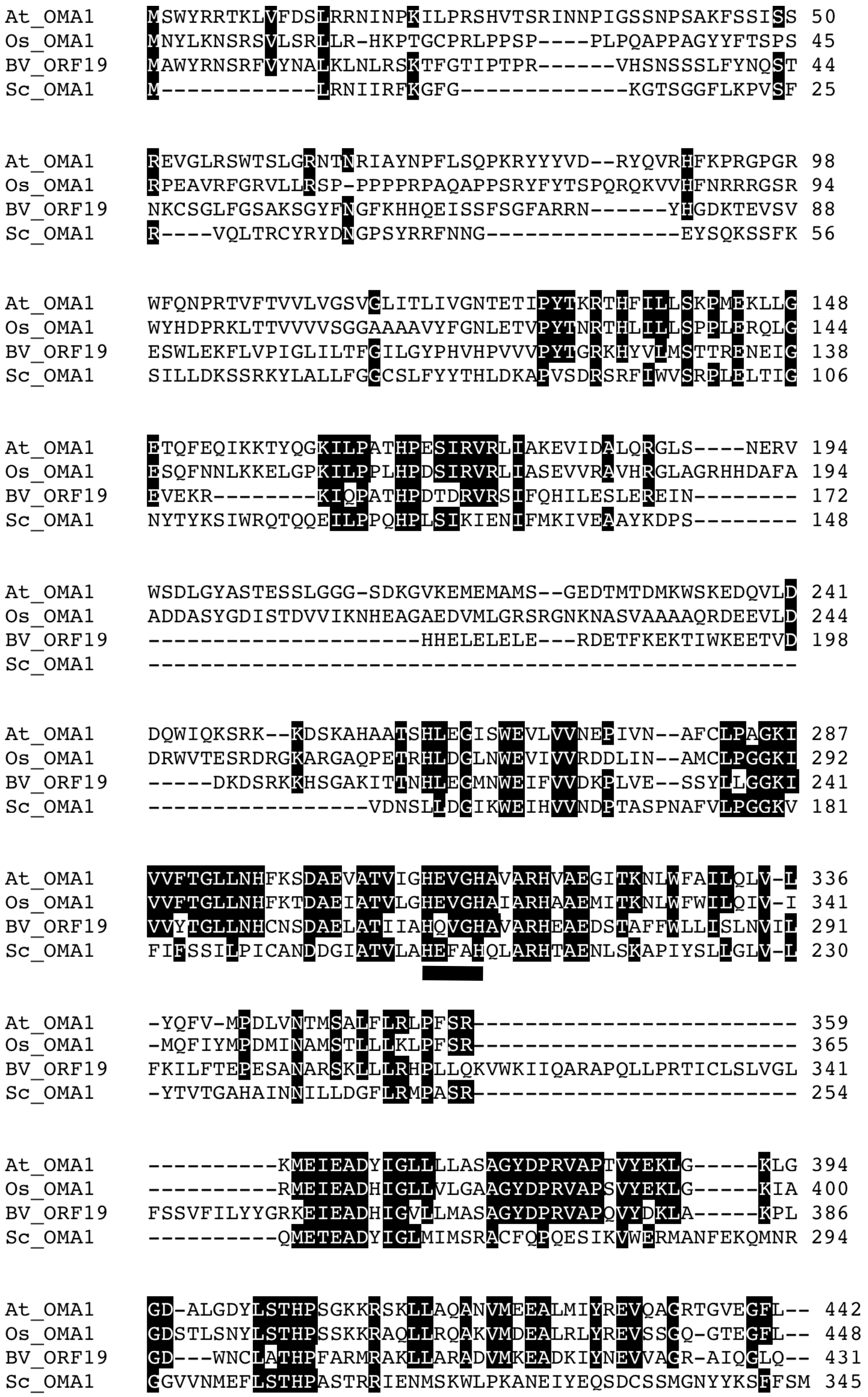

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At_OMA1     MSWYRRTKLVFDSLRRNINPKILPRSHVTSRINNPIGSSNPSAKFSSISS 50
Os_OMA1     MNYLKNSRSVLSRLLR-HKPTGCPRLPPSP----PLPQAPPAGYYFTSPS 45
BV_ORF19    MAWYRNSRFVYNALKLNLRSKTFGTIPTPR------VHSNSSSLFYNQST 44
Sc_OMA1     M------------LRNIIRFKGFG-------------KGTSGGFLKPVSF 25

At_OMA1     REVGLRSWTSLGRNTNRIAYNPFLSQPKRYYYVD--RYQVRHFKPRGPGR 98
Os_OMA1     RPEAVRFGRVLLRSP-PPPPRPAQAPPSRYFYTSPQRQKVVHFNRRRGSR 94
BV_ORF19    NKCSGLFGSAKSGYFNGFKHHQEISSFSGFARRN------YHGDKTEVSV 88
Sc_OMA1     R----VQLTRCYRYDNGPSYRRFNNG---------------EYSQKSSFK 56

At_OMA1     WFQNPRTVFTVVLVGSVGLITLIVGNTETIPYTKRTHFILLSKPMEKLLG 148
Os_OMA1     WYHDPRKLTTVVVVSGGAAAAVYFGNLETVPYTNRTHLILLSPPLERQLG 144
BV_ORF19    ESWLEKFLVPIGLILTFGILGYPHVHPVVVPYTGRKHYVLMSTTRENEIG 138
Sc_OMA1     SILLDKSSRKYLALLFGGCSLFYYTHLDKAPVSDRSRFIWVSRPLELTIG 106

At_OMA1     ETQFEQIKKTYQGKILPATHPESIRVRLIAKEVIDALQRGLS----NERV 194
Os_OMA1     ESQFNNLKKELGPKILPPLHPDSIRVRLIASEVVRAVHRGLAGRHHDAFA 194
BV_ORF19    EVEKR--------KIQPATHPDTDRVRSIFQHILESLEREIN-------- 172
Sc_OMA1     NYTYKSIWRQTQQEILPPQHPLSIKIENIFMKIVEAAYKDPS-------- 148

At_OMA1     WSDLGYASTESSLGGG-SDKGVKEMEMAMS--GEDTMTDMKWSKEDQVLD 241
Os_OMA1     ADDASYGDISTDVVIKNHEAGAEDVMLGRSRGNKNASVAAAAQRDEEVLD 244
BV_ORF19    ---------------------HHELELELE---RDETFKEKTIWKEETVD 198
Sc_OMA1     --------------------------------------------------

At_OMA1     DQWIQKSRK--KDSKAHAATSHLEGISWEVLVVNEPIVN--AFCLPAGKI 287
Os_OMA1     DRWVTESRDRGKARGAQPETRHLDGLNWEVIVVRDDLIN--AMCLPGGKI 292
BV_ORF19    -----DKDSRKKHSGAKITTNHLEGMNWEIFVVDKPLVE--SSYLLGGKI 241
Sc_OMA1     -----------------VDNSLLDGIKWEIHVVNDPTASPNAFVLPGGKV 181

At_OMA1     VVFTGLLNHFKSDAEVATVIGHEVGHAVARHVAEGITKNLWFAILQLV-L 336
Os_OMA1     VVFTGLLNHFKTDAEIATVLGHEVGHAIARHAAEMITKNLWFWILQIV-I 341
BV_ORF19    VVYTGLLNHCNSDAELATIIAHQVGHAVARHEAEDSTAFFWLLISLNVIL 291
Sc_OMA1     FIFSSILPICANDDGIATVLAHEFAHQLARHTAENLSKAPIYSLLGLV-L 230

At_OMA1     -YQFV-MPDLVNTMSALFLRLPFSR------------------------- 359
Os_OMA1     -MQFIYMPDMINAMSTLLLKLPFSR------------------------- 365
BV_ORF19    FKILFTEPESANARSKLLLRHPLLQKVWKIIQARAPQLLPRTICLSLVGL 341
Sc_OMA1     -YTVTGAHAINNILLDGFLRMPASR------------------------- 254

At_OMA1     ----------KMEIEADYIGLLLLASAGYDPRVAPTVYEKLG-----KLG 394
Os_OMA1     ----------RMEIEADHIGLLVLGAAGYDPRVAPSVYEKLG-----KIA 400
BV_ORF19    FSSVFILYYGRKEIEADHIGVLLMASAGYDPRVAPQVYDKLA-----KPL 386
Sc_OMA1     ----------QMETEADYIGLMIMSRACFQPQESIKVWERMANFEKQMNR 294

At_OMA1     GD-ALGDYLSTHPSGKKRSKLLAQANVMEEALMIYREVQAGRTGVEGFL-- 442
Os_OMA1     GDSTLSNYLSTHPSSKKRAQLLRQAKVMDEALRLYREVSSGQ-GTEGFL-- 448
BV_ORF19    GD---WNCLATHPFARMRAKLLARADVMKEADKIYNEVVAGR-AIQGLQ-- 431
Sc_OMA1     GGVVNMEFLSTHPASTRRIENMSKWLPKANEIYEQSDCSSMGNYYKSFFSM 345
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File S3. Multiple alignment of amino acid sequences of OMA1-homologous proteins from Arabidopsis (At_OMA1, At5g51740), rice (Os_OMA1, Os02g0735100), sugar beet (bvORF19, this study), and yeast (Sc_OMA1, S000001795). Position of the Zn^{2+} binding motif is shown by a horizontal line. The amino acid sequences were aligned using ClustalW (http://clustalw.ddbj.nig.ac.jp/index.php?lang=ja). The identity of amino acid sequences between bvORF19 and yeast OMA1 is 17%. The E-value obtained from a BLAST search using bvORF19 as a query is 1e-12 for yeast OMA1.