. <i>Cell Metabolism</i> , 2018 , 27, 559-571.e5	24.6	189
307	SATB2 in combination with cytokeratin 20 identifies over 95% of all colorectal carcinomas. <i>American Journal of Surgical Pathology</i> , 2011 , 35, 937-48	6.7	183
306	Immunofluorescence and fluorescent-protein tagging show high correlation for protein localization in mammalian cells. <i>Nature Methods</i> , 2013 , 10, 315-23	21.6	175
305	Integration of clinical data with a genome-scale metabolic model of the human adipocyte. <i>Molecular Systems Biology</i> , 2013 , 9, 649	12.2	167
304	A genome-wide transcriptomic analysis of protein-coding genes in human blood cells. <i>Science</i> , 2019 , 366,	33.3	131
303	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020 , 367,	33.3	130
302	High-resolution mapping of linear antibody epitopes using ultrahigh-density peptide microarrays. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1790-800	7.6	122
301	Standard guidelines for the chromosome-centric human proteome project. <i>Journal of Proteome Research</i> , 2012 , 11, 2005-13	5.6	121
300	A Protein Epitope Signature Tag (PrEST) library allows SILAC-based absolute quantification and multiplexed determination of protein copy numbers in cell lines. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, O111.009613	7.6	116
299	Toward a confocal subcellular atlas of the human proteome. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 499-508	7.6	112

298	PATCHED and p53 gene alterations in sporadic and hereditary basal cell cancer. <i>Oncogene</i> , 2001 , 20, 7770-8	9.2	112
297	Single-step recovery of a secreted recombinant protein by expanded bed adsorption. <i>Bio/technology</i> , 1994 , 12, 285-8		112
296	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016 , 24, 172-84	24.6	105
295	The human secretome. <i>Science Signaling</i> , 2019 , 12,	8.8	99
294	Affinity proteomics for systematic protein profiling of chromosome 21 gene products in human tissues. <i>Molecular and Cellular Proteomics</i> , 2003 , 2, 405-14	7.6	98
293	Antibodypedia, a portal for sharing antibody and antigen validation data. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 2028-37	7.6	95
292	Transcriptomics resources of human tissues and organs. <i>Molecular Systems Biology</i> , 2016 , 12, 862	12.2	95
291	Personal model-assisted identification of NAD and glutathione metabolism as intervention target in NAFLD. <i>Molecular Systems Biology</i> , 2017 , 13, 916	12.2	92
290	Stratification of Hepatocellular Carcinoma Patients Based on Acetate Utilization. <i>Cell Reports</i> , 2015 , 13, 2014-26	10.6	92
289	Molecular pathology in basal cell cancer with p53 as a genetic marker. <i>Oncogene</i> , 1997 , 15, 1059-67	9.2	92
288	Antibody suspension bead arrays within serum proteomics. <i>Journal of Proteome Research</i> , 2008 , 7, 3168-78		92
287	Proteome-wide epitope mapping of antibodies using ultra-dense peptide arrays. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1585-97	7.6	88
286	Proteome- and transcriptome-driven reconstruction of the human myocyte metabolic network and its use for identification of markers for diabetes. <i>Cell Reports</i> , 2015 , 11, 921-933	10.6	81
285	Affinity proteomics within rare diseases: a BIO-NMD study for blood biomarkers of muscular dystrophies. <i>EMBO Molecular Medicine</i> , 2014 , 6, 918-36	12	81
284	An atlas of human metabolism. <i>Science Signaling</i> , 2020 , 13,	8.8	78
283	Epitope mapping of antibodies using bacterial surface display. <i>Nature Methods</i> , 2008 , 5, 1039-45	21.6	77
282	Recombinant human factor VIII-specific affinity ligands selected from phage-displayed combinatorial libraries of protein A. <i>FEBS Journal</i> , 2001 , 268, 4269-77		77
281	The mechanism of binding staphylococcal protein A to immunoglobulin G does not involve helix unwinding. <i>Biochemistry</i> , 1996 , 35, 22-31	3.2	77

280	Genetic and nutrient modulation of acetyl-CoA levels in <i>Synechocystis</i> for n-butanol production. <i>Microbial Cell Factories</i> , 2015 , 14, 167	6.4	76
279	Large-scale Affinity Purification of Human Insulin-like Growth Factor I from Culture Medium of <i>Escherichia Coli</i> . <i>Nature Biotechnology</i> , 1987 , 5, 379-382	44.5	75
278	Using transcriptomics to improve butanol tolerance of <i>Synechocystis</i> sp. strain PCC 6803. <i>Applied and Environmental Microbiology</i> , 2013 , 79, 7419-27	4.8	73
277	Translation from a DMD exon 5 IRES results in a functional dystrophin isoform that attenuates dystrophinopathy in humans and mice. <i>Nature Medicine</i> , 2014 , 20, 992-1000	50.5	72
276	Immobilization and affinity purification of recombinant proteins using histidine peptide fusions. <i>FEBS Journal</i> , 1989 , 186, 563-9		72
275	Network analyses identify liver-specific targets for treating liver diseases. <i>Molecular Systems Biology</i> , 2017 , 13, 938	12.2	71
274	Metabolic network-based stratification of hepatocellular carcinoma reveals three distinct tumor subtypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018 , 115, E11874-E11883	11.5	71
273	Systems biology in hepatology: approaches and applications. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 365-377	24.2	70
272	A single-cell type transcriptomics map of human tissues. <i>Science Advances</i> , 2021 , 7,	14.3	69
271	A single fixation protocol for proteome-wide immunofluorescence localization studies. <i>Journal of Proteomics</i> , 2010 , 73, 1067-78	3.9	66
270	Profiling cancer testis antigens in non-small-cell lung cancer. <i>JCI Insight</i> , 2016 , 1, e86837	9.9	65
269	Complementing tissue characterization by integrating transcriptome profiling from the Human Protein Atlas and from the FANTOM5 consortium. <i>Nucleic Acids Research</i> , 2015 , 43, 6787-98	20.1	61
268	Expression of the RNA-binding protein RBM3 is associated with a favourable prognosis and cisplatin sensitivity in epithelial ovarian cancer. <i>Journal of Translational Medicine</i> , 2010 , 8, 78	8.5	61
267	A web-based tool for in silico biomarker discovery based on tissue-specific protein profiles in normal and cancer tissues. <i>Molecular and Cellular Proteomics</i> , 2008 , 7, 825-44	7.6	60
266	Anoctamin 2 identified as an autoimmune target in multiple sclerosis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, 2188-93	11.5	59
265	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301	17.4	59
264	The human liver-specific proteome defined by transcriptomics and antibody-based profiling. <i>FASEB Journal</i> , 2014 , 28, 2901-14	0.9	58
263	Secretagoin is a Ca ²⁺ -binding protein specifying subpopulations of telencephalic neurons. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009 , 106, 22492-7	11.5	58

262	Nuclear expression of the RNA-binding protein RBM3 is associated with an improved clinical outcome in breast cancer. <i>Modern Pathology</i> , 2009 , 22, 1564-74	9.8	57
261	Dissecting antibodies with regards to linear and conformational epitopes. <i>PLoS ONE</i> , 2015 , 10, e0121673	3.7	56
260	Antibody-based tissue profiling as a tool for clinical proteomics. <i>Clinical Proteomics</i> , 2004 , 1, 285-299	5	56
259	Selection of protein epitopes for antibody production. <i>BioTechniques</i> , 2005 , 38, 723-7	2.5	55
258	Developmental trajectory of the healthy human gut microbiota during the first 5 years of life. <i>Cell Host and Microbe</i> , 2021 , 29, 765-776.e3	23.4	55
257	Advancing cell biology through proteomics in space and time (PROSPECTS). <i>Molecular and Cellular Proteomics</i> , 2012 , 11, O112.017731	7.6	52
256	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1378-1391	7.6	51
255	Toward next generation plasma profiling via heat-induced epitope retrieval and array-based assays. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 2497-507	7.6	51
254	Affinity as a tool in life science. <i>BioTechniques</i> , 2008 , 44, 649-54	2.5	51
253	All individual domains of staphylococcal protein A show Fab binding. <i>FEMS Immunology and Medical Microbiology</i> , 1998 , 20, 69-78		51
252	Growth of Cyanobacteria Is Constrained by the Abundance of Light and Carbon Assimilation Proteins. <i>Cell Reports</i> , 2018 , 25, 478-486.e8	10.6	50
251	Defining the human adipose tissue proteome to reveal metabolic alterations in obesity. <i>Journal of Proteome Research</i> , 2014 , 13, 5106-19	5.6	49
250	Molecular correlates and prognostic significance of SATB1 expression in colorectal cancer. <i>Diagnostic Pathology</i> , 2012 , 7, 115	3	49
249	The human gastrointestinal tract-specific transcriptome and proteome as defined by RNA sequencing and antibody-based profiling. <i>Journal of Gastroenterology</i> , 2015 , 50, 46-57	6.9	48
248	Identifying anti-growth factors for human cancer cell lines through genome-scale metabolic modeling. <i>Scientific Reports</i> , 2015 , 5, 8183	4.9	48
247	Enhanced validation of antibodies for research applications. <i>Nature Communications</i> , 2018 , 9, 4130	17.4	48
246	Thiol-directed immobilization of recombinant IgG-binding receptors. <i>FEBS Journal</i> , 1989 , 186, 557-61		47
245	RBM3-regulated genes promote DNA integrity and affect clinical outcome in epithelial ovarian cancer. <i>Translational Oncology</i> , 2011 , 4, 212-21	4.9	46

244	Selective enrichment of monospecific polyclonal antibodies for antibody-based proteomics efforts. <i>Journal of Chromatography A</i> , 2004 , 1043, 33-40	4.5	46
243	ANLN is a prognostic biomarker independent of Ki-67 and essential for cell cycle progression in primary breast cancer. <i>BMC Cancer</i> , 2016 , 16, 904	4.8	46
242	Whole-Proteome Peptide Microarrays for Profiling Autoantibody Repertoires within Multiple Sclerosis and Narcolepsy. <i>Journal of Proteome Research</i> , 2017 , 16, 1300-1314	5.6	44
241	Contribution of antibody-based protein profiling to the human Chromosome-centric Proteome Project (C-HPP). <i>Journal of Proteome Research</i> , 2013 , 12, 2439-48	5.6	44
240	Drug Repositioning for Effective Prostate Cancer Treatment. <i>Frontiers in Physiology</i> , 2018 , 9, 500	4.6	43
239	Affibody Scaffolds Improve Sesquiterpene Production in <i>Saccharomyces cerevisiae</i> . <i>ACS Synthetic Biology</i> , 2017 , 6, 19-28	5.7	43
238	Low RBM3 protein expression correlates with tumour progression and poor prognosis in malignant melanoma: an analysis of 215 cases from the MalmDiet and Cancer Study. <i>Journal of Translational Medicine</i> , 2011 , 9, 114	8.5	43
237	A whole-genome bioinformatics approach to selection of antigens for systematic antibody generation. <i>Proteomics</i> , 2008 , 8, 2832-9	4.8	43
236	Multiple affinity domains for the detection, purification and immobilization of recombinant proteins. <i>Journal of Molecular Recognition</i> , 1996 , 9, 585-94	2.6	43
235	Integration of cardiac proteome biology and medicine by a specialized knowledgebase. <i>Circulation Research</i> , 2013 , 113, 1043-53	15.7	42
234	Detection of mutations in PCR products from clinical samples by surface plasmon resonance. <i>Journal of Molecular Recognition</i> , 1997 , 10, 7-17	2.6	42
233	The human cardiac and skeletal muscle proteomes defined by transcriptomics and antibody-based profiling. <i>BMC Genomics</i> , 2015 , 16, 475	4.5	41
232	Genetic instability in the 9q22.3 region is a late event in the development of squamous cell carcinoma. <i>Oncogene</i> , 1998 , 17, 1837-43	9.2	40
231	Mapping the Human Proteome Using Antibodies. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1455-1456	7.6	40
230	CSF profiling of the human brain enriched proteome reveals associations of neuromodulin and neurogranin to Alzheimer's disease. <i>Proteomics - Clinical Applications</i> , 2016 , 10, 1242-1253	3.1	40
229	Exploration of high-density protein microarrays for antibody validation and autoimmunity profiling. <i>New Biotechnology</i> , 2016 , 33, 582-92	6.4	39
228	Understanding the Representative Gut Microbiota Dysbiosis in Metformin-Treated Type 2 Diabetes Patients Using Genome-Scale Metabolic Modeling. <i>Frontiers in Physiology</i> , 2018 , 9, 775	4.6	39
227	Neuronal calcium-binding proteins 1/2 localize to dorsal root ganglia and excitatory spinal neurons and are regulated by nerve injury. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, E1149-58	11.5	39

226	Competitive elution of protein A fusion proteins allows specific recovery under mild conditions. <i>FEBS Journal</i> , 1994 , 224, 103-8		39
225	Facilitated in vitro refolding of human recombinant insulin-like growth factor I using a solubilizing fusion partner. <i>Nature Biotechnology</i> , 1991 , 9, 363-6	44.5	39
224	Dynamic changes in HIV-1 quasispecies from azidothymidine (AZT)-treated patients. <i>FASEB Journal</i> , 1992 , 6, 2843-7	0.9	39
223	Discovery of therapeutic agents for prostate cancer using genome-scale metabolic modeling and drug repositioning. <i>EBioMedicine</i> , 2019 , 42, 386-396	8.8	38
222	New Challenges to Study Heterogeneity in Cancer Redox Metabolism. <i>Frontiers in Cell and Developmental Biology</i> , 2017 , 5, 65	5.7	38
221	Expression of human skin-specific genes defined by transcriptomics and antibody-based profiling. <i>Journal of Histochemistry and Cytochemistry</i> , 2015 , 63, 129-41	3.4	38
220	High nuclear RBM3 expression is associated with an improved prognosis in colorectal cancer. <i>Proteomics - Clinical Applications</i> , 2011 , 5, 624-35	3.1	38
219	Structural changes in insulin-like growth factor (IGF) I mutant proteins affecting binding kinetic rates to IGF binding protein 1 and IGF-I receptor. <i>Biochemistry</i> , 1997 , 36, 4108-17	3.2	38
218	The lung-specific proteome defined by integration of transcriptomics and antibody-based profiling. <i>FASEB Journal</i> , 2014 , 28, 5184-96	0.9	37
217	The kidney transcriptome and proteome defined by transcriptomics and antibody-based profiling. <i>PLoS ONE</i> , 2014 , 9, e116125	3.7	37
216	Prognostic and treatment predictive significance of SATB1 and SATB2 expression in pancreatic and periampullary adenocarcinoma. <i>Journal of Translational Medicine</i> , 2014 , 12, 289	8.5	37
215	Generation and validation of affinity reagents on a proteome-wide level. <i>Journal of Molecular Recognition</i> , 2009 , 22, 57-64	2.6	37
214	Different Approaches to Stabilize a Recombinant Fusion Protein. <i>Nature Biotechnology</i> , 1989 , 7, 165-168	44.5	37
213	Affinity proteomic profiling of plasma, cerebrospinal fluid, and brain tissue within multiple sclerosis. <i>Journal of Proteome Research</i> , 2014 , 13, 4607-19	5.6	36
212	Affinity proteomics reveals elevated muscle proteins in plasma of children with cerebral malaria. <i>PLoS Pathogens</i> , 2014 , 10, e1004038	7.6	36
211	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. <i>Nature</i> , 2021 , 590, 649-654	50.4	36
210	Targeting CDK2 overcomes melanoma resistance against BRAF and Hsp90 inhibitors. <i>Molecular Systems Biology</i> , 2018 , 14, e7858	12.2	35
209	Automated magnetic preparation of DNA templates for solid phase sequencing. <i>Electrophoresis</i> , 1992 , 13, 547-51	3.6	35

208	The protein expression profile of ACE2 in human tissues		35
207	TCSBN: a database of tissue and cancer specific biological networks. <i>Nucleic Acids Research</i> , 2018 , 46, D595-D600	20.1	34
206	Antibody performance in western blot applications is context-dependent. <i>Biotechnology Journal</i> , 2014 , 9, 435-45	5.6	34
205	Expression of the global regulator SATB1 is an independent factor of poor prognosis in high grade epithelial ovarian cancer. <i>Journal of Ovarian Research</i> , 2012 , 5, 24	5.5	34
204	Mapping the subcellular protein distribution in three human cell lines. <i>Journal of Proteome Research</i> , 2011 , 10, 3766-77	5.6	34
203	High-throughput protein production--lessons from scaling up from 10 to 288 recombinant proteins per week. <i>Biotechnology Journal</i> , 2009 , 4, 51-7	5.6	34
202	Defining the Human Brain Proteome Using Transcriptomics and Antibody-Based Profiling with a Focus on the Cerebral Cortex. <i>PLoS ONE</i> , 2015 , 10, e0130028	3.7	34
201	Quantification and discovery of sequence determinants of protein-per-mRNA amount in human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8513	12.2	33
200	An engineered affibody molecule with pH-dependent binding to FcRn mediates extended circulatory half-life of a fusion protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 17110-5	11.5	33
199	A community standard format for the representation of protein affinity reagents. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1-10	7.6	33
198	Species-dependent binding of serum albumins to the streptococcal receptor protein G. <i>FEBS Journal</i> , 1990 , 193, 143-8		33
197	Integration of molecular profiles in a longitudinal wellness profiling cohort. <i>Nature Communications</i> , 2020 , 11, 4487	17.4	32
196	Comprehensive analysis of the genome transcriptome and proteome landscapes of three tumor cell lines. <i>Genome Medicine</i> , 2012 , 4, 86	14.4	31
195	Individual and stable autoantibody repertoires in healthy individuals. <i>Autoimmunity</i> , 2019 , 52, 1-11	3	30
194	Plasma profiling reveals three proteins associated to amyotrophic lateral sclerosis. <i>Annals of Clinical and Translational Neurology</i> , 2014 , 1, 544-53	5.3	30
193	Creation of an antibody-based subcellular protein atlas. <i>Proteomics</i> , 2010 , 10, 3984-96	4.8	30
192	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020 , 36, 2636-2642	7.2	29
191	Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. <i>EBioMedicine</i> , 2019 , 40, 471-487	8.8	29

190	A Systematic Investigation of the Malignant Functions and Diagnostic Potential of the Cancer Secretome. <i>Cell Reports</i> , 2019 , 26, 2622-2635.e5	10.6	28
189	Immunocapture strategies in translational proteomics. <i>Expert Review of Proteomics</i> , 2016 , 13, 83-98	4.2	28
188	Systems biology based drug repositioning for development of cancer therapy. <i>Seminars in Cancer Biology</i> , 2021 , 68, 47-58	12.7	28
187	Secretagogin is expressed in sensory CGRP neurons and in spinal cord of mouse and complements other calcium-binding proteins, with a note on rat and human. <i>Molecular Pain</i> , 2012 , 8, 80	3.4	27
186	Single-step trypsin cleavage of a fusion protein to obtain human insulin and its C peptide. <i>FEBS Journal</i> , 1996 , 236, 656-61		27
185	Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder. <i>Molecular Systems Biology</i> , 2020 , 16, e9469	12.2	27
184	PDGFB, a new candidate plasma biomarker for venous thromboembolism: results from the VEREMA affinity proteomics study. <i>Blood</i> , 2016 , 128, e59-e66	2.2	27
183	Novel Multiomics Profiling of Human Carotid Atherosclerotic Plaques and Plasma Reveals Biliverdin Reductase B as a Marker of Intraplaque Hemorrhage. <i>JACC Basic To Translational Science</i> , 2018 , 3, 464-480	8.7	27
182	Multiplexed analysis of the secretin-like GPCR-RAMP interactome. <i>Science Advances</i> , 2019 , 5, eaaw2778	14.3	26
181	High expression of RNA-binding motif protein 3 in esophageal and gastric adenocarcinoma correlates with intestinal metaplasia-associated tumours and independently predicts a reduced risk of recurrence and death. <i>Biomarker Research</i> , 2014 , 2, 11	8	26
180	Systematic validation of antibody binding and protein subcellular localization using siRNA and confocal microscopy. <i>Journal of Proteomics</i> , 2012 , 75, 2236-51	3.9	26
179	A pilot project to generate affinity reagents to human proteins. <i>Nature Methods</i> , 2008 , 5, 854-5	21.6	26
178	Critical role of somatostatin receptor 2 in the vulnerability of the central noradrenergic system: new aspects on Alzheimer's disease. <i>Acta Neuropathologica</i> , 2015 , 129, 541-63	14.3	25
177	Combination of novel HER2-targeting antibody 1E11 with trastuzumab shows synergistic antitumor activity in HER2-positive gastric cancer. <i>Molecular Oncology</i> , 2015 , 9, 398-408	7.9	24
176	High levels of WNT-5A in human glioma correlate with increased presence of tumor-associated microglia/monocytes. <i>Experimental Cell Research</i> , 2015 , 339, 280-8	4.2	23
175	Metabolic Network-Based Identification and Prioritization of Anticancer Targets Based on Expression Data in Hepatocellular Carcinoma. <i>Frontiers in Physiology</i> , 2018 , 9, 916	4.6	23
174	Type 2 diabetes and obesity induce similar transcriptional reprogramming in human myocytes. <i>Genome Medicine</i> , 2017 , 9, 47	14.4	23
173	Antibody-based protein profiling of the human chromosome 21. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M1111.013458	7.6	23

172	Insulin-like growth factors I and II are unable to form and maintain their native disulfides under in vivo redox conditions. <i>FEBS Letters</i> , 1999 , 443, 271-6	3.8	23
171	Surface display on staphylococci: a comparative study. <i>FEBS Letters</i> , 1996 , 390, 327-33	3.8	23
170	Immunoproteomics using polyclonal antibodies and stable isotope-labeled affinity-purified recombinant proteins. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1611-24	7.6	22
169	Elevated levels of circulating CDH5 and FABP1 in association with human drug-induced liver injury. <i>Liver International</i> , 2017 , 37, 132-140	7.9	22
168	Immunogens containing sequences from antigen Pf332 induce Plasmodium falciparum-reactive antibodies which inhibit parasite growth but not cytoadherence. <i>Parasite Immunology</i> , 1995 , 17, 341-52	2.2	22
167	Autoantibody targets in vaccine-associated narcolepsy. <i>Autoimmunity</i> , 2016 , 49, 421-433	3	22
166	Multi-Omic Data Interpretation to Repurpose Subtype Specific Drug Candidates for Breast Cancer. <i>Frontiers in Genetics</i> , 2019 , 10, 420	4.5	21
165	Improved production of a heterologous amylase in <i>Saccharomyces cerevisiae</i> by inverse metabolic engineering. <i>Applied and Environmental Microbiology</i> , 2014 , 80, 5542-50	4.8	20
164	Systems Biology Approaches to Understand the Host-Microbiome Interactions in Neurodegenerative Diseases. <i>Frontiers in Neuroscience</i> , 2020 , 14, 716	5.1	20
163	Analysis of Body-wide Unfractionated Tissue Data to Identify a Core Human Endothelial Transcriptome. <i>Cell Systems</i> , 2016 , 3, 287-301.e3	10.6	20
162	The Human Adrenal Gland Proteome Defined by Transcriptomics and Antibody-Based Profiling. <i>Endocrinology</i> , 2017 , 158, 239-251	4.8	19
161	Profiling post-centrifugation delay of serum and plasma with antibody bead arrays. <i>Journal of Proteomics</i> , 2013 , 95, 46-54	3.9	19
160	Tissue profiling of the mammalian central nervous system using human antibody-based proteomics. <i>Molecular and Cellular Proteomics</i> , 2009 , 8, 1612-22	7.6	19
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24	iNetModels 2.0: an interactive visualization and database of multi-omics data		1
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