Researcher Information Form

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Research Interest (1-2 Sentences)**:**
My research has involved the mechanism, function, and drug discovery of key proteins in ADP-ribosylation metabolism and signaling, with particular focus on the dynamic regulation of residue-specific ADP-ribosylations by two ADP-ribosylation reversal enzymes, ADP-ribosyl-acceptor hydrolase 3 (ARH3) and PAR glycohydrolase (PARG). I seek to address questions of (1) how ADP-ribosylation reversal enzymes specifically recognize ligands & substrates, (2) how they are assembled into a multi-protein complex for their specialized functions and regulation, and (3) how we can translate our findings to develop novel and tumor-selective cancer therapeutics.

Unique Resources/Techniques:
TR-FRET enzyme activity assay platforms
Biochemistry and monitoring of ADP-ribosylations
Nucleic acid/DNA repair enzymology
X-ray crystallography and Small Angle X-ray Scattering (SAXS)
Chemical library screening for drug discovery
Hit validation and structure-based optimization

Representative Publications (5 Maximum, May use Hyperlink)**:**

Houl, J., Ye, Z., Brosey, C., Balapiti-Modarage, L.P.F., Namjoshi, S., Bacolla, A., Laverty, D., Walker, B.L., Pourfarjam, Y., Warden, L.S., Chinnam, N.B., Moiani, D., Stegeman, R.A., Chen, M.K., Hung, M.C., Nagel, Z.D., Ellenberger, T., **Kim, I.K.**¶, Jones, D.E., Ahmed, Z.¶, and Tainer, J.A¶. (2019) Selective small-molecule poly(ADP-ribose) glycohydrolase inhibitor causes radiation sensitization, replication fork stalling, and cancer cell death. *Nature Communications*. 10 (1), 5654 (¶: Co-corresponding author), PMCID: PMC6906431.

Pourfarjam, Y., Ventura, J., Kurinov, I., Cho, A., Moss, J., and **Kim, I.K.** (2018). Structure of human ADP-ribosyl-acceptor hydrolase 3 bound to ADP-ribose reveals a conformational switch that enables specific substrate recognition. *Journal of Biological Chemistry*. 293, 12350-12359, PMCID: PMC6093245.

Pourfarjam, Y., Kasson, S., Tran, L., Ho, C. and **Kim, I.K.** (2020) PARG has a robust endo-glycohydrolase activity that releases protein-free poly(ADP-ribose) chains. *Biochemical and Biophysical Research Communications. in press*

Kim, I.K.[#], Stegeman, R.A., Brosey, C.A. & Ellenberger, T.[#] (2015). A quantitative assay reveals ligand specificity of the DNA scaffold repair protein XRCC1 and efficient disassembly of complexes of XRCC1 and the poly(ADP-ribose) polymerase 1 by poly(ADP-ribose) glycohydrolase. Journal of Biological Chemistry, 290(6), 3775-3783. ([#]Co-corresponding author), PMCID: PMC4319041.

Kim, I.K., Kiefer, J.R., Ho, C.M.W., Stegeman, R.A., Classen, S., Tainer, J.A. & Ellenberger, T. (2012). Structure of mammalian poly(ADP-ribose) glycohydrolase reveals a flexible tyrosine clasp as a substrate-binding element. Nature Structural & Molecular Biology, 19(6), 653-656, PMCID: PMC3381899.