

Masaki Sasai

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2887675/publications.pdf>

Version: 2024-02-01

70
papers

1,203
citations

516710

16
h-index

501196

28
g-index

74
all docs

74
docs citations

74
times ranked

1017
citing authors

#	ARTICLE	IF	CITATIONS
1	Generation of dynamic three-dimensional genome structure through phase separation of chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	7.1	30
2	Physics, Chemistry, or Biology; What Do You Want to Pursue?. Seibutsu Butsuri, 2022, 62, 140-142.	0.1	0
3	The Structural Rule Distinguishing a Superfold: A Case Study of Ferredoxin Fold and the Reverse Ferredoxin Fold. Molecules, 2022, 27, 3547.	3.8	1
4	Mechanism of autonomous synchronization of the circadian KaiABC rhythm. Scientific Reports, 2021, 11, 4713.	3.3	6
5	Stochastic epigenetic dynamics of gene switching. Physical Review E, 2020, 102, 042408.	2.1	10
6	Heterogeneous fluid-like movements of chromatin and their implications to transcription. Biophysical Reviews, 2020, 12, 461-468.	3.2	19
7	Single nucleosome imaging reveals loose genome chromatin networks via active RNA polymerase II. Journal of Cell Biology, 2019, 218, 1511-1530.	5.2	162
8	Organization of fast and slow chromatin revealed by single-nucleosome dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 19939-19944.	7.1	67
9	Effects of Stochastic Single-Molecule Reactions on Coherent Ensemble Oscillations in the KaiABC Circadian Clock. Journal of Physical Chemistry B, 2019, 123, 702-713.	2.6	8
10	Single-molecular and ensemble-level oscillations of cyanobacterial circadian clock. Biophysics and Physicobiology, 2018, 15, 136-150.	1.0	9
11	Heterogeneous Spatial Distribution of Transcriptional Activity in Budding Yeast Nuclei. Biophysical Journal, 2017, 112, 491-504.	0.5	11
12	Role of ATP Hydrolysis in Cyanobacterial Circadian Oscillator. Scientific Reports, 2017, 7, 17469.	3.3	12
13	Importance of consensus region of multiple-ligand templates in a virtual screening method. Biophysics and Physicobiology, 2016, 13, 149-156.	1.0	3
14	Cooperativity and modularity in protein folding. Biophysics and Physicobiology, 2016, 13, 281-293.	1.0	7
15	Liquid-like behavior of chromatin. Current Opinion in Genetics and Development, 2016, 37, 36-45.	3.3	122
16	Loose Mechanism of Eukaryotic Gene Regulation and Chromatin Dynamics. Seibutsu Butsuri, 2016, 56, 106-108.	0.1	0
17	Effects of Collective Histone State Dynamics on Epigenetic Landscape and Kinetics of Cell Reprogramming. Scientific Reports, 2015, 5, 16746.	3.3	23
18	VS-APPLE: A Virtual Screening Algorithm Using Promiscuous Protein-Ligand Complexes. Journal of Chemical Information and Modeling, 2015, 55, 1108-1119.	5.4	8

#	ARTICLE	IF	CITATIONS
19	Multiple coupled landscapes and non-adiabatic dynamics with applications to self-activating genes. Physical Chemistry Chemical Physics, 2015, 17, 29036-29044.	2.8	8
20	Coupling of Lever Arm Swing and Biased Brownian Motion in Actomyosin. PLoS Computational Biology, 2014, 10, e1003552.	3.2	12
21	Folding pathway of a multidomain protein depends on its topology of domain connectivity. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 15969-15974.	7.1	37
22	3P284 Epigenetic Dynamics of Cell Reprogramming(25. Nonequilibrium state & Biological) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 2014, 54, S296.	0.1	0
23	Time Scales in Epigenetic Dynamics and Phenotypic Heterogeneity of Embryonic Stem Cells. PLoS Computational Biology, 2013, 9, e1003380.	3.2	56
24	Eddy current and coupled landscapes for nonadiabatic and nonequilibrium complex system dynamics. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 14930-14935.	7.1	46
25	2P132 Dynamics of transcriptional apparatus in eukaryotic gene expression(08. Molecular genetics) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62 0.1	0.1	0
26	1PT217 Mean field theory of epigenetic dynamics of cell differentiation(The 50th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 0.1	0.1	0
27	2PT213 Transitions of the cell state in the early stage of differentiation from the pluripotent cell(The) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62 0.1	0.1	0
28	2PS010 Free energy landscape analysis of the actin-myosin VI interaction under the applied force(The) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 0.1	0.1	0
29	1PT166 Comparison of the conformational transitions of DHFR bound to the different ligands using the chameleon model(The 50th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2012, 52, S97.	0.1	0
30	1F1436 Stochastic epigenetic dynamics of cell differentiation(Mathematical biology 1,The 49th Annual) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 0.1	0.1	0
31	3G1036 Conformational transition of DHFR simulated with the chameleon model(3G Protein:) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62 S129. 0.1	0.1	0
32	2C1448 Statistical Mechanical Model of Signaling Pathways in Photoactive Yellow Protein(Protein:) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 62 0.1	0.1	0
33	3C1434 Molecular Dynamics Simulation of Interphase Chromosomes in Budding Yeast(3C Molecular) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 62 0.1	0.1	0
34	3H1112 The energy landscape perspective of oxygen binding of hemoglobin : a study with the chameleon model(3H Protein: Property 4,The 49th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2011, 51, S134.	0.1	0
35	The Fragment-based Consistency Score in Model Quality Assessment for De Novo Prediction of Protein Structures. Chem-Bio Informatics Journal, 2011, 11, 63-81.	0.3	0
36	2P047 The energy landscape perspective on the oxygen binding of hemoglobin : a study with chameleon model(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsurei, 2010, 50, S90.	0.1	0

#	ARTICLE	IF	CITATIONS
37	2P062 Statistical Mechanical Analysis of Folding Flexibility in Ribosomal Protein S6(The 48th Annual) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.1	0
38	2P150 Stochastic simulation of transcriptional control network in pluripotent cells(The 48th Annual) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
39	2P309 Oscillation mechanism of segmentation clock studied by a two-dimensional model of presomitic mesoderm(The 48th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2010, 50, S137.	0.1	0
40	1P187 Free energy landscape of the interaction between actin and myosin underlying the sliding movement of the myosin head(Molecular motor,The 48th Annual Meeting of the Biophysical Society of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
41	1P301 1H1355 Strategies of locomotion of unicellular and multicellular amoeboid cells(Mathematical) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 Butsuri, 2010, 50, S73.	0.1	0
42	1P314 Coordinated dynamics of phosphorylation and ATP hydrolysis in the simulated circadian oscillation of KaiC(Non-equilibrium state & Biological rhythm,The 48th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
43	Synchronization of Circadian Oscillation of Phosphorylation Level of KaiC In Vitro. Biophysical Journal, 2010, 98, 2469-2477.	0.5	26
44	3P-144 Free energy landscape of the interaction between actin and myosin underlying the sliding movement of the myosin head(Molecular motor,The 47th Annual Meeting of the Biophysical Society of) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
45	2P-248 Coordinated dynamics of phosphorylation and ATP hydrolysis in the simulated circadian oscillation of KaiC(Mathematical biology,The 47th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2009, 49, S146.	0.1	0
46	2P-098 Influence of cell cycles to the oscillation of segmentation clock : Simulation with a two-dimensional model(Molecular genetics & Gene expression,The 47th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
47	3P-053 Statistical Mechanical Theory of Protein Allostery(Protein:Property,The 47th Annual Meeting) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.1	0
48	2TA4-10 Strategies for chemotaxis of amoeboid cells(The 47th Annual Meeting of the Biophysical) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
49	2P-249 Entrainment of Circadian Oscillation of Phosphorylation Level of KaiC in vitro(Mathematical) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.1	0
50	Mechanism of Robust Circadian Oscillation of KaiC Phosphorylation In Vitro. Biophysical Journal, 2008, 95, 1773-1784.	0.5	27
51	2P-312 Simulation of circadian rhythm of KaiC with a model considering dual phosphorylation sites(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S123.	0.1	0
52	1P-127 Precise spatial patterns of Bicoid and Hunchback in the early Drosophila embryo(The 46th) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0
53	1S4-6 Roles of water in protein structure fluctuation and functioning(1S4 Water as a key player in) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50	0.1	0
54	2P-075 Multi-dimensional Landscape Theory of Diverse Folding Behaviors of Proteins(The 46th Annual) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	0.1	0

#	ARTICLE	IF	CITATIONS
55	2P-109 A coarse-grained wormlike chain DNA model for transcriptional control in eukaryote(The 46th) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.1	0
56	1P-126 Does the pre-steady state decoding mechanism in Drosophila embryo solve Bialek's paradox?(The 46th Annual Meeting of the Biophysical Society of Japan). Seibutsu Butsuri, 2008, 48, S40.	0.1	0
57	Effects of the DNA state fluctuation on single-cell dynamics of self-regulating gene. Journal of Chemical Physics, 2007, 127, 105107.	3.0	18
58	Roles of noise in single and coupled multiple genetic oscillators. Journal of Chemical Physics, 2007, 126, 115101.	3.0	45
59	2P144 Conformational change of motor proteins described by extended Go-like model(Molecular) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T	0.1	0
60	3P080 Protein Conformational Dynamics from a Viewpoint of Single-molecule Statistical Physics(Proteins-stability, folding, and other physicochemical properties,Poster Presentations). Seibutsu Butsuri, 2007, 47, S223.	0.1	0
61	1P013 A coarse-grained Langevin molecular dynamics approach to de novo structure prediction(Proteins-structure and structure-function relationship,Poster Presentations). Seibutsu Butsuri, 2007, 47, S26.	0.1	0
62	3P338 Effects of stochastic diffusion and cooperative binding of Bicoid on expression of hunchback in Drosophila embryo(Development and differentiation,Poster Presentations). Seibutsu Butsuri, 2007, 47, S287.	0.1	0
63	Monomer-Shuffling and Allosteric Transition in KaiC Circadian Oscillation. PLoS ONE, 2007, 2, e408.	2.5	45
64	3P339 Stochastic three-dimensional simulation of Bicoid and Hunchback in the early Drosophila embryo(Development and differentiation,Poster Presentations). Seibutsu Butsuri, 2007, 47, S287.	0.1	0
65	1P298 Monomer-shuffling and allosteric transition in KaiC circadian oscillation(Mathematical) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T 2007, 47, S98.	0.1	0
66	2P472 Correlation, response, and violation of the fluctuation-dissipation relation in gene networks(50. Non-equilibrium and complex system,Poster Session,Abstract,Meeting Program of EABS &) Tj ETQq0 0.0 rgBT /Overlock 10 T	0.0	0
67	1P588 Conformational change of proteins described by extended Go-like models(27. Molecular) Tj ETQq1 1 0.784314 rgBT /Overlock 10 T Butsuri, 2006, 46, S293.	0.1	0
68	Self-Consistent Proteomic Field Theory of Stochastic Gene Switches. Biophysical Journal, 2005, 88, 828-850.	0.5	101
69	On the model granularity to simulate protein dynamics: A biological physics view on biomolecular computing. Natural Computing, 2004, 3, 377-393.	3.0	10
70	Stochastic gene expression as a many-body problem. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2374-2379.	7.1	267