# Daisuke Kiga

List of Publications by Year
in descending order



| | | | |
|---|---|---|---|
| 49 papers | 1,345 citations | 687220 13 h-index | 377752 34 g-index |
| 50 all docs | 50 docs citations | 50 times ranked | 1140 citing authors |

| # | Article | IF | Citations |
|---|---|---|---|
| 1 | Comparative analysis of three studies measuring fluorescence from engineered bacterial genetic constructs. PLoS ONE, 2021, 16, e0252263. | 1.1 | 11 |
| 2 | Robust estimation of bacterial cell count from optical density. Communications Biology, 2020, 3, 512. | 2.0 | 86 |
| 3 | Comparison between Effects of Retroactivity and Resource Competition upon Change in Downstream Reporter Genes of Synthetic Genetic Circuits. Life, 2019, 9, 30. | 1.1 | 7 |
| 4 | Enhancement of Binding Affinity of Folate to Its Receptor by Peptide Conjugation. International Journal of Molecular Sciences, 2019, 20, 2152. | 1.8 | 9 |
| 5 | Horizontal transfer of code fragments between protocells can explain the origins of the genetic code without vertical descent. Scientific Reports, 2018, 8, 3532. | 1.6 | 13 |
| 6 | Escherichia coli expression, purification, and refolding of human folate receptor Î± (hFRÎ±) and Î² (hFRÎ²). Protein Expression and Purification, 2018, 149, 17-22. | 0.6 | 3 |
| 7 | A Highly Bioactive Lys-Deficient IFN Leads to a Site-Specific Di-PEGylated IFN with Equivalent Bioactivity to That of Unmodified IFN-Î±2b. ACS Synthetic Biology, 2018, 7, 2537-2546. | 1.9 | 0 |
| 8 | Constraint-based perturbation analysis with cluster Newton method: a case study of personalized parameter estimations with irinotecan whole-body physiologically based pharmacokinetic model. BMC Systems Biology, 2017, 11, 129. | 3.0 | 9 |
| 9 | A Bacterial Continuous Culture System Based on a Microfluidic Droplet Open Reactor. Analytical Sciences, 2016, 32, 61-66. | 0.8 | 6 |
| 10 | High-frequency Noise Attenuation of a Two-component System Responding to Short-pulse Input. , 2016, , . | | 2 |
| 11 | Two site genetic incorporation of varying length polyethylene glycol into the backbone of one peptide. Chemical Communications, 2015, 51, 14385-14388. | 2.2 | 6 |
| 12 | In vitro selection of a photoresponsive peptide aptamer to glutathione-immobilized microbeads. Journal of Bioscience and Bioengineering, 2015, 119, 137-139. | 1.1 | 4 |
| 13 | Synthetic Biology. , 2015, , 2449-2450. | | 0 |
| 14 | Experimental Evolution of a Green Fluorescent Protein Composed of 19 Unique Amino Acids without Tryptophan. Origins of Life and Evolution of Biospheres, 2014, 44, 75-86. | 0.8 | 1 |
| 15 | Multiple Amino Acid-Excluded Genetic Codes for Protein Engineering Using Multiple Sets of tRNA Variants. ACS Synthetic Biology, 2014, 3, 140-144. | 1.9 | 6 |
| 16 | General Applicability of Synthetic Gene-Overexpression for Cell-Type Ratio Control via Reprogramming. ACS Synthetic Biology, 2014, 3, 638-644. | 1.9 | 8 |
| 17 | 2P280 Effects of downstream reporter genes on synthetic genetic circuits(24. Mathematical) Tj ETQq1 1 0.784314 rgBT /Overlock 10 | 0.0 | 0 |
| 18 | Effects of downstream genes on synthetic genetic circuits. BMC Systems Biology, 2014, 8, S4. | 3.0 | 16 |

| # | Article | IF | Citations |
|---|---|---|---|
| 19 | An Observation Method for Autonomous Signaling-Mediated Synthetic Diversification in Escherichia coli. Methods in Molecular Biology, 2014, 1151, 69-74. | 0.4 | 0 |
| 20 | Synthetic Biology. , 2014, , 1-2. | | 0 |
| 21 | The number of amino acids in a genetic code. RSC Advances, 2013, 3, 12512. | 1.7 | 5 |
| 22 | Waddington Landscape Based Experimental Model of Phenotypic Diversification. Seibutsu Butsuri, 2013, 53, 319-320. | 0.0 | 0 |
| 23 | Cultivation of Synthetic Biology with the iGEM Competition. Journal of Advanced Computational Intelligence and Intelligent Informatics, 2013, 17, 161-166. | 0.5 | 0 |
| 24 | Synthetic Biology and Dual Use. Journal of Disaster Research, 2013, 8, 698-704. | 0.4 | 0 |
| 25 | Tunability of the ratio of cell states after the synthetic diversification by the diversity generator. Communicative and Integrative Biology, 2012, 5, 393-394. | 0.6 | 0 |
| 26 | Simplification of the genetic code: restricted diversity of genetically encoded amino acids. Nucleic Acids Research, 2012, 40, 10576-10584. | 6.5 | 18 |
| 27 | An aptazyme-based molecular device that converts a small-molecule input into an RNA output. Chemical Communications, 2012, 48, 7556. | 2.2 | 12 |
| 28 | Design strategy for an initial state-independent diversity generator. Chem-Bio Informatics Journal, 2012, 12, 39-49. | 0.1 | 0 |
| 29 | RTRACS: A Modularized RNA-Dependent RNA Transcription System with High Programmability. Accounts of Chemical Research, 2011, 44, 1369-1379. | 7.6 | 23 |
| 30 | 2SL-04 Tunable synthetic phenotypic diversification on Waddington's landscape through autonomous signaling(2SL Information processing of biological systems,The 49th Annual Meeting of the) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 297 T | | |
| 31 | Tunable synthetic phenotypic diversification on Waddingtonâ€™s landscape through autonomous signaling. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 17969-17973. | 3.3 | 38 |
| 32 | Construction of a genetic AND gate under a new standard for assembly of genetic parts. BMC Genomics, 2010, 11, S16. | 1.2 | 12 |
| 33 | RNA Oscillator: Limit Cycle Oscillations based on Artificial Biomolecular Reactions. New Generation Computing, 2009, 27, 107-127. | 2.5 | 8 |
| 34 | Design and Numerical Analysis of RNA Oscillator. Proceedings in Information and Communications Technology, 2009, , 201-212. | 0.2 | 1 |
| 35 | A design and feasibility study of reactions comprising DNA molecular machine that walks autonomously by using a restriction enzyme. Natural Computing, 2008, 7, 303-315. | 1.8 | 2 |
| 36 | Synthetic Biology. New Generation Computing, 2008, 26, 347-364. | 2.5 | 2 |

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|---|---|---|---|
| 37 | Experiments and simulation models of a basic computation element of an autonomous molecular computing system. Physical Review E, 2008, 78, 041921. | 0.8 | 40 |
| 38 | 2P280 Autonomous DNA computing in cell-sized liposome(Native and artificial) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 702 Td (biomembr | 0.0 | 0 |
| 39 | S02I1 Molecular computing and molecular communication : synthetic approach using biomolecules(Molecular Computing and Molecular Communication: New Computing and) Tj ETQq1 1 0.784314 rgBT /Overlock 10 Tf 50 | | |
| 40 | 1P335 Construction of in vitro proteosynthesis molecular automaton(Bioengineering,Poster) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 622 | 0.0 | 0 |
| 41 | A Realization of DNA Molecular Machine That Walks Autonomously by Using a Restriction Enzyme. , 2007, , 54-65. | | 5 |
| 42 | Cationâˆ'Ï€ Interaction in the Polyolefin Cyclization Cascade Uncovered by Incorporating Unnatural Amino Acids into the Catalytic Sites of Squalene Cyclase. Journal of the American Chemical Society, 2006, 128, 13184-13194. | 6.6 | 72 |
| 43 | DNA polymerase programmed with a hairpin DNA incorporates a multiple-instruction architecture into molecular computing. BioSystems, 2006, 83, 18-25. | 0.9 | 25 |
| 44 | Translation of â€˜rareâ€™ Codons in a Cell-free Protein Synthesis System from Escherichia coli. Journal of Structural and Functional Genomics, 2006, 7, 31-36. | 1.2 | 28 |
| 45 | An engineered Escherichia coli tyrosyl-tRNA synthetase for site-specific incorporation of an unnatural amino acid into proteins in eukaryotic translation and its application in a wheat germ cell-free system. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9715-9720. | 3.3 | 163 |
| 46 | Site-specific incorporation of an unnatural amino acid into proteins in mammalian cells. Nucleic Acids Research, 2002, 30, 4692-4699. | 6.5 | 231 |
| 47 | Shifted positioning of the anticodon nucleotide residues of amber suppressor tRNA species by Escherichia coli arginyl-tRNA synthetase. FEBS Journal, 2001, 268, 6207-6213. | 0.2 | 12 |
| 48 | Molecular Computation by DNA Hairpin Formation. Science, 2000, 288, 1223-1226. | 6.0 | 363 |
| 49 | State transitions by molecules. BioSystems, 1999, 52, 81-91. | 0.9 | 94 |