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Research Interests: Chemical and membrane biology, structure and function of membrane protein and membrane protein complex, infection and cancer, structure-based drug design, drug synthesis by novel enzymes.



About 20-30% of the total proteins of cells are membrane proteins, which play essential roles in chemical reactions of living organisms, involving in photosynthesis, nutrition transportation, signalling transduction, cell and cell interaction and communication. Especially, most of the membrane proteins are pharmaceutical targets.

We are currently interested in using cutting-edge technologies to determine structures of membrane proteins involved in O-antigen biosynthesis and lipopolysaccharide (LPS) exportation machinery, and using the structural information to design novel drugs.

SELECTED RECENT PUBLICATIONS

1. The 3-D structure of a novel periplasm-spanning platform required for assembly of group 1 capsular polysaccharides in *Escherichia coli*, Collins, R., Beis, K., Dong, C., Botting, C., McDonnell, C., Ford, R., Clarke, B., Whitfield, C. & Naismith, J. *Proc. Natl. Acad. Sci. USA*, 2007, **104**, 2390-2395
2. RmlC, a C3' and C5' carbohydrate epimerase, appears to operate via an intermediate with an unusual twist boat conformation, Dong, C., Major, L.L., Srikannathasan, V., Errey, J.C., Philp, D., Asuncion, M., Giraud, M.F., Lam, J., Graninger, M., Messner, P., McNeil, M.R., Field, R.A., Whitfield, C. & Naismith, J.H. *J. Mol. Biol.*, 2007, **365**, 146-159.
3. Wza the translocon for *E. coli* capsular polysaccharides defines a new class of membrane protein, Dong, C., Beis, K., Nesper, J., Brunkan-Lamontagne, A.L., Clarke, B.R., Whitfield, C. & Naismith, J.H. *Nature*, 2006, **444**, 226-229.
4. SUMO protease SENP1 induces isomerization of the scissile peptide bond, Shen, L., Tatham, M.H., Dong, C., Zagorska, A., Naismith, J.H. & Hay, R.T. *Nat. Struct. Mol. Biol.*, 2006, **13**, 1069-1077.
5. Tryptophan 7-halogenase (PrnA) structure suggests a mechanism for regioselective chlorination Dong, C., Flecks, S., Unversucht, S., Haupt, C., van Pee, K.H. & Naismith, J.H. *Science* 2005 309, 2216-2219.
6. Crystal structure and mechanism of a bacterial fluorinating enzyme, Dong, C., Huang, F., Deng, H., Schaffrath, C., Spencer, J.B., O'Hagan, D. & Naismith, J.H. *Nature*, 2004, **427**, 561-565.
7. High-resolution structures of RmlC from *Streptococcus suis* in complex with substrate analogs locate the active site of this class of enzyme, Dong, C., Major, L.L., Allen, A., Blankenfeldt, W., Maskell, D. & Naismith, J.H. *Structure.*, 2003, **11**, 715-723.
8. Structural basis of NEDD8 ubiquitin discrimination by the deNEDDylating enzyme NEDP1, Shen, L.N., Liu, H., Dong, C., Xirodimas, D., Naismith, J.H. & Hay, R.T. *EMBO J.*, 2005, **24**, 1341-1351.