**Protein Global Sequence Alignment**

**CRY\_Peas:**

mkrehnqehedas-mtgkseicweddggmdellavvgykvkssdmaevaqkleqleqamgnfqdqdeatiaqhls-ndtv-hynpadisnwlq---tmlsnfdsqpnpsvssssdndl-naipgkaiyantdsqteeslpsrkrvkrvgs-ssstestrpvvmvvetqekgiilvhtl-macaeaveqnnrpvaealvkqignlavsqegamrkvatyfaiglarriydvfpqhsvsdslqihfyetcpylkfahftanqaileafqgksr-vhvid-fsinqgmqwpalmqalalrpggppafrltgigppasdnsdhlqqvgwrlaqfaqti--h-vqfeyrgfvansladldasmlelrsp--etesvavnsvfelhklnarpgalekvfsvirqirpeivtv-veqeanhngpaf-ldrfteslhyystlfdslesslvepqdkamsevylgkqicnvvacegtdrverhetlnqwrnrfgsagfspvhlgsnafkqasmllalfaggdgykveendgclmlgwh-trpliatsawklaansmvvsh

**CRY\_mouse:**

m----------aspaag---------g-------vv--ivgs--------gligrswam-lf-----a------sggfkvkly---di---eqqqit-----d-------------alen-i-rk----emks-leqs-gslk-----gsls--ae--r--------q-----l--slisgc-------------------gnla---e-a---v-----eg-a-----vhiqecvpenl-----e----lkkkif-a-q--l------driv---ddrvi-lssssscl---l---p--sklf--sg---la-----h---v----kq---civahpvnppy--yv--pl-------vel-vphpet---a-------patmdrtyalmk---kigq-sp--vrvlke----idg--fvlnr----lqy---avis-e---------a---wrl------v---e-----e--e--------ivs----p----s-------dl-------d--lv-msd---rag-havr-vhrt----l—gdyapqc

**Total results:**

Matches: 121   
Mismatches: 105   
Gaps: 325  
Score: -309