(a)

```
AtS3H       MATSAISKLLVSDFASSVHIPSNYVRPISDRPNLSEVE-SSGDSIPLIDLRDLHGPNRAV   59
Zm2-ODD7    MAPAISKPLLTDLVAQIGKVPSSHIRPVGDRPDLANVDNESGAGIPLIDLKKLNGPERRK   60
OsS5H-1     MAPAIAKPLLSDLVAQSGQVPSSHIRPVGDRPDLDNVDHESGAGIPVIDLKQLDGPDRRK   60
            ** :  . ** . .*.  ::**.::**:.***:* :*: .** .**:***:.*.**:*

AtS3H       IVQQLASACSTYGFFQIKNHGVPDTTVNKMQTVAREFFHQPESERVKHYSADPTKTTRLS   119
Zm2-ODD7    VVEAIGKACESDGFFMVTNHGIPAAVVEGMLRVAREFFHLPESERLKCYSDDPNKAIRLS   120
OsS5H-1     VVEAIGSACETDGFFMVKNHGIPEEVVEGMLRVAREFFHMPESERLKCYSDDPKKAIRLS   120
            :*: :..**.: *** :.***:*  .*: *  ******* *****:* ** **.*: ***

AtS3H       TSFNVGADKVLNWRDFLRLHCFPIEDFIEEWPSSPISFREVTAEYATSVRALVLRLLEAI   179
Zm2-ODD7    TSFNVRTEKVSNWRDFLRLHCYPLQSFVDQWPSNPPSFRQVVGTYATEARALALRLLEAI   180
OsS5H-1     TSFNVRTEKVSNWRDFLRLHCYPLESFIDQWPSNPPSFRQVVGTYSREARALALRLLEAI   180
            ***** ::** **********:*::.*:::***.* ***:*.. *: ..***.*******

AtS3H       SESLGLESDHISNILGKHAQHMAFNYYPPCPEPELTYGLPGHKDPTVITVLLQDQVSGLQ   239
Zm2-ODD7    SESLGLERSHMVAAMGRHAQHMAVNYYPPCPQPELTYGLPGHKDPNAITLLLQDGVSGLQ   240
OsS5H-1     SESLGLERGHMVSAMGRQAQHMAVNYYPPCPQPELTYGLPGHKDPNAITLLLQDGVSGLQ   240
            ******* .*:   :*::*****.*******:*************..**:**** *****

AtS3H       VFKDDKWVAVSPIPNTFIVNIGDQMQVISNDKYKSVLHRAVVNTENERLSIPTFYFPSTD   299
Zm2-ODD7    VQRGGRWVAVNPVPNALVINIGDQMQALSNDRYKSVLHRVIVNSESERISVPTFYCPSPD   300
OsS5H-1     VQRNGRWVAVNPVPDALVINIGDQIQALSNDRYKSVLHRVIVNSESERISVPTFYCPSPD   300
            * :..:****.*:*:::::*****:*.:***:*******.:**:*.**:*:**** ** *

AtS3H       AVIGPAHELVNEQDSLAIYRTYPFVEYWDKFWNRSLATASCLDAFKAPTT-- 349
Zm2-ODD7    AVIAPADALVDD-GHPLAYRPFTYQEYYDAFWNMGLQSASCLDRFRPGGSLE 351
OsS5H-1     AVIAPAGALVDGALHPLAYRPFKYQAYYDEFWNMGLQSASCLDRFRPNDQAV 352
            ***.**  **:       ** : :  *:* *** .* :***** *:
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(b)

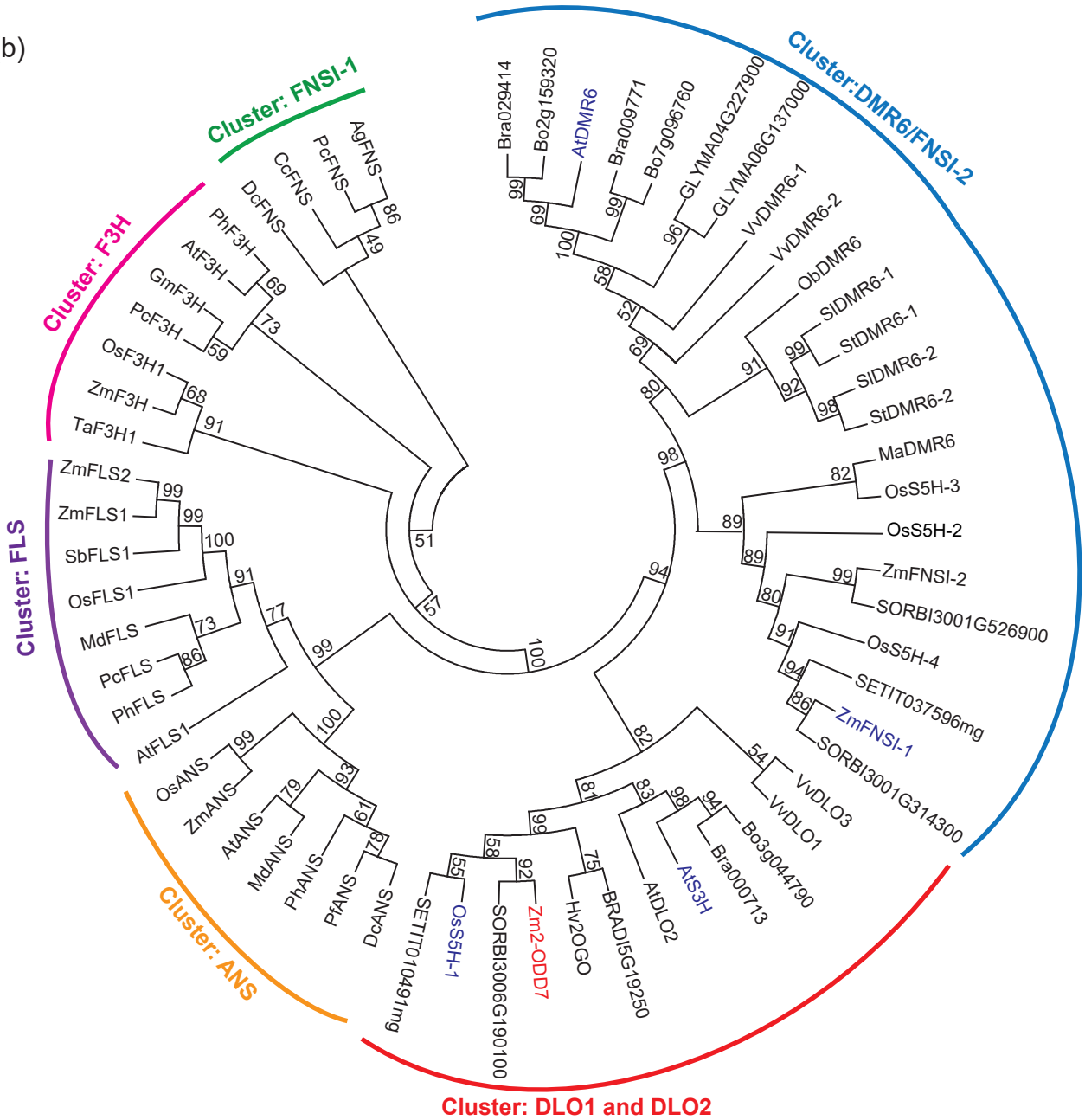

FIGURE 1 a) Amino acid sequences alignment of the predicted ZmSH (Zm2-ODD7, A0A1D6E1X8) with AtS3H (Q9ZSA8) and OsS5H-1 (Q7XUN0) proteins. b) Phylogenetic analysis of 2-oxoglutarate-Fe^{2+} dioxygenases involved in phenolic secondary metabolism, The phylogenetic tree was constructed with the aligned protein sequences with MEGA 11 (Tamura et al., 2021) using the maximum-likelihood analysis with bootstrap (10,000 replicates). The protein sequences were aligned using ClustalW implemented in MEGA 11. Different oxoglutarate-Fe^{2+} dioxygenases are clustered based on their major demonstrated activities. Proteins in blue correspond to the sequences of the characterized proteins, AtS3H (Q9ZSA8), ZmFNSI-1 (B4FZ24), AtDMR6 (NP_197841) and OsS5H-1 (Q7XUN0), used to search homologous sequences from angiosperm species. Zm2-ODD7 is in red.