

```

DLO1      MATSAISKLLVSDFASSV-HIPSNYVRPISDRPNLSEVESSGDSIPLIDLRLDHLHGPNRAV 59
DLO2      ---MAASKLLVSDIASVVDHVPSNYVRPVS DRPKMSEVQTS GDSIPLIDLHDLHGPNRAD 57
DMR6      ----MAAKLISTGFRHTT--LPENYVRPISDRPRLSEVSQLED-FPLIDL S---STDRSF 50
          :*: :.: . :*.*****:***.:***. * :***** ..*:

DLO1      IVQQLASACSTYGGFFQIKNHGVPD TTVNKMQTVAREFFHQPESE RVKHYSADPTKTTRLS 119
DLO2      IINQFAHACSSCGFFQIKNHGVP EETIKKMMNAAREFFRQSESERVKHYSADTKKTTRLS 117
DMR6      LIQQIHQACARFGFFQVINHG VNKQIIDEMVSVAREFFSMSMEEKMKLYSDDPTKTTRLS 110
          :*:*: **: *****: ***** . :.:* ..***** . .*::* ** *..*****

DLO1      TSFNVGADKVLNWRDFLRLHCFPIEDFIEEW PSSPISFREVTAEYATSVRALVLRLEAI 179
DLO2      TSFNVSKEKVS NWRDFLRLHCYPIEDFINEWPSTPISFREVTAEYATSVRALVLTLEAI 177
DMR6      TSFNVKKEEVNWRDYLRLHCYPIHKYVNEWPSNPPSFKEIVSKYSREVRV EGVGFKIEELI 170
          ***** :.* *****:*****:* ..:.* **:*:.*:.*:.* ** : : * *

          * *

DLO1      SESLGLESDHISNILGKHAQHMAFNYYPPCPEPELTYGLPGHKDPTVITVLLQD-QV SGL 238
DLO2      SESLGLAKDRVSN TIGKHGQHMAINYYPRCPQPELTYGLPGHKDANLITVLLQD-EV SGL 236
DMR6      SESLGLEKDYMKKVLGEQQQHMAVNYYPPCPEPELTYGLPAHTDPNALT ILLQD TTVCGL 230
          ***** .* :.: :*:.*.***.*** **:******.*.*. :*:*** *.*

          *

DLO1      QVFKDDKWVAVSPIPNTFIVNIGDQMQVISNDKYKSVLHRAV VNTENERLSIPTFFYPST 298
DLO2      QVFKDGKWI AVNPVPNTFIVNLGDQMQVISNEKYKSVLHRAV VNSDMERISIPTFYCPSE 296
DMR6      QILIDGQWF AVNPHPDAFVINIGDQLQALSNGVYKSVWHRAV Tntenprlsvasflcpad 290
          *.: *.:*.*.* *.:*:*:*:*:*:*:* * ** * **.*.: *:*:.* *

DLO1      DAVIGPAHEL VNEQ--DSLAIYRTYPFVEYWDKFWNRSLATASCLDAFKAPT T 349
DLO2      DAVISPAQELINEEE- DSPAIYRNFTYA EYFEKFWDTAFDTE SCIDSFKASTA 348
DMR6      CAVMSPAKPLWEAEDDETKPVYKDFTYAEY YKKFWSRNLDQEHCL ENFLNN-- 341
          **:.*: * : : :. :*: :.:*:*.*. : * :*: *

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Supplemental figure 5. Multiple alignment of Arabidopsis DMR6, DLO1 and DLO2. Alignment is created using the Clustal Omega tool. Asterisks above the alignment indicate catalytic residues.