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20 E T $\quad{ }^{30}$
40
APYPQAEKGMKRQV QG R GQK G T L E V D
 I A P Y P Q A E K G M K R Q V I T L P P A Q K D E A G Y R V E L L I G K MM D


 $V A P P Y P K A E A G F T R Q V I$ V | $V$ | $A$ |
| :--- | :--- |
| $V$ | $A$ | $P Y P K A D A G F T R Q Q I$ VA P Y PVAEKGMTRQV A PYPKA DA GYVRQVI I APFPAAESTMSRQVI

I APYPAPEKGMKRVVVI
A P
1 $\begin{array}{rl}\text { IK MF P Q A A A GQQRAA } \\ K & V \\ \text { K } & \end{array}$

 $V A P P Y P K A S E G M V R N V I$ | $V$ | $A$ | $P$ | $Y$ | $L$ | $Q$ | $E$ | $Q$ |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| $I$ | $M T$ | $R$ | $Q$ | $V$ | 1 |  |  |
| $I$ | $A$ | $P$ | $Y$ | $P$ | $K$ | $A$ | $E$ | $V$ A P Y P E A S K G M V V R S V I I A P Y P A A E K GMMTR Q V I V A P YP QA E E GYQRWVI $V$

I
I D F P P A A S E G Q A R H

LK A F P A A E A G M V R R HV I
L A A F P A A A E K G M MVV R H V
$\begin{array}{llllllllllll}L & A & A & F & P & K & A & E & G & D & M & V \\ L & H & V & I \\ A & P & Y & P & D & A & Q & A & G & M & V & R \\ V & Q & I\end{array}$
$V A P Y P E P K E G Q K R S V I$




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 $\square E M F P K A K E G F K Q V Y I Q L P D E K N E R D L K V E V G A G D E K T V D$ $M$ F P E P E S G Y V R Y I V E V $V$ R K T K N D Y D H K V E L L L I G K VS MFPK A EK G QV Q Y I I DVM H S D K D N L K K I EFFA G K I M E T D FPKEKKGYKRYVI AFPEAPAGQQRHV $L$ K A F P A A E Q GMVR HVL VAPYPKAAGNDNRNVI PFPAADFGFYRYMI
 Y P TVS SDQRQVVI MFPEM DNMTKHVFYVEPASNEADKRVELVVGKTDEKD
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 MS $\square W P K A E L G Y K R V V I Q L P T L K D E D A Y R V E L V P Q K T M K A D$ L P A K E D E S N Y K V E E L I G G K T M T V D

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## QUERY

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C CNQQMLTGELKQHSVKGWGYTYYQVDSISEGPSTRMACDR (IGPARLQHTLGSGYPYYRVTDIGPVAATKMACPS CNRHQLMGTLEQKDLQGWGYNYYDFSSDGKTDSTDMGCNQ CNKHGLS GELTQHTVKGWGYNYYQVDADHQGPSTMMACFD
CNRQMLSGSSEQHDVEGWGYSYYRVSNLEKGGSTMMACPE CNHQWF GGTLTQKTVDGFGYDYYETGDLTGPMSTMMGCDN CNDSWFGGSLTPSTVEGWGFDYFTDAASDRMSGTDMACPE CNHYRLA GRLTEETAKGWGYSYYTATVQPDADSTRMACTED CNARSLSK KQLVVGGWGYNYYVVDSDN G PS MMACPA CNKHGLTGELKQLSVVKGWGYNYYQVDSVNEGPSTMMACFD GNRYFFSGAIEEKNI EGWGYTRYVLSNIGPMAGTLMAVPD CNNYF $\square$ MG $\|$ MKSQDLQGWGYNYYEVESNGETAGTLMGCPG CNHHSFSGKDEK LDPLQGWGYSYYKVSDDKSGPTTMMACQE CNTYGLLAGQFEEKDLGGWGYNYYVFTTNGSVRSTMMACPD CNRHTFSSRLEKRTVDGWGYDYYVVTGVGVVASTRMACPD CNTRSLGG VVKQEELKGWGYNYYVVDKADNNISTMMACPE CNNTWYSGDLKEDDLQGWGYTYYKIEKITGPMSTRMGCLD CNRHSFSGQMVENFLPGVGYPYYRMPKIQGPLSTRMACPN CNNFFLTGGFEQKTVDGWGYDYYDFESNGNVGGTDMGCFD CNHDMINGKDEDKPLTGWGYEYYVLSQDSQPASTRMACPA CNRHGLDGSWEKKTVEGMGYTYYTFTSDGKAWSTMMGCPE CNHVSLGGKDTEHNLEGWGYTYYQVDSSGAGMSTMMGCPD RNRYFFAGRI EEETIKGWGFPRYVVSALGPMAGTDMADPD CNNYGLMGTLEKKDLQGWGYDYYVFQSNGDAFSTQMGCPD ANTYFFTGKIGEEQIIDDGWGFPRYVVSNLGGPMAGTLMAVSN CNRQRLGGSLEERTLEDWGYSYYRLDKVSGPASTLMACPD CNYFGLGGGSLEEKDLEDGWGYNYYVIFT TVGQMTSTQQMCDDD CNSFGLQGELEKKDLQGWGYNYYVFKTKGNVISTQMACPG GNRYFFAGKLETESIPGWGYDRYI LRKLGPMAGTLMAVPN SNHFFFGGSLEAKNIDGWGFTKYVVAKLGPMGGTLIGVDP GNRHMMGGSVEDKVLEGWGYSFYVV QLGMAASTRMMPPA CNTRSYHTDLKKKDLKGWGYDYFVVGKADQVISTDMGCDD CNSRGMDGRFEAREVQGWGYSYWVFGSQGRVLSTMMMCPP CNLVHLAGSFSEETAKGWGYPYYRVTLQPGLISTRRACAQ GNRHFIGGKDEEKTVEGWGYDYYVV QLGPMAGTDMMPDA $C N R V S L G G Q Q V E H D L \mid K G W G Y N Y F Q V E G Y G Q G A S T L M A C P D$

## QUERY <br> UniRef90_E3GBA1 UniRef90_UPI00029AFADE UniRef90_UPI000329F164 UniRef90-A4WCM2

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 GKAHPEFVVVGDGFMLRYNSKLPIVVYVPKDI EVRYRIWS GKTREDFVPVGDGFVLRYNSKLPIVIYAPKDVEVRYRLWS QKKEQRF VVGEGFLLRYNSKLPIVVYAPKDVEVRYRIWS
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 QKERFVQVQLGKDAGI RYNSKLPVVVYTPKSMTVKYRIWQ SQRHFVTVHL GDSALQRYNSKLPLVVYVPQGVQVKYRVWQ PAKRFITANGGDDATIRYNSKLPVVVYAPKDVDVKYRIWS NKKKFVQVNLGKDAAVRYNSKLPIVVYTPDTIVKVYRIWH RRPQFIAANVGDAAMQRYNSRLPIVVYVPKGVEVKYRIWQ
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 KAKHEEFVRIPGEYKLRYNSKLPMVIYQPKDAELRYRVWR KAKTEAFLSI PGSLKVNYDSRLPKVFYLPKGSELRYRIWR NAKRFVTANLGAESLRRYNSKLPLVIYAPEDLVVKYRI WR KEKKFVTSHPGDAGMLNYNSKLPVVVYTSENIDVVKRLWK KPNENRFVSGGQTLIVRYNSKLPIVVYAPKGYEVKYRIWK
 QDAQEAFVPVGSGYLLRYNSRLPIVVYVPNGFDVRYRLWY GSRKQAFVQVGGEPMLRYNSKLPLVIYAPADVEVRYRVW GTETSKFVAHGNGFVVRYNSKLPVVVYDPQGFELRYRTWQ K SKKDFVPVIGTGYMLRYNSKLPLVIYAPDDVEIRYRDWT


 K E EKEAFVQI RDELKKNYDSRLAKVFYLPKGSELRYRVWK ATPQSAFVIGGDGFLLRYNSRLPVVVYVPDGYEVRYRLWQ P EYRFVQSR T LIVRYNSRLPIVVYAPEGFDIKYKVWK KAKKTAF GSEKQRFVAAHHASFVAYNSQLPDVVYAPADVDVRYRVWK



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UniRef90_U3BFH5

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 $\square T P Y P K P T A A Q T R W V I Q L P G S P N P S D W R V Q L I A G R E V E A D$
 PYPAAGPCQKRTVI YL PQQDEQHHLRVQLI PGRHVRCD

 LS GYPQPAPGLQRWVIQLPKSSDPTDWRIQLIVGQEVTMD
$\square S G Y P A P K Q G \square K R W V I Q \square P K S D D P L D W R V Q L I V G K E V E M D$ APYPEPGADQSCCVIFPESKDDEEDYRLQLIPGLVLEDS APYPEPGPDQTCCI I LLEEKPDEENYRVELI PGRVMEDG

 PSPREGERRCLFVLDPLEESKDRMVELLPGRVETVDPYPAASAGMKRCVIYLDPSPREGQKRCLFVLEKKE YPEAKEGYDRY FUDPGEHHNDRMLELLPGRVEAVD
 YPEPAAGEKRVTFVLDPQFEENNCRLQLIDGRVVEMT $\square A P Y P T P \square E N Q K R Y V I H L P D E S N E E K L K V E L Q A T K N A M Q D$

EGEKRCCSFLTPLPSDNNRMLELQPGRVETVD $P K P T A N Q A V H I D K V D T L P E A S Q Y Q L Q V Q D G L N D M Q D$ YAEPVEGNKRIIVALDPFDEAAHCRLQLQPGRMVELD

A G LK R HEFTLPSLENESEKLIDFVINKQVTET AEAMQMNVIKLKPMKAPLDFKVEVVFAKKMQAD YTQTKEGFDPYRITAPQGSDAEDYYI ELIPSKLMKVD
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$N V F E E P$ PVSKMDPSEKKFDEAAFSKKEVETD

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 CNYKS ${ }^{\text {CHGSWREQTVQGWGLDVYTLNTNGEVETTVMECVD }}$ CNNYRGAGVLHQETVQGWGYRYLRADLSDKVLGSLMLCSN ANHQTDSGSI EQHTVEGWGAPFVHVKLAKEAAATLMQVHH ANHQALGGSIUQHSVEGWGATFFHVKLEKQAASTLMHVHD CNQRAFRGRFRASKLKGLGVSVYTVSDVGPMVSTLMACPG
 GCFYQLTGTVSEETLQSWGYPYYVVTDDDYPAQCSPSDPA
 $C N N T W L S G P G L T M T R S A A G K A D F S L K G P L V V M S T R M A C P D$
$C N T K S R S A K Y T K K L V E G M Q Y P Y Y E V G K L G N I D T T L M G C S E$ CNSYFFTGNLTNQNLKGFGYEYYKFKAKGLLAGTLMYCGD $C N Q K Q L S G P G M T M R M L P Q G K A L F E V K A P L R V I S T K M A C P E$
$C N N M R F G G K L E E K T L D G W G Y N Y Y V I D Q V G D P I T T L M G C P G$
$C N D$ CNVKRLSGPSLSMQRLPQGKADFEVSGPVLVLSTRMACSE CNRVWFGGKDETKTLEGWGYNYYVI EQVSDPASTMMACPN

 CNQYHLAGQLRMERFQGAERMLYSVAGAVKVMSTRMVCPD GNTYYINGCTTEEKFPGDDYTCYRVDLDDTYRSRCAVPPE PEHTYLQGVIEEQVIDGWGYSYFVV QMGHVIDAHPVSGG $D N H H F L G G K L E E K D V E G W G Y P Y Y I F S G D S Q M A Q T D M A F P G$
$G N S Y F I N G T V T E E V D G L G Y P C M V D L K E T Y K S R Y A V P P E ~$ CRKNKI GGQFNPNLVPGRGLMYWELDTNNK LYGEQGECGD CNSYGLLGK IE QKKDQETNUSYY LYDTDGNMRSTMMACPD FNINILGGGEVQELAALSS GHTCYKVALQQEHMASTRMMLPD CNRVWF GGKLETKTLEGWGYNYYI I AQVSD GNRYHIEGCIAGGNNEDMDYTDYRVTLGETRRSLYAVPPE CNQRRLMGEVQKKTSQGVTHYYWLESLMEAPMVTLPCIEA ASSATLGGTVEEMLLES GPTCYFVDLAEELVMTRGALHD CNSTALDGTLIKKPANGDESTHYVLDSYG DTQTMKACTS CNYQFLGGQMEEKNSAKFG DYYEFTGGDEVATSLMLCPD
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D SPPSLQFVGMQPLLVRYNSRLPCVVYVPEGFAVRYRLWK


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S P PVRRKVVMAERPFDPYNSKLPVVVYMPKEGELHYRVWT
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