

Gil Omenn

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.

380
papers

22,661
citations

66
h-index

141
g-index

470
ext. papers

26,258
ext. citations

10.6
avg. IF

6.54
L-index

#	Paper	IF	Citations
380	Distinguishing Admissions Specifically for COVID-19 from Incidental SARS-CoV-2 Admissions: A National EHR Research Consortium Study. 2022 ,		2
379	Personal Dense Dynamic Data Clouds Connect Systems Biomedicine to Scientific Wellness.. <i>Methods in Molecular Biology</i> , 2022 , 2486, 315-334	1.4	
378	Distinguishing Admissions Specifically for COVID-19 From Incidental SARS-CoV-2 Admissions: National Retrospective Electronic Health Record Study.. <i>Journal of Medical Internet Research</i> , 2022 , 24, e37931	7.6	4
377	Functional organization of the maternal and paternal human 4D Nucleome. <i>IScience</i> , 2021 , 24, 103452	6.1	4
376	Advances and Utility of the Human Plasma Proteome. <i>Journal of Proteome Research</i> , 2021 , 20, 5241-5263	3.6	16
375	Multinational characterization of neurological phenotypes in patients hospitalized with COVID-19. <i>Scientific Reports</i> , 2021 , 11, 20238	4.9	3
374	Progress Identifying and Analyzing the Human Proteome: 2021 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021 , 20, 5227-5240	5.6	7
373	International Comparisons of Harmonized Laboratory Value Trajectories to Predict Severe COVID-19: Leveraging the 4CE Collaborative Across 342 Hospitals and 6 Countries: A Retrospective Cohort Study 2021 ,		9
372	What Every Reader Should Know About Studies Using Electronic Health Record Data but May Be Afraid to Ask. <i>Journal of Medical Internet Research</i> , 2021 , 23, e22219	7.6	13
371	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021 , 39, 509-528	8.20	71
370	Validation of an internationally derived patient severity phenotype to support COVID-19 analytics from electronic health record data. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2021 , 28, 1411-1420	8.6	15
369	DUOX2 variants associate with preclinical disturbances in microbiota-immune homeostasis and increased inflammatory bowel disease risk. <i>Journal of Clinical Investigation</i> , 2021 , 131,	15.9	6
368	International Changes in COVID-19 Clinical Trajectories Across 315 Hospitals and 6 Countries: Retrospective Cohort Study. <i>Journal of Medical Internet Research</i> , 2021 , 23, e31400	7.6	2
367	International Analysis of Electronic Health Records of Children and Youth Hospitalized With COVID-19 Infection in 6 Countries. <i>JAMA Network Open</i> , 2021 , 4, e2112596	10.4	12
366	Identification of 13 Guanidinobenzoyl- or Aminidinobenzoyl-Containing Drugs to Potentially Inhibit TMPRSS2 for COVID-19 Treatment. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	2
365	IsoResolve: predicting splice isoform functions by integrating gene and isoform-level features with domain adaptation. <i>Bioinformatics</i> , 2021 , 37, 522-530	7.2	1
364	Multinational Prevalence of Neurological Phenotypes in Patients Hospitalized with COVID-19 2021 ,		3

363	Functions of Essential Genes and a Scale-Free Protein Interaction Network Revealed by Structure-Based Function and Interaction Prediction for a Minimal Genome. <i>Journal of Proteome Research</i> , 2021 , 20, 1178-1189	5.6	7
362	Ethical Principles, Constraints and Opportunities in Clinical Proteomics. <i>Molecular and Cellular Proteomics</i> , 2021 , 100046	7.6	15
361	Reflections on the HUPO Human Proteome Project, the Flagship Project of the Human Proteome Organization, at 10 Years. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100062	7.6	6
360	Integrative functional genomic analysis of intron retention in human and mouse brain with Alzheimer's disease. <i>Alzheimer's and Dementia</i> , 2021 , 17, 984-1004	1.2	9
359	Proteogenomic insights into the biology and treatment of HPV-negative head and neck squamous cell carcinoma. <i>Cancer Cell</i> , 2021 , 39, 361-379.e16	24.3	50
358	A proteogenomic portrait of lung squamous cell carcinoma. <i>Cell</i> , 2021 , 184, 4348-4371.e40	56.2	15
357	Proteogenomic characterization of pancreatic ductal adenocarcinoma. <i>Cell</i> , 2021 , 184, 5031-5052.e26	56.2	26
356	Insights from the First Phosphopeptide Challenge of the MS Resource Pillar of the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020 , 19, 4754-4765	5.6	4
355	Longitudinal analysis reveals transition barriers between dominant ecological states in the gut microbiome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 13839-13845	11.5	13
354	The role of the histone H3 variant CENPA in prostate cancer. <i>Journal of Biological Chemistry</i> , 2020 , 295, 8537-8549	5.4	23
353	CIDO, a community-based ontology for coronavirus disease knowledge and data integration, sharing, and analysis. <i>Scientific Data</i> , 2020 , 7, 181	8.2	41
352	Cellular, transcriptomic and isoform heterogeneity of breast cancer cell line revealed by full-length single-cell RNA sequencing. <i>Computational and Structural Biotechnology Journal</i> , 2020 , 18, 676-685	6.8	16
351	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020 , 182, 200-225.e35	56.2	139
350	Proteogenomic Characterization of Endometrial Carcinoma. <i>Cell</i> , 2020 , 180, 729-748.e26	56.2	122
349	Untargeted longitudinal analysis of a wellness cohort identifies markers of metastatic cancer years prior to diagnosis. <i>Scientific Reports</i> , 2020 , 10, 16275	4.9	4
348	Measurement of Organ-Specific and Acute-Phase Blood Protein Levels in Early Lyme Disease. <i>Journal of Proteome Research</i> , 2020 , 19, 346-359	5.6	8
347	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301	17.4	59
346	Identifying the Zoonotic Origin of SARS-CoV-2 by Modeling the Binding Affinity between the Spike Receptor-Binding Domain and Host ACE2. <i>Journal of Proteome Research</i> , 2020 , 19, 4844-4856	5.6	15

345	ClusterMine: A knowledge-integrated clustering approach based on expression profiles of gene sets. <i>Journal of Bioinformatics and Computational Biology</i> , 2020 , 18, 2040009	1	1
344	International electronic health record-derived COVID-19 clinical course profiles: the 4CE consortium. <i>Npj Digital Medicine</i> , 2020 , 3, 109	15.7	61
343	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020 , 19, 4735-4746	5.6	25
342	Multimic blood correlates of genetic risk identify presymptomatic disease alterations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 21813-21820	11.5	9
341	Improving Health Risk Assessment as a Basis for Public Health Decisions in the 21st Century. <i>Risk Analysis</i> , 2020 , 40, 2272-2299	3.9	1
340	Blood metabolome predicts gut microbiome diversity in humans. <i>Nature Biotechnology</i> , 2019 , 37, 1217-1223	14.3	95
339	Mass Spectrometry-Based Plasma Proteomics: Considerations from Sample Collection to Achieving Translational Data. <i>Journal of Proteome Research</i> , 2019 , 18, 4085-4097	5.6	56
338	Genetic Predisposition Impacts Clinical Changes in a Lifestyle Coaching Program. <i>Scientific Reports</i> , 2019 , 9, 6805	4.9	25
337	Progress on Identifying and Characterizing the Human Proteome: 2019 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2019 , 18, 4098-4107	5.6	32
336	Blinded Testing of Function Annotation for uPE1 Proteins by I-TASSER/COFACTOR Pipeline Using the 2018-2019 Additions to neXtProt and the CAF3 Challenge. <i>Journal of Proteome Research</i> , 2019 , 18, 4154-4166	5.6	12
335	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. <i>Journal of Proteome Research</i> , 2019 , 18, 4108-4116	5.6	37
334	Integrated Proteogenomic Characterization of Clear Cell Renal Cell Carcinoma. <i>Cell</i> , 2019 , 179, 964-983.e31	31.1	173
333	Multi-Omic Biological Age Estimation and Its Correlation With Wellness and Disease Phenotypes: A Longitudinal Study of 3,558 Individuals. <i>Journals of Gerontology - Series A Biological Sciences and Medical Sciences</i> , 2019 , 74, S52-S60	6.4	16
332	Accurate prediction of personalized olfactory perception from large-scale chemoinformatic features. <i>GigaScience</i> , 2018 , 7,	7.6	20
331	Reply to "Precision medicine in the clouds". <i>Nature Biotechnology</i> , 2018 , 36, 680-682	44.5	2
330	A similarity-based approach to leverage multi-cohort medical data on the diagnosis and prognosis of Alzheimer's disease. <i>GigaScience</i> , 2018 , 7,	7.6	3
329	Progress on Identifying and Characterizing the Human Proteome: 2018 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2018 , 17, 4031-4041	5.6	46
328	Prioritizing predictive biomarkers for gene essentiality in cancer cells with mRNA expression data and DNA copy number profile. <i>Bioinformatics</i> , 2018 , 34, 3975-3982	7.2	1

327	Structure and Protein Interaction-Based Gene Ontology Annotations Reveal Likely Functions of Uncharacterized Proteins on Human Chromosome 17. <i>Journal of Proteome Research</i> , 2018 , 17, 4186-4196	5.6	20
326	Launching the C-HPP neXt-CP50 Pilot Project for Functional Characterization of Identified Proteins with No Known Function. <i>Journal of Proteome Research</i> , 2018 , 17, 4042-4050	5.6	31
325	Chromosome 17 Missing Proteins: Recent Progress and Future Directions as Part of the neXt-MP50 Challenge. <i>Journal of Proteome Research</i> , 2018 , 17, 4061-4071	5.6	6
324	Nucleome Analysis Reveals Structure-Function Relationships for Colon Cancer. <i>Molecular Cancer Research</i> , 2017 , 15, 821-830	6.6	24
323	Functional proteogenomics reveals biomarkers and therapeutic targets in lymphomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017 , 114, 6581-6586	11.5	18
322	miRmine: a database of human miRNA expression profiles. <i>Bioinformatics</i> , 2017 , 33, 1554-1560	7.2	87
321	Systematic Proteogenomic Approach To Exploring a Novel Function for NHERF1 in Human Reproductive Disorder: Lessons for Exploring Missing Proteins. <i>Journal of Proteome Research</i> , 2017 , 16, 4455-4467	5.6	9
320	Advances in the Chromosome-Centric Human Proteome Project: looking to the future. <i>Expert Review of Proteomics</i> , 2017 , 14, 1059-1071	4.2	21
319	Mapping genetic variations to three-dimensional protein structures to enhance variant interpretation: a proposed framework. <i>Genome Medicine</i> , 2017 , 9, 113	14.4	31
318	Progress on the HUPO Draft Human Proteome: 2017 Metrics of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2017 , 16, 4281-4287	5.6	46
317	The Human Plasma Proteome Draft of 2017: Building on the Human Plasma PeptideAtlas from Mass Spectrometry and Complementary Assays. <i>Journal of Proteome Research</i> , 2017 , 16, 4299-4310	5.6	119
316	A wellness study of 108 individuals using personal, dense, dynamic data clouds. <i>Nature Biotechnology</i> , 2017 , 35, 747-756	44.5	235
315	Rapid molecular assays to study human centromere genomics. <i>Genome Research</i> , 2017 , 27, 2040-2049	9.7	16
314	The proteomes of the human eye, a highly compartmentalized organ. <i>Proteomics</i> , 2017 , 17, 1600340	4.8	4
313	Annotation of Alternatively Spliced Proteins and Transcripts with Protein-Folding Algorithms and Isoform-Level Functional Networks. <i>Methods in Molecular Biology</i> , 2017 , 1558, 415-436	1.4	2
312	Strategies for Genomic and Proteomic Profiling of Cancers. <i>Statistics in Biosciences</i> , 2016 , 8, 1-7	1.5	6
311	Highlights of the Biology and Disease-driven Human Proteome Project, 2015-2016. <i>Journal of Proteome Research</i> , 2016 , 15, 3979-3987	5.6	18
310	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016 , 15, 4091-4100	5.6	16

309	Identification of Organ-Enriched Protein Biomarkers of Acute Liver Injury by Targeted Quantitative Proteomics of Blood in Acetaminophen- and Carbon-Tetrachloride-Treated Mouse Models and Acetaminophen Overdose Patients. <i>Journal of Proteome Research</i> , 2016 , 15, 3724-3740	5.6	18
308	Linking MedDRA(□)-Coded Clinical Phenotypes to Biological Mechanisms by the Ontology of Adverse Events: A Pilot Study on Tyrosine Kinase Inhibitors. <i>Drug Safety</i> , 2016 , 39, 697-707	5.1	19
307	A proteogenomic approach to understand splice isoform functions through sequence and expression-based computational modeling. <i>Briefings in Bioinformatics</i> , 2016 , 17, 1024-1031	13.4	6
306	The Impact of Alternative Payment Models on Oncology Innovation and Patient Care. <i>Clinical Cancer Research</i> , 2016 , 22, 2335-41	12.9	4
305	A Network of Splice Isoforms for the Mouse. <i>Scientific Reports</i> , 2016 , 6, 24507	4.9	14
304	Genome-Wide Functional Annotation of Human Protein-Coding Splice Variants Using Multiple Instance Learning. <i>Journal of Proteome Research</i> , 2016 , 15, 1747-53	5.6	23
303	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016 , 15, 3961-3970	5.6	130
302	Metrics for the Human Proteome Project 2016: Progress on Identifying and Characterizing the Human Proteome, Including Post-Translational Modifications. <i>Journal of Proteome Research</i> , 2016 , 15, 3951-3960	5.6	60
301	MI-PVT: A Tool for Visualizing the Chromosome-Centric Human Proteome. <i>Journal of Proteome Research</i> , 2015 , 14, 3762-7	5.6	3
300	Functional Networks of Highest-Connected Splice Isoforms: From The Chromosome 17 Human Proteome Project. <i>Journal of Proteome Research</i> , 2015 , 14, 3484-91	5.6	26
299	Metrics for the Human Proteome Project 2015: Progress on the Human Proteome and Guidelines for High-Confidence Protein Identification. <i>Journal of Proteome Research</i> , 2015 , 14, 3452-60	5.6	74
298	Computational Inferences of the Functions of Alternative/Noncanonical Splice Isoforms Specific to HER2+/ER-/PR- Breast Cancers, a Chromosome 17 C-HPP Study. <i>Journal of Proteome Research</i> , 2015 , 14, 3519-29	5.6	10
297	State of the Human Proteome in 2014/2015 As Viewed through PeptideAtlas: Enhancing Accuracy and Coverage through the AtlasProphet. <i>Journal of Proteome Research</i> , 2015 , 14, 3461-73	5.6	57
296	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015 , 14, 3415-31	5.6	50
295	Human Endogenous Retrovirus Type K (HERV-K) Particles Package and Transmit HERV-K-Related Sequences. <i>Journal of Virology</i> , 2015 , 89, 7187-201	6.6	30
294	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 495-506	8.6	42
293	Combination of Multiple Spectral Libraries Improves the Current Search Methods Used to Identify Missing Proteins in the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015 , 14, 4959-66	5.6	13
292	Structural Bioinformatics Inspection of neXtProt PE5 Proteins in the Human Proteome. <i>Journal of Proteome Research</i> , 2015 , 14, 3750-61	5.6	11

291	Use of ENCODE resources to characterize novel proteoforms and missing proteins in the human proteome. <i>Journal of Proteome Research</i> , 2015 , 14, 603-8	5.6	16
290	Expansion of a novel endogenous retrovirus throughout the pericentromeres of modern humans. <i>Genome Biology</i> , 2015 , 16, 74	18.3	24
289	MIsoMine: a genome-scale high-resolution data portal of expression, function and networks at the splice isoform level in the mouse. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav045	5	14
288	N-Glycoproteomic Landscape of Human Lymphoid Cancers Reveals Novel Biomarkers and Potential Therapeutic Targets. <i>Blood</i> , 2015 , 126, 697-697	2.2	
287	Epithelial-mesenchymal transition-associated secretory phenotype predicts survival in lung cancer patients. <i>Carcinogenesis</i> , 2014 , 35, 1292-300	4.6	31
286	State of the human proteome in 2013 as viewed through PeptideAtlas: comparing the kidney, urine, and plasma proteomes for the biology- and disease-driven Human Proteome Project. <i>Journal of Proteome Research</i> , 2014 , 13, 60-75	5.6	106
285	Plasma proteomics, the Human Proteome Project, and cancer-associated alternative splice variant proteins. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 866-73	4	15
284	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014 , 32, 223-6	44.5	2053
283	Metrics for the Human Proteome Project 2013-2014 and strategies for finding missing proteins. <i>Journal of Proteome Research</i> , 2014 , 13, 15-20	5.6	113
282	The strategy, organization, and progress of the HUPO Human Proteome Project. <i>Journal of Proteomics</i> , 2014 , 100, 3-7	3.9	38
281	MetDisease--connecting metabolites to diseases via literature. <i>Bioinformatics</i> , 2014 , 30, 2239-41	7.2	17
280	A new class of protein cancer biomarker candidates: differentially expressed splice variants of ERBB2 (HER2/neu) and ERBB1 (EGFR) in breast cancer cell lines. <i>Journal of Proteomics</i> , 2014 , 107, 103-123	3.9	30
279	Distinct splice variants and pathway enrichment in the cell-line models of aggressive human breast cancer subtypes. <i>Journal of Proteome Research</i> , 2014 , 13, 212-27	5.6	30
278	Highlights of B/D-HPP and HPP Resource Pillar Workshops at 12th Annual HUPO World Congress of Proteomics: September 14-18, 2013, Yokohama, Japan. <i>Proteomics</i> , 2014 , 14, 975-88	4.8	13
277	Regulation of the human endogenous retrovirus K (HML-2) transcriptome by the HIV-1 Tat protein. <i>Journal of Virology</i> , 2014 , 88, 8924-35	6.6	46
276	Epigenetics: relevance and implications for public health. <i>Annual Review of Public Health</i> , 2014 , 35, 105-22	6	66
275	The emerging era of genomic data integration for analyzing splice isoform function. <i>Trends in Genetics</i> , 2014 , 30, 340-7	8.5	61
274	Novel bioinformatics method for identification of genome-wide non-canonical spliced regions using RNA-Seq data. <i>PLoS ONE</i> , 2014 , 9, e100864	3.7	10

273	Revisiting the identification of canonical splice isoforms through integration of functional genomics and proteomics evidence. <i>Proteomics</i> , 2014 , 14, 2709-18	4.8	28
272	A chromosome-centric human proteome project (C-HPP) to characterize the sets of proteins encoded in chromosome 17. <i>Journal of Proteome Research</i> , 2013 , 12, 45-57	5.6	31
271	The human eye proteome project. <i>Proteomics</i> , 2013 , 13, 2375-6	4.8	7
270	The biology/disease-driven human proteome project (B/D-HPP): enabling protein research for the life sciences community. <i>Journal of Proteome Research</i> , 2013 , 12, 23-7	5.6	87
269	Innovations in proteomic profiling of cancers: alternative splice variants as a new class of cancer biomarker candidates and bridging of proteomics with structural biology. <i>Journal of Proteomics</i> , 2013 , 90, 28-37	3.9	29
268	Genome wide proteomics of ERBB2 and EGFR and other oncogenic pathways in inflammatory breast cancer. <i>Journal of Proteome Research</i> , 2013 , 12, 2805-17	5.6	30
267	Current perspective on the global and United States cancer burden attributable to lifestyle and environmental risk factors. <i>Annual Review of Public Health</i> , 2013 , 34, 97-117	20.6	74
266	GeneEnvironment Interactions 2013 , 50-59		1
265	Healthcare information technology and economics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013 , 20, 212-7	8.6	26
264	HIV infection reveals widespread expansion of novel centromeric human endogenous retroviruses. <i>Genome Research</i> , 2013 , 23, 1505-13	9.7	51
263	Systematically differentiating functions for alternatively spliced isoforms through integrating RNA-seq data. <i>PLoS Computational Biology</i> , 2013 , 9, e1003314	5	58
262	On best practices: the Institute of Medicine scheme for developing, validating, and demonstrating clinical utility of omics-based diagnostic and predictive tests. <i>Proteomics - Clinical Applications</i> , 2013 , 7, 748-55	3.1	4
261	Evolution and medicine in undergraduate education: a prescription for all biology students. <i>Evolution; International Journal of Organic Evolution</i> , 2012 , 66, 1991-2006	3.8	23
260	Metscape 2 bioinformatics tool for the analysis and visualization of metabolomics and gene expression data. <i>Bioinformatics</i> , 2012 , 28, 373-80	7.2	288
259	Ratcheting up cancer potency estimates. <i>Environmental Science & Technology</i> , 2012 , 46, 2538-44	10.3	1
258	Standard guidelines for the chromosome-centric human proteome project. <i>Journal of Proteome Research</i> , 2012 , 11, 2005-13	5.6	121
257	New and improved proteomics technologies for understanding complex biological systems: addressing a grand challenge in the life sciences. <i>Proteomics</i> , 2012 , 12, 2773-83	4.8	49
256	The human proteome - a scientific opportunity for transforming diagnostics, therapeutics, and healthcare. <i>Clinical Proteomics</i> , 2012 , 9, 6	5	37

255	Bioinformatics for High-Throughput Toxico-Epigenomics Studies 2012 , 569-588		1
254	SRM targeted proteomics in search for biomarkers of HCV-induced progression of fibrosis to cirrhosis in HALT-C patients. <i>Proteomics</i> , 2012 , 12, 1244-52	4.8	25
253	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012 , 30, 221-3	44.5	244
252	Evolutionary molecular medicine. <i>Journal of Molecular Medicine</i> , 2012 , 90, 509-22	5.5	31
251	Metab2MeSH: annotating compounds with medical subject headings. <i>Bioinformatics</i> , 2012 , 28, 1408-10	7.2	27
250	The NIH National Center for Integrative Biomedical Informatics (NCIBI). <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2012 , 19, 166-70	8.6	12
249	Ontology-based combinatorial comparative analysis of adverse events associated with killed and live influenza vaccines. <i>PLoS ONE</i> , 2012 , 7, e49941	3.7	38
248	The HUPO Human Proteome Project (HPP), a Global Health Research Collaboration. <i>Central Asian Journal of Global Health</i> , 2012 , 1, 37	0.8	2
247	Functional implications of structural predictions for alternative splice proteins expressed in Her2/neu-induced breast cancers. <i>Journal of Proteome Research</i> , 2011 , 10, 5503-11	5.6	38
246	Identification of alternatively spliced transcripts using a proteomic informatics approach. <i>Methods in Molecular Biology</i> , 2011 , 696, 319-26	1.4	12
245	Identifying inhibitors of epithelial-mesenchymal transition by connectivity map-based systems approach. <i>Journal of Thoracic Oncology</i> , 2011 , 6, 1784-92	8.9	53
244	A high-confidence human plasma proteome reference set with estimated concentrations in PeptideAtlas. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.006353	7.6	341
243	The human proteome project: current state and future direction. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.009993	7.6	249
242	Enhancing the Teaching of Evolution in Public Health. <i>Evolution: Education and Outreach</i> , 2011 , 4, 567-573	3.6	3
241	Recent Workshops of the HUPO Human Plasma Proteome Project (HPPP): a bridge with the HUPO CardioVascular Initiative and the emergence of SRM targeted proteomics. <i>Proteomics</i> , 2011 , 11, 3439-43	4.8	12
240	The human proteome project: Current state and future direction. <i>Molecular and Cellular Proteomics</i> , 2011 ,	7.6	28
239	Making Credible Scientific Judgments about Important Health and Ecological Risks and Ways to Efficiently Reduce Those Risks. <i>Human and Ecological Risk Assessment (HERA)</i> , 2011 , 17, 800-806	4.9	5
238	Characterization of KRAS rearrangements in metastatic prostate cancer. <i>Cancer Discovery</i> , 2011 , 1, 35-43	24.4	83

237	Data management and data integration in the HUPO plasma proteome project. <i>Methods in Molecular Biology</i> , 2011 , 696, 247-57	1.4	15
236	Preanalytical Variables for Plasma and Serum Proteome Analyses 2011 , 269-289		10
235	Physician-Scientist: Linking Science, Medicine, and Public Policy 2011 , 269-287		
234	Alternative Splice Variants, a New Class of Protein Cancer Biomarker Candidates: Findings in Pancreatic Cancer and Breast Cancer with Systems Biology Implications. <i>Disease Markers</i> , 2010 , 28, 241-251	3.2	46
233	"Topological significance" analysis of gene expression and proteomic profiles from prostate cancer cells reveals key mechanisms of androgen response. <i>PLoS ONE</i> , 2010 , 5, e10936	3.7	29
232	Proteomic characterization of novel alternative splice variant proteins in human epidermal growth factor receptor 2/neu-induced breast cancers. <i>Cancer Research</i> , 2010 , 70, 3440-9	10.1	51
231	ConceptGen: a gene set enrichment and gene set relation mapping tool. <i>Bioinformatics</i> , 2010 , 26, 456-63	7.2	120
230	Quantitative proteomic profiling of prostate cancer reveals a role for miR-128 in prostate cancer. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 298-312	7.6	96
229	Metscape: a Cytoscape plug-in for visualizing and interpreting metabolomic data in the context of human metabolic networks. <i>Bioinformatics</i> , 2010 , 26, 971-3	7.2	148
228	Humoral autoimmunity against the extracellular domain of the neuroendocrine autoantigen IA-2 heightens the risk of type 1 diabetes. <i>Endocrinology</i> , 2010 , 151, 2528-37	4.8	27
227	Evolution in health and medicine Sackler colloquium: Making evolutionary biology a basic science for medicine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107 Suppl 1, 1800-7	11.5	149
226	Evolution in health and medicine Sackler colloquium: Evolution and public health. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107 Suppl 1, 1702-9	11.5	48
225	Bioinformatics and systems biology of cancers. <i>Progress in Molecular Biology and Translational Science</i> , 2010 , 95, 159-91	4	3
224	Multilayer and multimetric quality control: the Supercourse. <i>Journal of Cancer Education</i> , 2010 , 25, 478-83		5
223	WaveletQuant, an improved quantification software based on wavelet signal threshold de-noising for labeled quantitative proteomic analysis. <i>BMC Bioinformatics</i> , 2010 , 11, 219	3.6	16
222	NGSQC: cross-platform quality analysis pipeline for deep sequencing data. <i>BMC Genomics</i> , 2010 , 11 Suppl 4, S7	4.5	78
221	Re: Florian Jentzmik, Carsten Stephan, Kurt Miller, et al. Sarcosine in urine after digital rectal examination fails as a marker in prostate cancer detection and identification of aggressive tumours. <i>Eur Urol</i> 2010;58:12-8. <i>European Urology</i> , 2010 , 58, e29-30; author reply e31-2	10.2	16
220	Alternative splice variants, a new class of protein cancer biomarker candidates: findings in pancreatic cancer and breast cancer with systems biology implications. <i>Disease Markers</i> , 2010 , 28, 241-51	3.2	29

219	A landmark systems analysis of prion disease of the brain. <i>Molecular Systems Biology</i> , 2009 , 5, 254	12.2	2
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18	Integration of Pharmacogenomics into Medical Practice ¹³⁵⁻¹⁶¹		2
17	A study of glycoproteins in human serum and plasma reference standards (HUPO) using multilectin affinity chromatography coupled with RPLC-MS/MS ¹⁵⁹⁻¹⁸⁴		
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