Supporting Information Appendix

This file contains the aligned sequences of the c-terminal region of Bud6 from 46 fungi, and is shaded according to evolutionary sequence variation as analyzed with the CONSURF server. Magenta corresponds to the most conserved residues, teal the most variable. Numbering corresponds to that of the input sequence (residues 550-788 of S. cerevisiae Bud6). Organism and additional identifying information for each of the aligned sequences is provided after the alignment. See Fig. 3A in the main text for mapping of sequence conservation onto the Bud6^{core} structure and for further details.

ConSurf Color-Coded MSA

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C5JIM8|C5JIM8_AJEDS_758_999       -EGDAGRARVNAGKKELADESERIVARVDDLQDLVEDLRKDVVTRGVRPL
G8JM94|G8JM94_ERECY_505_740       ASTSSNRVYMEQSQTKLSELSDILLAKVDDLQDIIEGLRKDVAIRGAKPT
C4JTL0|C4JTL0_UNCRE_763_1005      -EGDAGRARINAGKKELADESEKLVARVDDLQDLVEDLRKDVVTRGVRPL
A5DT78|A5DT78_LODEL_567_805       SSQSSNRLYMESCQSKLSDESDKLLTKVDDLQDLMEEVRKDVAQRGVRVG
C0RYR4|C0RYR4_PARBP_747_990       -EGDACRARVNAGKKELADESEKIVARVDDLQDLVEDLRKDVVTRGVRPL
B8LVI6|B8LVI6_TALSN_772_1009      -EGDAGRARINSGKKELSDESERLVGRVDDLQDLVEDLRKDVVSRGVRPL
B2B176|B2B176_PODAN_778_1024      -EGDSGRAYVINGRKQLNTDSDRLVNKVDDLQDLVEDLRKDVVHRGVRPL
A7EXU2|A7EXU2_SCLS1_748_984       --GDSGRSYVNGGKKNLSEDSDKLVAQVDDLQDIVEDLRKDVVQRGVRPL
C5E095|C5E095_ZYGRC_627_861       -KSSSNNRYIETSQNRLSELSDALLSKVDDLQDVIEVLRKDVAVHGVKPS
G0VKP2|G0VKP2_NAUCC_499_733       -KTSANKVYMEKSQAELGEVSDSLLSRVDDLQDLIEVLRKDVADRGAEPS
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Q5BDQ6|Q5BDQ6_EMENI_663_900       -EGDAGRARVNLGKKELAEESERLVARVDDLQDLIEDLRKDVVSRGVRPL
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G8JM94|G8JM94_ERECY_505_740       RKKLDAVQNELKRATEDLGKMEAYINIEKPNWKMIWESELDKVCEEQQFL
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A5DT78|A5DT78_LODEL_567_805       EKQLKYIVKEIQDANKTLQQMSTYITSEKSTWKKIWESELDKVCEEQQFF
C0RYR4|C0RYR4_PARBP_747_990       PRQLEAVGRDISAVSKELKKMQEFLKREKPIWTKIWEKELQLVCEERDQL
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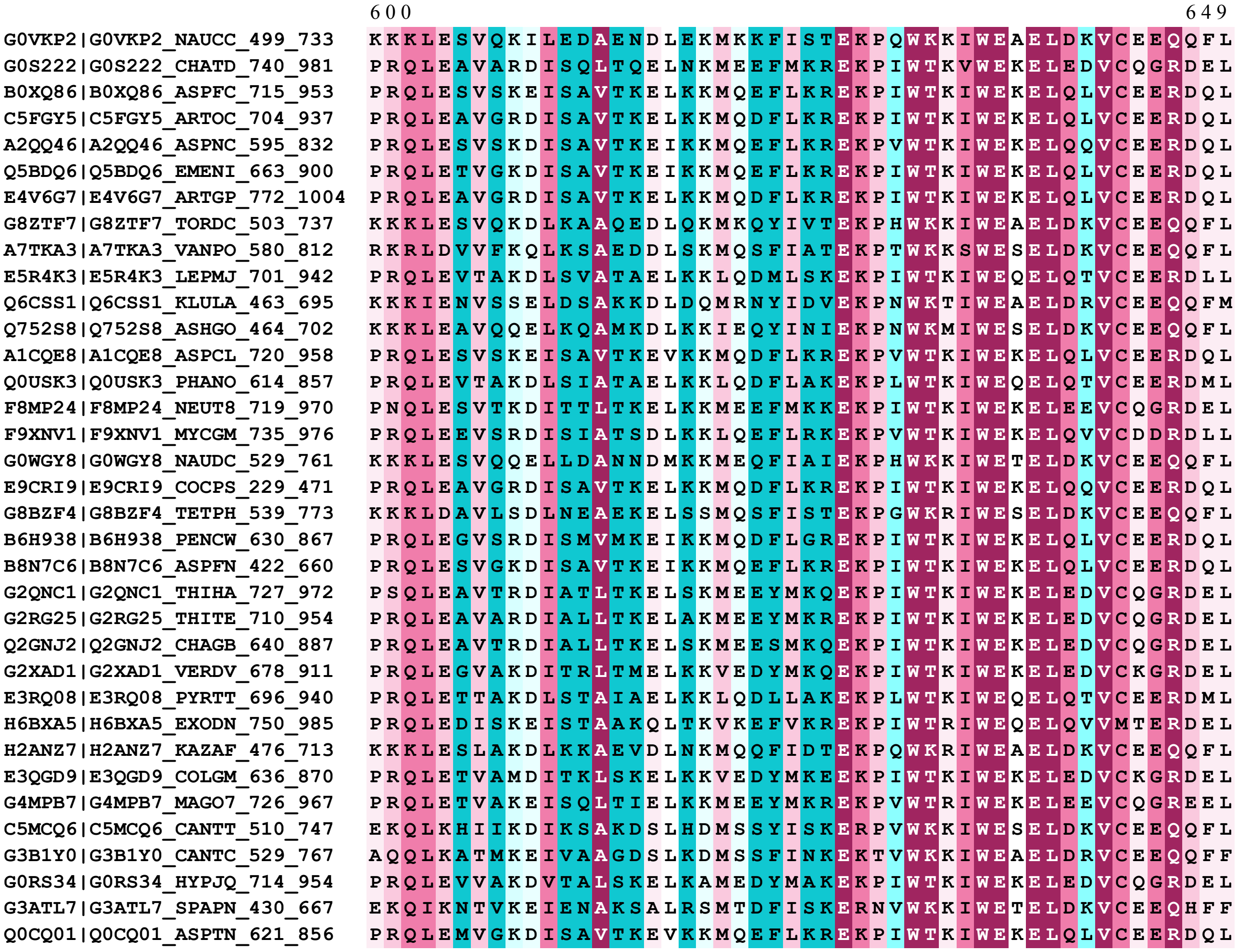

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C5FGY5|C5FGY5_ARTOC_704_937   PRQLEAVGRDISAVTKELKKMQDFLKREKPIWTKIWEKELQLVCEERDQL
A2QQ46|A2QQ46_ASPNC_595_832   PRQLESVSKDISAVTKEIKKMQEFLKREKPVWTKIWEKELQQVCEERDQL
Q5BDQ6|Q5BDQ6_EMENI_663_900   PRQLETVGKDISAVTKEIKKMQEFLKREKPIWTKIWEKELQLVCEERDQL
E4V6G7|E4V6G7_ARTGP_772_1004  PRQLEAVGRDISAVTKELKKMQDFLKREKPIWTKIWEKELQLVCEERDQL
G8ZTF7|G8ZTF7_TORDC_503_737   KKKLESVQKDLKAAQEDLQKMKQYIVTEKPHWKKIWEAELDKVCEEQQFL
A7TKA3|A7TKA3_VANPO_580_812   RKRLDVVFKQLKSAEDDLSKMQSFIATEKPTWKKSWESELDKVCEEQQFL
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F9XNV1|F9XNV1_MYCGM_735_976   PRQLEEVSRDISIATSDLKKLQEFLRKEKPVWTKIWEKELQVVCDDRDLL
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G4MPB7|G4MPB7_MAGO7_726_967   PRQLETVAKEISQLTIELKKMEEYMKREKPVWTRIWEKELEEVCQGREEL
C5MCQ6|C5MCQ6_CANTT_510_747   EKQLKHIIKDIKSAKDSLHDMSSYISKERPVWKKIWESELDKVCEEQQFL
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G3ATL7|G3ATL7_SPAPN_430_667   EKQIKNTVKEIENAKSALRSMTDFISKERNVWKKIWETELDKVCEEQHFF
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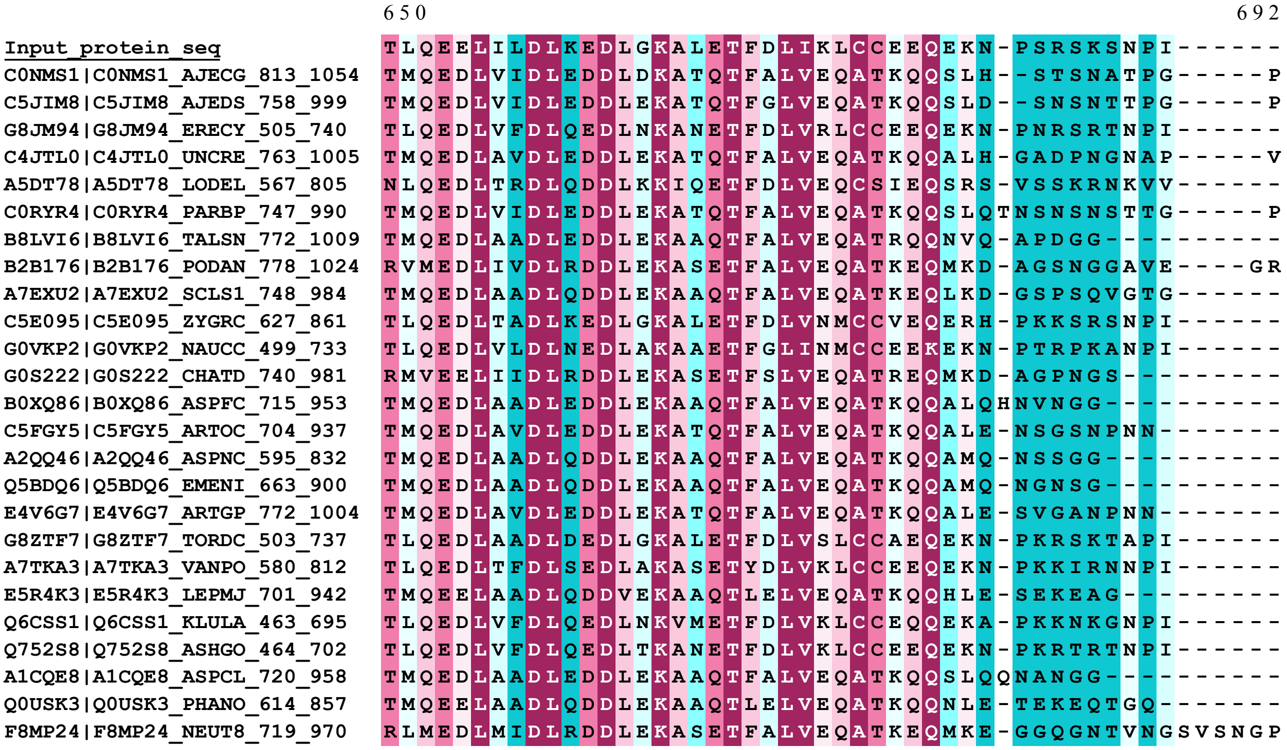

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A5DT78|A5DT78_LODEL_567_805   NLQEDLTRDLQDDLKKIQETFDLVEQCSIEQSRS-VSSKRNKVV------
C0RYR4|C0RYR4_PARBP_747_990   TMQEDLVIDLEDDLEKATQTFALVEQATKQQSLQTNSNSNSTTG-----P
B8LVI6|B8LVI6_TALSN_772_1009  TMQEDLAADLEDDLEKAAQTFALVEQATRQQNVQ-APDGG----------
B2B176|B2B176_PODAN_778_1024  RVMEDLIVDLRDDLEKASETFALVEQATKEQMKD-AGSNGGAVE----GR
A7EXU2|A7EXU2_SCLS1_748_984   TMQEDLAADLQDDLEKAAQTFALVEQATKEQLKD-GSPSQVGTG------
C5E095|C5E095_ZYGRC_627_861   TLQEDLTADLKEDLGKALETFDLVNMCCVEQERH-PKKSRSNPI------
G0VKP2|G0VKP2_NAUCC_499_733   TLQEDLVLDLNEDLAKAAETFGLINMCCEEKEKN-PTRPKANPI------
G0S222|G0S222_CHATD_740_981   RMVEELIIDLRDDLEKASETFSLVEQATREQMKD-AGPNGS---------
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E4V6G7|E4V6G7_ARTGP_772_1004  IAVRNVS-----RT--HN-PNIDPADAKDSVLGEVRALQPNHESRLEAIE
G8ZTF7|G8ZTF7_TORDC_503_737   --------------LPIPKPG-TLNVVRDQLLVEVQSLNPDHESRVEALE
A7TKA3|A7TKA3_VANPO_580_812   --------------LPIPKPG-TMNQVRDQLLVEVQSLNPNHEGRVDALE
E5R4K3|E5R4K3_LEPMJ_701_942   KGTRTASGRNMINAASFD-KAVDPRQARDGVLGEVKALQPNHESRLEAIE
Q6CSS1|Q6CSS1_KLULA_463_695   --------------LPIAKPG-TYNMIRDQVLTEVQNLNPDHDSRVEAIK
Q752S8|Q752S8_ASHGO_464_702   --------------LPLTKPG-TLTDLRDMVLMEVQNLNPDHESRVQAIE
A1CQE8|A1CQE8_ASPCL_720_958   VPLRNTS-----RNVGSG-PAIDPMKAKDGVLGEVRALQPNHESRLEAIE
Q0USK3|Q0USK3_PHANO_614_857   KGLRSASGRNAINAAALD-KVVDPREARDGVLGEVKALQPNHESRLEAIE
F8MP24|F8MP24_NEUT8_719_970   TPFGAFS--RGLKSISEKVTHADPSEAKEGVLGEVRALQPNHQSRLEAIE
F9XNV1|F9XNV1_MYCGM_735_976   TGVRSTS-----RTLVPI-PTADPAKAKDSVLGEVRALQPNHESRLEAIE
G0WGY8|G0WGY8_NAUDC_529_761   --------------LPILKPG-TFTEVRNQLLVDVLSITPDHESRLEAIG
E9CRI9|E9CRI9_COCPS_229_471   VSFRVAS-----RTLPLD-PSIDPVKAKDSVLGEVRALQPNHENRVEAIE
G8BZF4|G8BZF4_TETPH_539_773   --------------LPIPKPG-TLNQTRDQLLVDVQSLVPDHESRVDALE
B6H938|B6H938_PENCW_630_867   TAVRAPS-----RTLGID-PTIDPMKAKDGVLGEVRALQPNHESRLEAIE
B8N7C6|B8N7C6_ASPFN_422_660   VTLRNTS-----RNVVID-PAVDPMKAKDSVLGEVRALQPNHESRLEAIE
G2QNC1|G2QNC1_THIHA_727_972   IAARQFS--KGLNSIRENAALADPSAAKEGVLGEVRALQPNHENRLEAIE
G2RG25|G2RG25_THITE_710_954   ITARQFS--KGLNSIRDN-ALVDPTAAKEGVLGEVRALQPNHENRLEAIE
Q2GNJ2|Q2GNJ2_CHAGB_640_887   IVARQFS--KGLTSIRENAAAVDPNTAKEGVLGEVRALQPNHENRLEAIE
G2XAD1|G2XAD1_VERDV_678_911   --ARNFS--KGLNSLG---NSLDQNAAKEGVLGEVRALMPNHEDRLEAIE
E3RQ08|E3RQ08_PYRTT_696_940   GGMRSASGRNMLNAVAID-KVVDPRQARDGVLGEVKALQPNHEGRLEAIE
H6BXA5|H6BXA5_EXODN_750_985   ---------QGLKQLPFD-TDVDPHEAKSGMLDEVRALQPNHESRLEAIE
H2ANZ7|H2ANZ7_KAZAF_476_713   --------------LPILKPG-TFGQVREQVMLAVQSINPNYDSRIDALE
E3QGD9|E3QGD9_COLGM_636_870   --ARNFS--KGLNNLG---NSSDPNAAKDGVLGEVRALQPNHENRLEAIE
G4MPB7|G4MPB7_MAGO7_726_967   GVLRQFS--RGLENIGNN-AFVDPSAAKEGVLGEVRALQPNHENRLEAIE
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                              693                                              727
C5MCQ6|C5MCQ6_CANTT_510_747   ------------ANLYIPEPGESLHTAKDAVLNDIAALTPNHESRVEAIE
G3B1Y0|G3B1Y0_CANTC_529_767   ------------ANLPIPEPGENLHSIKDAVLSEVAALKPDHESRVDAIN
G0RS34|G0RS34_HYPJQ_714_954   --VRTFS--KGLNNLG---NSLDQNAAKEDMLGEVRALQPNHQDRLEAIE
G3ATL7|G3ATL7_SPAPN_430_667   ------------ANLYIPEPGESLHDIKDAVLNEVVALVPDHQSRVEAIE
Q0CQ01|Q0CQ01_ASPTN_621_856   VTLRNVS-----RN--ID-PSVDPLKAKDNVLGEVRALQPDHESRLEAIE
```

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                               728                                             776
Input_protein_seq              KAEKMWEMERKLKASNEFDDELENFVGNSNLKKS-GGFEEVERIRKQKDE
C0NMS1|C0NMS1_AJECG_813_1054   RAEKAREKELESRRIGPLQKELGKFVEEGKLKKS-GGFEEIERMRKAKDE
C5JIM8|C5JIM8_AJEDS_758_999    RAEKARQKELETRRVGPLQKELGKFVEEGKLKKS-GGFEEIERMRKAKED
G8JM94|G8JM94_ERECY_505_740    RAEKLREKELQYKDGNAFELELEDFVGSGAFKRA-GGIEEVERLRKERDE
C4JTL0|C4JTL0_UNCRE_763_1005   RAEKARQKELENRRVGKFQKELGAFVQQGKLKKS-GGFEEAERLRKAKDE
A5DT78|A5DT78_LODEL_567_805    RAEKLRQRERELARNDKFQEELGDFVEDGKLKKS-GGIEEIENMRKQRDQ
C0RYR4|C0RYR4_PARBP_747_990    RAEKARQKELKTRRVGPLQKELGKFVEEGKLKKS-GGFEEVERMRKAKDE
B8LVI6|B8LVI6_TALSN_772_1009   RAEKARQKELESRRVGLFQKELGQFVEEGKLKKS-GGFEETERLRRAKDE
B2B176|B2B176_PODAN_778_1024   RAEKLRQKELETRMQNPLKKELTNFVEEGRLKKS-GGVEEVERARKAKEE
A7EXU2|A7EXU2_SCLS1_748_984    RAEKLRQKELEGRRGNVLQKELTQFVEEGKLKKS-GGFEEVERQRIAKDA
C5E095|C5E095_ZYGRC_627_861    RAQKMWEREREYRDTDAFEDELGNFVEKGNLKTA-GGVEEVERIRKQKDE
G0VKP2|G0VKP2_NAUCC_499_733    KAQRLWQKEKEFKDGDEFEDELGNFVGNSNLKKS-GGVEEVERLRRQRDE
G0S222|G0S222_CHATD_740_981    RAEKARQKELERRMENPLKKELISFVEEGRLKKS-GGVEEVERARKAKDD
B0XQ86|B0XQ86_ASPFC_715_953    RAEKARQKELENRRIGLFQKELGAFVQEGKLKKS-GGVEEAERQRRVKDD
C5FGY5|C5FGY5_ARTOC_704_937    RAEKARQRELESRRGGEFQRELSNFVGAGKLKSNGGGFEELERVRKEKEE
A2QQ46|A2QQ46_ASPNC_595_832    RAEKARQKELETRRIGLFQKELGAFVEEGKLKKS-GGVEEAERLRRAKDD
Q5BDQ6|Q5BDQ6_EMENI_663_900    RAEKARQKELETRRVDLFQKELGTFVQEGKLKKS-GGFEEAERLRRAKDE
E4V6G7|E4V6G7_ARTGP_772_1004   RAEKARQRELESRRGGEFQKELSSFVGANKLKNT-GGFEELERVRKEKEE
G8ZTF7|G8ZTF7_TORDC_503_737    RAEKLWLKEREYRDNGEFEEELGHFVEKSSFKRS-GGVEEVERLRRQKDE
A7TKA3|A7TKA3_VANPO_580_812    KAQKLWQIEREYRDTDEFEDELGSFVEKSNFKKS-GGIEEIERLRREKDE
E5R4K3|E5R4K3_LEPMJ_701_942    RAEKARQRELETRNDDEFKRELGSFVEEGKLKKS-GGVEEVERMRKAKDE
Q6CSS1|Q6CSS1_KLULA_463_695    KAEKLRNREKEYKENEAFEDELGNFVEKGNFKKA-GGIEEIERLRKQKDE
Q752S8|Q752S8_ASHGO_464_702    RAEKLREKELQYKDSSVFESELVNFVGNNGFKRA-GGIEEVERIRRARDE
A1CQE8|A1CQE8_ASPCL_720_958    RAEKARQRELENRRIGLFQKELGAFVEEGKLKKS-GGVEEAERQRRVKDD
Q0USK3|Q0USK3_PHANO_614_857    RAEKARQRELATRNDDEFKRELGNFVEEGKLKKS-GGVEEVERLRKAKDE
F8MP24|F8MP24_NEUT8_719_970    RAEKLRQKELQTRMVNPLTKELASFVEEGKLKKS-GGVEEVERARKAKDD
F9XNV1|F9XNV1_MYCGM_735_976    RAERLRQRELETRREGEFQKELGNFVEEGKLKKS-GGVEEVERQRKSRED
G0WGY8|G0WGY8_NAUDC_529_761    KAEKLWQKEREYRAGDEFQDELGDFVEKSALKKS-GGVEEVERLREQKNR
E9CRI9|E9CRI9_COCPS_229_471    RAEKARQKELESRRIGQFQKELGAFVEGGKLKKS-GGFEEAERLRKAKDE
G8BZF4|G8BZF4_TETPH_539_773    KAQKIWQKERILKENDEFQEELGTFVGNASFKKT-GGIEEIERIRQQKNE
B6H938|B6H938_PENCW_630_867    RAEKARKKELETRRIGLFQKELGAFVEEGKLKKS-GGFEETERLRTAKDD
B8N7C6|B8N7C6_ASPFN_422_660    RAEKARQKELENRRIGLFQKELGAFVEEGKLKKS-GGVEETERLRRAKDD
G2QNC1|G2QNC1_THIHA_727_972    RAEKLRQKELERRRENPLTKELASFVEEGKLKKS-GGVEEVERARKAKDE
G2RG25|G2RG25_THITE_710_954    RAEKLRQKELERRRENPLKQELVSFVEEGKLKKS-GGVEEVERARKAKDD
Q2GNJ2|Q2GNJ2_CHAGB_640_887    RAEKLRQKELARRRENPLTKELATFVEEGKLKKS-GGVEEVERARKAKDD
G2XAD1|G2XAD1_VERDV_678_911    RAEKLRQRELATRNTNKLQQELTNFVEEGRLKKS-GGFEEVERARTAKDE
E3RQ08|E3RQ08_PYRTT_696_940    RAEKARQRDLETRNDDEFKRELGTFVEEGKLKKS-GGVEEAERLRKAKDE
H6BXA5|H6BXA5_EXODN_750_985    RAAKVRQRELESRRVGEFQREVEKFVEEGKLKKT-GGMDEVERRRKLKDE
H2ANZ7|H2ANZ7_KAZAF_476_713    KAEKLWEKEKQYKEDTAFRDELGRFVESSSLKKS-GGVEEIEKVRKQKDE
E3QGD9|E3QGD9_COLGM_636_870    RAEKLRQKELEGRKGNELQRELSSFVEEGKLKKS-GGFEEVERARKAKDD
G4MPB7|G4MPB7_MAGO7_726_967    RAEKLRQKELETRKGNALTKEITAFVGEGKLKKS-GGFEEVERARKAMDD
C5MCQ6|C5MCQ6_CANTT_510_747    RAEKIREKEREMMRLNKFQEELGDFVEDNRLKKS-GGIEELEKARQIKDS
G3B1Y0|G3B1Y0_CANTC_529_767    KAEKLRQKNKQMMDLTEFQEELGSFIDDSKLRKS-GGIDEIERQRQLKDS
G0RS34|G0RS34_HYPJQ_714_954    RAEKLRQKELKTRTTNPLHREMKAFVSEGKLKKS-GGFEEVERARLAKDE
G3ATL7|G3ATL7_SPAPN_430_667    RAEKLREKEREMMKLNQFQEELGDFVEDKKLKKS-GGIAEVEKMRSQKDS
Q0CQ01|Q0CQ01_ASPTN_621_856    RAEKARQKELENRRIGLFQKELGSFVQEGKLKKS-GGVEETERLRRAKDD
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                               777     788
Input_protein_seq              ANLRAYFGPGFT
C0NMS1|C0NMS1_AJECG_813_1054   RIRKEVW-----
C5JIM8|C5JIM8_AJEDS_758_999    RIRKEVW-----
G8JM94|G8JM94_ERECY_505_740    QNLRQNFG---G
C4JTL0|C4JTL0_UNCRE_763_1005   KIRKEAW-----
A5DT78|A5DT78_LODEL_567_805    ENLKSSFG---I
```

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                              7 7 7               7 8 8

C0RYR4|C0RYR4_PARBP_747_990   R I R K E V W - - - - -
B8LVI6|B8LVI6_TALSN_772_1009  R I R K E V W - - - - -
B2B176|B2B176_PODAN_778_1024  R I R R E V W - - - - -
A7EXU2|A7EXU2_SCLS1_748_984   R I R R E V W - - - - -
C5E095|C5E095_ZYGRC_627_861   N N L R A Y F G - - - G
G0VKP2|G0VKP2_NAUCC_499_733   E N L R A N F G - - - G
G0S222|G0S222_CHATD_740_981   Q I R R Q V W - - - - -
B0XQ86|B0XQ86_ASPFC_715_953   R I R K E V W - - - - -
C5FGY5|C5FGY5_ARTOC_704_937   S I R K E V W - - - - -
A2QQ46|A2QQ46_ASPNC_595_832   R I R K E V W - - - - -
Q5BDQ6|Q5BDQ6_EMENI_663_900   R N R K E M W - - - - -
E4V6G7|E4V6G7_ARTGP_772_1004  S I R R E V W - - - - -
G8ZTF7|G8ZTF7_TORDC_503_737   E N L R A N F G - - - G
A7TKA3|A7TKA3_VANPO_580_812   E N L R T T F G - - - -
E5R4K3|E5R4K3_LEPMJ_701_942   R A R K E N - - - - - -
Q6CSS1|Q6CSS1_KLULA_463_695   E N L R V N F G - - - -
Q752S8|Q752S8_ASHGO_464_702   E N L R S N F G L G A S
A1CQE8|A1CQE8_ASPCL_720_958   R I R K E V W - - - - -
Q0USK3|Q0USK3_PHANO_614_857   R A R K E N - - - - - -
F8MP24|F8MP24_NEUT8_719_970   R I R R E V W - - - - -
F9XNV1|F9XNV1_MYCGM_735_976   R T R K E I W - - - - -
G0WGY8|G0WGY8_NAUDC_529_761   E N L R A N F - - - - -
E9CRI9|E9CRI9_COCPS_229_471   K I R K E V W - - - - -
G8BZF4|G8BZF4_TETPH_539_773   E N L R A G L G - - - I
B6H938|B6H938_PENCW_630_867   R I R K E V W - - - - -
B8N7C6|B8N7C6_ASPFN_422_660   R I R R E V W - - - - -
G2QNC1|G2QNC1_THIHA_727_972   R I R R E V W - - - - -
G2RG25|G2RG25_THITE_710_954   R I R R E V W - - - - -
Q2GNJ2|Q2GNJ2_CHAGB_640_887   R I R R E V W - - - - -
G2XAD1|G2XAD1_VERDV_678_911   R I R R E V W - - - - -
E3RQ08|E3RQ08_PYRTT_696_940   R A R K E N F - - - - -
H6BXA5|H6BXA5_EXODN_750_985   A A R K E N W - - - - -
H2ANZ7|H2ANZ7_KAZAF_476_713   E N L R A V F G - T N I
E3QGD9|E3QGD9_COLGM_636_870   M I R K Q V W - - - - -
G4MPB7|G4MPB7_MAGO7_726_967   K I R R E V W - - - - -
C5MCQ6|C5MCQ6_CANTT_510_747   E N L K S S F G - - - I
G3B1Y0|G3B1Y0_CANTC_529_767   E N L K S S M G - - - G
G0RS34|G0RS34_HYPJQ_714_954   K I R R E V W - - - - -
G3ATL7|G3ATL7_SPAPN_430_667   E N L K S S F G - - - I
Q0CQ01|Q0CQ01_ASPTN_621_856   R I R K E V W - - - - -
```

1	2	3	4	5	6	7	8	9

Variable Average Conserved

X - Insufficient data - the calculation for this site was performed on less than 10% of the sequences.

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>Input_protein_seq
AKNSSNRMYMEKSQTELGDLSDTLLSKVDDLQDVIEIMRKDVAERRSQPAKKKLETVSKDLENAQADVLKLQEFIDTEKPHWKKTWEAELDKVCEEQQFL
TLQEELILDLKEDLGKALETFDLIKLCCEEQEKNPSRSKSNPILPIMRPGTFNQVREQVMVAVQSLNPDHDSRVEAIDKAEKMWEMERKLKASNEFDDEL
ENFVGNSNLKKSGGFEEVERIRKQKDEANLRAYFGPGFT
> C0NMS1 | C0NMS1_AJECG_813_1054 | SubName: Full=Bud site selection protein; - Ajellomyces
capsulata (strain G186AR / H82 / ATCC MYA-2454 / RMSCC 2432) (Darling's disease fungus)
(Histoplasma capsulatum)
EGDAGRARVNAGKKELADESERIVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEAVGRDIGAVSKELNKMKEFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLVIDLEDDLDKATQTFALVEQATKQQSLHSTSNATPGPNGLRNVSRNFPVDEPFDPMKAKDHLLGEVRALQPNHENRLEAIERAEKAREKELESRR
IGPLQKELGKFVEEGKLKKSGGFEEIERMRKAKDERIRKEVW
> C5JIM8 | C5JIM8_AJEDS_758_999 | SubName: Full=Actin-interacting protein; - Ajellomyces
dermatitidis (strain SLH14081) (Blastomyces dermatitidis)
EGDAGRARVNAGKKELADESERIVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEAVGRDISAVTKELKKMQEFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLVIDLEDDLEKATQTFGLVEQATKQQSLDSNSNTTPGPHGLRNVSRNFPIDEPLDPMKAKDYLLGEVRALQPNHENRLEAIERAEKARQKELETRR
VGPLQKELGKFVEEGKLKKSGGFEEIERMRKAKEDRIRKEVW
> G8JM94 | G8JM94_ERECY_505_740 | SubName: Full=Putative uncharacterized protein; - Eremothecium
cymbalariae (strain CBS 270.75 / DBVPG 7215 / KCTC 17166 / NRRL Y-17582) (Yeast)
ASTSSNRVYMEQSQTKLSELSDILLAKVDDLQDIIEGLRKDVAIRGAKPTRKKLDAVQNELKRATEDLGKMEAYINIEKPNWKMIWESELDKVCEEQQFL
TLQEDLVFDLQEDLNKANETFDLVRLCCEEQEKNPNRSRTNPILPLVKPGTMNELRDRLLSEVQSLNPDHESRVQAIQRAEKLREKELQYKDGNAFELEL
EDFVGSGAFKRAGGIEEVERLRKERDEQNLRQNFGG
> C4JTL0 | C4JTL0_UNCRE_763_1005 | SubName: Full=Putative uncharacterized protein; - Uncinocarpus
reesii (strain UAMH 1704)
EGDAGRARINAGKKELADESEKLVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEAVGRDISAVTKELKKMQDFLRREKPIWTKIWEKELQQVCEERDQLT
MQEDLAVDLEDDLEKATQTFALVEQATKQQALHGADPNGNAPVPGFRVPSRTLPPDAAIDPVKAKDSVLGEVRALQPNHENRVEAIERAEKARQKELENR
RVGKFQKELGAFVQQGKLKKSGGFEEAERLRKAKDEKIRKEAW
> A5DT78 | A5DT78_LODEL_567_805 | SubName: Full=Putative uncharacterized protein; - Lodderomyces
elongisporus (strain ATCC 11503 / CBS 2605 / JCM 1781 / NBRC 1676 / NRRL YB-4239) (Yeast)
(Saccharomyces elongisporus)
SSQSSNRLYMESCQSKLSDESDKLLTKVDDLQDLMEEVRKDVAQRGVRVGEKQLKYIVKEIQDANKTLQQMSTYITSEKSTWKKIWESELDKVCEEQQFF
NLQEDLTRDLQDDLKKIQETFDLVEQCSIEQSRSVSSKRNKVVANIPIPEPGESLHNIKDQVLVDIIQLKPDHESRVEAIERAEKLRQRERELARNDKFQ
EELGDFVEDGKLKKSGGIEEIENMRKQRDQENLKSSFGI
> C0RYR4 | C0RYR4_PARBP_747_990 | SubName: Full=Bud site selection protein; - Paracoccidioides
brasiliensis (strain Pb03)
EGDACRARVNAGKKELADESEKIVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEAVGRDISAVSKELKKMQEFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLVIDLEDDLEKATQTFALVEQATKQQSLQTNSNSNSTTGPQGFRAVSRNIPANEPFDPMKAKDHLLGEVRALLPNHKDRLEAIERAEKARQKELKT
RRVGPLQKELGKFVEEGKLKKSGGFEEVERMRKAKDERIRKEVW
> B8LVI6 | B8LVI6_TALSN_772_1009 | SubName: Full=Actin-interacting protein (Bud6/Aip3), putative; -
Talaromyces stipitatus (strain ATCC 10500 / CBS 375.48 / QM 6759 / NRRL 1006) (Penicillium
stipitatum)
EGDAGRARINSGKKELSDESERLVGRVDDLQDLVEDLRKDVVSRGVRPLPRQLEAVSKDISTVTKEVKKMQDFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLAADLEDDLEKAAQTFALVEQATRQQNVQAPDGGPVLRSTSRTLAIDQGVDPVKAKDGVLGEVRALQPNHESRLEAIERAEKARQKELESRRVGLF
QKELGQFVEEGKLKKSGGFEETERLRRAKDERIRKEVW
> B2B176 | B2B176_PODAN_778_1024 | SubName: Full=Predicted CDS Pa_3_9560; - Podospora anserina
(strain S / ATCC MYA-4624 / DSM 980 / FGSC 10383) (Pleurage anserina)
EGDSGRAYVINGRKQLNTDSDRLVNKVDDLQDLVEDLRKDVVHRGVRPLPRQLESVTKDITQLTKELNKMEEYMKQEKPVWTKIWEKELEDVCQGRDELR
VMEDLIVDLRDDLEKASETFALVEQATKEQMKDAGSNGGAVEGRPVLRQFSKGLNSINSNAFVDPRDAKEGVLGEVRALQPNHENRLEAIERAEKLRQKE
LETRMQNPLKKELTNFVEEGRLKKSGGVEEVERARKAKEERIRREVW
> A7EXU2 | A7EXU2_SCLS1_748_984 | SubName: Full=Putative uncharacterized protein; - Sclerotinia
sclerotiorum (strain ATCC 18683 / 1980 / Ss-1) (White mold) (Whetzelinia sclerotiorum)
GDSGRSYVNGGKKNLSEDSDKLVAQVDDLQDIVEDLRKDVVQRGVRPLPKQLETVAKDISQATMELKRMQDFLKRERPIWTKIWEKELETVCNDREEITM
QEDLAADLQDDLEKAAQTFALVEQATKEQLKDGSPSQVGTGRSLSKLNRIDPIDPAMAKEGVLDEVRALQPNHENRLEAIERAEKLRQKELEGRRGNVLQ
KELTQFVEEGKLKKSGGFEEVERQRIAKDARIRREVW
> C5E095 | C5E095_ZYGRC_627_861 | SubName: Full=ZYRO0G10868p; - Zygosaccharomyces rouxii (strain
ATCC 2623 / CBS 732 / NBRC 1130 / NCYC 568 / NRRL Y-229) (Candida mogii)
KSSSNNRYIETSQNRLSELSDALLSKVDDLQDVIEVLRKDVAVHGVKPSKKKLDSVQKELVLAENDLSMMQMFMQNEKPQWKKIWKAELEKVCEEQQFLT
LQEDLTADLKEDLGKALETFDLVNMCCVEQERHPKKSRSNPILPIPEPGTFHRVRDQVLNEVQALNPDHNERIEALERAQKMWEREREYRDTDAFEDELG
NFVEKGNLKTAGGVEEVERIRKQKDENNLRAYFGG
> G0VKP2 | G0VKP2_NAUCC_499_733 | SubName: Full=Uncharacterized protein; - Naumovozyma castellii
(strain ATCC 76901 / CBS 4309 / NBRC 1992 / NRRL Y-12630) (Yeast) (Saccharomyces castellii)
KTSANKVYMEKSQAELGEVSDSLLSRVDDLQDLIEVLRKDVADRGAEPSKKKLESVQKILEDAENDLEKMKKFISTEKPQWKKIWEAELDKVCEEQQFLT
LQEDLVLDLNEDLAKAAETFGLINMCCEEKEKNPTRPKANPILPILKPGTFHQVRDQMLMAVESINPDHESRLKALDKAQRLWQKEKEFKDGDEFEDELG
NFVGNSNLKKSGGVEEVERLRRQRDEENLRANFGG
> G0S222 | G0S222_CHATD_740_981 | SubName: Full=Putative uncharacterized protein; - Chaetomium
thermophilum (strain DSM 1495 / CBS 144.50 / IMI 039719)
EGDSGRAYVMNGRKRLNADSDRLVNKVDDLQDAVEDLRKDVVHRGVRPLPRQLEAVARDISQLTQELNKMEEFMKREKPIWTKVWEKELEDVCQGRDELR
MVEELIIDLRDDLEKASETFSLVEQATREQMKDAGPNGSIVPRQGAFGKPLFSNNAFIDPASAKEGVLGEVRALQPDHASRLEAIERAEKARQKELERRM
ENPLKKELISFVEEGRLKKSGGVEEVERARKAKDDQIRRQVW
> B0XQ86 | B0XQ86_ASPFC_715_953 | SubName: Full=Actin-interacting protein (Bud6/Aip3), putative; -
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Neosartorya fumigata (strain CEA10 / CBS 144.89 / FGSC A1163) (Aspergillus fumigatus)
EGDAGRARVNAGKKELADESERLVGRVDDLQDLVEDLRKDVVSRGVRPLPRQLESVSKEISAVTKELKKMQEFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLAADLEDDLEKAAQTFALVEQATKQQALQHNVNGGVALRNTSRNVVIDPAVDPMKAKDDVLGEVRALQPNHESRLEAIERAEKARQKELENRRIGL
FQKELGAFVQEGKLKKSGGVEEAERQRRVKDDRIRKEVW
> C5FGY5 | C5FGY5_ARTOC_704_937 | SubName: Full=YlBUD6; - Arthroderma otae (strain ATCC MYA-4605 /
CBS 113480) (Microsporum canis)
ARVQAGKKELADESEKLVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEAVGRDISAVTKELKKMQDFLKREKPIWTKIWEKELQLVCEERDQLTMQEDLA
VDLEDDLEKATQTFALVEQATKQQALENSGSNPNNVAVRTVSRTMNPHIDPADAKDSVLGEVRALQPNHESRLEAIERAEKARQRELESRRGGEFQRELS
NFVGAGKLKSNGGGFEELERVRKEKEESIRKEVW
> A2QQ46 | A2QQ46_ASPNC_595_832 | SubName: Full=Putative uncharacterized protein An08g01240; Flags:
Precursor; - Aspergillus niger (strain CBS 513.88 / FGSC A1513)
EGDAGRVRVNSGKKELAEESERLVARVDDLQDLVEDLRKDVVTRGVRPLPRQLESVSKDISAVTKEIKKMQEFLKREKPVWTKIWEKELQQVCEERDQLT
MQEDLAADLQDDLEKAAQTFALVEQATKQQAMQNSSGGPTLRNTSRNVVIDPAVDPMKAKDSVLGEVRALQPNHESRLEAIERAEKARQKELETRRIGLF
QKELGAFVEEGKLKKSGGVEEAERLRRAKDDRIRKEVW
> Q5BDQ6 | Q5BDQ6_EMENI_663_900 | SubName: Full=Polarisome component BudA (Eurofung); - Emericella
nidulans (strain FGSC A4 / ATCC 38163 / CBS 112.46 / NRRL 194 / M139) (Aspergillus nidulans)
EGDAGRARVNLGKKELAEESERLVARVDDLQDLIEDLRKDVVSRGVRPLPRQLETVGKDISAVTKEIKKMQEFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLAADLQDDLEKAAQTFALVEQATKQQAMQNGNSGPTLRNTSRNVVIDPAVDPMKAKDSVLGEVRALQPNHESRLEAIERAEKARQKELETRRVDLF
QKELGTFVQEGKLKKSGGFEEAERLRRAKDERNRKEMW
> E4V6G7 | E4V6G7_ARTGP_772_1004 | SubName: Full=Bud site selection protein 6; - Arthroderma
gypseum (strain ATCC MYA-4604 / CBS 118893) (Microsporum gypseum)
ARVQAGKKELADESEKLVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEAVGRDISAVTKELKKMQDFLKREKPIWTKIWEKELQLVCEERDQLTMQEDLA
VDLEDDLEKATQTFALVEQATKQQALESVGANPNNIAVRNVSRTHNPNIDPADAKDSVLGEVRALQPNHESRLEAIERAEKARQRELESRRGGEFQKELS
SFVGANKLKNTGGFEELERVRKEKEESIRREVW
> G8ZTF7 | G8ZTF7_TORDC_503_737 | SubName: Full=Putative uncharacterized protein TDEL0D03170; -
Torulaspora delbrueckii (strain ATCC 10662 / CBS 1146 / NBRC 0425 / NCYC 2629 / NRRL Y-866) (Yeast)
(Candida colliculosa)
AASSNRAYMDKSQSQLGEESDALLSRVDDLQDLIEILRKDVAARGAKPSKKKLESVQKDLKAAQEDLQKMKQYIVTEKPHWKKIWEAELDKVCEEQQFLT
LQEDLAADLDEDLGKALETFDLVSLCCAEQEKNPKRSKTAPILPIPKPGTLNVVRDQLLVEVQSLNPDHESRVEALERAEKLWLKEREYRDNGEFEEELG
HFVEKSSFKRSGGVEEVERLRRQKDEENLRANFGG
> A7TKA3 | A7TKA3_VANPO_580_812 | SubName: Full=Putative uncharacterized protein; - Vanderwaltozyma
polyspora (strain ATCC 22028 / DSM 70294) (Kluyveromyces polysporus)
NSSDRSYMEKSQTKLGDISDSLLTRVDDLQDVIEVLRKDVADRGVKPTRKRLDVVFKQLKSAEDDLSKMQSFIATEKPTWKKSWESELDKVCEEQQFLTL
QEDLTFDLSEDLAKASETYDLVKLCCEEQEKNPKKIRNNPILPIPKPGTMNQVRDQLLVEVQSLNPNHEGRVDALEKAQKLWQIEREYRDTDEFEDELGS
FVEKSNFKKSGGIEEIERLRREKDEENLRTTFG
> E5R4K3 | E5R4K3_LEPMJ_701_942 | SubName: Full=Putative uncharacterized protein; - Leptosphaeria
maculans (strain JN3 / isolate v23.1.3 / race Av1-4-5-6-7-8) (Blackleg fungus) (Phoma lingam)
GDSGRAYINAGKKTLQEDSEKIVNRVDDLQDLIEDLRKDVVMRGVRPLPRQLEVTAKDLSVATAELKKLQDMLSKEKPIWTKIWEQELQTVCEERDLLTM
QEELAADLQDDVEKAAQTLELVEQATKQQHLESEKEAGKGTRTASGRNMINAASFDKAVDPRQARDGVLGEVKALQPNHESRLEAIERAEKARQRELETR
NDDEFKRELGSFVEEGKLKKSGGVEEVERMRKAKDERARKEN
> Q6CSS1 | Q6CSS1_KLULA_463_695 | SubName: Full=KLLA0C18359p; - Kluyveromyces lactis (strain ATCC
8585 / CBS 2359 / DSM 70799 / NBRC 1267 / NRRL Y-1140 / WM37) (Yeast) (Candida sphaerica)
KSANRDYMEKSQSKLSEVSDNLLSKVDDLQDVIEALRKDVAIRGARTPKKKIENVSSELDSAKKDLDQMRNYIDVEKPNWKTIWEAELDRVCEEQQFMTL
QEDLVFDLQEDLNKVMETFDLVKLCCEQQEKAPKKNKGNPILPIAKPGTYNMIRDQVLTEVQNLNPDHDSRVEAIKKAEKLRNREKEYKENEAFEDELGN
FVEKGNFKKAGGIEEIERLRKQKDEENLRVNFG
> Q752S8 | Q752S8_ASHGO_464_702 | SubName: Full=AFR495Cp; - Ashbya gossypii (strain ATCC 10895 /
CBS 109.51 / FGSC 9923 / NRRL Y-1056) (Yeast) (Eremothecium gossypii)
ASTSANRVYMEQSHSKLSELSDSLLAKVDDLQDIIEALRKDVAIRGAKPTKKKLEAVQQELKQAMKDLKKIEQYINIEKPNWKMIWESELDKVCEEQQFL
TLQEDLVFDLQEDLTKANETFDLVKLCCEEQEKNPKRTRTNPILPLTKPGTLTDLRDMVLMEVQNLNPDHESRVQAIERAEKLREKELQYKDSSVFESEL
VNFVGNNGFKRAGGIEEVERIRRARDEENLRSNFGLGAS
> A1CQE8 | A1CQE8_ASPCL_720_958 | SubName: Full=Actin-interacting protein (Bud6/Aip3), putative; -
Aspergillus clavatus (strain ATCC 1007 / CBS 513.65 / DSM 816 / NCTC 3887 / NRRL 1)
EGDAGRSRVNSGKKELADESERLVGRVDDLQDLVEDLRKDVVSRGVRPLPRQLESVSKEISAVTKEVKKMQDFLKREKPVWTKIWEKELQLVCEERDQLT
MQEDLAADLEDDLEKAAQTFALVEQATKQQSLQQNANGGVPLRNTSRNVGSGPAIDPMKAKDGVLGEVRALQPNHESRLEAIERAEKARQRELENRRIGL
FQKELGAFVEEGKLKKSGGVEEAERQRRVKDDRIRKEVW
> Q0USK3 | Q0USK3_PHANO_614_857 | SubName: Full=Putative uncharacterized protein; - Phaeosphaeria
nodorum (strain SN15 / ATCC MYA-4574 / FGSC 10173) (Glume blotch fungus) (Septoria nodorum)
GDTGRAYINTGKKSLQDDSEKIVNRVDDLQDLVEDLRKDVVQRGVRPLPRQLEVTAKDLSIATAELKKLQDFLAKEKPLWTKIWEQELQTVCEERDMLTM
QEELAADLQDDLEKAAQTLELVEQATKQQNLETEKEQTGQKGLRSASGRNAINAAALDKVVDPREARDGVLGEVKALQPNHESRLEAIERAEKARQRELA
TRNDDEFKRELGNFVEEGKLKKSGGVEEVERLRKAKDERARKEN
> F8MP24 | F8MP24_NEUT8_719_970 | SubName: Full=Putative uncharacterized protein; - Neurospora
tetrasperma (strain FGSC 2508 / ATCC MYA-4615 / P0657)
EGDSGRAYVTKGRKLLNADSDWLVNKVDDLQDLIEDLRKDVVHRGVRPRPNQLESVTKDITTLTKELKKMEEFMKKEKPIWTKIWEKELEEVCQGRDELR
LMEDLMIDLRDDLEKASETFALVEQATKEQMKEGGQGNTVNGSVSNGPTPFGAFSRGLKSISEKVTHADPSEAKEGVLGEVRALQPNHQSRLEAIERAEK
LRQKELQTRMVNPLTKELASFVEEGKLKKSGGVEEVERARKAKDDRIRREVW
> F9XNV1 | F9XNV1_MYCGM_735_976 | SubName: Full=Putative uncharacterized protein; - Mycosphaerella
graminicola (strain CBS 115943 / IPO323) (Speckled leaf blotch fungus) (Septoria tritici)
NNTGRAYVNNGKKSLSDDSESIVNRVDDLQDLVEDLRKDVVTRGVRPLPRQLEEVSRDISIATSDLKKLQEFLRKEKPVWTKIWEKELQVVCDDRDLLTM
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QEELAADLEDDLEKAAQTFALVEQATKQQNLASPTANGGAVPTGVRSTSRTLVPIPTADPAKAKDSVLGEVRALQPNHESRLEAIERAERLRQRELETRR
EGEFQKELGNFVEEGKLKKSGGVEEVERQRKSREDRTRKEIW
> G0WGY8 | G0WGY8_NAUDC_529_761 | SubName: Full=Uncharacterized protein; - Naumovozyma dairenensis
(strain ATCC 10597 / BCRC 20456 / CBS 421 / NBRC 0211 / NRRL Y-12639) (Saccharomyces dairenensis)
KTSANRVYMDKSQNELGEVSDSLLSRVDDLQDIIEVIRKDVADRGAKPSKKKLESVQQELLDANNDMKKMEQFIAIEKPHWKKIWETELDKVCEEQQFLT
LQEELVLDLKEDLGKASETFTLINLCCEEQEKNPTRTKTNPILPILKPGTFTEVRNQLLVDVLSITPDHESRLEAIGKAEKLWQKEREYRAGDEFQDELG
DFVEKSALKKSGGVEEVERLREQKNRENLRANF
> E9CRI9 | E9CRI9_COCPS_229_471 | SubName: Full=Actin interacting protein; - Coccidioides posadasii
(strain RMSCC 757 / Silveira) (Valley fever fungus)
EGDAGRARVNAGKKELADESEKLVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEAVGRDISAVTKELKKMQDFLKREKPIWTKIWEKELQQVCEERDQLT
MQEDLAVDLEDDLEKATQTFALVEQATKQQALQSSNPDGNATVVSFRVASRTLPLDPSIDPVKAKDSVLGEVRALQPNHENRVEAIERAEKARQKELESR
RIGQFQKELGAFVEGGKLKKSGGFEEAERLRKAKDEKIRKEVW
> G8BZF4 | G8BZF4_TETPH_539_773 | SubName: Full=Putative uncharacterized protein TPHA0K01490; -
Tetrapisispora phaffii (strain ATCC 24235 / CBS 4417 / NBRC 1672 / NRRL Y-8282 / UCD 70-5) (Yeast)
(Fabospora phaffii)
AGSSTRSYIEKSQSKLGVVSDNLLSKVDDIQDIIEVLRKDVAVRGVNPSKKKLDAVLSDLNEAEKELSSMQSFISTEKPGWKRIWESELDKVCEEQQFLT
LQEDLAFDLVEDLKKASETFELVKLCCEEQEKYPKKVRTNPILPIPKPGTLNQTRDQLLVDVQSLVPDHESRVDALEKAQKIWQKERILKENDEFQEELG
TFVGNASFKKTGGIEEIERIRQQKNEENLRAGLGI
> B6H938 | B6H938_PENCW_630_867 | SubName: Full=Pc16g03380 protein; - Penicillium chrysogenum
(strain ATCC 28089 / DSM 1075 / Wisconsin 54-1255) (Penicillium notatum)
EGDAGRARVNTGKKELAAESERLVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEGVSRDISMVMKEIKKMQDFLGREKPIWTKIWEKELQLVCEERDQLT
MQEDLAADLQDDLEKATQTFALVEQATKEQVLTNATGGTAVRAPSRTLGIDPTIDPMKAKDGVLGEVRALQPNHESRLEAIERAEKARKKELETRRIGLF
QKELGAFVEEGKLKKSGGFEETERLRTAKDDRIRKEVW
> B8N7C6 | B8N7C6_ASPFN_422_660 | SubName: Full=Actin-interacting protein (Bud6/Aip3), putative; -
Aspergillus flavus (strain ATCC 200026 / FGSC A1120 / NRRL 3357 / JCM 12722 / SRRC 167)
EGDAGRARVNSGKKELGEESERLVARVDDLQDLVEDLRKDVVTRGVRPLPRQLESVGKDISAVTKEIKKMQEFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLAADLQDDVEKAAQTFALVEQATKEQTMQNNPSNGVTLRNTSRNVVIDPAVDPMKAKDSVLGEVRALQPNHESRLEAIERAEKARQKELENRRIGL
FQKELGAFVEEGKLKKSGGVEETERLRRAKDDRIRREVW
> G2QNC1 | G2QNC1_THIHA_727_972 | SubName: Full=Putative uncharacterized protein; - Thielavia
heterothallica (strain ATCC 42464 / BCRC 31852 / DSM 1799) (Myceliophthora thermophila)
EGESGHSYVANGRKKLNADSDRLVNKVDDLQDMVEDLRKDVVHRGVRPLPSQLEAVTRDIATLTKELSKMEEYMKQEKPIWTKIWEKELEDVCQGRDELR
LVEDLIVDLRDDLEKASETFALVEQATKEQMKDAGPGGVGGGIAARQFSKGLNSIRENAALADPSAAKEGVLGEVRALQPNHENRLEAIERAEKLRQKEL
ERRRENPLTKELASFVEEGKLKKSGGVEEVERARKAKDERIRREVW
> G2RG25 | G2RG25_THITE_710_954 | SubName: Full=Putative uncharacterized protein; - Thielavia
terrestris (strain ATCC 38088 / NRRL 8126) (Acremonium alabamense)
EGDAGHSYVIKGRKQLNADSDRLVNKVDDLQDMVEDLRKDVVHRGVRPLPRQLEAVARDIALLTKELAKMEEYMKREKPIWTKIWEKELEDVCQGRDELR
LAEDLIVDLRDDLEKASETFALVEQATKEQMKDAGPGGVGGGITARQFSKGLNSIRDNALVDPTAAKEGVLGEVRALQPNHENRLEAIERAEKLRQKELE
RRRENPLKQELVSFVEEGKLKKSGGVEEVERARKAKDDRIRREVW
> Q2GNJ2 | Q2GNJ2_CHAGB_640_887 | SubName: Full=Putative uncharacterized protein; - Chaetomium
globosum (strain ATCC 6205 / CBS 148.51 / DSM 1962 / NBRC 6347 / NRRL 1970) (Soil fungus)
EGNAGHAYVITGRKQLNQDSDRLVNRVDDLQDLVEDLRKDVVHRGVRPLPRQLEAVTRDIALLTKELSKMEESMKQEKPIWTKIWEKELEDVCQGRDELR
LVEDLIVDLRDDLEKASETFALVEQATKEQMKDAGGAGAGPGGVIVARQFSKGLTSIRENAAAVDPNTAKEGVLGEVRALQPNHENRLEAIERAEKLRQK
ELARRRENPLTKELATFVEEGKLKKSGGVEEVERARKAKDDRIRREVW
> G2XAD1 | G2XAD1_VERDV_678_911 | SubName: Full=Bud site selection protein; - Verticillium dahliae
(strain VdLs.17 / ATCC MYA-4575 / FGSC 10137)
YVSKGREQLNQDSDRLVTKVDDLQDTVEDLRKDVVHRGVRPLPRQLEGVAKDITRLTMELKKVEDYMKQEKPIWTKIWEKELEDVCKGRDELRLMEDLMV
DLQDDLEKASETFALVEAATKEQLKDNGTGASAGNARNFSKGLNSLGNSLDQNAAKEGVLGEVRALMPNHEDRLEAIERAEKLRQRELATRNTNKLQQEL
TNFVEEGRLKKSGGFEEVERARTAKDERIRREVW
> E3RQ08 | E3RQ08_PYRTT_696_940 | SubName: Full=Putative uncharacterized protein; - Pyrenophora
teres f. teres (strain 0-1) (Barley net blotch fungus) (Drechslera teres f. teres)
GDSGRAYINTGKKALQDDSEKIVNRVDDLQDLVEDLRKDVVLRGVRPLPRQLETTAKDLSTAIAELKKLQDLLAKEKPLWTKIWEQELQTVCEERDMLTM
QEELAADLQDDLEKAAQTLELVEQATKQQNLENEKEASGKGGMRSASGRNMLNAVAIDKVVDPRQARDGVLGEVKALQPNHEGRLEAIERAEKARQRDLE
TRNDDEFKRELGTFVEEGKLKKSGGVEEAERLRKAKDERARKENF
> H6BXA5 | H6BXA5_EXODN_750_985 | SubName: Full=Putative uncharacterized protein; - Exophiala
dermatitidis (strain ATCC 34100 / CBS 525.76 / NIH/UT8656) (Black yeast) (Wangiella dermatitidis)
KGDAGRAHINESKKVLSDDSEALVNRVDDLSDIVEELRKDVVTRGVRPLPRQLEDISKEISTAAKQLTKVKEFVKREKPIWTRIWEQELQVVMTERDELT
QQDELMNDLDGDLEDITNVFKLVEEATKQQNLQAASTGGRQGLKQLPFDTDVDPHEAKSGMLDEVRALQPNHESRLEAIERAAKVRQRELESRRVGEFQR
EVEKFVEEGKLKKTGGMDEVERRRKLKDEAARKENW
> H2ANZ7 | H2ANZ7_KAZAF_476_713 | SubName: Full=Putative uncharacterized protein KAFR0A06620; -
Kazachstania africana (strain ATCC 22294 / BCRC 22015 / CBS 2517 / CECT 1963 / NBRC 1671 / NRRL
Y-8276) (Yeast) (Kluyveromyces africanus)
SATGSAKAYMEKSQSELGQVSDGLLSRVDDLQDIIEILRKDVAERGARPSKKKLESLAKDLKKAEVDLNKMQQFIDTEKPQWKRIWEAELDKVCEEQQFL
TLQEDLIMDLNEDLNKAQETYNLIDLCFQEQEKNPQKVKVNPILPILKPGTFGQVREQVMLAVQSINPNYDSRIDALEKAEKLWEKEKQYKEDTAFRDEL
GRFVESSSLKKSGGVEEIEKVRKQKDEENLRAVFGTNI
> E3QGD9 | E3QGD9_COLGM_636_870 | SubName: Full=Actin interacting protein 3; - Colletotrichum
graminicola (strain M1.001 / M2 / FGSC 10212) (Maize anthracnose fungus) (Glomerella graminicola)
AYVHKGREQLNADSDRLVAKVDDLQDLVEDLRKDVVHRGVRPLPRQLETVAMDITKLSKELKKVEDYMKEEKPIWTKIWEKELEDVCKGRDELRLMEDLM
IDLQDDLEKASETFALVEQATKEQLKDNGTTASAGTARNFSKGLNNLGNSSDPNAAKDGVLGEVRALQPNHENRLEAIERAEKLRQKELEGRKGNELQRE
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LSSFVEEGKLKKSGGFEEVERARKAKDDMIRKQVW
> G4MPB7 | G4MPB7_MAGO7_726_967 | SubName: Full=Bud site selection protein 6; - Magnaporthe oryzae
(strain 70-15 / ATCC MYA-4617 / FGSC 8958) (Rice blast fungus) (Pyricularia oryzae)
AYVIKGRKQLNTDSDRLVTQVDDLQDIVEDLRKDVVTRGVRPRPRQLETVAKEISQLTIELKKMEEYMKREKPVWTRIWEKELEEVCQGREELRIMEELM
IDLQDDLEKASETFALVEQATKEQLKDAGAGNAAGPIGPGVLRQFSRGLENIGNNAFVDPSAAKEGVLGEVRALQPNHENRLEAIERAEKLRQKELETRK
GNALTKEITAFVGEGKLKKSGGFEEVERARKAMDDKIRREVW
> C5MCQ6 | C5MCQ6_CANTT_510_747 | SubName: Full=Putative uncharacterized protein; - Candida
tropicalis (strain ATCC MYA-3404 / T1) (Yeast)
SQNSNRAYMESCNSKLSDDSDLLITKVDDLQDVMEEMRKDVAQRGVRVSEKQLKHIIKDIKSAKDSLHDMSSYISKERPVWKKIWESELDKVCEEQQFLN
LQDDLIQDLQEDIKKIEETFGLIEQCSVEQTKGKSSKRNKIVANLYIPEPGESLHTAKDAVLNDIAALTPNHESRVEAIERAEKIREKEREMMRLNKFQE
ELGDFVEDNRLKKSGGIEELEKARQIKDSENLKSSFGI
> G3B1Y0 | G3B1Y0_CANTC_529_767 | SubName: Full=Putative uncharacterized protein; - Candida tenuis
(strain ATCC 10573 / BCRC 21748 / CBS 615 / JCM 9827 / NBRC 10315 / NRRL Y-1498 / VKM Y-70) (Yeast)
ATKSSNRIYMEKCHGRLSEESDSLLTKVDDLQDVMEGLRKDVAQRGVRVGAQQLKATMKEIVAAGDSLKDMSSFINKEKTVWKKIWEAELDRVCEEQQFF
NLQDDLTKDLEEDLAKIQETFDLVEQCSLEQSKQSSYRRNKVVANLPIPEPGENLHSIKDAVLSEVAALKPDHESRVDAINKAEKLRQKNKQMMDLTEFQ
EELGSFIDDSKLRKSGGIDEIERQRQLKDSENLKSSMGG
> G0RS34 | G0RS34_HYPJQ_714_954 | SubName: Full=Predicted protein; Flags: Fragment; - Hypocrea
jecorina (strain QM6a) (Trichoderma reesei)
EGDAGYAYVSNGRKQLNADSDRLVAKVDDLQDLVEDLRKDVVHRGVRPLPRQLEVVAKDVTALSKELKAMEDYMAKEKPIWTKIWEKELEDVCQGRDELR
IMEELLIDLRDDLEKASETFTLVEQATKEQMKDSGTGHSASTVRTFSKGLNNLGNSLDQNAAKEDMLGEVRALQPNHQDRLEAIERAEKLRQKELKTRTT
NPLHREMKAFVSEGKLKKSGGFEEVERARLAKDEKIRREVW
> G3ATL7 | G3ATL7_SPAPN_430_667 | SubName: Full=Putative uncharacterized protein; - Spathaspora
passalidarum (strain NRRL Y-27907 / 11-Y1)
SKDSNRSFMETCHTKLSEESDVLITKVDDLQDLVEELRKDVAQRGVRISEKQIKNTVKEIENAKSALRSMTDFISKERNVWKKIWETELDKVCEEQHFFK
VQDELTIDLEEDIKKMEETFTLIEQCSIEQSKGSTRKRNKVVANLYIPEPGESLHDIKDAVLNEVVALVPDHQSRVEAIERAEKLREKEREMMKLNQFQE
ELGDFVEDKKLKKSGGIAEVEKMRSQKDSENLKSSFGI
> Q0CQ01 | Q0CQ01_ASPTN_621_856 | SubName: Full=Putative uncharacterized protein; - Aspergillus
terreus (strain NIH 2624 / FGSC A1156)
EGDAGRARVNSGKKELAEESERIVARVDDLQDLVEDLRKDVVTRGVRPLPRQLEMVGKDISAVTKEVKKMQEFLKREKPIWTKIWEKELQLVCEERDQLT
MQEDLAADLQDDLEKAAQTFALVEQATKQQALQNANQGVTLRNVSRNIDPSVDPLKAKDNVLGEVRALQPDHESRLEAIERAEKARQKELENRRIGLFQK
ELGSFVQEGKLKKSGGVEETERLRRAKDDRIRKEVW
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