



**B**

```

1 MFSSSSRPSK EPLLFDIRLR NLDNDVLLIK GPPDEASSVL LSGTIVLSIT EPIQIKSLAL
61 RLFGRRLRLNI PTVLQTVHGP HKRYSKFERN IYSHFWDDFN IKSYPQONLYD NHNNGKITIS
121 SKSSTNLAAL PKRKRALSTA SLISSNGQTS ASKNYHTLVK GNYEFPFSAI IPGSLVESVE
181 GLPNAAVTYA LEATIERPKQ PDLICKKHLR VIRTLAIDAV ELSETVSVDN SWPEKVDYTI
241 SIPTKAI AIG SSTMINILIV PILKGLKLG P VRISLVENSQ YCGSYGGVIN QERMVAKLKL
301 KDPLKHVAQI KKRSLNEAA DEGVDTDTGE FQDKWEVRAL LNIPASLTKC SQDCRILSNI
361 KVRHKIKFTI SLLNPDGHIS ELRAALPVQL FISPFVNVV KTS•SDVIERTL KTFGPSYQVT
421 SQHDNSFSSK NFVDDSEEDV IFORSAS•ALQ LSSMPTIVSG STLNINSTDA EATAVADTTM
481 VTSLMVPPNY GNHVYDRVYG EVTNEDE TSA SASSAVESQ AIHNIQONLYI SDSNNSNNPI
541 LAPNPQIKIE DDSLNNCD SR GDSVNNSNLN LVNSNLTISE NWNNSPSAN RYNNIINAGL
601 NSPSLTPSFA HLSRRNSYSR QTSSTSLKND LELTDLSRVP SYDKAMKSDM IGEDLPPAYP
661 EEELGVQENK KIELERPQIL HHKSTSSLLP LPGSSKSSNN LKRSS•RTHL SHSPLPRNNS
721 GSSVSLQOLA RNNTDSSFNL NLSFTSAKSS TGSRHFPFNM TTSFTSNSSS KNSHFDKTD
781 STSDANKPRE EENYTSATHN RRSRSS•VRS NNSNSPLRQG TGSFANLMEM FTKRDRS*

```

**Figure S1. Locations of phosphorylation sites for Snf1 and Ypk1 in Rod1.** (A) Schematic diagram of Rod1 showing the relative positions of the six Snf1 (*green*) and two Ypk1 (*magenta*) phosphorylation sites. Arrestin fold (*blue*); V/PPxY (Rsp5-binding) motifs (*purple*). (B) Primary sequence of Rod1 with the six Snf1 consensus sites indicated by the double-underline and dotted Ser residue (*bold green*) and the two Ypk1 consensus sites indicated by the single-underline and the dotted Ser residue (*bold magenta*). Basic (R or K) residues (*bold blue*); hydrophobic residues (*bold black*); V/PPxY (Rsp5-binding) motifs (*purple*).