

Curriculum Vitae

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Donghyuk Kim

Research Interests

Systems Biology, Machine Learning, Metabolic Engineering, Bacterial Pathogen

Education

University of California, San Diego, California, USA, 2014

Degree : Ph.D., Bioengineering

Thesis : Systems Assessment of Regulator Components in Bacterial Transcription Initiation

Adviser : Dr. Bernhard O. Palsson, Systems Biology Research Group

Seoul National University, Seoul, Korea, 2006

Degree : B.S., Computer Science and Engineering

Thesis : Pattern Classification and Completion by Probabilistic Library Model

Adviser : Dr. Byung-Tak Zhang, Biointelligence Lab

Degree : B.S., Biological Sciences

Thesis : Designing Efficient siRNAs for Gene Silencing

Adviser : Dr. V. Narry Kim, RNomics Lab

Professional Experience

- **Associate Professor**, School of Energy and Chemical Engineering, UNIST, Ulsan, Korea, *Sep 2020 ~ Present*
- **Assistant Professor**, Department of Chemical Engineering, School of Energy and Chemical Engineering, UNIST, Ulsan, Korea, *Jul 2018 ~ Aug 2020*
- **Assistant Professor**, Department of Genetic Engineering, School of Life Sciences, Kyung Hee University, Yongin, Korea, *Mar 2016 ~ Jun 2018*
- **Post-Doctoral Researcher**, Systems Biology Research Group of Dr. Bernhard Palsson, Department of Bioengineering, University of California, San Diego, *Jun 2014 ~ Feb 2016*
- **Graduate Student Researcher**, Systems Biology Research Group of Dr. Bernhard Palsson, Department of Bioengineering, University of California, San Diego, *Sep 2009 ~ May 2014*
- **Research Assistant**, RNomics Lab of Dr. V. Narry Kim, School of Biological Sciences, Seoul National University, *Jan 2006 ~ Jan 2007*

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- **Research Assistant**, Biointelligence Lab, Computer Science and Engineering, Seoul National University, Seoul, Korea, 2005

Professional Activity

- **Member**, The Korean Society for Biotechnology and Bioengineering, *Sep 2017 ~ Present*
- **Member**, The Korean Society for Microbiology and Biotechnology, *Jan 2018 ~ Present*
- **Member**, The Microbiological Society of Korea, *Feb 2018 ~ Present*
- **Member**, The Korean Society of Industrial and Engineering Chemistry, *Sep 2017 ~ Present*
- **Editor**, Journal of Microbiology and Biotechnology, *Mar 2017 ~ Feb 2018*
- **Committee of Research Affairs**, Korean Society of Bioinformatics and Systems Biology, *Mar 2017 ~ Feb 2018*

Awards and Scholarships

- Recipient, Research grant for UNIST Waste-plastic Carbon-cycling Center, The Circle Foundation, Seoul, South Korea, Dec 2020 ~ Dec 2023
- Recipient, Scholarship for the graduate study, Samsung Scholarship, Seoul, South Korea, *Fall 2008 ~ Fall 2013*

Publications

1. Experimental promoter identification of a food-borne pathogen *Salmonella Enterica* Subsp. *Enterica* Serovar Typhimurium with near single base-pair resolution. Lee SM[#], Le HT[#], Taizhanova A, Nong LK, Park JY, Lee EJ, Palsson BO, Kim D. Front Microbiol. In press.
2. Blanket antimicrobial resistance gene database with structural information, BOARDS, provides insights on historical landscape of resistance prevalence and effects of mutations in enzyme structure. Ko S[#], Kim J[#], Lim J, Lee SM, Park JY, Woo J, Scott-Nevros ZK, Kim JR, Yoon H, Kim D*. mSystems. In press.
3. A deep learning-based framework for battery reusability verification: one-step state-of-health estimation of pack and constituent modules using a generative algorithm and graphical representation. Park S[#], Lim D[#], Lee H, Jung D, Choi Y*, Lim H*, Kim D*. J. Mater. Chem. A. 2023 Oct 17. doi:10.1039/D3TA03603K.
4. Design of synthetic promoters for cyanobacteria with generative deep-learning model. Seo E, Choi YN, Shin YR, Kim D, Lee JW. Nucleic Acids Res. 2023 May 29. doi: 10.1093/nar/gkad451.

5. Comparative genomic analysis and BTEX degradation pathways of a thermotolerant *Cupriavidus cauae* PHS1. Sathesh-Prabu C[#], Woo J[#], Kim Y[#], Kim SM, Lee SB, Jeon CO*, Kim D*, Lee SK*. J Microbiol Biotechnol. 2023 Apr 10. doi:0.41014/jmb.2301.01011.
6. The *Escherichia coli* Fur pan-regulon has few conserved but many unique regulatory targets. Gao Y[#], Bang I[#], Seif Y, Kim D*, Palsson BO*. Nucleic Acids Res. 2023 Apr 07. doi:10.1093/nar/gkad253.
7. Deep-learning based spatio-temporal generative model on assessing state-of-health for Li-ion batteries with partially-cycled profiles. Park S[#], Lee H[#], Scott-Nevros ZK, Lim D, Seo DH, Choi Y*, Lim H*, Kim D*. Mater Horiz. 2023 Feb 20. doi:10.1039/D3MH00013C.
8. Deep-learning optimized DEOCSU suite provides an iterable pipeline for accurate ChIP-exo peak calling. Bang I[#], Lee SM[#], Park S[#], Park JY, Nong LK, Gao Y, Palsson BO, Kim D. Brief Bioinform. 2023 Jan 25. doi:10.1093/bib/bbad024.
9. Model-driven experimental design workflow expands understanding of regulatory role of Nac in *Escherichia coli*. Park JY, Lee SM, Ebrahim A, Scott-Nevros ZK, Kim J, Yang L, Sastry A, Seo SW*, Palsson BO*, Kim D*. NAR Genom Bioinform. 2023 Jan 20. doi:10.1093/nargab/lqad006.
10. Characterization of *Klebsiella pneumoniae* bacteriophages, KP1 and KP12, with deep learning-based structure prediction. Kim YJ[#], Lee SM[#], Nong LK[#], Kim J, Kim SB, Kim D. Front Microbiol. 2023 Jan 24. doi:10.3389/fmicb.2022.990910.
11. A Machine Learning Approach Reveals a Microbiota Signature for Infection with *Mycobacterium avium* subsp. *paratuberculosis* in cattle. Lee SM[#], Park HT[#], Park S, Lee J, Kim D, Yoo HS*, Kim D*. Microbiol Spectr. 2023 Jan 19. doi:10.1128/spectrum.03134-22.
12. Revealing Causes for False-Positive and False-Negative Calling of Gene Essentiality in *Escherichia coli* Using Transposon Insertion Sequencing. Choe D, Kim U, Hwang S, Seo SW, Kim D, Cho S, Palsson B, Cho BK. mBio. 2022 Dec 12. doi:10.1128/msystems.00896-22.
13. ChEAP: ChIP-exo Analysis Pipeline and the investigation of *Escherichia coli* RpoN protein-DNA interactions. Bang I[#], Nong LK[#], Park JY, Le HT, Lee SM, Kim D. Comput Struct Biotechnol J. 2022 Dec 02. doi:10.1016/j.csbj.2022.11.053.
14. Characterization of an Entner-Doudoroff pathway-activated *Escherichia coli*. Kim YE[#], Cho KH[#], Bang I[#], Kim CH, Ryu YS, Kim Y, Choi EM, Nong LK, Kim D*, Lee SK*. Biotechnol Biofuels Bioprod. 2022 Nov 09. doi.org/10.1186/s13068-022-02219-6
15. Pan-genome analysis reveals comparative genomic features of central metabolic pathways in *Methylobacterium extorquens*. Lee GM, Scott-Nevros ZK, Lee SM, Kim D. Biotechnol Bioprocess Eng. 2022 Sep 29. doi:10.1007/s12257-022-0154-1.
16. Delineating transcriptional crosstalk between *Mycobacterium avium* subsp. *paratuberculosis* and human THP-1 cell at early stage of infection via dual RNA-seq analysis. Park HT[#], Lee SM[#], Ko S, Kim S, Park HE, Shin MK, Kim D*, Yoo HS*. Vet Res. 2022 Sep 13. doi:10.1186/s13567-022-01089-y.
17. Comparative genomic analysis of plasmids encoding metallo- β -Lactamase NDM-5 in *Enterobacteriaceae* Korean isolates from Companion dogs. Kyung SM, Choi SW, Lim J, Shim S, Kim S, Im YB, Lee NE, Hwang CY, Kim D, Yoo HS. Sci Rep. 2022 Jan 28. doi:10.1038/s41598-022-05585-1.

18. proChIPdb: a chromatin immunoprecipitation database for prokaryotic organisms. Decker K[#], Gao Y[#], Rychel K[#], Al Bulushi T, Chauhan S, Kim D, Cho BK, Palsson B. Nucleic Acids Res. 2022 Jan 7. doi:10.1093/nar/gkab1043.
19. Real-time PCR for *Salmonella* serotyping Rapid real-time PCR for *Salmonella* serotyping based on novel unique gene markers by pangenome analysis. Yang SM, Kim E, Kim D, Kim HB, Baek J, Ko S, Kim D, Yoon H, Kim HY. Front Microbiol. 2021 Sep 21. doi:10.3389/fmicb.2021.750379.
20. Enhanced production of nonanedioic acid from nonanoic acid by engineered *Escherichia coli*. Lee Y, Sathesh-Prabu C, Kwak GH, Bang I, Jung HW, Kim D, Lee SK. Biotechnol J. 2021 May 08. doi:10.1002/biot.202000416.
21. Genomic diversity of *Mycobacterium avium* subsp. *paratuberculosis*: pangenomic approach for highlighting unique genomic features with newly constructed complete genomes. Lim J[#], Park HT[#], Ko S, Park HE, Lee GM, Kim S, Shin MK, Yoo HS*, Kim D*. Vet Res. 2021 Mar 18. doi:10.1186/s13567-021-00905-1.
22. Alpha-2-macroglobulin as a new promising biomarker improving the diagnostic sensitivity of bovine paratuberculosis. Park HE, Park JS, Park HT, Choi JG, Shin J, Jung MH, Kang HL, Baik SC, Lee WK, Kim , Yoo HS*, Shin MK*. Front Vet Sci. 2021 Mar 05. doi:10.3389/fvets.2021.637716.
23. Genome-wide Identification of DNA-protein Interaction to Reconstruct Bacterial Transcription Regulatory Network. Park JY[#], Rimal H[#], Bang I, Nong LK, Kim D. Biotechnol Bioprocess Eng. 2020 Dec 29. doi:10.1007/s12257-020-0030-9.
24. Development of a genoserotyping method for *Salmonella Infantis* detection on the basis of pan-genome analysis. Yang SM, Baek J, Kim E, Kim HB, Ko S, Kim D, Yoon H*, Kim HY*. Microorganisms. 2020 Dec 29. doi:10.3390/microorganisms9010067.
25. Mechanism of tolerance improvement of *Escherichia coli* W against 3-hydroxypropionic acid by deletion of less-characterized transcription factor *yieP*. Nguyen-Vo TP[#], Ko S[#], Ryu H, Kim JR, Kim D*, Park S*. Sci Rep. 2020 Nov 04. doi:10.1038/s41598-020-76120-3.
26. Comparative genome analysis reveals an evolutionary trace in the genomes of *Erwinia pyrifoliae*, a black shoot blight pathogen in apple and pear. Lee GM, Ko S, Oh EJ, Song YR, Kim D*, Oh CS*. Plant Pathol J. 2020 Oct 1. doi:10.5423/PPJ.OA.06.2020.0097.
27. Adaptive laboratory evolution of *Escherichia coli* lacking cellular byproduct formation for enhanced acetate utilization through compensatory ATP consumption. Seong W, Han GH, Lim HS, Baek JI, Kim SJ, Kim D, Kim SK, Lee H, Kim H, Lee SG*, Lee DH*. Metab Eng. 2020 Sep 12. doi:10.1016/j.ymben.2020.09.005.
28. Genomic and phenotypic characterization of a lytic bacteriophage CF1 infecting multi-drug resistant *Citrobacter freundii*. Kim Y[#], Ko S[#], Yeon YE, Kim H, Oh CS, Ahn JK*, Kim D*. Biotechnol Bioprocess Eng. 2020 Jun 29. doi:10.1007/s12257-019-0505-8.
29. Metabolic role of pyrophosphate-linked phosphofructokinase *pfk* for C1 assimilation in *Methylobacterium alcalophilum* 20Z. Nguyen AD[#], Nam G[#], Kim D*, Lee EY*. Microb Cell Fact. 2020 Jun 16. doi:10.1186/s12934-020-01382-5.

30. Unlocking the biosynthesis of sesquiterpenoids from methane via the methylerythritol phosphate pathway in methanotrophic bacteria, using α -humulene as a model compound. Nguyen AD, Kim D, Lee EY. *Metab Eng*. 2020 May 5. doi:10.1016/j.ymben.2020.04.011.
31. Metabolic engineering of *Escherichia coli* for 2,3-butanediol production from a major cellulosic biomass sugar by using glucose-inducible gene expression system. Sathesh-Prabu C[#], Kim D[#], Lee SK. *Bioresour Technol*. 2020 Apr 10. doi:10.1016/j.biortech.2020.123361.
32. Near-complete genome sequence of a potential eukaryotic probiotic *Saccharomyces cerevisiae* KCCM 51299: Application of genomic data in the food industry. Hwang J[#], Bang I[#], Kim D, Shin SC, Chin YW, Kim TW, Kim HJ. *3 Biotech*. Accepted.
33. Comprehensive genomic analysis on the novel species *Sphingomonas panacis* DCY99T reveals insights into iron tolerance of ginseng. Kim YJ^{*,*}, Park JY[#], Balusamy SR, Huo Y, Nong LK, Le HT, Yang DC, Kim D*. *Int J Mol Sci*. 2020 Mar 16. doi:10.3390/ijms21062019.
34. Functional cooperation of the glycine synthase-reductase and Wood-Ljungdahl pathways for autotrophic growth of *Clostridium drakei*. Song Y, Lee JS, Shin J, Lee GM, Jin S, Kang SG, Lee JK, Kim DR, Lee EY, Kim SC, Cho S, Kim D*, Cho BK*. *Proc Natl Acad Sci U S A*. 2020 Mar 13. doi:10.1073/pnas.1912289117.
35. Increasing Prevalence of Extended-Spectrum B-Lactamases in the Environment and Livestock: Challenges to Mitigate Antimicrobial Resistance. Lee S, Mir RA, Park SH, Kim D, Kim HY, Boughton RK, Morris JG, Jeong KC. *Crit Rev Microbiol*. 2020 Jan 24. doi: 10.1080/1040841X.2020.1715339.
36. The *Escherichia coli* Transcriptome Mostly Consists of Independently Regulated Modules. Anand VS, Gao Y, Szubin R, Hefner Y, Xu S, Kim D, Choudhary KS, Yang L, King ZA, Palsson BO. *Nat Commun*. 2019 Dec 04. doi:10.1038/s41467-019-13483-w.
37. Genome-scale evaluation of core one-carbon metabolism in gammaproteobacterial methanotrophs grown on methane and methanol. Nguyen AD[#], Park JY[#], Hwang IY[#], Hamilton R, Kalyuzhnaya MG, Kim D*, Lee EY*. *Metab Eng*. 2019 Oct 15. pii: S1096-7176(19)30307-6. doi: 10.1016/j.ymben.2019.10.004.
38. Photoluminescent and internal reflection scattering of hyaluronic acid-zinc oxide-ginsenoside Rh2 nanoparticles and their potential Cas9 apoptotic mechanism towards cancer cell lines. Kim YJ^{*,*}, Perumalsamy H[#], Castro-Aceituno V, Kim D, Markus J, Lee S, Park SY, Kim S, Yang DC. *Int J Nanomedicine*. 2019 Sep 17;2019(14):8195-8208. doi:10.2147/IJN.S221328.
39. Cellular responses to reactive oxygen species can be predicted on multiple biological scales from molecular mechanisms. Yang L, Mih N, Anand A, Park JH, Tan J, Yurkovich JT, Monk JM, Lloyd CJ, Sandberg TE, Seo SW, Kim D, Anand VS, Phaneuf P, Gao Y, Broddrick JT, Chen K, Heckmann D, Szubin R, Hefner Y, Feist AM, Palsson BO. *Proc Natl Acad Sci U S A*. 2019 Jul 9;116(28):14368-14373. doi: 10.1073/pnas.1905039116.
40. Fermentation product with new equol-producing *Lactobacillus paracasei* as a probiotic candidate for prevention of skin and intestinal disorder. Kwon JE[#], Lim J[#], Bang I, Kim I, Kim D*, Kang SC*. *J Sci Food Agric*. 2019 Feb 14. doi.org/10.1002/jsfa.9648.
41. Comparative transcriptome analysis of a novel obligate *Methylobacter* sp. DH-1 reveals key differences in the transcriptional responses of C1 and secondary metabolite pathways during

- growth on methane and methanol. Nguyen AD, Kim D*, Lee EY*. BMC Genomics. 2019 Feb 12. doi.org/10.1186/s12864-019-5487-6.
42. Genomic characterization of a newly isolated rhizobacteria *Sphingomonas panacis* reveals plant growth promoting effect to rice. Kim YJ^{#,*}, Lim J[#], Sukweenadhi J, Seok JW, Lee SW, Park JC, Taizhanova A, Kim D*, Yang DC. Biotechnol Bioprocess Eng. 2019 Feb 08. doi.org/10.1007/s12257-018-0386-2.
43. Characterizing post-translational modifications in prokaryotic metabolism using a multi-scale workflow. Brunk E[#], Chang RL, Xia J, Hefzi H, Yurkovich J, Kim D, Buckmiller E, Wang H, Cho BK, Yang C, Palsson BO, Church GM*, Lewis NE^{#,*}. Proc Natl Acad Sci U S A. 2018 Oct 9. doi.org/10.1073/pnas.1811971115.
44. Genomic characterization of the lytic bacteriophage phiEaP-8 effective against both *Erwinia amylovora* and *Erwinia pyrifoliae* causing severe diseases in apple and pear. Park J, Lee GM, Kim D, Park DH, Oh CS. Plant Pathol J. 2018 Oct 1. doi.org/10.5423/PPJ.NT.06.2018.0100.
45. Basics of genome-scale metabolic modeling and applications on C1-utilization. Kabimoldayev I[#], Nguyen AD[#], Yang L[#], Park S, Lee EY, Kim D. FEMS Microbiol Lett. 2018 Sep 25. doi.org/10.1093/femsle/fny241.
46. Deciphering bacterial xylose metabolism and metabolic engineering of industrial microorganisms for use as efficient microbial cell factories. Kim D, Woo HM. Appl Microbiol Biotechnol. 2018 Sep 20. doi.org/10.1007/s00253-018-9353-2.
47. Systematic discovery of uncharacterized transcription factors in *Escherichia coli* K-12 MG1655. Gao Y, Yurkovich JT, Seo SW, Kabimoldayev I, Drager A, Chen K, Sastry A, Mih N, Yang L, Eichner J, Cho BK, Kim D*, Palsson BO*. Nucleic Acids Res. 2018 Aug 23. doi.org/10.1093/nar/gky752.
48. Draft genome sequence of lytic bacteriophage KP1 infecting *Klebsiella pneumoniae*. Kim Y[#], Bang I[#], Yeon YE, Park JY, Han BK, Kim H, Ahn JK, Kim D. Korean J Microbiol. 2018 Jul 2. doi.org/10.7845/kjm.2018.54.2.152.
49. Draft genome sequence of lytic bacteriophage CP3 infecting anaerobic bacterial pathogen *Clostridium perfringens*. Kim Y[#], Ko S[#], Yeon YE, Le HT, Han BK, Kim H, Oh CS, Kim D. Korean J Microbiol. 2018 Jul 2. doi:10.7845/kjm.2018.54.2.149.
50. Coordination-driven self-assembly and anticancer studies of thiophene-derived donor and arene ruthenium acceptors. Kim T[#], Song HS[#], Singh J, Kim D, Kim H, Kang SC*, Chi KW*. Inorganica Chimica Acta. 2018 May 28. doi:10.1016/j.ica.2018.05.035.
51. Systematic metabolic engineering of *Methylobacterium alcaliphilum* 20Z for 2,3-butanediol production from methane. Nguyen AD, Hwang IY, Lee OK, Kim D, Kalyuzhnaya MG, Mariyana R, Hadiyati S, Kim MS*, Lee YE*. Metab Eng. 2018 Apr 16. doi: 10.1016/j.ymben.2018.04.010.
52. Draft Genome Sequence of Lytic Bacteriophage CF1 Infecting *Citrobacter freundii* Isolates. Kim YJ, Ko S, Yeon YE, Lim J, Han BK, Kim H, Ahn JK, Kim D. Korean J Microbiol. 2018 Apr 1. doi:10.7845/kjm.2018.7099.
53. Draft Genome Sequence of Lytic Bacteriophage SA7 Infecting *Staphylococcus aureus* Isolates. Kim YJ, Lee GM, Taizhanova A, Han BK, Kim H, Ahn JK, Kim D. Korean J Microbiol. 2018 Apr 1. doi:10.7845/kjm.2018.7098.

54. Draft genome sequence of a bacterial plant pathogen *Erwinia pyrifoliae* strain EpK1/15 isolated from an apple twig showing black shoot blight. Lee GM, Oh EJ, Park J, Ko S, Park DH, Kim D*, Oh CS*. Korean J Microbiol, 2018 Apr 1. doi:10.7845/kjm.2018.7087.
55. Isolation and identification of novel equol-producing bacterial strains. Kwon JE, Lim J, Kim I, Kim D*, Kang SC*. PLoS One, 2018 Feb 15;13(2):e0192490. doi:10.1371/journal.pone.0192490
56. Systems assessment of transcriptional regulation on central carbon metabolism by Cra and CRP. Kim D^{#,*}, Seo SW[#], Gao Y[#], Nam H, Guzman GI, Cho BK, Palsson BØ*. Nucleic Acids Res. 2018 Jan 31. doi:10.1093/nar/gky069.
57. Multiple plasmid-borne virulence genes of *Clavibacter michiganensis* subsp. *capsici* critical for disease development in pepper. Hwang IS, Oh EJ, Kim D, Oh CS. New Phytol. 2017 Nov 14. doi:10.1111/nph.14896.
58. Global transcriptional regulatory network for *Escherichia coli* robustly connects gene expression to transcription factor activities. Fang X[#], Sastry A[#], Mih N, Kim D, Yurkovich JT, Lloyd CJ, Tan J, Gao Y, Yang L*, Palsson BO*. Proc Natl Acad Sci U S A. 2017 Sep 19;114(38):10286-10291. doi: 10.1073/pnas.1702581114. Epub 2017 Sep 5.
59. Coordination-Driven Self-Assembly Using Ditopic Pyridyl-Pyrazolyl Donor and p-Cymene Ru(II) Acceptors: [2]Catenane Synthesis and Anticancer Activities. Jo JH[#], Singh N[#], Kim D[#], Cho SM, Mishra A, Kim H, Kang SC*, Chi KW*. Inorg Chem. 2017 June 30. doi: 10.10
60. Highly efficient silver nanowire/PEDPT:PSS composite microelectrodes via poly(ethylene glycol) photolithography. Kim D, Ko Y, Kim W, Kim D, You J. Opt Mater Express. 2017 June 8;7(7):2272-2279. doi:10.1364/OME.7.002272.
61. Revealing the genome-scale transcriptional regulatory landscape of OmpR highlights its expanded regulatory roles and unexpected importance of narX under osmotic stress in *Escherichia coli* K-12 MG1655. Seo SW^{#,*}, Geo Y[#], Kim D[#], Szubin R, Cho BK, Palsson BO*. Sci Rep. 2017 May 19. doi:10.1038/s41598-017-02110-7.
62. Selective bio-oxidation of propane to acetone using methane-oxidizing *Methylobacter* sp. DH-1. Hur DH, Nguyen TT, Kim D, Lee EY. J Ind Microbiol Biotechnol. 2017 Mar 20. doi: 10.1007/s10295-017-1936-x.
63. Elucidation of bacterial translation regulatory networks. Jeong Y, Shin H, Seo SW, Kim D, Cho S, Cho BK. Curr Opin Sys Biol. 2017 Mar 8. doi:10.1016/j.coisb.2017.01.009.
64. Rice pectin methylesterase inhibitor28 (OsPMEI28) encodes a functional PME1 and its overexpression results in a dwarf phenotype through increased pectin methylesterification levels. Nguyen HP[#], Jeong HY[#], Jeon SH, Kim D, Lee C. J Plant Physiol. 2016 Nov 18. doi: 10.1016/j.jplph.2016.11.006.
65. Multi-omic data integration enables discovery of hidden biological regularities. Ebrahim A[#], Brunk E[#], Tan J[#], O'Brien EJ, Kim D, Szubin R, Lerman JA, Lechner A, Sastry A, Bordbar A, Feist AM, Palsson BO. Nat Commun. 2016 Oct 26;7:13091. doi: 10.1038/ncomms13091.
66. Genome-wide Reconstruction of OxyR and SoxRS Transcriptional Regulatory Networks under Oxidative Stress in *Escherichia coli* K-12 MG1655. Seo SW[#], Kim D[#], Szubin R, Palsson BØ. Cell Reports. 2015 Aug 25. DOI: http://dx.doi.org/10.1016/j.celrep.2015.07.043.

67. A systems biology definition of the core proteome of metabolism and expression is consistent with high-throughput data. Yang L[#], Tan J[#], O'Brien EJ, Monk JM, Kim D, Li H, Charusanti P, Ebrahim A, Lloyd C, Yurkovich JT, Du B, Dräger A, Thomas A, Sun Y, Ma D, Saunders MA, Palsson BØ. Proc Natl Acad Sci U S A. 2015 Aug 10. pii: 201501384.
68. Decoding the genome-wide GadEWX transcriptional regulatory landscape for acid resistance in *Escherichia coli*. Seo SW[#], Kim D[#], O'Brien EJ, Szubin R, Palsson BØ. Nat Commun. 2015 Aug 10;6:7970. doi: 10.1038/ncomms8970.
69. Deciphering the Fur transcriptional regulatory network highlights its complex role beyond iron metabolism in *Escherichia coli*. Seo SW[#], Kim D[#], Latif H[#], O'Brien EJ, Szubin R, Palsson BO. Nat Commun. 2014 Sep 15;5:4910. doi: 10.1038/ncomms5910.
70. Determining the control circuitry of redox metabolism at the genome-scale. Federowicz S, Kim D, Ebrahim A, Lerman JA, Nagarajan H, Cho BK, Zengler K, Palsson BØ. PLoS Genet. 2014 Apr 3;10(4):e1004264. doi: 10.1371/journal.pgen.1004264. eCollection 2014.
71. Genome-scale reconstruction of the sigma factor network in *Escherichia coli*: topology and functional states. Cho BK[#], Kim D[#], Knight EM, Zengler K, Palsson BO. BMC Biol. 2014 Jan 24;12(1):4. doi: 10.1186/1741-7007-12-4.
72. Structural Systems Biology Evaluation of Metabolic Thermotolerance in *Escherichia coli*. Chang RL, Andrews K, Kim D, Li Z, Godzik A, Palsson BO. Science. 2013 Jun 7;340(6137):1220-3. doi: 10.1126/science.1234012.
73. Multiple-omic data analysis of *Klebsiella pneumoniae* MGH 78578 reveals its transcriptional architecture and regulatory features. Seo JH[#], Hong JS[#], Kim D, Cho BK, Huang TW, Tsai SF, Palsson BO, Charusanti P. BMC Genomics. 2012 Nov 29;13:679. doi: 10.1186/1471-2164-13-679.
74. Network context and selection in the evolution to enzyme specificity. Nam H*, Lewis NE*, Lerman JA, Lee DH, Chang RL, Kim D, Palsson BO. Science. 2012 Aug 31;337(6098):1101-4. doi: 10.1126/science.1216861.
75. Comparative analysis of regulatory elements between *Escherichia coli* and *Klebsiella pneumoniae* by genome-wide transcription start site profiling. Kim D[#], Hong JS[#], Qiu Y, Nagarajan H, Seo JH, Cho BK, Tsai SF, Palsson BØ. PLoS Genet. 2012;8(8):e1002867. doi: 10.1371/journal.pgen.1002867. Epub 2012 Aug 9.
76. The PurR regulon in *Escherichia coli* K-12 MG1655. Cho BK, Federowicz SA, Embree M, Park YS, Kim D, Palsson BØ. Nucleic Acids Res. 2011 Aug;39(15):6456-64. doi: 10.1093/nar/gkr307. Epub 2011 May 13.
77. Functional links between clustered microRNAs: suppression of cell-cycle inhibitors by microRNA clusters in gastric cancer. Kim YK, Yu J, Han TS, Park SY, Namkoong B, Kim DH, Hur K, Yoo MW, Lee HJ, Yang HK, Kim VN. Nucleic Acids Res. 2009 Apr;37(5):1672-81. doi: 10.1093/nar/gkp002. Epub 2009 Jan 19.