

P2-HP1

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gi|4530499|K139 --MLTYEWAP-----ESYYCEKYSVSLPMGTIRQYIAERIIK--PKTK---TKEKPLWNVWMH-----EIAAREAMQVLG-----
gi|141342|phi-R67 --MLTYLFCDPSISFVPIWLVLTITTGSPQANRRCCIMTPNISITLNTHYIERYSETTLIDITNDLADRRIRHRLRKDK---KREKVMNIALT-----VDALTDCNVEN-----
gi|459180|HP1 -MSKQNAICIN-----HMEQYYYREEFKKLDVSTRTIDRLRQQVIIKIMKNDEGEETERLVLNDVIA-----VRNAKNAFQI-----
gi|1679810|S2 -MNGQNAICIN-----VQIHAYYYYLKKYNETLSLDKVRKRAAEEPIADKK---AERSSVLNIIA-----KQAAKQE-----
gi|5824357|WPhi EVNDYVIQYP-----IDAHTVKFELLLKPETAVVKVKENKLVIELRDPSKPNARVEKMFIPEFNRAVREEFYNTPVEQRDAWLLMMRI-----
gi|76820|P2 SK---QWTLN-----TDAIPYQEFKIIKKGTGAVRRIDKKLVIDITDPQSASGRAEYWYFPMNGLLKLYESPKEIRDGWLMLIGEPR
ruler 1.....10.....20.....30.....40.....50.....60.....70.....80.....90.....100.....110.....120.....130
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