

CLUSTAL 2.1 multiple sequence alignment

```

bsMutL_CTD      -----GAMDRVPIMYPIGQMHGTYILAQNENGLYIIDQHAAQER
ngMutL_CTD      TMGSSHHHHHSSGLVPRGSHSQSELPLGFIAQLLGIYILAQAEDSLLIIDMHAAAER
aqMutL_CTD      -----PLSQPVKTYKPTYEILGQMDETFILVKDSEYL YFVDQHLLLEER
hPMS2_CTD       -----IGQFNLGFIITKLNEDIFIVDQHATDEK
                ::* :   :*:::  : : : ::* *  *:
    
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```

bsMutL_CTD      IKYEYFR-EKVGVEPEVQEMIVPLTFHYSTNEALIEQHKQELESVGVFLESFGSNSYI
ngMutL_CTD      VNYEKMKRQRQENGLQSQHLLIPVTF AASHEECAALADHAETLAGFGLSDMGNTLA
aqMutL_CTD      INYEKLL365-----
hPMS2_CTD       YNFEMLQQHTVLQGQRLIAPQTLNLTAVNEAVLIENLEIFRKNGFDFVIDENAPVTERAK
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bsMutL_CTD      VRCHPAWFPKGEEAELIEEIIQVLDLDS-KNIDIKKLREEAAIMMSCKGSIKANRHLRNDL
ngMutL_CTD      VRAAPVMLGKSDVVSLARDVLGELAQVGSSTIASHENRILATMSCHGSIIRAGRRLTLPE
aqMutL_CTD      -----DENLACRISVKAGQKLSEEK366
hPMS2_CTD       LISLPTSKNWTFGPQDVDELIFMLSDSPGVMCRPSRVKQMFASRACRKSVMIGTALNTSE
                :*: * : . *  :
    
```

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bsMutL_CTD      IKALLDDL RSTSDPFTCPHGRPIIIHHSTYEMEKMFKRVM
ngMutL_CTD      MNALLRDMEN TPRSNCNHGRPTWVKLTLKELDTLFLRGQ
aqMutL_CTD      IRELIKTWRNLENPHVCPHGRPIYYKIPLREIYEKVG RNY
hPMS2_CTD       MKKLITHMGEMDHPWNCNHGRPTMRHIANLGVISQN----
                :. *: . . * **** : . :
    
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