

A. p27Kip1 (Human)

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      10      20      30      40      50      60
MSNVRVSNQS PSLERMDARQ AEHPKPSACR NLFGPVDHEE LTRDLEKHCR DMEEASQRKW

      70      80      90      100     110     120
NFDQFQNHKPL EGKYEQEVE KGSLEFYR PPRPPKGACK VPAQESQDVS GSRPAAPLIG

      130     140     150     160     170     180
APANSEDTLH VDPKTDPSDS QTGLAEQCAG IRKRPATDSS STQNKANRT EENVSDGSPN

      190
AGSVEQTPKK PGLRRQT

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B. p27 Kip1 (mouse)

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      10      20      30      40      50      60
MSNVRVSNQS PSLERMDARQ AEHPKPSACR NLFGPVDHEE LTRDLEKHCR DMEEASQRKW

      70      80      90      100     110     120
NFDQFQNHKPL EGRYEQEVE RGSLEFYR PPRPPKSACK VLAQESQDVS GSRQAVPLIG

      130     140     150     160     170     180
SQANSEDRHL VDQMPDSSDN PAGLAEQCPG MRKRPAEEDS SSQNKANRT EENVSDGSPN

      190
AGTVEQTPKK PGLRRQT

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C.

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p27kip1 mouse p27kip1 human
CLUSTAL 2.1 multiple sequence alignment
sp|P46414|CDN1B_MOUSE      MSNVRVSNQSPSLERMDARQAEHPKPSACRNLFQGPVNHEELTRDLEKHCR
sp|P46527|CDN1B_HUMAN    MSNVRVSNQSPSLERMDARQAEHPKPSACRNLFQGPVDHEELTRDLEKHCR
*****:*****

sp|P46414|CDN1B_MOUSE    DMEEASQRKWNFDQFQNHKPLEGKYEQEVERGSLPEFYRPPRPPKSACK
sp|P46527|CDN1B_HUMAN    DMEEASQRKWNFDQFQNHKPLEGKYEQEVEKGSLEFYRPPRPPKGACK
*****:*****

sp|P46414|CDN1B_MOUSE    VLAQESQDVSGSRQAVPLIGSQANSEDRHLVDQMPDSSDNPAGLAEQCPG
sp|P46527|CDN1B_HUMAN    VPAQESQDVSGSRPAAPLIGAPANSEDTLHVDPKTDPSDSQTGLAEQCAG
* ***** * ***** ***** * . * . * :*****

sp|P46414|CDN1B_MOUSE    MRKRPAEEDSSQNKANRT EENVSDGSPNAGTVEQTPKKPGLRRQT
sp|P46527|CDN1B_HUMAN    IRKRPAEDSSQNKANRT EENVSDGSPNAGSVEQTPKKPGLRRQT
*****:*****:*****:*****:*****:*****:*****:*****

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157 170 197 198

Supplemental figure 1. The alignment (C) of p27 human (A) and mouse (B) sequences.