

{MATRIX} Mascot Search Results

Protein View

Match to: **EEH42759.2** Score: **3021**
hypothetical protein PADG_07579 [Paracoccidioides brasiliensis Pb18]
 Found in search of 281474976710778.mgf

Nominal mass (M_r): **142545**; Calculated pI value: **5.34**
 NCBI BLAST search of **EEH42759.2** against nr
 Unformatted [sequence string](#) for pasting into other applications

Fixed modifications: Carbamidomethyl (C)
 Variable modifications: Oxidation (M)
 Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
 Sequence Coverage: **59%**

Matched peptides shown in **Bold Red**

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1 MTRGDETLA VAGILQGLAK DVPNSASFPF GGYKANNSTN GDVTKIKLPG
51 EESDGGKAVLE HELEDLIRRI VTMQSFVPPS RRSTRAPNFA SQQHSOLEGS
101 FKSLPESDTN YKEDIQFLN RVQLQAQEIQ LQKDVISKVR EELRNQEKRT
151 EEALGRVKID DVSILERELE KHQQANEAFQ KALREIGGII TQVANGDLSM
201 KVQIHPLEMD PEITTFKRTI NTMMDQLQVF GSEVSRVARE VGTEGILGGQ
251 AQISGVHGIW KELTENVNIM AKNLTDQVRE IATVTTAVAH GDLSQKIESQ
301 AKGEILELQQ TINTMVDQLR TFAIEVNRVA KDVGIEGVLG GQAQIDGVQG
351 KMHILTUNVN AMAENLTTQV RDIAMVTAV AKGDLTQKVQ ANCKGEILAL
401 KTIINSMDVQ LKQFAQEVTK IAKEVGTGTV LGGQATVHDV EGTWKDLTEN
451 VNGMAMNLTIT QVREIADVTT AVAKGDLTKK VTADVKGEL DLKNTINGMV
501 DRLNTFAFEV SKVAREVGTD GTLGGQAKVD NVEGKWKDLT DNVNTMAQNL
551 TSQVRGISDV TQAIKAGELS KKIEVHAQGE ILTLKVTINN MVDRLANFAH
601 ELKRVARDVG VEGKMGQQAN VEGISGRWKE ITEDVNTMAE NLTSQVRAFG
651 EITDAATDGD FTKLITVNAS GEMDELKRKI NKMVENLRDS IQRNTAAKEA
701 AELANRTKSE FLANMSHEIR TPMNGIIGMT QLTLOTDDLK PYPREMLNVV
751 HSLANSLTI IDDLIDISKI EANRMVIERI PPSMRGAVEN ALKTLAVKAN
801 EKILNLIYQV DSSIPDFVTG DPFLRQIIL NLVGNAIKFT ERGEVRVTIL
851 KSDREECRPN EYSFEFIVSD TGIGIEEDKL DLIFDTFQQA DGSTTRKFGG
901 TGLGLSISKR LVNLMGGDVM VTSEFGHGSK FHFTCVVEMA DQDISNIAAS
951 LFPYKNHRVL FIDRGETGGY AKEITNMLKQ LDLDPIVVTN ESQIPPPETQ
1001 DSSGKDSGHA YDVIIIVDSVN TAKSLRTYDE FKYIPIVLLC PVVSVNLKSA
1051 LDLGITSYMT TPCLPVDLGN GMIPALEGRS TPITTDHTRS FDILLAEEND
1101 VNQRVAVKIL ECKNHDVTVV SNGLOALEAI KORREFDVLM DVQMPVMGGF
1151 EATGKIREYE REHGLPRTPI IALTAAHMLG DREKCIQAM DEYLAKPLKH
1201 NQMVQMILKC VTIGDSLLEK SNEPSALGGG DOTHHLTRHT LVQSSEARSQ
1251 RLLMDSRALA AFGSSGANHG LNRKPDVST VRPFCDQLLS LC
  
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Figure S1. PbDrk1 identity confirmation. Mascot results. Peptide summary report of identified protein. Matched peptides are highlighted in red, in which its sequence coverage reaches 59% of the Drk1 sequence of *P. brasiliensis*.