Mathias Uhlen

List of Publications by Year in Descending Order

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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.

166 64 29,027 333 h-index g-index citations papers 362 38,509 6.75 9.5 L-index avg, IF ext. citations ext. papers

#	Paper	IF	Citations
333	Genome-wide annotation of protein-coding genes in pig BMC Biology, 2022, 20, 25	7.3	3
332	Circulating proteins reveal prior use of menopausal hormonal therapy and increased risk of breast cancer <i>Translational Oncology</i> , 2022 , 17, 101339	4.9	
331	Multiomics Analysis Reveals the Impact of Microbiota on Host Metabolism in Hepatic Steatosis <i>Advanced Science</i> , 2022 , e2104373	13.6	3
330	Polymorphisms in alpha 7 nicotinic acetylcholine receptor gene, CHRNA7, and its partially duplicated gene, CHRFAM7A, associate with increased inflammatory response in human peripheral mononuclear cells <i>FASEB Journal</i> , 2022 , 36, e22271	0.9	Ο
329	A Gene Co-Expression Network-Based Drug Repositioning Approach Identifies Candidates for Treatment of Hepatocellular Carcinoma <i>Cancers</i> , 2022 , 14,	6.6	1
328	Dynamics of the normal gut microbiota: A longitudinal one-year population study in Sweden <i>Cell Host and Microbe</i> , 2022 ,	23.4	7
327	Anthraquinone derivatives as ADP-competitive inhibitors of liver pyruvate kinase <i>European Journal of Medicinal Chemistry</i> , 2022 , 234, 114270	6.8	O
326	Prediction of drug candidates for clear cell renal cell carcinoma using a systems biology-based drug repositioning approach <i>EBioMedicine</i> , 2022 , 78, 103963	8.8	1
325	Spatiotemporal transcriptomic atlas of mouse organogenesis using DNA nanoball-patterned arrays <i>Cell</i> , 2022 , 185, 1777-1792.e21	56.2	14
324	Annotation of pituitary neuroendocrine tumors with genome-wide expression analysis. <i>Acta Neuropathologica Communications</i> , 2021 , 9, 181	7.3	0
323	Next generation plasma proteome profiling of COVID-19 patients with mild to moderate symptoms. <i>EBioMedicine</i> , 2021 , 74, 103723	8.8	3
322	Combined metabolic activators therapy ameliorates liver fat in nonalcoholic fatty liver disease patients. <i>Molecular Systems Biology</i> , 2021 , 17, e10459	12.2	5
321	A network-based approach reveals the dysregulated transcriptional regulation in non-alcoholic fatty liver disease. <i>IScience</i> , 2021 , 24, 103222	6.1	2
320	Identification of Endothelial Proteins in Plasma Associated With Cardiovascular Risk Factors. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2021 , 41, 2990-3004	9.4	2
319	Revealing the Molecular Mechanisms of Alzheimer's Disease Based on Network Analysis. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	1
318	Systematic analysis of gut microbiome reveals the role of bacterial folate and homocysteine metabolism in Parkinson's disease. <i>Cell Reports</i> , 2021 , 34, 108807	10.6	13
317	Multi-omics approaches for revealing the complexity of cardiovascular disease. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	3

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316	Association of CSF proteins with tau and amyloid levels in asymptomatic 70-year-olds. <i>Alzheimerks Research and Therapy</i> , 2021 , 13, 54	9	2	
315	Revealing the Metabolic Alterations during Biofilm Development of Based on Genome-Scale Metabolic Modeling. <i>Metabolites</i> , 2021 , 11,	5.6	1	
314	Blood protein profiles related to preterm birth and retinopathy of prematurity. <i>Pediatric Research</i> , 2021 ,	3.2	4	
313	iNetModels 2.0: an interactive visualization and database of multi-omics data. <i>Nucleic Acids Research</i> , 2021 , 49, W271-W276	20.1	8	
312	Altered perivascular fibroblast activity precedes ALS disease onset. <i>Nature Medicine</i> , 2021 , 27, 640-646	50.5	19	
311	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	
310	Informing Pharmacokinetic Models With Physiological Data: Oral Population Modeling of L-Serine in Humans. <i>Frontiers in Pharmacology</i> , 2021 , 12, 643179	5.6	О	
309	Integrative transcriptomic analysis of tissue-specific metabolic crosstalk after myocardial infarction. <i>ELife</i> , 2021 , 10,	8.9	6	
308	Next generation plasma proteome profiling to monitor health and disease. <i>Nature Communications</i> , 2021 , 12, 2493	17.4	15	
307	A porcine brain-wide RNA editing landscape. <i>Communications Biology</i> , 2021 , 4, 717	6.7	1	
306	Combined Metabolic Activators Accelerates Recovery in Mild-to-Moderate COVID-19. <i>Advanced Science</i> , 2021 , 8, e2101222	13.6	11	
305	A single-cell type transcriptomics map of human tissues. <i>Science Advances</i> , 2021 , 7,	14.3	69	
304	Disorganization and degeneration of liver sympathetic innervations in nonalcoholic fatty liver disease revealed by 3D imaging. <i>Science Advances</i> , 2021 , 7,	14.3	2	
303	Addressing the heterogeneity in liver diseases using biological networks. <i>Briefings in Bioinformatics</i> , 2021 , 22, 1751-1766	13.4	6	
302	Dramatic changes in blood protein levels during the first week of life in extremely preterm infants. <i>Pediatric Research</i> , 2021 , 89, 604-612	3.2	6	
301	Allergome-wide peptide microarrays enable epitope deconvolution in allergen-specific immunotherapy. <i>Journal of Allergy and Clinical Immunology</i> , 2021 , 147, 1077-1086	11.5	2	
300	Small Bispecific Affinity Proteins for Simultaneous Target Binding and Albumin-Associated Half-Life Extension. <i>Molecular Pharmaceutics</i> , 2021 , 18, 328-337	5.6	О	
299	Longitudinal plasma protein profiling of newly diagnosed type 2 diabetes. <i>EBioMedicine</i> , 2021 , 63, 1031	487 .8	6	

298	Systems biology based drug repositioning for development of cancer therapy. <i>Seminars in Cancer Biology</i> , 2021 , 68, 47-58	12.7	28
297	Discovery of Functional Alternatively Spliced Transcripts in Human Cancers. <i>Cancers</i> , 2021 , 13,	6.6	3
296	Inflammation and Apolipoproteins Are Potential Biomarkers for Stratification of Cutaneous Melanoma Patients for Immunotherapy and Targeted Therapy. <i>Cancer Research</i> , 2021 , 81, 2545-2555	10.1	3
295	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics. <i>Nature</i> , 2021 , 590, 649-654	50.4	36
294	Stratification of patients with clear cell renal cell carcinoma to facilitate drug repositioning. <i>IScience</i> , 2021 , 24, 102722	6.1	2
293	Secretome screening reveals immunomodulating functions of IFNET, PAP and GDF-7 on regulatory T-cells. <i>Scientific Reports</i> , 2021 , 11, 16767	4.9	0
292	Systems Analysis Reveals Ageing-Related Perturbations in Retinoids and Sex Hormones in Alzheimer's and Parkinson's Diseases. <i>Biomedicines</i> , 2021 , 9,	4.8	2
291	Targeted proteomics analysis of plasma proteins using recombinant protein standards for addition only workflows. <i>BioTechniques</i> , 2021 , 71, 473-483	2.5	2
2 90	Immunoglobulin A Autoreactivity toward Brain Enriched and Apoptosis-Regulating Proteins in Saliva of Athletes after Acute Concussion and Subconcussive Impacts. <i>Journal of Neurotrauma</i> , 2021 , 38, 2373-2383	5.4	1
289	High throughput generation of a resource of the human secretome in mammalian cells. <i>New Biotechnology</i> , 2020 , 58, 45-54	6.4	7
288	Spatial Characterization of the Human Centrosome Proteome Opens Up New Horizons for a Small but Versatile Organelle. <i>Proteomics</i> , 2020 , 20, e1900361	4.8	2
287	An atlas of the protein-coding genes in the human, pig, and mouse brain. <i>Science</i> , 2020 , 367,	33.3	130
286	An atlas of human metabolism. Science Signaling, 2020, 13,	8.8	78
285	Genome-Scale Metabolic Modeling of Glioblastoma Reveals Promising Targets for Drug Development. <i>Frontiers in Genetics</i> , 2020 , 11, 381	4.5	8
284	Proximity Ligation Assay as a Tool for Antibody Validation in Human Tissues. <i>Journal of Histochemistry and Cytochemistry</i> , 2020 , 68, 515-529	3.4	5
283	Whole-genome sequence association analysis of blood proteins in a longitudinal wellness cohort. <i>Genome Medicine</i> , 2020 , 12, 53	14.4	12
282	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020 , 36, 2636-2642	7.2	29
281	Expression and regulation of FRMD6 in mouse DRG neurons and spinal cord after nerve injury. <i>Scientific Reports</i> , 2020 , 10, 1880	4.9	3

280	Classification of clear cell renal cell carcinoma based on alternative splicing. Heliyon, 2020, 6, e03440	3.6	3
279	The acute effect of metabolic cofactor supplementation: a potential therapeutic strategy against non-alcoholic fatty liver disease. <i>Molecular Systems Biology</i> , 2020 , 16, e9495	12.2	16
278	Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder. <i>Molecular Systems Biology</i> , 2020 , 16, e9469	12.2	27
277	Profiles of histidine-rich glycoprotein associate with age and risk of all-cause mortality. <i>Life Science Alliance</i> , 2020 , 3,	5.8	3
276	A systems biology approach for studying neurodegenerative diseases. <i>Drug Discovery Today</i> , 2020 , 25, 1146-1159	8.8	8
275	Applications of Genome-Wide Screening and Systems Biology Approaches in Drug Repositioning. <i>Cancers</i> , 2020 , 12,	6.6	8
274	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301	17.4	59
273	Facets of individual-specific health signatures determined from longitudinal plasma proteome profiling. <i>EBioMedicine</i> , 2020 , 57, 102854	8.8	13
272	Improvements of a high-throughput protein purification process using a calcium-dependent setup. <i>Protein Expression and Purification</i> , 2020 , 175, 105698	2	5
271	Enhanced Validation of Antibodies Enables the Discovery of Missing Proteins. <i>Journal of Proteome Research</i> , 2020 , 19, 4766-4781	5.6	8
270	Systems Biology Approaches to Understand the Host-Microbiome Interactions in Neurodegenerative Diseases. <i>Frontiers in Neuroscience</i> , 2020 , 14, 716	5.1	20
269	Human Immune System Variation during 1 Year. <i>Cell Reports</i> , 2020 , 32, 107923	10.6	11
268	Longitudinal Plasma Protein Profiling Using Targeted Proteomics and Recombinant Protein Standards. <i>Journal of Proteome Research</i> , 2020 , 19, 4815-4825	5.6	4
267	Integration of molecular profiles in a longitudinal wellness profiling cohort. <i>Nature Communications</i> , 2020 , 11, 4487	17.4	32
266	The protein expression profile of ACE2 in human tissues. <i>Molecular Systems Biology</i> , 2020 , 16, e9610	12.2	405
265	Cerebrospinal Fluid Levels of Kininogen-1 Indicate Early Cognitive Impairment in Parkinson's Disease. <i>Movement Disorders</i> , 2020 , 35, 2101-2106	7	4
264	Improvement in the Current Therapies for Hepatocellular Carcinoma Using a Systems Medicine Approach. <i>Advanced Biology</i> , 2020 , 4, e2000030	3.5	6
263	Multiplexed analysis of the secretin-like GPCR-RAMP interactome. <i>Science Advances</i> , 2019 , 5, eaaw2778	B 14.3	26

262	Chromophore pre-maturation for improved speed and sensitivity of split-GFP monitoring of protein secretion. <i>Scientific Reports</i> , 2019 , 9, 310	4.9	3
261	Screening a Resource of Recombinant Protein Fragments for Targeted Proteomics. <i>Journal of Proteome Research</i> , 2019 , 18, 2706-2718	5.6	14
260	Multi-Omic Data Interpretation to Repurpose Subtype Specific Drug Candidates for Breast Cancer. <i>Frontiers in Genetics</i> , 2019 , 10, 420	4.5	21
259	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
258	Quantification and discovery of sequence determinants of protein-per-mRNA amount in 29 human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8513	12.2	33
257	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
256	Individual and stable autoantibody repertoires in healthy individuals. <i>Autoimmunity</i> , 2019 , 52, 1-11	3	30
255	Cell Type-Specific Expression of Testis Elevated Genes Based on Transcriptomics and Antibody-Based Proteomics. <i>Journal of Proteome Research</i> , 2019 , 18, 4215-4230	5.6	15
254	The Potential Use of Metabolic Cofactors in Treatment of NAFLD. <i>Nutrients</i> , 2019 , 11,	6.7	18
253	Systematic Development of Sandwich Immunoassays for the Plasma Secretome. <i>Proteomics</i> , 2019 , 19, e1900008	4.8	6
252	Single-cell RNA-seq variant analysis for exploration of genetic heterogeneity in cancer. <i>Scientific Reports</i> , 2019 , 9, 9524	4.9	15
251	Systems biology perspective for studying the gut microbiota in human physiology and liver diseases. <i>EBioMedicine</i> , 2019 , 49, 364-373	8.8	13
250	A Systems-Based Map of Human Brain Cell-Type Enriched Genes and Malignancy-Associated Endothelial Changes. <i>Cell Reports</i> , 2019 , 29, 1690-1706.e4	10.6	10
249	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues. <i>Molecular Systems Biology</i> , 2019 , 15, e8503	12.2	235
248	Absolute Quantification of Apolipoproteins Following Treatment with Omega-3 Carboxylic Acids and Fenofibrate Using a High Precision Stable Isotope-labeled Recombinant Protein Fragments Based SRM Assay. <i>Molecular and Cellular Proteomics</i> , 2019 , 18, 2433-2446	7.6	8
247	A genome-wide transcriptomic analysis of protein-coding genes in human blood cells. <i>Science</i> , 2019 , 366,	33.3	131
246	The human secretome. <i>Science Signaling</i> , 2019 , 12,	8.8	99
245	Phenotypic Screen with the Human Secretome Identifies FGF16 as Inducing Proliferation of iPSC-Derived Cardiac Progenitor Cells. <i>International Journal of Molecular Sciences</i> , 2019 , 20,	6.3	9

(2018-2019)

244	Characterization of heterogeneous redox responses in hepatocellular carcinoma patients using network analysis. <i>EBioMedicine</i> , 2019 , 40, 471-487	8.8	29
243	Pyruvate kinase L/R is a regulator of lipid metabolism and mitochondrial function. <i>Metabolic Engineering</i> , 2019 , 52, 263-272	9.7	17
242	Discovery of KIRREL as a biomarker for prognostic stratification of patients with thin melanoma. <i>Biomarker Research</i> , 2019 , 7, 1	8	13
241	Targeting CDK2 overcomes melanoma resistance against BRAF and Hsp90 inhibitors. <i>Molecular Systems Biology</i> , 2018 , 14, e7858	12.2	35
240	Systems biology in hepatology: approaches and applications. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2018 , 15, 365-377	24.2	70
239	Mining the Human Tissue Proteome for Protein Citrullination. <i>Molecular and Cellular Proteomics</i> , 2018 , 17, 1378-1391	7.6	51
238	Broad Views of Non-alcoholic Fatty Liver Disease. <i>Cell Systems</i> , 2018 , 6, 7-9	10.6	8
237	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
236	How many human proteoforms are there?. Nature Chemical Biology, 2018, 14, 206-214	11.7	324
235	TCSBN: a database of tissue and cancer specific biological networks. <i>Nucleic Acids Research</i> , 2018 , 46, D595-D600	20.1	34
234	In situ protein detection with enhanced specificity using DNA-conjugated antibodies and proximity ligation. <i>Modern Pathology</i> , 2018 , 31, 253-263	9.8	11
233	Drug Repositioning for Effective Prostate Cancer Treatment. Frontiers in Physiology, 2018 , 9, 500	4.6	43
232	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
231	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
230	Ca2+-binding protein NECAB2 facilitates inflammatory pain hypersensitivity. <i>Journal of Clinical Investigation</i> , 2018 , 128, 3757-3768	15.9	9
229	Translational study reveals a two-faced role of RBM3 in pancreatic cancer and suggests its potential value as a biomarker for improved patient stratification. <i>Oncotarget</i> , 2018 , 9, 6188-6200	3.3	9
228	Transcriptome profiling of the interconnection of pathways involved in malignant transformation and response to hypoxia. <i>Oncotarget</i> , 2018 , 9, 19730-19744	3.3	0
227	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

226	A systems-approach reveals human nestin is an endothelial-enriched, angiogenesis-independent intermediate filament protein. <i>Scientific Reports</i> , 2018 , 8, 14668	4.9	10
225	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
224	Integration of Transcriptomics and Antibody-Based Proteomics for Exploration of Proteins Expressed in Specialized Tissues. <i>Journal of Proteome Research</i> , 2018 , 17, 4127-4137	5.6	11
223	Enhanced validation of antibodies for research applications. <i>Nature Communications</i> , 2018 , 9, 4130	17.4	48
222	ESS: A Tool for Genome-Scale Quantification of Essentiality Score for Reaction/Genes in Constraint-Based Modeling. <i>Frontiers in Physiology</i> , 2018 , 9, 1355	4.6	8
221	Novel Multiomics Profiling of Human Carotid Atherosclerotic Plaques and Plasma Reveals Biliverdin Reductase B as Marker of Intraplaque Hemorrhage. <i>JACC Basic To Translational Science</i> , 2018 , 3, 464-4	4 80 7	27
220	Surface Display of Small Affinity Proteins on Synechocystis sp. Strain PCC 6803 Mediated by Fusion to the Major Type IV Pilin PilA1. <i>Journal of Bacteriology</i> , 2018 , 200,	3.5	7
219	A systematic search strategy identifies cubilin as independent prognostic marker for renal cell carcinoma. <i>BMC Cancer</i> , 2017 , 17, 9	4.8	17
218	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
217	FZD-GB ignalling axis points to a role of FZD in CNS angiogenesis. <i>Cellular Signalling</i> , 2017 , 32, 93-103	4.9	18
216	Response to: Should we ignore western blots when selecting antibodies for other applications?. <i>Nature Methods</i> , 2017 , 14, 215-216	21.6	10
215	Personal model-assisted identification of NAD and lalutathione metabolism as intervention target in NAFLD. <i>Molecular Systems Biology</i> , 2017 , 13, 916	12.2	92
214	The Human Adrenal Gland Proteome Defined by Transcriptomics and Antibody-Based Profiling. <i>Endocrinology</i> , 2017 , 158, 239-251	4.8	19
213	Machine learning in computational biology to accelerate high-throughput protein expression. <i>Bioinformatics</i> , 2017 , 33, 2487-2495	7.2	6
212	Affinity Proteomics Exploration of Melanoma Identifies Proteins in Serum with Associations to T-Stage and Recurrence. <i>Translational Oncology</i> , 2017 , 10, 385-395	4.9	7
211	A subcellular map of the human proteome. <i>Science</i> , 2017 , 356,	33.3	1183
210	Network analyses identify liver-specific targets for treating liver diseases. <i>Molecular Systems Biology</i> , 2017 , 13, 938	12.2	71
209	Human protein secretory pathway genes are expressed in a tissue-specific pattern to match processing demands of the secretome. <i>Npj Systems Biology and Applications</i> , 2017 , 3, 22	5	18

(2016-2017)

208	Improving the economics of NASH/NAFLD treatment through the use of systems biology. <i>Drug Discovery Today</i> , 2017 , 22, 1532-1538	8.8	16
207	A pathology atlas of the human cancer transcriptome. <i>Science</i> , 2017 , 357,	33.3	1481
206	Type 2 diabetes and obesity induce similar transcriptional reprogramming in human myocytes. <i>Genome Medicine</i> , 2017 , 9, 47	14.4	23
205	Antibody Validation in Bioimaging Applications Based on Endogenous Expression of Tagged Proteins. <i>Journal of Proteome Research</i> , 2017 , 16, 147-155	5.6	14
204	Affibody Scaffolds Improve Sesquiterpene Production in Saccharomyces cerevisiae. <i>ACS Synthetic Biology</i> , 2017 , 6, 19-28	5.7	43
203	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
202	Identification of a Novel Autoimmune Peptide Epitope of Prostein in Prostate Cancer. <i>Journal of Proteome Research</i> , 2017 , 16, 204-216	5.6	14
201	Flow-cytometric screening of aggregation-inhibitors using a fluorescence-assisted intracellular method. <i>Biotechnology Journal</i> , 2017 , 12, 1600364	5.6	1
200	New Challenges to Study Heterogeneity in Cancer Redox Metabolism. <i>Frontiers in Cell and Developmental Biology</i> , 2017 , 5, 65	5.7	38
199	A novel RNA sequencing data analysis method for cell line authentication. <i>PLoS ONE</i> , 2017 , 12, e01714.	35 _{3.7}	18
198	Elevated levels of FN1 and CCL2 in bronchoalveolar lavage fluid from sarcoidosis patients. <i>Respiratory Research</i> , 2016 , 17, 69	7.3	5
197	Liver: Phenotypic and genetic variance: a systems approach to the liver. <i>Nature Reviews Gastroenterology and Hepatology</i> , 2016 , 13, 439-40	24.2	6
196	Integrated Network Analysis Reveals an Association between Plasma Mannose Levels and Insulin Resistance. <i>Cell Metabolism</i> , 2016 , 24, 172-84	24.6	105
195	Exploration of high-density protein microarrays for antibody validation and autoimmunity profiling. <i>New Biotechnology</i> , 2016 , 33, 582-92	6.4	39
194	Immunocapture strategies in translational proteomics. Expert Review of Proteomics, 2016, 13, 83-98	4.2	28
193	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
192	Comparative anatomical distribution of neuronal calcium-binding protein (NECAB) 1 and -2 in rodent and human spinal cord. <i>Brain Structure and Function</i> , 2016 , 221, 3803-23	4	12
191	Exploring the role of neuropeptide S in the regulation of arousal: a functional anatomical study. Brain Structure and Function, 2016 , 221, 3521-46	4	13

190	Profiling cancer testis antigens in non-small-cell lung cancer. JCI Insight, 2016, 1, e86837	9.9	65
189	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
188	Transcriptomics resources of human tissues and organs. <i>Molecular Systems Biology</i> , 2016 , 12, 862	12.2	95
187	Gene-specific correlation of RNA and protein levels in human cells and tissues. <i>Molecular Systems Biology</i> , 2016 , 12, 883	12.2	230
186	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
185	Stratification of responders towards eculizumab using a structural epitope mapping strategy. <i>Scientific Reports</i> , 2016 , 6, 31365	4.9	11
184	Autoantibody targets in vaccine-associated narcolepsy. <i>Autoimmunity</i> , 2016 , 49, 421-433	3	22
183	Multiplexed protein profiling by sequential affinity capture. <i>Proteomics</i> , 2016 , 16, 1251-6	4.8	6
182	A proposal for validation of antibodies. <i>Nature Methods</i> , 2016 , 13, 823-7	21.6	312
181	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
180	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
179	Affinity proteomics discovers decreased levels of AMFR in plasma from Osteoporosis patients. <i>Proteomics - Clinical Applications</i> , 2016 , 10, 681-90	3.1	7
178	Proteomics. Tissue-based map of the human proteome. <i>Science</i> , 2015 , 347, 1260419	33.3	6576
177	Loss of ASRGL1 expression is an independent biomarker for disease-specific survival in endometrioid endometrial carcinoma. <i>Gynecologic Oncology</i> , 2015 , 137, 529-37	4.9	17
176	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
175	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
174	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
173	The human cardiac and skeletal muscle proteomes defined by transcriptomics and antibody-based profiling. <i>BMC Genomics</i> , 2015 , 16, 475	4.5	41

(2014-2015)

172	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
171	Genetic and nutrient modulation of acetyl-CoA levels in Synechocystis for n-butanol production. <i>Microbial Cell Factories</i> , 2015 , 14, 167	6.4	76
170	Heat differentiated complement factor profiling. <i>Journal of Proteomics</i> , 2015 , 126, 155-62	3.9	9
169	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
168	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
167	Neuropeptide S- and Neuropeptide S receptor-expressing neuron populations in the human pons. <i>Frontiers in Neuroanatomy</i> , 2015 , 9, 126	3.6	17
166	Schip1 is a novel podocyte foot process protein that mediates actin cytoskeleton rearrangements and forms a complex with Nherf2 and ezrin. <i>PLoS ONE</i> , 2015 , 10, e0122067	3.7	12
165	The Urinary Bladder Transcriptome and Proteome Defined by Transcriptomics and Antibody-Based Profiling. <i>PLoS ONE</i> , 2015 , 10, e0145301	3.7	18
164	Overexpression of functional human oxidosqualene cyclase in Escherichia coli. <i>Protein Expression and Purification</i> , 2015 , 115, 46-53	2	7
163	Dissecting antibodies with regards to linear and conformational epitopes. <i>PLoS ONE</i> , 2015 , 10, e01216	73 3.7	56
162	Expression of human skin-specific genes defined by transcriptomics and antibody-based profiling. Journal of Histochemistry and Cytochemistry, 2015 , 63, 129-41	3.4	38
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19	Mapping the nucleolar proteome reveals a spatiotemporal organization related to intrinsic protein disorder	1
18	Facets of individual-specific health signatures determined from longitudinal plasma proteome profiling	2
17	The protein expression profile of ACE2 in human tissues	35
16	Combined Metabolic Activators accelerates recovery in mild-to-moderate COVID-19	7
15	Integrative transcriptomic analysis of tissue-specific metabolic crosstalk after myocardial infarction	1
14	A deep proteome and transcriptome abundance atlas of 29 healthy human tissues	1
13	Profiles of circulating histidine-rich glycoprotein associate with chronological age and risk of all-cause mortality	2
12	The human secretome Ithe proteins secreted from human cells	6
11	Spatiotemporal dissection of the cell cycle with single-cell proteogenomics	3

10	Multiplexed Analysis of the Secretin-like GPCR-RAMP Interactome	3
9	iNetModels 2.0: an interactive visualization and database of multi-omics data	1
8	RMetD2: a tool for integration of relative transcriptomics data into Genome-scale metabolic models	1
7	Global and temporal state of the human gut microbiome in health and disease	2
6	Multi-omics analysis reveals the impact of microbiota on host metabolism in hepatic steatosis	1
5	Combined Metabolic Activators Reduces Liver Fat in Nonalcoholic Fatty Liver Disease Patients	2
4	Next generation plasma proteome profiling of COVID-19 patients with mild to moderate symptoms	1
3	Systems analysis reveals ageing-related perturbations in retinoids and sex hormones in Alzheimer and Parkinson diseases	1
2	Combined Metabolic Activators Improves Cognitive Functions in Alzheimer∄ Disease	2
1	Combined Metabolic Activators Improve Cognitive Functions without Altering Motor Scores in Parkinson Disease	1