```
ADH1          MSIPETQKGVIFYESHGKLEHKDIPVPKPKANELLINVKYSGVCHTDLHAWHGDWPLPVK  60
AFLA_048690   MSIPEMQWAQVAEQKGGPLIYKQIPVPKPGPDEILVKVRYSGVCHTDLHALKGDWPLPVK  60
              ***** *          * *  * ******  * *   * ***********  ********

ADH1          LPLVGGHEGAGVVVGMGENVKGWKIGDYAGIKWLNGSCMACEYCELGNESNCPHADLSGY  120
AFLA_048690   MPLVGGHEGAGVVVARGDLVTEFEIGDHAGLKWLNGSCLACEFCKQADEPLCPNASLSGY  120
               *************  *  *    *** ** ******* *** *    *  ** * ****

ADH1          THDGSFQQYATADAVQAAHIPQGTDLAQVAPILCAGITVYKALKSANLMAGHWVAISGAA  180
AFLA_048690   TVDGTFQQYAIGKATHASKLPKNVPLDAVAPVLCAGITVYKGLKESGVRPGQTVAIVGAG  180
              * ** *****   *  *   *    *  *** ********* **      *  *** **

ADH1          GGLGSLAVQYAKAMGYRVLGIDGGEGKEELFRSIGGEVFIDFTKEKDIVGAVLKATDG--  238
AFLA_048690   GGLGSLALQYAKAMGIRVVAIDGGEEKQAMCEQLGAEAYVDFTKTQDLVADVKAATPEGL  240
              ******* ******* **  ***** *        * *   ****  * *  *  **

ADH1          GAHGVINVSVSEAAIEASTRYVRANGTTVLVGMPAGAKCCSDVFNQVVKSISIVGSYVGN  298
AFLA_048690   GAHAVILLAVAEKPFQQAAEYVRSRGTVVAIGLPAGAFLRAPVFNTVVRMINIKGSYVGN  300
              *** **   * *        ***  ** *  * ****     *** **  * * ******

ADH1          RADTREALDFFARGLVKSPIKVVGLSTLPEIYEKMEKGQIVGRYVVDTSK  348
AFLA_048690   RQDGVEAVDFFARGLIKAPFKTAPLQDLPKIFELMEQGKIAGRYVLEIPE  350
              * *  ** ******* * * *   *  ** * * ** * * ****
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