



**Supplementary information, Figure S10. Structural comparison between the active NAIP5 and a modeled inactive NAIP5**

The structure of inactive NAIP5 (gray) was modeled using the program of MODELLER [53] with the inactive NLRC4 (PDB code: 4KXF). The NOD module (containing NBD and HD1) of the FliC<sub>D0L</sub>-bound NAIP5 was used as the template to align with the modeled structure of inactive NAIP5. The relative positioning of LRR and NBD in inactive NAIP5 could act to block the surface (highlighted within the red rectangle frame) where the C-terminal side of FliC-C (the longer helix) binds. For clarity, all the structural domains of NAIP5 are shown in cyan except that NTD, BIR1 and BIR2 are shown in orange, blue and yellow, respectively. “N” and “C” represent N- and C-terminus of FliC<sub>D0L</sub>, respectively.

**Reference:**

53. A. Fiser, A. Sali, Modeller: generation and refinement of homology-based protein structure models. *Methods Enzymol* **374**, 461-491 (2003)10.1016/S0076-6879(03)74020-8).