

ADH1 MSIPETQKGVIFYESHGKLEHKDIPVVPKPKANELLINVKYSGVCHTDLHAWHGDWPLPVK 60
AFLA_048690 MSIPEMQWAQVAEQKGGPLIYKQIPVVPKPGPDEILVKVRYSGVCHTDLHALKGDWPLPVK 60
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ADH1 LPLVGGHEGAGVVVGMGENVKGWKIGDYAGIKWLNGSCMACEYCELGNESNCPHADLSGY 120
AFLA_048690 MPLVGGHEGAGVVVARGDLVTEFEIGDHAGLKWLNGSCLACEFCKQADEPLCPNASLSGY 120
***** *

ADH1 THDGSFQQYATADAVQAAHIPQGTDLAQVAPILCAGITVYKALKSANLMAGHWVAISGAA 180
AFLA_048690 TVDGTFFQQYAIGKATHASKLPKNVPLDAVAPVLCAGITVYKGLKESGVRPGQTVVAIVGAG 180
* *

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

ADH1 GAHGVINVSVSEAAIEASTRYVRANGTTVLVGMPAGAKCCSDVFNQVVKSIISIVGSYVGN 298
AFLA_048690 GAHAVILLAVAEKPFQQAAEYVRSRGTVVAIGLPAGAFRLRAPVFNTVVRMINIKGSYVGN 300
* *

ADH1 RADTREALDFFARGLVKSPIKVVGLSTLPEIYEKMEKGQIVGRYVVDTSK 348
AFLA_048690 RQDGVEAVDFFARGLIKAPFKTAPLQDLPKIFELMEQGKIAGRYVLEIPE 350
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