

STE24  
 Candida\_STE24  
 Aspergillus\_STE24  
 Coccidioides  
 Neurospora  
 Os\_STE24  
 Hv\_STE24  
 AT\_STE24  
 Homo\_STE24  
 Mus\_STE24  
 Bos\_STE24  
 Gallus\_STE24  
 Xenopus\_STE24  
 Tetraodon\_STE24  
 Strongylocentrotus\_STE24  
 Drosophila  
 AtCpMPL  
 OsCpMPL  
 Synechocystis  
 Crocosphaera  
 Anabaena  
 Thermosynechococcus  
 Synechococcus  
 Streptomyces  
 Mycobacterium  
 Trichodesmium  
 htpX  
 Haemophilus  
 Desulfitobacterium  
 Nitrobacter  
 Methanosarcina  
 Wolinella  
 Photobacterium  
 a-proteobacterium  
 Nitrococcus  
 Pseudomonas  
 Azotobacter  
 Chromobacterium  
 Bordetella  
 Flavobacterium  
 Ustilago  
 Cryptococcus  
 Omalp  
 Candida  
 MRPRP-1  
 Mus  
 Pstrongylocentrotus  
 Gibberella  
 Aspergillus  
 AtMPL  
 OsMPL  
 ORF19  
 yfgC

EITAVLAHEI GHWQKNE IVNMVIFS QLHTFLIFSL  
 ETVAVLAHEI GHWKLNE LPKMITMMQGHFLIFSL  
 EVVAVLSHEL GHWSLGH TTKLFAIAQSHMFYIFAL  
 EVVAVLSHEL GHWSLGH TTKLFGIAQFHMFIYIFAL  
 EVVAVLAHEL GHWKLGH TTSLFGISQAHFFAIFSL  
 EIVSVIAHEL GHWKLNE TVYSFVAVQLLMFLQFGG  
 EIVSVLAHEL GHWKLNE TAYSFVAVQLLTFMQFGG  
 EIVAVIAHEL GHWKLNE TTYSFIAVQILAFLOFGG  
 EVLAVLGHEL GHWKLGH TVKNI IISQMNSFLCFFL  
 EVLAVLGHEL GHWKLGH TVKNI IISQMNSFLCFFL  
 EVLAVLGHEL GHWKLGH TVKNI IISQMNSFLCFFL  
 EVLAVLGHEL GHWKLGH TVKNI IISQMNSFLCFFL  
 EVLAVLGHEL GHWKLGH TVKNI IISQMNSFLCFFL  
 EILAVLGHEL GHWKLGH TVKNI IISQMNSFLCFFL  
 EVLAVLAHEL GHWKLGH NLKNI IISQVNLILCLFL  
 EVLAVLGHEL GHWKLGH TVKNI IIMQVHLFLMFLV  
 ELQAVLAHEL GH LKCDHGVWLT FANILT - - LGAYT  
 ELQAVLAHEL GH LKCDHGVWLT FANILT - - MGAYS  
 EIQAVMAHEL GH LKCEHGVYLT LANIMV - - LAAGL  
 EIQGVMAHEL GH LKCEHGVYLT LANIMV - - LGASL  
 EIQAVIAHEL GH LKCDHGVYLT PVNLLV - - LAASA  
 ELQAVLAHEL GH LKCEHGVYLT IANLLL - - FAASQ  
 EIQAVIAHEL GH LKCEHGVYLT MANLLM - - LSTSL  
 EMRAVIGHEV GH ALSGH SVYRT ILLFLTSLALRVA  
 EMRFVMGHEL GH ALSGH AVYRT MMMHLRLARSFG  
 ELKTVLAHEL GH IKCGH PILLNQMA TWAMG IASAIT  
 EAEAVIAHEI SH IANGDMVTMT LIQGVVNTFVIFI  
 EAEAVLAHEI SH ISNGDMVTMALLQGVLNTFVIFL  
 ELEGVLAHEI MAHIKNRD ILI STLAA - VMAGVI TTL  
 ELAGVIAHEI LAHIKHD TLLMTITA - TIAGAI SML  
 ELEAVLAHEI SHVKNRDMAVLT IAS - FLS SVAFYI  
 ELAVVMGHEI AHAIARE GAERLSVSMA SELGRNLI  
 QLAVVIGHEI GHVIAQH SNERLSRSQLANAGLELT  
 QLAVVMGHEI GHVIAEH GNERMSIATLSNLGLQIT  
 QLAVVIGHEV GHVLAGH ANERLSTNAATQTGLDLL  
 ELAAVMGHEI AHALREH GREAMSKAYGVQVASQ - I  
 ELAAVMGHEI AHALREH GREALSKAYAVEMAKQGA  
 ELAAVIGHEI SHALREH TRENMSQAYAQMGGLGLV  
 ELAAVIGHEI AHALREH ARERV SQQMATSI GLSVL  
 GLAMILGHEI LAHALANE GAQRMTAQGGQIVGAG  
 GLATVIGHEV AHQVARE SAEKMSGYKVVLLFGTFL  
 GLATVIGHEI AHQVARE PAERMSSMKVLFALGLLL  
 GIATVLAHEFAHQVARE TAENLSKAPIYSLGLGLV  
 GIATVLSHEFAHQVARE TAENLSKAPLYSLGLIIL  
 QLSFLLGHEI AHAVLGH AA EKAGMVHLDFLGMIF  
 QLSFLLGHEI AHAVLGH AA EKASLVHLDFLGMIF  
 QLGTVLAHEMAHVVLNE SAEMASFFEFDFL FMIVV  
 ALAAVIGHEI AHNTA SHASERLSA AWVGNLTA GSL  
 GLAAVIGHEI AHVVAHE TGERMSN - - - NFVTMGV  
 EVATVIGHEV GHAVARE VAEGITKNLWF AI - LQLV  
 EIAVIGHEV GHAIARE AAEMITKNLWF AI - LQIV  
 ELATIIAHQV GHAVARE EAEDSTAFFWLLI SLNVI  
 QLAVMAHEI SHVTQRE LARAMEDQQRSA PLTWVG

File S4. See next page for the legend.

File S4. Multiple alignment of ~35 amino acid residues surrounding the Zn<sup>2+</sup> binding motif of peptidase M48 proteins, a protein family to which yeast OMA1 belongs. The position of the Zn<sup>2+</sup> binding motif is shown by a horizontal line. Note that only bvORF19 (indicated by ORF19 in the alignment) contains HQxxH, instead of HEXxH that is present in the other members. Data from: STE24, *Saccharomyces cerevisiae*, CAA89647; *Candida*\_STE24, *Candida albicans*, XP\_713382; *Aspergillus*\_STE24, *Aspergillus fumigatus*, XP\_752066; *Coccidioides*, *Coccidioides immitis*, EAS28348; *Neurospora*, *Neurospora crassa*, CAC28689; OsSTE24, *Oryza sativa*, Os02g0680400; HvSTE24, *Hordeum vulgare*, CAL26913; ATSTE24, *Arabidopsis thaliana*, At4g01320; Homo\_STE24, *Homo sapiens*, NP\_005848; Mus\_STE24, *Mus musculus*, NP\_766288; Bos\_STE24, *Bos taurus*, XP\_882083; Gallus\_STE24, *Gallus gallus*, XP\_417720; Xenopus\_STE24, *Xenopus laevis*, AAH82484; Tetradon\_STE24, *Tetraodon nigroviridis*, CAG10466; *Strongylocentrotus*\_STE24, *Strongylocentrotus purpuratus*, XP\_001177479; *Drosophila*\_STE24, *Drosophila melanogaster*; AtCpMPL, *Arabidopsis thaliana*, At3g27110; OsCpMPL, *Oryza sativa*, Os01g0970700; *Synechocystis*, *Synechocystis* sp. PCC 6803, NP\_440889, *Crocospaera*, *Crocospaera watsonii*, NP\_681428; *Anabaena*, *Anabaena variabilis*, YP\_321952; *Thermosynechococcus*, *Thermosynechococcus elongatus*, NP\_681428; *Synechococcus*, *Synechococcus* sp. JA-3-3Ab, YP\_473883; *Streptomyces*, *Streptomyces avermitilis*, NP\_826653; *Mycobacterium*, *Mycobacterium tuberculosis*, NP\_216493; *Trichodesmium*, *Trichodesmium erythraeum*, YP\_721635; htpX, *Escherichia coli*, AAA62779; *Haemophilus*, *Haemophilus influenzae*, NP\_438878; *Desulfitobacterium*, *Desulfitobacterium hafniense*, ZP\_01369144; *Nitrobacter*, *Nitrobacter hamburgensis*, YP\_575597; *Methanosarcina*, *Methanosarcina mazei*, NP\_635158; yfgC, *Escherichia coli*, AAC75547; *Desulfovibrio*, *Desulfovibrio desulfuricans*, YP\_386603; *Wolinella*, *Wolinella succinogenes*, NP\_907498; *Photobacterium*, *Photobacterium profundum*, YP\_132334; a-proteobacterium, a-proteobacterium HTCC2255, ZP\_01448796; *Nitrococcus*, *Nitrococcus mobilis*, ZP\_01126393; *Pseudomonas*, *Pseudomonas aeruginosa*, NP\_253322; *Azotobacter*, *Azotobacter vinelandii*, ZP\_00416091; *Chromobacterium*, *Chromobacterium violaceum*, NP\_899823; *Bordetella*, *Bordetella bronchiseptica*, NP\_888655; *Flavobacterium*, *Flavobacterium* sp. MED217, ZP\_01061128; *Ustilago*, *Ustilago maydis*, XP\_757961; *Cryptococcus*, *Cryptococcus neoformans*, XP\_569916; Oma1p, *Saccharomyces cerevisiae*, P36163; *Candida*, *Candida glabrata*, XP\_446463; MPRP-1, *Homo sapiens*, BAC79381; *Mus*, *Mus musculus*, NP\_080185; *Strongylocentrotus*, *Strongylocentrotus purpuratus*, XP\_799173; *Gibberella*, *Gibberella zeae*, XP\_390368; *Aspergillus*, *Aspergillus nidulans*, XP\_659454; AtMPL, *Arabidopsis thaliana*, At5g51740 (AtOMA1); OsMPL, *Oryza sativa*, Os02g0735100 (OsOMA1). Multiple alignment was done by using ClustalX (<http://www.clustal.org/clustal2/>).