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SbDLDH-1   ------------------------------MATSLLRLSRPRRALPLLPISSLRQP----------------------LSTQSHAPSPTPSSARRLPHFLSFLAAAAAAAAGGATVALCDSGLDH--HRVGGKDSTDLVVRGERKLV
OsLDH      ----------------------------MATAAAALLRLSRSRR--PLLPLSSLRLPPPAP---------------YHHHSHSQTPPSSSSSHARLPAFLSFLAAAAA---AGGTTVALCDSGID---HRVGGKESTELVVRGERKRV
AtLDH      -------------------------MAFASKFARSKTILSFLRPCRQLHSTPKSTGDVT--------------------VLSPVKGRRRLPTCWSSSLFPLAIAASATSFAYLNLSNPSISESSSALDSRDITVGGKDSTEAVVKGEYKQV
SbDLDH-4.1 MDSRLRQSLLEKHPPPMADVHEPLVRRKRKKVLVDYLVQFRWILVIFVVLPISSLIYFNIFLGDMWSAMKSEKKRQKQHDENVQKVVKRLKQRNPKKDGLVCTARKPWIAVGMRNVDYKRARHFEVDLSSFRNILEIDKERMVAKVEPLV
SbDLDH-4.2 ----------------MADVHEPLVRRKRKKVLVDYLVQFRWILVIFVVLPISSLIYFNIFLGDMWSAMKSEKKRQKQHDENVQKVVKRLKQRNPKKDGLVCTARKPWIAVGMRNVDYKRARHFEVDLSSFRNILEIDKERMVAKVEPLV
SbDLDH-3   ------------------------------------------------------------------------------------------------------------------------------------------MRNVDYKRARHFQVDLSAFRNILEIDTERMVAKVEPLV
SbDLDH-2   ------------------------------MARREAARLLRRLGPLAVESPTRGMPR--------------------CQHESANHIVNSCRRFHWIPSLQRPLCGPTTCRGIYEGQSSANKACEVQKRTFGSAATATHIQRNPAYSQL

SbDLDH-1   PQEFIDELASFLGDNMTLDYEERSFHGTPQNSFHKAINVPDVVVFPSSQDEVQKIVMACNKYKVPIVPYGGATSIEGHTLAPHGGVCIDMTLMKKIKSLNVEDMDVVVEPGVGWIELNEYLKPYGLFFPLDPGKNLAIVGNCIFTCFEGF
OsLDH      PNEFIDELASFLGENLTVDYEERHYHGTPQNSFHKAVNVPDVVVFPRSQDEVQKIVMACNKYKVPIVPYGGATSIEGHTLAPHGGVCINMSLMKKIKSLHVEDMDVVVEPGVGWIELNEYLKPYGLFFPLDPG-----------------
AtLDH      PKELISQLKTILEDNLTTDYDERYFHGKPQNSFHKAVNIPDVVVFPRSEEEVSKILKSCNEYKVPIVPYGGATSIEGHTLAPKGGVCIDMSLMKRVKALHVEDMDVIVEPGIGWLELNEYLEEYGLFFPLDPG-----------------
SbDLDH-4.1 NMGQITRATCPMNLALAVVAELDDLTVGGLINGYGIEGSSHLYGLFSDTVVAMEVVLADGRVVRATKDNEYSDLFYG---IPWSQGTLGFLVSAEIKLIPIKEYMKLTYIPVKG-SLKEIAQAYADSFAPRDGD----------------
SbDLDH-4.2 NMGQITRATCPMNLALAVVAELDDLTVGGLINGYGIEGSSHLYGLFSDTVVAMEVVLADGRVVRATKDNEYSDLFYG---IPWSQGTLGFLVSAEIKLIPIKEYMKLTYIPVKG-SLKEIAQAYADSFAPRDGD----------------
SbDLDH-3   SMGQITKATCPMNLSLAVAPEFDDLTVGGLINSYGISGGSHIYGLFTDTVVAMEVVLADGQVVRATMDNEHSDLFLWHAMVPRHDWAPCFSRDQAHSCQGIHEAH--IYTPVRG-TLKEIAEAYADSFVPRDGD----------------
SbDLDH-2   SSDDVSYFKSVLGENGVVQDEDR-VAVANVDWMGKYRGASQLLLLPKNTAEVSKILSYCNTRRLAVVPQGGNTGLVGGSVPVYDEVIVGLAGMDKIISFDNVNGILTCEAGCVLESLSNFVENEGFIMPLDLGAKG----------------

SbDLDH-1   KCMFSSHYHSVERSIEPSSYLEDGPGATIGGMCATRCSGSLAVRYGTMRDNVINLRAVLPNGDVVKTGSRARKSAAGYDLARLIIGSEGTLGVITEVTLRLQKLPSHSVVAMCNFKTIKDAADVAIATMLS-GIQVSRVELLDEVQIKAI
OsLDH      ------------------------PGATIGGMCATRCSGSLAVSL-----------------------------------------------------------------------------------------------------
AtLDH      ------------------------PGASIGGMCATRCSGSLAVRYGTMRDNVISLKVVLPNGDVVKTASRARKSAAGYDLTRLIIGSEGTLGVITEITLRLQKIPQHSVVAVCNFPTVKDAADVAIATMMS-GIQVSRVELLDEVQIRAI
SbDLDH-4.1 ---------------------PAKVPDFVEGMVYTESEGVMMTGVYASKE-----EAKKKGNKINCVGWWFKPWFYQHAQTALKRGEFVEYIPTREYYHRHTRCLYWEGKLILPFG-----DQFWFRFLLG-WLMPPKVSLLKATQGEAI
SbDLDH-4.2 ---------------------PAKVPDFVEGMVYTESEGVMMTGVYASKE-----EAKKKGNKINCVGWWFKPWFYQHAQTALKRGEFVEYIPTREYYHRHTRCLYWEGKLILPFG-----DQFWFRFLLG-WLMPPKVSLLKATQGEAI
SbDLDH-3   ---------------------PAKVPDFVEGMVYSSSEGVTMTGVYASEE-----EAKKKGNRINRVGWWFKPWFYQYAETALKRGEFVEYIPTREYYHRHTRSLYWEGKLIIPFG-----DQFWFRFLLG-WLMPPKISLLKITQGEAI
SbDLDH-2   -------------------------SCHIGGNVSTNAGGLRFIRYGSLHGSVLGLEVVLADGTILDMLTTLRKDNTGYDLKHLFIGSEGSLGVVTKISVLTPAKLPSTNVAFLSCNDYKSCQKLLLAARRSLGEILSAFEFMDHHCINLA

SbDLDH-1   N--MANGKN-LPEVPTLMFEFIGTEAYAL-----EQTLLVQKIANKHHGSDFVFVEEPDAKAELWKIRKEALWAGFAMKPDYEAMITDVCVPLS---RLAECISTSKRLLDASPLTCLVIAHAGDGNFHTIILFDPSQDDQQKEAERLNH
OsLDH      ----------------------------------------------------------------------------------------------------------------------------------------------------
AtLDH      N--MANGKN-LTEAPTLMFEFIGTEAYTR-----EQTQIVQQIASKHNGSDFMFAEEPEAKKELWKIRKEALWACYAMAPGHEAMITDVCVPLS---HLAELISRSKKELDASSLLCTVIAHAGDGNFHTCIMFDPSSEEQRREAERLNH
SbDLDH-4.1 RNYYHDNHV-IQDMLVPLYKVGDALEFVH-----REMEVYPLWLCPHRLYKLPVKTMVYPEPGFEHQHRQGDTSYAQMFTDVGVYYAPGAVLRGEEFNGAEAVHRLEQWLIENHSYQPQYAVSELNEKDFWRMFDASHYEHCRHKYGAVG
SbDLDH-4.2 RNYYHDNHV-IQDMLVPLYKVGDALEFVH-----REMEVYPLWLCPHRLYKLPVKTMVYPEPGFEHQHRQGDTSYAQMFTDVGVYYAPGAVLRGEEFNGAEAVHRLEQWLIENHSYQPQYAVSELNEKDFWRMFDASHYEHCRHKYGAVG
SbDLDH-3   RNYYHDNHV-IQDVLVPLHKVSDALEFAH-----RELEVYPVWLCPHRLYKLPVKTMVHPEPGFEQHRRKGDTSYAQMFTDVGFYYAPASVLRGEEFNGAEAVHRLEQWLIRNHGYQAQYAVSELSEKDFWRMFDPSHYEHCRRKYGAVG
SbDLDH-2   MRHLEGVHNPLPASPYKFYVLIETTGSDESYDKTKLEAFLLRSMEDGLVADGVIAQDISQASNFWRIREGISEASVKVG---AVYKYDLSIPVEKLYDIVEEMRCRLG----DSAEVLGYGHLGDGNLHLNIVSSKYDDSTLG---RIEP

SbDLDH-1   FMVDTALSMEGTCTGEHGVGTGKMKYLEKELGIESLRTMKRIKGALDPNNIMNPGKLIPPHVCI
OsLDH      ----------------------------------------------------------------
AtLDH      FMVHSALSMDGTCTGEHGVGTGKMKYLEKELGIEALQTMKRIKKTLDPNDIMNPGKLIPPHVCF
SbDLDH-4.1 TFMSVYYKSKKGRKTEKEVQEAEAAILEPAYADEA-----------------------------
SbDLDH-4.2 TFMSVYYKSKKGRKTEKEVQEAEAAILEPAYADEA-----------------------------
SbDLDH-3   SFMSAHYKSKK-RQKERGGGARS-----------------------------------------
SbDLDH-2   FVYEWTSAQRGSISAEHGLGLMKAEKIHYSKSPEAVQLMASIKKLLDPNSILNPYKVLPQSVL-
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Figure S5