



## Markus Covert

Shriram Chair of the Department of Bioengineering, Professor of Bioengineering and, by courtesy, of Chemical and Systems Biology

### CONTACT INFORMATION

- **Chair's Office**

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### Bio

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#### BIO

Our focus is on building computational models of complex biological processes, and using these models to guide an experimental program. Such an approach leads to a relatively rapid identification and validation of previously unknown components and interactions. Biological systems of interest include metabolic, regulatory and signaling networks as well as cell-cell interactions. Current research involves the dynamic behavior of NF-kappaB, an important family of transcription factors whose aberrant activity has been linked to oncogenesis, tumor progression, and resistance to chemotherapy.

#### ACADEMIC APPOINTMENTS

- Professor, Bioengineering
- Professor (By courtesy), Chemical and Systems Biology
- Member, Bio-X
- Member, Cardiovascular Institute
- Faculty Fellow, Sarafan ChEM-H

#### ADMINISTRATIVE APPOINTMENTS

- Shriram Chair, Stanford Bioengineering, (2023- present)

#### HONORS AND AWARDS

- The Grimwade Medal for Biochemistry and Molecular Biology, University of Melbourne (2025)
- Allen Distinguished Investigator Award, Paul G. Allen Frontiers Group (2013-2016)
- Director's Pioneer Award, NIH (2009-2014)

#### PROFESSIONAL EDUCATION

- Ph.D., UCSD , Bioengineering/ Bioinformatics (2003)
- M.S., UCSD , Bioengineering (2002)
- B.S., Brigham Young University , Chemical Engineering (1997)

## LINKS

- Lab Website: <https://www.covert.stanford.edu/>

## Research & Scholarship

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### CURRENT RESEARCH AND SCHOLARLY INTERESTS

Our focus is on building computational models of complex biological processes, and using these models to guide an experimental program. Such an approach leads to a relatively rapid identification and validation of previously unknown components and interactions. Biological systems of interest include metabolic, regulatory and signaling networks as well as cell-cell interactions. Current research involves the dynamic behavior of NF-kappaB, an important family of transcription factors whose aberrant activity has been linked to oncogenesis, tumor progression, and resistance to chemotherapy.

## Teaching

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### COURSES

#### 2025-26

- Systems Biology: BIOE 101, BIOE 210 (Aut)

#### 2024-25

- Systems Biology: BIOE 101, BIOE 210 (Aut)

#### 2023-24

- Systems Biology: BIOE 101, BIOE 210 (Aut)

#### 2022-23

- Bioengineering Departmental Research Colloquium: BIOE 393 (Aut)
- Systems Biology: BIOE 101, BIOE 210 (Aut)

### STANFORD ADVISEES

#### Med Scholar Project Advisor

Sean Cheah

#### Doctoral Dissertation Reader (AC)

Eliel Akinbami, Frida Bjoerklund, Linus Hein, Yulin Huang, Micah Lawrence, Lorenzo Magni, Gustavo Santiago-Reyes, George Walters-Marrah

#### Postdoctoral Faculty Sponsor

Rong Ma

#### Doctoral Dissertation Advisor (AC)

Annabelle Fowler, Mia Grahm, Riley Juenemann, Cyrus Knudsen, Heena Saqib, Hyunjae Woo, Mica Yang

#### Doctoral (Program)

Eliel Akinbami

### GRADUATE AND FELLOWSHIP PROGRAM AFFILIATIONS

- Bioengineering (Phd Program)
- Biomedical Data Science (Phd Program)
- Chemical and Systems Biology (Phd Program)

## Publications

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### PUBLICATIONS

- **Cross-evaluation of *E. coli*'s operon structures via a whole-cell model suggests alternative cellular benefits for low- versus high-expressing operons.** *Cell systems*  
Sun, G., DeFelice, M. M., Gillies, T. E., Ahn-Horst, T. A., Andrews, C. J., Krummenacker, M., Karp, P. D., Morrison, J. H., Covert, M. W.  
2024
- **Whole-cell modeling of *E. coli* colonies enables quantification of single-cell heterogeneity in antibiotic responses.** *PLoS computational biology*  
Skalnik, C. J., Cheah, S. Y., Yang, M. Y., Wolff, M. B., Spangler, R. K., Talman, L., Morrison, J. H., Peirce, S. M., Agmon, E., Covert, M. W.  
2023; 19 (6): e1011232
- **Whole-cell modeling of *E. coli* confirms that in vitro tRNA aminoacylation measurements are insufficient to support cell growth and predicts a positive feedback mechanism regulating arginine biosynthesis.** *Nucleic acids research*  
Choi, H., Covert, M. W.  
2023
- **A multiplexed epitope barcoding strategy that enables dynamic cellular phenotypic screens.** *Cell systems*  
Kudo, T., Lane, K., Covert, M. W.  
2022
- **Simultaneous cross-evaluation of heterogeneous *E. coli* datasets via mechanistic simulation.** *Science (New York, N.Y.)*  
Macklin, D. N., Ahn-Horst, T. A., Choi, H., Ruggero, N. A., Carrera, J., Mason, J. C., Sun, G., Agmon, E., DeFelice, M. M., Maayan, I., Lane, K., Spangler, R. K., Gillies, et al  
2020; 369 (6502)
- **Engineered Fluorescent *E. coli* Lysogens Allow Live-Cell Imaging of Functional Prophage Induction Triggered inside Macrophages.** *Cell systems*  
Bodner, K. n., Melkonian, A. L., Barth, A. I., Kudo, T. n., Tanouchi, Y. n., Covert, M. W.  
2020
- **Deep Learning Automates the Quantitative Analysis of Individual Cells in Live-Cell Imaging Experiments.** *PLoS computational biology*  
Van Valen, D. A., Kudo, T., Lane, K. M., Macklin, D. N., Quach, N. T., DeFelice, M. M., Maayan, I., Tanouchi, Y., Ashley, E. A., Covert, M. W.  
2016; 12 (11)
- **High-sensitivity measurements of multiple kinase activities in live single cells.** *Cell*  
Regot, S., Hughey, J. J., Bajar, B. T., Carrasco, S., Covert, M. W.  
2014; 157 (7): 1724-1734
- **A Whole-Cell Computational Model Predicts Phenotype from Genotype** *CELL*  
Karr, J. R., Sanghvi, J. C., Macklin, D. N., Gutschow, M. V., Jacobs, J. M., Bolival, B., Assad-Garcia, N., Glass, J. I., Covert, M. W.  
2012; 150 (2): 389-401
- **Viruses in multi-scale ocean models: challenges and opportunities** *FRONTIERS IN MARINE SCIENCE*  
Talmy, D., Howard-Varona, C., Eveillard, D., Covert, M., Sullivan, M. B.  
2025; 12
- **The EcoCyc database (2025).** *EcoSal Plus*  
Karp, P. D., Paley, S., Caspi, R., Kothari, A., Krummenacker, M., Midford, P. E., Moore, L. R., Subhraveti, P., Gama-Castro, S., Tierrafria, V. H., Lara, P., Muñoz-Rascado, L., Bonavides-Martinez, et al  
2025: eesp00192024
- **Integrating multiplexed imaging and multiscale modeling identifies tumor phenotype conversion as a critical component of therapeutic T cell efficacy.** *Cell systems*  
Hickey, J. W., Agmon, E., Horowitz, N., Tan, T. K., Lamore, M., Sunwoo, J. B., Covert, M. W., Nolan, G. P.  
2024; 15 (4): 322-338.e5
- **The EcoCyc Database (2023).** *EcoSal Plus*

Karp, P. D., Paley, S., Caspi, R., Kothari, A., Krummenacker, M., Midford, P. E., Moore, L. R., Subhraveti, P., Gama-Castro, S., Tierrafria, V. H., Lara, P., Muñoz-Rascado, L., Bonavides-Martinez, et al  
2023: eesp00022023

- **An expanded whole-cell model of E. coli links cellular physiology with mechanisms of growth rate control.** *NPJ systems biology and applications*  
Ahn-Horst, T. A., Mille, L. S., Sun, G., Morrison, J. H., Covert, M. W.  
2022; 8 (1): 30
- **Microbial metabolites in the marine carbon cycle.** *Nature microbiology*  
Moran, M. A., Kujawinski, E. B., Schroer, W. F., Amin, S. A., Bates, N. R., Bertrand, E. M., Braakman, R., Brown, C. T., Covert, M. W., Doney, S. C., Dyhrman, S. T., Edison, A. S., Eren, et al  
2022; 7 (4): 508-523
- **Vivarium: an interface and engine for integrative multiscale modeling in computational biology.** *Bioinformatics (Oxford, England)*  
Agmon, E., Spangler, R. K., Skalnik, C. J., Poole, W., Peirce, S. M., Morrison, J. H., Covert, M. W.  
2022
- **The E. coli Whole-Cell Modeling Project.** *EcoSal Plus*  
Sun, G., Ahn-Horst, T. A., Covert, M. W.  
2021: eESP00012020
- **A forecast for large-scale, predictive biology: Lessons from meteorology.** *Cell systems*  
Covert, M. W., Gillies, T. E., Kudo, T., Agmon, E.  
2021; 12 (6): 488-496
- **Building Structural Models of a Whole Mycoplasma Cell.** *Journal of molecular biology*  
Maritan, M., Autin, L., Karr, J., Covert, M. W., Olson, A. J., Goodsell, D. S.  
2021: 167351
- **A Protocol to Engineer Bacteriophages for Live-Cell Imaging of Bacterial Prophage Induction Inside Mammalian Cells.** *STAR protocols*  
Bodner, K., Melkonian, A. L., Covert, M. W.  
2020; 1 (2): 100084
- **Stress-mediated exit to quiescence restricted by increasing persistence in CDK4/6 activation.** *eLife*  
Yang, H. W., Cappell, S. D., Jaimovich, A., Liu, C., Chung, M., Daigh, L. H., Pack, L. R., Fan, Y., Regot, S., Covert, M., Meyer, T.  
2020; 9
- **The Enemy of My Enemy: New Insights Regarding Bacteriophage-Mammalian Cell Interactions.** *Trends in microbiology*  
Bodner, K. n., Melkonian, A. L., Covert, M. W.  
2020
- **A Protocol to Engineer Bacteriophages for Live-Cell Imaging of Bacterial Prophage Induction Inside Mammalian Cells** *STAR Protocols*  
Bodner, K., Melkonian, A. L., Covert, M. W.  
2020
- **Deep learning for cellular image analysis.** *Nature methods*  
Moen, E., Bannon, D., Kudo, T., Graf, W., Covert, M., Van Valen, D.  
2019
- **NF-kappaB signaling dynamics is controlled by a dose-sensing autoregulatory loop.** *Science signaling*  
DeFelice, M. M., Clark, H. R., Hughey, J. J., Maayan, I., Kudo, T., Gutschow, M. V., Covert, M. W., Regot, S.  
2019; 12 (579)
- **Techniques for Studying Decoding of Single Cell Dynamics.** *Frontiers in immunology*  
Jeknić, S., Kudo, T., Covert, M. W.  
2019; 10: 755
- **Escalating Threat Levels of Bacterial Infection Can Be Discriminated by Distinct MAPK and NF-kappaB Signaling Dynamics in Single Host Cells.** *Cell systems*  
Lane, K., Andres-Terre, M., Kudo, T., Monack, D. M., Covert, M. W.

2019

- **Simultaneous Cross-Evaluation of Heterogeneous E. coli Datasets via Mechanistic Simulation**  
Covert, M.  
CELL PRESS.2019: 451A
- **Combinatorial processing of bacterial and host-derived innate immune stimuli at the single-cell level.** *Molecular biology of the cell*  
Gutschow, M. V., Mason, J. C., Lane, K. M., Maayan, I., Hughey, J. J., Bajar, B. T., Amatya, D. N., Valle, S. D., Covert, M. W.  
2018: mbcE18070423
- **Live-cell measurements of kinase activity in single cells using translocation reporters** *NATURE PROTOCOLS*  
Kudo, T., Jeknic, S., Macklin, D. N., Akhter, S., Hughey, J. J., Regot, S., Covert, M. W.  
2018; 13 (1): 155–69
- **Combining Comprehensive Analysis of Off-Site Lambda Phage Integration with a CRISPR-Based Means of Characterizing Downstream Physiology** *MBIO*  
Tanouchi, Y., Covert, M. W.  
2017; 8 (5)
- **Measuring Signaling and RNA-Seq in the Same Cell Links Gene Expression to Dynamic Patterns of NF- $\kappa$ B Activation.** *Cell systems*  
Lane, K., Van Valen, D., DeFelice, M. M., Macklin, D. N., Kudo, T., Jaimovich, A., Carr, A., Meyer, T., Pe'er, D., Boutet, S. C., Covert, M. W.  
2017; 4 (4): 458-469 e5
- **High-resolution imaging and computational analysis of haematopoietic cell dynamics in vivo.** *Nature communications*  
Koechlein, C. S., Harris, J. R., Lee, T. K., Weeks, J., Fox, R. G., Zimdahl, B., Ito, T., Blevins, A., Jung, S., Chute, J. P., Chourasia, A., Covert, M. W., Reya, et al  
2016; 7: 12169-?
- **Why Build Whole-Cell Models?** *Trends in cell biology*  
Carrera, J., Covert, M. W.  
2015; 25 (12): 719-722
- **NetworkPainter: dynamic intracellular pathway animation in Cytobank** *BMC BIOINFORMATICS*  
Karr, J. R., Guturu, H., Chen, E. Y., Blair, S. L., Irish, J. M., Kotecha, N., Covert, M. W.  
2015; 16
- **Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models.** *PLoS computational biology*  
Karr, J. R., Williams, A. H., Zucker, J. D., Raue, A., Steiert, B., Timmer, J., Kreutz, C., Wilkinson, S., Allgood, B. A., Bot, B. M., Hoff, B. R., Kellen, M. R., Covert, et al  
2015; 11 (5)
- **Summary of the DREAM8 Parameter Estimation Challenge: Toward Parameter Identification for Whole-Cell Models.** *PLoS computational biology*  
Karr, J. R., Williams, A. H., Zucker, J. D., Raue, A., Steiert, B., Timmer, J., Kreutz, C., Wilkinson, S., Allgood, B. A., Bot, B. M., Hoff, B. R., Kellen, M. R., Covert, et al  
2015; 11 (5): e1004096
- **Single-cell variation leads to population invariance in NF- $\kappa$ B signaling dynamics.** *Molecular biology of the cell*  
Hughey, J. J., Gutschow, M. V., Bajar, B. T., Covert, M. W.  
2015; 26 (3): 583-590
- **NetworkPainter: dynamic intracellular pathway animation in Cytobank.** *BMC bioinformatics*  
Karr, J. R., Guturu, H., Chen, E. Y., Blair, S. L., Irish, J. M., Kotecha, N., Covert, M. W.  
2015; 16: 172-?
- **WholeCellSimDB: a hybrid relational/HDF database for whole-cell model predictions** *DATABASE-THE JOURNAL OF BIOLOGICAL DATABASES AND CURATION*  
Karr, J. R., Phillips, N. C., Covert, M. W.  
2014

- **Nonlytic viral spread enhanced by autophagy components** *PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA*  
Bird, S. W., Maynard, N. D., Covert, M. W., Kirkegaard, K.  
2014; 111 (36): 13081-13086
- **Nonlytic viral spread enhanced by autophagy components.** *Proceedings of the National Academy of Sciences of the United States of America*  
Bird, S. W., Maynard, N. D., Covert, M. W., Kirkegaard, K.  
2014; 111 (36): 13081-13086
- **The future of whole-cell modeling** *CURRENT OPINION IN BIOTECHNOLOGY*  
Macklin, D. N., Ruggero, N. A., Covert, M. W.  
2014; 28: 111-115
- **Incorporation of flexible objectives and time-linked simulation with flux balance analysis.** *Journal of theoretical biology*  
Birch, E. W., Udell, M., Covert, M. W.  
2014; 345: 12-21
- **WholeCellSimDB: a hybrid relational/HDF database for whole-cell model predictions.** *Database : the journal of biological databases and curation*  
Karr, J. R., Phillips, N. C., Covert, M. W.  
2014; 2014
- **Accelerated discovery via a whole-cell model.** *Nature methods*  
Sanghvi, J. C., Regot, S., Carrasco, S., Karr, J. R., Gutschow, M. V., Bolival, B., Covert, M. W.  
2013; 10 (12): 1192-1195
- **Accelerated discovery via a whole-cell model** *NATURE METHODS*  
Sanghvi, J. C., Regot, S., Carrasco, S., Karr, J. R., Gutschow, M. V., Bolival, B., Covert, M. W.  
2013; 10 (12): 1192-?
- **Towards a whole-cell modeling approach for synthetic biology** *CHAOS*  
Purcell, O., Jain, B., Karr, J. R., Covert, M. W., Lu, T. K.  
2013; 23 (2)
- **Single-Cell and Population NF-kappa B Dynamic Responses Depend on Lipopolysaccharide Preparation** *PLOS ONE*  
Gutschow, M. V., Hughey, J. J., Ruggero, N. A., Bajar, B. T., Valle, S. D., Covert, M. W.  
2013; 8 (1)
- **WholeCellKB: model organism databases for comprehensive whole-cell models.** *Nucleic acids research*  
Karr, J. R., Sanghvi, J. C., Macklin, D. N., Arora, A., Covert, M. W.  
2013; 41 (Database issue): D787-92
- **Accelerated discovery via a whole-cell model** *Nature Methods.*  
Sanghvi, J. C., Regot, S., Carrasco, G. S., Karr, J. R., Gutschow, M. V., Bolival, B., Covert, M.  
2013
- **WholeCellViz: data visualization for whole-cell models.** *BMC bioinformatics*  
Lee, R., Karr, J. R., Covert, M. W.  
2013; 14 (1): 253-?
- **WholeCellKB: model organism databases for comprehensive whole-cell models** *NUCLEIC ACIDS RESEARCH*  
Karr, J. R., Sanghvi, J. C., Macklin, D. N., Arora, A., Covert, M. W.  
2013; 41 (D1): D787-D792
- **Single-cell and population NF- $\kappa$ B dynamic responses depend on lipopolysaccharide preparation.** *PloS one*  
Gutschow, M. V., Hughey, J. J., Ruggero, N. A., Bajar, B. T., Valle, S. D., Covert, M. W.  
2013; 8 (1)
- **Determining Host Metabolic Limitations on Viral Replication via Integrated Modeling and Experimental Perturbation** *PLOS COMPUTATIONAL BIOLOGY*

- Birch, E. W., Ruggero, N. A., Covert, M. W.  
2012; 8 (10)
- **Neuron-to-neuron transmission of alpha-synuclein fibrils through axonal transport** *ANNALS OF NEUROLOGY*  
Freundt, E. C., Maynard, N., Clancy, E. K., Roy, S., Bousset, L., Sourigues, Y., Covert, M., Melki, R., Kirkegaard, K., Brahic, M.  
2012; 72 (4): 517-524
  - **Competing pathways control host resistance to virus via tRNA modification and programmed ribosomal frameshifting** *MOLECULAR SYSTEMS BIOLOGY*  
Maynard, N. D., Macklin, D. N., Kirkegaard, K., Covert, M. W.  
2012; 8
  - **High-throughput, single-cell NF-kappa B dynamics** *CURRENT OPINION IN GENETICS & DEVELOPMENT*  
Lee, T. K., Covert, M. W.  
2010; 20 (6): 677-683
  - **Single-cell NF-kappa B dynamics reveal digital activation and analogue information processing** *NATURE*  
Tay, S., Hughey, J. J., Lee, T. K., Lipniacki, T., Quake, S. R., Covert, M. W.  
2010; 466 (7303): 267-U149
  - **The virus as metabolic engineer** *BIOTECHNOLOGY JOURNAL*  
Maynard, N. D., Gutschow, M. V., Birch, E. W., Covert, M. W.  
2010; 5 (7): 686-694
  - **A Forward-Genetic Screen and Dynamic Analysis of Lambda Phage Host-Dependencies Reveals an Extensive Interaction Network and a New Anti-Viral Strategy** *PLOS GENETICS*  
Maynard, N. D., Birch, E. W., Sanghvi, J. C., Chen, L., Gutschow, M. V., Covert, M. W.  
2010; 6 (7)
  - **Computational modeling of mammalian signaling networks** *WILEY INTERDISCIPLINARY REVIEWS-SYSTEMS BIOLOGY AND MEDICINE*  
Hughey, J. J., Lee, T. K., Covert, M. W.  
2010; 2 (2): 194-209
  - **Genome-scale metabolic networks** *WILEY INTERDISCIPLINARY REVIEWS-SYSTEMS BIOLOGY AND MEDICINE*  
Terzer, M., Maynard, N. D., Covert, M. W., Stelling, J.  
2009; 1 (3): 285-297
  - **A Noisy Paracrine Signal Determines the Cellular NF-kappa B Response to Lipopolysaccharide** *SCIENCE SIGNALING*  
Lee, T. K., Denny, E. M., Sanghvi, J. C., Gaston, J. E., Maynard, N. D., Hughey, J. J., Covert, M. W.  
2009; 2 (93)
  - **A dynamic network of transcription in LPS-treated human subjects** *BMC SYSTEMS BIOLOGY*  
Seok, J., Xiao, W., Moldawer, L. L., Davis, R. W., Covert, M. W.  
2009; 3
  - **Integrating metabolic, transcriptional regulatory and signal transduction models in Escherichia coli** *BIOINFORMATICS*  
Covert, M. W., Xiao, N., Chen, T. J., Karr, J. R.  
2008; 24 (18): 2044-2050
  - **Integrated Flux Balance Analysis Model of Escherichia coli** *Bioinformatics*.  
Covert, M. W., Xiao, N., Chen, T. J., Karr, J. R.  
2008; 18 (24): 2044-2050
  - **Achieving stability of lipopolysaccharide-induced NF-kappa B activation** *SCIENCE*  
Covert, M. W., Leung, T. H., Gaston, J. E., Baltimore, D.  
2005; 309 (5742): 1854-1857
  - **Integrated regulatory and metabolic models** *Computational Systems Biology, Academic Press, New York*  
Covert, M.W.  
2005

- **Computational Systems Biology. *Integrated regulatory and metabolic models***  
Covert, M. W.  
Academic Press.2005
- **Integrating high-throughput and computational data elucidates bacterial networks *NATURE***  
Covert, M. W., Knight, E. M., Reed, J. L., Herrgard, M. J., Palsson, B. O.  
2004; 429 (6987): 92-96
- **Reconstruction of microbial transcriptional regulatory networks *CURRENT OPINION IN BIOTECHNOLOGY***  
Herrgard, M. J., Covert, M. W., Palsson, B. O.  
2004; 15 (1): 70-77
- **Identifying constraints that govern cell behavior: A key to converting conceptual to computational models in biology? *BIOTECHNOLOGY AND BIOENGINEERING***  
Covert, M. W., Famili, I., Palsson, B. O.  
2003; 84 (7): 763-772
- **Reconciling gene expression data with known genome-scale regulatory network structures *3rd International Conference on Systems Biology 2002***  
Herrgard, M. J., Covert, M. W., Palsson, B. O.  
COLD SPRING HARBOR LAB PRESS, PUBLICATIONS DEPT.2003: 2423-34
- **Constraints-based models: Regulation of gene expression reduces the steady-state solution space *JOURNAL OF THEORETICAL BIOLOGY***  
Covert, M. W., Palsson, B. O.  
2003; 221 (3): 309-325
- **Transcriptional regulation in constraints-based metabolic models of *Escherichia coli* *JOURNAL OF BIOLOGICAL CHEMISTRY***  
Covert, M. W., Palsson, B. O.  
2002; 277 (31): 28058-28064
- **Genome-scale metabolic model of *Helicobacter pylori* 26695 *9th International Conference on Microbial Genomes***  
Schilling, C. H., Covert, M. W., Famili, I., Church, G. M., Edwards, J. S., Palsson, B. O.  
AMER SOC MICROBIOLOGY.2002: 4582-93
- **Metabolic modelling of microbes: the flux-balance approach *Environ Microbiol.***  
Edwards, J. S., Covert, M. W., Palsson, B. O.  
2002; 3 (4): 133-40
- **Regulation of gene expression in flux balance models of metabolism *JOURNAL OF THEORETICAL BIOLOGY***  
Covert, M. W., Schilling, C. H., Palsson, B.  
2001; 213 (1): 73-88
- **Metabolic modeling of microbial strains in silico *TRENDS IN BIOCHEMICAL SCIENCES***  
Covert, M. W., Schilling, C. H., Famili, I., Edwards, J. S., Goryanin, I. I., Selkov, E., Palsson, B. O.  
2001; 26 (3): 179-186
- **Encyclopedia of Microbiology. *Genomic Engineering of Bacterial Metabolism***  
Edwards, J. S., Schilling, C. H., Covert, M. W., Smith, S. J., Palsson, B. O.  
Academic Press.2000