

A

CLUSTAL W (1.83) multiple sequence alignment

```

PPGK      MTSTGPETSETPGATTQRHGFIDVGGSGIKGGIVDLDTGQLIGDR--IKLLTPQPATPL
GLKA      -----MLTLCLDIGGTKIAAGLADPAGTLVHTAQRPTPAYGGAEQVWA
           :  :*:**:*  *  .*:.*      :      :      .

PPGK      AVAKTIAEVVNGFG--WRGPLGVITYPGVVTHGVRTAANVDKSWIGTNARDTIGAELGGQQ
GLKA      AVAEMIADALGVAGGAVGGVGIASAGPIDLHSGRVS PINIGSWGGFPLRDRVAAAVPGVP
           ***:  **:..  *  *  :*:  .*  :      *:.  ** *  **  :.*  :  *

PPGK      VTILNDADAAGLAETRYGAGKNNPGLVLLTFGTGIGSAVIHN-----GTL
GLKA      VRLGGDGVCMALGEHWLGAGRG-ARFLLGLVVSTGVGGGLVLDGAPCLGRTGNAGHVGHV
           *  :  .*  .  .*.*  ***:.  .  :::  *...**:*...:  :      *  :

PPGK      IPNTEFGHLEVGGKEAEERAASS-----VKEKNDWTYP-----
GLKA      VVDPDGSPCPCGGRGCVETIASGPSLARWARANGWSAPPGAGAKELAEAAGAGDPVALRA
           :  :.:  .  **:  .  *  **.  .  *.*:  *

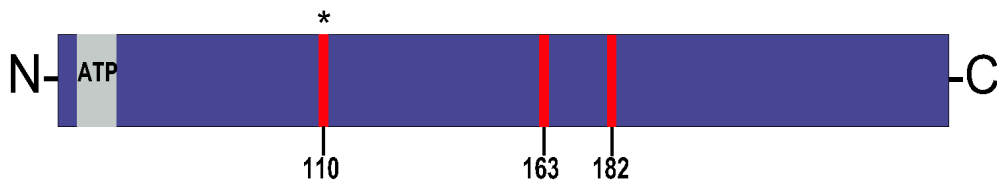
PPGK      --KWAKQVIRVLIAIENAIWPDFIAGGGISR-----KADKWVPLENRTPVV
GLKA      FRRGAAALAAMIASVGAVCDLDAVIGGGVAKSGRLLFEPLRAALADHARLDFLAGLRVV
           :  *  :  :.:  :.  **  :  ***:  :      **:  :      **

PPGK      PAALQNTAGIVGAAMASVADTTH
GLKA      PAELGGAAGLVGAARLAAIA---
           ** *  .:***:****  :.

```

B

GLKA (302 aa)



PPGK (265 aa)

