

Jignesh M Patel

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

1,776
citations

567281

15
h-index

794594

19
g-index

37
all docs

37
docs citations

37
times ranked

1613
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | TALE: A Tool for Approximate Large Graph Matching. , 2008, , . | | 206 |
| 2 | Identification of Cross-Species Shared Transcriptional Networks of Diabetic Nephropathy in Human and Mouse Glomeruli. Diabetes, 2013, 62, 299-308. | 0.6 | 163 |
| 3 | Energy management for MapReduce clusters. Proceedings of the VLDB Endowment, 2010, 3, 129-139. | 3.8 | 157 |
| 4 | Partition based spatial-merge join. SIGMOD Record, 1996, 25, 259-270. | 1.2 | 138 |
| 5 | BitWeaving. , 2013, , . | | 97 |
| 6 | Discovery-driven graph summarization. , 2010, , . | | 91 |
| 7 | Learning Generalized Linear Models Over Normalized Data. , 2015, , . | | 81 |
| 8 | Model Selection Management Systems. SIGMOD Record, 2016, 44, 17-22. | 1.2 | 77 |
| 9 | Practical methods for constructing suffix trees. VLDB Journal, 2005, 14, 281-299. | 4.1 | 69 |
| 10 | To Join or Not to Join?. , 2016, , . | | 58 |
| 11 | Efficient Evaluation of All-Nearest-Neighbor Queries. , 2007, , . | | 55 |
| 12 | On energy management, load balancing and replication. SIGMOD Record, 2010, 38, 35-42. | 1.2 | 54 |
| 13 | Wimpy node clusters. , 2010, , . | | 52 |
| 14 | Towards Multi-tenant Performance SLOs. , 2012, , . | | 49 |
| 15 | OASIS. , 2003, , 910-921. | | 49 |
| 16 | Efficient and Accurate Discovery of Patterns in Sequence Data Sets. IEEE Transactions on Knowledge and Data Engineering, 2011, 23, 1154-1168. | 5.7 | 40 |
| 17 | WideTable. Proceedings of the VLDB Endowment, 2014, 7, 907-918. | 3.8 | 36 |
| 18 | Towards energy-efficient database cluster design. Proceedings of the VLDB Endowment, 2012, 5, 1684-1695. | 3.8 | 33 |

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 19 | Fibrillar Collagen Quantification With Curvelet Transform Based Computational Methods. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 198. | 4.1 | 32 |
| 20 | Practical Suffix Tree Construction. , 2004, , 36-47. | | 31 |
| 21 | miBLAST: scalable evaluation of a batch of nucleotide sequence queries with BLAST. <i>Nucleic Acids Research</i> , 2005, 33, 4335-4344. | 14.5 | 30 |
| 22 | Role of Live-coding in Learning Introductory Programming. , 2018, , . | | 24 |
| 23 | Dictionary-Based Compression for Long Time-Series Similarity. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2010, 22, 1609-1622. | 5.7 | 20 |
| 24 | Towards Multi-Tenant Performance SLOs. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2014, 26, 1447-1463. | 5.7 | 18 |
| 25 | Toward GPUs being mainstream in analytic processing. , 2015, , . | | 17 |
| 26 | Design and evaluation of storage organizations for read-optimized main memory databases. <i>Proceedings of the VLDB Endowment</i> , 2013, 6, 1474-1485. | 3.8 | 16 |
| 27 | Quickstep. <i>Proceedings of the VLDB Endowment</i> , 2018, 11, 663-676. | 3.8 | 16 |
| 28 | A Padded Encoding Scheme to Accelerate Scans by Leveraging Skew. , 2015, , . | | 14 |
| 29 | The Role of Declarative Querying in Bioinformatics. <i>OMICS A Journal of Integrative Biology</i> , 2003, 7, 89-91. | 2.0 | 12 |
| 30 | Scaling-up in-memory datalog processing. <i>Proceedings of the VLDB Endowment</i> , 2019, 12, 695-708. | 3.8 | 9 |
| 31 | Implications of Emerging 3D GPU Architecture on the Scan Primitive. <i>SIGMOD Record</i> , 2015, 44, 18-23. | 1.2 | 8 |
| 32 | Live-coding vs Static Code Examples. , 2020, , . | | 8 |
| 33 | Efficient and accurate discovery of patterns in sequence datasets. , 2010, , . | | 6 |
| 34 | Accurate modeling of the hybrid hash join algorithm. <i>Performance Evaluation Review</i> , 1994, 22, 56-66. | 0.6 | 5 |
| 35 | What Do Students Feel about Learning Programming Using Both English and Their Native Language?. , 2017, , . | | 3 |
| 36 | Impact of Bilingual CS Education on Student Learning and Engagement in a Data Structures Course. , 2019, , . | | 2 |

| # | ARTICLE | IF | CITATIONS |
|----|---|-----|-----------|
| 37 | BatchGenAna: a batch platform for large-scale genomic analysis of mammalian small RNAs. <i>Bioinformatics</i> , 2009, 3, 336-348. | 0.5 | 0 |