Guillermo H Lopez-Campos

List of Publications by Year
in descending order

64 papers	1,091 citations	393982 19 h-index	433756 31 g-index
67 all docs	67 docs citations	67 times ranked	2230 citing authors

#	Article	IF	Citations
1	Host adaptive immunity deficiency in severe pandemic influenza. Critical Care, 2010, 14, R167.	2.5	145
2	Colon cancer molecular subtypes identified by expression profiling and associatedto stroma, mucinous type and different clinical behavior. BMC Cancer, 2012, 12, 260.	1.1	110
3	Exposome informatics: considerations for the design of future biomedical research information systems. Journal of the American Medical Informatics Association: JAMIA, 2014, 21, 386-390.	2.2	63
4	Patient-Reported Outcomes and Therapeutic Affordances of Social Media: Findings From a Global Online Survey of People With Chronic Pain. Journal of Medical Internet Research, 2015, 17, e20.	2.1	59
5	The Presence of HIV-1 Tat Protein Second Exon Delays Fas Protein-mediated Apoptosis in CD4+ T Lymphocytes. Journal of Biological Chemistry, 2013, 288, 7626-7644.	1.6	47
6	Secondary Use and Analysis of Big Data Collected for Patient Care. Yearbook of Medical Informatics, 2017, 26, 28-37.	0.8	45
7	Genome Sequence of Lactococcus garvieae 21881, Isolated in a Case of Human Septicemia. Journal of Bacteriology, 2011, 193, 4033-4034.	1.0	37
8	Genome Sequence of Lactococcus garvieae 8831, Isolated from Rainbow Trout Lactococcosis Outbreaks in Spain. Journal of Bacteriology, 2011, 193, 4263-4264.	1.0	37
9	Oligonucleotide array for simultaneous detection of respiratory viruses using a reverse-line blot hybridization assay. Journal of Medical Virology, 2005, 76, 256-264.	2.5	32
10	An artificial neural network improves the non-invasive diagnosis of significant fibrosis in HIV/HCV coinfected patients. Journal of Infection, 2011, 62, 77-86.	1.7	31
11	Semaphorin and plexin gene expression is altered in the prefrontal cortex of schizophrenia patients with and without auditory hallucinations. Psychiatry Research, 2015, 229, 850-857.	1.7	31
12	Targeting of cathepsin S reduces cystic fibrosis-like lung disease. European Respiratory Journal, 2019, 53, 1801523.	3.1	31
13	Global Transcriptome Analysis of Lactococcus garvieae Strains in Response to Temperature. PLoS ONE, 2013, 8, e79692.	1.1	30
14	Temporal Profiling of the Coding and Noncoding Murine Cytomegalovirus Transcriptomes. Journal of Virology, 2011, 85, 6065-6076.	1.5	28
15	EHR Big Data Deep Phenotyping. Yearbook of Medical Informatics, 2014, 23, 206-211.	0.8	28
16	Direct association between pharyngeal viral secretion and host cytokine response in severe pandemic influenza. BMC Infectious Diseases, 2011, 11, 232.	1.3	24
17	Characterization of Plasmids in a Human Clinical Strain of Lactococcus garvieae. PLoS ONE, 2012, 7, e40119.	1.1	23
18	Intubated patients developing tracheobronchitis or pneumonia have distinctive complement system gene expression signatures in the pre-infection period: A pilot study. Medicina Intensiva, 2012, 36, 257-263.	0.4	22

#	ARTICLE	IF	CITATIONS
19	Microarray Detection and Characterization of Bacterial Foodborne Pathogens. SpringerBriefs in Food, Health and Nutrition, 2012, , .	0.5	21
20	Changes in the cellular microRNA profile by the intracellular expression of HIV-1 Tat regulator: A potential mechanism for resistance to apoptosis and impaired proliferation in HIV-1 infected CD4+ T cells. PLoS ONE, 2017, 12, e0185677.	1.1	21
21	Overlapping pathogenic signalling pathways and biomarkers in preeclampsia and cardiovascular disease. Pregnancy Hypertension, 2020, 20, 131-136.	0.6	19
22	Glucocorticoid resistance of migration and gene expression in a daughter MDA-MB-231 breast tumour cell line selected for high metastatic potential. Scientific Reports, 2017, 7, 43774.	1.6	18
23	Oligonucleotide microarray design for detection and serotyping of human respiratory adenoviruses by using a virtual amplicon retrieval software. Journal of Virological Methods, 2007, 145, 127-136.	1.0	16
24	Nanoinformatics: developing new computing applications for nanomedicine. Computing (Vienna/New) Tj ETQq0 0 0 rgBT /Overlock 10 T	3.2	15
25	The New Role of Biomedical Informatics in the Age of Digital Medicine. Methods of Information in Medicine, 2016, 55, 392-402.	0.7	14
26	Analysis of the genome content of Lactococcus garvieae by genomic interspecies microarray hybridization. BMC Microbiology, 2010, 10, 79.	1.3	11
27	Transcriptomic depression of immunological synapse as a signature of ventilator-associated pneumonia. Annals of Translational Medicine, 2018, 6, 415-415.	0.7	11
28	Person-generated Data in Self-quantification. Methods of Information in Medicine, 2017, 56, 40-45.	0.7	10
29	Progress in Characterizing the Human Exposome: a Key Step for Precision Medicine. Yearbook of Medical Informatics, 2020, 29, 115-120.	0.8	9
30	A Primer in Knowledge Management for Nanoinformatics in Medicine. Lecture Notes in Computer Science, 2008, , 66-72.	1.0	8
31	Training Health Professionals in Bioinformatics. Methods of Information in Medicine, 2010, 49, 299-304.	0.7	8
32	Biomedical Informatics Methods for Personalized Medicine and Participatory Health. , 2014, , 347-394.		8
33	Lactococcus garvieae: a small bacteria and a big data world. Health Information Science and Systems, 2015, 3, S5.	3.4	8
34	How does temperature influences the development of lactococcosis? Transcriptomic and immunoproteomic <i>inÂvitro</i> approaches. Journal of Fish Diseases, 2017, 40, 1285-1297.	0.9	8
35	A method for automatically extracting infectious disease-related primers and probes from the literature. BMC Bioinformatics, 2010, 11, 410.	1.2	7
36	A Non-canonical Pathway with Potential for Safer Modulation of Transforming Growth Factor-Î²1 in Steroid-Resistant Airway Diseases. IScience, 2019, 12, 232-246.	1.9	7

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37	Tripartite motif-containing 55 identified as functional candidate for spontaneous cardiac hypertrophy in the rat locus cardiac mass 22. Journal of Hypertension, 2016, 34, 950-958.	0.3	5
38	Involvement of human monogenic cardiomyopathy genes in experimental polygenic cardiac hypertrophy. Physiological Genomics, 2018, 50, 680-687.	1.0	5
39	New Approaches in Data Integration for Systems Chemical Biology. Current Topics in Medicinal Chemistry, 2013, 13, 591-601.	1.0	4
40	Is Precision Medicine different from Personalised Medicine? A Biomedical informatics perspective. Studies in Health Technology and Informatics, 2014, 202, 20-3.	0.2	4
41	Proposal for a Standardised Reporting Guideline to Annotate Health-related Self-Quantification Experiments. Studies in Health Technology and Informatics, 2014, 202, 79-82.	0.2	4
42	Time dependent expression of the blood biomarkers EIF2D and TOX in patients with schizophrenia. Brain, Behavior, and Immunity, 2019, 80, 909-915.	2.0	3
43	An Integrative Biomedical Informatics Approach to Elucidate the Similarities Between Pre-Eclampsia and Hypertension. Studies in Health Technology and Informatics, 2019, 264, 988-992.	0.2	3
44	Microarrays and Colon Cancer in the Road for Translational Medicine. Current Bioinformatics, 2011, 6, 145-162.	0.7	3
45	Biomedical Informatics and the Digital Component of the Exposome. Studies in Health Technology and Informatics, 2017, 245, 496-500.	0.2	3
46	Characterizing the Scope of Exposome Research Through Topic Modeling and Ontology Analysis. Studies in Health Technology and Informatics, 2019, 264, 1530-1531.	0.2	2
47	Microarray Data Analysis and Management in Colorectal Cancer. Lecture Notes in Computer Science, 2005, , 391-400.	1.0	2
48	Comment on 'Discovering hospital admission patterns using models learnt from electronic hospital records'. The importance of using the right codes. Bioinformatics, 2016, 32, 2079-2080.	1.8	1
49	Phexpo: a package for bidirectional enrichment analysis of phenotypes and chemicals. JAMIA Open, 2020, 3, 173-177.	1.0	1
50	Use of informatics to characterise the exposome of COVID-19. BMJ Health and Care Informatics, 2021, 28, e100371.	1.4	1
51	Immunoinformatics and Systems Biology in Personalized Medicine. Methods in Molecular Biology, 2014, 1184, 457-475.	0.4	1
52	INDIV-3D. A new model for INdividual Data Integration and Visualisation using spatial coordinates. Studies in Health Technology and Informatics, 2013, 190, 172-4.	0.2	1
53	29Whole genome and transcriptome approach in a polygenic model for cardiac hypertrophy identifies Trim55 as a new candidate gene in quantitative trait locus cardiac mass 22. Cardiovascular Research, 2014, 103, S4.1-S4.	1.8	0
54	Construction of a Physical Factor Resource for Exposome Informatics Research. Studies in Health Technology and Informatics, 2021, 281, 1079-1080.	0.2	0

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55	Machine Learning Algorithms Reveals Country-Specific Metagenomic Taxa from American Gut Project Data. Studies in Health Technology and Informatics, 2021, 281, 382-386.	0.2	0
56	BIKMAS: A Knowledge Engineering System for Bioinformatics. Lecture Notes in Computer Science, 2002, , 435-440.	1.0	0
57	A Bioinformatic Approach to Epigenetic Susceptibility in Non-disjunctional Diseases. Lecture Notes in Computer Science, 2005, , 120-129.	1.0	0
58	BioMedical Informatics: its role in merging participatory health and personalised medicine. , 0, , .		0
59	An "in silico" Bench to Bedside Approach to Investigating Sepsis Biomarkers. Studies in Health Technology and Informatics, 2020, 270, 1195-1196.	0.2	0
60	Linking Genome and Exposome: Computational Analysis of Human Variation in Chemical-Target Interactions. Studies in Health Technology and Informatics, 2020, 270, 1331-1332.	0.2	0
61	Integration of Annotated Phenotype, Gene and Chemical Text Data to Advance Exposome Informatics. Studies in Health Technology and Informatics, 2022, , .	0.2	0
62	Exploring Molecular Mechanisms Within Biomedical Literature. Studies in Health Technology and Informatics, 2022, , .	0.2	0
63	A Comparative Analysis of Phenotypes Derived from Genes or Biomedical Literature in COVID-19. Studies in Health Technology and Informatics, 2022, , .	0.2	0
64	A Copula Type-Model for Examining the Role of Microbiome as a Potential Tool in Diagnosis. Mathematical Problems in Engineering, 2022, 2022, 1-16.	0.6	0