```
logo
gelK       ....MAEATEAAHTTGKRLKMCLAASGGGHLRQILDLESVWREHDYFFVTEDTALGRSLAEKHPVELVGHYALGQARLGHPFKMLGGALRNLRQSLAIVRRHKPDVVIST   106
dpsK       ....MAEANAVDGKASKPLKMCLAASGGGHLRQILDLESVWREHDYFFVTEDTALGRSLAEKHPVELVEHYALGQAKLGHPLRMLGGAWRNLRQSLSILRRHKPDVVIST   106
spsK       MGDGMAEATVTEAKAGKPLKMCLAASGGGHLRQILDLESVWKEHDYFFVTEDTALGRSLAEKHSVALVDHYALGQAKLGHPLRMLGGAWRNLRQSLSIIRKHKPDVVIST   110
consensus      !!!!*    ***!*!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!*!*!! !!!!!!!*!!!!**!!!!!*!!!!!!!*! !*!!!!!!!!!

logo
gelK       GAGAVYFTALFAKLFGAKFIHIESFARFDHPSAFGKMVKGIATISIVQSPALKQIWPDAELFDPFRMLDTPRPPKQALTFATVGATLPFPRLVQAVLDLKRAGGLPGKLI   216
dpsK       GAGAVYFTALLAKLSGAKFVHIESFARFDHPSAFGKMVKGIATVTIVQSAALKETWPDAELFDPFRLLDTPRPPKQALIFATVGATLPFPRLVQAVLDLKRAGGLPGKLI   216
spsK       GAGAVYFTALLAKLSGAKFVHIESFARFDHPSAFGKMVKGIATVTIVQSAALKQTWPDAELFDPFRLLDTPRPPKQALTFATVGATLPFPRLVQAVLDLKRAGGLPGKLV   220
consensus  !!!!!!!!!!*!!!*!!!!*!!!!!!!!!!!!!!!!!!!!!!!!**!!!!*!!!**!!!!!!!!!!!!*!!!!!!!!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!!!!!!*

logo
gelK       LQYGDQALTDPGIPDVEIRPTIPFDELQLMLRDADIVICHGGTGSLVTALRAGCRVIAFPRRFDLGEHYDDHQEEIAQTFADRGLLQAVRDERELGAAVAAAKATEPRLA   326
dpsK       LQYGDQDLPDPGIPDVEIRRTIPFDDLQLLLRDADMVICHGGTGSLVTALRAGCRVVAFPRRHDLGEHYDDHQEEIAQTFADRGLLQAVRDERQLGAAVEAAKATEPQLA   326
spsK       LQYGDQDLADPGIPDVEIRRTIPFDDLQLLLRDADMVICHGGTGSLVTALRAGCRVVAFPRRHDLGEHYDDHQEEIAQTFADRGLLHAVRDERELGAAVEAAKATEPQLA   330
consensus  !!!!!!*! !!!!!!!!!!*!!!!!*!!!!*!!!!!*!!!!!!!!!!!!!!!!!!!!!!!!*!!!!!*!!!!!!!!!!!!!!!!!!!
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