

# Hana El-Samad

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/593395/publications.pdf>

Version: 2024-02-01

67  
papers

5,155  
citations

172457

29  
h-index

149698

56  
g-index

77  
all docs

77  
docs citations

77  
times ranked

6736  
citing authors

#	ARTICLE	IF	CITATIONS
1	The Vision for <i>GEN Biotechnology</i>: From Precision Biology to Engaging a Broad Audience. , 2022, 1, 21-25.		2
2	Competitive Displacement of <i>De Novo</i> Designed HeteroDimers Can Reversibly Control Protein-Protein Interactions and Implement Feedback in Synthetic Circuits. , 2022, 1, 91-100.		4
3	Generosity of Spirit. , 2022, 1, 113-114.		0
4	The Human Right to Our Bodies. , 2022, 1, 207-207.		0
5	Fund Black scientists. Cell, 2021, 184, 561-565.	28.9	107
6	Stress-induced growth rate reduction restricts metabolic resource utilization to modulate osmo-adaptation time. Cell Reports, 2021, 34, 108854.	6.4	12
7	Biological feedback control-Respect the loops. Cell Systems, 2021, 12, 477-487.	6.2	35
8	Director Lander, the time is now. Science, 2021, 373, 7-7.	12.6	3
9	De novo design of tyrosine and serine kinase-driven protein switches. Nature Structural and Molecular Biology, 2021, 28, 762-770.	8.2	14
10	Orthogonal control of mean and variability of endogenous genes in a human cell line. Nature Communications, 2021, 12, 292.	12.8	11
11	Optogenetic Control Reveals Differential Promoter Interpretation of Transcription Factor Nuclear Translocation Dynamics. Cell Systems, 2020, 11, 336-353.e24.	6.2	37
12	Multidimensional Characterization of Parts Enhances Modeling Accuracy in Genetic Circuits. ACS Synthetic Biology, 2020, 9, 2917-2926.	3.8	15
13	De novo design of protein logic gates. Science, 2020, 368, 78-84.	12.6	151
14	Multi-kinase control of environmental stress responsive transcription. PLoS ONE, 2020, 15, e0230246.	2.5	12
15	Assembly of Genetic Circuits with the Mammalian ToolKit. Bio-protocol, 2020, 10, e3547.	0.4	3
16	Multi-kinase control of environmental stress responsive transcription. , 2020, 15, e0230246.		0
17	Multi-kinase control of environmental stress responsive transcription. , 2020, 15, e0230246.		0
18	Multi-kinase control of environmental stress responsive transcription. , 2020, 15, e0230246.		0

#	ARTICLE	IF	CITATIONS
19	Multi-kinase control of environmental stress responsive transcription. , 2020, 15, e0230246.		0
20	Modular and tunable biological feedback control using a de novo protein switch. Nature, 2019, 572, 265-269.	27.8	96
21	De novo design of bioactive protein switches. Nature, 2019, 572, 205-210.	27.8	190
22	Design and Analysis of a Proportional-Integral-Derivative Controller with Biological Molecules. Cell Systems, 2019, 9, 338-353.e10.	6.2	67
23	A Toolkit for Rapid Modular Construction of Biological Circuits in Mammalian Cells. ACS Synthetic Biology, 2019, 8, 2593-2606.	3.8	49
24	Synthetic transcriptional synergy. Science, 2019, 364, 531-532.	12.6	1
25	Control theoretical concepts for synthetic and systems biology. Current Opinion in Systems Biology, 2019, 14, 50-57.	2.6	16
26	A population shift between two heritable cell types of the pathogen <i>Candida albicans</i> is based both on switching and selective proliferation. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 26918-26924.	7.1	10
27	Complexity-aware simple modeling. Current Opinion in Microbiology, 2018, 45, 47-52.	5.1	1
28	Real-Time Genetic Compensation Defines the Dynamic Demands of Feedback Control. Cell, 2018, 175, 877-886.e10.	28.9	67
29	Robust Synthetic Circuits for Two-Dimensional Control of Gene Expression in Yeast. ACS Synthetic Biology, 2017, 6, 545-554.	3.8	63
30	Model-guided optogenetic study of PKA signaling in budding yeast. Molecular Biology of the Cell, 2017, 28, 221-227.	2.1	20
31	Tradeoffs in adapting biological systems. European Journal of Control, 2016, 30, 68-75.	2.6	5
32	Low Dimensionality in Gene Expression Data Enables the Accurate Extraction of Transcriptional Programs from Shallow Sequencing. Cell Systems, 2016, 2, 239-250.	6.2	130
33	Transcriptional rewiring over evolutionary timescales changes quantitative and qualitative properties of gene expression. ELife, 2016, 5, .	6.0	54
34	The Impact of Different Sources of Fluctuations on Mutual Information in Biochemical Networks. PLoS Computational Biology, 2015, 11, e1004462.	3.2	8
35	Population Diversification in a Yeast Metabolic Program Promotes Anticipation of Environmental Shifts. PLoS Biology, 2015, 13, e1002042.	5.6	110
36	Systematic analysis of asymmetric partitioning of yeast proteome between mother and daughter cells reveals ageing factors and mechanism of lifespan asymmetry. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 11977-11982.	7.1	51

#	ARTICLE	IF	CITATIONS
37	Using Dynamic Noise Propagation to Infer Causal Regulatory Relationships in Biochemical Networks. ACS Synthetic Biology, 2015, 4, 258-264.	3.8	17
38	A master equation and moment approach for biochemical systems with creation-time-dependent bimolecular rate functions. Journal of Chemical Physics, 2014, 141, 214108.	3.0	6
39	Dynamic characterization of growth and gene expression using high-throughput automated flow cytometry. Nature Methods, 2014, 11, 443-448.	19.0	40
40	Delayed Ras/PKA signaling augments the unfolded protein response. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14800-14805.	7.1	45
41	Multicellular Architecture of Malignant Breast Epithelia Influences Mechanics. PLoS ONE, 2014, 9, e101955.	2.5	16
42	Building robust functionality in synthetic circuits using engineered feedback regulation. Current Opinion in Biotechnology, 2013, 24, 790-796.	6.6	27
43	Msn2 Coordinates a Stoichiometric Gene Expression Program. Current Biology, 2013, 23, 2336-2345.	3.9	51
44	Conformational biosensors reveal GPCR signalling from endosomes. Nature, 2013, 495, 534-538.	27.8	713
45	Basic leucine zipper transcription factor Hac1 binds DNA in two distinct modes as revealed by microfluidic analyses. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3084-93.	7.1	61
46	A non-memoryless stochastic simulation algorithm for modeling diffusion-reactions on biological membranes. , 2012, , .		0
47	Synergistic dual positive feedback loops established by molecular sequestration generate robust bimodal response. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, E3324-33.	7.1	76
48	Modeling and simulation of cellular functions. Molecular Biology of the Cell, 2012, 23, 972-972.	2.1	0
49	Stochastic Modeling of Cellular Networks. Methods in Cell Biology, 2012, 110, 111-137.	1.1	10
50	Cellular Noise Regulons Underlie Fluctuations in Saccharomyces cerevisiae. Molecular Cell, 2012, 45, 483-493.	9.7	143
51	Noise rules. Nature, 2011, 480, 188-189.	27.8	7
52	Can a Systems Perspective Help Us Appreciate the Biological Meaning of Small Effects?. Developmental Cell, 2011, 21, 11-13.	7.0	2
53	In silico feedback for in vivo regulation of a gene expression circuit. Nature Biotechnology, 2011, 29, 1114-1116.	17.5	263
54	A data-integrated method for analyzing stochastic biochemical networks. Journal of Chemical Physics, 2011, 135, 214110.	3.0	10

#	ARTICLE	IF	CITATIONS
55	Homeostatic adaptation to endoplasmic reticulum stress depends on Ire1 kinase activity. <i>Journal of Cell Biology</i> , 2011, 193, 171-184.	5.2	140
56	Coordinate control of gene expression noise and interchromosomal interactions in a MAP kinase pathway. <i>Nature Cell Biology</i> , 2010, 12, 954-962.	10.3	59
57	Combinatorial, site-specific requirement for heterochromatic silencing factors in the elimination of nucleosome-free regions. <i>Genes and Development</i> , 2010, 24, 1758-1771.	5.9	52
58	BiP Binding to the ER-Stress Sensor Ire1 Tunes the Homeostatic Behavior of the Unfolded Protein Response. <i>PLoS Biology</i> , 2010, 8, e1000415.	5.6	369
59	Tuning the Activation Threshold of a Kinase Network by Nested Feedback Loops. <i>Science</i> , 2009, 324, 509-512.	12.6	48
60	Not all quiet on the noise front. <i>Nature Chemical Biology</i> , 2009, 5, 699-704.	8.0	17
61	Defining Network Topologies that Can Achieve Biochemical Adaptation. <i>Cell</i> , 2009, 138, 760-773.	28.9	1,354
62	Algorithms for Discriminating Between Biochemical Reaction Network Models: Towards Systematic Experimental Design. <i>Proceedings of the American Control Conference</i> , 2007, , .	0.0	8
63	Bound attractant at the leading vs. the trailing edge determines chemotactic prowess. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 13349-13354.	7.1	95
64	Regulated Degradation Is a Mechanism for Suppressing Stochastic Fluctuations in Gene Regulatory Networks. <i>Biophysical Journal</i> , 2006, 90, 3749-3761.	0.5	68
65	Module-Based Analysis of Robustness Tradeoffs in the Heat Shock Response System. <i>PLoS Computational Biology</i> , 2006, 2, e59.	3.2	89
66	Coherence Resonance: A Mechanism for Noise Induced Stable Oscillations in Gene Regulatory Networks. , 2006, , .		3
67	Module-Based Analysis of Robustness Tradeoffs in the Heat Shock Response System. <i>PLoS Computational Biology</i> , 2005, preprint, e59.	3.2	0