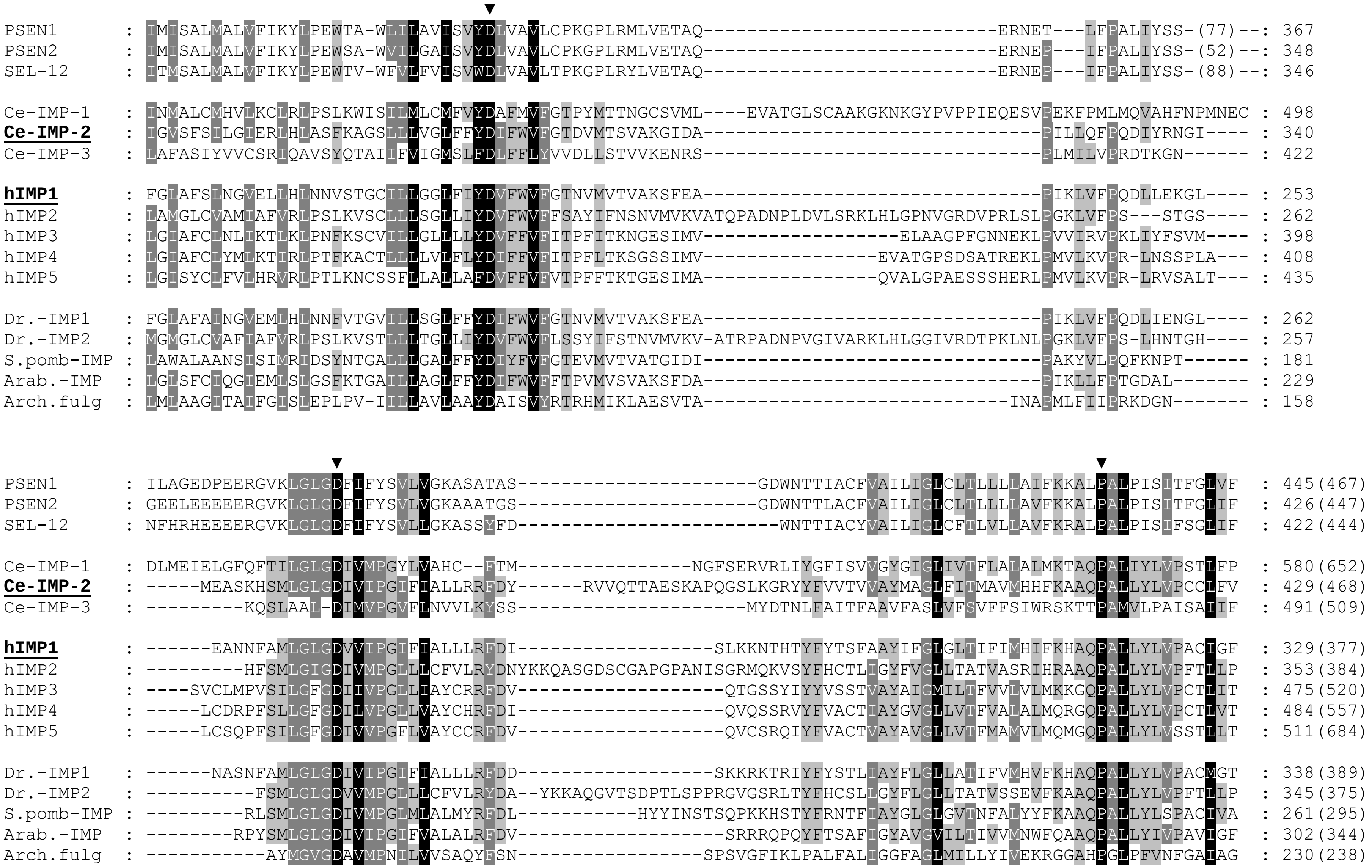

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                                            ▼
PSEN1      : IMISALMALVFIKYLPEWTA-WLILAVISVYDLVAVLCPKGPLRMLVETAQ---------------------------ERNET---LFPALIYSS-(77)--: 367
PSEN2      : IMISALMALVFIKYLPEWSA-WVILGAISVYDLVAVLCPKGPLRMLVETAQ---------------------------ERNEP---IFPALIYSS-(52)--: 348
SEL-12     : ITMSALMALVFIKYLPEWTV-WFVLFVISVWDLVAVLTPKGPLRYLVETAQ---------------------------ERNEP---IFPALIYSS-(88)--: 346

Ce-IMP-1   : INMALCMHVLKCLRLPSLKWISILMLCMFVYDAFMVFGTPYMTTNGCSVML----EVATGLSCAAKGKNKGYPVPPIEQESVPEKFPMLMQVAHFNPMNEC : 498
Ce-IMP-2   : IGVSFSILGIERLHLASFKAGSLLLVGLFFYDIFWVFGTDVMTSVAKGIDA-------------------------------PILLQFPQDIYRNGI---- : 340
Ce-IMP-3   : LAFASIYVVCSRIQAVSYQTAIIFVIGMSLFDLFFLYVVDLLSTVVKENRS-------------------------------PLMILVPRDTKGN------ : 422

hIMP1      : FGLAFSLNGVELLHLNNVSTGCILLGGLFIYDVFWVFGTNVMVTVAKSFEA-------------------------------PIKLVFPQDLLEKGL---- : 253
hIMP2      : LAMGLCVAMIAFVRLPSLKVSCLLLSGLLIYDVFWVFFSAYIFNSNVMVKVATQPADNPLDVLSRKLHLGPNVGRDVPRLSLPGKLVFPS---STGS---- : 262
hIMP3      : LGIAFCLNLIKTLKLPNFKSCVILLGLLLLYDVFFVFITPFITKNGESIMV------------------ELAAGPFGNNEKLPVVIRVPKLIYFSVM---- : 398
hIMP4      : LGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFVFITPFLTKSGSSIMV----------------EVATGPSDSATREKLPMVLKVPR-LNSSPLA--- : 408
hIMP5      : LGISYCLFVLHRVRLPTLKNCSSFLLALLAFDVFFVFVTPFFTKTGESIMA----------------QVALGPAESSSHERLPMVLKVPR-LRVSALT--- : 435

Dr.-IMP1   : FGLAFAINGVEMLHLNNFVTGVILLSGLFFYDIFWVFGTNVMVTVAKSFEA-------------------------------PIKLVFPQDLIENGL---- : 262
Dr.-IMP2   : MGMGLCVAFIAFVRLPSLKVSTLLLTGLLIYDVFWVFLSSYIFSTNVMVKV-ATRPADNPVGIVARKLHLGGIVRDTPKLNLPGKLVFPS-LHNTGH---- : 257
S.pomb-IMP : LAWALAANSISIMRIDSYNTGALLLGALFFYDIYFVFGTEVMVTVATGIDI-------------------------------PAKYVLPQFKNPT------ : 181
Arab.-IMP  : LGLSFCIQGIEMLSLGSFKTGAILLAGLFFYDIFWVFFTPVMVSVAKSFDA-------------------------------PIKLLFPTGDAL------- : 229
Arch.fulg  : LMLAAGITAIFGISLEPLPV-IILLAVLAAYDAISVYRTRHMIKLAESVTA----------------------------INAPMLFIIPRKDGN------- : 158


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PSEN1      : ILAGEDPEERGVKLGLGDFIFYSVLVGKASATAS----------------------GDWNTTIACFVAILIGLCLTLLLLAIFKKALPALPISITFGLVF : 445(467)
PSEN2      : GEELEEEEERGVKLGLGDFIFYSVLVGKAAATGS----------------------GDWNTTLACFVAILIGLCLTLLLLAVFKKALPALPISITFGLIF : 426(447)
SEL-12     : NFHRHEEEERGVKLGLGDFIFYSVLLGKASSYFD------------------------WNTTIACYVAILIGLCFTLVLLAVFKRALPALPISIFSGLIF : 422(444)

Ce-IMP-1   : DLMEIELGFQFTILGLGDIVMPGYLVAHC--FTM----------------NGFSERVRLIYGFISVVGYGIGLIVTFLALALMKTAQPALIYLVPSTLFP : 580(652)
Ce-IMP-2   : -----MEASKHSMLGLGDIVIPGIFIALLRRFDY------RVVQTTAESKAPQGSLKGRYYFVVTVVAYMAGLFITMAVMHHFKAAQPALLYLVPCCLFV : 429(468)
Ce-IMP-3   : ---------KQSLAAL-DIMVPGVFLNVVLKYSS---------------------MYDTNLFAITFAAVFASLVFSVFFSIWRSKTTPAMVLPAISAIIF : 491(509)

hIMP1      : ------EANNFAMLGLGDVVIPGIFIALLLRFDI------------------SLKKNTHTYFYTSFAAYIFGLGLTIFIMHIFKHAQPALLYLVPACIGF : 329(377)
hIMP2      : ---------HFSMLGIGDIVMPGLLLCFVLRYDNYKKQASGDSCGAPGPANISGRMQKVSYFHCTLIGYFVGLLTATVASRIHRAAQPALLYLVPFTLLP : 353(384)
hIMP3      : ----SVCLMPVSILGFGDIIVPGLLIAYCRRFDV-------------------QTGSSYIYYVSSTVAYAIGMILTFVVLVLMKKGQPALLYLVPCTLIT : 475(520)
hIMP4      : -----LCDRPFSLLGFGDILVPGLLVAYCHRFDI-------------------QVQSSRVYFVACTIAYGVGLLVTFVALALMQRGQPALLYLVPCTLVT : 484(557)
hIMP5      : -----LCSQPFSILGFGDIVVPGFLVAYCCRFDV-------------------QVCSRQIYFVACTVAYAVGLLVTFMAMVLMQMGQPALLYLVSSTLLT : 511(684)

Dr.-IMP1   : ------NASNFAMLGLGDIVIPGIFIALLLRFDD------------------SKKRKTRIYFYSTLIAYFLGLLATIFVMHVFKHAQPALLYLVPACMGT : 338(389)
Dr.-IMP2   : ----------FSMLGLGDVVMPGLLLCFVLRYDA--YKKAQGVTSDPTLSPPRGVGSRLTYFHCSLLGYFLGLLTATVSSEVFKAAQPALLYLVPFTLLP : 345(375)
S.pomb-IMP : ---------RLSMLGLGDIVMPGLMLALMYRFDL-----------HYYINSTSQPKKHSTYFRNTFIAYGLGLGVTNFALYYFKAAQPALLYLSPACIVA : 261(295)
Arab.-IMP  : --------RPYSMLGLGDIVIPGIFVALALRFDV-------------------SRRRQPQYFTSAFIGYAVGVILTIVVMNWFQAAQPALLYIVPAVIGF : 302(344)
Arch.fulg  : -----------AYMGVGDAVMPNILVVSAQYFSN-----------------SPSVGFIKLPALFALIGGFAGLMILLYIVEKRGGAHPGLPFVNFGAIAG : 230(238)
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