JERRY M. PARKS

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EDUCATION

2008	Ph.D. Chemistry, Duke University, Advisor: Weitao Yang
2001	M.S. Chemistry, Southern Methodist University, Advisor: George P. Ford
1999	B.S. Chemistry, Texas Christian University

PROFESSIONAL POSITIONS

2020 – present	Group Leader, Molecular Biophysics, Biosciences Division, ORNL
2015 – 2020	R & D Staff, Biosciences Division, Oak Ridge National Laboratory
2015 – present	Joint Faculty, Department of Biochemistry and Cellular and Molecular Biology, University of Tennessee
2015 – present	Adjunct Assistant Professor, Genome Science and Technology Graduate Program, University of Tennessee
2009 – 2015	R & D Associate, Biosciences Division, Oak Ridge National Laboratory
2008 – 2009	Postdoctoral Research Associate, Center for Molecular Biophysics, Biosciences Division, Oak Ridge National Laboratory, Advisor: Jeremy C. Smith

Awards

2020	ORNL Team Award for Outstanding Scholarly Output
2014	ORNL Nominee for the Blavatnik Award for Young Scientists, Chemistry Category
2013	ORNL Director's Award for Outstanding Team Accomplishment "for groundbreaking research in biotic and abiotic mechanisms of mercury methylation in the environment, leading to high-impact publications in *Science* and *Nature Geoscience*"
2013	UT-Battelle Team Award for Scientific Research
2013	ORNL Significant Event Award – For the discovery of genes and proteins required for bacterial mercury methylation

Selected recent publications

Ishida T, Parks JM, and Smith JC. Insight into the Catalytic Mechanism of GH11 Xylanase: Computational Analysis of Substrate Distortion based on a Neutron Structure. *J Am Chem Soc*. **2020**, In press. **DOI**: 10.1021/jacs.0c02148

Aranha MP, Jewel YSM, Beckman RA, Weiner LM, Mitchell JC, Parks JM, and Smith JC. Combining 3D modeling with artificial intelligence to increase specificity and precision in peptide:MHC binding predictions. *J Immunol*. **2020**, 205, 1962-1977.

Cooper CJ, Zheng, K, Rush KW, Johs A, Sanders BC, Pavlopoulos G, Kyrpides NC, Podar M, Ovchinnikov S, Ragsdale SW, and Parks JM. Structure determination of the HgcAB complex using metagenome sequence data: Insight into the mechanism of mercury methylation. *Commun Biol.* **2020**, 3, 320.

Cross KL, Campbell JH, Balachandran M, Campbell AG, Cooper SJ, Griffen A, Heaton M, Joshi S, Klingeman D, Leys E, Yang Z, Parks JM, and Podar M. Targeted isolation and cultivation of uncultivated bacteria by reverse genomics. *Nat Biotechnol,* **2019**, 37, 1314-1321.

Hwang H, Paracini N, Parks JM, Lakey JH and Gumbart JC. Distribution of mechanical stress in the *Escherichia coli* cell envelope. *BBA Biomembranes*, **2018**, 1860, 2566-2575.

Cooper SJ, Krishnamoorthy G, Wolloscheck D, Nguyen J, Walker JK, Rybenkov VV, Parks JM and Zgurskaya HI. Molecular properties that define the activities of antibiotics in *Escherichia coli* and *Pseudomonas aeruginosa*. *ACS Infect. Dis*, **2018**, 4, 1223–1234.

Dajnowicz S. Parks JM, Hu X, Johnston RC, Kovalevsky A and Mueser TC. Hyperconjugation promotes catalysis in a pyridoxal 5'-phosphate-dependent enzyme. *ACS Catal*, **2018**, 8, 6733–6737.

Langan PS, Vandavasi VG, Cooper SJ, Weiss KL, Ginell SL, Parks JM, and Coates L. Substrate binding induces conformational changes in a class A β-lactamase that prime it for catalysis. *ACS Catal*, **2018**, 8, 2428-2437.

Dajnowicz S, Johnston RC, Parks JM, Blakeley MP, Keen DA, Weiss KL, Gerlits O, Kovalevsky A, and Mueser TC. Direct visualization of critical hydrogen atoms in a pyridoxal 5'-phosphate enzyme. *Nat Commun*, **2017**, 8, 955.

Abdali N, Parks JM, Haynes KM, Chaney JL, Green AT, Wolloscheck D, Walker JK, Rybenkov VV, Baudry J, Smith JC and Zgurskaya HI. Reviving antibiotics: Efflux pump inhibitors that interact with AcrA, a membrane fusion protein of the AcrAB-TolC multidrug efflux pump. *ACS Infect Dis*, **2017**, 3, 89–98.

Wan Q, Parks JM, Hanson BL, Fischer SZ, Ostermann A, Schrader TE, Graham DE, Coates L, Langan P and Kovalevsky A. Direct determination of protonation states and visualization of hydrogen bonding in a glycoside hydrolase with neutron crystallography, *Proc Nat Acad Sci USA*, **2015**, 112, 12384–12389.

Smith SD, Bridou R, Johs A, Parks JM, Elias DA, Hurt Jr, RA, Brown SD. Podar M and Wall JD. Site-directed mutagenesis of HgcA and HgcB reveals amino acid residues important for mercury methylation. *Appl Environ Microbiol*, **2015**, 81, 3205–3217.

Parks JM, Johs A, Podar M, Bridou R, Hurt Jr, RA, Smith SD, Tomanicek SJ, Qian Y, Brown SD, Brandt CC, Palumbo AV, Smith JC, Wall JD, Elias DA and Liang L. The genetic basis for bacterial mercury methylation, *Science*, **2013**, 339**,** 1332–1335.