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Fig. S1. Alignment of the amino acid sequences of the human ADO and the zebrafish orthologues Adoa. The human ADO shares 54.1 % similarity with the zebrafish Adoa. >NP\_116193.2 2-aminoethanethiol dioxygenase [Homo sapiens], >NP\_001008634.1 2-aminoethanethiol (cysteamine) dioxygenase a [Danio rerio].

| CLUSTAL O(1.2.4) MULTIPLE SEQUENCE ALIGNMENT |                                                             |     |  |
|----------------------------------------------|-------------------------------------------------------------|-----|--|
| NP_116193.2                                  | MPRDNMASLIQRIARQACLTFRGSGGGGASDRDAASGPEAPMQGFPENLSKLKSLLTQ  | 60  |  |
| NP_001008634.1                               | MPRNNKSLIQKIASQAYATFTNCSSSAIE-----DNNKVFLHQAADLVALLSD       | 49  |  |
|                                              | ***:* :****:* ** ** ..... : * * : . * :**:                  |     |  |
| NP_116193.2                                  | LRAEDLNIAPRKATLQPLPPNLPPVTYMHYETDGFSLGVFLKSGTSIPLHDHPGMHGM  | 120 |  |
| NP_001008634.1                               | IRAADLKIAPTK-VSTSSPVPPVTYMHICETDVFSGVFLKSGASIPLDHPGMHGM     | 108 |  |
|                                              | :** **:* ** . :. * :***** ** **:******:*****                |     |  |
| NP_116193.2                                  | LKVLYGTVRISCMKLDAGGGQRPRLPPEQQFEPPLQPREREAVRPGVLRSAEYTEAS   | 180 |  |
| NP_001008634.1                               | LKVLYGKVSIRCYDKLKAESD-----TERHFDPLLAFQDDVRRALRSSGQFSELS     | 162 |  |
|                                              | *****.* * * **** . .: *::*** : : ** ..** .::* *             |     |  |
| NP_116193.2                                  | GPCILTPHRDNLHQIDAVEGPAAFLDILAPPYDPDDGRDCHYRVLEPVRPKEASSSACD | 240 |  |
| NP_001008634.1                               | GPCVLSPFKDNLHEIDAVDGAAFLDILAPPYDPDDGRDCHYRVLQTAGKKSEQ----S  | 218 |  |
|                                              | ***:*:*.*:****:****:* *****: . * . .                        |     |  |
| NP_116193.2                                  | LPREVWLLLETPQADDFWCEGEYPGPKVFP                              | 270 |  |
| NP_001008634.1                               | GDDEAWLLEIPQDDFWCGGEYPGPVETI                                | 248 |  |
|                                              | *.***** ** ***** *****:*                                    |     |  |

Fig. S2. Alignment of the amino acid sequences of the human ADO and the zebrafish orthologues Adob. The human ADO shares 54.4 % similarity with Adob. >NP\_998358.2 2-aminoethanethiol (cysteamine) dioxygenase b [Danio rerio].

| CLUSTAL O(1.2.4) MULTIPLE SEQUENCE ALIGNMENT |                                                               |     |  |
|----------------------------------------------|---------------------------------------------------------------|-----|--|
| NP_116193.2                                  | MPRDNMASLIQRIARQACLTFRGSGGGGASDRDAASGPPEAPMQPGFPENLSKLSLLTQ   | 60  |  |
| NP_998358.2                                  | MPRDNMTSTVQKIAKQALATFRNPSVI-----GEHNKVFLNQSKLSLLAE            | 47  |  |
|                                              | *****:* :*:***:*** ***. . . : * ** *****: :                   |     |  |
| NP_116193.2                                  | LRAEDLNIAPRKATLQPLPP--NLPPVTYMHIIYETDGFSLGVFLLKSGTSIPLHDHPGMH | 118 |  |
| NP_998358.2                                  | VRAADLKIAARTPESAPVPHQRAPPVTYMHICETDSFSMGVFLKLTGASIPLDHPGMY    | 107 |  |
|                                              | :** **:* ** . *:* ***** ***.**:******:*****:*****:            |     |  |
| NP_116193.2                                  | GMLKVLVYGTVRISCMDKLDAGGGQRPALPPEQQFEPPLQPREREAVRPGVLSRAEYTE   | 178 |  |
| NP_998358.2                                  | GMLKVIYGVKVRISCFDRLDK-----PRDGASGVQFNPLMPFQVGLRPSVLKSVGEFTE   | 162 |  |
|                                              | *****:*.*****:*:*** ** **:**** * :* :*:*.**:* .*:**           |     |  |
| NP_116193.2                                  | ASGPCILTPHRDNLHQIDAVEGPAAFLDILAPPYDPPDGRDCHYYRVLEPVRPKEASSSA  | 238 |  |
| NP_998358.2                                  | DSSPCVLSPPQDNHQIDAVDGPATAFLDILAPPYDPDEGRDCHYYKVLQAHSEADKKSE   | 222 |  |
|                                              | *.***:*:~*:~*:*****:~*:~*:*****:~*:~*:*****:~*:~*:~* .*.~*    |     |  |
| NP_116193.2                                  | CDLPREVWLLLETPQADDFWCEGEPYPGPKVFP                             | 270 |  |
| NP_998358.2                                  | VQDQGVDVWLMEIQPSEFWCGGEPYPGPKVTL                              | 254 |  |
|                                              | : :***:* ** .:*** *****                                       |     |  |

