**S6 Table. Sequence alignment of AurI.**

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| AurI-StFRB508 1 MEFIEFHTLD YSATPHAWVA DLYGLRKEVF ADRLNWKVNI KNDIEFDEYD 50 ||.||||.|| |||||||||| ||:||||||| |||||||||| ||||||||||AurI-PB-St2 1 MESIEFHALD YSATPHAWVA DLHGLRKEVF ADRLNWKVNI KNDIEFDEYD 50AurI-StFRB508 51 NERTTYLIGT WKGVPLAGLR LINTLDPYMV EGPFRDFFRC APPKQALMAE 100 |||||||||| |||||||||| |||||||||| |||||||||| .|||||||||AurI-PB-St2 51 NERTTYLIGT WKGVPLAGLR LINTLDPYMV EGPFRDFFRC EPPKQALMAE 100AurI-StFRB508 101 SSRFFVDKTR SRQLGLAHLP LTEMLLLCMH NHAARSGLES IITVVSNAMG 150 |||||||||| |||||||||| |||||||||| |||||||||| ||||||:|||AurI-PB-St2 101 SSRFFVDKTR SRQLGLAHLP LTEMLLLCMH NHAARSGLES IITVVSSAMG 150AurI-StFRB508 151 RIVRNAGWHY EVMDSGEAAP GEKVLLLNMP ISDANRQRLL SSIARKCPLS 200 |||||||||| ||||:||||| |||||||||| |||||||||| ||||||||||AurI-PB-St2 151 RIVRNAGWHY EVMDTGEAAP GEKVLLLNMP ISDANRQRLL SSIARKCPLS 200AurI-StFRB508 201 SAQLNSWPQR LNPLHTALYE PQRISA 226 |||||.|||| ||||||||.| ||||||AurI-PB-St2 201 SAQLNHWPQR LNPLHTALCE PQRISA 226 |

“|” indicates positions which have a single, fully conserved residue. “:” indicates conservation between groups of strongly similar properties. “.”indicates conservation between groups of weakly similar properties. The yellow color highlights the eight different amino acids. GenBank accession numbers for the protein sequences: AurI-StFRB508: BAM94429.1, AurI-PB-St2: ETD40527.1.