

Human_Hs_aldh1a1	1 M-SSSGT-----PD-----LPVLLTDLKIQYTKIFINNEWHDSVSGKKFPVFNPAATEEELCQ	51
Human_Hs_aldh1a2	1 M-TSSK IEMPGEVKADPAALMA-----SLHLLPSPTPNLEIKYTKIFINNEWQNSSESGRVFPVYNPATGEQVCE	68
Human_Hs_aldh1a3	1 MATANGAVENGQPDRAKPPA-----LPRPIRNLEVKFTKIFINNEWHESKSGKKFATCNPSTRQICE	62
SeaLily_Mr_aldh1-a	1 M-----NLQLVFSRPFLLSVNRGFFVHSYSMSQLNSAPEVKFTQLFINNEFVNSVSGKTFPTLNPCTGEKICD	68
Starfish_Pp_aldh1a-a	1-----MAPPQVKYTQLFINNEFVNSVSGKTFPTLNPCTGEKICD	39
Starfish_Pp_aldh1a-b	-----MAPVEVKYTQIFINNEFVNSVSGKTFPTLNPATGKKTC	39
Starfish_Pp_aldh1a-c	1-----MAAPEVRFTQIFINNEFVNSVSGKTFPCINPINQKKVTD	39
BrittleStar_Af_aldh1a	1-----MAAPEVRFTQIFINNEFVNSVSGKTFPCINPINQKKVTD	39
Human_Hs_aldh1a1	52 VEEGDKEDVDKAVKAAARQAFQIGSPWRTMDASERGRLLYKLLADLIERDRLLLATMESMNGGKLYSNAYLNDLACGI	127
Human_Hs_aldh1a2	69 VQEADKADIDKAVQAARLAFSLGSPWRRMDASERGRLLDLKADLVERDRAVLATMESLNGGKPFLLQAFYVDLQGGVI	144
Human_Hs_aldh1a3	63 VEEGDKPDVDKAVEAAQVAFQRCSPWRRLDALSRGRLLHQADLVERDRATLAALETMDTGKPFLLHAFFIDLEGCI	138
SeaLily_Mr_aldh1-a	69 VQEGDKADVDLAVKAAAREAFKLGSPWRRLDPTKRAKHMTKLAEELLEQNKDQLSALETLDNGMPYFESQ-MWVDSFV	143
Starfish_Pp_aldh1a-a	40 IQEGDKADVDLAVKAAAREAVKLGSPWRTMDAQDRGKLMQKLADLFERDAEHIASLDTLDNGTLTYTMMY-GCVQGSV	114
Starfish_Pp_aldh1a-b	1-----MDASKRALYLLKLAELLKRDKLEYLASLETLDNGLIIAGSR-SCVDRAV	47
Starfish_Pp_aldh1a-c	40 VQEGDKADADKAVRAAQDAFKLGSAWRRMDATGRARLLNKLADLIERDREYLVNLETMDNGMTVMNAT-GSVMGCA	114
BrittleStar_Af_aldh1a	40 IQEGDKADVDKAVQAARDAFKLGSPWRRMDAAARGRLMLKLADLVERDADYISKLETSDNGMLVKNAAGCVEMAV	114
Human_Hs_aldh1a1	128 KTLRYCAGWADKIQGRTIPIDGNFITYTRHEPIGVCGQIPWNFPLVMLIWKIGPALSCGNTVVVKPAEQTPLTAL	203
Human_Hs_aldh1a2	145 KTFRYIYAGWADKIHGMTIPVDGDYFTFTRHEPIGVCGQIPWNFPLLMFAWKIAPALCCGNTVVIKPAEQTPLSAL	220
Human_Hs_aldh1a3	139 RTLRIFAGWADKIQGKTIPDODNVFCFTRHEPIGVCGAITPWNFPLMLVWKLAPALCCGNTMVLKPAEQTPLTAL	214
SeaLily_Mr_aldh1-a	144 NTLTYFAGWADKIVHGKTIPIDGDYFCYTRHEPIGVCGAIPWNYPMMDMLGWKVPALACGNTMVIKPAEQTPLTAL	219
Starfish_Pp_aldh1a-a	115 EVLRYFAGWADKIHGKTIPKGDYFCYTRHEPIGVCGAIPWNFPTMELSWKLGPALCCGNSLIKPAEQTPLSAL	190
Starfish_Pp_aldh1a-b	48 GLHYIYAGWADKITGKTIPIDGSFICYTRYEPKGVVAATPWNAPIVVTRKMATALACGNTVVLKPAEQTPLTAL	123
Starfish_Pp_aldh1a-c	115 KFLRYGAGYADKLHGKVVPLDGDYFCYSRYEPIGVVAAIPWNFPCLLTGAKLSALTGVNTLVIKPAEQSPLTAL	190
BrittleStar_Af_aldh1a	115 SVLRYIYGGYADKIHGKTIPIDGDYFCYTRHEPIGVCGAIPWNFPIEMASWKMGPALACGNTMVIKPAEQTPLTAL	190
Human_Hs_aldh1a1	204 HVASLIKEAGFPPGVVNVIPGYCPTAGAAISSHMDIDKVAFTGSTEVGKLIKEAAGKSNLKRVTLELGGKSPCIVL	279
Human_Hs_aldh1a2	221 YMGALIKEAGFPPGVVNVIPGYCPTAGAAIASHIGIDKIAFTGSTEVGKLIKEAAGRSNLKRVTLELGGKSPNIF	296
Human_Hs_aldh1a3	215 YLGSLIKEAGFPPGVVNVIPGYCPTVGAASSHPQINKIAFTGSTEVGKLVKEAASRSNLKRVTLELGGKNPCIVC	290
SeaLily_Mr_aldh1-a	220 HIASLIKEAGFPPGVVNIIPGYCPTAGAAISEHMDVDKVAFTGSTEVGRLIQQAAGKSNLKRVALELGGKSPNIVF	295
Starfish_Pp_aldh1a-a	191 HIASLIKEAGFPAAGVNIIPGYCPTAGAAISEHMDVDKVAFTGSTEIGRLIQAASGTSNLKRVSLEMGKSPNIF	266
Starfish_Pp_aldh1a-b	124 YLASLIKEAGFPPGVVNVIPGYCPTAGAALEHMDVDVITFTGSTEVGKLIQQAAGKSNLKHVCLLELGGKSPNVF	199
Starfish_Pp_aldh1a-c	191 YIASLAKEAGFPPGVVNVIPGYCPTAGAAITGSMVDVMTFTGSTEVGRIIQRAAGDSNLKKIHLELGGKSPNVF	266
BrittleStar_Af_aldh1a	191 YLASLVKEAGFPPGVVNVIPGYCPTAGAAISEHMNDKVAFTGSTEIGKIIQQAAGKSNLKRVSLEMGKSPNIVF	266
Human_Hs_aldh1a1	280 ADADLDNAVEFAHHGVFYHQCCQCI AASRI FVEESIYDEFVRRSVERAKKYILGNPLTPGVTTQGPQIDKEQYDKIL	355
Human_Hs_aldh1a2	297 ADADLDYAVEQAHQGVFFNQCCQCTAGSRI FVEESIYEEFVRRSVERAKRRVVGSPFDPPTTEQGPQIDKKQYKIL	372
Human_Hs_aldh1a3	291 ADADLDLAVECAHQGVFFNQCCQCTAASRVFVEEQVYSEFVRRSVEYAKKRPVGDYFDVKTTEQGPQIDQKQFDKIL	366
SeaLily_Mr_aldh1-a	296 ADSDLDFAVDEAHEAVMCNECCQCSAGSRTFVQEGIYDEFVKKSIEMAKARVIGDPYVEGTQSGPQIDEEQFTKVL	371
Starfish_Pp_aldh1a-a	267 ADADLDYAVEESHEAIFNNMCECCSAGSRTFVQEGIYDEFVKKSVRAKRRVVGDPFEEKTESGPQIDQDQMDKIL	342
Starfish_Pp_aldh1a-b	200 ADADLDYAVETSHRALFAHSQCIC IAGSRTFVQEDIYDEFVKKSTERAKKRVVGDPYNDKSES GPVIDEGQVTRIL	275
Starfish_Pp_aldh1a-c	267 ADCDLDYAVEMSHYGVFLHSQVCCAGSRTFVQEDIYDEFVKKSKERAERKRVVGDPYDVKTEGGPQIDQDQDKIL	342
BrittleStar_Af_aldh1a	267 ADCDLDYAVEEAHEALFFNMCECCSAGSRTFVQEGIYDEFVKKSVRAKTRVVGPNYDDKTENGPDQDEQDKIM	342
Human_Hs_aldh1a1	356 DLI ESGKKEGAKLECGGGPWGNKG YFVQPTVFSNVTDEMR IAKEE IFGPVQQIMKFSLDDV IKRANNTFYGLSAG	431
Human_Hs_aldh1a2	373 ELIQSGVAEGAKLECGGKGLGRKGFFI EPTVFSNVTDMR IAKEE IFGPVQEI LRFKTMDEVI ERANNSDFGLVAA	448
Human_Hs_aldh1a3	367 ELI ESGKKEGAKLECGGSAMEDKGLFI KPTVFSVTDNMR IAKEE IFGPVQPI LKFKSI EEVI KRANSTDYGLTAA	442
SeaLily_Mr_aldh1-a	372 EKIKSGKNEGATLGGCGSRHGDKGFFLESTVFSVDSDEMS IAKEE IFGPVQVILKFKTI EEVI ERAHKTHYGLAGA	447
Starfish_Pp_aldh1a-a	343 SYVEI GKKEGAKLECGGQRI GDKG YFVQSTVFSNVTNEMRVAQEE IFGPVQLLIKFKTLDEVLKANNTQYGLAGG	418
Starfish_Pp_aldh1a-b	276 GMI ESGKEGAKLQCGGRI SDRKGNFI ESTVFSVTDDDME IAREE IFGPVQQLIKFKTLDEVI ERANNTSYGLAAA	351
Starfish_Pp_aldh1a-c	343 ELI ESGKKEGAKLMCGGQKRGDCGY FVESTVFSVTDDDMR IAKEE IFGPVQQLIKFKTI EEVVERANNTQYGLAGA	418
BrittleStar_Af_aldh1a	343 ELI EAGKKEGAKLQCGGKQ--KDGWFI ESTVFSVTDNMR IAREE IFGPVQTI LKFKTL EEVI ERANDTQYGLAAA	416
Human_Hs_aldh1a1	432 VFTKDIDKALITISALQAGTVVWVNCYGVVSAQCFPGGFKMSGNGRELGEYGFHEYTEVKTIVTKISQKNS	501
Human_Hs_aldh1a2	449 VFTNDINKALTVSSAMQAGTVWVNCYNALNAQSPFGGFKMSGNGREMGEFGLREYSEVKTIVTKIPQKNS	518
Human_Hs_aldh1a3	443 VFTKNDLDAKLALASLESCTVWVNCYNALYAQAPFGGFKMSGNGRELGEYALAEYTEVKTIVTKILGDKNP	512
SeaLily_Mr_aldh1-a	448 VFTKIDTAMTVASHLSAGTVVWVNCYNVGGPQTFFGGYKQSGVGRDLGEDSLKEYYEVKTIVIKVPQKNS	517
Starfish_Pp_aldh1a-a	419 VFTKDIDKALTIANSLQAGTITVNNYSGGGANAPFGGYKMSGIGRDLGEDALHEYYQVKTIVIKVPVKNS	488
Starfish_Pp_aldh1a-b	352 VITKIDKALTMANSVRAGVWVNTYVSLDPSAPFGGYKMSGIGREGGEESLLEFSEIKTVVIKIPQKNS	421
Starfish_Pp_aldh1a-c	419 VFTKIDKALTIVANTIRAGLIWVNNYGLFSPMIFPGGYKMSGVGRREGGEDGFKEYCEVKTIVIKVPQKNS	488
BrittleStar_Af_aldh1a	417 VFSKDIDKALITISNSVRAGTVWVNNYNSAQTFPGGYKMSGNGRELGEALHEYYEVKTIVIKIPQKNS	486

- Homotetrameric interface
- NAD binding site
- Catalytic residues

Figure S1. The alignment of echinoderm and human *aldh1a* genes.

Functional domain residues of the Human *aldh1a1* gene were predicted using the NCBI conserved domains search (<https://www.ncbi.nlm.nih.gov/Structure/cdd/wrpsb.cgi>). Green, red and blue shade respectively indicates the alignment of homotetrameric interface, the NAD binding site and the catalytic residues. The percentage of the identical over aligned residues across human and each echinoderm *aldh1a* genes is indicated below.

Homotetrameric interface: Sea lily; 50/61 (82.0%), Starfish 1; 48/61 (78.7%), Starfish 2; 41/59 (69.5%), Starfish 3; 38/61 (62.3%) and Brittle star; 49/61 (80.3%). NAD binding site: Sea lily; 18/18 (100%), Starfish 1; 16/18 (88.9%), Starfish 2; 16/18 (88.9%), Starfish 3; 18/18 (100%) and Brittle star; 16/18 (88.9%). Catalytic residues: Sea lily; 4/4 (100%), Starfish 1; 4/4 (100%), Starfish 2; 4/4 (100%), Starfish 3; 4/4 (100%) and Brittle star; 4/4 (100%).