Hillel Kugler

List of Publications by Year
in descending order

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49 papers	1,068 citations	516710 16 h-index	454955 30 g-index
58 all docs	58 docs citations	58 times ranked	535 citing authors

#	Article	IF	Citations
1	SYNTHESIZING STATE-BASED OBJECT SYSTEMS FROM LSC SPECIFICATIONS. International Journal of Foundations of Computer Science, 2002, 13, 5-51.	1.1	130
2	Synthesis Revisited: Generating Statechart Models from Scenario-Based Requirements. Lecture Notes in Computer Science, 2005, , 309-324.	1.3	80
3	Smart Play-out of Behavioral Requirements. Lecture Notes in Computer Science, 2002, , 378-398.	1.3	74
4	The Rhapsody Semantics of Statecharts (or, On the Executable Core of the UML). Lecture Notes in Computer Science, 2004, , 325-354.	1.3	63
5	Formalizing UML Models and OCL Constraints in PVS. Electronic Notes in Theoretical Computer Science, 2005, 115, 39-47.	0.9	63
6	Multiple instances and symbolic variables in executable sequence charts. , 2002, , .		45
7	A method to identify and analyze biological programs through automated reasoning. Npj Systems Biology and Applications, 2016, 2, .	3.0	42
8	A scenario-based approach to modeling development: A prototype model of C. elegans vulval fate specification. Developmental Biology, 2008, 323, 1-5.	2.0	32
9	Mechano-logical model of C. elegans germ line suggests feedback on the cell cycle. Development (Cambridge), 2015, 142, 3902-11.	2.5	28
10	Synthesizing State-Based Object Systems from LSC Specifications. Lecture Notes in Computer Science, 2001, , 1-33.	1.3	27
11	Compositional Synthesis of Reactive Systems from Live Sequence Chart Specifications. Lecture Notes in Computer Science, 2009, , 77-91.	1.3	25
12	Biocharts: a visual formalism for complex biological systems. Journal of the Royal Society Interface, 2010, 7, 1015-1024.	3.4	24
13	SMT-Based Analysis of Biological Computation. Lecture Notes in Computer Science, 2013, , 78-92.	1.3	22
14	Supporting UML-based development of embedded systems by formal techniques. Software and Systems Modeling, 2008, 7, 131-155.	2.7	21
15	A model of stem cell population dynamics: in silico analysis and in vivo validation. Development (Cambridge), 2012, 139, 47-56.	2.5	18
16	Modeling and Verification of a Telecommunication Application Using Live Sequence Charts and the Play-Engine Tool. Lecture Notes in Computer Science, 2005, , 414-428.	1.3	17
17	Modeling and verification of a telecommunication application using live sequence charts and the Play-Engine tool. Software and Systems Modeling, 2008, 7, 157-175.	2.7	16
18	Automated Synthesis and Analysis of Switching Gene Regulatory Networks. BioSystems, 2016, 146, 26-34.	2.0	16

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19	Specifying and executing requirements. , 2002, , .		15
20	Some Methodological Observations Resulting from Experience Using LSCs and the Play-In/Play-Out Approach. Lecture Notes in Computer Science, 2005, , 26-42.	1.3	13
21	Functional Analysis of Large-Scale DNA Strand Displacement Circuits. Lecture Notes in Computer Science, 2013, , 189-203.	1.3	10
22	A model of stem cell population dynamics: in silico analysis and in vivo validation. Journal of Cell Science, 2012, 125, e1-e1.	2.0	9
23	Deductive Verification of UML Models in TLPVS. Lecture Notes in Computer Science, 2004, , 335-349.	1.3	9
24	Formal Modelling of C. elegans Development. A Scenario-Based Approach. Natural Computing Series, 2004, , 151-173.	2.2	9
25	BRE:IN - A Backend for Reasoning About Interaction Networks with Temporal Logic. Lecture Notes in Computer Science, 2019, , 289-295.	1.3	8
26	Symbolic Approximation of the Bounded Reachability Probability in Large Markov Chains. Lecture Notes in Computer Science, 2014, , 388-403.	1.3	8
27	Synthesizing Biological Theories. Lecture Notes in Computer Science, 2011, , 579-584.	1.3	8
28	Smart play-out. , 2003, , .		7
29	Temporal Reasoning on Incomplete Paths. Lecture Notes in Computer Science, 2018, , 28-52.	1.3	7
30	Formal Analysis of Network Motifs Links Structure to Function in Biological Programs. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 261-271.	3.0	7
31	Design of network-based biocomputation circuits for the exact cover problem. New Journal of Physics, 2021, 23, 085004.	2.9	7
32	Model Checking Using SMT and Theory of Lists. Lecture Notes in Computer Science, 2011, , 282-297.	1.3	7
33	Multiple instances and symbolic variables in executable sequence charts. ACM SIGPLAN Notices, 2002, 37, 83-100.	0.2	6
34	Formal Semantics and Verification of Network-Based Biocomputation Circuits. Lecture Notes in Computer Science, 2021, , 464-485.	1.3	5
35	Solving Exact Cover Instances with Molecular-Motor-Powered Network-Based Biocomputation. ACS Nanoscience Au, 2022, 2, 396-403.	4.8	4
36	Switching Gene Regulatory Networks. Lecture Notes in Computer Science, 2015, , 131-144.	1.3	3

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37	How computational models contribute to our understanding of the germ line. Molecular Reproduction and Development, 2016, 83, 944-957.	2.0	3
38	â€œDonâ€™t Careâ€•Modeling: A Logical Framework for Developing Predictive System Models. , 2007, , 343-357.		3
39	Some Thoughts on the Semantics of Biocharts. Lecture Notes in Computer Science, 2010, , 185-194.	1.3	3
40	Temporal Logic Based Synthesis of Experimentally Constrained Interaction Networks. Lecture Notes in Computer Science, 2019, , 89-104.	1.3	3
41	Unifying Modelling and Programming: A Systems Biology Perspective. Lecture Notes in Computer Science, 2016, , 131-133.	1.3	2
42	Accelerating Smart Play-Out. Lecture Notes in Computer Science, 2010, , 477-488.	1.3	2
43	Modeling the C. elegans germline stem cell genetic network using automated reasoning. BioSystems, 2022, 217, 104672.	2.0	2
44	Biocharts: Unifying Biological Hypotheses with Models and Experiments. , 2013, , .		1
45	Synthesizing reactive systems from LSC requirements using the play-engine. , 2007, , .		0
46	Crafting game-models using reactive system design. , 2008, , .		0
47	TEMPO: Thermal-Efficient Management of Power in High-Throughput Network Switches. , 2019, , .		0
48	Runtime Verification and Refutation for Biological Systems. Lecture Notes in Computer Science, 2013, , 384-385.	1.3	0
49	Mechano-logical model of C. elegans germ line suggests feedback on the cell cycle. Journal of Cell Science, 2015, 128, e1.2-e1.2.	2.0	0