

## Protein Global Sequence Alignment

### CRY\_Peas:

mkrehnqehedas-mtgkseicweddggmdellavvgykvkssdmaevaqlqleqamgnfqdqdeatiaqls-ndtv-  
hynpadisnwlq---tmlsnfdsqpnpsvssssdndl-naipgkaiyantdsqteeslpsrkrkrvgs-ssstestrpvmvvetqekgiilvhtl-  
macaeaveqnnrpvaealvkqignlavsqegamrkvatyfaiglarriydvfpqhsvsdslqihfyetcpylkfahftanqaileafqgksr-  
vhvid-fsinqgmqwpalmqalalrpggppafrltgigppasdnsdhlqqvgwrlaqfaqi--h-vqfeyrgfvansladldasmlerlsp--  
etesvavnsvfelhklнарpgalekvfsvirqirpeivtv-veqeanhngpaf-  
ldrfteslhyystlfdslesslvepqdkamsevylgkqicnvacegtdrverhetlnqwrnrfgsagfspvhlgsnafkqasmllalfaggdgykve  
endgclmlgwh-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-lsssscl---l---p--sklf--sg---la-----h---v---kq---civahpvnpvy--  
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