

# Structural basis for activation and inhibition of the pro-neurodegenerative NADase SARM1

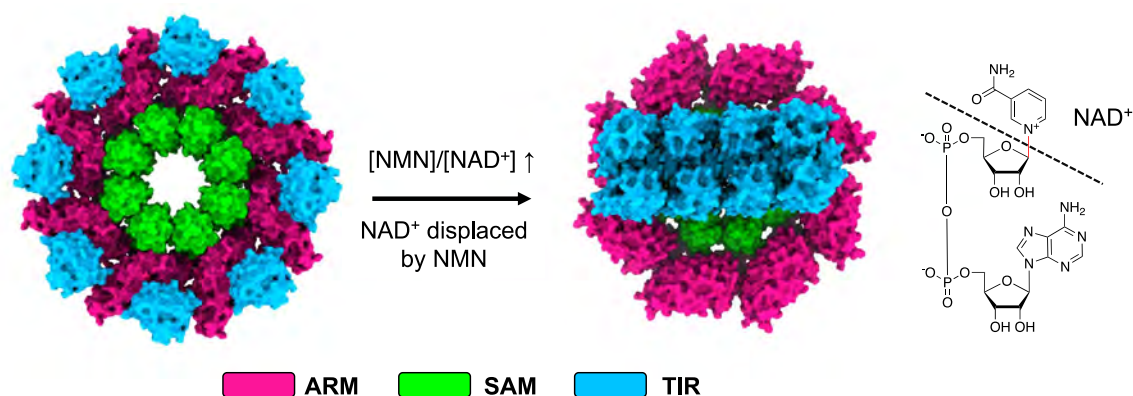
Y. Shi<sup>1</sup>, J. Nanson<sup>2</sup>, W. Gu<sup>2</sup>, V. Masic<sup>1</sup>, T. Mosaib<sup>1</sup>, M. Landsberg<sup>2</sup>, B. Kobe<sup>2</sup> and T. Ve<sup>1</sup>

<sup>1</sup>Institute for Glycomics, Griffith University, Goldcoast, QLD 4215, Australia, <sup>2</sup>School of Chemistry and Molecular Biosciences, University of Queensland, QLD 4072, Australia.

t.ve@griffith.edu.au

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Axonal degeneration is responsible for disease progression and accumulation of disability in many neurodegenerative conditions. Sterile alpha and Toll/interleukin-1 receptor motif-containing 1 (SARM1) is an octameric nicotinamide adenine dinucleotide (NAD<sup>+</sup>)-cleaving enzyme whose activation triggers axon destruction [1-3]. Using crystallography, cryo-EM, NMR, biochemical and cellular assays, we demonstrate that SARM1 is activated by an increase in the ratio of nicotinamide mononucleotide (NMN) to NAD<sup>+</sup> and show that both metabolites compete for binding to the allosteric armadillo repeat (ARM) domain of SARM1 [4]. We show that NMN binding triggers a reorientation of the ARM domains, which disrupts autoinhibitory intramolecular interactions and enables its catalytic Toll/interleukin-1 receptor (TIR) domains to form two-stranded assemblies [5]. The active site spans two molecules in these assemblies, explaining the requirement of TIR domain self-association for NADase activity and axon degeneration [5]. We also show that a potent orthosteric small-molecule inhibitor of SARM1 undergoes base exchange with the nicotinamide moiety of NAD<sup>+</sup> to produce the bona fide inhibitor 1AD and we report structures of SARM1 in complex with 1AD [5]. Our results reveal mechanisms of SARM1 activation, substrate binding and inhibition, and provide rational avenues for the design of new therapeutics targeting SARM1.



**Figure 1.** SARM1 activation mechanism. Cryo-EM structures of SARM1 in inactive (left) and active (right) states.

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