

# Yves A Lussier

## List of Publications by Year in descending order

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190  
papers

6,214  
citations

76326

40  
h-index

82547

72  
g-index

201  
all docs

201  
docs citations

201  
times ranked

8637  
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated Encoding of Clinical Documents Based on Natural Language Processing. Journal of the American Medical Informatics Association: JAMIA, 2004, 11, 392-402.	4.4	430
2	Lung microbiome and disease progression in idiopathic pulmonary fibrosis: an analysis of the COMET study. Lancet Respiratory Medicine, the, 2014, 2, 548-556.	10.7	353
3	Development and Validation of a Brief Version of the Dyadic Adjustment Scale With a Nonparametric Item Analysis Model.. Psychological Assessment, 2005, 17, 15-27.	1.5	329
4	Panmicrobial Oligonucleotide Array for Diagnosis of Infectious Diseases. Emerging Infectious Diseases, 2007, 13, 73-81.	4.3	298
5	MicroRNA Expression Characterizes Oligometastasis(es). PLoS ONE, 2011, 6, e28650.	2.5	242
6	Peripheral Blood Mononuclear Cell Gene Expression Profiles Predict Poor Outcome in Idiopathic Pulmonary Fibrosis. Science Translational Medicine, 2013, 5, 205ra136.	12.4	242
7	Oligo- and Polymetastatic Progression in Lung Metastasis(es) Patients Is Associated with Specific MicroRNAs. PLoS ONE, 2012, 7, e50141.	2.5	181
8	Information theory applied to the sparse gene ontology annotation network to predict novel gene function. Bioinformatics, 2007, 23, i529-i538.	4.1	148
9	Up-regulation of a HOXA-PBX3 homeobox-gene signature following down-regulation of miR-181 is associated with adverse prognosis in patients with cytogenetically abnormal AML. Blood, 2012, 119, 2314-2324.	1.4	145
10	Network Modeling Identifies Molecular Functions Targeted by miR-204 to Suppress Head and Neck Tumor Metastasis. PLoS Computational Biology, 2010, 6, e1000730.	3.2	140
11	Microbes Are Associated with Host Innate Immune Response in Idiopathic Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2017, 196, 208-219.	5.6	130
12	Essential Role of Pre-B-Cell Colony Enhancing Factor in Ventilator-induced Lung Injury. American Journal of Respiratory and Critical Care Medicine, 2008, 178, 605-617.	5.6	111
13	Genomic assessment of a multikinase inhibitor, sorafenib, in a rodent model of pulmonary hypertension. Physiological Genomics, 2008, 33, 278-291.	2.3	100
14	<i>GO-Module</i>: functional synthesis and improved interpretation of Gene Ontology patterns. Bioinformatics, 2011, 27, 1444-1446.	4.1	97
15	Chronic Intestinal Inflammation Induces Stress-Response Genes in Commensal Escherichia coli. Gastroenterology, 2011, 141, 1842-1851.e10.	1.3	81
16	ExprTarget: An Integrative Approach to Predicting Human MicroRNA Targets. PLoS ONE, 2010, 5, e13534.	2.5	80
17	The Emergence of Genome-Based Drug Repositioning. Science Translational Medicine, 2011, 3, 96ps35.	12.4	79
18	Structure bidimensionnelle de l'attachement amoureux: Anxiété face à l'abandon et évitement de l'intimité.. Canadian Journal of Behavioural Science, 2003, 35, 56-60.	0.6	78

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19	Single Sample Expression-Anchored Mechanisms Predict Survival in Head and Neck Cancer. PLoS Computational Biology, 2012, 8, e1002350.	3.2	75
20	MAP17 Is a Necessary Activator of Renal Na <sup>+</sup> /Glucose Cotransporter SGLT2. Journal of the American Society of Nephrology: JASN, 2017, 28, 85-93.	6.1	71
21	Non-Myosin Light Chain Kinase Isoform Is a Viable Molecular Target in Acute Inflammatory Lung Injury. American Journal of Respiratory Cell and Molecular Biology, 2011, 44, 40-52.	2.9	69
22	Disambiguating Ambiguous Biomedical Terms in Biomedical Narrative Text: An Unsupervised Method. Journal of Biomedical Informatics, 2001, 34, 249-261.	4.3	68
23	Identification of Jak-STAT signaling involvement in sarcoidosis severity via a novel microRNA-regulated peripheral blood mononuclear cell gene signature. Scientific Reports, 2017, 7, 4237.	3.3	67
24	Simvastatin Attenuates Radiation-Induced Murine Lung Injury and Dysregulated Lung Gene Expression. American Journal of Respiratory Cell and Molecular Biology, 2011, 44, 415-422.	2.9	62
25	Translational bioinformatics: linking knowledge across biological and clinical realms: Figure 1. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 354-357.	4.4	61
26	Deregulation of a Hox Protein Regulatory Network Spanning Prostate Cancer Initiation and Progression. Clinical Cancer Research, 2012, 18, 4291-4302.	7.0	61
27	GADD45a is a novel candidate gene in inflammatory lung injury via influences on Akt signaling. FASEB Journal, 2009, 23, 1325-1337.	0.5	60
28	Role of sphingolipids in murine radiation-induced lung injury: protection by sphingosine 1-phosphate analogs. FASEB Journal, 2011, 25, 3388-3400.	0.5	57
29	Computational Approaches to Phenotyping: High-Throughput Phenomics. Proceedings of the American Thoracic Society, 2007, 4, 18-25.	3.5	56
30	Murine Lung Responses to Ambient Particulate Matter: Genomic Analysis and Influence on Airway Hyperresponsiveness. Environmental Health Perspectives, 2008, 116, 1500-1508.	6.0	54
31	Does Anger Towards the Partner Mediate and Moderate the Link Between Romantic Attachment and Intimate Violence?. Journal of Family Violence, 2005, 20, 349-361.	3.3	53
32	Variants Affecting Exon Skipping Contribute to Complex Traits. PLoS Genetics, 2012, 8, e1002998.	3.5	53
33	Wnt7a is a novel inducer of $\beta$ 2-catenin-independent tumor-suppressive cellular senescence in lung cancer. Oncogene, 2015, 34, 5317-5328.	5.9	51
34	Genome-Wide Association Study in African Americans with Acute Respiratory Distress Syndrome Identifies the Selectin P Ligand Gene as a Risk Factor. American Journal of Respiratory and Critical Care Medicine, 2018, 197, 1421-1432.	5.6	50
35	Protein interaction network underpins concordant prognosis among heterogeneous breast cancer signatures. Journal of Biomedical Informatics, 2010, 43, 385-396.	4.3	49
36	Early exposure to violence, relationship violence, and relationship satisfaction in adolescents and emerging adults: The role of romantic attachment.. Psychological Trauma: Theory, Research, Practice, and Policy, 2017, 9, 127-137.	2.1	48

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37	The Mitochondrial Cardiolipin Remodeling Enzyme Lysocardiolipin Acyltransferase Is a Novel Target in Pulmonary Fibrosis. American Journal of Respiratory and Critical Care Medicine, 2014, 189, 1402-1415.	5.6	47
38	The discriminatory cost of ICD-10-CM transition between clinical specialties: metrics, case study, and mitigating tools. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 708-717.	4.4	46
39	Use of consomic rats for genomic insights into ventilator-associated lung injury. American Journal of Physiology - Lung Cellular and Molecular Physiology, 2007, 293, L292-L302.	2.9	43
40	Network models of genome-wide association studies uncover the topological centrality of protein interactions in complex diseases. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 619-629.	4.4	43
41	Complex-disease networks of trait-associated single-nucleotide polymorphisms (SNPs) unveiled by information theory. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 295-305.	4.4	42
42	Replication Analysis for Severe Diabetic Retinopathy. , 2012, 53, 2377.		42
43	â€N-of-1- <i>pathways</i> ™ unveils personal deregulated mechanisms from a single pair of RNA-Seq samples: towards precision medicine. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 1015-1025.	4.4	42
44	A functional genomic model for predicting prognosis in idiopathic pulmonary fibrosis. BMC Pulmonary Medicine, 2015, 15, 147.	2.0	42
45	Particulate Matter Induces Cardiac Arrhythmias via Dysregulation of Carotid Body Sensitivity and Cardiac Sodium Channels. American Journal of Respiratory Cell and Molecular Biology, 2012, 46, 524-531.	2.9	40
46	Evidence Suggesting That Discontinuous Dosing of ALK Kinase Inhibitors May Prolong Control of ALK+ Tumors. Cancer Research, 2015, 75, 2916-2927.	0.9	40
47	The effect of ketone bodies on renal ammoniogenesis. Journal of Clinical Investigation, 1971, 50, 1781-1791.	8.2	38
48	Information visualization techniques in bioinformatics during the postgenomic era. Drug Discovery Today Biosilico, 2004, 2, 237-245.	0.7	37
49	Integration of curated databases to identify genotype-phenotype associations. BMC Genomics, 2006, 7, 257.	2.8	37
50	PhenoGO: an integrated resource for the multiscale mining of clinical and biological data. BMC Bioinformatics, 2009, 10, S8.	2.6	32
51	Kinase inhibition-related adverse events predicted from in vitro kinome and clinical trial data. Journal of Biomedical Informatics, 2010, 43, 376-384.	4.3	32
52	Dynamic changes of RNA-sequencing expression for precision medicine: N-of-1-pathways Mahalanobis distance within pathways of single subjects predicts breast cancer survival. Bioinformatics, 2015, 31, i293-i302.	4.1	30
53	The complexity and challenges of the International Classification of Diseases, Ninth Revision, Clinical Modification to International Classification of Diseases, 10th Revision, Clinical Modification transition in EDs. American Journal of Emergency Medicine, 2015, 33, 713-718.	1.6	29
54	N-of-1-pathways MixEnrich: advancing precision medicine via single-subject analysis in discovering dynamic changes of transcriptomes. BMC Medical Genomics, 2017, 10, 27.	1.5	29

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55	An Integrative Genomic Approach to Uncover Molecular Mechanisms of Prokaryotic Traits. PLoS Computational Biology, 2006, 2, e159.	3.2	28
56	Bio-Ontology and text: bridging the modeling gap. Bioinformatics, 2006, 22, 2421-2429.	4.1	28
57	PhenoGO: assigning phenotypic context to gene ontology annotations with natural language processing. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2006, , 64-75.	0.7	28
58	Protein-network modeling of prostate cancer gene signatures reveals essential pathways in disease recurrence. Journal of the American Medical Informatics Association: JAMIA, 2011, 18, 392-402.	4.4	27
59	Physician nurse care: A new use of UMLS to measure professional contribution. International Journal of Medical Informatics, 2018, 113, 63-71.	3.3	27
60	Advantages of genomic complexity: bioinformatics opportunities in microRNA cancer signatures: Figure 1. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 156-160.	4.4	26
61	Rhinovirus Infections in Individuals with Asthma Increase ACE2 Expression and Cytokine Pathways Implicated in COVID-19. American Journal of Respiratory and Critical Care Medicine, 2020, 202, 753-755.	5.6	25
62	Discovery of protein interaction networks shared by diseases. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2007, , 76-87.	0.7	25
63	PHENOGO: ASSIGNING PHENOTYPIC CONTEXT TO GENE ONTOLOGY ANNOTATIONS WITH NATURAL LANGUAGE PROCESSING. , 2005, , .		24
64	Curvilinear associations between neuroticism and dyadic adjustment in treatment-seeking couples.. Journal of Family Psychology, 2013, 27, 232-241.	1.3	24
65	Developing a "personalome"™ for precision medicine: emerging methods that compute interpretable effect sizes from single-subject transcriptomes. Briefings in Bioinformatics, 2019, 20, 789-805.	6.5	24
66	A genome-by-environment interaction classifier for precision medicine: personal transcriptome response to rhinovirus identifies children prone to asthma exacerbations. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 1116-1126.	4.4	23
67	Association of circulating transcriptomic profiles with mortality in sickle cell disease. Blood, 2017, 129, 3009-3016.	1.4	22
68	Comprehensive viral oligonucleotide probe design using conserved protein regions. Nucleic Acids Research, 2008, 36, e3-e3.	14.5	21
69	An Integrated Genomic Approach to the Assessment and Treatment of Acute Myeloid Leukemia. Seminars in Oncology, 2011, 38, 215-224.	2.2	21
70	The Transition to ICD-10-CM: Challenges for Pediatric Practice. Pediatrics, 2014, 134, 31-36.	2.1	21
71	Rethinking the role and impact of health information technology: informatics as an interventional discipline. BMC Medical Informatics and Decision Making, 2016, 16, 40.	3.0	21
72	DISCOVERY OF PROTEIN INTERACTION NETWORKS SHARED BY DISEASES. , 2006, , .		21

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73	Comparative Gastrointestinal Blood Loss Associated with Placebo, Aspirin, and Nabumetone as Assessed by Radiochromium ( <sup>51</sup> Cr). Journal of Clinical Pharmacology, 1989, 29, 225-229.	2.0	19
74	Integrative genomics analyses unveil downstream biological effectors of disease-specific polymorphisms buried in intergenic regions. Npj Genomic Medicine, 2016, 1, .	3.8	19
75	New autosomal recessive mutations in aquaporinâ€² causing nephrogenic diabetes insipidus through deficient targeting display normal expression in <i>Xenopus</i> oocytes. Journal of Physiology, 2010, 588, 2205-2218.	2.9	18
76	Correlates of psychopathic personality traits in community couples. Personality and Mental Health, 2011, 5, 186-199.	1.2	18
77	Translating Mendelian and complex inheritance of Alzheimer's disease genes for predicting unique personal genome variants. Journal of the American Medical Informatics Association: JAMIA, 2012, 19, 306-316.	4.4	18
78	Towards a PBMC âœvirogram assayâ€•for precision medicine: Concordance between ex vivo and in vivo viral infection transcriptomes. Journal of Biomedical Informatics, 2015, 55, 94-103.	4.3	18
79	Differential transcriptomics in sarcoidosis lung and lymph node granulomas with comparisons to pathogen-specific granulomas. Respiratory Research, 2020, 21, 321.	3.6	17
80	Concordance of deregulated mechanisms unveiled in underpowered experiments: PTBP1 knockdown case study. BMC Medical Genomics, 2014, 7, S1.	1.5	16
81	Metrics and tools for consistent cohort discovery and financial analyses post-transition to ICD-10-CM. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 730-737.	4.4	16
82	Terminology model discovery using natural language processing and visualization techniques. Journal of Biomedical Informatics, 2006, 39, 626-636.	4.3	15
83	Breakthroughs in genomics data integration for predicting clinical outcome. Journal of Biomedical Informatics, 2012, 45, 1199-1201.	4.3	15
84	Analysis of aggregated cellâ€•cell statistical distances within pathways unveils therapeutic-resistance mechanisms in circulating tumor cells. Bioinformatics, 2016, 32, i80-i89.	4.1	15
85	kMEn: Analyzing noisy and bidirectional transcriptional pathway responses in single subjects. Journal of Biomedical Informatics, 2017, 66, 32-41.	4.3	15
86	Visualizing information across multidimensional post-genomic structured and textual databases. Bioinformatics, 2005, 21, 1659-1667.	4.1	14
87	Evaluation of high-throughput functional categorization of human disease genes. BMC Bioinformatics, 2007, 8, S7.	2.6	14
88	Challenges and remediation for Patient Safety Indicators in the transition to ICD-10-CM. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 19-28.	4.4	14
89	Topological Analysis of Large-scale Biomedical Terminology Structures. Journal of the American Medical Informatics Association: JAMIA, 2007, 14, 788-797.	4.4	13
90	Identifying Clinically Disruptive International Classification of Diseases 10th Revision Clinical Modification Conversions to Mitigate Financial Costs Using an Online Tool. Journal of Oncology Practice, 2014, 10, 97-103.	2.5	13

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91	Complex genetics of pulmonary diseases: lessons from genome-wide association studies and next-generation sequencing. <i>Translational Research</i> , 2016, 168, 22-39.	5.0	13
92	Testing for differentially expressed genetic pathways with single-subject N-of-1 data in the presence of inter-gene correlation. <i>Statistical Methods in Medical Research</i> , 2018, 27, 3797-3813.	1.5	13
93	Endothelial eNAMPT drives EndMT and preclinical PH: rescue by an eNAMPT-neutralizing mAb. <i>Pulmonary Circulation</i> , 2021, 11, 1-14.	1.7	13
94	People, organizational, and leadership factors impacting informatics support for clinical and translational research. <i>BMC Medical Informatics and Decision Making</i> , 2013, 13, 20.	3.0	12
95	Comparison and impact of COVID-19 for patients with cancer: a survival analysis of fatality rate controlling for age, sex and cancer type. <i>BMJ Health and Care Informatics</i> , 2021, 28, e100341.	3.0	12
96	Mining OMIM for insight into complex diseases. <i>Studies in Health Technology and Informatics</i> , 2004, 107, 753-7.	0.3	12
97	Partitioning knowledge bases between advanced notification and clinical decision support systems. <i>Decision Support Systems</i> , 2007, 43, 1274-1286.	5.9	11
98	Robust methods for accurate diagnosis using pan-microbiological oligonucleotide microarrays. <i>BMC Bioinformatics</i> , 2009, 10, S11.	2.6	11
99	A Sphingosine 1-Phosphate 1 Receptor Agonist Modulates Brain Death-Induced Neurogenic Pulmonary Injury. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2011, 45, 1022-1027.	2.9	11
100	Prognostic implication of pulmonary function at the beginning of postoperative radiotherapy in non-small cell lung cancer. <i>Radiotherapy and Oncology</i> , 2014, 113, 374-378.	0.6	10
101	eQTL networks unveil enriched mRNA master integrators downstream of complex disease-associated SNPs. <i>Journal of Biomedical Informatics</i> , 2015, 58, 226-234.	4.3	10
102	Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses. , 2018, , .		10
103	Effect of the addition of temsirolimus to cetuximab in cetuximab-resistant head and neck cancers: Results of the randomized PII MAESTRO study.. <i>Journal of Clinical Oncology</i> , 2014, 32, 6089-6089.	1.6	10
104	Putting data integration into practice: using biomedical terminologies to add structure to existing data sources. <i>AMIA ... Annual Symposium proceedings</i> , 2003, , 125-9.	0.2	10
105	Mechanism-anchored profiling derived from epigenetic networks predicts outcome in acute lymphoblastic leukemia. <i>BMC Bioinformatics</i> , 2009, 10, S6.	2.6	9
106	Curation-free biomodules mechanisms in prostate cancer predict recurrent disease. <i>BMC Medical Genomics</i> , 2013, 6, S4.	1.5	9
107	The mechanism of cancer drug addiction in ALK-positive T-Cell lymphoma. <i>Oncogene</i> , 2020, 39, 2103-2117.	5.9	9
108	GENESTRACE: PHENOMIC KNOWLEDGE DISCOVERY VIA STRUCTURED TERMINOLOGY. , 2004, , .		9



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109	Genestrace: phenomic knowledge discovery via structured terminology. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2005, , 103-14.	0.7	9
110	La nature et les corrélats de l'attachement au sein des relations de couple.. Canadian Journal of Behavioural Science, 1994, 26, 551-565.	0.6	8
111	Identification of common microRNA-mRNA regulatory biomodules in human epithelial cancer. Science Bulletin, 2010, 55, 3576-3589.	1.7	8
112	Current methodologies for translational bioinformatics. Journal of Biomedical Informatics, 2010, 43, 355-357.	4.3	8
113	Scalability and cost of a cloud-based approach to medical NLP. , 2011, , .		8
114	Genetic Interactions between Chromosomes 11 and 18 Contribute to Airway Hyperresponsiveness in Mice. PLoS ONE, 2012, 7, e29579.	2.5	8
115	Novel disease syndromes unveiled by integrative multiscale network analysis of diseases sharing molecular effectors and comorbidities. BMC Medical Genomics, 2018, 11, 112.	1.5	8
116	Evaluating single-subject study methods for personal transcriptomic interpretations to advance precision medicine. BMC Medical Genomics, 2019, 12, 96.	1.5	8
117	Role of FAM18B in diabetic retinopathy. Molecular Vision, 2014, 20, 1146-59.	1.1	8
118	The use of a <sup>51</sup> Cr technique to detect gastrointestinal microbleeding associated with nonsteroidal antiinflammatory drugs. Seminars in Arthritis and Rheumatism, 1988, 17, 40-45.	3.4	7
119	Natural language processing and visualization in the molecular imaging domain. Journal of Biomedical Informatics, 2007, 40, 270-281.	4.3	7
120	Simulation of ICD-9 to ICD-10-CM Transition for Family Medicine: Simple or Convolved?. Journal of the American Board of Family Medicine, 2016, 29, 29-36.	1.5	7
121	Clinical Ontologies for Discovery Applications. , 2007, , 101-119.		7
122	Abstract 3405: MicroRNA expression characterizes oligometastasis(es). , 2012, , .		7
123	Towards mechanism classifiers: expression-anchored Gene Ontology signature predicts clinical outcome in lung adenocarcinoma patients. AMIA ... Annual Symposium proceedings, 2012, 2012, 1040-9.	0.2	7
124	Emergence of pathway-level composite biomarkers from converging gene set signals of heterogeneous transcriptomic responses. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 484-495.	0.7	7
125	ARTS: automated randomization of multiple traits for study design. Bioinformatics, 2014, 30, 1637-1639.	4.1	6
126	Exploring Wound-Healing Genomic Machinery with a Network-Based Approach. Pharmaceuticals, 2017, 10, 55.	3.8	6



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127	Semantic Modeling for Exposomics with Exploratory Evaluation in Clinical Context. Journal of Healthcare Engineering, 2017, 2017, 1-10.	1.9	6
128	MicroRNA and protein-coding gene expression analysis in idiopathic pulmonary fibrosis yields novel biomarker signatures associated to survival. Translational Research, 2021, 228, 1-12.	5.0	6
129	INTERPRETING PERSONAL TRANSCRIPTOMES: PERSONALIZED MECHANISM-SCALE PROFILING OF RNA-SEQ DATA. , 2012, , .		6
130	PatientNarr: Towards generating patient-centric summaries of hospital stays. , 2014, , .		6
131	Generating executable knowledge for evidence-based medicine using natural language and semantic processing. AMIA ... Annual Symposium proceedings, 2006, , 56-60.	0.2	6
132	An integrative model for in-silico clinical-genomics discovery science. Proceedings, 2002, , 469-73.	0.6	6
133	Interpreting personal transcriptomes: personalized mechanism-scale profiling of RNA-seq data. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2013, , 159-70.	0.7	6
134	Interpretation of 'Omics dynamics in a single subject using local estimates of dispersion between two transcriptomes. AMIA ... Annual Symposium proceedings, 2019, 2019, 582-591.	0.2	6
135	Detection of practice pattern trends through Natural Language Processing of clinical narratives and biomedical literature. AMIA ... Annual Symposium proceedings, 2007, , 120-4.	0.2	5
136	Biomolecular Systems of Disease Buried Across Multiple GWAS Unveiled by Information Theory and Ontology. Summit on Translational Bioinformatics, 2010, 2010, 31-5.	0.7	5
137	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2019, 24, 308-319.	0.7	5
138	SEMANTIC WEBS FOR LIFE SCIENCES: SESSION INTRODUCTION. , 2005, , .		4
139	Improving the Human Readability of Arden Syntax Medical Logic Modules Using a Concept-oriented Terminology and Object-oriented Programming Expressions. CIN - Computers Informatics Nursing, 2006, 24, 220-225.	0.5	4
140	Stromal microenvironment processes unveiled by biological component analysis of gene expression in xenograft tumor models. BMC Bioinformatics, 2010, 11, S11.	2.6	4
141	ICD-10 procedure codes produce transition challenges. AMIA Summits on Translational Science Proceedings, 2018, 2017, 35-44.	0.4	4
142	Selected proceedings of the 2009 Summit on Translational Bioinformatics. BMC Bioinformatics, 2009, 10, I1.	2.6	3
143	The rise of translational bioinformatics. Genome Biology, 2012, 13, 319.	9.6	3
144	Editorial: Big Data for Health. IEEE Journal of Biomedical and Health Informatics, 2015, 19, 1191-1192.	6.3	3

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145	binomialRF: interpretable combinatoric efficiency of random forests to identify biomarker interactions. BMC Bioinformatics, 2020, 21, 374.	2.6	3
146	Precision drug repurposing via convergent eQTL-based molecules and pathway targeting independent disease-associated polymorphisms. , 2018, , .		3
147	Personalized beyond Precision: Designing Unbiased Gold Standards to Improve Single-Subject Studies of Personal Genome Dynamics from Gene Products. Journal of Personalized Medicine, 2021, 11, 24.	2.5	3
148	Integration of Neuroimaging and Microarray Datasets through Mapping and Model-Theoretic semantic Decomposition of Unstructured phenotypes. Cancer Informatics, 2009, 8, CIN.S1046.	1.9	2
149	Activity of Temsirolimus Added to Cetuximab in Patients With Cetuximab-Resistant, Recurrent/Metastatic Head-and-Neck Cancer: Results of the Randomized Phase 2 Maestro-HN Study. International Journal of Radiation Oncology Biology Physics, 2014, 88, 510.	0.8	2
150	“Single-subject studies”-derived analyses unveil altered biomechanisms between very small cohorts: implications for rare diseases. Bioinformatics, 2021, 37, i67-i75.	4.1	2
151	A tool for abstracting relevant classes of concepts: the Common Ancestry Summarizer. Studies in Health Technology and Informatics, 2004, 107, 449-53.	0.3	2
152	Epithelial cell responses to rhinovirus identify an early-life “onset asthma phenotype in adults. Journal of Allergy and Clinical Immunology, 2022, 150, 604-611.	2.9	2
153	Ontologies for natural language processing. , 2005, , .		1
154	Cascading Policies Provide Fault Tolerance for Pervasive Clinical Communications. , 2005, 2005, 209-212.		1
155	Stimulating Effect of External Myo-Inositol on the Expression of Mutant Forms of Aquaporin 2. Journal of Membrane Biology, 2010, 236, 225-232.	2.1	1
156	In Silico cancer cell versus stroma cellularity index computed from species-specific human and mouse transcriptome of xenograft models: towards accurate stroma targeting therapy assessment. BMC Medical Genomics, 2014, 7, S2.	1.5	1
157	Convergent downstream candidate mechanisms of independent intergenic polymorphisms between co-classified diseases implicate epistasis among noncoding elements. , 2018, , .		1
158	A Single-Subject Method to Detect Pathways Enriched With Alternatively Spliced Genes. Frontiers in Genetics, 2019, 10, 414.	2.3	1
159	Microbes mediated host innate immune response in idiopathic pulmonary fibrosis. , 2016, , .		1
160	Natural language processing in the molecular imaging domain. AMIA ... Annual Symposium proceedings, 2005, , 1143.	0.2	1
161	COPD Hospitalization Risk Increased with Distinct Patterns of Multiple Systems Comorbidities Unveiled by Network Modeling. AMIA ... Annual Symposium proceedings, 2014, 2014, 855-64.	0.2	1
162	Convergent downstream candidate mechanisms of independent intergenic polymorphisms between co-classified diseases implicate epistasis among noncoding elements. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 524-535.	0.7	1

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163	Single subject transcriptome analysis to identify functionally signed gene set or pathway activity. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2018, 23, 400-411.	0.7	1
164	Word-of-Mouth Innovation: Hypothesis Generation for Supplement Repurposing based on Consumer Reviews. AMIA ... Annual Symposium proceedings, 2017, 2017, 689-695.	0.2	1
165	MOLECULAR BIOINFORMATICS FOR DISEASE “ SESSION INTRODUCTION. , 2008, , .		0
166	Selected proceedings of the First Summit on Translational Bioinformatics 2008. BMC Bioinformatics, 2009, 10, 11.	2.6	0
167	Particulate Matter Exacerbates Cardiac Arrhythmias And Respiratory Dysynchrony In Mice With Heart Failure Via Heightened Carotid Body Sensitivity. , 2010, , .		0
168	Multivariate Genomic Analyses Predict The Presence Of Pulmonary Hypertension In Chuvash Polycythemia. , 2010, , .		0
169	Novel Candidate Genes Associated With The Protective Effects Of SEW-2871 On Brain Death-Induced Acute Lung Injury. , 2011, , .		0
170	Critical Role Of Sphingolipid Pathway Components In Murine Radiation-Induced Lung Injury: Protection By Sphingosine 1 Phosphate Analogues. , 2011, , .		0
171	Gene Co-Expression Modules In Peripheral Blood Mononuclear Cells Predict Clinical Outcome Of Idiopathic Pulmonary Fibrosis. , 2011, , .		0
172	Gene Expression Profiling In Peripheral Blood Mononuclear Cells Correlates Chuvash Polycythemia Progression To Pulmonary Hypertension. , 2011, , .		0
173	Peripheral Blood Mononuclear Cells Gene Expression Patterns Predict Mortality In Patients With Idiopathic Pulmonary Fibrosis. , 2011, , .		0
174	Hypothesis Generation from Heterogeneous Datasets. , 2014, , 81-98.		0
175	Reading Between the Genes: Computational Models to Discover Function from Noncoding DNA. , 2018, , .		0
176	Clinical Decision Support Systems. Best Practices, 2002, , .	0.0	0
177	An integrative genomic approach to uncover molecular mechanisms of prokaryotic traits. PLoS Computational Biology, 2005, preprint, e159.	3.2	0
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