Theresa L Walunas

List of Publications by Year
in descending order

46 papers	9,558 citations	236925 25 h-index	265206 42 g-index
50 all docs	50 docs citations	50 times ranked	9815 citing authors

#	Article	IF	Citations
1	Identifying Contextual Factors and Strategies for Practice Facilitation in Primary Care Quality Improvement Using an Informatics-Driven Model: Framework Development and Mixed Methods Case Study. JMIR Human Factors, 2022, 9, e32174.	2.0	8
2	Metadata Correction: Identifying Contextual Factors and Strategies for Practice Facilitation in Primary Care Quality Improvement Using an Informatics-Driven Model: Framework Development and Mixed Methods Case Study. JMIR Human Factors, 2022, 9, e40674.	2.0	0
3	Remdesivir for Severe Coronavirus Disease 2019 (COVID-19) Versus a Cohort Receiving Standard of Care. Clinical Infectious Diseases, 2021, 73, e4166-e4174.	5.8	135
4	A Taxonomy for External Support for Practice Transformation. Journal of the American Board of Family Medicine, 2021, 34, 32-39.	1.5	6
5	Does coaching matter? Examining the impact of specific practice facilitation strategies on implementation of quality improvement interventions in the Healthy Hearts in the Heartland study. Implementation Science, 2021, 16, 33.	6.9	21
6	Evaluation of structured data from electronic health records to identify clinical classification criteria attributes for systemic lupus erythematosus. Lupus Science and Medicine, 2021, 8, e000488.	2.7	6
7	Remdesivir Versus Standard-of-Care for Severe Coronavirus Disease 2019 Infection: An Analysis of 28-Day Mortality. Open Forum Infectious Diseases, 2021, 8, ofab278.	0.9	31
8	Pleiotropy of systemic lupus erythematosus risk alleles and cardiometabolic disorders: A phenome-wide association study and inverse-variance weighted meta-analysis. Lupus, 2021, 30, 1264-1272.	1.6	2
9	Neptune: an environment for the delivery of genomic medicine. Genetics in Medicine, 2021, 23, 1838-1846.	2.4	3
10	Development of preclinical and clinical models for immune-related adverse events following checkpoint immunotherapy: a perspective from SITC and AACR. , 2021, 9, e002627.		15
11	A Polygenic and Phenotypic Risk Prediction for Polycystic Ovary Syndrome Evaluated by Phenome-Wide Association Studies. Journal of Clinical Endocrinology and Metabolism, 2020, 105, 1918-1936.	3.6	40
12	Using Electronic Health Records to Measure Quality Improvement Efforts: Findings from a Large Practice Facilitation Initiative. Joint Commission Journal on Quality and Patient Safety, 2020, 46, 11-17.	0.7	6
13	Effects of 2 Forms of Practice Facilitation on Cardiovascular Prevention in Primary Care. Medical Care, 2020, 58, 344-351.	2.4	14
14	Contrasting Perspectives of Practice Leaders and Practice Facilitators May Be Common in Quality Improvement Initiatives. Journal for Healthcare Quality: Official Publication of the National Association for Healthcare Quality, 2020, 42, e32-e38.	0.7	3
15	Identifying Practice Facilitation Delays and Barriers in Primary Care Quality Improvement. Journal of the American Board of Family Medicine, 2020, 33, 655-664.	1.5	32
16	Lung Cancer Survival in Patients With Autoimmune Disease. JAMA Network Open, 2020, 3, e2029917.	5.9	16
17	Making work visible for electronic phenotype implementation: Lessons learned from the eMERGE network. Journal of Biomedical Informatics, 2019, 99, 103293.	4.3	27
18	Challenges to electronic clinical quality measurement using third-party platforms in primary care practices: the healthy hearts in the heartland experience. JAMIA Open, 2019, 2, 423-428.	2.0	8

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19	Harmonizing Clinical Sequencing and Interpretation for the eMERGE III Network. American Journal of Human Genetics, 2019, 105, 588-605.	6.2	99
20	Qualitative evaluation of a cardiovascular quality improvement programmereveals sizable data inaccuracies in small primary care practices. BMJ Open Quality, 2019, 8, e000702.	1.1	1
21	Assessing the Concordance of Clinical Classification Criteria for Lupus Between Electronic Health Records and a Physician Curated Registry. Studies in Health Technology and Informatics, 2019, 264, 1466-1467.	0.3	0
22	BD-09â€...Preliminary report: rule-based algorithms using systemic lupus international collaborating clinics (SLICC) classification criteria to identify patients with systemic lupus erythematosus (SLE) from electronic health record (EHR) data. , 2018, , .		0
23	Practice Facilitatorsâ€™ and Leadersâ€™ Perspectives on a Facilitated Quality Improvement Program. Annals of Family Medicine, 2018, 16, S65-S71.	1.9	15
24	Engaging Primary Care Practices in Studies of Improvement: Did You Budget Enough for Practice Recruitment?. Annals of Family Medicine, 2018, 16, S72-S79.	1.9	15
25	Design of healthy hearts in the heartland (H3): A practice-randomized, comparative effectiveness study. Contemporary Clinical Trials, 2018, 71, 47-54.	1.8	20
26	Disease Outcomes and Care Fragmentation Among Patients With Systemic Lupus Erythematosus. Arthritis Care and Research, 2017, 69, 1369-1376.	3.4	33
27	Payment Reform Needed to Address Health Disparities of Undiagnosed Diabetic Retinopathy in the City of Chicago. Ophthalmology and Therapy, 2017, 6, 123-131.	2.3	10
28	Design and implementation of a privacy preserving electronic health record linkage tool in Chicago. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 1072-1080.	4.4	101
29	The Genetic Basis of Laboratory Adaptation in *Caulobacter crescentus*. Journal of Bacteriology, 2010, 192, 3678-3688.	2.2	166
30	Living with Genome Instability: the Adaptation of Phytoplasmas to Diverse Environments of Their Insect and Plant Hosts. Journal of Bacteriology, 2006, 188, 3682-3696.	2.2	356
31	Identification of Open Reading Frames Unique to a Select Agent: Ralstonia solanacearum Race 3 Biovar 2. Molecular Plant-Microbe Interactions, 2006, 19, 69-79.	2.6	121
32	The complete genome sequence of *Lactobacillus bulgaricus* reveals extensive and ongoing reductive evolution. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 9274-9279.	7.1	382
33	Comparative genome analysis ofBacillus cereusgroup genomes withBacillus subtilis. FEMS Microbiology Letters, 2005, 250, 175-184.	1.8	73
34	Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis. Nature, 2003, 423, 87-91.	27.8	740
35	Genome Analysis of *F. nucleatum sub spp vincentii* and Its Comparison With the Genome of *F. nucleatum* ATCC 25586. Genome Research, 2003, 13, 1180-1189.	5.5	72
36	The ERGOTM genome analysis and discovery system. Nucleic Acids Research, 2003, 31, 164-171.	14.5	207

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37	Whole-genome comparative analysis of three phytopathogenic Xylella fastidiosa strains. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 12403-12408.	7.1	94
38	Draft Sequencing and Comparative Genomics of Xylella fastidiosa Strains Reveal Novel Biological Insights. Genome Research, 2002, 12, 1556-1563.	5.5	70
39	Genome Sequence and Analysis of the Oral Bacterium <i>Fusobacterium nucleatum</i> Strain ATCC 25586. Journal of Bacteriology, 2002, 184, 2005-2018.	2.2	311
40	Cutting Edge: The Ets1 Transcription Factor Is Required for the Development of NK T Cells in Mice. Journal of Immunology, 2000, 164, 2857-2860.	0.8	86
41	The Ets-1 Transcription Factor Is Required for the Development of Natural Killer Cells in Mice. Immunity, 1998, 9, 555-563.	14.3	338
42	CTLA-4 ligation blocks CD28-dependent T cell activation.. Journal of Experimental Medicine, 1996, 183, 2541-2550.	8.5	732
43	CD28/B7 SYSTEM OF T CELL COSTIMULATION. Annual Review of Immunology, 1996, 14, 233-258.	21.8	2,466
44	CTLA-4: a negative regulator of autoimmune disease.. Journal of Experimental Medicine, 1996, 184, 783-788.	8.5	369
45	Absence of B7-dependent responses in CD28-deficient mice. Immunity, 1994, 1, 501-508.	14.3	359
46	CTLA-4 can function as a negative regulator of T cell activation. Immunity, 1994, 1, 405-413.	14.3	1,949