Supplementary Figure 1

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                α1(A)               β1(A)     α2(B)         β2(B)   α3(C)
                HHHHH             EEEEEEE HHHHHHHHHHHH     EEEEE   HHHHHH
                                          ●●●                    ♦♦
LDHA_HUMAN   MATLKDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKG
LDHA_BOVIN   MATLKDQLIQNLLKEEHVPQNKITIVGVGAVGMACAISILMKDLADEVALVDVMEDKLKG
LDHA_PIG     MATLKDQLIHNLLKEEHVPHNKITVVGVGAVGMACAISILMKELADEIALVDVMEDKLKG
LDHA_RABIT   MAALKDQLIHNLLKEEHVPQNKITVVGVGAVGMACAISILMKDLADELALVDVMEDKLKG
LDHA_MOUSE   MATLKDQLIVNLLKEEQAPQNKITVVGVGAVGMACAISILMKDLADELALVDVMEDKLKG
LDHA_RAT     MAALKDQLIVNLLKEEQVPQNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKG
LDHA_MONDO   MGTVKDQLILNVLKEEQTPHNKITVVGVGAVGMACAISILMKDLADELALVDVIEDKLKG
             *.::***** *:****:.*:****:*****************:****:*****:******

                            β3(C)          β4(D)               α4(D)
             HHHHHHH GGG    EEEE   GGGG    EEEE       TT  HHHHHHHHHHHHHHH
                                   ♦           ●♦♦ ●●     ●         ♦   ♦
LDHA_HUMAN   EMMDLQHGSLFLRTPKIVSGKDYNVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFI
LDHA_BOVIN   EMMDLQHGSLFLRTPKIVSGKDYNVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFI
LDHA_PIG     EMMDLQHGSLFLRTPKIVSGKDYNVTANSRLVVITAGARQQEGESRLNLVQRNVNIFKFI
LDHA_RABIT   EMMDLQHGSLFLRTPKIVSGKDYSVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFI
LDHA_MOUSE   EMMDLQHGSLFLKTPKIVSSKDYCVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFI
LDHA_RAT     EMMDLQHGSLFLKTPKIVSSKDYSVTANSKLVIITAGARQQEGESRLNLVQRNVNIFKFI
LDHA_MONDO   EMMDLQHGSLFLKTPKIVSSKDYAVTANSKLVVITAGARQQEGESRLNLVQRNVNIFKFI
             ************:******.*** *****:**:***************************

               α4(E)    β5(E)      α5(1F)         β6(F)       α6(2F)
             HHHHHHH    EEEE    HHHHHHHHHHHH   GGGEEE   HHHHHHHHHHHHHHH
                            ●●●                      ●    ●  ●
LDHA_HUMAN   IPNVVKYSPNCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
LDHA_BOVIN   IPNIVKYSPNCKLLVVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
LDHA_PIG     IPNIVKYSPNCKLLVVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
LDHA_RABIT   IPNVVKYSPHCKLLVVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
LDHA_MOUSE   IPNIVKYSPHCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
LDHA_RAT     IPNVVKYSPQCKLLIVSNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
LDHA_MONDO   IPNIVKYSPNCKLLVVSNPVDILTYVAWKLSGFPKNRVIGSGCNLDSARFRYLMGEKLGI
             ***:*****:****:**************:**************************:**:

                    β7(G)    β8(H)   β9(J)β10 α7               α8(1G)(2G)
              GGG    EE    TT EE GGG EETTEEHHHH      TT TT  HHHHHHHHHHHHH
                         ●
LDHA_HUMAN   HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDKEQWKEVHKQVVESAYE
LDHA_BOVIN   HPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELGTDADKEQWKAVHKQVVDSAYE
LDHA_PIG     HPLSCHGWILGEHGDSSVPVWSGVNVAGVSLKNLHPELGTDADKEHWKAVHKQVVDSAYE
LDHA_RABIT   HALSCHGWILGEHGDSSVPVWSGMNVAGVSLKTLHPELGTDADKEQWKQVHKQVVDSAYE
LDHA_MOUSE   HALSCHGWVLGEHGDSSVPVWSGVNVAGVSLKSLNPELGTDADKEQWKEVHKQVVDSAYE
LDHA_RAT     HPLSCHGWVLGEHGDSSVPVWSGVNVAGVSLKSLNPQLGTDADKEQWKDVHKQVVDSAYE
LDHA_MONDO   HSSSCHGWILGEHGDSSVPVWSGVNVAGVSLKSLHPALGTDSDSEQWKDVHKQVVESAYE
             *. *****:**************:********.*:* **** *.*:** ******:****

                           α9(3G)         β11(K)               β12(L)
             HHHHH    HHHHHHHHHHHHHHH    EEEEEEEE TT TT    EEEEEEEEEETTEE
                    ●   ●
LDHA_HUMAN   VIKLKGYTSWAIGLSVADLAESIMKNLRRVHPVSTMIKGLYGIKDDVFLSVPCILGQNGI
LDHA_BOVIN   VIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKEDVFLSVPCILGQNGI
LDHA_PIG     VIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKEDVFLSVPCILGQNGI
LDHA_RABIT   VIKLKGYTTWAIGLSVADLAESIMKNLRRVHPISTMLKGLYGIKEDVFLSVPCVLGQNGI
LDHA_MOUSE   VIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGINEDVFLSVPCILGQNGI
LDHA_RAT     VIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGIKEDVFLSVPCILGQNGI
LDHA_MONDO   VIKLKGYTSWAIGLSVADLAESIMKNLRRVHPISTMIKGLYGINEDVFLSVPCILGQNGI
             ********:***********************:***:******::*********:*****

             β13(M)        α10(H)
             EEEE     HHHHHHHHHHHHHHHHHHH

LDHA_HUMAN   SDLVKVTLTSEEEARLKKSADTLWGIQKELQF
LDHA_BOVIN   SDVVKVTLTHEEEACLKKSADTLWGIQKELQF
LDHA_PIG     SDVVKVTLTPEEEAHLKKSADTLWGIQKELQF
LDHA_RABIT   SDVVKVTLTSEEEAHLKKSADTLWGIQKELQF
LDHA_MOUSE   SDVVKVTLTPEEEARLKKSADTLWGIQKELQF
LDHA_RAT     SDVVKVTLTPDEEARLKKSADTLWGIQKELQF
LDHA_MONDO   SDVVKVTLTTEEESRLKQSADTLWGIQKELQF
             **:****** :**: **:**************
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Multiple sequence alignment of human (UniProtKB accession code: P00338), bovine (UniProtKB accession code: P19858; 93.7% sequence identity), porcine (UniProtKB accession code: P00339; 92.8% sequence identity), rabbit (UniProtKB accession code: P13491; 93.7% sequence identity), murine (UniProtKB accession code: P06151, 93.9% sequence identity), rat (UniProtKB accession code: P04642; 94.3% sequence identity) and opposum (UniProtKB accession code: Q9XT87; 90.9% sequence identity) LDH-A. The active site loop is highlighted in yellow and the catalytic residue His193 is highlighted in orange. Other active site pocket residues are marked with a rhombus or dot depending on their proximity to the adenine or oxamate/nicotinamide moieties, respectively. Secondary structure elements are shown above the sequences whereby E denotes for β-strand, H for α-helix, G for 3_{10} helix and T for β-turn. A sequential and the historical (in brackets) nomenclature are shown for secondary structure elements.