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Structural and Functional Implications of the Heterodimeric GTPase Latch that Docks SRP to its Receptor.

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Ffh (SRP54) & FtsY (SR α) are structurally homologous Signal Recognition Particle GTPases that interact directly during co-translational targeting to the membrane. Assembly of the targeting complex is primed by GTP binding to both proteins, and, subsequent to release of the translating ribosome to the translocon, GTP hydrolysis drives their disengagement. The structure of the GMPPCP stabilized complex of the 'NG' GTPase domains of Ffh and FtsY has been determined at 2.05 Å resolution¹. The two proteins form an extensive and symmetric interface that buries both active sites from solvent and that is coupled to an interdomain conformational change that may act allosterically to signal assembly to the accessory domains of the targeting complex. The two bound nucleotides are integral to formation of the interface, and interact directly. Disengagement of this molecular 'latch' is regulated by stimulation of GTP hydrolysis, and by placing it within the context provided by recent structures of the SRP/ribosome complex² and intact SRP54³, a specific hypothesis for its mechanism can be proposed.

1. Focia *et al* (2004) *Science* **303** 373
2. Van den Berg *et al* (2004) *Nature* **427** 36
3. Rosendal *et al* (2003) *PNAS* **100** 14701