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Education:

1988-1993: B.S., Biochemistry and Biophysics, University of Science and Technology of China, P.R.China
1993-1996: M.S., Biophysics, crystallography, Institute of Biophysics, Chinese Academy of Sciences, P.R.China
1996-2001: Ph.D., Biophysics, crystallography, The Ohio State University
2001-2006: Protein crystallography, Research Associate, Howard Hughes Institute at site of University of Washington, WA

Academic Appointments:

2001-2006: Research Associate, Howard Hughes Medical Institute, WA
2006-2011: Assistant Professor, Oklahoma State University, OK
2011-2016: Associate Professor, Oklahoma State University, OK
2016-present: Professor, Oklahoma State University, OK

Awards and Honors:

2000: Chung Soo Yoo Award, Pittsburgh Diffraction Conference, PA

Other Experience and Professional Memberships:

1997-present: American Crystallography Association member
1997-present: American Biophysical Society member

Research Funding:

Current:

- 2014-2019: NIH RO1AI079217, UTHSCSA, "Poxvirus Immune Evasion Mechanisms", Awarded: \$409,930, Role: Co-PI
 - 2014-2014: OCAST HR14-068, "Structure and function studies on the signaling complex of interleukin 18", Awarded: \$135,000, Role: PI
 - R21AI1133589, NIH, "Non-vesicular lipid transport by poxvirus A6 protein", Awarded: \$418,314, Role: MPI
 - R15CA219907, NIH, "Structure/function studies of anti-cancer Hsp90 inhibitors that target the C-terminal domain", Awarded: \$427,491, Role: MPI
- Past:

- 2014-2017: NIH R21AI113539, "Structure-function studies on a key signaling module from interleukin 17 receptor", Awarded: \$395,195, Role: PI
- 2009-2014: NIH/NIAID 1R01AI081928-01, "Structure-function studies on IL-18, IL-18 binding proteins and receptors", Awarded: \$1,343,644, Role: PI
- 2011-2014: OCAST. HR11-118, "Structure function studies on ROC dimeric GTPase", Role: PI, \$135,000
- 2008-2012: NIH/NINDS 1R15 NS062287-01A1, "Structural insights into the mechanism of the novel dimeric ROC GTPase from LRRK2", Awarded: \$221,550, Role: PI

Selected Publications:

1. Krumm B, Meng X, Xiang Y, Deng J. Identification of small molecule inhibitors of interleukin-18. 2017. *Sci Rep.* 7:483.
2. Hu Y, Wang Y, Deng J#, Jiang H#. The structure of a prophenoloxidase (PPO) from *Anopheles gambiae* provides new insights into the mechanism of PPO activation. 2016. *BMC Biol.* 14:2. (# correspondence authors contributing equally).
3. Meng X, Krumm B, Li Y, Deng J#, Xiang Y#. Structural basis for antagonizing a host restriction factor by C7 family of poxvirus host-range proteins. 2015. *Proc Natl Acad Sci U S A.* 112:14858-14863. (#correspondence authors, contributing equally).
4. Kolli S, Meng X, Wu X, Shengjuler D, Cameron C, Xiang Y, Deng J. Structure –function analysis of vaccinia virus H7 protein reveals a novel phosphoinositide binding fold essential for poxvirus replication. 2015. *J Virol*, 89:2209-19.
5. Krumm B, Xiang Y, Deng J. Structural Biology of IL-1 superfamily: key cytokines in the regulation of immune and inflammatory responses. 2014. *Protein Sci*, 23:526-538.
6. Meng X, Wu X, Yan B, Deng J, Xiang Y. Analysis of the role of vaccinia virus H7 in virion membrane biogenesis with an H7-deletion mutant. 2013. *J Virol*, 87:8247-8253.
7. Zhang B, Liu C, Qian W, Han Y, Li X, Deng J. Crystal structure of IL-17 Receptor B SEFIR domain. 2013. *J Immunol*, 190:2320-2326.
8. Krumm B, Meng X, Xiang Y and Deng J. A Unique Bivalent Binding and Inhibition Mechanism by the Yatapoxvirus Interleukin 18 Binding Protein. 2012. *Plos Pathogens*, e1002876.
9. Peng X, Wang Y, Kolli, S, Deng J*, Li L, Wang Z, Raj JU, Gou D*. Physical and functional interactions between the ID1 and p65 for activation of NF-kB. 2012. *Am J Physiol Cell Physiol*, 303:C267-C277. (* Correspondence Authors).
10. Liu C, Swaidani S, Qian W, Kang Z, Sun P, Han Y, Wang C, Gulen MF, Yin W, Zhang C, Fox PL, Aronica M, Hamilton TA, Misra S, Deng J, Li X. A CC' loop decoy peptide blocks the interaction between Act1 and IL-17RA to attenuate IL-17- and IL-25-induced inflammation. 2011. *Sci Signal*, 4(197):ra72.
11. Li Y, Meng X, Xiang Y, Deng J. Structure function studies of vaccinia virus host-range protein K1 reveal a novel functional surface for ankyrin-repeat proteins. 2010. *J Virol*, 84:3331-3338.
12. Li Y, Wang Y, Jiang H, Deng J. Crystal structure of *Manduca sexta* prophenoloxidase provides insights into the mechanism of type 3 copper enzymes. 2009. *Proc Natl Acad Sci U S A*, 106:17002-17006.
13. Li Y, Dunn L, Greggio E, Krumm B, Jackson G, Cookson M, Lewis P, Deng J. The R1441C mutation alters the folding properties of the ROC domain of LRRK2. 2009. *Biochimica et Biophysica Acta - Molecular Basis of Disease*, 1792:1194-1197.
14. Krumm B, Meng X, Li Y, Xiang Y, Deng J. Structural Basis for Antagonism of Human Interleukin-18 by Poxvirus Interleukin-18 Binding Protein. 2008. *Proc Natl Acad Sci U S A*, 105: 20711-20715.
15. Deng J*, Lewis PA, Greggio E, Sluch E, Beilina A, Cookson MR. Structure of the ROC domain from the Parkinson's disease-associated leucine-rich repeat kinase 2 reveals a dimeric GTPase. 2008. *Proc Natl Acad Sci U S A*, 105: 1499-1504. (*correspondence).