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1801 ctaggacaataaagccacttgttgggaaacagatgattcagggggtcccatgtccatagg
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- 1861 tgatttgctctatcaacgatttccccccaaagggcgctttgccgaggctggttggggtgg
- 1921 agacttgggataccgcctggcgtggatggaggaggcgatgagggggccctggaagccagc
- 1981 ccctgagcctggcgtgtaaggcgattacacatcttcctggggtcatattttctgtgagcg
- 2041 tttatctttcatgcctgccgcgctaggattttccccctgccgtgcaagacatctttgctc
- 2101 ggtctggggagggcgttagccatttgcccgggtgggggggtcccgtgttctgcaaagt
- 2161 getetgeacttgeecegggttaggteecggaeggeegeeteeagtgeecaccactaac
- 25 A Y S S V P V
- 32 S N M N S G L G S M N S M N T Y M T M N
- 2281 TCAGCAACATGAACTCAGGCCTGGGCTCCATGAACTCCATGAACACCTACATGACCATGA
- 52 T M T T S G N M T P A S F N M S Y A N P
- 2341 ACACCATGACTACGAGCGGCAACATGACCCCGGCGTCCTTCAACATGTCCTATGCCAACC
- 72 G L G A G L S P G A V A G M P G G S A G
- 2401 CGGGCCTAGGGGCCGGCCTGAGTCCCGGCGCAGTAGCCGGCATGCCGGGGGGCTCGGCGG
- 92 A M N S M T A A G V T A M G T A L S P S
- 2461 GCGCCATGAACAGCATGACTGCGGCCGGCGTGACGCCATGGGTACGGCGCTGAGCCCGA
- 112 G M G A M G A Q Q A A S M N G L G P Y A
- $2521\ GCGGCATGGGCGCCATGGGTGCGCAGCAGGCGGCCTCCATGAATGGCCTGGGCCCCTACG$
- 132 A A M N P C M S P M A Y A P S N L G R S
- 2581 CGGCCGCCATGAACCCGTGCATGAGCCCCATGGCGTACGCGCCGTCCAACCTGGGCCGCA
- 152 RAGGGGDAKTFKRSYPHAKP
- 2641 GCCGCGCGGGGGGGGGGGGCGACGCCAAGACGTTCAAGCGCAGCTACCCGCACGCCAAGC
- 172 PYSYISLITMAIQQAPSKML
- 2701 CGCCCTACTCGTACATCTCGCTCATCACCATGGCCATCCAGCAGGCGCCCAGCAAGATGC
- 192 TLSEIYQWIMDLFPYYRQNQ
- 2761 TCACGCTGAGCGAGATCTACCAGTGGATCATGGACCTCTTCCCCTATTACCGGCAGAACC
- 212 Q R W Q N S I R H S L S F N D C F V K V
- 2821 AGCAGCGCTGGCAGAACTCCATCCGCCACTCGCTGTCCTTCAATGACTGCTTCGTCAAGG
- $232 \quad A \quad R \quad S \quad P \quad D \quad K \quad P \quad G \quad K \quad G \quad S \quad Y \quad W \quad T \quad L \quad H \quad P \quad D \quad S \quad G$
- 2881 TGGCACGCTCCCGGACAAGCCGGGCAAGGGCTCCTACTGGACGCTGCACCCGGACTCCG
- 252 NMFENGCYLRRQKRFKCEKQ
- 2941 GCAACATGTTCGAGAACGGCTGCTACTTGCGCCGCCAGAAGCGCTTCAAGTGCGAGAAGC
- 272 P G A G G G G G S G S G G S G A K G G P
- 292 E S R K D P S G A S N P S A D S P L H R
- 3061 CTGAGAGCCGCAAGGACCCCTCTGGCGCCTCTAACCCCAGCGCCGACTCGCCCCTCCATC
- $312 \hspace{0.1cm} G \hspace{0.1cm} V \hspace{0.1cm} H \hspace{0.1cm} G \hspace{0.1cm} K \hspace{0.1cm} T \hspace{0.1cm} G \hspace{0.1cm} Q \hspace{0.1cm} L \hspace{0.1cm} E \hspace{0.1cm} G \hspace{0.1cm} A \hspace{0.1cm} P \hspace{0.1cm} A \hspace{0.1cm} P \hspace{0.1cm} G \hspace{0.1cm} P \hspace{0.1cm} A \hspace{0.1cm} A \hspace{0.1cm} S$
- 332 P Q T L D H S G A T A T G G A S E L K T
- 3181 GCCCCCAGACTCTGGACCACAGTGGGGGCGACGGCGACAGGGGGCGCCTCGGAGTTGAAGA
- 352 P A S S T A P P I S S G P G A L A S V P
- 3241 CTCCAGCCTCCTCAACTGCGCCCCCATAAGCTCCGGGCCCGGGGCGCTGGCCTCTGTGC
- 372 A S H P A H G L A P H E S Q L H L K G D
- 3301 CCGCCTCTCACCCGGCACACGGCTTGGCACCCCACGAGTCCCAGCTGCACCTGAAAGGGG
- 392 PHYSFNHPFSINNLMSSSEQ
- 3361 ACCCCCACTACTCCTTCAACCACCCGTTCTCCATCAACAACCTCATGTCCTCCTCGGAGC
- 412 Q H K L D F K A Y E Q A L Q Y S P Y G S
- 3421 AGCAGCATAAGCTGGACTTCAAGGCATACGAACAGGCACTGCAATACTCGCCTTACGGCT
- 432 T L P A S L P L G S A S V T T R S P I E
- 3481 CTACGTTGCCCGCCAGCCTGCCTCTAGGCAGCGCCTCGGTGACCACCAGGAGCCCCATCG
- 452 PSALEPAYYOGVYSRPVLNT
- 3541 AGCCCTCAGCCCTGGAGCCGGCGTACTACCAAGGTGTGTATTCCAGACCCGTCCTAAACA
- 472 S \*
- 3601 CTTCCTAG