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Matching the proteome to the genome

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Supplementary Fig. S3

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          *           20           *           40           *           60
Dhan-ICL1 : ----MPYTKIDVNEEKFQDQVKEIQQWKEPRWAKTKRIYQAEDIAKRRSSLKVDY : 54
Calb-ICL1 : ----MPYTPIDIQKEADEQKEVAEIKKWWSEPRWRKTKRIYSAEDIAKRRGTLKINH : 54
Ppas-ICL1 : ---MSGPYTKIDLKDEQDFQNQIKEIEEWWSQPRWAKTKRIYNAEDIAKRRSSLS-SVP : 56
Ncra-ICL1 : MAANNMVNPAVDPALDELEAKEVEEVKKWWSDSRWROTTRPFTAEQIVSKRGNLKIEY : 59
Gzea-ICL1 : MASQNMNTNPSINPDIDELEQKEVEAVKTTWSDSRWROTTRPFTAEQIVSKRCYLPIDY : 59
Cglo-ICL1 : MAANNMVNPAVDPNRDELEALEVDQIKKWWSDPRWRYTTRPFTAEQIVSKRGNLKIEY : 59
Mgri-ICL1 : MASKNMVNPAVEPSMDDLFAREVAEVKQWWSDPWRWYTKRPFTAEQIVSKRGNLKIEY : 59
Afum-ICL1 : MGF-----LEDEQKYWDDVQAVKAWKDSRWRYTKRPYTAEQIVAKRGNLKIEY : 50
Anig-ICL1 : MAS-----FEEEDRKYLDDVQAVQKWWQDSRWRYTKRPFTAEQIVAKRGNLKIEY : 50
Aory-ICL1 : MGF-----LEDEKKYLDDVQAVKAWWTDSDRWRYTKRPFSAEQIVAKRGNLKIEY : 50
Pchr-ICL1 : MGL-----HEDEDRQYAAEVQAVQSWWSDSRWRYTKRPFTAEQIVAKRGNLKIDY : 50
Anid-ICL1 : MSY-----IEEEDQRWDEVAAVKNWWSDSRWRYTKRPFTAEQIVAKRGNLKIEY : 50
Cimm-ICL1 : MSL-----VEQEEQYWEVEAVKQWWSDSRWRYTKRPFTAEQIVAKRGNLKIEY : 51
Pnod-ICL1 : MSH-----ADAEDAQEQKEVQEVKQWWTDSRWRYTRRPFTAEQIVAKRGNLKIY : 50
Fpal-ICL1 : -----MSNRAAEQAEVARVEQWWDKDPFRNRVTRPYTAAQVSKRGTLPISY : 47
Ccin-ICL1 : -----MSSRAAEQAEVAEVERWWSKSPREARVNRPYTAAQVSKRGTLPIN : 47
Cneo-ICL1 : -----MSSKAEEDAQEVKAEFAFAKSPREARTTRPYTAAQVSKRGTLPISY : 47
Umay-ICL1 : -----MADQELKQEAEEVEAVKQWWSKSPREAHITRPYTAEQVSKRGTLPQTY : 48
Ylip-ICL1 : -----MSQQRNNEVEEIKKWWSSPRWKHTKRVYSPEDIASRRGTLPVPO : 46
Scer-ICL1 : -MPIVPGNTKNDFAALQAKLDADAAEIEKWWSDSRWSKTKRNYTSARDIARRGTFPPIEY : 59
Cgla-ICL1 : -MPVFN-SEANEFQALQARIDADAKEIEQWWSSEPRWNTKRTYSAREIARRGTFPPLTY : 58
Klac-ICL1 : -MVSVKASAAEKKEFLQSQID---EIEKWWSEPRWKTTRKRIYSAYEIAKRRGSKPNTF : 55
Agos-ICL1 : -MSPSVRDARNDLASLQQQAAAEAEIDRRWWSQPRWAGTKRVYTAEDIVRRGTFPVVEY : 59

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          *           80           *           100           *           120
Dhan-ICL1 : PSSNQAKKLYKLLQEHDKN--KSASFTFGALDPVQVTQMAKYLDSIYVSGWQCSSTASTS : 112
Calb-ICL1 : PSSQQADKLFKLLQKHDAD--KTVSFTFGALDPIHVAQMAKYLDSIYVSGWQCSSTASTS : 112
Ppas-ICL1 : ASNQQAQKLFKLLGEHAKN--ETASFTFGALDPIHITQMAKYLDTIYVSGWQCSSTASTS : 114
Ncra-ICL1 : ASNAQAKKLWKILDRFAK--RDASYTYGCLPTMVTQMAKYLDTVYVSGWQSSSTASSS : 117
Gzea-ICL1 : ASNTQAKKLWKILHRFEN--RDASYTYGCLPTMVTQMAKYLDTVYVSGWQSSSTASSS : 117
Cglo-ICL1 : ASNAQSKKLWNILENRFQT--KDasYTYGCLPTAVTQMAKYLDTVYVSGWQSSSTASSS : 117
Mgri-ICL1 : PSNAQSKKLWKILGRFQK--RDASYTYGCLPTMVTQMAKYLDTVYVSGWQSSSTASSS : 117
Afum-ICL1 : PSNDQSKKLWKILSNFEK--KVASFTYGCLEPTMLTQMAKYLDTVYVSGWQSSSTASST : 108
Anig-ICL1 : PSNAMSKKLWKILSNFEK--KVPSFTYGCLEPTMLTQMAKYLDTVYVSGWQSSSTASST : 108
Aory-ICL1 : PSNVQSKKLWKILSNFEN--KVASFTYGCLEPTMVTQMAKYLDTVYVSGWQSSSTASST : 108
Pchr-ICL1 : PSNVQAKKLWGIVSNFNQ--KQASFTYGCLEPTMITQMKFLDTIYVSGWQSSSTASST : 108
Anid-ICL1 : PSNVQAKKLWGILERNFN--KEASFTYGCLEPTMVTQMAKYLDTVYVSGWQSSSTASST : 108
Cimm-ICL1 : PSNVQSKKLWKILVEKFKT--KTASFTYGCLEPTMVTQMKYLDTVYVSGWQSSSTASST : 109
Pnod-ICL1 : PSNSQSKKLWNIVEQRFN--NDVSYTYGCLDPMVTQMAKYLDTVYVSGWQCSSTASST : 108
Fpal-ICL1 : PSDVLAQKLWASLTQHYKN--GTPSHTYCALDPVQVTQMAKYLETVYVSGWQSSSTASSS : 105
Ccin-ICL1 : PSDVQGKKLWKLLSEHAKN--GTPSHTYCALDPVQVTQMAKYLETVYVSGWQSSSTASSS : 105
Cneo-ICL1 : PSDVQAKKLWKILESKARGEGGCTATYCALDPVQLTQMAKYLETVYVSGWQCSSTASSS : 107
Umay-ICL1 : PSDVQAKKLWKILLEDHASK--GTTSHTYCALDPVQVTQMAKHELETVYVSGWQSSSTASST : 106
Ylip-ICL1 : ASSQADKLFKLLQEHKKN--HTASHTYCALDPVQVTQMAKYLDSIYVSGWQCSSTASTS : 104
Scer-ICL1 : PSSVMAKLFKVLKHHNE--GTVSKTFGALDPVQISQMAKYLDTIYISGWQCSSTASTS : 117
Cgla-ICL1 : PSSVMAKLVYKVLKHHKE--GTVSRTFGALDPVQVQMAKFLDTIYVSGWQCSSTASTS : 116
Klac-ICL1 : PSTVMSQKLFKILGEHAKN--GTVSKTFGALDPVQVTQMSKYLDTIYVSGWQCSSTASTS : 113
Agos-ICL1 : PSSVMAKLVETLARHSRN--GTVSQTFGVLDVQVTQMKYLDTIYVSGWQCSATASTS : 117

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	*	140	*	160	*	180	
Dhan-ICL1	:	NEFSPDLADYPM	DTVPNKVEHLWFA	-	QLFHDRKQREERLNL-SKEERAKTPY	-	TDFLRPI : 169
Calb-ICL1	:	NEFSPDLADYPM	DTVPNKVEHLWFA	-	QLFHDRKQREERLTL-SKEERAKTPY	-	IDFLRPI : 169
Ppas-ICL1	:	NEFSPDLADYPM	DTVPNKVERLILRRQ	LFHDRKQREERLSV-SKQERAKLPY	-	TDFLRPI	: 172
Ncra-ICL1	:	DEFGPDLADYPYT	TVPNKVGHLFMA	-	QLFHDRKQREERLSV-PKQREKLAN	-	IDYLRPI : 174
Gzea-ICL1	:	DEFGPDLADYPYT	TVPNKVGHLFMA	-	QLFHDRKQREERLSV-PKEORANLLN	-	IDYLRPI : 174
Cglo-ICL1	:	DEFGPDLADYPYT	TVPNKVGHLFMA	-	QLFHDRKQREERLSV-PKARTKLAN	-	IDYLRPI : 174
Mgri-ICL1	:	DEFGPDLADYPYT	TVPNKVSHLFMA	-	QLFHDRKQREERLSA-PKSEERSKLQN	-	IDYLRPI : 174
Afum-ICL1	:	DEFGPDLADYPM	NTVPNKVNQLFMA	-	QLFHDRKQREERITT-PKDORSKLPN	-	IDYLRPI : 165
Anig-ICL1	:	DEFGPDLADYPM	NTVPNKVNQLFLA	-	QLFHDRKQREERITT-PKEORGKVAN	-	VDYLRPI : 165
Aory-ICL1	:	DEFGPDLADYPM	NTVPNKVNQLWMA	-	QLFHDRKQREERITT-PKEKRGNVAN	-	IDYLRPI : 165
Pchr-ICL1	:	DEFGPDLADYPM	DTVPNKVNQLFMA	-	QLFHDRKQREERVTT-PAGORGNVAN	-	VDYLRPI : 165
Anid-ICL1	:	DEFGPDLADYPM	NTVPNKVNHLWMA	-	QLFHDRKQREERMIT-PKDRHKVAN	-	VDYLRPI : 165
Cimm-ICL1	:	DEFGPDLADYPM	NTVPNKVNQLWMA	-	QLFHDRKQREERLRN-PKEKRASLAN	-	IDYLRPI : 166
Pnod-ICL1	:	DEFGPDLADYPYT	TVPNKVGHLFMA	-	QLFHDRKQREERLTT-PKADRAKLAN	-	TDFLRPI : 165
Fpal-ICL1	:	NEFGPDLADYPS	NTVPNKVEHLFMA	-	QLFHDRKQREERARNL-SEAE LAQTPV	-	IDYLRPI : 162
Ccin-ICL1	:	NEFGPDLADYPS	NTVPNKVEHLFMA	-	QLFHDRKQREERARM-SDAELANTPV	-	IDYLRPI : 162
Cneo-ICL1	:	IEFGPDLADYPS	NTVPNKVAQLFTA	-	QLYHDKRQREERTSAA-LANGQDPGER	-	IDYLRPI : 164
Umay-ICL1	:	NEFGPDLADYPYN	TVPLKVEHLFMA	-	QLFHDRKQREERTNL-SPEORAKTPV	-	IDYLRPI : 163
Ylip-ICL1	:	NEFSPDLADYPM	DTVPNKVEHLWFA	-	QLFHDRKQREERLSL-PESERSKLPAPV	-	VDYLRPI : 162
Scer-ICL1	:	NEFGPDLADYPM	DTVPNKVEHLFKA	-	QLFHDRKQREERASKAKSQEELDEMGA	-	IDYLRPI : 176
Cgla-ICL1	:	NEFGPDLADYPM	DTVPNKVEHLFKA	-	QLFHDRKQREERAKATSQEELDAMGPA	-	IDYLRPI : 175
Klac-ICL1	:	NEFGPDLADYPM	DTVPNKVEHLFKA	-	QLFHDRKQREERICDGTIEE-----SEI	-	IDYLRPI : 167
Agos-ICL1	:	NEFGPDLADYPM	DTVPNKVEHLFMA	-	QLFHDRKQREERALSCTTQRELDQIGPE	-	IDYLRPI : 176

	*	200	*	220	*	240	
Dhan-ICL1	:	IADADTGHGGITAI	IKLTKLVERGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 229
Calb-ICL1	:	IADADTGHGGITAI	IKLTKMFIERGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 229
Ppas-ICL1	:	IADADTGHGGITAI	IKLTKMFIERGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 232
Ncra-ICL1	:	VADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 234
Gzea-ICL1	:	VADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 234
Cglo-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 234
Mgri-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 234
Afum-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 225
Anig-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 225
Aory-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 225
Pchr-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 225
Anid-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 225
Cimm-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 226
Pnod-ICL1	:	IADADTGHGGLTAV	MKLTKLEIEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 225
Fpal-ICL1	:	IADADTGHGGLTAV	MKLTAKMFEVKGGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 222
Ccin-ICL1	:	VADADTGHGGLTAV	MKLTKMEVEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 222
Cneo-ICL1	:	VADADTGHGGLTAV	MRLTKMMEVSGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLV		: 224
Umay-ICL1	:	VADADTGHGGLTAV	MKLTKLEVEKGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLI		: 223
Ylip-ICL1	:	IADADTGHGGLTAV	VKLTKMEIERGAAGIHIEDQ	APGTTKCGHMAGKVLVPVQ	EHINRLI		: 222
Scer-ICL1	:	VADADAGHGGLTAV	FKLTKMEIERGAAGIHIEDQ	TSTNKKCGHMAGRCVIVPQ	EHVNRV		: 236
Cgla-ICL1	:	IADADAGHGGLTAV	FKLTKMEIERGAAGIHIEDQ	TSTNKKCGHMAGRCVIVPQ	EHINRLV		: 235
Klac-ICL1	:	VADADAGHGGLTAV	FKLTKMEIERGAAGIHIEDQ	TSTNKKCGHMAGRCVIVPQ	EHINRLI		: 227
Agos-ICL1	:	VADADTGHGGLTAV	FKLTKMEIERGAAGIHIEDQ	SSSNKKCGHMAGRCVIVPQ	EHISRLV		: 236

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                *           260           *           280           *           300
Dhan-ICL1 : AIRASADILGSDLLCVARTDSEAAATLLTSTIDHRDHYFVLGATNPESP--DLAALMAEAE : 287
Calb-ICL1 : AIRASADIFGSNLLAVARTDSEAAATLLTSTIDHRDHYFIIIGATNPEAG--DLAALMAEAE : 287
Ppas-ICL1 : AIRTSADLFGSDLLAVARTDSEAAATLLTSTIDKRDHYFVIGATNPDIP--DLIDVLTEAE : 290
Ncra-ICL1 : AIRAQAADIMGSDLLCIARTDAEAAATLITTTIDPRDHAFILGCTNPDLE--PLADLMMKAE : 292
Gzea-ICL1 : AIRAQAADIMGSDLLAIARTDAEAAATLLSTNIDPRDHAFILGSTNSTLK--PLNDLMIAAE : 292
Cglo-ICL1 : AIRAQAADIMGSDLLAIARTDAEAAATLITTTIDPRDHAFILGSTNPNLQ--PLNDLMVAEE : 292
Mgri-ICL1 : AIRAQAADIMGVDLLAIARTDAEAAATLITTTIDPRDHAFILGCTNPSLQ--PLADLMNTAE : 292
Afum-ICL1 : AIRAQAADIMGTDLLAIARTDSEAAATLITSTIDHRDHAFIVGSTNPNLQ--PLNDLMVLAEE : 283
Anig-ICL1 : AIRAQAADIMGTDLLAIARTDSEAAATLITSTIDYRDHAFVVGSTNPNLQ--PLNDLMVVAEE : 283
Aory-ICL1 : AIRAQAADIMGTDLLAIARTDAEAAATLITSTIDHRDHAFIVGSTNPNLQ--PLVDLMVVAEE : 283
Pchr-ICL1 : AIRAQAADIMGSDLLAIARTDSEAAATLITSTIDHRDHAFIVGSTNSSLQ--PLNDLMVVAEE : 283
Anid-ICL1 : AIRAQAADIMGTDLLAIARTDSEAAATLITSTIDHRDHPFIIGSTNPDIQ--PLNDLMVMAEE : 283
Cimm-ICL1 : AIRAQAADIMGTDLLAIARTDSEAAATLITSTIDPRDHAFVVGSTNPTLE--PLNDLMIAAE : 284
Pnod-ICL1 : AIRAQAADIMGTDLLAVARTDSEAAATLITSTIDPRDHYIIMGCTNPALQ--PLGELMYAAEE : 283
Fpal-ICL1 : AIRLQFDIMGVNNLVIARTDSEAAATLITTNVDERDHAFILGSTNPDLR--PLNTLLNEAE : 280
Ccin-ICL1 : AIRLQYDIMGVENLVVARTDSEAAATLITSNIDDRDHPFIQGSTNPSLP--PLNNVMVEAE : 280
Cneo-ICL1 : AMRLQCDIMGTTNLVVCRTDSEAAATLLSTNIDPRDHSFILGSTNPSLP--PLNDLMIAAE : 282
Umay-ICL1 : AIRLQYDIMGVENLVVARTDSEAAATLITTNVDERDHSFILGTTHTELE--PLVDILNRAE : 281
Ylip-ICL1 : AIRASADIFGSNLLAIARTDSEAAATLITSSIDYRDHYFIAGATNPKDAG--HLVDVMVAEE : 280
Scer-ICL1 : TIRMCADIMHSDLIVVARTDSEAAATLITSTIDTRDHYFIVGATNPNIE--PFAEVLNDAI : 294
Cgla-ICL1 : TIRMCADIMHSELVIVARTDSEAAATLITSTIDTRDHYFVVGATNPDIE--PFAEYMDRAI : 293
Klac-ICL1 : TCRMAADVLGSDLILVARTDSEAAATLLSSTADSRDHYFILGASNPVAVKGPPLNDLLNKAI : 287
Agos-ICL1 : TIRMCADVMSNLLVIVARTDSEAAATLLSSNIDARDHYIIVGASNPEVT-VPLIEVLDAAQ : 295

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                *           320           *           340           *           360
Dhan-ICL1 : SNGIYGDKLASTIEVEWTKKAGLKLFFHEAVIDEIN-NGNFSNKQALIKKFTDKVNPLSATS : 346
Calb-ICL1 : SKGIYGNELAAIESEWTKKAGLKLFFHEAVIDEIK-NGNYSNKDALIKKFTDKVNPLSHTS : 346
Ppas-ICL1 : LQGGYGAELSQLLEADWSKKAGLKLFFHEAVFEADKSSSVKDKQAAKDKFSAKVGPLTGT : 350
Ncra-ICL1 : ABGKTGAQLQAIEDDWLAKADLKRFDVAVLDTAKG-KFSNAKDLAAKYQAAVKGKQ-IS : 350
Gzea-ICL1 : ATCKSGAELQRIEDEWLAKANLSSFDDAVAAAIDAG-SFSDKAGIKQEYTSRAKGG---S : 348
Cglo-ICL1 : RACKSGDALQAIEDKWLAQANLKRFDVAVLDAI AAS-GSANAKGLADQYRSATQKQ-LS : 350
Mgri-ICL1 : QSGKTGDQLQAIEDEWMAKANLKRFDVAVDVINSSSSIRNPKDVAAKYLQAAKGG---S : 349
Afum-ICL1 : QAGKTGEELQAIEDQWIAQAGLKLFFDDAVVDTKAG-VHVNKDALIKELYLTAAGKGG---S : 339
Anig-ICL1 : QACKNGNELQAIEDQWVAQAGLKLFFSEAVIDTINKS-SSGNKKALIDEYLKKAAGKGG---S : 339
Aory-ICL1 : QACKQGDDELQAIEDQWVAQAGLKLFFNDAVIEAINKG-AHSNKQSLIDQYLKAAKGGGG---S : 339
Pchr-ICL1 : QACKNGAQLQAIEDQWISQAGLKLFFSEAVIDTINSG-SHANKKSLIDQYLSASKGGGG---S : 339
Anid-ICL1 : QACKNGAELQAIEDEWLAKAGLKLFFNDAVVDANNNS-PLPNKKAIEKYLQSKGGGG---S : 339
Cimm-ICL1 : RACKNGAELQAIEDSWTAKAGLKRFDVAVIDQIKAS-SAANKQATTDAFLREIKGGGG---S : 340
Pnod-ICL1 : QACKNGAQLQAIEDAWTKKANLKLFFHEAVIDTINAG-VHVNKQDLIQQLQKSKGGGG---S : 339
Fpal-ICL1 : RACKTGAALAEVEEQWLAANKLQLFPEVLANALKAQ--TGANQVKLEQFHRVVAHL---S : 335
Ccin-ICL1 : AQCKTGDQLQAIEDGWLKAANLQLFQALQAL-AN--EGASRSTVEKLVARVSRLL---S : 334
Cneo-ICL1 : MECKYQELQKIEDAWTKQAGLKLFFPDVLAAL-SK--HGVSSKKITEFREQSIGT---S : 336
Umay-ICL1 : ABGADGPKLIALEEEWLAQAQPVRYGDVAEAL-EK--KGG-KAEAEAFRKEVVGL---S : 334
Ylip-ICL1 : LEGKQGAALQAVEDEWNRKAGVKLFFHEAFADENVAG-SYSNKAELIAEFNKKVTPLSNTP : 339
Scer-ICL1 : MSGASQELADIEQKWCARDAGLKLFFHEAVIDEIERSALSNKQE-LIKKFTSKVGPLTETS : 353
Cgla-ICL1 : MACVSCDELQKLEAAWTEKAGLKLFFHEAFADENVKSSVSNKQE-IIKKFNKVGPLTETS : 352
Klac-ICL1 : LDGATIDDLQTIKEWLAQADVKLFFHEVFADAQ--AAGKQDS-VIDQFNSKVNPLSETS : 344
Agos-ICL1 : QACASGDRLAQLLEEDWCKKAKLRLFFHEAFADQVNASPSIKDKAGVIAKFNQIQFGPQTGAS : 355

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          *           380           *           400           *           420
Dhan-ICL1 : NKEARKLAREILGKD----VFDFDVARAREGYRYRQGGTQCAVMRGOAYAPYADMIWME : 402
Calb-ICL1 : HKEAKKLAKELTGKD----IYFNWDVARAREGYRYRQGGTQCAVMRGRAPYADLIWME : 402
Ppas-ICL1 : HKEAAKLAKELGEE----VFDFWEAPKVRREGYRYRQGGTECAIMRARAYSPYADLVWME : 406
Ncra-ICL1 : NREARAIARQLLGQE----IFFDWEESPRTREGYRYRLKGGCDCSINRAISYAPYCDAIWME : 406
Gzea-ICL1 : NEEARAVARQLLGRD----IFFDWDAPRTREGYFRLKGGCDCAVNRAIAYAPYCDAIWME : 404
Cglo-ICL1 : NAEARAVARGILGKD----VHFDWDAPRTREGYRYRLKGGCDCSVNRAIAYAPYCDAIWME : 406
Mgri-ICL1 : NREARAIASSLGVPE----LFFDWDSPRTREGYFRLKGGCDCAINRAIAYAPYADAIWME : 405
Afum-ICL1 : NSEARAIAGKITGVD----IYWDWDAPRTREGYRYRQGGTQCAINRAVAYAPFADLIWME : 395
Anig-ICL1 : NREARAIADITGVD----IYWDWDAPRTREGYRYRQGGTQCAVNRAIAYGPFADLIWME : 395
Aory-ICL1 : NLEARAIAKNITGQD----IYFNWDAPRTREGYRYRQGGTQCAINRGLAYAPFADLIWME : 395
Pchr-ICL1 : NTEARAIKNTLTVGVD----IYWNWDSPRTREGYRYRQGGTQCAVNRAIAYAPFADLIWME : 395
Anid-ICL1 : NLEARAIAGEIAGTD----IYFDWEAPRTREGYRYRQGGTQCAINRAVAYAPFADLIWME : 395
Cimm-ICL1 : NKEARAIARQLLGTD----IFFDWDAPRTREGYRYRQGGTQCAINRAVAFAPFADLIWME : 396
Pnod-ICL1 : NSEARAIAGLITGVD----VYFNWEAARTREGYRYRQGGTQCAINRAVAYAPYCDMIWME : 395
Fpal-ICL1 : YPDVAVAVAKKEFGLR--SAPFDWDAPRTREGYRYRQGGTQCAVNRAIAFAPYADLIWME : 393
Ccin-ICL1 : WSQAVAVAKKEFGLK--QVPYWNWDAPRTREGYRYRQGGTECAIHRAVAFAPYADLIWME : 392
Cneo-ICL1 : HASTLQLAQ-SFGLPPSATPYWSDTPRSREGYRYRQGGTQCAINRAIAFAPYADLIWME : 395
Umay-ICL1 : LIKSKAKAK-SLGVGVD----INFWDACRTREGYRYRQGGTDCAINRAIAFAPYADLIWME : 389
Ylip-ICL1 : ALEARALAAARLLGKD----IYFNWEAARVREGYRYRQGGTQCAVNRAIAYAPYADLIWME : 395
Scer-ICL1 : HREAKKLAKELLGHE----IFFDWEELPRVREGLYRMRGGTQCSIMRARAFAPYADLVWME : 409
Cgla-ICL1 : HREAKKLAKELLGKD----LFFDWDLPRVREGLYRMRGGTQCSVMRARAFAPYADLVWME : 408
Klac-ICL1 : IYEMQALAKELLGTE----LFFDWDLPRGREGLYRMRGGTQCSVMRARAFAPYADLCWME : 400
Agos-ICL1 : IREMRKILGRELLGQD----VYFDWDLPRAREGLYRMRGGTQCAIMRARAFAPYADLVWFE : 411

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          *           440           *           460           *           480
Dhan-ICL1 : SALPDKFAQAEFAEGVKAKEVDQWLAYNLSPSFNWNRAMP-NEQETYIKRLSELGYVWQ : 461
Calb-ICL1 : SALPDYAQAEFADGVKAAVEDQWLAYNLSPSFNWNRAMP-DEQETYIKRLGKLGWVWQ : 461
Ppas-ICL1 : SKVPDYQAEAVDFAKGVKFTFTQTNWLAYNLSPSFNWNRAMP-DEQETYIKRLGKLGYNWQ : 465
Ncra-ICL1 : SKLPDYAQAEEFAKGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIRRLAKLGYCWQ : 465
Gzea-ICL1 : SKLPDFAQAEQFAQGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIRRLAKLGYCWQ : 463
Cglo-ICL1 : SKLPDKFAQAEFARGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIRRLATLGYCWQ : 465
Mgri-ICL1 : SKLPDYEQAEFAEGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIRRLAGLGYCWQ : 464
Afum-ICL1 : SKLPDYAQAQAEFADGVHAWVPECKLAYNLSPSFNWKTAMP-EEQETYIKRLGALGYAWQ : 454
Anig-ICL1 : SKLPDYAQAQAEFADGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIRRLGALGYCWQ : 454
Aory-ICL1 : SKLPDYAQAQAEFAEGHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIKRLGALGYCWQ : 454
Pchr-ICL1 : SKLPDYNQAQAEFADGVHAWVPECKLAYNLSPSFNWKTAMP-NEQETYIKRLGELGYAWQ : 454
Anid-ICL1 : SKLPDYKQAQAEFADGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIKRLGALGYAWQ : 454
Cimm-ICL1 : SKLPDYAQAQAEFAEGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIRRLGELGYCWQ : 455
Pnod-ICL1 : SKLPDFAQAEFADGVHAWVPECKLAYNLSPSFNWKTAMP-DEQETYIRRLAKLGYCWQ : 454
Fpal-ICL1 : TKKPIYAQAQAEFADGVHAWVPECKLAYNLSPSFNWKTAMP-GLNEQDMKAFVWDLGKLGFCWQ : 453
Ccin-ICL1 : TKKPILAQAQAEFAAGVHAWVPECKLAYNLSPSFNWKTAMP-QDMQAYVWDLGKLGFCWQ : 451
Cneo-ICL1 : TKKPIYAQAQAEFAEGVHAWVPECKLAYNLSPSFNWKTAMP-AGLGKEMKEYVWDLGKLGFCWQ : 455
Umay-ICL1 : TKKPILAQAQAEFSEGKAAVEHQWLAYNLSPSFNWKTAMP-DAKLSTEQMSYVWDLGKLGFCWQ : 449
Ylip-ICL1 : SKLPDYAQAQAEFAEGVKAKEVDQWLAYNLSPSFNWKTAMP-EDQETYIRRLAKLGYVWQ : 454
Scer-ICL1 : SNYPDFQAQAEFAEGVKEKFPDQWLAYNLSPSFNWKTAMP-SV-DEQHTFIORLGDLYIWO : 468
Cgla-ICL1 : SNYPDFEQAREFAEGVKAKEVDQWLAYNLSPSFNWKTAMP-SV-DEQATFIERLQGLGYIWO : 467
Klac-ICL1 : SNYPDYEQAQAEFAEGVTAKEFGKWMAYNLSPSFNWKTAMP-SV-DEQETFIORLGDLYIWO : 459
Agos-ICL1 : SNYPDFQAQAEFAQGVREKFPDQWLAYNLSPSFNWKTAMP-PP-KEQENYIORLGETGYVWQ : 470

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          *           500           *           520           *           540
Dhan-ICL1 : FITLAGLHTTALAVDDFANQYSQIGMRAYGOTIQAPEIEKGVVVKHOKWSGAEYIDGLL : 521
Calb-ICL1 : FITLAGLHTTALAVDDFSNQYSQIGMKAYGOTVQOPEIEKGVVVKHOKWSGATYIDGLL : 521
Ppas-ICL1 : FITLAVLHTTALAVDDFSRDYQKIGMKAYGQVQAKEIEDGIEIVKHOKWSGAEYIDGLL : 525
Ncra-ICL1 : FITLAGLHTTALISDQFAKAYSKI GMRAYGELVQEPETDNGVDVVKHOKWSGATYVDELQ : 525
Gzea-ICL1 : FITLAGLHTTALISDQFAKAYSTVGMRAYGELVQEPEDQKVDVVKHOKWSGATYVDELQ : 523
Cglo-ICL1 : FITLAGLHTTALISDRFARAYSQO GMRAYGELVQEPEMELGVDVVKHOKWSGATYVDELQ : 525
Mgri-ICL1 : FITLAGLHTTALISDRFARAYSEVGMRAYGELVQEPEMELGVDVVKHOKWSGATYVDELQ : 524
Afum-ICL1 : FITLAGLHTTALISDQFARAYAKQGMRAYGELVQEPEMEQQVDVVT HOKWSGANYVDNML : 514
Anig-ICL1 : FITLAGLHTTALITDQFAKAYAKQGMRAYGELVQEPEMEQQVDVVT HOKWSGANYVDNML : 514
Aory-ICL1 : FITLAGLHTTALISDQFAKAYSKQGMRAYGELVQEPEMEQQVDVVT HOKWSGANYVDNLL : 514
Pchr-ICL1 : FITLAGLHTTALISHQFAKAYSQNGMRAYGELVQEPEMEQQVDVVT HOKWSGANYVDNML : 514
Anid-ICL1 : FITLAGLHTTALISDTFAKAYAKQGMRAYGELVQEPEMANGVDVVT HOKWSGANYVDNML : 514
Cimm-ICL1 : FITLAGLHTTALISDQFAKAYAKQGMRAYGELVQEPEMENKVDVVT HOKWSGANYVDELL : 515
Pnod-ICL1 : FITLAGLHQSALMADTFASKAYAKQGMRAYGELVQEPENKVDVVT HOKWSGANYVDNML : 514
Fpal-ICL1 : FITLAGLHSNAYISDLFAKAFATEGMKAYVELVORREREIGCDVLT HOKWSGADYMDNLM : 513
Ccin-ICL1 : FITLAGLHSNAYISDLFAQNFAGTKGMKAYVELVOSREREIGCDVLT HOKWSGADYADSLI : 511
Cneo-ICL1 : FITLAGLHSNAYINDLFAAFSKEGMKAYVELVOSREREIGCDVLT HOKWSGADYADAML : 515
Umay-ICL1 : FITLGLHSNAYISDLFAAGFAKEGMKAYVELVORKEREIGCDVLT HOKWSGANFVDACL : 509
Ylip-ICL1 : FITLAGLHTNALISDKFAKAYSERGMKAYGGEIQOPEIQDQCEVVKHOKWSGAEYIDGITL : 514
Scer-ICL1 : FITLAGLHTNALAVHNF SRDFAKDGMKAYAQNVOQREMDGVDVLKHOKWSGAEYIDGLL : 528
Cgla-ICL1 : FITLAGLHTTALAIHKFSEDFAREGMKAYAQNVOQIEMDEGVDVLKHOKWSGAEYIDGLL : 527
Klac-ICL1 : FITLAGLHTSGLAIEQFSKNFAKLGMKAYAODIQKELDNGIDMVKHOKWSGAEYIDGLL : 519
Agos-ICL1 : FITLAGLHTNALAIDNFSREFSRFGMRAYAQGIQOREMDEGVDVLKHOKWAGAEYVDSIL : 530

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          *           560           *
Dhan-ICL1 : KMVTGGVSS TAAMGAGVTEDFKKEAAGK----- : 550
Calb-ICL1 : KMVSGGVST TAAMGQGVTEDFKESKAKA----- : 550
Ppas-ICL1 : KLTGGGLSS TAAMGAGVTEDFKDH----- : 550
Ncra-ICL1 : KMVTGGVSS TAAMGKGVTEDFQH----- : 548
Gzea-ICL1 : KMVTGGISS TAAMGAGVTEDFK----- : 546
Cglo-ICL1 : KMVTGGVSS TAAMGRGVTEDFQH----- : 548
Mgri-ICL1 : KMVTGGVSS TAAMGKGVTEDFQH----- : 547
Afum-ICL1 : KMLTGGVSS TAAMGKGVTEDFKH----- : 538
Anig-ICL1 : KMVTGGISS TAAMGKGVTEDFKH----- : 538
Aory-ICL1 : KMVTGGVSS TAAMGKGVTEDFKH----- : 538
Pchr-ICL1 : KMVSGGVSS TAAMGKGVTEDFKN----- : 538
Anid-ICL1 : KMITGGVSS TAAMGKGVTEDFKS----- : 538
Cimm-ICL1 : KMVTGGISS TSMGKGVTEDFK----- : 538
Pnod-ICL1 : KMVSGGVSS TAAMGKGVTEDFK----- : 537
Fpal-ICL1 : KTVTGGVSS TAAMGKGVTEDFKSKL----- : 539
Ccin-ICL1 : KTVTGGVSS TAAMGAGVTEDFKSKL----- : 537
Cneo-ICL1 : MTVTGGVSS TAAMGKGVTEDFVDDKTKDALHKL : 549
Umay-ICL1 : NTVLK-AAST TSMGKGVTEDFK----- : 531
Ylip-ICL1 : RMVTGGITST AAMGAGVTEDFKSKL----- : 540
Scer-ICL1 : KLAQGGVSATAAMGTGVTEDFKENG VVK----- : 557
Cgla-ICL1 : KLAQGGVSATAAMGQGVTEDFKSNL----- : 553
Klac-ICL1 : RLAQGGLAATAAMGQGVTEDFK----- : 542
Agos-ICL1 : KLAQGGVSS TSMGKGVTEDFGSSNGAKL----- : 560

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Legend to Supplementary Fig. S3.

Sequence alignment of fungal microbody-located isocitrate lyases (ICL1).

The following accession numbers were used:

Yeast species:

Dhan, *Debaryomyces hansenii* (CAG87204); Calb, *Candida albicans* (EAK93039); Ppas, *Pichia pastoris* (CAC34630);

Filamentous ascomycetes:

Ncra, *Neurospora crassa* (EAA31618); Gzea, *Gibberella zeae* (EAA70122); Cglo, *Chaetomium globosum* (EAQ85852); Mgri, *Magnaporthe grisea* (AAN28719); Afum, *Aspergillus fumigatus* (EAL89442); Anig, *Aspergillus niger* (ABC73716); Aory, *Aspergillus oryzae* (BAE54710); Pchr, *Penicillium chrysogenum* (Pc22g03660); Anid, *Aspergillus nidulans* (EAA62727); Cimm, *Coccidioides immitis* (AAK72548); Pnod, *Phaeosphaeria nodorum* (EAT86690).

Basidiomycetes:

Fpal, *Fomitopsis palustris* (BAD93181); Ccin, *Coprinopsis cinerea* (CAA67367); Cneo, *Cryptococcus neoformans* (AAW45191) and Umay, *Ustilago maydis* (EAK85334).

Yeast species:

Ylip, *Yarrowia lipolytica* (CAG82243); Scer, *Saccharomyces cerevisiae* (AAB64601); Cgla, *Candida glabrata* (CAG60786, minus the first 23 amino acids); Klac, *Kluyveromyces lactis* (CAH01411) and Agos, *Ashbya gossypii* (AAS51854).

Sequences were aligned using the Clustal_X programme (Thompson et al. 1997). Gaps were introduced to maximize the similarity. Residues that are similar in all 23 proteins are represented by white letters that are shaded black. Similar residues in at least 18 of the proteins are shown as white letters that are shaded dark grey, while those that are similar in at least 14 of the proteins are shown as black letters that are shaded light grey. Putative PTS1 sequences are shaded red, while an internal sequence in ICL1 of filamentous ascomycetes that weakly resembles the PTS2 consensus is shaded yellow.