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110
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VECNEEGYHIHVVIGGPGLNPRNLGLFNNVLYHLVTENVK LEPSSSE $\square$ HYHLVAEQGNVSGTEISNWLKRWASFLTRHMA AEHNDEGFHVHVVV GGPFVTPRNVCNDVETGFNKVL VECPTAGYHMHVLLNHPKGSNQTYGRKVNELVCRGV DTF LEPSSGEVHYHLVVNQGDMVGREFSNWLRTWKVFMAGYV | $L$ | $E P S S G E M H Y H L V V N Q A D M V G R E C S N W L R T W K V F M A G Y L$ |
| :--- | :--- | :--- | :--- |
| $L$ | $P C T S E Y H F H$ |
| $E$ | $V V G A E G L T$ | LEPCTSEYHFHLVVGAEGLTGRDYSYWLRQLGRFMFQYVS MEESPGGLHCHGWCASMMCSTRQLADALTSGFKQLGRSMY




QUERY
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UniRef90-A7J3Q4
UniRef90-H2ESE4
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[^1]QUERY
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[^0]:    lupas 21
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