

University of Groningen

Matching the proteome to the genome

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Supplementary Fig. S2

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*          20          *          40          *          60
Aory : -----MAPAPRVIVVGGGLSGLSAAHTVYLNNGN-VLVLDKQAEFFGGNSTKATSGIN : 51
Anig : -----MATAPRVIVVGGGLSGLSAAHTVYLNNGN-VLVLDKQAEFFGGNSTKATSGIN : 51
Ater : -----MATPPRVIVVGGGLSGLSAAHTVYLNNGN-VLVLDKQAEFFGGNSTKATSGIN : 51
Afum : -----MATPPRVIVVGGGLSGLSAAHTVYLNNGN-VLVLDKQAEFFGGNSTKATSGIN : 51
Pchr : -----MAAPQVIVVGGGLSGLSAAHTIYLNNGN-VLVLDKQAEFFGGNSTKATSGIN : 50
Anid : -----MAPRVIVVGGGLSGLSAAHTVYLNNGS-VLVLDKQAEFFGGNSTKATSGIN : 49
Acap : ----- : -
Cimm : -----MATPQRVIVVGGGLSGLSAAHTVYLNNGN-VLVLDKQSEFFGGNSTKATSGIN : 51
Cglo : -----MAPSVIVVGGGLSGLSAAHTIYLAGGN-VVLDKQGEFFGGNSTKATSGIN : 49
Ncra : -----MAPRVIVVGGGLSGLSAAHTIYLAGGN-VVLDKQGEFFGGNSTKATSGIN : 49
Mgri : -----MPSRVIVVGGGLSGLSAAHTIYLAGGN-VVLDKQGEFFGGNSTKATSGIN : 49
Gzea : -----MAPRVIVVGGGLSGLSAAHTIYLAGGN-VVLDKQGEFFGGNSTKATSGIN : 49
Sscl : -----MAPRVIVVGGGLSGLSAAHTIYLAGGN-VVLDKQAEFFGGNSTKATSGIN : 49
Pnod : -----MPQNVIVVGGGLSGLSAAHTIYLAGGN-VVLDKNNFMGGNSTKATSGIN : 49
Calb : ----MSTASIPSNPILIVGGGLAGLSAAHQAYLRGAN-VVLDKSEFSLGNSGKATSGIN : 55
Dhan : ----MSNIPENPVIIVGGGLAGLSAAHQAYLRGAN-IILLDKQGEFSLGNSGKATSGIN : 53
Cneo : ----MSKVKVIIVGGGLSGLSAAHTVLERGGN-VLLLDKNSFMGGNSTKATSGIN : 50
Ccin : ----MAQVIVVGGGLAGLSAAHTLLERGAS-VLLLDKQPEFMGGNSTKATSGIN : 48
Umay : ----MSRVIVVGGGLSGLSAAHTLYERGAN-VLVLDKPNFFGGNSTKATSGIN : 48
Otau : ----MAEQVIVVGGGLAGLSAAHTVLEHGAR-VVLDKCEFLGNSGKATSGIN : 49
Lmaj : MPPSQPPVEGGANRIIVGGGLAGVCAAHASLQHGGV-VLLLDKSAFLGGNSTKASSGIA : 59
Scer : ----MSLSPVVVIGTGLAGLAAANELVNKYNIPTILKASSIGGNSIKASSGIN : 51

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*          80          *          100          *          120
Aory : GALTRTQVDLGIQDSVKTFYEDTLKSARDKARPE-----LIKVLTYKSAAAWEWLMDV : 104
Anig : GALTRTQVDLGIADSVKQFYDDTLKSARDKARPE-----LIKVLTYKSAAAWEWLDQV : 104
Ater : GALTRTQVDLGIQDSVKTFYEDTLKSARDKARPE-----LIKVLTYKSAAAWEWLDQV : 104
Afum : GALTRTQVDLGIQDSVKTFYEDTLKSARDKARPE-----LIKVLTYKSAAAWEWLDQV : 104
Pchr : GALTRTQVDLGIQDSVKQFYEDTLKSARDKARPD-----LIKVLTYKSASAVEWLDQV : 103
Anid : GALTRTQVDLNIIRDSVKQFYDDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQV : 102
Acap : -----VKGFYEDTIQSARDKARLD-----LIKVLTYNSASAIHWLQEI : 38
Cimm : GALTRTQIEELGIGDSVKQFYEDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQV : 104
Cglo : GALTRTQVEHGIQDSVKQFYDDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQV : 102
Ncra : GALTRTQVELGIQDSVKQFYDDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQV : 102
Mgri : GALTRTQVEHGIQDSVKQFYDDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQV : 102
Gzea : GALTRTQVDGIPDSVKQFYDDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQE : 102
Sscl : GALTRTQVDQKIQDSVKQFYDDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQV : 102
Pnod : GALTRTQVDHIGDSVKQFYDDTLKSARDKARPD-----LIKVLTYKSAAAWEWLDQV : 102
Calb : GALTRTQVNLKIPDSVEQFYQDTLASAKDRAHPE-----LIKVLTYNSADAVHWLQEV : 108
Dhan : GSLTRTQVNLSTKDSVEQFYEDTLKTAKDRANPD-----LIKVLTYNSADAVHWLQEV : 106
Cneo : GANTQAQQTLPDTSAKFFADTKKSARELARD-----LIRVLTYSKGDVAVNWLIER : 103
Ccin : GAGTNSQRHLNIPDTPETFADTKKSARELARD-----LIRVLTYSKGDVAVNWLDQK : 101
Umay : GAGTATQAEQIPDSAKTFEEDTKKSARELARD-----LIKVLTKSGEAVNWMDR : 101
Otau : GALTRTQARLNIPDSADKFEDDILKGAAGVGHTEAPAHTIPLAKVLAQSGSSVDWLCEK : 109
Lmaj : GTPTQAQIDAGVLDGVKLFTEDTNRSFHGVQAGEKPGVSPFLVSEMARLSGPSLDWLVRY : 119
Scer : GACTETQRHFHIEDSPRLFEDDTIKSAKGGKVQE-----LMAKLANDSPLAIEWLKNE : 104

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*          140          *          160          *          180
Aory : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELTE-KEPERVQIVKKARV : 163
Anig : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELTE-SEPDRVQIIVKKARV : 163
Ater : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-AEPHRVQIVKKARV : 163
Afum : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELSE-KEPERVQIIVKKARV : 163
Pchr : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-SEPGRVQIVKKANV : 162
Anid : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELSE-SDPDRVQIIVKKARV : 161
Acap : FKLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELTC-SEPDRVQIVKKARV : 97
Cimm : FDLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELTE-KEPNRVQIVKKARV : 163
Cglo : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-TEPHRVQIIVKKARV : 161
Ncra : FKLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-TEPERVQIIVKKARV : 161
Mgri : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-TEPHRVEIVKKARV : 161
Gzea : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-SEPGRVEIVKKARV : 161
Sscl : FGLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-AEPERVQIIVKKARV : 161
Pnod : FNLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYALMQRLEELAE-AEPERVQIVKKAKV : 161
Calb : FDLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYRLLERLEELSE-TEPDRVVILKNSQV : 167
Dhan : FGLDLTIIVSRLGGHSPRTHRGHDAKFPGMATYKLLLEKLENLSE-SEPHRVMIKKSQV : 165
Cneo : FNLDLTIIVSRLGGHSEKTRTHRG-TQEFPGMTIYALMEKLEELMAA-QHPDRVKILKKAQV : 161
Ccin : FQDLDSKVARLGGHSPRTHRG-DAQFPGMVMTYAQMERLEELAV-SDPDRVQIIVKKARV : 159
Umay : FALDLTIIVSRLGGHSPRTHRG-GAQFPGMTIYALMEKLEELAE-AEPDRVQIIVKKARV : 159
Otau : FKLDLTIIVSRLGGHSPRTHRG-KEPEFGMTIYALMEGLEKVMEDSNGETARITKAE : 168
Lmaj : FNCDLSKLGFMGGHSPRTHRG-KEPEFGMTIYALMGLAEVQK-VDPARARITKARV : 177
Scer : FDLDLTIIVSRLGGHSPRTHRGSSGLPFGFELVSALENNKLEAE-TKPELVKILNLDKQV : 163

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*          200          *          220          *          240
Aory : TSVNKTGNT---VTGVTYE--YDGETHTADG-IVILATGGYAADFG-DG-SLLKQHRPDT : 215
Anig : TSINKSGNH---VTGVTYE--YDGETHTADG-VVVLATGGYAADFG-DG-SLLKQHRPDT : 215
Ater : TSINKSGNH---VTGVTYE--RDGQSHSADG-VVVLATGGYAADFG-DG-SLLKQHRPDT : 215
Afum : TKVNKSGNT---ITGVTYE--LNGETKTADG-VVILATGGYAADFG-DG-SLLKQHRPDT : 215
Pchr : TSINKSGNH---VTGVTYE--INGEEKVADG-VVVLATGGYAADFS-DT-SLLKQHRPDT : 214
Anid : TAVNKDGN---VTGVTFE--VDGETKTADG-VVILATGGYAADFG-DS-SLLKQHRPDT : 213
Acap : TAVNKEGNK---ITGVTYE--YNGETHKADG-VVVLATGGYAADFT-ED-SLLKQHRPDT : 149
Cimm : TGINREGNK---VTGVTYE--YNGESHADG-VVVLATGGYAADFT-EN-SLLKQHRPDT : 215
Cglo : TGLNKQGN---ITGVQYE--HNGENLSIDG-PVVLATGGYAADFS-DS-SLLKQHRPDT : 213
Ncra : TSLNKEGNK---VTGVKYE--VNGETQSLDG-PVVLATGGYAADFT-ED-SLLKQHRPDT : 213
Mgri : TNLNKEGNK---VTGVTYE--HDGQKHTMDG-PVVLATGGYAADFS-ET-SLLKQHRPDT : 213
Gzea : TELNKEGNK---VTGVKYE--HNGEIVSIDG-PVVLATGGYAADFS-DS-SLLKQHRPDT : 213
Sscl : TGLKKEGNK---ITGVNYE--FGGEPFVEG-PVVLATGGYAADFT-ET-SLLKQHRPDT : 213
Pnod : TSVNIENNR---ALGVTYE--FNGEETLEG-PVILATGGYAADFT-AD-SLLKQHRPDT : 213
Calb : IDLIMEQDN---KVVGVKYNLKD KSKHELYG-PVILSTGGYAADFT-KN-SLRKYRPI : 222
Dhan : IDLIKLDDEFKIVGVKYLKDLTKLKHLLG-PVIMATGGYAADFT-KN-SLRKYRPI : 222
Cneo : TKLLQ-EDGK--VIGVDYE--RDGKHYTEYG-PVVLATGGYAADFT-AD-SLLQOYRPEY : 213
Ccin : TKLLKDESGA--VVGVEYS--HADKHTAYG-PVVLATGGYAADFT-ED-SLLKQHRPDT : 212
Umay : TKLVH-QNGE--VTGVVEYE--YOGQHTESG-PVVLATGGYAADFDDVN-SLLKQHRPDT : 212
Otau : KRLLTD-GSG-TVIGVEYE--KDGVLNQEYG-PVVIATGGFGADYKPD--SLLKQHRPDT : 221
Lmaj : VRLVHRPLDG-PVTGVVFD-REGNQHMERG-AVVIATGGFAADFAQDSSLIARFAPQL : 234
Scer : VDIHEKDG---ISAVVYED-KNGEKHMVSANDVVFCSGGFGFS-----KEMLEKYEAPQL : 214

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*          260          *          280          *          300
Aory : FGLSSTNGTTHATGDGQKMLMEIGANGIDMDKVQVHPTGLVDPKD-----PTAKFKFLA : 268
Anig : FGLSSTNGTTHATGDGQKMLMEIGANGIDMDKVQVHPTGLVDPKD-----PTAKFKFLA : 268
Ater : FGLSSTNGTTHATGDGQKMLMEIGANGIDMDKVQVHPTGLVDPKD-----PTAKFKFLA : 268
Afum : FGLSSTNGTTHATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PTAKFKFLA : 268
Pchr : FGLSSTNGTTHATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PGAKFKFLA : 267
Anid : FGLSSTNGTTHATGDGQKMLMSIGANGIDMDKVQVHPTGLVDPKD-----PTAKFKFLA : 266
Acap : FHLSTNGVHATGDGQKMLMAIGANGIDMDKVQVHPTGLIDPKD-----PDSKWKFLA : 202
Cimm : FNLSTNGVHATGDGHKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PTSCKWKFLA : 268
Cglo : FGLASTNGVHATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PGSKWKFLA : 266
Ncra : YGLATTNGTTHATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PNSKWKFLA : 266
Mgri : YGLATTNGSHTATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PGSKWKFLA : 266
Gzea : YGLATTNGTTHATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PGSKWKFLA : 266
Sscl : YDLASTNGVHATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PGSKWKFLA : 266
Pnod : YDLSTNGVHATGDGHKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PTAKTKFLA : 266
Calb : IDLPSTNGGHTATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PDAKVKFLA : 282
Dhan : IDLPSTNGGHTATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PDAKVKFLA : 282
Cneo : YNLPTTNGDHTCTGDGHKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PDAKVKFLA : 266
Ccin : WNLPTTNGDHTCTGDGHKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PDAKVKFLA : 265
Umay : VHLPTTNGDHTCTGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PDAKVKFLA : 265
Otau : QALPTTNGDHTCTGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PDSKWKFLA : 274
Lmaj : TKFSTTNGDHTATGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----PNNHVKFLA : 287
Scer : VNLPTTNGDHTCTGDGQKMLMAIGANGIDMDKVQVHPTGLVDPKD-----RSSWKFLA : 267

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*          320          *          340          *          360
Aory : AEALRGGGLLN--SDGQRFSDDELCHRDIYVSGQMWKEKEKGNPRLVNLNSKASNVLDLDFH : 327
Anig : AEALRGGGLLN--SDGQRFSDDELCHRDIYVSGQMWKEKEKGNPRLVNLNSKASNVLDLDFH : 327
Ater : AEALRGGGLLN--SDGQRFSDDELCHRDIYVSGQMWKEKEKGNPRLVNLNSKASNVLDLDFH : 327
Afum : AEALRGGGLLN--SDGQRFSDDELCHRDIYVSGQMWKEKEKGNPRLVNLNSKASNVLDLDFH : 327
Pchr : AEALRGGGLLN--SDGQRFSDDELCHRDIYVSGQMWKEKEKGNPRLVNLNSKASNVLDLDFH : 326
Anid : AEALRGGGLLN--SDGERFSDDELCHRDIYVSGQMWKEKEKGNPRLVNLNSKASNVLDLDFH : 325
Acap : AEALRGGGLLN--SEGQRFADDELCHRDIYVSGEMWKEKEKGNPRLVNLNSKASNVLDLDFH : 261
Cimm : AEALRGGGLLN--KDGQRFADDELCHRDIYVSGEMWKEKEKGNPRLVNLNSKASNVLDLDFH : 327
Cglo : AEALRGGGLLN--ADGDRFCDELCHRDIYVSGMMWKEKDKGNPRLVNLNSKASNVLDLDFH : 325
Ncra : AEALRGGGLLN--GDGDRFCDELCHRDIYVSGMIHKEKDKGNPRLVNLNSKASNVLDLDFH : 325
Mgri : AEALRGGGLLN--ADGDRFCDELCHRDIYVSGMMWKEKDKGNPRLVNLNSKASNVLDLDFH : 325
Gzea : AEALRGGGLLN--ADGDRFCDELCHRDIYVSGMMWKEKDKGNPRLVNLNSKASNVLDLDFH : 325
Sscl : AEALRGGGLLN--GDGDRFCDELCHRDIYVSGEMWKEKDKGNPRLVNLNSKASNVLDLDFH : 325
Pnod : AEALRGGGLLN--NKGKRFCDDELCHRDIYVSGMMWKEKDKGNPRLVNLNSKASNVLDLDFH : 325
Calb : AEALRGGGLLN--SKGERFVDELCHRDIYVSGEMDKQIKQGNPRLVNLNSKASNVLDLDFH : 341
Dhan : AEALRGGGLLN--NKGKRFVDELCHRDIYVSGEMDKQIKQGNPRLVNLNSKASNVLDLDFH : 341
Cneo : AEALRGGGLLN--RDGERFVDELCHRDIYVSGKMWKE---NDKFPVRLVNLNSKASNVLDLDFH : 322
Ccin : AEALRGGGLLN--NTGARFVDELCHRDIYVSGKIWE---NGKFPVRLVNLNSKASNVLDLDFH : 321
Umay : AEALRGGGLLN--NEGKRFVDELCHRDIYVSGRMWD---NNKFPVRLVNLNSKASNVLDLDFH : 321
Otau : AEALRGGGLLN--ANGKRFVDELCHRDIYVSGEMNR--NK--GFFRLVNLNSKASNVLDLDFH : 329
Lmaj : AEALRGGGLLN--KHGQRFVDELCHRDIYVSGAAMLK--HDSASEFYLLNLSKASNVLDLDFH : 344
Scer : AESLRGLGGGLLN--PITGRFVDELCHRDIYVSGAAIQKVCQEDNRALVLMGKMYTDLKNN : 327

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*          380          *          400          *          420
Aory : TRHYSGRGLMKKIS-GKELAK-EIGCGEAA LKKTFFQEYNATAEGKQKDP----- : 374
Anig : TRHYSGRGLMKKMT-GKELAK-EIGCGEAA LKKTFFDDYNLIAEGKKKDP----- : 374
Ater : TRHYSGRGLMRKMT-GKELAK-EIGCGEAA LKKTFFDEYNLIAEGKKKDP----- : 374
Afum : TRHYSGRGLMKKMT-GKELAK-EIGCGEAA LKKTFFDEYNLIAEGKKKDP----- : 374
Pchr : TRHYSGRGLMKKMT-GAELVA-EIGCGEAA LKKTFFDEYNLIAEGKKKDP----- : 373
Anid : TRHYSGRGLMKKMT-GKELAK-EIGCGEAA LKKTFFEDYNIAEGKKKDP----- : 372
Acap : TRHYSGRGLMKKMT-GKELAK-DIGCGEAA LKKTFFDEYNQIADGKKKDP----- : 308
Cimm : TRHYSGRGLMKKMT-GKELAR-EIGCGEAA LKKTFFDDYNQIAEGKKKDP----- : 374
Cglo : TRHYSGRGLMKKMT-GKELAK-EIGCTPDH LKKTFFQTYNATAEGKQKDP----- : 372
Ncra : TRHYSGRGLMKKMT-GQELAK-EIGCTPEH LKKTFFQTYNATAEGKQKDP----- : 372
Mgri : TRHYSGRGLMKKMT-GQOLAK-EIGCTPEH LKKTFFTTYNATAEGKQKDP----- : 372
Gzea : TRHYSGRGLMKKMT-GKELAK-EIGCTPEH LKKTFFSTYNDIADGKQKDP----- : 372
Sscl : TRHYSGRGLMKKMT-GKELAK-EIGCTPDH LKKTFFKKNKIAEGKEKDP----- : 372
Pnod : TRHYSGRGLMKKMS-GAELAK-EIGVSDK LQAEFQSYNATAKGEKKDE----- : 372
Calb : VKHYTORGLMRTVS-GKELVE-EMGCSEDI VKQQLDITYNKAASGAIKDP----- : 388
Dhan : IKHYTORNLMTLS-GDELIK-EIGCNKETV DKQFEKYNKAASGETEDE----- : 388
Cneo : CKHYVGRGLMKKFNSGEELAK-EIGCSPEA LKKTFFDDHNRYAKNPGTDP----- : 370
Ccin : CKHYVGRGLMKRFDSGEALAK-EFGVAPAV LKKTFFEDYNQSVRTK-KDP----- : 368
Umay : CKHYVGRGLMKRFDSANDLAK-EMGIPAEL QSTFFQDYEAIAKGEKKCP----- : 369
Otau : CKHYVGRGIMKRHDSGAEVAK-ELGISPQK LADTFAKYNAAARTKNCP----- : 376
Lmaj : CKHYVGRGLMKRYASGYEFACT-ATNKPPEA LAATYEQYKKAAVNAASRGADSAAAGAAK : 403
Scer : LDFYMFKRLVQKLTLSQVVSEYNLPITVAQL CEELQTYSSFTTKADPLG----- : 376

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*          440          *          460          *          480
Aory : -----WGKRFFHNLFPD--INDTFHVALMEPVLHF : 402
Anig : -----WNKRFFHNLPFS--IDDDFHVALMEPVLHF : 402
Ater : -----WNKRFFHNM PFS--IDDTFHVALMEPVLHF : 402
Afum : -----WGKRFFHNM PFD--INDEFHVSLMEPVLHF : 402
Pchr : -----WNKRFFHNM PFK--LDDEFHVSLMEPVLHF : 401
Anid : -----WNKRFFHNL PFS--IDDEFHVSLMEPVLHF : 400
Acap : -----FGKKYFHNGPMS--VDDTFYVALMQPVLHF : 336
Cimm : -----FGKKYFHNL PFS--VDDTFHVAVMEPVLHF : 402
Cglo : -----WGKKFFHNLPLD--ISDDFHVSLMEPVLHF : 400
Ncra : -----WGKKFFHNL PVD--INDDFHVSIMEPVLHF : 400
Mgri : -----WGKKFFHNL PLD--INDDFHVSLMEPVLHF : 400
Gzea : -----WGKKFFHNL PVD--VDDDFHVAVMEPVLHF : 400
Sscl : -----YGKKFFHNGPLD--IDDDFHVAVMEPVLHF : 400
Pnod : -----WNKKFFHNL PFD--INDTFHVAVMEPVLHF : 400
Calb : -----FGKKYFPATPFEYSPDAKYHVSFITPVLHF : 418
Dhan : -----FGKQYFPNTPFEFTTDSKYHVSFITRVLHF : 418
Cneo : -----FGKKFFSGGDFS--MSDTYHAAIMTPVLHY : 398
Ccin : -----FGKKFFQGEWK--FDDFFHVAIMTPVLHY : 395
Umay : -----WGKKFFSNSDLR--MNQAFYVALMTPVLHY : 397
Otau : -----FGKKFFTAP-FE-MNDFHSAIVCTVVHY : 404
Lmaj : RGFSLFGFGEKRAATGTAVAKDSSRGTDPQEGKTVFRNVDAFS-MDGPLYVAWIAPVVHY : 462
Scer : -----RTVILNEFGSDVTPETVVFVIGEVTPVVFH : 405

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*          500          *          520          *          540
Aory : TMGGIEINEHAQVLNSE-KKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 461
Anig : TMGGIEINEHAQVLNSE-KEAFDGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 461
Ater : TMGGIEINEHAQVLNSE-KKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 461
Afum : TMGGIEINEHAQVLNSE-KKPFNGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 461
Pchr : TMGGIEINEHAQVLNSE-QKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 460
Anid : TMGGIEINDRAEVLNSE-HKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 459
Acap : TMGGIEINDKAQVLNSE-KKPFEGLFACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 395
Cimm : TMGGIEINDKAQVLNKE-GKPFEGLFVCGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 461
Cglo : TMGGIEINDKAQVLNKE-QKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 459
Ncra : TMGGIEINDKAQVLNSE-QKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 459
Mgri : TMGGVEINDKSEVLGQD-KKPIEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDTA : 459
Gzea : TMGGIEINDKAQVLNQE-QKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDTA : 459
Sscl : TMGGIEINDAQVLNQE-GKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 459
Pnod : TMGGIEINDQAQVLNSE-GKPFEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSA : 459
Calb : TMGGVKINDKTOVIADN-DSPFEGLYACGEVAGGVHGHNRLLGGSLLACVVYGRVAGDQA : 477
Dhan : TMGGVKINGKTEVLYDD-NEPFNGLYACGEVAGGVHGHNRLLGGSLLACVVYGRVAGDQA : 477
Cneo : TMGGLETGINAAVHNAN-GGEVEGLYACGELAGGVHGANRLGGSLLGCVVYGRVAGDSV : 457
Ccin : TMGGLETDAESRVLGTN-GKPIPLGLFAAGEVAGGVHGANRLGGSLLGCVVYGRVAGDSA : 454
Umay : TMGGLETDPESRVVDNQ-GKPIAGLFAAGEIAGGVHGANRLGGSLLGCVVYGRVAGDSA : 456
Otau : TMGGLETINTDSQIVGPR--GPIPLGLGAGEVAGGVHGHNRLLGGSLLGCVVYGRVAGSAV : 462
Lmaj : TMGGLETINERAQVLDAKTKKPIPLGLYACGEVAGGVHGHNRLLGGSLLGCVVYGRVAGSAV : 522
Scer : TMGGLETINVAQVIGKNDERLLKGLYACGEVAGGVHGANRLGGSLLGCVVYGRVAGSAV : 465

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*          560          *          580          *          600

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Aory : SQHLFQKLVSGGASSA-----AQR LGQISLHTD-----PSTPGKLSV : 498
Anig : SQYLFQKLLSGGASTA-----AQR LGQISLHTD-----PSTPGKLSV : 498
Ater : SQHLFQKLLSGGASSA-----QQR LGQISLHTD-----PATPGKLSV : 498
Afum : SQYLFKKLTSG-STTA-----QQR LGQISLHTD-----PSTPGKLSV : 497
Pchr : SQHLFQKLLANGSSAA-----SQR LGQISLHTD-----PSTPGKLSV : 497
Anid : SEYLFKKLVAGGGSSA-----QQR LGQISLHTD-----PATPGKLSV : 496
Acap : SQYLFQELLSNPSALA-----SRR LNQISLHTD-----PSQPGKLSV : 432
Cimm : SEYLFQQVLSNPGATA-----QSR LNQISLHTD-----PSQPGKLSV : 498
Cglo : SNFLFQQALKGSTG-----AAR LGQIALHTD-----PSTPGKLSV : 494
Ncra : SNYLFQEALKGNAG-----AAR LGQIALHTD-----PSQPGKLSV : 494
Mgri : SNYLFQALSGGAG-A-----AQR LGQISLHTD-----PTQPGKLSV : 495
Gzea : SNYLFQNALKGGAGSA-----AER VQGISLHTD-----PSIPNQVTV : 496
Sscl : SNYLFQNALKGNLS-S-----ASR LGQISLHTD-----PSQPGKLSV : 495
Pnod : SKYLFQQALNSSGGSA-----VNR LGQISLHTD-----PSQPGKLSV : 496
Calb : SSSYKFKHLSFGDGDSIASAS-----QR LKMINLHTD-----PSN-GRIFI : 516
Dhan : SGYLLQKLGAAASNDA SRAAGNAAQESSGSGPV-----SRLQQVNFHTD-----PNHPQRITI : 529
Cneo : SSYLLSSLANTDANVKAA-----KRLGTIINHIVETKIKLDPE SKALQLSFI : 503
Ccin : ASYLLQQTQS--AAVRKAG-----GRLDALAGQL----- : 480
Umay : SSYLLRNLA---TGKAT-----AR LGQISNHL--ETRVRADPNTKTIITIFI : 497
Otau : SRHLMSTAIRALRSG-----QTTAMNRVANLNDKIN----- : 493
Lmaj : TKYLLATYMGFFSN-----NRLNTIYSHLAI----- : 548
Scer : ANDRK----- : 470

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*          620          *          640          *          660
Aory : EWSGA-----AGSGAQIPAGAGTPAAAATEPAKASATPAGASSTA---KANDPKKFEI : 547
Anig : EWGGS-----GAAGGQIAAGAGTPAAAAAQAKSAATPAGAAETA---KPKEPAKFSI : 547
Ater : EWNGA-----AAGGSAPQVAAAAPTAAAAAAPAEAAPAASG-----PKKFEI : 540
Afum : EWNGA-----AASGAGGAQVTAAPAVQTGGQGAPAPAAAAS-----KPNDISNFKI : 544
Pchr : EWGGA-----ATGGSPLAALAAPAAAAAEEAPASKP-----DPANFKV : 536
Anid : EWNGAGAA-----KASGTNPAVSTAPLPANADAPAETS KPPTKA-----PKKFTI : 541
Acap : EWTTPSG-----ASGASTSVQAAPVAATSPSTASAASAKAADG-----AADIANKV : 481
Cimm : EWTAPGD-----GKGQGVQAQISAPKADASATPAPAAASTPAE-----ADISDFKV : 545
Cglo : EWAG-----ASSTEAPK-----AQAVLASVPAAKQES-----SEAKPFAI : 529
Ncra : QWGG-----ESGAQATAN-----TEAPKKDTAAAPPK-----ENPKAFTI : 530
Mgri : EWG-----SGAGAAA-----ASTQSGAGNVAATQAESAKP-----NNPKFKI : 533
Gzea : SWGAPG-----AASGSGAPSKVDEHASVAAGPNPVKEDGAKAAKP-----NDPKAFKV : 544
Sscl : EWDSQS-----SSSGDKVAQQSQT SAGPVMKNGADSSDPGKVS KP-----TKPSEFKI : 543
Pnod : EWGNGVSTSQGATDGQSKVDQKQFSSAPVMSSNADSNDPGKVS KP-----NKPSQFTI : 550
Calb : DTN-GNGGE---GNTASTSTPDNGSSSSAAAPPPPQKKAPKQPK-----PEFSV : 562
Dhan : DWLDSKQDQ---ESSAEQLLQKHNNQQQQPQQQPQQQQEQQQEQSKEKKDNAGPFEI : 586
Cneo : SWGDETGDQNKDAGGAQVPASSAPGQKGDRTAAEIEPEALPTPPAK-----KGS DKG : 556
Ccin : -----GAPSSQPS-----PAAAPT SAAA-----APV GKT : 504
Umay : GFGDQLSST SAAQSQSSAIPAPVASGQ-----PAQTDKAVQQAGSAA-----AAQQTIL : 545
Otau : -----PPAMSAAPAAAASAASGG----- : 510
Lmaj : -----EDLPPVPKAAAPT KPAVAPAASKEAHAGSDASPA-----AAVDGEKHK : 591
Scer : ----- : -

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*          680          *          700          *          720
Aory : PETEYSMEEIAKHNNKDDLLWIVVKGVVLDVTNWLDEHPGGANALFNFMGRDATEEFAMLH : 607
Anig : PEKEYSMEEIAKHNNKDDLLWIVVKGVVLDVTNWLDEHPGGANALFNFMGRDATEEFAMLH : 607
Ater : PETEYSMEEVAKHNNKDDLLWIVVKGVVLDVTNWLDEHPGGANALFNFMGRDATEEFAMLH : 600
Afum : PEKEYTMEEVAKHNNKDDLLWIVVKGVVLDVTNWLDEHPGGANALFNFMGRDATEEFAMLH : 604
Pchr : PETEYTMEEVAKHNSKEDLWVVVKGITLIDL TNVWDEHPGGANALYNFMGRDATEEFAMLH : 596
Anid : PETEYSMEEVAKHNNKDDLLWIVVKGITLIDLVTNWLDEHPGGANALFNFMGRDATEEFAMLH : 601
Acap : PNKEFTMEEVAKHNNKDDLLWIVVKGVVMDVSNWLDEHPGGAQALF SHMGKDATEEFAMLH : 541
Cimm : PEKEFTMEEVAKHNNKDDLLWIVVKGVVMDVSNWLDEHPGGAQALF SHMGKDATEEFAMLH : 605
Cglo : PEKEYTMEEIAKHNNKEDLWVVVKGVVLDL TNWLEEHHPGGQALNFMGRDATEEFAMLH : 589
Ncra : PDKEYTMEEVAKHNNKEDLWVVVKGVVLDL TNWLEEHHPGGVQALNFMGRDATEEFAMLH : 590
Mgri : PEKEFTMEEVAKHNNKDDLLWVVVKGVVMDLSDWLEEHHPGGQALNFMGRDATEEFAMLH : 593
Gzea : PEKEYTMEEIAEHNTKDNVWVVVKGVVLDLSDWLEEHHPGGVQALNFMGRDATEEFAMLH : 604
Sscl : PEKEFTMEEVAKHNNKEDLWVVVKGVVMDVSNWLDEHPGGQALMFMGRDATEEFAMLH : 603
Pnod : PDKEFTSLEEIAKHNNKDDLLWIAVKGITVMDVTNWTDEHPGGQALF SHMGKDATEEFAMLH : 610
Calb : PDKEFTAEEVAQHNNKPGDCWCICIKNVVLDLTPFLGDHPGGKESTANFAGRDATESEFAMLH : 622
Dhan : PSKEFTTEEVAKHNNKEDCWCICIKNVVLDLTPFLKDHPPGGEQSTLNFAGKDATESEFAMLH : 646
Cneo : DKKEYTLEEVAKHNTKEDCWCVVVIGEQVLDVTNFLDHPGGVKA TMLYAGRDATEEFDMIH : 616
Ccin : AEA EYTVVEVAKHNTKDDVWVIIDGQVLDVTNFLADHPGGKATLLYAGRDATEEFNMLH : 564
Umay : EEKEYTMEEVAKHTSEDDVWVVVEGQVLDVNSGFLDDHPGGKATMLYAGRDATEEFLMLH : 605
Otau : GSRALTMDEINKNHTEGDLWVIIEGNVYDLTKFLPDHPGGKATMLFAGKDATEEFNMLH : 570
Lmaj : GLKRYTRAEVAKHNNKESDCWCICIVRGLVNLTEFLPDHPGGKQSVLMYAGGDATKEEDLVH : 651
Scer : ----- : -

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Aory : DDEVIPKYA-AQIVIGRVKGQTPSLEL : 633
 Anig : DDEVIPKYA-GHIVIGRVKGQTP---- : 629
 Ater : DDEVIPKYA-SHIVIGRVKGQKPTLEI : 626
 Afum : DDEVIPKYA-SQIVIGRVKGQTPSLEF : 630
 Pchr : DDEVIPKYA-AQTVIGRVKGQTPSLEL : 622
 Anid : DDEVIPKYA-PHIVIGRVKGQTPSLEY : 627
 Acap : DDEVIPKYA-SHIVIGRVKGQTPSLEY : 567
 Cimm : DDEVIPKYA-SQIVIGRVKGQTPSLKF : 631
 Cglo : DDEVIPKYA-PSQVIGRVKGQKVTLEI : 615
 Ncra : DDEVIPKYA-PEQVIGRVKGQKVTLEV : 616
 Mgri : DDEVIPKYA-PSQVIGRVKGVKPTLEI : 619
 Gzea : DDEVIPKYA-PQQVIGRVKGQEVTLPEP : 630
 Sscl : DDEVIPKYA-ASQVIGRVKGVKPTLEI : 629
 Pnod : DDEVIPKYA-PEIVIGRVKGQEVTLLEY : 636
 Calb : DDDFIPKYV-ANCVLGRLLKGTSELQL : 648
 Dhan : EDNVIVRYA-KSCVLGRLLKGTPELDI : 672
 Cneo : PPNAIAKYA-PDTVIGTIKS----- : 635
 Ccin : DAKVIPRYA-PDTVIGRVKKP----- : 584
 Umay : DRKVIQKYA-ADTVIGRVKA----- : 624
 Otau : PPNVLKKYLSPDAKIGTVLC----- : 590
 Lmaj : QPEVIDKYT-PDAIIGVVSD----- : 670
 Scer : ----- : -

Legend to Supplementary Fig. S2.

Sequence alignment of fumarate reductase-cytochrome b5 fusion proteins.

The following accession numbers were used:

Filamentous ascomycetes:

Aory, *Aspergillus oryzae* (BAE55635); Anig, *Aspergillus niger* (CAL00488); Ater, *Aspergillus terreus* (EAU32005); Afum, *Aspergillus fumigatus* (EAL85317); Pchr, *Penicillium chrysogenum* (Pc12g03090); Anid, *Aspergillus nidulans* (EAA64250); Acap, *Ajellomyces capsulatus* (EDN06793; an incomplete ORF); Cimm, *Coccidioides immitis* (EAS29974); Cglo, *Chaetomium globosum* (EAQ93149); Ncra, *Neurospora crassa* (EAA36475); Mgri, *Magnaporthe grisea* (AAX07713); Gzea, *Gibberella zeae* (EAA76084); Sscl, *Sclerotinia sclerotiorum* (EDO03741) and Pnod, *Phaeosphaeria nodorum* (EAT88472).

Yeast species:

Calb, *Candida albicans* (EAL03566) and Dhan, *Debaryomyces hansenii* (CAG86843)

Basidiomycetes:

Cneo, *Cryptococcus neoformans* (AAW45754); Ccin, *Coprinopsis cinerea okayama* (EAU91547) and Umay, *Ustilago maydis* (EAK85801).

Other sequences:

Otau, the marine alga *Ostreococcus tauri* (CAL56480, minus amino acids 1-24) and Lmaj, the parasite *Leishmania major* (CAJ07044).

Control:

Scer, the short fumarate reductase YEL047c from *Saccharomyces cerevisiae* (NP_010867) that lacks the cytochrome b5 moiety and the putative PTS2 sequence.

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 22 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 13 of the proteins are shown as black letters that are shaded light grey. Putative PTS2 sequences are in red.