



Supplemental Data

Figure 1.

Sequence alignment of PduO-like ATRs. Secondary structure and numbering of hATR is indicated above the alignment, and conserved residues (red on white) and invariant residues (white on red) are highlighted. Sequences are from human (AAH05054.1), mouse (BAE28544.1), xenopus (AAI06514.1), *C.elegans* (AAA21165.2), *Bacillus Halodurans* (10174212) PDBcode:2AH6, *Bacillus Subtilis* Yvqk PDBcode:1RTY, *Sulfolobus Tokodaii* (St2180) PDBcode:1WVT, *Sulfolobus Tokodaii* St1454 PDBcode:1WOZ, *Thermoplasma Acidophilum* TA0546 PDBcode 1NOG, *Mycobacterium Tuberculosis* PDBcode:2GDG. *Pyrococcus horikoshi* OT3 PH0671 PDBcode:1WY1.