

{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 **Red**

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1 MTRGDETLA VAGILQGLAK DVPNSASFPF GGYKANNSTN GDVTKIKLPG
51 EESDGKAVLE HELEDLIRRI VTMQSFVPPS RRSTRAPNFA SQQHSOLEGS
101 FKSLPESDTN YKEDIQFLLN RVQLQAQEIQ LQKDVISKVR EELRNQEKRT
151 EEALGRVKID DVSILEREELR KHQQANEAFQ KALREIGGII TQVANGDLSM
201 KVQIHPLEMD PEITTFKRTI NTMMDQLQVF GSEVSRVARE VGTEGILGGQ
251 AQISGVHGIW KELTENVNIM AKNLTDQVRE IATVTTAVAH GDLSQKIRSQ
301 AKGEILELQQ TINTMVDQLR TFAIEVNRVA KDVGIEGVLG GQAQIDGVQG
351 KKNELTVNVN AMAENLTTQV RDIAMVTAV AKGDLTQKVG ANCKGEILAL
401 KTIINSMVDQ LKQFAQEVTK IAKEVGTGTV LGGQATVRDV EGTMKDLTEN
451 VNGMAMNLTQ QVREIADVTT AVAKGDLTKK VTADVKGKEL DLKNTINGMV
501 DRLNTFAFEV SKVAREVGTD GTLGGQAKVD NVEGKWKDLT DNVNTMAQNL
551 TSQVRGISDV TQAIKAGELS KKIEVHAQGE ILTLKVTINN MVDRLANFAH
601 ELKRVARVDG VEGKMGQQAN VEGISGRWKE ITEDVNTMAE NLTSQVRAFG
651 EITDAATDGD FTKLITVNAS GEMDELKRKI NKMVSNLRDS IQRNTAAREA
701 AELANRTKSE FLANMSHEIR TFMNGIIGMT QLTLDTDDLK PYPREMLNVV
751 HSLANSLTI IDDILDISKI EANRMVIERI PPSMRGAVFN ALKTLAVKAN
801 EKILNLIYQV DSSIPDFVTG DPFRLRQIIL NLVGNAIKFT ERGEVRVTIL
851 KSDREECRPN EYSFEFIVSD TGIGIEEDKL DLIFDTFQQA DGSTTRKFGG
901 TGLGLSISKR LVNLMGGDVM VTSEFGHGSK FHFTCVVEMA DQDISNIAAS
951 LFPYKNHRVL FIDRGETGGY AKEITNMLKQ LDLDFIVVTN ESQIPPPETQ
1001 DSSGKDSGHA YDVIIVDSVN TAKSLRITYDE FKYIPIVLLC PVVSVNLKSA
1051 LDLGITSYMT TPCLPVDLGN GMIPALEGRS TPITTDHTRS FDILLAEDND
1101 VNQRVAVKIL EKCNHDVTVV SNGLQALEAI KORRFVDILM DVQMPVMGGF
1151 EATGKIREYE REHGLPRTPI IALTAHMLG DREKCIQAQM DEYLAKPLKH
1201 NQMVMILKC VTLDGSLLEK SNEPSALOGG 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*.