SUPPORTING INFORMATION PROTEIN SCIENCE, FOR THE RECORD MANUSCRIPT:

Structural insights into SAM domain-mediated tankyrase oligomerization Paul A. DaRosa, Sergey Ovchinnikov, Wenqing Xu, Rachel E. Klevit

Supporting Information Figure S1: Sequence alignment of hTNKS1/2 SAM domains and orthologues.

Supporting Information Figure S2: Mutant, but not wild-type TNKS2 can be purified from *Escherichia Coli*



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Sequence alignment showing the sterile alpha motif domain (SAM) and linker regions of TNKS1/2 and some of their orthologues. The SAM domain is well conserved. Human TNKS1 and TNKS2 SAM domains are 75 percent conserved. The positions of the five predicted helices (H1, H2, H3, H4, and H5) of the SAM domain are shown below the sequences (based on our model). Green boxes indicate residues on the surface generated between H2-H4 (mid-loop surface) that are at the predicted oligomeric interface; red boxes indicate residues on the H5 oligomeric interface (end-helix surface). Intensity of blue color indicates the degree of conservation at each position.



Supporting Information Figure S2: Mutant, but not wild-type TNKS2 can be purified from *Escherichia Coli*

Coomassie-stained SDS-PAGE gel of full-length TNKS2 purification. While both wild-type and mutants proteins were detectibly expressed, only mutant protein was retained in the soluble fraction. Whereas the wild-type protein could not be purified, the Y920E mutant protein could be purified using Ni-NTA resin in 20 mM Tris pH 7.6, 500 mM NaCl. Pre, cells before induction with IPTG; Post, after induction with 50 mg/L IPTG; sup, supernatant/soluble fraction after lysis and centrifugation; pellet, insoluble fraction after centrifugation; load, sample loaded onto Ni-NTA (same as "sup", but filtered through 0.22 µm filter); FT, flow-through/unbound material eluted from the Ni-NTA during protein binding in the presence of 5 mM imidazole; wash, wash step with 30 mM imidazole; elution, elution of protein with 500 mM imidazole, resin, boiled in SDS-PAGE sample loading buffer after elution. The Y920E mutant was eluted from the Ni-NTA in a soluble form and did not aggregate on the column resin.