|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Family | Gene name | Other names | NCBI gene ID | NCBI protein ID | Phytozome ID | Splice variants | Chrm | AA | Protein molecular weight (kDa) |
| ALDH2 | ALDH2B4 | ALDH2; ALDH2A | 823955 | NP\_190383.1 | AT3G48000 | 0 | 3 | 538 | 58.60 |
| ALDH2B7 | ALDH2B | 838991 | NP\_564204.1 | AT1G23800 | 2 | 1 | 534 | 58.16 |
| ALDH2C4 | ALDH1A; REF1 | 822042 | NP\_566749.1 | AT3G24503 | 0 | 3 | 501 | 54.37 |
| ALDH3 | ALDH3F1 | F23E13.140; F23E13\_140 | 829782 | NP\_195348.2 | AT4G36250 | 0 | 4 | 484 | 53.62 |
| ALDH3H1 | ALDH4 | 841020 | NP\_175081.1 | AT1G44170 | 3 | 1 | 484 | 53.16 |
| ALDH3I1 | ALDH3 | 829573 | NP\_567962.1 | AT4G34240 | 4 | 4 | 550 | 60.18 |
| ALDH5 | ALDH5F1 | ENF1; SSADH; SSADH1 | 844282 | NP\_178062.1 | AT1G79440 | 0 | 1 | 528 | 56.57 |
| ALDH6 | ALDH6B2 | MMSD | 815903 | NP\_179032.1 | AT2G14170 | 3 | 2 | 607 | 65.94 |
| ALDH7 | ALDH7B4 | F15I1.19; F15I1\_19 | 841849 | NP\_175812.1 | AT1G54100 | 2 | 1 | 508 | 54.22 |
| ALDH10 | ALDH10A8 | F25A4.11; F25A4\_11 | 843831 | NP\_001185399.1 | AT1G74920 | 2 | 1 | 496 | 53.98 |
| ALDH10A9 | BADH | 823972 | NP\_190400.1 | AT3G48170 | 0 | 3 | 503 | 54.92 |
| ALDH11 | ALDH11A3 | F27D4.18; F27D4\_18; NP-GAPDH | 816962 | NP\_001189589.1 | AT2G24270 | 4 | 2 | 496 | 53.07 |
| ALDH12 | ALDH12A1 | ATP5CDH; K19B1.14; K19B1\_14; P5CDH | 836373 | NP\_568955.1 | AT5G62530 | 0 | 5 | 556 | 61.78 |
| ALDH18 | ALDH18B1 | TP5CS; T5I7.10; T5I7\_10 | 818566 | NP\_181510.1 | AT2G39800 | 4 | 2 | 717 | 77.71 |
| ALDH18B2 | P5CS2 | 824727 | NP\_191120.2 | AT3G55610 | 2 | 3 | 726 | 78.88 |
| ALDH22 | ALDH22A1 | T8E24.4; T8E24\_4 | 819849 | NP\_974242.1 | AT3G66658 | 2 | 3 | 596 | 66.01 |

Table. S1. *Arabidopsis thaliana* ALDH superfamily.

Table. S2. Primers used in this study.

|  |  |  |
| --- | --- | --- |
| Gene | Sequence (5’->3’) | Accession Number |
| *AtALDH2B4* | Forward primer | CTAGAGACATGGGACAATGG | AT3G48000 |
| Reverse primer | AGTCCATGAATCTTATCCGC |
| *AtALDH2B7* | Forward primer | CCAGTGAAAGTTGAACACAC | AT1G23800 |
| Reverse primer | TTCAGACACTTGAGCAATCA |
| *AtALDH2C4* | Forward primer | GTGCAGCAGATAAAATCCAC | AT3G24503 |
| Reverse primer | GGGAAATTCCAAGGGATGAT |
| *AtALDH3F1* | Forward primer | AAATACCGTGCTTCTCAAGT | AT4G36250 |
| Reverse primer | ATCAGGTCCTCCTTCGATAA |
| *AtALDH3H1* | Forward primer | GACTCGGATACCGATTTGAA | AT1G44170 |
| Reverse primer | AAGATATAGTCCGGCGAAAC |
| *AtALDH3I1* | Forward primer | CCCAGTTTGAAAAATCGACC | AT4G34240 |
| Reverse primer | AACTCTGAGATAACGTCGTG |
| *AtALDH5F1* | Forward primer | AAGGTCTAATTGGAGGCAAG | AT1G79440 |
| Reverse primer | TTCCCATACATGCAACATCA |
| *AtALDH6B2* | Forward primer | TGACGGAAGAGATATTGTGG | AT2G14170 |
| Reverse primer | TTGTAACACTCCATGTCTGG |
| *AtALDH7B4* | Forward primer | ACACGCATTCCCTTAGTATC | AT1G54100 |
| Reverse primer | TTGCATTGTTTCCACTCAAC |
| *AtALDH10A8* | Forward primer | TTCTTGTTCACGAAAGCATC | AT1G74920 |
| Reverse primer | TTGCTAACTACAGGACCAAG |
| *AtALDH10A9* | Forward primer | TGGTCCTGTTGTCAGTAAAG | AT3G48170 |
| Reverse primer | TAAATGCTCAGGACGAACTC |
| *AtALDH11A3* | Forward primer | TACTGCGAATAAAGGGAGTG | AT2G24270 |
| Reverse primer | AACCAAACCTCTCACTCATC |
| *AtALDH12A1* | Forward primer | TTTCCGTGTGAGGGAATAAG | AT5G62530 |
| Reverse primer | CTGGTGGACTGAGTTTTACA |
| *AtALDH18B1* | Forward primer | ATATGGAAGATCCAATCGGC | AT2G39800 |
| Reverse primer | GAAGTACGCCTAATGGTGAT |
| *AtALDH18B2* | Forward primer | CGACTAAGTTGACTCGTTCT | AT3G55610 |
| Reverse primer | CGATACGCTTAACGTCTTTG |
| *AtALDH22A1* | Forward primer | CTCATGGGAAAGATACGGAG | AT3G66658 |
| Reverse primer | GTGGCAGGTTCATAACATTG |
| *Actin-2* | Forward primer | TTGGGATGAACCAGAAGGAT | At3G18780 |
| Reverse primer | TCCATATCATCCCAGTTGCT |

Table. S4. *Arabidopsis thaliana* ALDH protein superfamily localization.

|  |  |  |
| --- | --- | --- |
| Gene name | Localization | Reference |
| ALDH2B4 | Mitochondria | Wei et al. (2009) |
| ALDH2B7 | Mitochondria |  |
| ALDH2C4 | Cytosol | Nair et al. (2004) |
| ALDH3F1 | Cytosol | Nair et al. (2011) |
| ALDH3H1 | Cytosol | Nair et al. (2011) |
| ALDH3I1 | Chloroplasts | Sunkar et al. (2003); Kotchoni et al. (2006) |
| ALDH5F1 | Mitochondria | Bouché et al. (2003); Bouché and Fromm (2004); Toyokura et al. (2011) |
| ALDH6B2 | Mitochondria | - |
| ALDH7B4 | Cytosol | Kotchoni et al. (2006) |
| ALDH10A8 | Leucoplasts | Missihoun et al. (2011) |
| ALDH10A9 | Peroxisomes | Missihoun et al. (2011) |
| ALDH11A3 | - |  |
| ALDH12A1 | Mitochondria | Deuschle et al. (2001, 2004); Miller et al. (2009) |
| ALDH18B1 | - |  |
| ALDH18B2 | - |  |
| ALDH22A1 | Cytosol | Krich et al. (2005) |

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
|   | ALDH2B4 | ALDH2B7 | ALDH2C4 | ALDH3F1 | ALDH3H1 | ALDH3I1 | ALDH5F1 | ALDH6B2 | ALDH7B4 | ALDH10A8 | ALDH10A9 | ALDH11A3 | ALDH12A1 | ALDH18B1 | ALDH18B2 | ALDH22A1 |
| ALDH2B4 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| ALDH2B7 | 0,0748631178 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| ALDH2C4 | 0,7581100652 | 0,6457847964 |   |   |   |   |   |   |   |   |   |   |   |   |   |   |
| ALDH3F1 | 0,6476852116 | 0,4680559594 | 0,7503595256 |   |   |   |   |   |   |   |   |   |   |   |   |   |
| ALDH3H1 | 0,7029452971 | 0,2217818903 | 0,0937698039 | 0,0005916589 |   |   |   |   |   |   |   |   |   |   |   |   |
| ALDH3I1 | 0,3659853653 | 0,6548067857 | 0,1545439050 | 0,0725075196 | 0,0000080073 |   |   |   |   |   |   |   |   |   |   |   |
| ALDH5F1 | 0,0064546770 | 0,4049227517 | 0,0000000000 | 0,2864619838 | 0,5211936780 | 0,8518367934 |   |   |   |   |   |   |   |   |   |   |
| ALDH6B2 | 0,0008234884 | 0,7502807481 | 0,0000000000 | 0,4068152318 | 0,5166255755 | 0,7758042807 | 0,0000093515 |   |   |   |   |   |   |   |   |   |
| ALDH7B4 | 0,0064282148 | 0,0009796858 | 0,0000000000 | 0,6055557855 | 0,2484368541 | 0,1383307152 | 0,0000000000 | 0,0000001807 |   |   |   |   |   |   |   |   |
| ALDH10A8 | 0,0688918701 | 0,0041170748 | 0,0000000000 | 0,7342902406 | 0,0581338239 | 0,0428840250 | 0,0000000000 | 0,0000004422 | 0,0000000299 |   |   |   |   |   |   |   |
| ALDH10A9 | 0,0312153021 | 0,6866566369 | 0,0000000000 | 0,2742937502 | 0,1180396226 | 0,1940114444 | 0,0000000000 | 0,0000479423 | 0,0000000000 | 0,0000000000 |   |   |   |   |   |   |
| ALDH11A3 | 0,0280190340 | 0,5421288455 | 0,0000000000 | 0,7866485865 | 0,8405086515 | 0,8404209614 | 0,0000000070 | 0,0000018723 | 0,0000000483 | 0,0000000000 | 0,0002330063 |   |   |   |   |   |
| ALDH12A1 | 0,0002848217 | 0,8647462978 | 0,0071624157 | 0,9087779503 | 0,4545404221 | 0,2595822008 | 0,0087720526 | 0,0013363144 | 0,0001805334 | 0,0073564969 | 0,0075157256 | 0,0087892843 |   |   |   |   |
| ALDH18B1 | 0,0483819120 | 0,5134339279 | 0,0081017850 | 0,9881065411 | 0,4232049854 | 0,9000673477 | 0,7112620242 | 0,6829958998 | 0,9072712670 | 0,1111250796 | 0,2564578227 | 0,9215577136 | 0,1071841456 |   |   |   |
| ALDH18B2 | 0,5395711814 | 0,4950795390 | 0,1369108808 | 0,2356686916 | 0,0631480235 | 0,0949548207 | 0,4793970344 | 0,9043756190 | 0,6685419088 | 0,3902499540 | 0,9072281154 | 0,6789423449 | 0,5241029971 | 0,8731796332 |   |   |
| ALDH22A1 | 0,0851185769 | 0,6656832385 | 0,3691796711 | 0,9982662159 | 0,9393735787 | 0,4856387053 | 0,0598678011 | 0,3295065292 | 0,1981599679 | 0,8027995797 | 0,6196974428 | 0,4815724809 | 0,9379807695 | 0,2906885086 | 0,5027529552 |   |

Table. S5. Evolutionary constraint (dN/dS).

Table. S6. All the sequences of used for phylogenetic tree construction.

>AtALDH2B4

MAARRVSSLLSRSFSASSPLLFRSQGRNCYNGGILRRFGTSSAAAEEIINPSVQVSHTQLLINGNFVDSASGKTFPTLDP

RTGEVIAHVAEGDAEDINRAVKAARTAFDEGPWPKMSAYERSRVLLRFADLVEKHSEELASLETWDNGKPYQQSLTAEIP

MFARLFRYYAGWADKIHGLTIPADGNYQVHTLHEPIGVAGQIIPWNFPLLMFAWKVGPALACGNTIVLKTAEQTPLTAFY

AGKLFLEAGLPPGVLNIVSGFGATAGAALASHMDVDKLAFTGSTDTGKVILGLAANSNLKPVTLELGGKSPFIVFEDADI

DKAVELAHFALFFNQGQCCCAGSRTFVHEKVYDEFVEKSKARALKRVVGDPFRKGIEQGPQIDLKQFEKVMKYIKSGIES

NATLECGGDQIGDKGYFIQPTVFSNVKDDMLIAQDEIFGPVQSILKFSDVDEVIKRANETKYGLAAGVFTKNLDTANRVS

RALKAGTVWVNCFDVFDAAIPFGGYKMSGNGREKGIYSLNNYLQIKAVVTALNKPAWI

>AtALDH2B7

MASRRVSSLLSRSFMSSSRSIFSLRGMNRGAQRYSNLAAAVENTITPPVKVEHTQLLIGGRFVDAVSGKTFPTLDPRNGE

VIAQVSEGDAEDVNRAVAAARKAFDEGPWPKMTAYERSKILFRFADLIEKHNDEIAALETWDNGKPYEQSAQIEVPMLAR

VFRYYAGWADKIHGMTMPGDGPHHVQTLHEPIGVAGQIIPWNFPLLMLSWKLGPALACGNTVVLKTAEQTPLSALLVGKL

LHEAGLPDGVVNIVSGFGATAGAAIASHMDVDKVAFTGSTDVGKIILELASKSNLKAVTLELEESHHSFVCEDADVDQAV

ELAHFALFFNQGQCCCAGSRTFVHERVYDEFVEKAKARALKRNVGDPFKSGIEQGPQVDSEQFNKILKYIKHGVEAGATL

QAGGDRLGSKGYYIQPTVFSDVKDDMLIATDEIFGPVQTILKFKDLDEVIARANNSRYGLAAGVFTQNLDTAHRLMRALR

VGTVWINCFDVLDASIPFGGYKMSGIGREKGIYSLNNYLQVKAVVTSLKNPAWL

>AtALDH2C4

MENGKCNGATTVKLPEIKFTKLFINGQFIDAASGKTFETIDPRNGEVIATIAEGDKEDVDLAVNAARYAFDHGPWPRMTG

FERAKLINKFADLIEENIEELAKLDAVDGGKLFQLGKYADIPATAGHFRYNAGAADKIHGETLKMTRQSLFGYTLKEPIG

VVGNIIPWNFPSIMFATKVAPAMAAGCTMVVKPAEQTSLSALFYAHLSKEAGIPDGVLNIVTGFGSTAGAAIASHMDVDK

VSFTGSTDVGRKIMQAAAASNLKKVSLELGGKSPLLIFNDADIDKAADLALLGCFYNKGEICVASSRVFVQEGIYDKVVE

KLVEKAKDWTVGDPFDSTARQGPQVDKRQFEKILSYIEHGKNEGATLLTGGKAIGDKGYFIQPTIFADVTEDMKIYQDEI

FGPVMSLMKFKTVEEGIKCANNTKYGLAAGILSQDIDLINTVSRSIKAGIIWVNCYFGFDLDCPYGGYKMSGNCRESGMD

ALDNYLQTKSVVMPLHNSPWM

>AtALDH3F1

MEAMKETVEESLREMRETFASGRTRSLKWRKAQIGAIYEMVKDNEDKICNALFQDLGKLSTEAFRDELGVVLRTATVAIN

CLDKWAVPKHSKLPLLFYPAKGKVISEPYGTVLVLSSWNFPISLSLDPLIGAIAAGNTVLLKSSELSPNASAFLAKTIPA

YLDTKAIKVIEGGPDVATILLQHQWDKIFFTGSPKIGRIIMAAAAQHLTPVTLELGGKCPTIVDHTISKNIKSVVKRIAG

GKWGSCNGQACISVDYVLIEKSFAPTLIDMLKPTIKSFFGENPKESGCLSRIANKHHVQRLSRLLSDPRVQASIVYGGSI

DEDKLYVEPTILLDPPLDSEIMNEEIFGPILPIITVRDIQESIGIINTKPKPLAIYAFTNDENLKTRILSETSSGSVTFN

DVMIQYMCDALPFGGVGESGIGRYHGKYSFDCFSHEKAIMEGSLGMDLEARYPPWNNFKLTFIRLAFREAYFKLILLMLG

LKR

>AtALDH3H1

MAAKKVFGSAEASNLVTELRRSFDDGVTRGYEWRVTQLKKLMIICDNHEPEIVAALRDDLGKPELESSVYEVSLLRNSIK

LALKQLKNWMAPEKAKTSLTTFPASAEIVSEPLGVVLVISAWNYPFLLSIDPVIGAISAGNAVVLKPSELAPASSALLTK

LLEQYLDPSAVRVVEGAVTETSALLEQKWDKIFYTGSSKIGRVIMAAAAKHLTPVVLELGGKSPVVVDSDTDLKVTVRRI

IVGKWGCNNGQACVSPDYILTTKEYAPKLIDAMKLELEKFYGKNPIESKDMSRIVNSNHFDRLSKLLDEKEVSDKIVYGG

EKDRENLKIAPTILLDVPLDSLIMSEEIFGPLLPILTLNNLEESFDVIRSRPKPLAAYLFTHNKKLKERFAATVSAGGIV

VNDIAVHLALHTLPFGGVGESGMGAYHGKFSFDAFSHKKAVLYRSLFGDSAVRYPPYSRGKLRLLKALVDSNIFDLFKVL

LGLA

>AtALDH3I1

MTKLLEINHIQTLCFAKGFSPARLNVATSPFLISRRGGGGYCSNACIPYRLKFTCYATLSAVVKEQASDFRGKEAALLVD

ELRSNFNSGRTKSYEWRISQLQNIARMIDEKEKCITEALYQDLSKPELEAFLAEISNTKSSCMLAIKELKNWMAPETVKT

SVTTFPSSAQIVSEPLGVVLVISAWNFPFLLSVEPVIGAIAAGNAVVLKPSEIAPAASSLLAKLFSEYLDNTTIRVIEGG

VPETTALLDQKWDKIFFTGGARVARIIMAAAARNLTPVVLELGGKCPALVDSDVNLQVAARRIIAGKWACNSGQACIGVD

YVITTKDFASKLIDALKTELETFFGQNALESKDLSRIVNSFHFKRLESMLKENGVANKIVHGGRITEDKLKISPTILLDV

PEASSMMQEEIFGPLLPIITVQKIEDGFQVIRSKSKPLAAYLFTNNKELEKQFVQDVSAGGITINDTVLHVTVKDLPFGG

VGESGIGAYHGKFSYETFSHKKGVLYRSFSGDADLRYPPYTPKKKMVLKALLSSNMFAAILAFFGFSKDS

>AtALDH5F1

MVIGAAARVAIGGCRKLISSHTSLLLVSSQCRQMSMDAQSVSEKLRSSGLLRTQGLIGGKWLDSYDNKTIKVNNPATGEI

IADVACMGTKETNDAIASSYEAFTSWSRLTAGERSKVLRRWYDLLIAHKEELGQLITLEQGKPLKEAIGEVAYGASFIEY

YAEEAKRVYGDIIPPNLSDRRLLVLKQPVGVVGAITPWNFPLAMITRKVGPALASGCTVVVKPSELTPLTALAAAELALQ

AGVPPGALNVVMGNAPEIGDALLTSPQVRKITFTGSTAVGKKLMAAAAPTVKKVSLELGGNAPSIVFDDADLDVAVKGTL

AAKFRNSGQTCVCANRVLVQDGIYDKFAEAFSEAVQKLEVGDGFRDGTTQGPLINDAAVQKVETFVQDAVSKGAKIIIGG

KRHSLGMTFYEPTVIRDVSDNMIMSKEEIFGPVAPLIRFKTEEDAIRIANDTIAGLAAYIFTNSVQRSWRVFEALEYGLV

GVNEGLISTEVAPFGGVKQSGLGREGSKYGMDEYLEIKYVCLGDMNRH

>AtALDH6B2

MVRVKQKNLESYRSNGTYPPTWRNPTTSFAPDQHRVSIHSSLKSKTKRRRLYKEADDNTKLRSSSSTTTTTTTMLLRISG

NNLRPLRPQFLALRSSWLSTSPEQSTQPQMPPRVPNLIGGSFVESQSSSFIDVINPATQEVVSKVPLTTNEEFKAAVSAA

KQAFPLWRNTPITTRQRVMLKFQELIRKNMDKLAMNITTEQGKTLKDSHGDIFRGLEVVEHACGMATLQMGEYLPNVSNG

VDTYSIREPLGVCAGICPFNFPAMIPLWMFPVAVTCGNTFILKPSEKDPGASVILAELAMEAGLPDGVLNIVHGTNDTVN

AICDDEDIRAVSFVGSNTAGMHIYARAAAKGKRIQSNMGAKNHGLVLPDANIDATLNALLAAGFGAAGQRCMALSTVVFV

GDAKSWEDKLVERAKALKVTCGSEPDADLGPVISKQAKERICRLIQSGVDDGAKLLLDGRDIVVPGYEKGNFIGPTILSG

VTPDMECYKEEIFGPVLVCMQANSFDEAISIINKNKYGNGAAIFTSSGAAARKFQMDIEAGQIGINVPIPVPLPFFSFTG

NKASFAGDLNFYGKAGVDFFTQIKTVTQQWKDIPTSVSLAMPTSQKQ

>AtALDH7B4 A new protein sequence entered manually

MGSANNEYEFLSEIGLTSHNLGSYVAGKWQANGPLVSTLNPANNQPIAQVVEASLEDYEQGLKACEEAAKIWMQVTAPKR

GDIVRQIGDALRSKLDYLGRLLSLEMGKILAEGIGEVQEVIDMCDFAVGLSRQLNGSVIPSERPNHMMLEMWNPLGIVGV

ITAFNFPCAVLGWNACIALVCGNCVVWKGAPTTPLITIAMTKLVAEVLEKNNLPGAIFTAMCGGAEIGEAIAKDTRIPLV

SFTGSSRVGSMVQQTVNARSGKTLLELSGNNAIIVMDDADIQLAARSVLFAAVGTAGQRCTTCRRLLLHESVYDKVLEQL

LTSYKQVKIGNPLEKGTLLGPLHTPESKKNFEKGIEVIKSQGGKILTGGKAVEGEGNFVEPTIIEISADAAVVKEELFAP

VLYVLKFKSFGEAVAINNSVPQGLSSSIFTRNPENIFRWIGPLGSDCGIVNVNIPTNGAEIGGAFGGEKATGGGREAGSD

SWKQYMRRSTCTINYGNELPLAQGINFG

>AtALDH10A8

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IAAKVNERKTDLAKLEALDCGKPLDEAVWDMDDVAGCFEFYADLAEGLDAKQKAPVSLPMESFKSYVLKQPLGVVGLITP

WNYPLLMAVWKVAPSLAAGCTAILKPSELASVTCLELADICREVGLPPGVLNVLTGFGSEAGAPLASHPGVDKIAFTGSF

ATGSKVMTAAAQLVKPVSMELGGKSPLIVFDDVDLDKAAEWALFGCFWTNGQICSATSRLLVHESIASEFIEKLVKWSKN

IKISDPMEEGCRLGPVVSKGQYEKILKFISTAKSEGATILHGGSRPEHLEKGFFIEPTIITDVTTSMQIWREEVFGPVLC

VKTFASEDEAIELANDSHYGLGAAVISNDTERCDRISEAFEAGIVWINCSQPCFTQAPWGGVKRSGFGRELGEWGLDNYL

SVKQVTLYTSNDPWGWYKSPN

>AtALDH10A9

MAITVPRRQLFIGGQWTEPVLRKTLPVVNPATEDIIGYIPAATSEDVELAVEAARKAFTRNNGKDWARATGAVRAKYLRA

IAAKVIERKSELANLEAIDCGKPLDEAAWDMDDVAGCFEYYADLAEGLDAKQKTPLSLPMDTFKGYILKEPIGVVGMITP

WNYPLLMAVWKVAPSLAAGCTAILKPSELASLTCLELADICREVGLPPGVLNILTGLGTEAGAPLASHPHVDKIVFTGST

TTGSSIMTSAAKLVKPVSLELGGKSPIIVFDDVDIDKAVEWTMFGCFWTNGQICSATSRLLVHERIADEFLDKLVKWTKN

IKISDPFEEGCRLGPVVSKGQYERVLKFVSNARNEGATVLCGGVRPEHLKKGYFVEPAIVSNVTTSMEIWREEVFGPALC

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SVKQVTQYISDEPWGWYKPPSKL

>AtALDH11A3

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LHKAAAILKDNKAPMAESLVKEIAKPAKDSVTEVVRSGDLISYCAEEGVRILGEGKFLLSDSFPGNDRTKYCLTSKIPLG

VVLAIPPFNYPVNLAVSKIAPALIAGNSLVLKPPTQGAVSCLHMVHCFHLAGFPKGLISCITGKGSEIGDFLTMHPAVNC

ISFTGGDTGISISKKAGMIPLQMELGGKDACIVLDDADLDLVASNIIKGGFSYSGQRCTAVKVVLVMESVADELVEKVKA

KVAKLTVGPPEENSDITAVVSESSANFIEGLVMDAKEKGATFCQEYKREGNLIWPLLLDNVRPDMRIAWEEPFGPVVPVL

RINSVEEGINHCNASNFGLQGCVFTKDINKAILISDAMETGTVQINSAPARGPDHFPFQGLKDSGIGSQGVTNSINLMTK

VKTTVINLPTPSYSMG

>AtALDH12A1

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KVAEVDESGTQPFVDSLSQCPKHGLHNPFKSPERYLLYGDISTKAAHMLALPKVADFFARLIQRVAPKSYQQAAGEVFVT

RKFLENFCGDQVRFLARSFAIPGNHLGQQSHGYRWPYGPVTIVTPFNFPLEIPLLQLMGALYMGNKPLLKVDSKVSIVME

QMMRLLHYCGLPAEDVDFINSDGKTMNKILLEANPRMTLFTGSSRVAEKLALDLKGRIRLEDAGFDWKVLGPDVQEVDYV

AWQCDQDAYACSGQKCSAQSMLFVHENWSKTPLVSKLKELAERRKLEDLTIGPVLTFTTEAMLEHMENLLQIPGSKLLFG

GKELKNHSIPSIYGALEPTAVYVPIEEILKDNKTYELVTKEIFGPFQIVTEYKKDQLPLVLDALERMHAHLTAAVVSNDP

IFLQEVIGNSVNGTTYAGLRGRTTGAPQNHWFGPAGDPRGAGIGTPEAIKLVWSCHREVIYDYGPVPQGWELPPST

>AtALDH18B1

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ADLQKPQTELDGKACAGVGQSSLMAYYETMFDQLDVTAAQLLVNDSSFRDKDFRKQLNETVKSMLDLRVIPIFNENDAIS

TRRAPYQDSSGIFWDNDSLAALLALELKADLLILLSDVEGLYTGPPSDPNSKLIHTFVKEKHQDEITFGDKSRLGRGGMT

AKVKAAVNAAYAGIPVIITSGYSAENIDKVLRGLRVGTLFHQDARLWAPITDSNARDMAVAARESSRKLQALSSEDRKKI

LLDIADALEANVTTIKAENELDVASAQEAGLEESMVARLVMTPGKISSLAASVRKLADMEDPIGRVLKKTEVADGLVLEK

TSSPLGVLLIVFESRPDALVQIASLAIRSGNGLLLKGGKEARRSNAILHKVITDAIPETVGGKLIGLVTSREEIPDLLKL

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KAPYEDSSGIFWDNDSLSALLALELKADLLVLLSDVEGLYSGPPSDPHSKLIHTYIKEKHQNEITFGDKSRVGRGGMTAK

VKAAVHAADAGIPVVITSGFAAENIINVLQGQRIGTLFHKDAHEWVQVKEVDAREMAVAARECSRRLQAISSEERKQILL

KIADDLEANEKIIRTENEADVAVAQQAGYENSLVARLALKPGKIASLANNVRIIANMEDPIGQVLKRTELSDGLILEKTS

SPLGVLLIVFESRPDALVQIASLAIRSGNGLLLKGGKEAKRSNAILHKVITEAIPDTVGGKLIGLVTSREEIPELLKLDD

VIDLVIPRGSNKLVSQIKSSTKIPVLGHADGVCHVYVDKSANVEMARGIVLDAKLDYPAACNAMETLLIHKDLIEKGWLN

DIVVDLRTEGVKLYGGPRASSLLNIPQAHSFHHEYSSLACTVEIVDDVYAAIEHINLYGSAHTDSIIAEDKEVANVFLRQ

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>GmALDH18B5

MENTDPCRHFLKDVKRIIIKVGTAVVTRQDGRLAVGKLGALCEQIKELNSLGYEIILVSSGAVGLGRQRLRYRKLINSSF

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TSSSLGVLLIVFESRPDALVQIASLAIRSGNGLLLKGGKEAKRSNAILHKVITEAIPDIVGSKLIGLVTSRAEIPELLKL

DDVIDLVIPRGSNKLVTQIKSSTKIPVLGHADGICHVYVDKSADLEMARRIVLDAKIDYPAGCNAMETLLVHKDLVEKGW

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>GmALDH22A1

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>GmALDH22A2

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EGEQCLKPEYRSSGRAMLHKRAKVEFHPLGVIGAIVSWNYPFHNIFNPMLAAVFSGNGVVIKISEHASWSGCFYFRIIQS

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>GmALDH22A3

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>GmALDH22A4

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VRAVLQSSGQNCAGAERFYVHREIYSSFVSLVTKIVKSVTAGPPLVGKYDMGALCMHEHSEKLEGLVNDALDKGAEIVAR

GSFGHIGEDAVDQYFPPTVIVNVNHTMRLMQEEAFGPIMPIMKFSSDEEVVRLANESKYGLGCAVFSGNQSRAREIASQI

HAGVAAVNDFASTYMCQSLPFGGVKHSGFGRFGGVEGLRACCLVKAVAEDRWWPFVKTKIPKPIQYPVAENGFEFQESLV

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>OsALDH2B1 Os06g0270900 [Oryza sativa Japonica Group]

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PYAQAANIEVPMVARLMRYYAGWADKIHGLVVPADGPHHVQVLHEPIGVAGQIIPWNFPLLMFAWKVGPALACGNTVVLK

TAEQTPLSALFASKLLHEAGLPDGVVNVVSGFGPTAGAALASHMDVDKIAFTGSTDTGKVVLELAARSNLKSVTLELGGK

SPFIIMDDADVDHAVELAHFALFFNQGQCCCAGSRTFVHERIYDEFVEKAKARALKRVVGDPFKNGVEQGPQIDDEQFNK

ILRYIKYGVDSGANLVTGGDRLGDKGYYIQPTIFSDVQDNMRIAQEEIFGPVQSILKFNDLNEVIKRANASQYGLAAGVF

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>OsALDH2B5 Os02g0730000 [Oryza sativa Japonica Group]

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DGGKTLEQTTGTEVPMVARYMRYYGGWADKIHGLVVPADGPHHVQVLHEPIGVAGQIIPWNFPLLMFAWKVGPALACGNA

VVLKTAEQTPLSALFVASLLHEAGLPDGVLNVVSGFGPTAGAALSSHMGVDKLAFTGSTGTGKIVLELAARSNLKPVTLE

LGGKSPFIVMDDADVDQAVELAHRALFFNQGQCCCAGSRTFVHERVYDEFVEKARARALQRVVGDPFRTGVEQGPQIDGE

QFKKILQYVKSGVDSGATLVAGGDRAGSRGFYIQPTVFADVEDEMKIAQEEIFGPVQSILKFSTVEEVVRRANATPYGLA

AGVFTQRLDAANTLARALRVGTVWVNTYDVFDAAVPFGGYKMSGVGREKGVYSLRNYLQTKAVVTPIKDAAWL

>OsALDH2C1 Os01g0591000 [Oryza sativa Japonica Group]

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GVVGHIVPWNYPTTMFFFKASPALAAGCTMVVKPAEQTPLSALFYAHLAKLAGVPDGVLNVVPGFGPTAGAAISSHMDID

KVSFTGSTEVGRLVMEAAAKSNLKPVSLELGGKSPVIVFDDADLDTAVNLVHMASYTNKGEICVAGSRIYVQEGIYDAFV

KKATEMAKKSVVGDPFNPRVHQGPQIDKEQYEKILKYIDIGKREGATLVTGGKPCGENGYYIEPTIFTDVKEEMSIAQEE

IFGPVMALMKFKTVEEAIQKANSTRYGLAAGIVTKNIDVANTVSRSIRAGAIWINCYLGFDPDVPFGGYKMSGFGKDMGM

DALEKYLHTKAVVTPLYNTPWL

>OsALDH2C2 Os01g0591300 [Oryza sativa Japonica Group]

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HMDVDSVAFTGSAEIGRAIMESAARSNLKNVSLELGGKSPMIVFDDADVDMAVSLSSLAVFFNKGEICVAGSRVYVQEGI

YDEFVKKAVEAAKNWKVGDPFDAATNMGPQVDKVQFERVLKYIEIGKNEGATLLTGGKPTGDKGYYIEPTIFVDVKEEMT

IAQEEIFGPVMSLMKFKTVEEAIEKANCTKYGLAAGIVTKNLNIANMVSRSVRAGTVWVNCYFAFDPDAPFGGYKMSGFG

RDQGMVAMDKYLQVKTVITAVPDSPWY

>OsALDH2C3 putative cytosolic aldehyde dehydrogenase [Oryza sativa Japonica Group]

MASESESNGHHHAGDEARAENSGAGCLHGGDDGGGTPRTTPEIRYTKLFINGRFVDAASGKTFETRDPRTGDVIARVAEG

DKEDVDLAVKAAREAFDHGEWPRMSGSERGRVMAKYAEVVERHADELAALESLDAGKPLAAARAVDVGECVGILRYFAGA

ADKIHGETLKMSRQLQGYTLREPLGVAGLIVPWNFPAIMFFSKVSPALAAGCTVVVKPAEQTPLSALFLAHLSKQAGVPD

GVINVVTGFGPTAGAAISSHMDVDVVAFTGSTEVGRLIMEASAKSNLKPVALELGGKSPFIVFDDADLDKAVELAIGGNF

FNKGEACVAGSRVFVQEGIYDRFEQKLADTMKSWVVGDPFDPRVNQGPQVDKAQYERVLGYIEQGKAEGATVLTGGKPCG

KKGYYIEPTIFTNVKDDMVIAREEIFGPVMCLMKFKTVEEAIERANGTRYGLAAGLVTRDIDVANRMARSIRAGVVWVNC

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>OsALDH3E1 Os02g0646500 [Oryza sativa Japonica Group]

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LQNLKKWASPEKVDVPLISFPCNARVVPEPIGVVLIFSCWNLPIGLALEPLSGAIAAGNAVVLKPSEFAPSTAAFLAANI

PKYLDANAVKVVQGGAEVGEELMEHRWDKVLFTGNARVGRIIMTKAAKHLTPVALELGSKCPCIVDCLDSKRECQVAVNR

IIGAKWSTCAGQACVAIDYILVEEQFAPFLIELLKSTLKRFFTEPEYMARILNEKHFHRLTNLLEDDQVKSSIVHGGNAD

PKTLWIEPTIVLNPPFDSDIMMEEIFGPLLPIITVKKTEDCIAFLKSKPKPLAIYAFTNNEKLKQRIVAETSSGSVLFND

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>OsALDH3E2 Os04g0540600 [Oryza sativa Japonica Group]

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LKDKSVAASVLHGGTLDAKNLCIEPTILLNPPLDSAIMTEEIFGPLLPIITVKKIEDSIAFVRARPRPLAVYAFTKNAAL

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QLYRYNYVGFVLTFLGLKK

>OsALDH3E3 Os02g0647900 [Oryza sativa Japonica Group]

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ILVKSIKYTLQNLKKWAASERAESPLVAFPATAMVVPEPLGVVLVFSCWNLPLGLALEPLSGAIAAGNAVVLKPSELAPS

TAAFLAANIPRYLDSRAVKVVLGGPNVGEELMEHRWDKVLFTGSARIGRIIMAKAVKHLTPVALELGSKCPCIVDWLDSK

RDRQIAVNRIIGAKWSTCAGQACIAIDHVIVEERFAPILIELLKSTLKRFMAKPGGMARILNAKHFERLSGYLEDNRVAA

SVVHGGYMDPKKLNIEPTLLLNPPADSDVMTEEVFGPILPIITVKKIEDCIAYLKSKPKPIAMYAFTNNERLKRRIVEET

SSGSVTFNDAVVQYALESVPFGGVGHSGFGQYHGKYSFELFSHKKAVFKRSFLIEFMFRYPPWDERKIGTLRHVFSYNYF

LLFFNLLGFRR

>OsALDH3H1 aldehyde dehydrogenase family protein, expressed [Oryza sativa Japonica Group]

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KWGCNNGQACISPDFIITTKSFAPKLLEALEKVLEKFYGRDPLRSSDLSRIVNSNHFNRLKKLMDDENVSDKIVFGGQRD

EHQLKIAPTIFMDVPLDSGIMKEEIFGPLLPIITVDKIHESFALINSMTKALAAYLFTKDSKLQEQYEAAISAGGMLVND

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PRGK

>OsALDH3H2 Os11g0186200 [Oryza sativa Japonica Group]

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DSSCIKVVEGGVPETTALLEQKWDKIFYTGSGNVGRIVMAAAAKHLTPVALELGGKCPAIVDSNTDLHVTMKRLAVGKWG

CNNGQACIAPDYVITTKSFAPELVDSLKRVLKRFYGEDPLQSEDLSRIVNSNHFRRLTNLIEDKKVAQKIVYGGQTDEKQ

LKIAPTVLLDVPLDTTLMAEEIFGPLLPIVTVDKIEDSIQFINSRTKPLAAYLFTKDKKLQEEFVSNVPAGGMLVNDVAL

HLANPHLPFGGVGDSGIGSYHGKFSFDCFTHKKAVLIRGFGGEATARYPPYTIEKQKILRGLINGSFFALILALLGFPKE

RR

>OsALDH5F1 RecName: Full=Succinate-semialdehyde dehydrogenase, mitochondrial; AltName: Full=Aldehyde dehydrogenase family 5 member F1; AltName: Full=NAD(+)-dependent succinic semialdehyde dehydrogenase; Flags: Precursor

MAMAMAMRRAAALGARHILAASSTSSSGVLLRRHMSVDAGAAMEKVRAAGLLRTQGLIGGKWVDAYDGKTIEVQNPATGE

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YFAEEAKRIYGDIIPPTLSDRRLLVLKQPVGVVGAVTPWNFPLAMITRKVGPALACGCTVVVKPSEFTPLTALAAADLAL

QAGIPAGAINVVMGNAPEIGDALLQSTQVRKITFTGSTAVGKKLMAGSANTVKKVSLELGGNAPCIVFDDADIDVAIKGS

LAAKFRNSGQTCVCANRILVQEGIYEKFASAFIKAVQSLKVGNGLEESTSQGPLINEAAVQKVEKFINDATSKGANIMLG

GKRHSLGMSFYEPTVVGNVSNDMLLFREEVFGPVAPLVPFKTEEDAIRMANDTNAGLAAYIFTKSIPRSWRVSEALEYGL

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>OsALDH6B1 Os07g0188800 [Oryza sativa Japonica Group]

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VSNVSNGIDTFSIREPLGVCAGICPFNFPAMIPLWMFPIAVTCGNTFVLKPSEKDPGAAMMLAELAMEAGLPKGVLNIVH

GTHDVVNNICDDEDIKAVSFVGSNIAGMHIYSRASAKGKRVQSNMGAKNHAIILPDADRDATLNALIAAGFGAAGQRCMA

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>OsALDH7B6 Os09g0440300 [Oryza sativa Japonica Group]

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VITAFNFPCAVLGWNACIALVCGNCVVWKGAPTTPLITIAMTKIVASVLERNNLPGSIFTAFCGGADIGQAISLDTRIPL

VSFTGSTKVGLMVQQQVNARFGKCLLELSGNNAIIVMDDADIQLAVRSVLFAAVGTAGQRCTTCRRLLLHESIYRTFLDQ

LVEVYKQVRIGDPLENGTLLGPLHTPASRDAFLKGIQTIRSQGGKILYGGSAIESEGNFVQPTIVEISPSAPVVREELFG

PVLYVMKVQNLKEAVEINNSVPQGLSSSIFTKRPDIIFKWIGPHGSDCGIVNVNIPTNGAEIGGAFGGEKATGGGREAGS

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>OsALDH10A5 Os04g0464200 [Oryza sativa Japonica Group]

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KSIKISDPLEEGCRLGSVVSEGQYQKIMKFISTARCEGATILYGGARPQHLKRGFFIEPTIITNVSTSMQIWREEVFGPV

ICVKEFRTEREAVELANDTHYGLAGAVISNDLERCERISKAIQSGIVWINCSQPCFVQAPWGGNKRSGFGRELGQWGLDN

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>OsALDH10A9 Os08g0424500 [Oryza sativa Japonica Group]

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>OsALDH11A3 Os08g0440800 [Oryza sativa Japonica Group]

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PLGVVLAIPPFNYPVNLAVSKIGPALIAGNALVLKPPTQGAVAALHMVHCFHLAGFPKGLINCVTGKGSEIGDFLTMHPG

VNCISFTGGDTGIAISKKAGMVPLQMELGGKDACVVLEDADLDLVAANIVKGGFSYSGQRCTAVKVVLIMESVADIVVEK

VKAKLAKLTVGPPEADSDITPVVTESSANFIEGLVMDAKEKGATFCQEYRREGNLIWPLLLDHVRPDMRIAWEEPFGPVL

PVIRINSVEEGIHHCNASNFGLQGCVFTKDINKAIMISDAMETGTVQINSAPARGPDHFPFQGLKDSGIGSQGITNSINM

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>OsALDH12A1 hypothetical protein OsJ\_19352 [Oryza sativa Japonica Group]

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NHSIPEIYGAFKPTAVFVPLSEILKSGNFELVTREIFGPFQVVTEYSDDELELVLEACERMNAHLTAAVVSNDPLFLQEV

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>OsALDH18B1 Os05g0455500 [Oryza sativa Japonica Group]

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Table. S7. AtALDH proteins N-glycosylation sites.

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH2B4 50 NPSV 0.6740 (8/9) + WARNING: PRO-X1.**

**AtALDH2B4 401 NATL 0.6011 (6/9) +**

**AtALDH2B4 458 NETK 0.6336 (9/9) ++**

**----------------------------------------------------------------------**

**---------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH2C4 421 NNTK 0.5898 (8/9) +**

**----------------------------------------------------------------------**

**(Threshold=0.5)**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH3F1 149 NASA 0.5993 (6/9) +**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH3I1 231 NTTI 0.6870 (9/9) ++**

**AtALDH3I1 274 NLTP 0.2650 (8/9) --**

**AtALDH3I1 465 NDTV 0.5169 (5/9) +**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH5F1 67 NKTI 0.7232 (9/9) ++**

**AtALDH5F1 176 NLSD 0.7066 (9/9) ++**

**AtALDH5F1 450 NDTI 0.4462 (6/9) -**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH6B2 15 NGTY 0.7224 (9/9) ++**

**AtALDH6B2 24 NPTT 0.6586 (8/9) + WARNING: PRO-X1.**

**AtALDH6B2 196 NITT 0.7474 (9/9) ++**

**AtALDH6B2 236 NVSN 0.6461 (9/9) ++**

**AtALDH6B2 316 NDTV 0.4772 (4/9) -**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH7B4 135 NGSV 0.6987 (9/9) ++**

**AtALDH7B4 417 NNSV 0.4807 (6/9) -**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH10A8 410 NDSH 0.3912 (6/9) -**

**AtALDH10A8 423 NDTE 0.5651 (5/9) +**

**AtALDH10A8 443 NCSQ 0.5043 (3/9) +**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH10A9 382 NVTT 0.5721 (7/9) +**

**AtALDH10A9 415 NDSQ 0.4262 (8/9) -**

**AtALDH10A9 448 NCSQ 0.5780 (6/9) +**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH12A1 32 NHSI 0.6784 (9/9) ++**

**AtALDH12A1 347 NWSK 0.6090 (7/9) +**

**AtALDH12A1 406 NHSI 0.3920 (8/9) -**

**AtALDH12A1 432 NKTY 0.6320 (9/9) ++**

**AtALDH12A1 492 NGTT 0.3962 (8/9) -**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH18B1 77 NSSF 0.5947 (9/9) ++**

**AtALDH18B1 124 NDSS 0.7233 (9/9) ++**

**AtALDH18B1 138 NETV 0.6790 (9/9) ++**

**AtALDH18B1 176 NDSL 0.6343 (8/9) +**

**AtALDH18B1 331 NVTT 0.6788 (9/9) ++**

**AtALDH18B1 501 NTTK 0.6198 (8/9) +**

**AtALDH18B1 651 NAST 0.4218 (7/9) -**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH18B2 77 NSSF 0.5944 (9/9) ++**

**AtALDH18B2 176 NDSL 0.5933 (7/9) +**

**AtALDH18B2 266 NISK 0.7893 (9/9) +++**

**AtALDH18B2 501 NSTK 0.5390 (5/9) +**

**AtALDH18B2 651 NAST 0.4236 (7/9) -**

**----------------------------------------------------------------------**

**----------------------------------------------------------------------**

**SeqName Position Potential Jury N-Glyc**

 **agreement result**

**----------------------------------------------------------------------**

**AtALDH22A1 455 NDSR 0.4917 (6/9) -**

**AtALDH22A1 588 NVSR 0.5391 (4/9) +**

**----------------------------------------------------------------------**

Table. S8. Prediction of secondary structure of the identified AtALDH proteins.

ALDH2B4

SOPMA :

 Alpha helix (Hh) : 223 is 41.45%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 87 is 16.17%

 Beta turn (Tt) : 42 is 7.81%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 186 is 34.57%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH2B7

Alpha helix (Hh) : 236 is 44.19%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 84 is 15.73%

 Beta turn (Tt) : 40 is 7.49%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 174 is 32.58%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH2C4

SOPMA :

 Alpha helix (Hh) : 200 is 39.92%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 91 is 18.16%

 Beta turn (Tt) : 41 is 8.18%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 169 is 33.73%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH3F1

Alpha helix (Hh) : 217 is 44.83%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 75 is 15.50%

 Beta turn (Tt) : 34 is 7.02%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 158 is 32.64%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH3H1

Alpha helix (Hh) : 210 is 43.39%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 80 is 16.53%

 Beta turn (Tt) : 34 is 7.02%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 160 is 33.06%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH3I1

Alpha helix (Hh) : 234 is 42.55%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 90 is 16.36%

 Beta turn (Tt) : 41 is 7.45%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 185 is 33.64%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH5F1

Alpha helix (Hh) : 246 is 46.59%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 87 is 16.48%

 Beta turn (Tt) : 47 is 8.90%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 148 is 28.03%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH6B2

 Alpha helix (Hh) : 203 is 33.44%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 119 is 19.60%

 Beta turn (Tt) : 48 is 7.91%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 237 is 39.04%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH7B4

 Alpha helix (Hh) : 220 is 43.31%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 88 is 17.32%

 Beta turn (Tt) : 23 is 4.53%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 177 is 34.84%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH10A8

Alpha helix (Hh) : 214 is 43.15%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 86 is 17.34%

 Beta turn (Tt) : 39 is 7.86%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 157 is 31.65%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH10A9

Alpha helix (Hh) : 214 is 42.54%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 80 is 15.90%

 Beta turn (Tt) : 37 is 7.36%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 172 is 34.19%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH11A3

 Alpha helix (Hh) : 207 is 41.73%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 92 is 18.55%

 Beta turn (Tt) : 34 is 6.85%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 163 is 32.86%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH12A1

 Alpha helix (Hh) : 223 is 40.11%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 75 is 13.49%

 Beta turn (Tt) : 30 is 5.40%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 228 is 41.01%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH18B1

Alpha helix (Hh) : 355 is 49.51%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 133 is 18.55%

 Beta turn (Tt) : 50 is 6.97%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 179 is 24.97%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH18B2

Alpha helix (Hh) : 370 is 50.96%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 129 is 17.77%

 Beta turn (Tt) : 48 is 6.61%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 179 is 24.66%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

ALDH22A1

 Alpha helix (Hh) : 261 is 43.79%

 310  helix (Gg) : 0 is 0.00%

 Pi helix (Ii) : 0 is 0.00%

 Beta bridge (Bb) : 0 is 0.00%

 Extended strand (Ee) : 75 is 12.58%

 Beta turn (Tt) : 38 is 6.38%

 Bend region (Ss) : 0 is 0.00%

 Random coil (Cc) : 222 is 37.25%

 Ambiguous states (?) : 0 is 0.00%

 Other states : 0 is 0.00%

Table. S9. Procheck Ramachandran plot analysis.

AtALDH2B7



AtALDH3H1



AtALDH5F1

